

**Studi Mekanisme Mutasi Virus Influenza A Membentuk Subtipe
H5N1 pada Manusia Secara *In silico***

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DEPARTEMEN KIMIA

DEPOK

2008

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H5N1 pada Manusia Secara *In silico***

**Skripsi ini diajukan sebagai salah satu syarat
untuk memperoleh gelar Sarjana Sains**

Oleh:

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**SKRIPSI : Studi Mekanisme Mutasi Virus Influenza A Membentuk Subtipe
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Prof Dr. Usman Sumo F. Tambunan

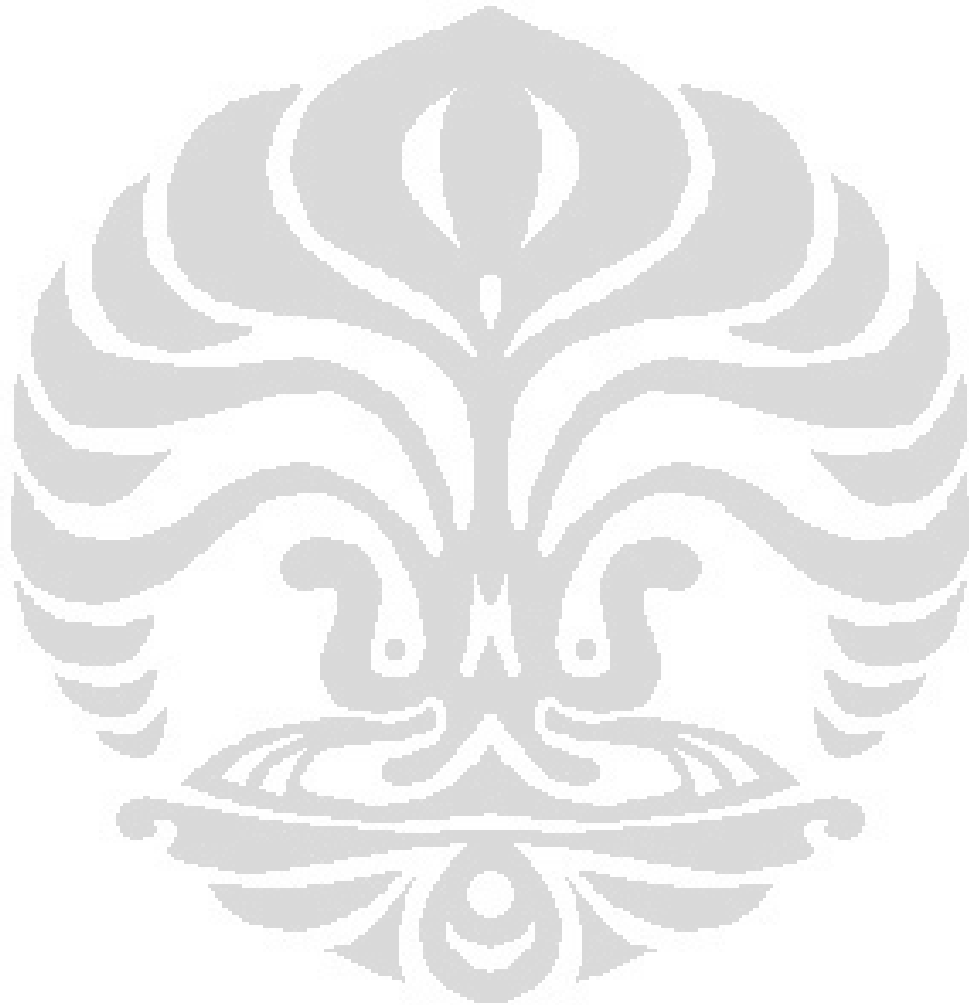
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Penguji I : Prof. Dr. Sumi Hudyono Pws

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Penguji III : Dra. Sri Handayani MBiomed



Tak akan pernah cukup waktu untuk menjadi sempurna, tapi akan selalu ada waktu untuk menyempurnakan (Nur Salim Ridlo)

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Semoga skripsi ini bermanfaat bagi kita semua.

Penulis

2008

ABSTRAK

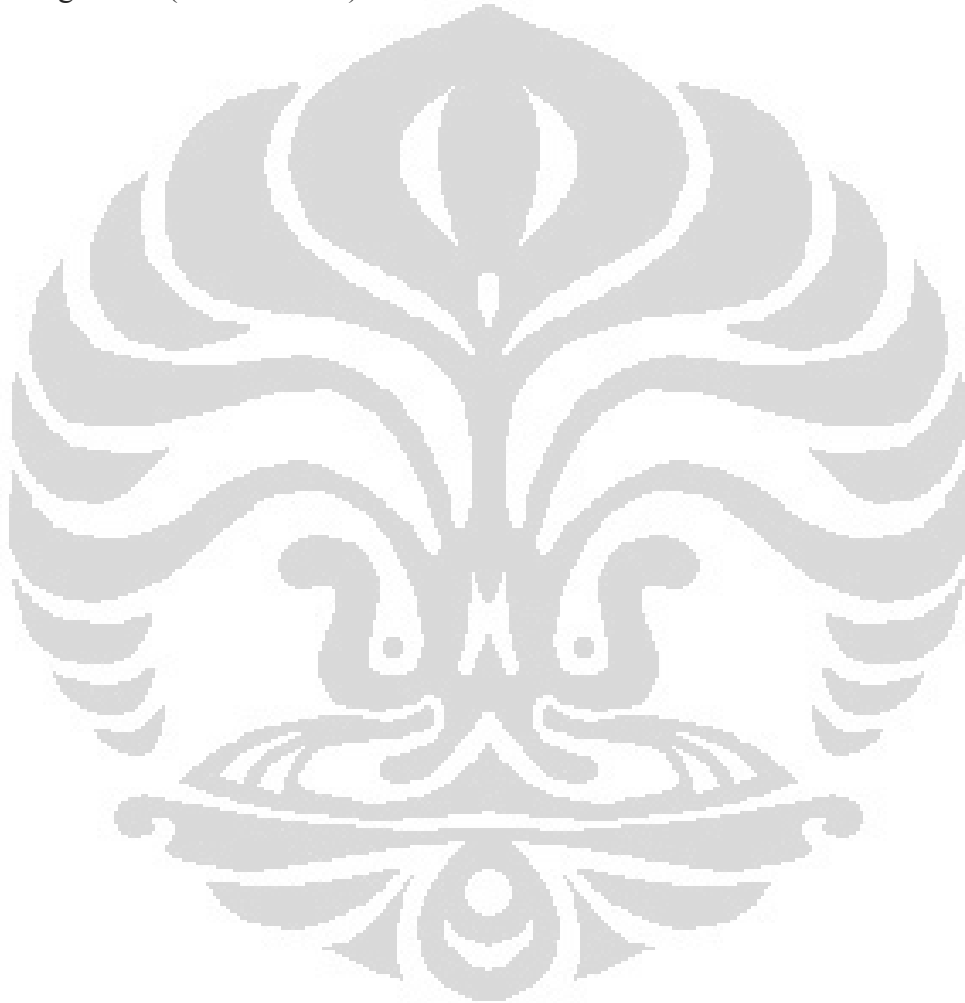
Kemampuan virus Influenza A dalam menginfeksi manusia sangat bergantung pada *receptor binding* yang dimilikinya. Protein yang berfungsi sebagai *receptor binding* pada virus ini adalah *haemagglutinin*. Virus Influenza A akan mampu menginfeksi manusia dan dapat menyebar antar manusia apabila protein *haemagglutinin* telah mengenali SA α -2,6 Gal sebagai *receptor* pada manusia. Virus Influenza A sub tipe H5N1 telah ditemukan dapat menginfeksi manusia namun belum mampu menular antar manusia. Dari hasil analisis mutasi terhadap sekuan *haemagglutinin* didapatkan bahwa sekuen protein *haemagglutinin* pada virus H5N1 belum menyamai sekuen protein *haemagglutinin* pada virus Influenza A yang telah menjadi pandemik yaitu sub tipe H1N1, H2N2, dan H3N2 sehingga belum mampu menyebar antar manusia. Sekuan utama yang mendukung penyebaran pada manusia adalah asam amino posisi 226 dan 228 pada protein *Haemagglutinin*. Pada saat virus menjadi pandemik maka asam amino posisi 226 telah berubah menjadi Leu dan pada posisi 228 telah berubah menjadi Ser. Sedangkan pada virus H5N1 masih berupa Gln pada posisi 226 dan Gly pada posisi 228 yang merupakan pengenalan SA α -2,3 Gal *receptor* pada burung. Selain pada posisi tersebut perbedaan juga ditemukan pada posisi 251 dan posisi 258. Pada sub tipe yang telah menjadi pandemik sekuen posisi 251 adalah Leu dan posisi 258 adalah Phe, sedangkan pada H5N1 Phe pada 251 dan Tyr pada 258. Dari hasil ini dapat diprediksi sekuen H5N1 yang dapat menjadi pandemik yaitu apabila telah terjadi perubahan pada sekuen posisi 226 dan 228 serta didukung dengan perubahan pada posisi 251 dan 258.

Kata Kunci : *haemagglutinin*, Influenza A H5N1, Mutasi, SA α -2,3 Gal. SA α -2,6

Gal

xi + 266 hlm;gbr;tab;lamp

Bibliografi 46 (1990 - 2008)



DAFTAR ISI

KATA PENGANTAR.....	i
ABSTRAK.....	v
DAFTAR ISI.....	vii
Daftar Gambar.....	x
Daftar Tabel.....	xi
Daftar Lampiran.....	xii
BAB I PENDAHULUAN.....	1
1.1 Latar Belakang.....	1
1.2 Tujuan Penelitian.....	5
1.3 Batasan Penelitian.....	5
BAB II TINJAUAN PUSTAKA.....	7
2.1 Virus Influenza.....	7
2.1.1 Mutasi virus.....	11
2.1.2 Avian Influenza A subtype H5N1.....	11
2.1.3 Haemagglutinin (HA).....	13
2.1.4 Neuraminidase.....	15

2.1.5 Polymerase B2 protein (PB2), Polymerase B1 protein (PB1), dan Polymerase A protein (PA).....	17
2.1.6 Protein M2.....	17
2.1.7 Protein NS1 dan NS2	17
2.2 Host.....	17
2.2.1 Definisi.....	17
2.2.2 Antibodi dan Antigen.....	18
2.2.3 Sistem Imun	19
2.2.4 Penamaan	21
2.3 Bioinformatika.....	22
2.3.1 Definisi.....	22
2.3.2 Format FASTA	23
2.3.3 GenBank Flatfile Format.....	24
2.3.4 Sequence Alignment.....	24
2.3.5 Database Similarity Searching.....	25
2.3.6 BLAST	26
2.3.7 Pohon Filogenetik	27
BAB III METODE PENELITIAN.....	29
3.1 Pencarian Genom dan Database protein	29

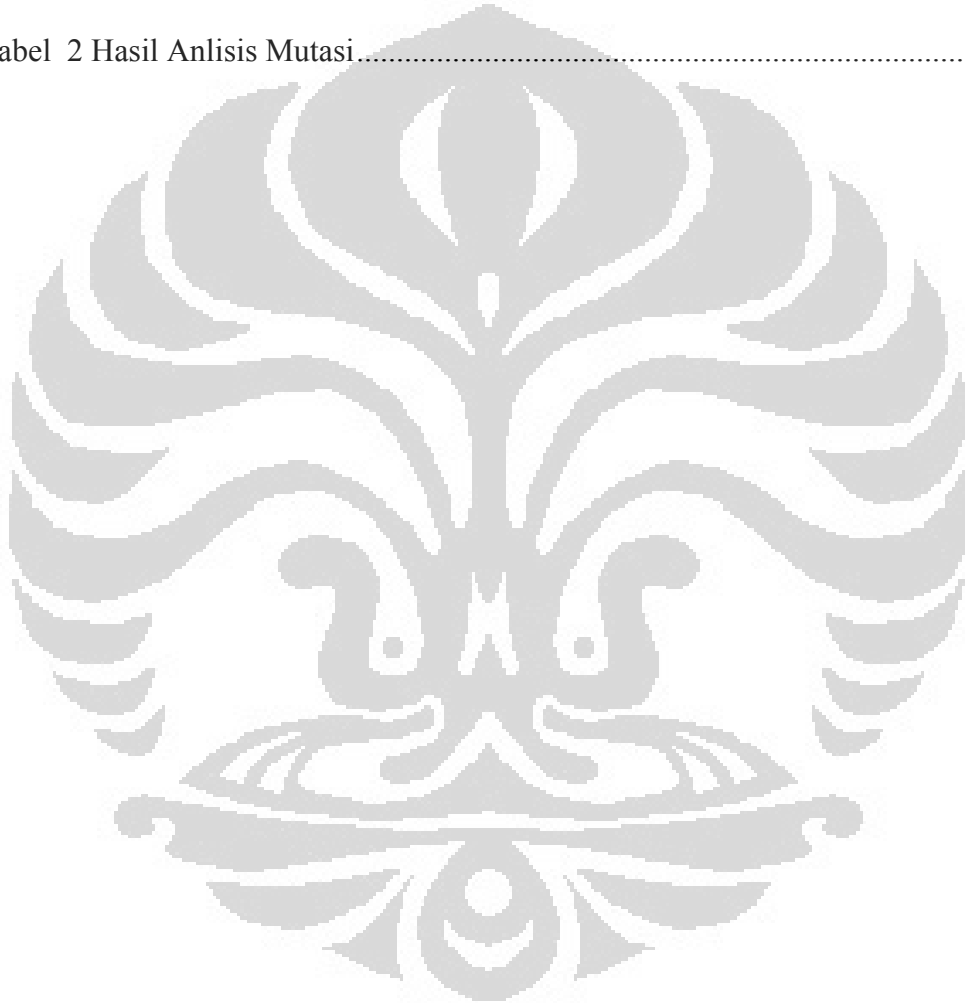
3.2 Database Similarity Searching.....	30
3.3 Sequence Alignment Genom.....	30
3.4 Analisis Mutasi	30
3.5 Prediksi struktur 3 dimensi	31
3.6 Analisis Filogenetik	31
BAB IV HASIL DAN PEMBAHASAN.....	32
4.1 Pencarian Sekuen Protein.....	32
4.2 Multiple Sequence Alignments.....	33
4.3 Penentuan Conserved Region	34
4.4 Analisis Pohon Filogenetik.....	35
4.5 Analisis Mutasi	36
4.6 Prediksi Struktur Tiga Dimensi.....	40
BAB V KESIMPULAN DAN SARAN.....	43
5.1 Kesimpulan	43
5.2 Saran.....	44
DAFTAR PUSTAKA.....	45
LAMPIRAN	50

Daftar Gambar

Gambar 1 Perkembangan mutasi (evolusi) virus Influenza A yang menjadi pandemik.....	2
Gambar 2 Struktur virus influenza.....	8
Gambar 3 Mekanisme masuk dan penggandan virus dalam sel <i>host</i>	9
Gambar 4 Struktur virus influenza A H5N1	13
Gambar 5 Molekul Haemagglutinin	15
Gambar 6 Neuraminidase.....	16
Gambar 7 Interaksi antibodi dengan antigen	19
Gambar 8 Bioinformatik	23
Gambar 9 struktur tiga dimensi protein <i>Haemagglutinin</i>	42

Daftar Tabel

Tabel 1 Virus famili <i>Orthomyxoviridae</i>	7
Tabel 2 Hasil Analisis Mutasi.....	37



Daftar Lampiran

Lampiran 1. Informasi Genetik Virus H5N1 <i>Hemagglutinin</i> dalam Format GBFF.....	51
Lampiran 2. Daftar Kode Dua Puluh Asam Amino	52
Lampiran 3 : Sekuen Protein Virus Influenza A subtipe H1N1, H2N2, H3N2, dan H5N1 dalam Format Fasta	53
Lampiran 4 : Hasil Alignment.....	179
Lampiran 5 : Conserve Region	253
Lampiran 6 : Pohon filogenetik.....	266

BAB I

PENDAHULUAN

1.1 Latar Belakang

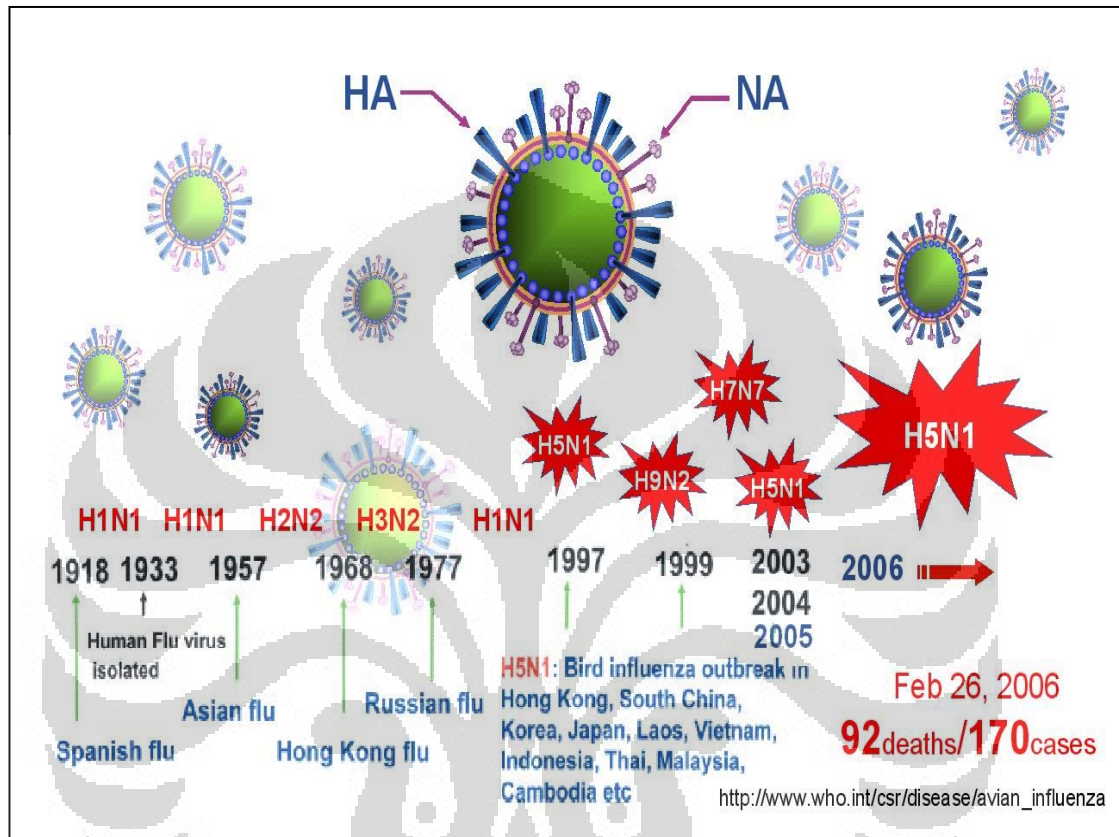
Avian Influenza atau sering disingkat AI merupakan salah satu penyakit yang telah menyebabkan banyak kematian di dunia. Sampai saat ini tiga sub tipe *avian influenza* pandemik telah menyebabkan puluhan juta orang meninggal. Sub tipe baru dari virus influenza A yang merupakan ancaman bagi kehidupan manusia telah muncul kembali dan telah menyebabkan kematian bagi manusia. Virus ini pertama kali muncul di Asia pada tahun 1997 dan kini dikenal dengan virus influenza A sub tipe H5N 1.

(www.en.wikipedia/influenza, diakses pada hari Rabu 13 agustus 2008 pukul 16:59)

Virus *avian influenza* sub tipe H5N1 tergolong famili *Orthomyxoviridae*, yang terdiri dari genom tunggal bersegmen. Antigen virus influenza tersusun atas beberapa komponen. Komponen pertama adalah antigen internal yang terdiri atas genome RNA dan protein M. Komponen kedua adalah antigen eksternal permukaan glikoprotein yang tersusun atas *haemagglutinin* (HA) dan *neuraminidase* (NA).

Berdasarkan perbedaan lapisan permukaan glikoprotein, *haemagglutinin* (HA) dan *neuraminidase* (NA) virus influenza A dikelompokkan dalam beberapa sub tipe. *Haemagglutinin* merupakan antigen yang diperlukan oleh virus untuk melekat pada membran sel inang (*host*) . Enzim *neuraminidase* berperan dalam penetrasi virus dan lepasnya virus dari sel yang diinfeksi. Virus influenza A terdiri dari 16 *haemagglutinin* dan 9 *neuraminidase* (de Jong., 2005).

Dalam perkembangannya virus influenza A telah bermutasi membentuk beberapa subtipe yang menjadi pandemik.



Gambar 1 Perkembangan mutasi (evolusi) virus Influenza A yang menjadi pandemik.

(sumber : <http://wisdom.eu-egge.fr/avianflu/pictures/>)

Virus influenza pandemik yang pertama kali muncul adalah H1N1, subtipe ini pertama kali muncul pada tahun 1918. Virus inilah yang lebih dikenal dengan *Spanish flu*. Virus ini telah menyebabkan kematian sekitar 50 juta orang diseluruh dunia (Stevens et al 2006). Subtipe kedua yang muncul menjadi pandemik adalah H2N2 , subtipe inilah yang dikenal sebagai *Asian flu* pada tahun 1956 yang berkembang di China, Singapura, Hong Kong, dan USA. Hasil mutasi dari H2N2

adalah subtipe H3N2 yang dikenal dengan *Russian flu* yang berkembang pada tahun 1977-1978. Pada tahun 1968-1969 H3N2 muncul di Hong Kong dan dikenal dengan *Hong Kong Flu* (www.en.wikipedia, diakses pada hari Rabu 13 agustus 2008 pukul 17:05).

Pada tahun 1999 dan 2003 muncul virus subtipe H9N2 yang menginfeksi tiga orang yang berumur satu, empat, dan lima tahun di Hong Kong. Semuanya dapat disembuhkan, tapi pada tahun 2007 H9N2 menginfeksi bayi berumur sembilan bulan di Hong Kong ([people daily online march,2007](http://people.daily.online.march)). Kemudian muncul subtipe H7N7 yang memiliki *Highly pathogenic strains (HPAI)* and *low pathogenic strains (LPAI)*. H7N7 bisa menginfeksi manusia, burung, babi, paus, dan kuda dan berpotensi menjadi pandemik (www.en.wikipedia, diakses pada hari Rabu 13 agustus 2008 pukul 17:05).

Pada tahun 1997 avian influenza H5N1 pertama kali menyerang dan menewaskan 6 orang dari 18 orang penduduk yang terinfeksi di Hongkong. Pada saat ini, masalah penting yang dikhawatirkan oleh para ahli adalah kemungkinan munculnya subtipe baru virus influenza yang mampu menular antarmanusia. Hal ini dapat terjadi sehubungan dengan adanya virus subtipe baru yang mungkin terbentuk akibat mutasi atau reassortasi (*reassortment*) virus avian influenza asal unggas dan virus *human influenza* (Horimoto T, Kawaoka Y. 2001).

Virus influenza A subtipe H5N1, yang juga dikenal sebagai A(H5N1) atau H5N1 merupakan subtipe dari virus influenza A yang dapat menyebabkan penyakit pada manusia dan beberapa spesies hewan lainnya. *Strain* H5N1 yang beradaptasi pada burung disebut juga HPAI A H5N1 yaitu *highly pathogenic avian influenza*

virus dari tipe A pada subtipe H5N1, merupakan agen kausatif H5N1 flu yang biasa dikenal sebagai avian influenza atau flu burung. Flu burung merupakan epizootic (sebuah epidemic dalam non manusia) dan panzootic (mempengaruhi beberapa spesies) (www.en.wikipedia, diakses pada hari Rabu 13 agustus 2008 pukul 17:08).

Saat ini virus subtipe H5N1 yang paling dikhawatirkan akan menjadi pandemik dan memungkinkan terbentuknya *strain* yang mampu menular antar manusia. Namun sampai saat ini belum ditemukan *strain* yang mampu menular dari manusia ke manusia (Tambunan et al , 2008)

Beradaptasinya virus *avian influenza* dalam populasi manusia disebabkan berubahnya kemampuan virus tersebut. Avian influenza akan mampu menginfeksi manusia apabila kemampuan pelekatannya telah berubah dari α -2,3 SA Gal menjadi α -2,6 SA Gal. Pada saat menginfeksi burung (*avian*) maka virus tersebut akan berikatan dengan α -2,3 SA Gal, sedangkan pada saat virus mampu menginfeksi manusia maka virus akan mengenali α -2,6 SA Gal sebagai agen untuk berikatannya. Kemampuan virus dalam menginfeksi sangat terkait dengan protein *haemagglutininya* karena fungsi pelekatan virus pada inangnya dipegang oleh protein ini.

Pada penelitian-penelitian sebelumnya telah dipelajari mutasi yang terjadi pada virus H5N1 yang dilihat dari protein *haemagglutinin* dan *neuraminidase*. Namun belum ada yang mengungkapkan mekanisme terjadinya virus H5N1 yang kini telah menyebabkan kematian diberbagai negara. Terbentuknya subtipe virus baru ini disebabkan mutasi yang dialami oleh virus sebelumnya. Mutasi ini bisa diakibatkan

oleh *antigenic drift* maupun *antigenic shift*. Ini bisa terjadi apabila satu sel terinfeksi dua jenis virus yang masih dalam satu famili (Gurtler, 2007).

Dengan terus ditemukannya virus Influenza subtipe baru yang merupakan hasil mutasi dari virus sebelumnya maka perlu dipelajari mekanisme mutasi yang terjadi pada virus influenza terutama pada subtipe H5N1. Dengan diketahinya mekanisme mutasi yang terjadi pada virus maka akan dapat diprediksi subtipe virus yang akan muncul kemudian dan dapat dilakukan penanganan lebih awal.

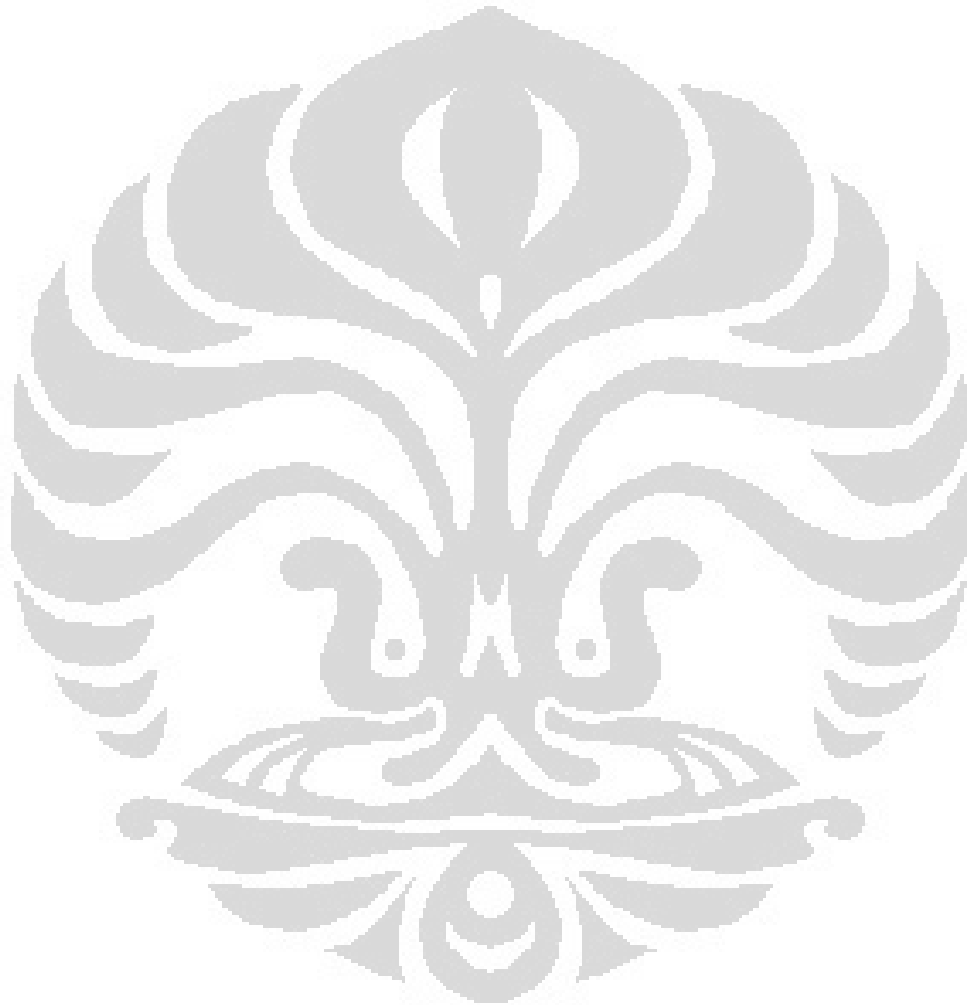
1.2 Tujuan Penelitian

Melihat dari perkembangannya sampai kini telah ditemukan beberapa virus influenza A yang telah menjadi pandemik. Masing-masing subtipe ini muncul pada tahun yang berbeda bahkan ada virus yang mampu bertahan puluhan tahun. Oleh karena itu dalam penelitian ini akan dicari asal-usul dari virus H5N1 yang sekarang dikhawatirkan akan menjadi pandemik serta mempelajari mekanisme mutasi yang terjadi pada virus tersebut hingga membentuk virus subtipe H5N1 yang mampu menginfeksi manusia.

1.3 Batasan Penelitian

Namun demikian seiring dengan telah terbentuknya banyak subtipe dari virus influenza A yang berarti juga telah terjadi banyak mutasi maka pada penelitian ini penulis memfokuskan pada mutasi yang telah dialami virus hingga membentuk virus H5N1. Pada penelitian ini, penulis hanya menganalisis mutasi dari segi perubahan asam amino pada masing-masing *sequence*. Penelitian ini akan difokuskan

untuk mempelajari mekanisme mutasi virus pada Influenza A H5N1 dari virus asalnya secara *in silico*, menggunakan seperangkat komputer yang terhubung langsung ke internet.



BAB II

TINJAUAN PUSTAKA

2.1 Virus Influenza

Virus influenza termasuk dalam famili *Orthomyxoviridae*, yang memiliki genom tunggal bersegmen. Antigen virus influenza terdiri dari beberapa komponen yaitu antigen internal, terdiri dari genom RNA dan protein M dan antigen eksternal yang terdapat pada permukaan, yaitu *haemagglutinin* (HA) dan neuraminidase (NA). Antigen yang terdapat pada lapisan permukaan merupakan pembeda atau yang menjadi perbedaan antar virus influenza. Berikut ini digambarkan jenis virus famili *Orthomyxoviridae* :

Tabel 1 Virus famili *Orthomyxoviridae*

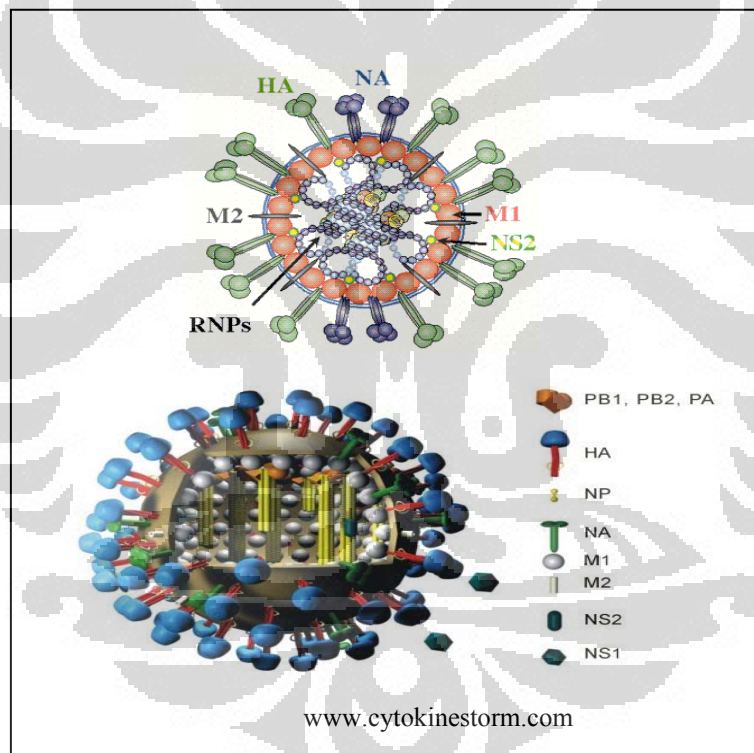
Family (Subfamily)	Genus	Type Species	Hosts
<i>Orthomyxoviridae</i>	<i>Influenza A virus</i>	<i>Influenza A virus</i>	Vertebrates
	<i>Influenza B virus</i>	<i>Influenza B virus</i>	Vertebrates
	<i>Influenza C virus</i>	<i>Influenza C virus</i>	Vertebrates

Ada tiga tipe virus influenza yang telah dikenal banyak orang yaitu A, B, dan C. Influenza A dan B memiliki 8 segman sebagai berikut :

1. Polymerase B2 protein (PB2)
2. Polymerase B1 protein (PB1)
3. Polymerase A protein (PA)

4. Haemagglutinin (H atau HA)
5. Nucleocapsid protein (NP)
6. Neuraminidase (NA atau N)
7. Matrix protein (M),terdiri dari M1 dan M2
8. Non-structural protein, terdiri dari NS1 dan NS2

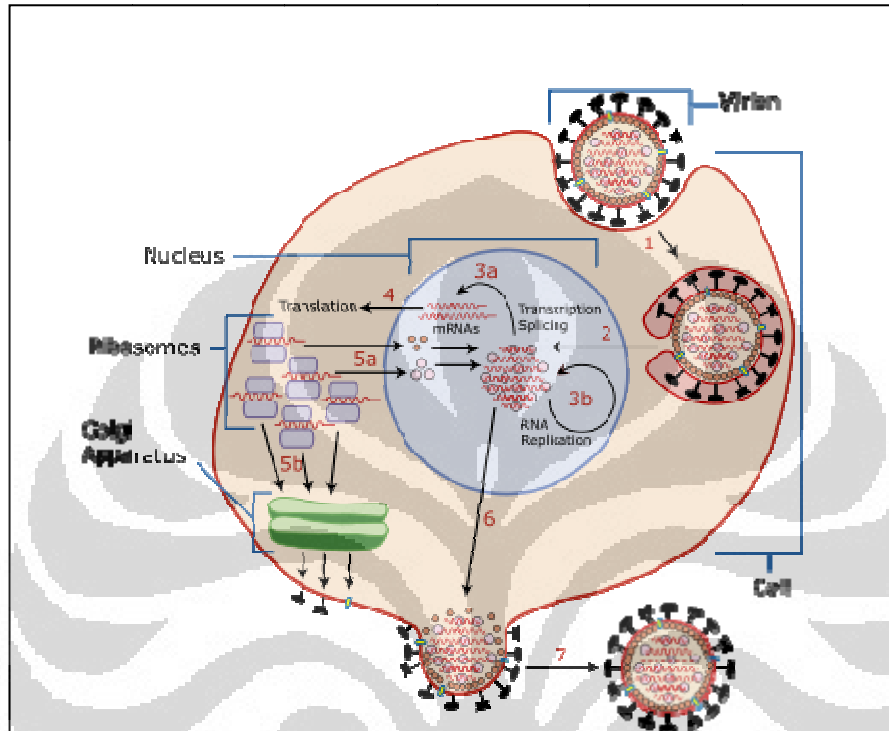
sedangkan influenza C hanya memiliki 7 segmen yaitu permukaannya hanya terdiri dari satu glikoprotein. Struktur virus ditunjukkan dalam gambar 2.



Gambar 2 Struktur virus influenza.

RNA aktif (RNA polymerase) yang berfungsi untuk replikasi dan transkripsi tersusun atas PB2, PB1, dan PA. ini mempunyai aktifitas endonuklease dan terikat pada RNP. Protein NS1 dan NS2 berfungsi dalam regulasi virus didalam sel yang telah terinfeksi. Virus ini dibungkus oleh membran yang berupa lipid bilayer yang

terdiri dari HA(H), NA(N), dan matrik. Berikut ini digambarkan tahapan dari replikasi virus.



Gambar 3 Mekanisme masuk dan penggandaan virus dalam sel *host*.

Replikasi virus terdiri dari beberapa tahap. Tahap pertama *haemagglutinin* virus influenza terikat pada gula *sialic acid* pada bagian permukaan sel, umumnya pada bagian hidung dan paru-paru dari mamalia atau burung. Tahap kedua virus masuk kedalam sel melalui endositosis, dalam keasaman endosom *haemagglutinin* dari virus berdifusi memasuki dan melepaskan molekul viral RNA (vRNA), protein aksesoris, dan RNA-polimerase kedalam sitoplasma. Tahap ketiga protein yang dilepaskan pada tahap kedua dan vRNA menuju ke inti sel dan RNA polimerase mulai mentranskripsikan rantai komplemennya (Viral RNA (vRNA) dikopi dari (-) sense menjadi (+) cRNA dan mRNA). Tahap keempat vRNA dikeluarkan kembali

kedalam sitoplasma dan mulai ditranslasikan. Tahap kelima viral protein yang baru terbentuk kembali lagi ke inti sel untuk membentuk vRNA lagi atau viral protein yang baru terbentuk dikeluarkan menuju apparatus golgi pada permukaan selnya (dalam hal ini *Haemagglutinin* dan Neuraminidasenya) . Tahap keenam vRNA dan inti viral meninggalkan inti sel menuju membran. Tahap terakhir virus meninggalkan sel dan membentuk virus baru (<http://en.wikipedia.org/wiki/Orthomyxoviridae> diakses pada Selasa 19 Agustus 2008 pukul 12.50).

Influenza A terdefinisi dalam 16 HA dan 9 NA, secara teori ada 16 x 9 sub tipe, dan sampai sekarang telah ditemukan 105 sub tipe dari virus influenza A dan semuanya endemik pada burung air. Namun demikian beberapa sub tipe telah ditemukan dalam ayam dan mamalia (Cinati, et al. 2007).

Pada manusia telah terdeteksi tiga sub tipe :H1N1, H2N2, dan H3N2 yang menjadi pandemik. H1N1 yang dikenal dengan *Spanish flu* pada tahun 1918-1919 telah menyebabkan 40 juta orang meninggal, *Asian flu* (H2N2) pada tahun 1957 menyebabkan 2 sampai 4 juta orang meninggal, dan *Hong Kong influenza* (H3N2) pada tahun 1968 mengakibatkan 1 sampai 2 juta orang meninggal (Cinati et al, 2007).

Sampai saat ini H1N1 dan H3N2 masih terdapat dalam populasi manusia tetapi merepresentasikan jenis *lower pathogenic*. Walaupun menyebabkan banyak kematian pada orang-orang tua pada saat gelombang musim dingin datang (Cinati et al .2007).

Sampai 1997 virus flu burung yang dikenal tidak bisa bertransmisi ke manusia karena tidak adanya reseptor untuk sel pada manusia. Namun pada musim panas 1997

di Hong Kong *strain* flu burung A H5N1 ditemukan telah bertransmisi kedalam tubuh manusia yang menyebabkan 18 orang terinfeksi dan 6 di antaranya meninggal. Analisa genetik dari antigen pada virus tersebut ternyata berbeda dengan H5N1 pada umumnya. Perbedaan yang utama terdapat pada keberadaan glikosilasi residu 152 pada *haemagglutininnya* (Kodihali et al 1999).

2.1.1 Mutasi virus

Mutasi merupakan perubahan susunan genetik yang mengakibatkan terbentuknya struktur baru. Pada virus mutasi umumnya terjadi pada saat terjadinya replikasi didalam sel *host*. Pada saat pengkopian rantai RNA kadang terjadi kesalahan yang disebabkan karena adanya proses replikasi lain yang berlangsung didalam sel yang sama sehingga menghasilkan susunan RNA yang baru dan akan terbentuk virus dengan genetik yang baru pula. Jika mutasi ini menyebabkan virus menjadi kebal terhadap antibodi maka akan terjadi virus baru yang lebih berbahaya (Art Anderson, 2000).

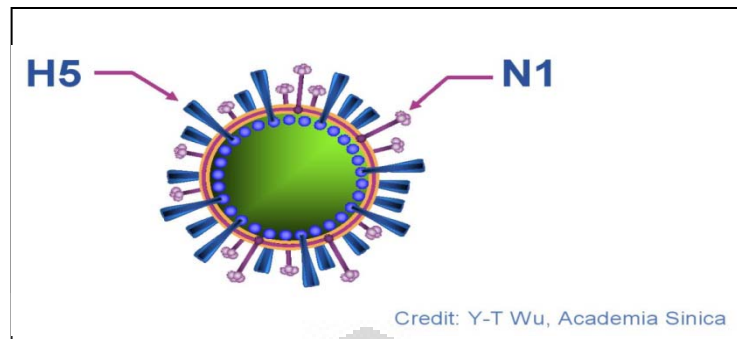
2.1.2 Avian Influenza A sub tipe H5N1

Virus H5N1 merupakan virus influenza tipe A, termasuk kelompok (famili) *Orthomyxoviridae*. Seringkali dalam referensi WHO, virus influenza ini dituliskan sebagai virus HPAI A/H5N1, "*Highly Pathogenic Avian Influenza*". Virus tipe A sub tipe H5N1 bersifat sangat patogen dan merupakan penyebab flu H5N1 atau yang lebih dikenal dengan avian influenza atau juga flu burung. Burung liar di seluruh dunia membawa virus H5N1 pada ususnya tetapi biasanya tidak menyebabkan sakit

pada burung tersebut. Penyakit ini bersifat endemik pada populasi burung terutama di Asia Tenggara. Satu *strain* dari HPAI A (H5N1) telah menyebar ke seluruh dunia setelah pertama kali muncul di Asia (<http://www3.niaid.nih.gov/>).

Virus H5N1 tidak dengan mudah menular antarmanusia dan jika seseorang telah terinfeksi maka virus tersebut sangat sulit untuk dapat menyebar atau menular antarmanusia. Hingga saat ini belum ada bukti berbasis molekular adanya transmisi antarmanusia atau penularan melalui transmisi udara (*airborne transmission*) oleh virus HPAI A(H5N1) ke manusia . Sejah ini semua kasus flu burung yang terjadi adalah karena kontak fisik dengan burung yang telah terinfeksi oleh virus tersebut. Walaupun demikian, dikhawatirkan adanya kemungkinan bahwa virus H5N1 dapat menular dan menyebar antarmanusia karena H5N1 dapat bermutasi (<http://www3.niaid.nih.gov/>).

Untuk melihat adanya perbedaan antara *strain* virus influenza yang satu dengan yang lain dapat dilakukan dengan cara melihat tiga jenis *sites* yang terdapat pada *haemagglutinin* virus influenza. Cara lain untuk mengetahui *strain* atau serotipe suatu virus yaitu dengan cara membuat pseudovirus atau virus buatan yang mengandung HA (*haemagglutinin*) dari virus influenza tetapi tidak punya kemampuan untuk menginfeksi. Kemudian pseudovirus tersebut diinkubasikan dalam darah tikus yang mengandung antibodi (niaidnews@niad.nih.gov).



Gambar 4 Struktur virus influenza A H5N1

2.1.3 Haemagglutinin (HA)

Haemagglutinin (HA atau H) adalah glikoprotein yang terdiri dari 3 situs glikosilasi, mempunyai berat molekul 76000. *Haemagglutinin* terdapat di membran dan merupakan bagian utamanya dan memiliki 5 antigen yang dominan yang terdapat di permukaan. *Haemagglutinin* ini merupakan homotrimer dan masing-masing merupakan polipeptida tunggal yang terpisah menjadi HA1 dan HA2. *Haemagglutinin* inilah yang nantinya akan berikatan dengan “*sialic acid*”. Ini adalah antigen yang utama pada virus. Sejuah ini telah diketahui ada 16 jenis antigen *Haemagglutinin* (HA). Subtipe ini diberi nama H1 sampai H16. H16 hanya baru ditemukan pada virus influenza A yang diisolasi dari burung gagak berkepala hitam yang ada di Swedia dan Norwegia (www.wikipedia.org).

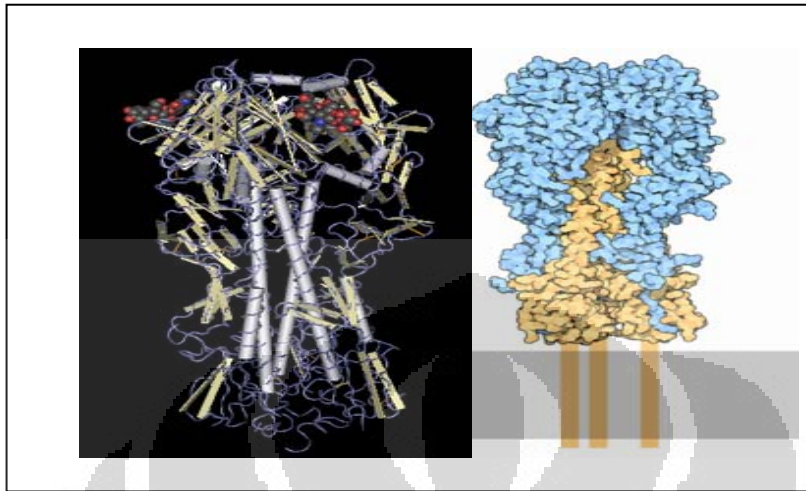
Namun demikian, sampai saat ini hanya H1, H2, dan H3 yang mampu menyebar antar manusia dan menjadi pandemik. Perubahan pengenalan dari *sialic acid* pada glukosanya dari α 2-3 (*avian*) menjadi α 2-6 (human) merupakan penyebab utama dari virus influenza A untuk menginfeksi spesies baru dan merubah *host* (Stevens et al 2006).

Pada *haemagglutinin* untuk subtipe H3, dan H2 ada dua buah posisi yang menentukan kemampuan pengenalan *receptor* yaitu pada posisi 226 dan 228 (berdasarkan penomoran pada H3). Pada virus yang hanya mengenali SA α -2,3 Gal posisi 226 merupakan Gln sedangkan untuk virus yang mampu mengenali SA α -2,6 Gal merupakan Leu. Sementara pada posisi 228 pengenal SA α -2,3 Gal adalah Gly dan pengenal SA α -2,6 Gal merupakan Ser (Gamblin et al,2004).

Haemagglutinin memiliki dua fungsi utama yaitu untuk mengenali sel target pada vertebrata yang akan berikatan dengan virus dan membantu masuknya genom viral kedalam sel melalui penggabungan membran endosom pada *host* dengan membran viral (White 1997).

Mutasi yang terjadi pada antigen akan mengurangi atau mencegah penetralan oleh antibodi, hal ini memungkinkan terjadinya subtipe baru yang menyebar dalam populasi non-imun. Fenomena ini dikenal dengan "*antigenic drift*". Mutasi yang disebabkan oleh *antigenic drift* menerangkan strain virus influenza pada musim epidemik influenza yang terjadi pada musim dingin (beriklim dingin). Respon imun terhadap antigen HA diikuti produksi antibodi penetralan yang merupakan dasar penyembuhan infeksi oleh setiap individu.(Gurtler et al 2007).

Atigenic shift merupakan perpindahan antigen yang terjadi pada saat sebuah sel terinfeksi dua virus yang berbeda tipe. Genome ini mengalami pertukaran pada saat terjadi replikasi didalam sel, misalnya H1 yang digantikan oleh H5 yang menghasilkan virus influenza dengan subtipe baru. (Gurtler at al 2007)



Gambar 5 Molekul Haemagglutinin

2.1.4 Neuraminidase

Seperti HA, neuraminidase (NA atau N) merupakan glikoprotein yang juga ditemukan pada permukaan virus. Memiliki struktur tetramer dan berat molekul rata-rata 220000. Molekul NA menampilkan bagian utamanya pada permukaan luar dari sel, menempel pada lipid bilayer, dan memiliki ekor sitoplasma yang kecil (Gurtler et al 2007).

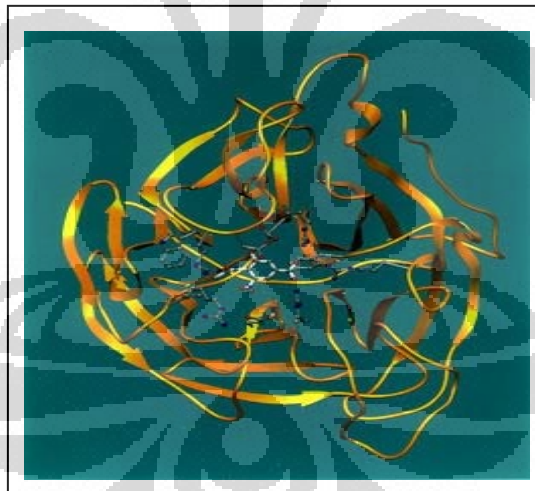
NA berfungsi seperti enzim yang memisahkan antara molekul HA dengan “*sialic acid*”, dari molekul NA yang lain, dan dari glikoprotein dan glikolipid pada permukaan sel. NA juga merupakan antigen yang berperan penting pada penetrasi saat virus memasuki lapisan mucin pada epithelium (Gurtler et al 2007).

Dari data *Swiss-Prot* ada 137 tipe neuraminidase dari berbagai jenis spesies sampai 18 oktober 2006. Sembilan diantara sub tipe NA terdapat pada virus Influenza, dan sebagian besarnya terdapat pada spesies bebek dan ayam. Sub tipe N1 dan N2

telah diketahui terdapat pada manusia dan N3 atau N7 telah diidentifikasi pada beberapa kasus kematian akibat virus influenza (www.eng.wikipedia.org)

Antigenic drift juga memungkinkan terjadi pada NA. NA membawa residu asam amino yang penting, dan jika mengalami mutasi dapat bertahan pada NA inhibitor (Gurtler et al 2007).

Ketika asam amino arginin (R) pada posisi 292 digantikan oleh lisin (K) misalnya maka kekebalan akan terbentuk. Mutasi ini terjadi ketika satu buah nukleotida berubah yaitu dari AGA menjadi AAA pada gen NA. Posisi 292 sangat signifikan karena mutasi pada posisi ini dapat membentuk *neuraminidase* yang kebal (*resistant*) terhadap inhibitor seperti zanamivir dan osetamivir (Gurtler et al 2007).



Gambar 6 Neuraminidase

2.1.5 Polymerase B2 protein (PB2), Polymerase B1 protein (PB1), dan Polymerase A protein (PA)

Protein PB1, PB2, dan PA merupakan RNA-RNA polymerase aktif yang mampu melakukan replikasi dan transkripsi dan replikasi. Fungsi dari protein ini adalah sebagai enzim yang akan menggandakan rantai RNA pada virus pada saat terjadi replikasi didalam sel inang (Gutler 2006).

2.1.6 Protein M2

Merupakan protein matrik yang terdapat dibawah kapsid. Saat protein virus. Fungsi protein M2 pada saat replikasi adalah mempengaruhi keadaan didalam sel seperti pH sehingga proses pemasukkan RNA kedalam inti sel akan berjalan lancar (Gutler 2006).

2.1.7 Protein NS1 dan NS2

Protein NS1 merupakan M-RNA yang memiliki berat molekul 26000. Protein ini akan membantu transport Viral RNA ke ribosom untuk ditranslasikan. Sedangkan NS2 merupakan molekul yang lebih kecil dengan berat molekul 11000. Protein ini dipercaya memiliki fungsi memfasilitasi transport RNP yang baru disintesis dari intisel menuju sitoplasma untuk mempercepat penggandaan virus (Gutler 2006).

2.2 Host

2.2.1 Definisi

Dalam ilmu virologi *host* merupakan organisme tempat menempelnya virus. Didalam *host* inilah virus dapat disebut sebagai makhluk hidup karena virus akan

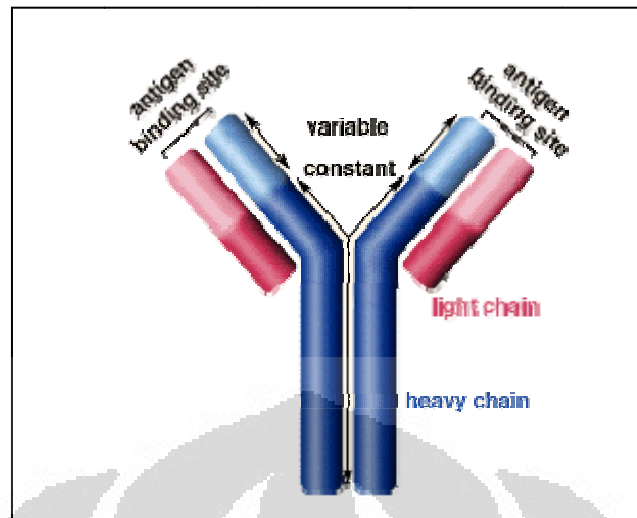
mengalami replikasi atau perkembangbiakan. Ada dua jenis *host* yaitu *host* primer dan *host* sekunder. *Host* primer merupakan *host* dimana virus akan bereplikasi atau bereproduksi secara seksual. Sedangkan *host* sekunder merupakan *host* yang ditempati oleh virus atau bakteri dalam waktu yang singkat saja, atau merupakan perantara. Dalam pengertian ini manusia merupakan *host* primer (www.eng.wikipedia.org)

Jenis *host* untuk virus influenza famili *Orthomyxoviridae* juga berbeda-beda berdasarkan tipenya. Influenza A dapat menginfeksi mamalia termasuk manusia, kuda, babi dan burung. Virus tipe inilah yang telah menjadi pandemik karena dapat menginfeksi lebih dari satu jenis makhluk hidup. Influenza B dan C hanya menginfeksi mamalia. Namun dengan adanya mutasi pada virus mengakibatkan virus dapat menginfeksi *host* yang baru. Umumnya virus yang mengalami mutasi adalah influenza tipe A yang kini telah membentuk subtipe H5N1 yang menjadi ancaman bagi manusia.

2.2.2 Antibodi dan Antigen

Antibodi adalah molekul protein dan dihasilkan oleh sistem imun sebagai respon terhadap antigen (Abbas et al., 1994). Antibodi yang sering dikenal dengan istilah *immunoglobulins* merupakan protein globulin gamma yang ditemukan didalam darah atau dalam cairan lain didalam tubuh makhluk hidup. Antibodi akan merespon senyawa-senyawa asing yang masuk kedalam tubuh dan akan menetralsirnya (www.en.wikipedia.org/antibody).

Setiap antibodi tersusun atas empat polipeptida yang membentuk huruf “Y”.



Gambar 7 Interaksi antibodi dengan antigen

Sementara antigen merupakan senyawa asing yang umumnya berupa protein. Suatu molekul dapat dikatakan antigen apabila molekul tersebut mempunyai sifat *immunogenicity* dan *antigenicity*. *Immunogenicity* sendiri adalah kemampuan suatu molekul untuk menginduksi respon imunitas spesifik dan antigen yang mempunyai sifat ini sering disebut sebagai *immunogen*. Sedangkan *antigenicity* adalah kemampuan suatu molekul untuk bereaksi secara spesifik dengan produk-produk yang dihasilkan oleh respon imunitas yang diinduksinya (Kuby, 1992; Kelgert, 1996).

2.2.3 Sistem Imun

Mekanisme pertahanan yang bersifat spesifik terhadap makromolekul tertentu disebut dengan *specific* atau *adaptive immunity*. Senyawa yang dapat memicu respon *specific immunity* dikenal dengan antigen. Antigen memicu timbulnya antibodi yang merupakan respon imunitas dari *specific immunity* (Abbas et al, 1994).

Antibodi disekresikan oleh limfosit . Limfosit terbagi atas dua kelas, yakni B limfosit dan T limfosit. B limfosit adalah satu-satunya limfosit yang dapat memproduksi antibodi. Kelas kedua yang merupakan T limfosit, tidak dapat memproduksi antibodi, sehingga untuk mengenali suatu antigen diperlukan suatu reseptor. Reseptor antigen T limfosit merupakan molekul membran yang secara struktur mirip dengan antibodi (Abbas, et al., 1994)

T limfosit terbagi atas dua jenis yaitu cytotoxic T cell dan helper T cell. Kedua jenis sel T ini hanya dapat mengenali antigen yang berupa peptida dan yang berikatan dengan protein hasil pengkodean senyawa MHC (Major Histocompatibility Complex). MHC merupakan komponen integral dari ligan yang dapat dikenali oleh T cell. Terdapat dua kelas MHC, yaitu kelas I yang merupakan fragmen peptida dari protein intraselular dan kelas II yang merupakan fragmen peptida dari protein ekstraseluler.

Helper T cell mensekresikan protein hormon yang disebut dengan cytokine yang fungsinya untuk mengaktivasi *macrophage*, sel B, dan mengaktifkan *inflammatory* leukosit. Cytotoxic T cell melisis sel yang menghasilkan antigen asing , seperti sel yang terinfeksi dengan virus dan mikroba intraseluler lainnya (Abbas, et al., 1994). Epitepe *sequence* yang tidak terlalu panjang, tanpa adanya keseluruhan *sequence* virus, dapat menstimulasi memori spesifik dari Cytotoxic T Lymphocyte (CTL) (Thomson, et al., 1997).

Sistem *mononuclear phagocyte* merupakan sistem imun yang terdiri atas kumpulan sel yang memiliki fungsi utama untuk proses fagositosis. Sel pertama yang meninggalkan sumsum tulang belakang melalui darah dan belum sepenuhnya

terdiferensiasi disebut dengan monosit. Monosit yang sampai di dalam jaringan disebut dengan *macrophage* (Abbas, et al, 1994)

Fungsi *macrophage* adalah untuk memfagositosis partikel asing seperti mikroba dan makromolekul, termasuk antigen. *Macrophage* dapat memproduksi *cytokine*. *Cytokine* ini kemudian mengaktifkan *inflammatory cell* dan bertanggung jawab terhadap efek *inflammatory* seperti demam (Abbas, et al., 1994).

2.2.4 Penamaan

Virus Influenza memiliki aturan penamaan sendiri berstandar international. Dapat dilihat pada contoh di bawah ini.

A/Chicken/Indonesia/CDC370P/2006(H5N1)

- **A** menunjukkan spesies dari virus influenza (A, B atau C).
- **Chicken** adalah asal spesies virus tersebut diisolasi.
- **Indonesia** adalah lokasi spesifik virus tersebut diisolasi.
- **CDC370P** adalah kode strain.
- **2006** menunjukkan tahun diambilnya sample.
- **H5** menunjukkan jenis hemmaglutinin yang dikandung.
- **N1** menunjukkan jenis neuraminidase yang dikandung.

Pada sistem ini berlaku pada virus yang diambil dari sample hewan, sedangkan pada manusia tidak disebutkan spesies inangnya. Seperti pada contoh dibawah ini.

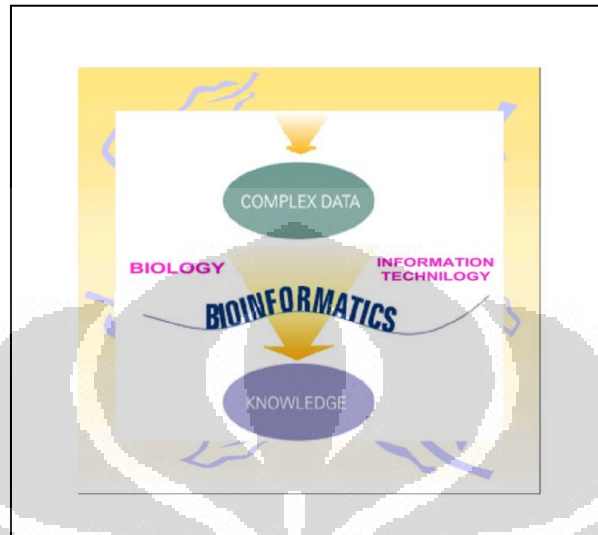
A/Indonesia/CDC669P/2006(H5N1)

2.3 Bioinformatika

2.3.1 Definisi

Bioinformatika merupakan perkawinan antara ilmu biologi dan ilmu teknik informatika. Bioinformatika melakukan analisa data genomik/proteomik yang kompleks, untuk menghasilkan pengetahuan biologi molekuler yang koheren. Bioinformatika adalah aplikasi dari alat komputasi dan analisis untuk menangkap dan menginterpretasikan data-data biologi. Ilmu ini merupakan ilmu baru yang merangkum berbagai disiplin ilmu termasuk ilmu komputer, matematika, fisika, kimia, biologi dan ilmu kedokteran yang kesemuanya saling menunjang dan saling bermanfaat satu sama lainnya (Utama, 2003).

Pesatnya perkembangan teknologi informasi dan peningkatan ilmu komputer, khususnya pada bidang biologi molekuler, menjadikan bioinformatika sebagai ilmu yang membuka sudut pandang baru dalam menyelesaikan persoalan biologi molekuler (Baxevanis dan Oullette, 2005).



Gambar 8 Bioinformatik

2.3.2 Format FASTA

Format FASTA terdiri atas *definition line* dan *sequence* asam amino atau nukleotida. Format ini merupakan format input (*query sequence*) untuk berbagai program analisis bioinformatika. Format FASTA tergolong kurang informatif dibandingkan format lainnya, namun format ini lebih praktis jika dipakai untuk data-data primer pada manusia (Baxevanis dan Oullete, 2001).

Dalam format FASTA penamaan protein pada *sequence* menggunakan kode satu huruf (*one letter code*). Penamaan protein memiliki dua jenis pengkodean, yaitu *1-letter code* dan *3-letter code*. Sebagai contoh, untuk Triptophan digunakan W sebagai *1-letter code* dan Trp sebagai *3-letter code*. Semua format dalam

bioinformatika, termasuk format FASTA menggunakan *1-letter code* (Claveire dan Notredame, 2001).

2.3.3 GenBank Flatfile Format

Format penyimpanan data yang paling umum digunakan adalah format *GenBank Flatfile Format* (GBFF), yang merupakan format elementer penyimpanan informasi dalam *GenBank*. *GenBank* merupakan suatu institusi yang menyimpan dan mengelola database urutan DNA suatu gen dan ekspresi asam aminonya. Urutan DNA diperoleh dari berbagai penelitian yang dengan sukarela mempublikasikan hasil penelitiannya untuk masyarakat umum. *GenBank* didirikan oleh *National Center for Biotechnology Information* (NCBI) bersama dengan *DNA Data Bank of Japan* dan *European Bioinformatics Institute* (EBI) (Baxevanis dan Oullette, 2001).

2.3.4 Sequence Alignment

Sequence Alignment merupakan metode penjajaran dua atau lebih *sequence* DNA atau asam amino menggunakan algoritma tertentu dengan bantuan komputer, sehingga didapatkan area yang memiliki urutan relatif identik satu sama lain. Metode ini berfungsi mencari kesamaan (konservatifitas) dan homologi antar *sequence* nukleotida DNA. Konservatifitas menunjukkan adanya hubungan evolusi antara dua atau lebih *sequence* nukleotida yang mengalami perubahan, seperti substitusi, insersi, dan delesi. Suatu area *sequence* nukleotida yang tidak memiliki kesamaan dengan

sequence nukleotida yang lain menunjukkan telah terjadinya substitusi (Baxevanis dan Ouellette, 2001).

Berdasarkan jumlah *sequence* yang digunakan, *sequence alignment* dibagi menjadi dua jenis, yaitu *pairwise alignment* jika melibatkan dua *sequence* dan *multiple sequence alignment* jika melibatkan lebih dari dua *sequence*. *Multiple sequence alignment* memberikan hasil yang lebih akurat dan representatif dibandingkan *pairwise sequence alignment*, karena peningkatan jumlah input *sequence* meningkatkan kepercayaan dan akurasi output. Peningkatan jumlah *sequence* yang dimasukkan berarti meningkatkan kompleksitas proses *sequence alignment* (Baxevanis dan Ouellette, 2001).

2.3.5 Database Similarity Searching

Sequence alignment digunakan untuk membandingkan pasangan *sequence* yang spesifik. Untuk suatu *sequence* yang belum diketahui pembandingnya digunakan *database similarity searching*, yang mana *sequence* tersebut dicari kecocokannya dengan *sequence* yang terdapat dalam database dan hasilnya berupa suatu daftar (*hit list*) beserta berbagai nilai dan statistik. (Baxevanis dan Ouellette, 2001)

Dikarenakan jumlah database yang begitu besar maka untuk melakukan pencarian dengan cara *sequence alignment* satu demi satu akan memakan waktu yang sangat lama, walaupun cara tersebut memberikan hasil yang paling baik. Salah satu pendekatan yang digunakan untuk meningkatkan kecepatan pencarian adalah dengan memecah *sequence* menjadi sejumlah rangkaian huruf yang disebut *word*. Prinsip

dasarnya adalah dua *sequence* yang berhubungan mengandung setidaknya satu word yang terdapat pada keduanya (*word hit*) (Baxevanis dan Oullette, 2001).

Program pertama kali yang dipakai secara luas dalam database *similarity searching* adalah FASTA (Lipman dan Pearson, 1985). Program FASTA tidak melakukan *sequence alignment* untuk tiap *word hit* yang terjadi, tetapi terlebih dahulu mencari bagian-bagian yang mengandung beberapa *word hit* yang berdekatan. Kompromi antara kecepatan dan sensitivitas dapat diatur dengan menentukan parameter ukuran word. Meningkatkan nilai *ktup*, akan menurunkan jumlah *word hit* yang terjadi tetapi meningkatkan kecepatan. (Baxevanis dan Ouellette, 2001).

2.3.6 BLAST

Program *Basic Local Alignment Search Tool* (*BLAST*) memperbaiki pencarian berdasarkan metode *word* dengan memperkenalkan konsep *neighborhood word*. Ada beberapa jenis *BLAST* sesuai tipe *sequence query* dan *subject*, protein atau nukleotida. Jika tipe *sequence* berbeda, *sequence* nukleotida akan terlebih dahulu ditranslasikan oleh program. *BLASTp* digunakan untuk *query* protein terhadap *subject* protein, *BLASTn* digunakan untuk *query* nukleotida (ditranslasikan) terhadap *subject* protein, *TBLASTn* digunakan untuk *query* protein terhadap *subject* nukleotida (ditranslasikan), yang terakhir adalah *TBLASTX* dimana *sequence query* dan *subject* merupakan nukleotida, tetapi keduanya ditranslasikan terlebih dahulu dan dibandingkan sebagai protein. (Baxevanis dan Ouellette, 2001).

2.3.7 Pohon Filogenetik

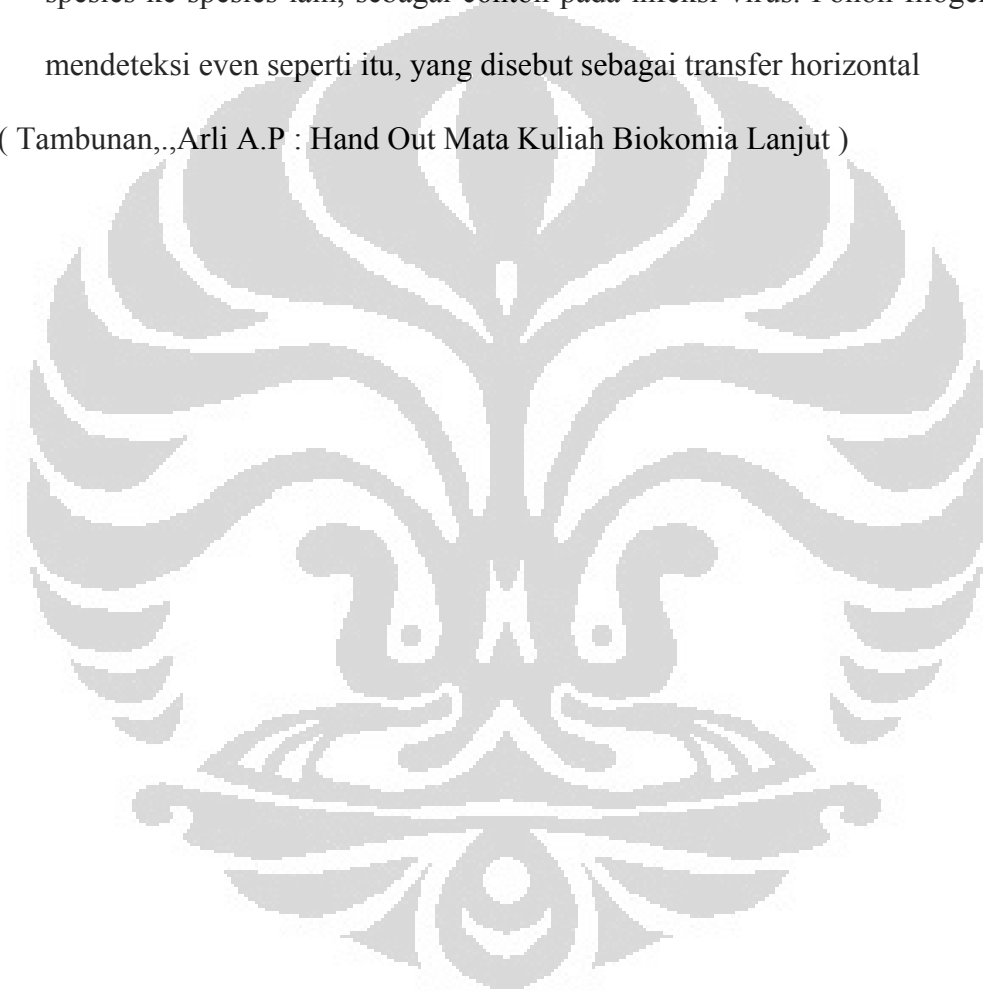
Filogeni bermanfaat untuk merekonstruksi sejarah kehidupan dan menjelaskan diversitas dari makhluk hidup. Hal ini dapat direpresentasikan sebagai pohon genealogi yang besar (pohon kehidupan). Prinsip filogeni adalah mencoba untuk mengklasifikasikan makhluk hidup berdasarkan tingkat similaritasnya. Dalam konteks ini, diasumsikan bahwa semakin similar kedua spesies (seperti manusia dan kera), semakin dekat *common ancestor* mereka. Filogenetik adalah filogeni khusus yang bergantung pada perbandingan gen-gen ekuivalen dari beberapa spesies untuk merekonstruksi pohon genealogi dan mengetahui kekerabatan di antara mereka. Sejarah molekuler yang bisa dijabarkan oleh filogenetiks adalah sangat kaya. Ketika famili protein dipelajari, ternyata ditemukan mutasi, delesi, duplikasi, spesiasi, kehilangan/penambahan fungsi, inaktivasi, dan berbagai even lainnya. Dalam konteks analisa bioinformatika, ada tiga alasan utama mengapa filogenetiks digunakan:

- Menentukan relasi terdekat dari organisme yang diteliti. Sebagai contoh, jika suatu bakteri baru dipelajari, RNA ribosomnya dapat *disequencing* dan dijabarkan pada pohon filogenetik untuk dibandingkan dengan RNA ribosom yang diketahui. Hal ini dapat memberikan gambaran mengenai identitas bakteri tersebut.
- Menemukan fungsi dari gen. Jika suatu gen baru dipelajari, maka pohon filogenetik dapat digunakan untuk memastikan apakah gen tersebut ortolog dengan gen pada spesies lain (Ortolog adalah gen-gen yang berasal dari

organisme berbeda, yang memiliki gen dari *common ancestor* yang sama, namun dipisahkan oleh even spesiasi).

- Melacak asal-usul dari gen: Sebagian besar gen pada genome melakukan perjalanan melalui waktu evolusi. Namun, gen individu dapat loncat dari satu spesies ke spesies lain, sebagai contoh pada infeksi virus. Pohon filogenik dapat mendeteksi even seperti itu, yang disebut sebagai transfer horizontal

(Tambunan,,Arli A.P : Hand Out Mata Kuliah Biokomia Lanjut)



BAB III

METODE PENELITIAN

Penelitian dilakukan di Laboratorium Bioinformatika Departemen Kimia Fakultas Matematika dan Ilmu Pengetahuan Alam Universitas Indonesia

3.1 Pencarian Genom dan Database protein

Peralatan yang digunakan untuk memperoleh genom virus influenza A adalah komputer yang terhubung ke internet dengan program *Internet Browser* seperti *Internet Explorer* atau *Mozilla FireFox* yang terintegrasi pada sistem operasi Microsoft Windows XP. Selain itu juga mempergunakan situs *google* yang menyediakan layanan *search engine* (www.google.com). Bahan yang digunakan adalah *sequence* avian influenza A yang dapat diperoleh dari GenBank yang dikeluarkan oleh *National Center for Biotechnology Information* dari *Influenza Sequence Database* yang dikeluarkan oleh Los Alamos National Laboratory. Pencarian genom didapat dalam format GBFF pada website Los Alamos National Laboratory <http://www.ncbi.nlm.nih.gov>.

Untuk menggunakan *sequence-sequence* yang telah didapat dalam *soft ware* maka *sequence-sequence* ini dirubah dalam bentuk FASTA yang telah tersedia pada situs <http://www.ncbi.nlm.nih.gov>. Format FASTA inilah yang akan digunakan untuk analisis selanjutnya dengan berbagai *software* bioinformatika.

3.2 Database Similarity Searching

Dilakukan pencarian *sequence* yang memiliki kemiripan dengan *sequence* yang telah didapatkan dari hasil pencarian genom dengan menggunakan *Basic Local Alignment Search Tool (BLAST)* yang juga bisa diakses dari *National Center for Biotechnology Information (NCBI)*.

3.3 Sequence Alignment Genom

Dilakukan *sequence alignment* pada gen yang dikira punya *conserved region* yang tinggi yang menyusun protein strukturan kapsid.

Sequence alignment dilakukan dengan software ClustalW versi 1.83. *Sequence alignment* dilakukan dengan menggunakan program ClustalW produksi *European Molecular Biology Laboratory*, program text editor Microsoft Word Office produksi Microsoft. Bahan yang digunakan adalah file *sequence* genom dari virus influenza dalam format FASTA.

File dalam format FASTA yang berisikan *sequence-sequence* yang akan diolah dimasukkan sebagai input *sequence*. Selanjutnya parameter-parameter operasi alignment ditentukan, lalu *multiple sequence alignment* dijalankan. Setelah selesai file output disimpan dalam format ClustalW.

3.4 Analisis Mutasi

Analisi mutasi dilakukan dengan *Amino Track toolbox* yang tersedia di situs <http://www.apps.sbri.org/AminoTrack/>. Program ini digunakan untuk indentifikasi mutasi pada protein viral.

3.5 Prediksi struktur 3 dimensi

Setelah ditemukan mutasi yang terjadi maka digunakan program online yang bias di akses di <http://ps2.life.nctu.edu.tw> untuk memprediksi struktur 3 dimensi dari *sequence* yang mengalami mutasi.

3.6 Analisis Filogenetik

Analisis filogenetik digunakan untuk melacak asal-usul virus H5N1. Data yang digunakan untuk analisis filogenetik ini adalah data hasil output dari alignment dengan program clustal W yang memiliki extention .dnl dengan menggunakan program ArboDraw untuk menampilkan pohon filogenik yang dihasilkan.

BAB IV

HASIL DAN PEMBAHASAN

4.1 Pencarian Sekuen Protein

Protein virus influenza yang digunakan sebagai bahan penelitian adalah semua sekuen protein yang terdapat pada virus *avian influenza* subtype H1N1, H2N2, H3N2, dan H5N1 dengan host *avian* dan *human*. Pemilihan sub tipe ini berdasarkan kemampuan virus dalam penyebarannya pada populasi manusia. Dalam hal ini H1N1, H2N2, dan H3N2 merupakan sub tipe yang telah mampu menyebar antar manusia dan telah menjadi pandemic, sementara H5N1 merupakan virus *avian* yang dikhawatirkan akan menjadi pandemic karena telah mampu menginfeksi manusia namun belum ada kasus yang menunjukkan kemampuan H5N1 menyebar antar manusia. Sekuen protein diperoleh dari *database GenBank* yang dikeluarkan oleh *National Center Biotechnology Information* melalui *Influenza Virus Resource (IVR-NCBI)* dengan alamat situs: <http://ncbi.nlm.nih.gov/genomes/FLU/Database.html>.

Dalam situs ini terdapat *influenza data search* yang kemudian dilakukan *advanced search* sesuai dengan spesifikasi yang kita inginkan. Penulis menggunakan spesifikasi Influenza A dengan inang manusia dan burung yang berada dalam database dengan segmen yang kita inginkan. Data yang diambil adalah data perwakilan dari data yang ada. Pada pemilihan data untuk protein *Haemagglutinin* dipilih sekuen yang *full length* dan diambil seratus sekuen sebagai sampel apabila datanya lebih dari seratus sekuen. Data yang diambil sebagai sampel adalah sekuen

yang awal diisolasi, pertengahan, dan sekuen yang tahun terakhir diisolasi dengan asumsi telah mewakili mutasi yang terjadi pada sekuen virus tersebut. Begitu juga dengan sekuen *Neuraminidase* dan sekuen protein yang lain.

Format yang ada pada *GenBank* IVR-NCBI adalah format GBFF (Gen Bank Flatfile Format) yaitu format yang berisi data lengkap sekuen tersebut dari mulai identitas host sampai dengan nukleotida dan proteinnya. Format GBFF terdiri atas *Header*, *Feature*, serta sekuen nukleotida. *Header* berisi data-data identitas organisme dari mana sampel virus diambil, seperti nama gen, waktu diambil, nomor akses. Sedangkan *feature* berisi informasi biologi yang terpenting, seperti nama genus, spesies, jaringan, kromosom, dan sebagainya. Sedangkan bagian terakhir adalah susunan lengkap asam aminonya (Lampiran 1). Sekuen protein yang ada terdiri dari urutan huruf-huruf, setiap huruf merupakan kode dari suatu asam amino (Lampiran 2). Agar lebih memudahkan penggunaannya dalam *software* maupun *server* dalam penelitian, semua sekuen protein diubah ke dalam format FASTA (Lampiran 3). Format FASTA ini juga telah tersedia didalam *Gen Bank* yang dikeluarkan oleh NCBI.

4.2 Multiple Sequence Alignments

Sequence Alignment merupakan metode penjajaran dua atau lebih sekuens DNA atau asam amino sehingga didapatkan area yang memiliki urutan relatif identik satu sama lain. Metode ini berfungsi mencari kesamaan (konservatifitas) dan homologi antar sekuens protein. Sekuen protein virus yang disimpan dalam format FASTA masing-masing dimasukkan sebagai *input* program ClustalX versi 1.83 untuk

proses *multiple sequence alignments*. ClustalX memudahkan melihat perbedaan sekuen asam amino sehingga dapat dikaitkan dengan variasi genetik dari virus sehingga dapat ditentukan satu perwakilan untuk setiap protein. Dengan menggunakan *Sequence Alignment* ini juga penulis menentukan sekuen hemagglutinin yang merupakan HA1 karena sekuen yang ada didatabase merupakan sekuen total dari protein *haemagglutinin* tanpa memperlihatkan bagian HA1 dan HA2-nya. Dengan *software* inilah penjabaran terhadap semua segmen virus dilakukan. Hasil dari *software* ini adalah berupa *file* dengan extension *.aln dan *.dnd. Asam amino yang sama pada semua protein diberikan tanda asterisk (*) untuk mempermudah melihat kesamaan yang terdapat pada semua sekuen (Lampiran 4).

4.3 Penentuan Conserved Region

Hasil *multiple alignments* dapat pula dilihat menggunakan program BioEdit versi 7.0.9.0 dengan *query* berupa file dalam format ClustalX yang disimpan (*.aln). Selanjutnya program BioEdit digunakan untuk menentukan *conserved region* dari hasil *alignments*.

Pemisahan *conserved region* dari hasil *alignment* dapat dilakukan dengan memasukkan sekuen-sekuen hasil *alignment*, dan kemudian menentukan parameter *conserved region* yang ingin diperoleh. Parameter yang digunakan pada penelitian ini menggunakan parameter *default* pada program tersebut. *Conserved region* merupakan daerah yang memiliki kemiripan antar nukleotida atau asam amino yang rapat sehingga jika dipisahkan, dapat membentuk subsekuen-subsekuen yang serupa. Untuk membatasi diskontinuitas tersebut, dapat ditentukan batasan jumlah

maksimum yang diperbolehkan ada dalam tiap segmen yang ditemukan. Selain itu dibatasi juga jumlah diskontinuitas yang berurutan. Dengan membatasi diskontinuitas, hasil yang akan ditampilkan oleh program hanyalah bagian-bagian sekuen yang masuk dalam kategori tersebut.

Hasil pencarian *conserved region* untuk protein *haemagglutinin* pada H5N1 didapat 8 sekuen *conserved region* yaitu, untuk sub tipe H1N1 didapat 3 *conserved region*, dan untuk sub tipe H2N2 didapat 7 *conserved region*, serta untuk H3N2 didapat 8 *conserved region* yang terdapat pada lampiran 5. Dari *conserved region* yang didapatkan terlihat ada beberapa *conserved region* yang berada pada posisi yang sama pada virus H5N1, H1N1, H2N2, dan H3N2. Hasil pencarian *conserved region* untuk protein yang lain juga terdapat dalam lampiran 5.

4.4 Analisis Pohon Filogenetik

Penggambaran pohon filogenetik untuk semua sekuen protein dilakukan dengan *software* ArboDraw yang bisa dilakukan secara *offline*. Input dari *software* ini adalah hasil dari *alignment* dengan format **dnd*. Hasil penggambaran pohon filogenetik untuk masing-masing protein dapat dilihat pada lampiran 6. Berdasarkan pohon filogenetik yang diperoleh didapatkan bahwa protein *haemagglutinin* pada virus influenza A sub tipe H5N1 memiliki kekerabatan yang lebih dekat dengan sub tipe H1N1 dibandingkan dengan sub tipe H2N2 atau pun H3N2. Dari pohon filogenetik ini juga dapat dilihat bahwa sekuen protein *haemagglutinin* pada H5N1 dengan host *Avian* dan *Human* masih terletak dalam satu grup yang menandakan bahwa belum ada sekuen *haemagglutinin* yang mengalami mutasi secara signifikan.

Sedangkan untuk protein *Neuraminidase* sekuen protein dari subtipe H5N1 juga lebih dekat dengan H1N1 karena masih dalam satu subtipe yaitu N1. Untuk pohon filogenetik dari masing-masing protein bisa dilihat pada lampiran 6.

4.5 Analisis Mutasi

Secara umum perbedaan virus influenza A yang menginfeksi manusia dan burung adalah pada pengenalan reseptornya. Virus influenza yang mampu menginfeksi manusia akan mengenali α -2,6-linked sialic acid (SA α – 2,3 Gal) sebagai tempat berikatannya, sedangkan avian influenza akan mengenali α -2,6-linked sialic acid (SA α – 2,6 Gal) sebagai tempat berikatannya (Kongchanagul et al 2008).

Pada manusia *receptor* SA α – 2,6Gal berada pada jalur udara bagian atas sementara SA α – 2,3Gal berada pada alveoli dan terminal bronkilous (Shinya et al, 2006). Virus yang mempunyai afinitas yang baik terhadap kedua *receptor* ini akan sangat berbahaya bagi manusia, virus itu akan mampu berikatan dengan SA α – 2,6Gal pada permukaan saluran pernafasan yang berarti akan mudah menginfeksi dan juga akan berikatan dengan α – 2,3Gal yang berada pada paru-paru sehingga akan menginfeksi organ bagian dalam (Glaser et al, 2005).

Secara fungsional protein *haemagglutinin* yang berada pada kapsid viruslah yang berperan sebagai *receptor binding*. Sekuen yang berfungsi sebagai *receptor binding* pada protein *haemagglutinin* adalah sekuen nomer 116 sampai 261 dengan penomoran berdasarkan pada penomoran sekuen H3 (Gamblin et al 2004). Dengan

demikian mutasi yang akan diamati adalah mutasi pada protein *haemagglutinin* terutama pada *reseptor binding sites*.

Dalam berikatan dengan protein *haemagglutinin* dari virus *receptor SA $\alpha - 2,3 Gal$* dan *SA $\alpha - 2,6 Gal$* mempunyai konformasi spesifik yaitu *cis* atau *trans*. Pada H5 ikatan antara protein *haemagglutinin* dengan *SA $\alpha - 2,6 Gal$* yang merupakan *receptor* pada manusia menunjukkan ketidakstabilan untuk kedua konformasi tersebut (Auewarakul et al, 2007).

Analisis yang digunakan untuk mengamati mutasi yang terjadi adalah dengan software AminoTrac™. *Software* ini akan menunjukkan sekuen yang mengalami perubahan. *Input* dari software ini adalah sekuen yang telah disimpan dalam file dengan format fasta. Sementara *outpunya* adalah hasil yang berupa urutan sekuen asam amino dalam file excel. Sekuen yang dipilih sebagai input untuk analisis mutasi ini adalah sekuen yang dianggap mewakili subtipe nya masing-masing yaitu (A/South Carolina/1/18 (H1N1)) untuk subtipe H1, (A/Kayano/57(H2N2)) untuk mewakili subtipe H2, (A/Beijing/1/68(H3N2)) sebagai perwakilan untuk subtipe H3, dan (A/Hong Kong/482/97(H5N1)) sebagai perwakilan untuk subtipe H5. Hasil dari analisis mutasi dari sekuen pada *Receptor Binding Domain (RBD)* dengan *software* AminoTrack adalah sebagai berikut :

Tabel 2 Hasil Analisis Mutasi

a. *Heamagglutinin*

No AA	134	136	139	190	191	195	225	226	228	251	258
H3	G	S	C		Q	Y		L	S	L	F
H1	G	S	C	D	Q	Y	D	Q	G	L	F
H2	G	S	C		Q	Y		L	S	L	F
H5	G	S	C	E	Q	Y	G	Q	G	F	Y
H5 Ind.	G	G	C	E	Q	Y	G	Q	G	F	Y

b. Neuraminidase

NO AA	190	191	258	264	269	328	346	350	358	396	397	401
H2N2	K	A	L	K	S	T	E	P	D	N	R	V
H3N2	K	A	L	K	S	T	E	Q	D	N	R	V
H1N1	M	G	L	K	I	N	S	N	R	V	R	V
H5N1	I	S	F	R	V	S	L	Y	K	X	K	I
H5N1 Ind.	I	S	F	R	V	S	L	Y	K	X	K	I

Pada protein *haemagglutinin* ada tiga area yang merupakan *receptor binding site* yaitu pada 190 helix (residu 190-198), 130 loop (residu 134-138) dan 220 loop (residu 221-228). Dari hasil analisis sekuen protein *haemagglutinin* pada bagian *receptor binding domain* dihasilkan data bahwa pada residu 134 dan 136 yang termasuk kedalam 130 loop pada subtipe H5N1 telah menyamai subtipe lainnya yang menjadi pandemik. Begitu juga pada residu nomer 191 dan 195, pada residu ini H5N1 juga telah sama dengan H1N1, H2N2, dan H3N2. Namun demikian pada H5N1 posisi yang paling menentukan pada protein *haemagglutinin* yang paling berperan dalam penyebarannya pada manusia belum berubah, yaitu pada posisi 226 dan 228. Residu pada posisi 226 masih *Gln* dan pada 228 masih *Gly* sementara pada virus influenza yang menjadi pandemik adalah *Leu* dan *Ser*.

Pada saat virus influenza A menginfeksi manusia maka virus tersebut terlebih dahulu harus mengenali SA α -2,6 *Gal* sebagai *receptor* yang terletak pada bagian permukaan saluran pernafasan, tanpa mampu mengenali *receptor* ini maka virus influenza A tidak akan mampu menginfeksi manusia. Setelah mampu menginfeksi virus influenza A akan berbahaya karena umumnya virus ini mengenali SA α -2,3 *Gal*

yang merupakan *receptor* yang terdapat pada paru-paru manusia. Inilah hal yang utama yang menyebabkan virus influenza A berbahaya bagi manusia sehingga menjadikan virus tersebut menjadi pandemik.

Pada kasus virus influenza A subtipe H5N1 yang kini telah mampu menginfeksi manusia namun belum memiliki kemampuan untuk menyebar antar manusia dapat disimpulkan bawa virus subtipe ini belum sepenuhnya mampu mengenali SA α -2,6 Gal sebagai *receptor* utama pada manusia. Hal ini disebabkan karena mutasi yang terjadi pada protein *haemagglutinin* dari subtipe H5N1 belum benar-benar dapat mengenali SA α -2,6 Gal. Berdasarkan dari penelitian yang dilakukan penulis sekuen asam amino dari haemagglutinin H5 dan H1 pada posisi yang menentukan pengenalan terhadap SA α -2,6 Gal yaitu pada posisi 226 dan 228 masih belum berubah dari mengenali SA α -2,3 Gal menjadi SA α -2,6 Gal. Dalam penelitian ini juga didapatkan perbedaan antara virus influenza A subtipe yang telah menjadi pandemik yaitu H1N1, H2N2, H3N2 dengan subtipe H5N1 yaitu pada sekuen asam amino posisi 251 dan 258. Pada subtipe yang menjadi pandemik asam amino 251 adalah *Leu* sedangkan pada H5N1 adalah *Phe*, sementara pada posisi 258 untuk subtipe pandemik adalah *Phe* dan pada H5N1 adalah *Tyr*. Perbedaan lain antara H1 dan H5 adalah pada posisi 225 dan 190. Untuk H1 terdapat *Asp* pada posisi 190 dan 225 sedangkan pada H5 terdapat *Glu* pada 190 dan *Gln* pada 225. Posisi inilah yang telah mendukung pengenalan H1 dengan *receptor* pada manusia (Gamblin et al,2004).

Sedangkan pada protein *neuraminidase* pada subtipe H5N1 dan H1N1 merupakan *neuraminidase* yang satu tipe sehingga untuk melihat perbedaanya akan

lebih dilihat antara H1N1 dan H5N1. Dari hasil analisis mutasi didapatkan perbedaan pada posisi 190, 191, 258, 264, 269, 328, 346, 350, 358, 396, 397, 401. Bila dibandingkan dengan dengan tipe lain yang telah pandemik maka didapatkan posisi 258, 264, 397, 401 yang pada H1 sama dengan tipe lainnya namun pada H5 berbeda dengan tipe lainnya.

Terkait dengan kemungkinan virus subtipe H5N1 menjadi pademik maka dapat dilihat dari mutasi yang terjadi, apabila semua receptor binding yang terkait dengan pengenalan receptor SA α -2,6 Gal telah berubah sepenuhnya sehingga memungkinkan penyebaran antar manusia. Pada asam amino yang masih berbeda dengan asam amino pada subtipe virus yang telah menjadi pandemik juga tidak bisa diabaikan karena perbedaan ini juga memiliki potensi dalam hal mempengaruhi kemampuan virus untuk menular antar manusia.

Bila dibandingkan dengan virus subtipe H5N1 yang menyebar di Indonesia dapat dilihat pada hasil analisis dengan AminoTrack. Dari sini bisa dilihat bahwa pada protein *haemagglutinin* virus H5N1 yang di Indonesia memiliki kesamaan dengan virus H5N1 yang menyebar didunia terutama pada bagian *conserve region*. Dengan demikian maka dapat disimpulkan bahwa virus subtipe H5N1 yang menyebar di Indonesia memiliki sifat yang sama dengan virus subtipe H5N1 diwilayah lain dan belum memiliki kemampuan menyebar antar manusia.

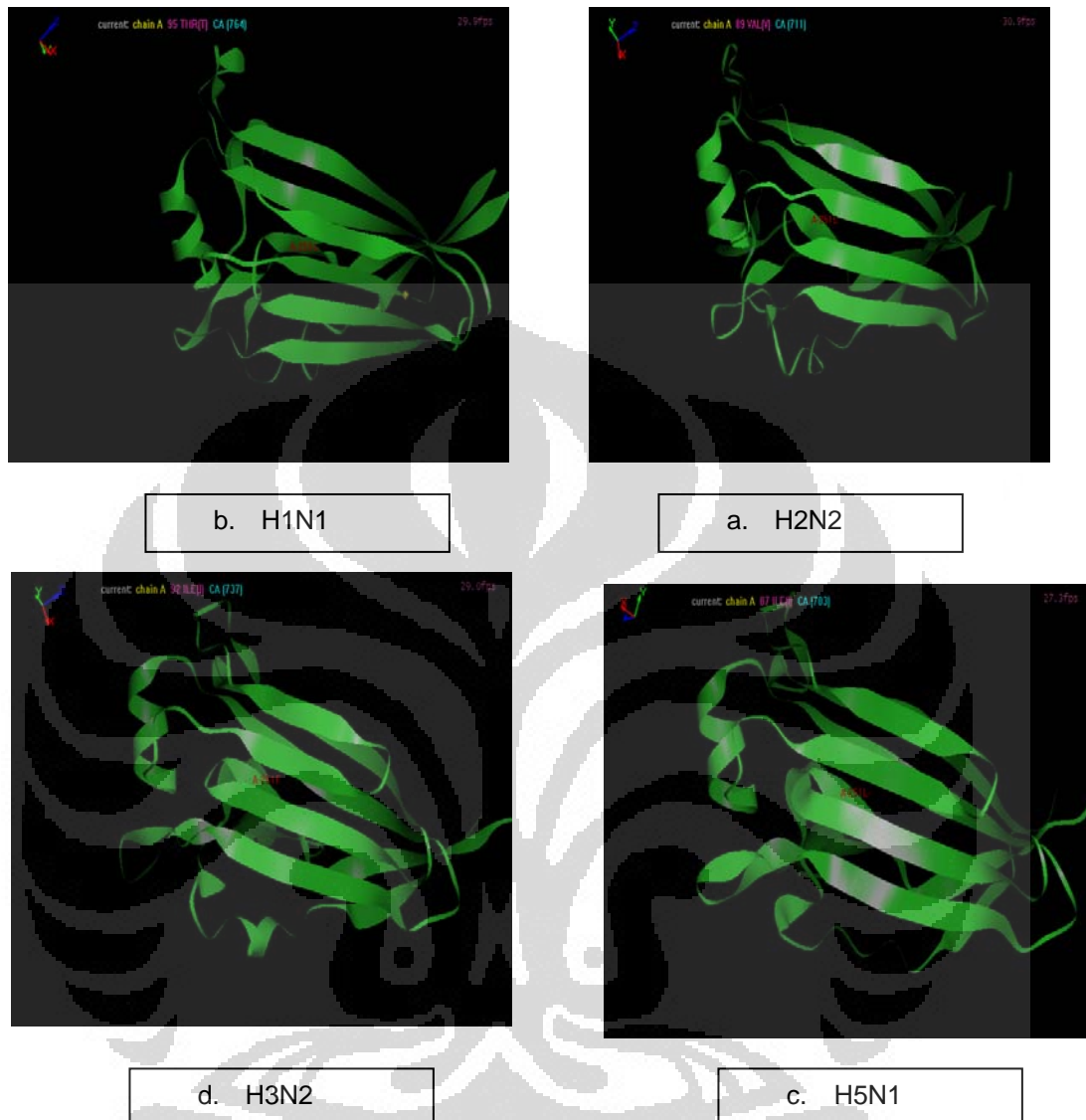
4.6 Prediksi Struktur Tiga Dimensi

Untuk meyakinkan bahwa sekuen yang dianalisis menggunakan AminoTrack merupakan sekuan yang tepat maka untuk setiap sekuen dari masing-masing subtipe

ini dilakukan prediksi struktur tiga dimensinya. Dalam penentuan struktur tiga dimensi digunakan *software* online yang bisa diakses melalui <http://ps2.life.nctu.edu.tw>. Input dari *software* ini adalah sekuen protein dalam format FASTA. Sekuen yang dipilih untuk diprediksi struktur tiga dimensi adalah sekuen *Haemagglutinin* yang merupakan *Receptor Binding Domain* (RBD) seperti yang digunakan pada analisis mutasi. Hasil prediksi dari *software* ini didasarkan pada data yang telah tersimpan dalam *Protein Data Bank* (PDB).

Output dari prediksi struktur tiga dimensi adalah file dalam format *.pdb yang bisa akan dibuka dengan *software* noc-3. Berikut ini adalah hasil prediksi struktur tiga dimensi dari RBD untuk masing-masing subtipe.

Dari hasil prediksi struktur tiga dimensi terlihat kemiripan antara struktur H1N1, H2N2, H3N2, dan H5N1. Kemiripan ini dapat dilihat dari struktur α -*helix* dan β -*sheet* dari masing-masing struktur tersebut. Hal ini dapat meyakinkan bahwa sekuen yang dianalisis dengan menggunakan AminoTrack adalah sekuen yang memiliki fungsi sama untuk masing-masing subtipe.



Gambar 9 struktur tiga dimensi protein *Haemagglutinin*

BAB V

KESIMPULAN DAN SARAN

5.1 Kesimpulan

Hasil penentuan dari analisis filogenetik didapatkan bahwa sekuen *haemagglutinin* dan *neuraminidase* untuk virus influenza A subtipe H5N1 lebih mirip dengan virus influenza A subtipe H1N1 dibanding dengan subtipe lain yang telah menjadi pandemik yaitu H2N2 dan H3N2. Berdasarkan analisis mutasi dengan AminoTrack didapatkan bahwa subtipe H5N1 belum menjadi pandemik karena virus ini belum sepenuhnya mampu mengenali *receptor SA α -2,6 Gal* yang merupakan *receptor* yang terdapat pada saluran pernafasan bagian atas pada manusia (hidung).

Ketidakmampuan virus subtipe H5N1 menyebar antar manusia adalah karena belum terjadinya mutasi pada posisi 226 dan 228 pada protein *haemagglutinin*. Posisi inilah yang merupakan *receptor binding* yang membedakan kemampuan mengenali *receptor SA α -2,3 Gal* dengan *SA α -2,6 Gal*. Pada host *avian* posisi 226 adalah *Gln* sementara pada host *human* merupakan *Leu*. Sedangkan pada posisi 228 adalah *Glu* untuk *avian* dan *Ser* untuk *human*. Berdasarkan analisis mutasi dengan AminoTrack didapatkan bahwa pada virus H5N1 asam amino posisi 226 dan 228 masih merupakan asam amino yang mengenali *SA α -2,3 Gal*. Hal lain yang mendukung ketidakmampuan H5N1 dalam mengenali *SA α -2,6 Gal* adalah asam amino posisi 251 dan 258 yang masih berbeda dengan asam amino pada subtipe yang telah

menjadi pandemik. Selain itu perbedaan pada sekuen protein neuraminidase juga ikut berperan pada ketidakmampuan virus H5N1 dalam penyebarannya pada manusia.

Begitu juga dengan virus influenza A subtipe H5N1 di Indonesia. Virus yang menyebar di Indonesia masih memiliki kesamaan sekuen dengan virus H5N1 lainnya dalam hal sekuen haemagglutinin terutama pada conserve region. Dengan demikian dapat disimpulkan virus yang menyebar di Indonesia akan menjadi pandemik apabila asam amino pada posisi yang telah dibahas telah mengalami mutasi baik secara *antigenic drift* maupun *antigenic sift*. Dari hasil penelitian ini maka dapat dilakukan perancangan vaksin untuk virus dengan sekuen *haemagglutinin* yang diprediksi bisa menjadi pandemik.

5.2 Saran

Melakukan penelitian lebih lanjut untuk mutasi yang terjadi pada sekuen protein lain dan pengaruhnya terhadap kemampuan penyebaran virus antar manusia serta peranannya dalam patogenitasnya secara *in silico*. Melakukan penelitian perancangan primer dan vaksin secara *in silico* untuk sekuen *hemagglutinin* yang telah diprediksikan akan menjadi pandemik.

Melakukan penelitian secara *in vitro* untuk uji patogenitas virus influenza A subtipe H5N1 hasil yang memiliki sekuen pandemic dari hasil prediksi secara *in silico*.

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<http://en.wikipedia.org/wiki/H1N1.htm> (diakses pada Rabu,13 agustus 2008 pukul 17:02)

<http://en.wikipedia.org/wiki/H2N2.htm> (diakses pada Rabu,13 agustus 2008 pukul 17:04)

<http://en.wikipedia.org/wiki/H3N2.htm> (diakses pada Rabu,13 agustus 2008 pukul 17:08)

<http://en.wikipedia.org/wiki/H9N2.htm> (diakses pada Rabu,13 agustus 2008 pukul 17:09)

<http://en.wikipedia.org/wiki/H7N7.htm> (diakses pada Rabu,13 agustus 2008 pukul 17:10)

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LAMPIRAN

Lampiran 1. Informasi Genetik Virus H5N1 Hemagglutinin dalam Format GBFF

1: hemagglutinin [In...[gi:124098927]

LOCUS ABM90478 552 aa linear VRL 24-JAN-2007

DEFINITION hemagglutinin [Influenza A virus (A/Indonesia/CDC1032/2007(H5N1))].

ACCESSION ABM90478

VERSION ABM90478.1 GI:124098927

DBSOURCE accession [CY019384.1](#)

KEYWORDS .

SOURCE Influenza A virus (A/Indonesia/CDC1032/2007(H5N1))

ORGANISM [Influenza A virus \(A/Indonesia/CDC1032/2007\(H5N1\)\)](#)
Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
Influenzavirus A.

REFERENCE 1 (residues 1 to 552)

AUTHORS Balish,A., Deyde,V., Garten,R., Lindstrom,S., Shu,B., Smith,C.,
Smith,E. and Xu,X.

TITLE Avian Influenza Associated with Outbreaks in Indonesia

JOURNAL Unpublished

REFERENCE 2 (residues 1 to 552)

AUTHORS Balish,A., Deyde,V., Garten,R., Lindstrom,S., Shu,B., Smith,C.,
Smith,E. and Xu,X.

TITLE Direct Submission

JOURNAL Submitted (24-JAN-2007) WHO Collaborating Center for Surveillance,
Epidemiology and Control of Influenza, Influenza Branch, Centers
for Disease Control and Prevention, 1600 Clifton Road NE, Atlanta,
GA 30333, USA

COMMENT Method: conceptual translation.

FEATURES Location/Qualifiers

source 1..552
/organism="Influenza A virus
(A/Indonesia/CDC1032/2007(H5N1))"
/strain="A/Indonesia/CDC1032/2007"
/serotype="H5N1"
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/db_xref="taxon:[421471](#)"
/segment="4"
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causes membrane fusion of the viral membrane with the host
membrane. Fusion occurs after the host cell internalises
the virus by endocytosis; pfam00509"
/db_xref="CDD:[64376](#)"

[CDS](#) 1..552
/gene="HA"
/coded_by="CY019384.1:<1..1659"

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121 swsdheassg vssacpylgs psffrnvwl ikknstypti kksynnntqe dlviwgihh
181 pnneeeqtrl yqnpptyisi gtstlnqrlv pkiatrskvn gqsgrmefwv tilkpndain
241 fesngnfiaf eyaykivkkg dsaimksele yscnctkcqt pmgainssmp fhnipltig
301 ecpsykssr llatglrns pqrresrkrk glfgaiagf eggwqgmvdg wygyhhsneq
361 gsgyaadkes tqkaidgvtn kvnsiidkmn tqfeavref nlierriell nkkmedgfd
421 vwtynaellv lmenertidf hdsnvknlyd kvrlqrdna kelngccef yhkcdnecme
481 sirngtynyp qyseearlkr eeisgvkles igtyqilsy stvasslala imiaglslwm
541 csngslqrci ci

Lampiran 2. Daftar Kode Dua Puluh Asam Amino

No	Kode satu huruf	Kode tiga huruf	Nama
1	A	Ala	Alanin
2	R	Arg	Arginin
3	N	Asn	Asparagin
4	D	Asp	Asam aspartat
5	C	Cys	Sistein
7	Q	Gln	Glutamin
6	E	Glu	Asam glutamat
8	G	Gly	Glisin
9	H	His	Histidin
10	I	Ile	Isoleusin
11	L	Leu	Leusin
12	K	Lys	Lisin
13	M	Met	Metionin
14	F	Phe	Fenilalanin
15	P	Pro	Prolin
16	S	Ser	Serin
17	T	The	Treonin
18	W	Trp	Triptofan
19	Y	Tyr	Tirosin
20	V	Val	Valin

Lampiran 3 : Sekuen Protein Virus Influenza A subtipe H1N1, H2N2, H3N2, dan H5N1 dalam Format Fasta

Haemagglutinin

H1N1

```
>gi|4325039|gb|AAD17229.1| hemagglutinin [Influenza A virus (A/South Carolina/1/18 (H1N1))]
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KCN I AGWLLGNPECDLLTASSWSYI VETPNSENGACYPGDFI DYEELREQLSSVSSFEKFEI FPKTSSW
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GI I TSDAPVHDCNTKCCQTPHGA I NSSLPFQNI HPVTI GECPKYVRSTKLRMATGLRNI PSI QSRGLFGAI
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I ENLNKKVDDGFLDI WTYNAELLVLENERLDFHDSNVRNLYEKVKSOLKNNAKEI GNGCFEFYHKCDD
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QCRI CI
>gi|94960371|gb|ABF47955.1| hemagglutinin [Influenza A virus (A/WSN/1933 TS61(H1N1))]
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KCN I TGWLLGNPECDLLPARSWSYI VETPNSENGACYPGDFI DYEELREQLSSVSSLERFEI FPKESSW
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I I TSNASMHECNTKCCQTPQGS I NSNLPFQNI HPVTI GECPKYVRSTKLRMTGLRNI PSI QYRGLFGAI A
GFI EGGWTGMI DGWYGYHHQNEOGSGYAADQKSTQNAI NRI TNKVN SVI EKMNTQFTAVGKEFNLEKRM
ENLNKKVDDGFLDI WTYNAELLVLENERLDFHDLNVKNLYEKVKSOLKNNAKEI GNGCFEFYHKCDNE
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CRI CI
>gi|89782156|gb|ABD77796.1| hemagglutinin [Influenza A virus (A/Wilson-
Smith/33(H1N1))]
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AGFI EGGWTGMI DGWYGYHHQNEOGSGYAADQKSTQNAI NGI TNKVN SVI EKMNTQFTAVGKEFNLEKRM
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QCRI CI
>gi|194352371|gb|ACF54598.1| hemagglutinin [Influenza A virus (A/WSN/1933(H1N1))]
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CRI CI
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Smith/1933(H1N1))]
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CRI CI
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CRI CI
```

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>gi|194304803|gb|ACF41834.1| hemagglutinin [Influenza A virus (A/Puerto
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 ENLNKKVDDGFLDI WTYNAELLV LLENERTLDFHDSNVKNLYEKVKSOLKNNAKEI GNGCFEFYHKCDNE
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 CRI CI

>gi|133754189|gb|AB038384.1| hemagglutinin [Influenza A virus (A/Philippines/1935(H1N1))]
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 PKHNHTTKGVTAACSHAGKSSFYRNLLWL TTKEDSYPKLNKSYVNNKKGKKEVLVWGVHHPSSSKEQOTLYO
 NENAYVSVVSSNYNRRFTPEI AERP KVRDQAGRMNYYWTL LKPGDTI I FEANGNLI APYAFALSRGFGS
 GI I TSNASMHECNTKCCQTP LGAI NSSLPFQNI HPVTI GECPKYVRS AKLRMTGLRNI PSI QSRGLFGAI
 AGFI EGGWTGMI DGWYGYHHQNEOGSGYAADQKSTQNAI NGI TNKVNSVI EKMMI QFTAVGKEFNKLEKR
 MENLNKKVDDGFLDI WTYNAELLV LLENERTLDFHDSNVKNLYEKVKSOLKNNAKEI GNGCFEFYHKCDN
 ECMESVRNGTYDYPKYSEESKLNREKI DGVKLESMGVYOI LAI YSTVASSLVLLVSLGAI SFWMCSNGSL
 QCRI CI

>gi|89148077|gb|ABD62781.1| hemagglutinin [Influenza A virus (A/Melbourne/35(H1N1))]
 MKARLLVLLCALAADADTI CI GYHANNSTDTVDTVLEKNVTVTHSVNLLLED SHNGKLCRLKGI APLQLG
 KCNI AGWLLGNPECDPLLPVRSWSYI VETPNSENGI CYPGDFI DYEELREQLSSVSSFERFEI FPKESSW
 PKHNHTTKGVTAACSHAGKSSFYRNLLWL TTKEDSYPKLNKSYVNNKKGKKEVLVWGVHHPSSSKEQOTLYO
 NENAYVSVVSSNYNRRFTPEI AERP KVRDQAGRMNYYWTL LKPGDTI I FEANGNLI APYAFALSRGFGS
 GI I TSNASMHECNTKCCQTP LGAI NSSLPFQNI HPVTI GECPKYVRS AKLRMTGLRNI PSI QSRGLFGAI
 AGFI EGGWTGMI DGWYGYHHQNEOGSGYAADQKSTQNAI NGI TNKVNSVI EKMMI QFTAVGKEFNKLEKR
 MENLNKKVDDGFLDI WTYNAELLV LLENERTLDFHDSNVKNLYEKVKSOLKNNAKEI GNGCFEFYHKCDN
 ECMESVRNGTYDYPKYSEESKLNREKI DGVKLESMGVYOI LAI YSTVASSLVLLVSLGAI SFWMCSNGSL
 QCRI CI

>gi|133754132|gb|AB038351.1| hemagglutinin [Influenza A virus (A/Henry/1936(H1N1))]
 MKARLLVLLCALAADADTI CI GYHANNSTDTVDTVLEKNVTVTHSVNLLLED SHNGKLCRLKGI APLQLG
 KCNI AGWLLGNPECDPLLPVRSWSYI VETPNSENGI CYPGAFI DYEELREQLSSVSSFERFEI FPKESSW
 PNHNHTNI GVTACSHAGKSSFYRNLLWL TTKGGSYPKLNKSYVNNKKGKKEVLVWGI HHPNSKDOOTLYO

NENAYVSVSSNYNRRFTPEI AERPEVRDQAGRMNYWTLLEPGDTI MFEANGNLVAPWYAFALSRGFGS
 GI I TSNASMHECCTKQTPQGA I NSSLPFQNI HPVTI GECPKYVRS AKLRMTGLRNI PSI QSRGLFGAI
 AGFI EGGWTGMI DGWYGYHHQNEOGSGYAADQKSTQNAI NGI TNKVNSVI EKMNTQFTAVGKEFNLEKR
 MENLNKKVDDGFLDI WTYNAELLVLENERLDFHDSNVKNLYEKVKSOLKNNAKEI GNGCFEFYHKCDN
 ECMESVRNGTYDPKYSEESKLNREKI DGVKLESMGVYQI LAI YSTVASSLVLLVSLGAI SFWMCSNGSL
 QCRI CI
 >gi |86788144|gb|ABD15258.1| hemagglutinin [Influenza A virus (A/Denver/57(H1N1))]
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 I I TSNAPLDECDTKCQTPQGA I NSSLPFQNI HPVTI GECPKYVRS AKLRMTGLRNI PSVQSRGLFGAI A
 GFI EGGWTGMMDGWYGYHHQNEOGSGYAADQKSTQNAI NGI TNKVNSVI EKMNTQFTAVGKEFNKLEKRM
 ENLNKKVDDGFDI WTYNAELLVLENERLDFHDSNVKNLYEKVKNQLRNNAKELGNGCFEFYHKCDNE
 CMESVKNGTYDPKYSEESKLNREKI DGVKLESMGVYRI LAI YSTVASSLVLLVSLGAI SFWMCSNGSLQ
 CRI CI
 >gi |189303378|gb|ACD85764.1| hemagglutinin [Influenza A virus
 (A/Oklahoma/02/2008(H1N1))]
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 I I NSNAPMDKCDKACQTPQGA I NSSLPFQNVHPVTI GECPKYVRS AKLRMTGLRNI PSI QSRGLFGAI A
 GFI EGGWTGMVDGWYGYHHQNEOGSGYAADQKSTQNAI NGI TNKVNSVI EKMNTQFTAVGKEFNKLERM
 ENLNKKVDDGFI DI WTYNAELLVLENERLDFHDSNVKNLYEKVKSOLKNNAKEI GNGCFEFYHKCDNE
 CMESVKNGTYDPKYSEESKLNREKI DGVKLESMGVYQI LAI YSTVASSLVLLVSLGAI SFWMCSNGSLQ
 CRI CI
 >gi |189303362|gb|ACD85756.1| hemagglutinin [Influenza A virus
 (A/Fiori da/09/2008(H1N1))]
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 ENAYVSVSSHYSRKFTPEI AKRPKVRDQEGRI NYYWTLLEPGDTI I FEANGNLI APRYAFALSRGFGSG
 I I NSNAPMDKCDKACQTPQGA I NSSLPFQNVHPVTI GECPKYVRS AKLRMTGLRNI PSI QSRGLFGAI A
 GFI EGGWTGMVDGWYGYHHQNEOGSGYAADQKSTQNAI NGI TNKVNSVI EKMNTQFTAVGKEFNKLERM
 ENLNKKVDDGFI DI WTYNAELLVLENERLDFHDSNVKNLYEKVKSOLKNNAKEI GNGCFEFYHKCDNE
 CMESVKNGTYDPKYSEESKLNREKI DGVKLESMGVYQI LAI YSTVASSLVLLVSLGAI SFWMCSNGSLQ
 CRI CI
 >gi |189303368|gb|ACD85759.1| hemagglutinin [Influenza A virus (A/New
 Jersey/10/2008(H1N1))]
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 ENAYVSVSSHYSRKFTPEI AKRPKVRDQEGRI NYYWTLLEPGDTI I FEANGNLI APRYAFALSRGFGSG
 I I NSNAPMDKCDKACQTPQGA I NSSLPFQNVHPVTI GECPKYVRS AKLRMTGLRNI PSI QSRGLFGAI A
 GFI EGGWTGMVDGWYGYHHQNEOGSGYAADQKSTQNAI NGI TNKVNSVI EKMNTQFTAVGKEFNKLERM
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 CRI CI
 >gi |189303386|gb|ACD85768.1| hemagglutinin [Influenza A virus (A/North
 Carolina/04/2008(H1N1))]
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 I I NSNAPMDKCDKACQTPQGA I NSSLPFQNVHPVTI GECPKYVRS AKLRMTGLRNI PSI QSRGLFGAI A
 GFI EGGWTGMVDGWYGYHHQNEOGSGYAADQKSTQNAI NGI TNKVNSVI EKMNTQFTAVGKEFNKLERM
 ENLNKKVDDGFI DI WTYNAELLVLENERLDFHDSNVKNLYEKVKSOLKNNAKEI GNGCFEFYHKCDNE
 CMESVKNGTYDPKYSEESKLNREKI DGVKLESMGVYQI LAI YSTVASSLVLLVSLGAI SFWMCSNGSLQ
 CRI CI
 >gi |189303392|gb|ACD85771.1| hemagglutinin [Influenza A virus
 (A/Georgia/06/2008(H1N1))]
 MKVKLLVLLCTFTATYADTI CI GYHANNSTDTVDTVLEKNVTVTHSVNLLLENSHNGKLCLLKGI APLQLG
 NCSVAGWI LGNPECELLI SKESWSYI VEKPNPENGTCYPGHFADYEELREQLSSVSSFERFEI FPKESSW
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 I I NSNAPMDKCDKACQTPQGA I NSSLPFQNVHPVTI GECPKYVRS AKLRMTGLRNI PSI QSRGLFGAI A
 GFI EGGWTGMVDGWYGYHHQNEOGSGYAADQKSTQNAI NGI TNKVNSVI EKMNTQFTAVGKEFNKLERM
 ENLNKKVDDGFI DI WTYNAELLVLENERLDFHDSNVKNLYEKVKSOLKNNAKEI GNGCFEFYHKCDNE
 CMESVKNGTYDPKYSEESKLNREKI DGVKLESMGVYQI LAI YSTVASSLVLLVSLGAI SFWMCSNGSLQ
 CRI CI
 >gi |189303390|gb|ACD85770.1| hemagglutinin [Influenza A virus
 (A/Georgia/05/2008(H1N1))]
 MKVKLLVLLCTFTATYADTI CI GYHANNSTDTVDTVLEKNVTVTHSVNLLLENSHNGKLCLLKGI APLQLG
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II NSNAPMDKCDAKCQTPOGAI NSSLPFQNVHPVTI GECPKYVRSTKLRMVTGLRNI PSI QSRGLFGAI A
 GFIEGGWTGMVDGWYGYHHQNEOGSGYAADQKSTQNAI NGI TXKVNSVI EKMNTQFTAVGKEFNKLERM
 ENLNKKVDDGFI DI WTYNAELLVLENERLDFHDSNVKNLYEKVKSOLKNNAKEI GNGCFEFYHKCNDE
 CMESVKNGTYDYPKYSEESKLNREKI DGVKLESMGVYQI LAI YSTVASSLVLLVSLGAI SFWMCSNGSLQ
 CRI CI

>gi |189303388|gb|ACD85769.1| hemagglutinin [Influenza A virus (A/North
 Carolina/05/2008(H1N1))]

MKVKLLVLLCTFTATYADTI CI GYHANNSTDTVDTVLEKNVTVTHSVNLLNSHNGKLCLLKGI APLQLG
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 I I NSNAPMDKCDAKCQTPOGAI NSSLPFQNVHPVTI GECPKYVRSAKLRMVTGLRNI PSI QSRGLFGAI A
 GFIEGGWTGMVDGWYGYHHQNEOGSGYAADQKSTQNAI NGI TNKVNSVI EKMNTQFTAVGKEFNKLERM
 ENLNKKVDDGFI DI WTYNAELLVLENERLDFHDSNVKNLYEKVKSOLKNNAKEI GNGCFEFYHKCNDE
 CMESVKNGTYDYPKYSEESKLNREKI DGVKLESMGVYQI LAI YSTVASSLVLLVSLGAI SFWMCSNGSLQ
 CRI CI

>gi |189303376|gb|ACD85763.1| hemagglutinin [Influenza A virus
 (A/Wyoming/10/2008(H1N1))]

MKVKLLVLLCTFTATYADTI CI GYHANNSTDTVDTVLEKNVTVTHSVNLLNSHNGKLCLLKGI APLQLG
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 ENAYVSVSSSHYSRKFTPEI AKRPKVRDQEGRI NYYWTLLEPGDTI I FEANGNLI APRYAFALSRGFGSG
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 GFIEGGWTGMVDGWYGYHHQNEOGSGYAADQKSTQNAI NGI TNKVNSVI EKMNTQFTAVGKEFNKLERM
 ENLNKKVDDGFI DI WTYNAELLVLENERLDFHDSNVKNLYEKVKSOLKNNAKEI GNGCFEFYHKCNDE
 CMESVKNGTYDYPKYSEESKLNREKI DGVKLESMGVYQI LAI YSTVASSLVLLVSLGAI SFWMCSNGSLQ
 CRI CI

>gi |189303382|gb|ACD85766.1| hemagglutinin [Influenza A virus
 (A/Indiana/04/2008(H1N1))]

MKVKLLVLLCTFTATYADTI CI GYHANNSTDTVDTVLEKNVTVTHSVNLLNSHNGKLCLLKGI APLQLG
 NCSVAGWI LGNPECELLI SKESWSYI VEKPNPENGTCYPGHFADYEELREQLSSVSSFERFEI FPKESSW
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 I I NSNAPMDKCDAKCQTPOGAI NSSLPFQNVHPVTI GECPKYVRSAKLRMVTGLRNI PSI QSRGLFGAI A
 GFIEGGWTGMVDGWYGYHHQNEOGSGYAADQKSTQNAI NGI TNKVNSVI EKMNTQFTAVGKEFNKLERM
 ENLNKKVDDGFI DI WTYNAELLVLENERLDFHDSNVKNLYEKVKSOLKNNAKEI GNGCFEFYHKCNDE
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 CRI CI

>gi |193084911|gb|ACF10345.1| hemagglutinin [Influenza A virus
 (A/Vermont/01/2008(H1N1))]

MKVKLLVLLCTFTATYADTI CI GYHANNSTDTVDTVLEKNVTVTHSVNLLNSHNGKLCLLKGI APLQLG
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 GFIEGGWTGMVDGWYGYHHQNEOGSGYAADQKSTQNAI NGI TNKVNSVI EKMNTQFTAVGKEFNKLERM
 ENLNKKVDDGFI DI WTYNAELLVLENERLDFHDSNVKNLYEKVKSOLKNNAKEI GNGCFEFYHKCNDE
 CMESVKNGTYDYPKYSEESKLNREKI DGVKLESMGVYQI LAI YSTVASSLVLLVSLGAI SFWMCSNGSLQ
 CRI CI

>gi |194294065|gb|ACF40127.1| hemagglutinin [Influenza A virus (A/New
 Jersey/13/2008(H1N1))]

MKVKLLVLLCTFTATYADTI CI GYHANNSTDTVDTVLEKNVTVTHSVNLLNSHNGKLCLLKGI APLQLG
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 GFIEGGWTGMVDGWYGYHHQNEOGSGYAADQKSTQNAI NGI TNKVNSVI EKMNTQFTAVGKEFNKLERM
 ENLNKKVDDGFI DI WTYNAELLVLENERLDFHDSNVKNLYEKVKSOLKNNAKEI GNGCFEFYHKCNDE
 CMESVKNGTYDYPKYSEESKLNREKI DGVKLESMGVYQI LAI YSTVASSLVLLVSLGAI SFWMCSNGSLQ
 CRI CI

>gi |189303380|gb|ACD85765.1| hemagglutinin [Influenza A virus
 (A/Oklahoma/03/2008(H1N1))]

MKVKLLVLLCTFTATYADTI CI GYHANNSTDTVDTVLEKNVTVTHSVNLLNSHNGKLCLLKGI APLQLG
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 CMESVKNGTYDYPKYSEESKLNREKI DGVKLESMGVYQI LAI YSTVASSLVLLVSLGAI SFWMCSNGSLQ
 CRI CI

>gi |189303400|gb|ACD85775.1| hemagglutinin [Influenza A virus
 (A/Illinois/06/2008(H1N1))]

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I I NSNAPMDKCDKACQTPQAI NSSLPFQNVHPVTI GECPKYVRSAKLRMTGLRNI PSI QSRGLFGAI A
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 ENLNKKVDDGFI DI WTYNAELLVLENERLDFHDSNVKNLYEKVKSOLKNNAKEI GNGCFEFYHKCNDE
 CMESVKNGTYDYPKYSEESKLNREKI DGVKLESMGVYQI LAI YSTVASSLVLLVSLGAI SFWMCSNGSLQ
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 >gi |194294069|gb|ACF40129.1| hemagglutinin [Influenza A virus (A/South
 Carolina/01/2008(H1N1))]
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 PXHTVTGVSASCSHNGESSFYRNLLWLTGKNGLYPNLSKSYANNKEKEVLVWGVVHHPNI GDQKTLTYHT
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 GFI EGGWTGMVDGWYGYHHQNEOGSGYAADQKSTQNAI NGI TNKVNSVI EKMNTQFTAVGKEFNKLERM
 ENLNKKVDDGFI DI WTYNAELLVLENERLDFHDSNVKNLYEKVKSOLKNNAKEI GNGCFEFYHKCNDE
 CMESVKNGTYDYPKYSEESKLNREKI DGVKLESMGVYQI LAI YSTVASSLVLLVSLGAI SFWMCSNGSLQ
 CRI CI
 >gi |112787546|gb|ABI20826.1| hemagglutinin [Influenza A virus (A/Hickox/1940(H1N1))]
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 KCNI AGWI LGNPECESLLSKRSWSYI AETPNSENGTCYPGDFADYEELREQLSSVSSFERFEI FPKERSW
 PNHNI NI GVTAACSHAGKSSFYKNLLWLTGKDGSYPNLNKSYVNKKEKEVLVWGVVHHPNI ENOKTLYR
 KENAYVSVSSNYNRRFTPEI AERPKVARGOAGRMNYWTLLEPGDTI I FEANGNLI APWYAFALSRGLSG
 GI I TSNASMDECDTKCQTPQAI NSSLPFQNI HPFTI GECPKYVRSKLRMTGLRNI PSI QSRGLFGAI A
 AGFI EGGWAGMI DGWYGYHHQNEOGSGYAADQKSTQNAI NGI TNKVNSVI EKMNTQFTAVGKEFNKLEKR
 MENLNKKVDDGFLDI WTYNAELLVLENERLDFHDSNVKNLYEKVKSOLRNNAKEI GNGCFEFYHKCN
 ECMESVKNGTYDYPKYSEESKLNREKI DGVKLESMGVYQI LAI YSTVASSLVLLVSLGAI SFWMCSNGSL
 QCRI CI
 >gi |89152215|gb|ABD62843.1| hemagglutinin [Influenza A virus (A/Bel/1942(H1N1))]
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 KCNI AGWI LGNPECESLLSERSWSYI VETPNSENGTCYPGDFI DYEELREQLSSVTSFERFEI FPKETSW
 PKHNTTKGVTAACSHAGKCSFYRNLLWLTGKDGSYPNLNKSYVNKKEKEVLVWGVVHHPNI KDQOTLYQ
 KENAYVSVSSNYNRRFTPEI AERPKVARGOAGRMNYWTLLEPGDTI I FEANGNLI APWYAFALSRGFGS
 GI I TSNASMHECDTKCQTPQAI NSSLPFQNI HPVTI GECPKYVRSKLRMTGLRNI PSI QSRGLFGAI A
 AGFI EGGWTGMI DGWYGYHHQNEOGSGYAADQKSTQNAI NGI TNKVNSVI EKMNTQFTAVGKEFNKLEKR
 MENLNKKVDDGFLDI WTYNAELLVLENERLDFHDSNVKNLYEKVKSOLRNNAKEI GNGCFEFYHKCN
 ECMESVKNGTYDYPKYSEESKLNREKI DGVKLESMGVYQI LAI YSTVASSLVLLVSLGAI SFWMCSNGSL
 QCRI CI
 >gi |89903056|gb|ABD79101.1| hemagglutinin [Influenza A virus (A/Weiss/43(H1N1))]
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 KENAYVSVSSNYNRRFTPEI AERPKVARGOAGRMNYWTLLEPGDTI I FEANGNLI APWYAFALSRGFGS
 GI I TSNASMHECDTKCQTPQAI NSSLPFQNI HPVTI GECPKYVRSKLRMTGLRNI PSI QSRGLFGAI A
 AGFI EGGWTGMI DGWYGYHHQNEOGSGYAADQKSTQNAI NGI TNKVNSVI EKMNTQFTAVGKEFNKLEKR
 MENLNKKVDDGFLDI WTYNAELLLVLENERLDFHDSNVKNLYEKVKSOLRNNAKEI GNGCFEFYHKCN
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 QCRI CI
 >gi |133752882|gb|AB038054.1| hemagglutinin [Influenza A virus
 (A/AA/Marton/1943(H1N1))]
 MKARLLVLLCALAATDADTI CI GYHANNSTDTVDTVLEKNVTVTHSVNLLSHNGKLCRLKGI APLQLG
 KCNI AGWI LGNPECESLLSERSWSYI VETPNSENGTCYPGDFI DYEELREQLSSVSSFERFEI FSKESSW
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 KENAYVSVSSNYNRRFTPEI AERPKVARGOAGRMNYWTLLEPGDTI MFEANGNLI APWYAFALSRGFGS
 GI I TSNASMHECDTKCQTPQAI NSSLPFQNI HPVTI GECPKYVRSKLRMTGLRNI PSI QSRGLFGAI A
 AGFI EGGWTGMI DGWYGYHHQNEOGSGYAADQKSTQNAI NGI TNKVNSVI EKMNTQFTAVGKEFNKLEKR
 MENLNKKVDDGFLDI WTYNAELLLVLENERLDFHDSNVKNLYEKVKSOLRNNAKEI GNGCFEFYHKCN
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 QCRI CI
 >gi |133754170|gb|AB038373.1| hemagglutinin [Influenza A virus (A/Iowa/1943(H1N1))]
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 KCNI AGWI LGNPECESLLSERSWSYI VETPNSENGTCYPGDFI DYEELREQLSSVSSFERFEI FSKESSW
 PKHTTGGVTAACSHAGKSSFYRNLLWLTGKDGSYPNLNKSYVNKKEKEVLVWGVVHHPNI KDQOTLYQ
 ENAYVSVSSNYNRRFTPEI AERPKVARGOAGRI NYYWTLLEPGDTI MFEANGNLI APWYAFALSRGFGSG
 I I TSNASMHECDTKCQTPQAI NSSLPFQNI HPVTI GECPKYVRSKLRMTGLRNI PSI QSRGLFGAI A
 GFI EGGWTGMI DGWYGYHHQNEOGSGYAADQKSTQNAI NGI TNKVNSVI EKMNTQFTAVGKEFNKLEKR
 ENLNKKVDDGFLDI WTYNAELLVLENERLDFHDSNVKNLYEKVKSOLRNNAKEI GNGCFEFYHKCN
 CMESVKNGTYDYPKYSEESKLNREKI DGVKLESMGVYQI LAI YSTVASSLVLLVSLGAI SFWMCSNGSLQ
 CRI CI
 >gi |145278810|gb|ABP49327.1| hemagglutinin [Influenza A virus
 (A/AA/Huston/1945(H1N1))]
 MKARLLVLLCALAATDADTI CI GYHANNSTDTVDTVLEKNVTVTHSVNLLSHNGKLCRLKGI APLQLR
 KCNI AGWI LGNPECESLLSERSWSYI VETPNSENGTCYPGDFI DYEELREQLSSVSSFERFEI FPKESSW
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 KENAYVSVSSNYNRRFTPEI AERPKVARGOAGRMNYWTLLEPGDTI MFEANGNLI APWYAFALSRGFGS
 GI I TSNASMHECDTKCQTPQAI NSSLPFQNI HPVTI GECPKYVRSKLRMTGLRNI PSI QSRGLFGAI A
 AGFI EGGWTGMI DGWYGYHHQNEOGSGYAADQKSTQNAI NGI TNKVNSVI EKMNTQFTAVGKEFNKLEKR
 MENLNKKVDDGFLDI WTYNAELLLVLENERLDFHDSNVKNLYEKVKSOLRNNAKEI GNGCFEFYHKCN
 ECMESVKNGTYDYPKYSEESKLNREKI DGVKLESMGVYQI LAI YSTVASSLVLLVSLGAI SFWMCSNGSL

QCRI CI
 >gi|89903075|gb|ABD79112.1|hemagglutinin [Influenza A virus (A/Cam/46(H1N1))]
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 PEHNI DI GVTAACSHAGKSSFYKNLLWLTEKDGSPNLSKYVNNKEKEVLI LWGVHHPNI ENOKTLR
 KENAYVSVSSNYNRRFTPEI AERPKVRGOAGRI NYWTLLLEPGDTI I FEANGNLI APWYAFALNRGI GS
 GI I TSNASMDECDTKCQTPQAI NSSLPFQNI HPVTI GECPKYVVRSTKLRMTGLRNI PSI QSRGLFGAI
 AGFI EGGWTDGMI DGWYGYHHQNEQSGYAADQKSTQNAI NGI TNKVNSVI EKMTQFTAVGKEFNKLEKR
 MENLNKKVDDGFLDI WTYNAELLVLENERLDFHDSNVKNLYEKVKQLRNNAKEI GNGCFEFYHKCN
 ECMESVKNGTYPKYSEESKLNREKI DGVKLESMGVYQI LAI YSTVASSLVLLVSLGAI SFWMCSNGSL
 QCRI CI
 >gi|89782382|gb|ABD77807.1|hemagglutinin [Influenza A virus
 (A/FortMonmouth/1/47(H1N1))]
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 KENAYVSVSSNYNRRFTPEI AERPKVRGOAGRI NYWTLLLEPGDTI I FEANGNLI APWYAFALSRGFGS
 GI I TSNASMDECDTKCQTPQAI NSSLPFQNI HPVTI GECPKYVVRSTKLRMTGLRNI PSI QSRGLFGAI
 AGFI EGGWTDGMI DGWYGYHHQNEQSGYAADQKSTQNAI NGI TNKVNSVI EKMTQFTAVGKEFNKLEKR
 MENLNKKVDDGFLDI WTYNAELLVLENERLDFHDSNVKNLYEKVKQLRNNAKEI GNGCFEFYHKCN
 ECMESVKNGTYPKYSEESKLNREKI DGVKLESMGVYQI LAI YSTVASSLVLLVSLGAI SFWMCSNGSL
 QCRI CI
 >gi|406042|gb|AAA67338.1|hemagglutinin [Influenza A virus (A/Fort
 Monmouth/1/1947(H1N1))]
 MKAKLLI LLLCALSDADDTI CI GYHANNSTDTVDTVLEKNVTVTHSVNLLLED SHNGKLCRLKGI APLQLG
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 PKHNI TRGVTAACSHAGKSSFYKNLLWLTETNGSYPKLSKYVNNKEKEVLIWLVGVHHPNI EDOKTLR
 KENAYVSVSSNYNRRFTPEI AERPKVRGOAGRI NYWTLLLEPGDTI I FEANGNLI APWYAFALSRGFGS
 GI I TSNASMDECDTKCQTPQAI NSSLPFQNI HPVTI GECPKYVVRSTKLRMTGLRNI PSI QSRGLFGAI
 AGFI EGGWTDGMI DGWYGYHHQNEQSGYAADQKSTQNAI NGI TNKVNSVI EKMTQFTAVGKEFNKLEKR
 MENLNKKVDDGFLDI WTYNAELLVLENERLDFHDSNVKNLYEKVKQLRNNAKEI GNGCFEFYHKCN
 ECMESVKNGTYPKYSEESKLNREKI DGVKLESMGVYQI LAI YSTVASSLVLLVSLGAI SFWMCSNGSL
 QCRI CI
 >gi|125976162|gb|ABN59401.1|hemagglutinin [Influenza A virus
 (A/AI bany/4835/1948(H1N1))]
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 PKHNI TRGVTAACSHAGKSSFYKNLLWLTETNGSYPKLSKYVNNKEKEVLIWLVGVHHPNI EDOKTLR
 KENAYVSVSSNYNRRFTPEI AERPKVRGOAGRI NYWTLLLEPGDTI I FEANGNLI APWYAFALSRGFGS
 GI I TSNASMDECDTKCQTPQAI NSSLPFQNI HPVTI GECPKYVVRSTKLRMTGLRNI PSI QSRGLFGAI
 AGFI EGGWTDGMI DGWYGYHHQNEQSGYAADQKSTQNAI NGI TNKVNSVI EKMTQFTAVGKEFNKLEKR
 MENLNKKVDDGFLDI WTYNAELLVLENERLDFHDSNVKNLYEKVKQLRNNAKEI GNGCFEFYHKCN
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 QCRI CI
 >gi|125976219|gb|ABN59434.1|hemagglutinin [Influenza A virus (A/Roma/1949(H1N1))]
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 PKHNI TRGVTAACSHAGKSSFYKNLLWLTETNGSYPKLSKYVNNKEKEVLIWLVGVHHPNI EDOKTLR
 KENAYVSVSSNYNRRFTPEI AERPKVRGOAGRI NYWTLLLEPGDTI I FEANGNLI APWYAFALSRGFGS
 GI I TSNASMDECDTKCQTPQAI NSSLPFQNI HPVTI GECPKYVVRSTKLRMTGLRNI PSI QSRGLFGAI
 AGFI EGGWTDGMI DGWYGYHHQNEQSGYAADQKSTQNAI NGI TNKVNSVI EKMTQFTAVGKEFNKLEKR
 MENLNKKVDDGFLDI WTYNAELLVLENERLDFHDSNVKNLYEKVKQLRNNAKEI GNGCFEFYHKCN
 ECMESVKNGTYPKYSEESKLNREKI DGVKLESMGVYQI LAI YSTVASSLVLLVSLGAI SFWMCSNGSL
 QCRI CI
 >gi|89114296|gb|ABD61735.1|hemagglutinin [Influenza A virus (A/Fort Worth/50(H1N1))]
 MKAKLLI LLLCALSDADDTI CI GYHANNSTDTVDTVLEKNVTVTHSVNLLLED SHNGKLCRLKGI APLQLG
 KCNI AGWV LGNPECESLLSNRSWSYI AETPNSENGACYPGDFADYEELREQLSSVSSFERFEI FPKERSW
 PKHNTI RGVTAACSHAGKSSFYKNLLWLTETNGSYPALSTSYVNNKEKEVLIWLVGVHHPNI EEOQTLR
 KDNAYVSVSSNYNRRFTPEI AKRPKVRDOPGRMNYWTLLLEPGDTI I FEATGNLI APWYAFALSRGFGS
 GI I TSNAPMDECDTKCQTPQAI NSSLPFQNI HPVTI GECPKYVVRSTKLRMTGLRNI PSI QSRGLFGAI
 AGFI EGGWTDGMI DGWYGYHHQNEQSGYAADQKSTQNAI NGI TNKVNSVI EKMTQFTAVGKEFNKLEKR
 MENLNKKVDDGFLDI WTYNAELLVLENERLDFHDSNVKNLYEKVKQLRNNAKEI GNGCFEFYHKCN
 ECMESVKNGTYPKYSEESKLNREKI DGVKLESMGVYQI LAI YSTVASSLVLLVSLGAI SFWMCSNGSL
 QCRI CI
 >gi|145278791|gb|ABP49316.1|hemagglutinin [Influenza A virus
 (A/AI bany/4836/1950(H1N1))]
 MKAKLLI LLLCALSDADDTI CI GYHANNSTDTVDTVLEKNVTVTHSVNLLLED SHNGKLCRLKGI APLQLG
 KCNI AGWI LGNPECESLLSKRSWSYI AETPNSENGACYPGDFADYEELREQLSSVSSFERFEI FPKERSW
 PKHNI TRGVTAACSHAGKSSFYKNLLWLTETNGSYPNLSKYVNNKEKEVLIWLVGVHHPNI EDOKTLR
 KENAYVSVSSNYNRRFTPEI AERPKVRGOAGRI NYWTLLLEPGDTI I FEANGNLI APWYAFALSRGFGS
 GI I TSNASMDECDTKCQTPQAI NSSLPFQNI HPVTI GECPKYVVRSTKLRMTGLRNI PSI QSRGLFGAI
 AGFI EGGWTDGMI DGWYGYHHQNEQSGYAADQKSTQNAI NGI TNKVNSVI EKMTQFTAVGKEFNKLEKR
 MENLNKKVDDGFLDI WTYNAELLVLENERLDFHDSNVKNLYEKVKQLRNNAKEI GNGCFEFYHKCN
 ECMESVKNGTYPKYSEESKLNREKI DGVKLESMGVYQI LAI YSTVASSLVLLVSLGAI SFWMCSNGSL
 QCRI CI
 >gi|145279077|gb|ABP49481.1|hemagglutinin [Influenza A virus
 (A/AI bany/12/1951(H1N1))]

MKARLLI LLCALSATDADTI CI GYHANNSTDTVDTVLEKNVTVTHSVNLLLED SHNGKLCRLKGI APLQLG KCNI AGWI LGNPECESLLSNRSWSYI AETPNSENGTCYPGDFADYEELREQLSSVSSFERFEI FPKERSW PKHNI TRGVTAAACSHAKKSSFYKNLLWLTEANGSYPNLSKSYVNNKEKEVLVWGVHHPNSI EDORTLYR KENAYVSVSSNYNRRFTPEI AERPKVRGOAGRMNYWTLLEPGDKI I FEANGNLI APWYAFALSRGLGS GI I TSNASMDECDTKCQTPQGA I NSSLPFQNI HPVTI GECPKYVRSTKLRMTGLRNI PSI QSRGLFGAI AGFI EGGWTGMVDGWYGYHHQNEQSGYAADQKSTQNAI NGI TNKVNSVI EKMTQFTAVGKEFNKLEKR MENLNKKVDDGFLDI WTYNAELLVLENERLDFHDSNVKNLYEKVKQLRNNAKEI GNGCFEFYHKCDN ECMESVKNGTYDYPKYSEESKLNREKI DGVKLESMGVYQI LAI YSTVASSLVLLVSLGAI SFWMCSNGSL QCRI CI

>gi |146760085|gb|ABQ44471.1| hemagglutinin [Influenza A virus (A/Al bany/14/1951(H1N1))]

MKARLLI LLCALSATDADTI CI GYHANNSTDTVDTVLEKNVTVTHSVNLLLED SHNGKLCRLKGI APLQLG KCNI AGWI LGNPECESLLSNRSWSYI AETPNSENGTCYPGDFADYEELREQLSSVSSFERFEI FPKERSW PKHNI TRGVTAAACSHAKKSSFYKNLLWLTEANGSYPNLSKSYVNNKEKEVLVWGVHHPNSI EDORTLYR KENAYVSVSSNYNRRFTPEI AERPKVRGOAGRMNYWTLLEPGDKI I FEANGNLI APWYAFALSRGLGS GI I TSNASMDECDTKCQTPQGA I NSSLPFQNI HPVTI GECPKYVRSTKLRMTGLRNI PSI QSRGLFGAI AGFI EGGWTGMVDGWYGYHHQNEQSGYAADQKSTQNAI NGI TNKVNSVI EKMTQFTAVGKEFNKLEKR MENLNKKVDDGFLDI WTYNAELLVLENERLDFHDSNVKNLYEKVKQLRNNAKEI GNGCFEFYHKCDN ECMESVKNGTYDYPKYSEESKLNREKI DGVKLESMGVYQI LAI YSTVASSLVLLVSLGAI SFWMCSNGSL QCRI CI

>gi |146133734|gb|ABQ01311.1| hemagglutinin [Influenza A virus (A/Al bany/1618/1951(H1N1))]

MKARLLI LLCALSATDADTI CI GYHANNSTDTVDTVLEKNVTVTHSVNLLLED SHNGKLCRLKGI APLQLG KCNI AGWI LGNPECESLLSNRSWSYI AETPNSENGTCYPGDFADYEELREQLSSVSSFERFEI FPKERSW PKHNI TRGVTAAACSHAKKSSFYKNLLWLTEANGSYPNLSKSYVNNKEKEVLVWGVHHPNSI EDORTLYR KENAYVSVSSNYNRRFTPEI AERPKVRGOAGRMNYWTLLEPGDKI I FEANGNLI APWYAFALSRGLGS GI I TSNASMDECDTKCQTPQGA I NSSLPFQNI HPVTI GECPKYVRSTKLRMTGLRNI PSI QSRGLFGAI AGFI EGGWTGMVDGWYGYHHQNEQSGYAADQKSTQNAI NGI TNKVNSVI EKMTQFTAVGKEFNKLEKR MENLNKKVDDGFLDI WTYNAELLVLENERLDFHDSNVKNLYEKVKQLRNNAKEI GNGCFEFYHKCDN ECMESVKNGTYDYPKYSEESKLNREKI DGVKLESMGVYQI LAI YSTVASSLVLLVSLGAI SFWMCSNGSL QCRI CI

>gi |148897951|gb|ABR15808.1| hemagglutinin [Influenza A virus (A/Al bany/13/1951(H1N1))]

MKARLLI LLCALSATDADTI CI GYHANNSTDTVDTVLEKNVTVTHSVNLLLED SHNGKLCRLKGI APLQLG KCNI AGWI LGNPECESLLSNRSWSYI AETPNSENGTCYPGDFADYEELREQLSSVSSFERFEI FPKERSW PKHNI TRGVTAAACSHAKKSSFYKNLLWLTEANGSYPNLSKSYVNNKEKEVLVWGVHHPNSI EDORTLYR KENAYVSVSSNYNRRFTPEI AERPKVRGOAGRMNYWTLLEPGDKI I FEANGNLI APWYAFALSRGLGS GI I TSNASMDECDTKCQTPQGA I NSSLPFQNI HPVTI GECPKYVRSTKLRMTGLRNI PSI QSRGLFGAI AGFI EGGWTGMVDGWYGYHHQNEQSGYAADQKSTQNAI NGI TNKVNSVI EKMTQFTAVGKEFNKLEKR MENLNKKVDDGFLDI WTYNAELLVLENERLDFHDSNVKNLYEKVKQLRNNAKEI GNGCFEFYHKCDN ECMESVKNGTYDYPKYSEESKLNREKI DGVKLESMGVYQI LAI YSTVASSLVLLVSLGAI SFWMCSNGSL QCRI CI

>gi |134047484|gb|AB052280.1| hemagglutinin [Influenza A virus (A/Mal aya/302/1954(H1N1))]

MKARLLI LLCALSATDADTI CI GYHANNSTDTVDTVLEKNVTVTHSVNLLLED SHNGKLCRLKGI APLQLG KCNI AGWI LGNPECESLLSNRSWSYI AETPNSENGTCYPGDFADYEELREQLSSVSSFERFEI FPKERSW PKHNI TRGVTAAACSHAKKSSFYKNLLWLTEANGSYPNLSKSYVNDREKEVLVWGVHHPNSI EDORTLYR KENAYVSVSSNYNRRFTPEI AERPKVRGQPRMNYWTLLEPGDKI I FEANGNLI APWYAFALSRGPGS GI I TSNASMDECDTKCQTPQGA I NSSLPFQNI HPVTI GECPKYVRSTKLRMTGLRNI PSI QSRGLFGAI AGFI EGGWTGMVDGWYGYHHQNEQSGYAADQKSTQNAI NGI TNKVNSVI EKMTQFTAVGKEFNKLEKR MENLNKKVDDGFLDI WTYNAELLVLENERLDFHDSNVKNLYEKVKQLRNNAKEI GNGCFEFYHKCDN ECMESVKNGTYDYPKYSEESKLNRAKI DGVKLESMGVYQI LAI YSTVASSLVLLVSLGAI SFWMCSNGSL QCRI CI

>gi |89112489|gb|ABD60966.1| hemagglutinin [Influenza A virus (A/Mal aya/54(H1N1))]

MKARLLI LLCALSATDADTI CI GYHANNSTDTVDTVLEKNVTVTHSVNLLLED SHNGKLCRLKGI APLQLG KCNI AGWI LGNPECESLLSNRSWSYI AETPNSENGTCYPGDFADYEELREQLSSVSSFERFEI FPKERSW PKHNI TRGVTAAACSHAKKSSFYKNLLWLTEANGSYPNLSKSYVNDREKEVLVWGVHHPNSI EDORTLYR KENAYVSVSSNYNRRFTPEI AERPKVRGQPRMNYWTLLEPGDKI I FEANGNLI APWYAFALSRGPGS GI I TSNASMDECDTKCQTPQGA I NSSLPFQNI HPVTI GECPKYVRSTKLRMTGLRNI PSI QSRGLFGAI AGFI EGGWTGMVDGWYGYHHQNEQSGYAADQKSTQNAI NGI TNKVNSVI EKMTQFTAVGKEFNKLEKR MENLNKKVDDGFLDI WTYNAELLVLENERLDFHDSNVKNLYEKVKQLRNNAKEI GNGCFEFYHKCDN ECMESVKNGTYDYPKYSEESKLNRAKI DGVKLESMGVYQI LAI YSTVASSLVLLVSLGAI SFWMCSNGSL QCRI CI

>gi |324122|gb|AAA43171.1| hemagglutinin [Influenza A virus (A/Leni ngrad/1954/1(H1N1))]

MKARLLI LLCALSATDADTI CI GYHANNSTDTVDTVLEKNVTVTHSVNLLLED SHNGKLCRLKGI APLQLG KCNI AGWI LGNPECESLLSNRSWSYI AETPNSENGTCYPGDFADYEELREQLSSVSSFERFEI FPKERSW PKHNI TRGVTAAACSHAKKSSFYKNLLWLTEANGSYPNLSKSYVNDREKEVLVWGVHHPNSI EDOKTI YR KENAYVSVSSNYNRRFTPEI AERPKVRGQAGRI NYWTLLEPGDTI I FEANGNLI APWYAFALNRGFGS GI I TSNASMDECDTKCQTPQGA I NSSLPFQNI HPVTI GECPKYVRSTKLRMTGLRNI PSI QSRGLFGAI AGFI EGGWTGMVDGWYGYHHQNEQSGYAADQKSTQNAI NGI TNKVNSVI EKMTQFTAVGKEFNKLEKR MENLNKKVDDGFLDI WTYNAELLVLENERLDFHDSNVKNLYEKVKQLRNNAKEI GNGCFEFYHKCDN ECMESVKNGTYDYPKYSEESKLNREKI DGVKLESMGVYQI LAI YSTVASSLVLLVSLGAI SFWMCSNGSL QCRI CI

>gi |189303366|gb|ACD85758.1| hemagglutinin [Influenza A virus (A/Memphis/07/2008(H1N1))]

MKARLLI LLCALSATDADTI CI GYHANNSTDTVDTVLEKNVTVTHSVNLLLED SHNGKLCRLKGI APLQLG

NCSVAGWI LGNPECELLI SKESWSYI VEKPNPENGTCYPGHFADYEELREQLSSVSSFERFEI FPKESSW
 PXHTVTGVSASCSHNGESSFYRNLLWLTGKNGLYPNLSKSYANNKEKEVLVWVGHPPNI GDQKALYHT
 ENAYVSVSSHYSRKFPEI AKRPKVRDQEGRI NYYWTLLEPGDTI I FEANGNLI APRYAFALSRGFGSG
 I I NSNAPMDKCDKACQTPQGA I NSSLPFQNVHPVTI GECPKYVRSAKLRMVTGLRNI PSI QSRGLFGAI A
 GF I EGGWTGMVDGWYGYHHQNEQSGYAADQKSTQNAI NGI TNKVNSVI EKMNTQFTAVGKEFNKLERM
 ENLNKKVDDGFI DI WTYNAELLVLENERLDFHDSNVKNLYEKVKSQKNNAKEI GNGCFEFYHKCNDE
 CMESVKNGTIDYDPKYSEESKLNREKI DGVKLESMGVYQI LAI YSTVASSLVLLVSLGAI SFWMCSNGSLO
 CRI CI

>gi |170786954|gb|ACB11800.2| hemagglutinin [Influenza A virus (A/New
 Jersey/04/2008(H1N1))]

MKVKLLVLLCTFTATYADTI CI GYHANNSTDTVDTVLEKNVTVTHSVNLLNSHNGKLCLLKGI APLQLG
 NCSVAGWI LGNPECELLI SKESWSYI VEKPNPENGTCYPGHFADYEELREQLSSVSSFERFEI FPKESSW
 PXHTVTGVSASCSHNGESSFYRNLLWLTGKNGLYPNLSKSYANNKEKEVLVWVGHPPNI GDQKALYHT
 ENAYVSVSSHYSRKFPEI AKRPKVRDQEGRI NYYWTLLEPGDTI I FEANGNLI APRYAFALSRGFGSG
 I I NSNAPMDKCDKACQTPQGA I NSSLPFQNVHPVTI GECPKYVRSAKLRMVTGLRNI PSI QSRGLFGAI A
 GF I EGGWTGMVDGWYGYHHQNEQSGYAADQKSTQNAI NGI TNKVNSVI EKMNTQFTAVGKEFNKLERM
 ENLNKKVDDGFI DI WTYNAELLVLENERLDFHDSNVKNLYEKVKSQKNNAKEI GNGCFEFYHKCNDE
 CMESVKNGTIDYDPKYSEESKLNREKI DGVKLESMGVYQI LAI YSTVASSLVLLVSLGAI SFWMCSNGSLO
 CRI CI

>gi |188076427|gb|ACD47240.1| hemagglutinin [Influenza A virus
 (A/Alaska/03/2008(H1N1))]

MKVKLLVLLCTFTATYADTI CI GYHANNSTDTVDTVLEKNVTVTHSVNLLNSHNGKLCLLKGI APLQLG
 NCSVAGWI LGNPECELLI SKESWSYI VEKPNPENGTCYPGHFADYEELREQLSSVSSFERFEI FPKESSW
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 ENAYVSVSSHYSRKFPEI AKRPKVRDQEGRI NYYWTLLEPRDTI I FEANGNLI APRYAFALSRGFGSG
 I I NSNAPMDKCDKACQTPQGA I NSSLPFQNVHPVTI GECPKYVRSAKLRMVTGLRNI PSI QSRGLXGAI A
 GF I EGGWTGMVDGWYGYHHQNEQSGYAADQKSTQNAI NGI TNKVNSVI EKMNTQFTAVGKEFNKLERM
 ENLNKKVDDGFI DI WTYNAELLVLENERLDFHDSNVKNLYEKVKSQKNNAKEI GNGCFEFYHKCNDE
 CMESVKNGTIDYDPKYSEESKLNREKI DGVKLESMGVYQI LAI YSTVASSLVLLVSLGAI SFWMCSNGSLO
 CRI CI

>gi |189303398|gb|ACD85774.1| hemagglutinin [Influenza A virus
 (A/Nebraska/01/2008(H1N1))]

MKVKLLVLLCTFAATYADTI CI GYHANNSTDTVDTVLEKNVTVTHSVNLLNSHNGKLCLLKGI APLQLG
 NCSVAGWI LGNPECELLI SKESWSYI VEKPNPENGTCYPGHFADYEELREQLSSVSSFERFEI FPKESSW
 PNHTVTGVSASCSHNGESSFYRNLLWLTGKNGLYPNLSKSYANNKEKEVLVWVGHPPNI GDQKALYHT
 ENAYVSVSSHYSRKFPEI AKRPKVRDQEGRI NYYWTLLEPGDTI I FEANGNLI APRYAFALSRGFGSG
 I I NSNAPMDKCDKACQTPQGA I NSSLPFQNVHPVTI GECPKYVRSAKLRMVTGLRNI PSI QSRGFFGAI A
 GF I EGGWTGMVDGWYGYHHQNEQSGYAADQKSTQNAI NGI TNKVNSVI EKMNTQFTAVGKEFNKLERM
 ENLNKKVDDGFI DI WTYNAELLVLENERLDFHDSNVKNLYEKVKSQKNNAKEI GNGCFEFYHKCNDE
 CMESVKNGTIDYDPKYSEESKLNREKI DGVKLESMGVYQI LAI YSTVASSLVLLVSLGAI SFWMCSNGSLO
 CRI CI

>gi |188076425|gb|ACD47239.1| hemagglutinin [Influenza A virus (A/New
 Jersey/08/2008(H1N1))]

MKVKLLVLLCTFTATYADTI CI GYHANNSTDTVDTVLEKNVTVTHSVNLLNSHNGKLCLLKGI APLQLG
 NCSVAGWI LGNPECELLI SKESWSYI VEKPNPENGTCYPGHFADYEELREQLSSVSSFERFEI FPKESSW
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 ENAYVSVSSHYSRKFPEI AKRPKVRDQEGRI NYYWTLLEPGDTI I FEANGNLI APRYAFALSRGFGSG
 I I NSNAPMDKCDKACQTPQGA I NSSLPFQNVHPVTI GECPKYVRSAKLRMVTGLRNI PSI QSRGLFGAI A
 GF I EGGWTGMVDGWYGYHHQNEQSGYAADQKSTQNAI NGI TNKVNSVI EKMNTQFTAVGKEFNKLERM
 ENLNKKVDDGFI DI WTYNAELLVLENERLDFHDSNVKNLYEKVKSQKNNAKEI GNGCFEFYHKCNDE
 CMESVKNGTIDYDPKYSEESKLNREKI DGVKLESMGVYQI LAI YSTVASSLVLLVSLGAI SFWMCSNGSLO
 CRI CI

>gi |194294063|gb|ACF40126.1| hemagglutinin [Influenza A virus
 (A/I daho/01/2008(H1N1))]

MKVKLLVLLCTFTATYADTI CI GYHANNSTDTVDTVLEKNVTVTHSVNLLNSHNGKLCLLKGI APLQLG
 NCSVAGWI LGNPECELLI SKESWSYI VEKPNPENGTCYPGHFADYEELREQLSSVSSFERFEI FPKESSW
 PNHTVTGVSASCSHNGESSFYRNLLWLTGKNGLYPNLSKSYANNKEKEVLVWVGHPPNI GDQNTLYHT
 ENAYVSVSSHYSRKFPEI AKRPKVRDQEGRI NYYWTLLEPGDTI I FEANGNLI APRYAFALSRGFGSG
 I I NSNAPMDKCDKACQTPQGA I NSSLPFQNVHPVTI GECPKYVRSAKLRMVTGLRNI PSI QSRGLFGAI A
 GF I EGGWTGMVDGWYGYHHQNEQSGYAADQKSTQNAI NGI TNKVNSVI EKMNTQFTAVGKEFNKLERM
 ENLNKKVDDGFI DI WTYNAELLVLENERLDFHDSNVKNLYEKVKSQKNNAKEI GNGCFEFYHKCNDE
 CMESVKNGTIDYDPKYSEESKLNREKI DGVKLESMGVYQI LAI YSTVASSLVLLVSLGAI SFWMCSNGSLO
 CRI CI

>gi |188076441|gb|ACD47247.1| hemagglutinin [Influenza A virus
 (A/I daho/02/2008(H1N1))]

MKVKLLVLLCTFTATYADTI CI GYHANNSTDTVDTVLEKNVTVTHSVNLLNSHNGKLCLLKGI APLQLG
 NCSVAGWI LGNPECELLI SKESWSYI VEKPNPENGTCYPGHFADYEELREQLSSVSSFERFEI FPKESSW
 PKHTVTGVSASCSHNGESSFYRNLLWLTGKNGLYPNLSKSYANNKEKEVLVWVGHPPNI GDQKALYHT
 ENAYVSVSSHYSRKFPEI AKRPKVRDQEGRI NYYWTLLEPGDTI I FEANGNLI APRYAFALSRGFGSG
 I I NSNAPMDKCDKACQTPQGA I NSSLPFQNVHPVTI GECPKYVRSAKLRMVTGLRNI PSI QSRGLFGAI A
 GF I EGGWTGMVDGWYGYHHQNEQSGYAADQKSTQNAI NGI TNKVNSVI EKMNTQFTAVGKEFNKLERM
 ENLNKKVDDGFI DI WTYNAELLVLENERLDFHDSNVKNLYEKVKSQKNNAKEI GNGCFEFYHKCNDE
 CMESVKNGTIDYDPKYSEESKLNREKI DGVKLESMGVYQI LAI YSTVASSLVLLVSLGAI SFWMCSNGSLO
 CRI CI

>gi |170181783|gb|ACB11806.1| hemagglutinin [Influenza A virus (A/New
 Jersey/05/2008(H1N1))]

MKVKLLVLLCTFTATYADTI CI GYHANNSTDTVDTVLEKNVTVTHSVNLLNSHNGKLCLLKGI APLQLG

NCSVAGWI LGNPECELLI SKESWSYI VEKPNPENGTCYPGHFADYEELREQLSSVSSFERFEI FPKESSW
 PNHTVTGVSASCSHNGESSFYRNLLWLTXKNGLYPNLSKSYANNKEKEVLVWVGHPPNI GDQKTYHT
 ENAYVSVSSHYSRKFPEI AKRPKVRDQEGRI NYYWTLLEPGDTI I FEANGNLI APRYAFALSRGFGSG
 I I NSNAPMDKCDAKCQTPQGA I NSSLPFQNVHPVTI GECPKYVRSAKLRMTGLRNI PSI QSRGLFGAI A
 GFI EGGWTGMVDGWYGYHHQNEQSGYAADQKSTQNAI NGI TNKVNSVI EKMNTQFTAVGKEFNKLERM
 ENLNKKVDDGFI DI WTYNAELLVLENERLDFHDSNVKNLYEKVKSQKNNAKEI GNGCFEFYHKCNDE
 CMESVKNGTYDYPKYSEESKLNREKI DGVKLESMEVYQI LAI YSTVASSLVLLVSLGAI SFWMCSNGSLO
 CRI CI

>gi |193084897|gb|ACF10338.1| hemagglutinin [Influenza A virus
 (A/Mi ssi ssi ppi /06/2008(H1N1))]

MKVKLLVLLCTFAATYADTI CI GYHANNSTDTVDTVLEKNVTVTHSVNLLNSHNGKLCLLKGI APLQLG
 NCSVAGWI LGNPECELLI SKESWSYI VEKPNPENGTCYPGHFADYEELREQLSSVSSFERFEI FPKESSW
 PNHTVTGVSASCSHNGESSFYRNLLWLTGKNGLYPNLSKSYANNKEKEVLVWVGHPPNI GGQKALYHT
 ENAYVSVSSHYSRKFPEI AKRPKVRDQEGRI NYYWTLLEPGDTI I FEANGNLI APRYAFALSRGFGSG
 I I NSNAPMDKCDAKCQTPQGA I NSSLPFQNVHPVTI GECPKYVRSAKLRMTGLRNI PSI QSRGLFGAI A
 GFI EGGWTGMVDGWYGYHHQNEQSGYAADQKSTQNAI NGI TNKVNSVI EKMNTQFTAVGKEFNKLERM
 ENLNKKVDDGFI DI WTYNAELLVLENERLDFHDSNVKNLYEKVKSQKNNAKEI GNGCFEFYHKCNDE
 CMESVKNGTYDYPKYSEESKLNREKI DGVKLESMEVYQI LAI YSTVASSLVLLVSLGAI SFWMCSNGSLO
 CRI CI

>gi |189303374|gb|ACD85762.1| hemagglutinin [Influenza A virus
 (A/Mi ssi ssi ppi /06/2008(H1N1))]

MKVKLLVLLCTFAATYADTI CI GYHANNSTDTVDTVLEKNVTVTHSVNLLNSHNGKLCLLKGI APLQLG
 NCSVAGWI LGNPECELLI SKESWSYI VEKPNPENGTCYPGHFADYEELRQLSSVSSFERFEI FPKESSW
 PNHTVTGVSASCSHNGESSFYRNLLWLTGKNGLYPNLSKSYANNKEKEVLVWVGHPPNI GBQKALYHT
 ENAYVSVSSHYSRKFPEI AKRPKVRDQEGRI NYYWTLLEPGDTI I FEANGNLI APRYAFALSRGFGSG
 I I NSNAPMDKCDAKCQTPQGA I NSSLPFQNVHPVTI GECPKYVRSAKLRMTGLRNI PSI QSRGLFGAI A
 GFI EGGWTGMVDGWYGYHHQNEQSGYAADQKSTQNAI NGI TNKVNSVI EKMNTQFTAVGKEFNKLERM
 ENLNKKVDDGFI DI WTYNAELLVLENERLDFHDSNVKNLYEKVKSQKNNAKEI GNGCFEFYHKCNDE
 CMESVKNGTYDYPKYSEESKLNREKI DGVKLESMEVYQI LAI YSTVASSLVLLVSLGAI SFWMCSNGSLO
 CRI CI

>gi |188076459|gb|ACD47256.1| hemagglutinin [Influenza A virus (A/New
 Jersey/09/2008(H1N1))]

MKVKLLVLLCTFAATYADTI CI GYHANNSTDTVDTVLEKNVTVTHSVNLLNSHNGKLCLLKGI APLQLG
 NCSVAGWI LGNPECELLI SKESWSYI VEKPNPENGTCYPGHFADYEELREQLSSVSSFERFEI FPKESSW
 PNHTVTGVSASCSHNGESSFYRNLLWLTGKNGLYPNLSKSYANNKEKEVLVWVGHPPNI GDQKALYHT
 ENAYVSVSSHYSRKFPEI AKRPKVRDQEGRI NYYWTLLEPGDTI I FEANGNLI APRYAFALSRGFGSG
 I I NSNAPMDKCDAKCQTPQGA I NSSLPFQNVHPVTI GECPKYVRSAKLRMTGLRNI PSI QSRGLFGAI A
 GFI EGGWTGMVDGWYGYHHQNEQSGYAADQKSTQNAI NGI TNKVNSVI EKMNTQFTAVGKEFNKLERM
 ENLNKKVDDGFI DI WTYNAELLVLENERLDFHDSNVKNLYEKVKSQKNNAKEI GNGCFEFYHKCNDE
 CMESVKNGTYDYPKYSEESKLNREKI DGVKLESMEVYQI LAI YSTVASSLVLLVSLGAI SFWMCSNGSLO
 CRI CI

>gi |189303372|gb|ACD85761.1| hemagglutinin [Influenza A virus
 (A/Hawai i /06/2008(H1N1))]

MKVKLLVLLCTFAATYADTI CI GYHANNSTDTVDTVLEKNVTVTHSVNLLNSHNGKLCLLKGI APLQLG
 NCSVAGWI LGNPECELLI SKESWSYI VEKPNPENGTCYPGHFADYEELREQLSSVSSFERFEI FPKESSW
 PNHTVTGVSASCSHNGESSFYRNLLWLTGKNGLYPNLSKSYANNKEKEVLVWVGHPPNI GNQKALYHT
 ENAYVSVSSHYSRKFPEI AKRPKVRDQEGRI NYYWTLLEPGDTI I FEANGNLI APRYAFALSRGFGSG
 I I NSNAPMDKCDAKCQTPQGA I NSSLPFQNVHPVTI GECPKYVRSAKLRMTGLRNI PSI QSRGLFGAI A
 GFI EGGWTGMVDGWYGYHHQNEQSGYAADQKSTQNAI NGI TNKVNSVI EKMNTQFTAVGKEFNKLERM
 ENLNKKVDDGFI DI WTYNAELLVLENERLDFHDSNVKNLYEKVKSQKNNAKEI GNGCFEFYHKCNDE
 CMESVKNGTYDYPKYSEESKLNREKI DGVKLESMEVYQI LAI YSTVASSLVLLVSLGAI SFWMCSNGSLO
 CRI CI

>gi |188076435|gb|ACD47244.1| hemagglutinin [Influenza A virus (A/New
 York/01/2008(H1N1))]

MKVKLLVLLCTFAATYADTI CI GYHANNSTDTVDTVLEKNVTVTHSVNLLNSHNGKLCLLKGI APLQLG
 NCSVAGWI LGNPECELLI SKESWSYI VEKPNPENGTCYPGHFADYEELREQLSSVSSFERFEI FPKESSW
 PNHTVTGVSASCSHNGESSFYRNLLWLTGKNGLYPNLSKSYANNKEKEVLVWVGHPPNI GBQKALYHT
 ENAYVSVSSHYSRKFPEI AKRPKVRDQEGRI NYYWTLLEPGDTI I FEANGNLI APRYAFALSRGFGSG
 I I NSNAPMDKCDAKCQTPQGA I NSSLPFQNVHPVTI GECPKYVRSAKLRMTGLRNI PSI QSRGLFGAI A
 GFI EGGWTGMVDGWYGYHHQNEQSGYAADQKSTQNAI NGI TNKVNSVI EKMNTQFTAVGKEFNKLERM
 ENLNKKVDDGFI DI WTYNAELLVLENERLDFHDSNVKNLYEKVKSQKNNAKEI GNGCFEFYHKCNDE
 CMESVKNGTYDYPKYSEESKLNREKI DGVKLESMEVYQI LAI YSTVASSLVLLVSLGAI SFWMCSNGSLO
 CRI CI

>gi |194294061|gb|ACF40125.1| hemagglutinin [Influenza A virus
 (A/Wi sconi n/01/2008(H1N1))]

MKVKLLVLLCTFAATYADTI CI GYHANNSTDTVDTVLEKNVTVTHSVNLLNSHNGKLCLLKGI APLQLG
 NCSVAGWI LGNPECELLI SKESWSYI VEKPNPENGTCYPGHFADYEELREQLSSVSSFERFEI FPKESSW
 PNHTVTGVSASCSHNGESSFYRNLLWLTGKNGLYPNLSKSYANNKEKEVLVWVGHPPDI GDQKTYHT
 ENAYVSVSSHYSRKFPEI AKRPKVRDQEGRI NYYWTLLEPGDTI I FEANGNLI APRYAFALSRGFGSG
 I I NSNAPMDKCDAKCQTPQGA I NSSLPFQNVHPVTI GECPKYVRSAKLRMTGLRNI PSI QSRGLFGAI A
 GFI EGGWTGMVDGWYGYHHQNEQSGYAADQKSTQNAI NGI TNKVNSVI EKMNTQFTAVGKEFNKLERM
 ENLNKKVDDGFI DI WTYNAELLVLENERLDFHDSNVKNLYEKVKSQKNNAKEI GNGCFEFYHKCNDE
 CMESVKNGTYDYPKYSEESKLNREKI DGVKLESMEVYQI LAI YSTVASSLVLLVSLGAI SFWMCSNGSLO
 CRI CI

>gi |170181707|gb|ACB11768.1| hemagglutinin [Influenza A virus
 (A/I ndi ana/01/2008(H1N1))]

MKVKLLVLLCTFAATYADTI CI GYHANNSTDTVDTVLEKNVTVTHSVNLLNSHNGKLCLLKGI APLQLG

NCSVAGWI LGNPECELLI SKESWSYI VEKPNPENGTCYPGHFADYEELREQLSSVSSFERFEI FPKESSW
 PNHTVTGVSASCSHNGESSFYRNLLWLTGKNGLYPNLSKSYANNKEKEVLVWVGHHPNI GDQKALYHT
 ENAYVSVSSHYSRKFPEI AKRPKVRDQEGRI NYHWTLLEPGDTI I FEANGNLI APRYAFALSRGFGSG
 I I NSNAPMDKCDKACQTPQGA I NSSLPFQNVHPVTI GECPKYVRSAKLRMVTGLRNI PSI QSRGLFGAI A
 GF I EGGWTGMVDGWYGYHHQNEQSGYAADQKSTQNAI NGI TNKVNSVI EKMNTQFTAVGKEFNKLERRM
 ENLNKKVDDGFI DI WTYNAELLVLENERLDFHDSNVKNLYEKVKSQKNNAKEI GNGCFEFYHKCNDE
 CMESVKNGTIDYDPKYSEESKLNREKI DGVKLESMGVYQI LAI YSTVASSLVLLVSLGAI SFWMCSNGSLO
 CRI CI

>gi |189303370|gb|ACD85760.1| hemagglutinin [Influenza A virus
 (A/Hawai i /05/2008(H1N1))]

MKVKLLVLLCTFTATYADTI CI GYHANNSTDTVDTVLEKNVTVTHSVNLLLEDNHNGKLCLLKGI APLQLG
 NCSVAGWV LGNPECELLI SKESWSYI VEKPNPENGTCYPGHFADYEELREQLSSVSSFERFEI FPKESSW
 PNHTVTGVSASCSHNGESSFYRNLLWLTGKNGLYPNLSKSYANNKKEVLVWVGHHPNI GBQMTLYHK
 ENAYVSVSSHYSRKFPEI AKRPKVRDQEGRI NYHWTLLEPGDTI I FEANGNLI APRYAFALSRGFGSG
 I I NSNAPMDKCDKACQTPQGA I NSSLPFQNVHPVTI GECPKYVRSAKLRMVTGLRNI PSI QSRGLFGAI A
 GF I EGGWTGMVDGWYGYHHQNEQSGYAADQKSTQNAI NGI TNKVNSVI EKMNTQFTAVGKEFNKLERRM
 ENLNKKVDDGFI DI WTYNAELLVLENERLDFHDSNVKNLYEKVKSQKNNAKEI GNGCFEFYHKCNDE
 CMESVKNGTIDYDPKYSEESKLSREKI DGVKLESMGVYQI LAI YSTVASSLVLLVSLGAI SFWMCSNGSLO
 CRI CI

>gi |189303360|gb|ACD85755.1| hemagglutinin [Influenza A virus (A/New
 York/03/2008(H1N1))]

MKVKLLVLLCTFTATYADTI CI GYHANNSTDTVDTVLEKNVTVTHSVNLLLENSHNGKLCLLKGLAPLQLG
 NCSVAGWI LGNPECELLI SKESWSYI VEKPNPENGTCYPGHFADYEELREQLSSVSSFERFEI FPKESSW
 PNHTVTGVSASCSHNGESSFYRNLLWLTGKNGLYPNLSKSYANNKEKEVLVWVGHHPNI GBQKALYHT
 ENAYVSVSSHYSRKFPEI AKRPKVRDQEGRI NYHWTLLEPGDTI I FEANGNLI APRYAFALSRGFGSG
 I I NSNAPMDKCDKACQTPQGA I NSSLPFQNVHPVTI GECPKYVRSAKLRMVTGLRNI PSI QSRGLFGAI A
 GF I EGGWTGMVDGWYGYHHQNEQSGYAADQKSTQNAI NGI TNKVNSVI EKMNTQFTAVGKEFNKLERRM
 ENLNKKVDDGFI DI WTYNAELLVLENERLDFHDSNVKNLYEKVKSQKNNAKEI GNGCFEFYHKCNDE
 CMESVKNGTIDYDPKYSEESKLNREKI DGVKLESMGVYQI LAI YSTVASSLVLLVSLGAI SFWMCSNGSLO
 CRI CI

>gi |170181715|gb|ACB11772.1| hemagglutinin [Influenza A virus (A/New
 Jersey/06/2008(H1N1))]

MKVKLLVLLCTFTATYADTI CI GYHANNSTDTVDTVLEKNVTVTHSVNLLLENSHNGKLCLLKGI APLQLG
 NCSVAGWI LGNPECELLI SKESWSYI VEKPNPENGTCYPGHFADYEELREQLSSVSSFERFEI FPKESSW
 PNHTVTGVSASCSHNGESSFYRNLLWLTGKNGLYPNLSKSYANNKEKEVLVWVGHHPNI GDQKTYHT
 ENAYVSVSSHYSRKFPEI AKRPKVRDQEGRI NYHWTLLEPGDTI I FEANGNLI APRYAFALSRGFGSG
 I I NSNAPMDKCDKACQTPQGA I NSSLPFQNVHPVTI GECPKYVRSAKLRMVTGLRNI PSI QSRGLFGAI A
 GF I EGGWTGMVDGWYGYHHQNEQSGYAADQKSTQNAI NGI TNKVNSVI EKMNTQFTAVGKEFNKLERRM
 ENLNKKVDDGFI DI WTYNAELLVLENERLDFHDSNVKNLYEKVKSQKNNAKEI GNGCFEFYHKCNDE
 CMESVKNGTIDYDPKYSEESKLNREKI DGVKLESMGVYQI LAI YSTVASSLVLLVSLGAI SFWMCSNGSLO
 CRI CI

>gi |193084905|gb|ACF10342.1| hemagglutinin [Influenza A virus (A/New
 York/05/2008(H1N1))]

MKVKLLVLLCTFTATYADTI CI GYHANNSTDTVDTVLEKNVTVTHSVNLLLENSHNGKLCLLKGI APLQLG
 NCSVAGWI LGNPECELLI SKESWSYI VEKPNPENGTCYPGHFADYEELREQLSSVSSFERFEI FPKESSW
 PNHTVTGVSASCSHNGESSFYRNLLWLTGKNGLYPNLSKSYANNKEKEVLVWVGHHPNI GDQKALYHT
 ENAYVSVSSHYSRKFPEI AKRPKVRDQEGRI NYHWTLLEPGDTI I FEANGNLI APRYAFALSRGFGSG
 I I NSNAPMDKCDKACQTPQGA I NSSLPFQNVHPVTI GECPKYVRSAKLRMVTGLRNI PSI QSRGLFGAI A
 GF I EGGWTGMVDGWYGYHHQNEQSGYAADQKSTQNAI NGI TNKVNSVI EKMNTQFTAVGKEFNKLERRM
 ENLNKKVDDGFI DI WTYNAELLVLENERLDFHDSNVKNLYEKVKSQKNNAKEI GNGCFEFYHKCNDE
 CMESVKNGTIDYDPKYSEESKLNREKI DGVKLESMGVYQI LAI YSTVASSLVLLVSLGAI SFWMCSNGSLO
 CRI CI

>gi |189303384|gb|ACD85767.1| hemagglutinin [Influenza A virus (A/North
 Carol i na/02/2008(H1N1))]

MKVKLLVLLCTFTATYADTI CI GYHANNSTDTVDTVLEKNVTVTHSVNLLLENSHNGKLCLLKGI APLQLG
 NCSVAGWI LGNPECELLI SKESWSYI VEKPNPENGTCYPGHFADYEELREQLSSVSSFERFEI FPKESSW
 PNHTVTGVSASCSHNGESSFYRNLLWLTGKNGLYPNLSKSYANNKEKEVLVWVGHHPNI VBQKTYHT
 ENAYVSVSSHYSRKFPEI AKRPKVRDQEGRI NYHWTLLEPGDTI I FEANGNLI APRYAFALSRGFGSG
 I I NSNAPMDKCDKACQTPQGA I NSSLPFQNVHPVTI GECPKYVRSAKLRMVTGLRNI PSI QSRGLFGAI A
 GF I EGGWTGMVDGWYGYHHQNEQSGYAADQKSTQNAI NGI TNKVNSVI EKMNTQFTAVGKEFNKLERRM
 ENLNKKVDDGFI DI WTYNAELLVLENERLDFHDSNVKNLYEKVKSQKNNAKEI GNGCFEFYHKCNDE
 CMESVKNGTIDYDPKYSEESKLNREKI DGVKLESMGVYQI LAI YSTVASSLVLLVSLGAI SFWMCSNGSLO
 CRI CI

>gi |112789450|gb|ABI 21541.1| hemagglutinin [Influenza A virus
 (A/Nanchang/16/1996(H1N1))]

MKAKLLVLLCTFTATYADTI CI GYHANNSTDTVDTVLEKNVTVTHSVNLLLEDHNGKLCLLKGI APLQLG
 NCSVAGWI LGNPECESLI SKESWSYI VETPNPENGTCYPGFADYEELREQLSSVSSFERFEI FPKESSW
 PNHTVTGVSASCSHNGKSSFYRNLLWLTGKNGLYPNLSKSYANNKEKEVLVWVGHHPNI GVQRAI YHT
 ENAYVSVSSHYSRKFPEI AKRPKVRDQEGRI NYHWTLLEPGDTI I FEANGNLI APRYAFALSRGFGSG
 I I TSNAPMNECDKACQTPQGA I NSSLPFQNVHPVTI GECPKYVRSAKLRMVTGLRNI PSI QSRGLFGAI A
 GF I EGGWTGMI DGWYGYHHQNEQSGYAADQKSTQNAI NGI TNKVNSVI EKMNTQFTAVGKEFNKLERRM
 ENLNKKVDDGFI DI WTYNAELLVLENERLDFHDSNVKNLYEKVKSQKNNAKEI GNGCFEFYHKCNDE
 CMESVKNGTIDYDPKYSEESKLNREKI DGVKLESMGVYQI LAI YSTVASSLVLLVSLGAI SFWMCSNGSLO
 CRI CI

>gi |112789469|gb|ABI 21552.1| hemagglutinin [Influenza A virus
 (A/Nanchang/17/1996(H1N1))]

MKAKLLVLLCTFTATYADTI CI GYHANNSTDTVDTVLEKNVTVTHSVNLLLEDHNGKLCLLKGI APLQLG

NCSVAGWI LGNPECESLI SKESWSYI VETPNPENGTCYPGYFADYEELREQLSSVSSFERFEI FPKESSW
 PNHTVTGVSASC SHNGKSSFYRNLLWLTEKNGLYPNLSKSYVNNKEKEVLVWGVHHPNSI GQORAI YHT
 ENAYVSVVSSHYSRRFTPEI AKRPKVRDQEGRI NYYWTLLEPGDTI I FEANGNLI APWYAFALSRGFGS
 I I TSNA PMDECDACKQTPQGA I NSSLPFQNVHPVTI GECPKYVRS AKLRMVTGLRNI PSI QSRGLFGAI A
 GFI EGGWTGMI DGWYGYHHQNEQSGYAADQKSTQNAI NGI TNKVNSVI EKMTQFTAVGKEFNKLERM
 ENLNKKVDDGFLDI WTYNAELLVLENERLDFHDSNVKNLYEKVKSQLKNNAKEI GNGCFEFYHKCNNE
 CMESVKNGTYPKYSEESKLNREKI DGVKLESMGVYQI LAI YSTVASSLVLLVSLGAI SFWMCSNGSLQ
 CRI CI
 >gi |134047389|gb|AB052225.1| hemagglutinin [Influenza A virus
 (A/Memphis/15/1996(H1N1))]
 MKAKLLVLLCAFTATYADTI CI GYHANNSTDTVDTVLEKNVTVTHSVNLLLED SHNGKLCRLKGTAPLQLG
 NCSVAGWI LGNPECESLFSKESWSYI AETPNPENGTCYPGYFADYEELREQLSSVSSFERFEI FPKESSW
 PNHTVTGVTASC SHNGKSSFYKNLLWLTEKNGLYPNLSKSYVNNKEKEVLVWGVHHPNSI GQORAI YH
 TENAYVSVVSSHYSRRFTPEI AKRPKVRDQEGRI NYYWTLLEPGDTI I FEANGNLI APWYAFALSRGFGS
 GI I TSNA SMGECDAKQTPQGA I NSSLPFQNVHPVTI GECPKYVRS TKLRMVTGLRNI PSI QSRGLFGAI
 AGFI EGGWTGMI DGWYGYHHQNEQSGYAADKSTQNAI DGI TNKVNSVI EKMTQFTAVGKEFNKLERR
 MENLNKKVDDGFLDI WTYNAELLVLENERLDFHDSNVKNLYEKVKSQLKNNAKEI GNGCFEFYHKCND
 ECMESVKNGTYPKYSEESKLNREKI DGVKLESMGVYQI LAI YSTVASSLVLLVSLGAI SFWMCSNGSL
 QCRI CI
 >gi |120434212|gb|ABM22290.1| hemagglutinin [Influenza A virus
 (A/Memphis/7/1996(H1N1))]
 MKAKLLVLLCAFTATYADTI CI GYHANNSTDTVDTVLEKNVTVTHSVNLLLED SHNGKLCRLKGTAPLQLG
 NCSVAGWI LGNPECESLFSKESWSYI AETPNPENGTCYPGYFADYEELREQLSSVSSFERFEI FPKESSW
 PNHTVTGVTASC SHNGKSSFYKNLLWLTEKNGLYPNLSKSYVNNKEKEVLVWGVHHPNSI GQORAI YH
 TENAYVSVVSSHYSRRFTPEI AKRPKVRDQEGRI NYYWTLLEPGDTI I FEANGNLI APWYAFALSRGFGS
 GI I TSNA SMGECDAKQTPQGA I NSSLPFQNVHPVTI GECPKYVRS TKLRMVTGLRNI PSI QSRGLFGAI
 AGFI EGGWTGMI DGWYGYHHQNEQSGYAADKSTQNAI DGI TNKVNSVI EKMTQFTAVGKEFNKLERR
 MENLNKKVDDGFLDI WTYNAELLVLENERLDFHDSNVKNLYEKVKSQLKNNAKEI GNGCFEFYHKCN
 ECMESVKNGTYPKYSEESKLNREKI DGVKLESMGVYQI LAI YSTVASSLVLLVSLGAI SFWMCSNGSL
 QCRI CI
 >gi |94959685|gb|ABF47649.1| hemagglutinin [Influenza A virus (A/New
 York/653/1996(H1N1))]
 MKAKLLVLLCAFTATYADTI CI GYHANNSTDTVDTVLEKNVTVTHSVNLLLED SHNGKLCRLKGTAPLQLG
 NCSVAGWI LGNPECESLFSKESWSYI AETPNPENGTCYPGYFADYEELREQLSSVSSFERFEI FPKESSW
 PNHTVTGVTASC SHNGKSSFYKNLLWLTEKNGLYPNLSKSYVNNKEKEVLVWGVHHPNSI GQORAI YH
 TENAYVSVVSSHYSRRFTPEI AKRPKVRDQEGRI NYYWTLLEPGDTI I FEANGNLI APWYAFALSRGFGS
 GI I TSNA SMGECDAKQTPQGA I NSSLPFQNVHPVTI GECPKYVRS TKLRMVTGLRNI PSI QSRGLFGAI
 AGFI EGGWTGMI DGWYGYHHQNEQSGYAADKSTQNAI DGI TNKVNSVI EKMTQFTAVGKEFNKLERR
 MENLNKKVDDGFLDI WTYNAELLVLENERLDFHDSNVKNLYEKVKSQLKNNAKEI GNGCFEFYHKCN
 ECMESVKNGTYPKYSEESKLNREKI DGVKLESMGVYQI LAI YSTVASSLVLLVSLGAI SFWMCSNGSL
 QCRI CI
 >gi |94959704|gb|ABF47660.1| hemagglutinin [Influenza A virus (A/New
 York/640/1996(H1N1))]
 MKAKLLVLLCAFTATYADTI CI GYHANNSTDTVDTVLEKNVTVTHSVNLLLED SHNGKLCRLKGTAPLQLG
 NCSVAGWI LGNPECESLFSKESWSYI AETPNPENGTCYPGYFADYEELREQLSSVSSFERFEI FPKESSW
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 GI I TSNA SMGECDAKQTPQGA I NSSLPFQNVHPVTI GECPKYVRS TKLRMVTGLRNI PSI QSRGLFGAI
 AGFI EGGWTGMI DGWYGYHHQNEQSGYAADKSTQNAI DGI TNKVNSVI EKMTQFTAVGKEFNKLERR
 MENLNKKVDDGFLDI WTYNAELLVLENERLDFHDSNVKNLYEKVKSQLKNNAKEI GNGCFEFYHKCN
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 QCRI CI
 >gi |112787584|gb|ABI20848.1| hemagglutinin [Influenza A virus (A/New
 York/646/1996(H1N1))]
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 TENAYVSVVSSHYSRRFTPEI AKRPKVRDQEGRI NYYWTLLEPGDTI I FEANGNLI APWYAFALSRGFGS
 GI I TSNA SMGECDAKQTPQGA I NSSLPFQNVHPVTI GECPKYVRS TKLRMVTGLRNI PSI QSRGLFGAI
 AGFI EGGWTGMI DGWYGYHHQNEQSGYAADKSTQNAI DGI TNKVNSVI EKMTQFTAVGKEFNKLERR
 MENLNKKVDDGFLDI WTYNAELLVLENERLDFHDSNVKNLYEKVKSQLKNNAKEI GNGCFEFYHKCN
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 QCRI CI
 >gi |109914458|gb|ABG47829.1| hemagglutinin [Influenza A virus (A/New
 York/626/1996(H1N1))]
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 TENAYVSVVSSHYSRRFTPEI AKRPKVRDQEGRI NYYWTLLEPGDTI I FEANGNLI APWYAFALSRGFGS
 GI I TSNA SMGECDAKQTPQGA I NSSLPFQNVHPVTI GECPKYVRS TKLRMVTGLRNI PSI QSRGLFGAI
 AGFI EGGWTGMI DGWYGYHHQNEQSGYAADKSTQNAI DGI TNKVNSVI EKMTQFTAVGKEFNKLERR
 MENLNKKVDDGFLDI WTYNAELLVLENERLDFHDSNVKNLYEKVKSQLKNNAKEI GNGCFEFYHKCN
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 QCRI CI
 >gi |89033079|gb|ABD59848.1| HA [Influenza A virus (A/TW/3355/97(H1N1))]
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 NCSVAGWI LGNPECELLI SKESWSYI VETPNPENGTCYPGFADYEELREQLSSVSSFERFEI FPKESSW

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>gi |14587051|gb|AAK70452.1|AF386776_1 hemagglutinin [Influenza A virus (A/Hong Kong/1035/98 (H1N1))]

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>gi |14587053|gb|AAK70453.1|AF386777_1 hemagglutinin [Influenza A virus (A/Hong Kong/1035/98 (H1N1))]

MKAKLLVLLCTFTATYADTI CI GYHANNSTDTVDTVLEKNVTVTHSVNLLDRHNGKLCLLKGI APLQLG NCSVAGWI LGNPECELLI SKESWSYI VETPNPENGTCYPGYFADYEELREQLSSVSSFERFEI FPKESSW PNHTVTGVSASCSHNGKSSFYRNLWLTCKKGLYPNLSKSYVNNKEKEVLVWGVHHPNSNI GDORAI YHT ENAYVSVSSHYSRRFTPEI AKRPKVRDQEGRI NYYWTLLEPGDTI I FEANGNLI APWYAFALSRGFGSG I I TSNAPMDECDACKQTPQGA I NSSLPFQNVHPVTI GECPKYVRSAKLRMVTGLRNI PSI QSRGLFGAI A GFI EGGWTGMI DGWYGYHHQNEQSGYAADQKSTQNAI NGI TNKVNSI I EKMNTQFTAVGKEFNKLERM ENLNKKVDDGFLDI WTYNAELLVLENERLDFHDSNVKNLYEKVKSOLKNNAKEI GNGCFEFYHKCNNE CMESVKNGTYDPKYSEESKLNREKI DGVKLESMGVYQI LAI YSTVASSLVLLVSLGAI SFWMCSNGSLQ CRI CI

>gi |14587061|gb|AAK70457.1|AF386781_1 hemagglutinin [Influenza A virus (A/Hong Kong/1134/98 (H1N1))]

MKAKLLVLLCTFTATYADTI CI GYHANNSTDTVDTVLEKNVTVTHSVNLLDSDHNGKLCLLKGI APLQLG NCSVAGWI LGNPECELLI PKESWSYI VETPNPENGTCYPGYFADYEELREQLSSVSSFERFEI FPKESSW PNHTVTGVSASCSHNGKSSFYRNLWLTCKKGLYPNLSKSYVNNKEKEVLVWGVHHPNSNI GDORAI YHT ENAYVSVSSHYSRRFTPEI VKRPKVRDQEGRI NYYWTLLEPGDTI I FEANGNLI APWYAFALSRGFGSG I I TSNAPMDECDACKQTPQGA I NSSLPFQNVHPVTI GECPKYVRSAKLRMVTGLRNI PSI QSRGLFGAI A GFI EGGWTGMI DGWYGYHHQNEQSGYAADQKSTQNAI NGI TNKVNSI I EKMNTQFTAVGKEFNKLERM ENLNKKVDDGFLDI WTYNAELLVLENERLDFHDSNVKNLYEKVKSOLKNNAKEI GNGCFEFYHKCNNE CMESVKNGTYDPKYSEESKLNREKI DGVKLESMGVYQI LAI YSTVASSLVLLVSLGAI SFWMCSNGSLQ CRI CI

>gi |14587049|gb|AAK70451.1|AF386775_1 hemagglutinin [Influenza A virus (A/Hong Kong/1131/98 (H1N1))]

MKAKLLVLLCTFTATYADTI CI GYHANNSTDTVDTVLEKNVTVTHSVNLLDSDHNGKLCLLKGI APLQLG NCSVAGWI LGNPECELLI SKESWSYI VETPNPENGTCYPGYFADYEELREQLSSVSSFERFEI FPKESSW PNHTVTGVSASCSHNGKSSFYRNLWLTCKKGLYPNLSKSYVNNKEKEVLVWGVHHPNSNI GDORAI YHT ENAYVSVSSHYSRRFTPEI AKRPKVRDQEGRI NYYWTLLEPGDTI I FEANGNLI APWYAFALSRGFGSG I I TSNAPMDECDACKQTPQGA I NSSLPFQNVHPVTI GECPKYVRSAKLRMVTGLRNI PSI QSRGLFGAI A GFI EGGWTGMI DGWYGYHHQNEQSGYAADQKSTQNAI NGI TNKVNSI I EKMNTQFTAVGKEFNKLERM ENLNKKVDDGFLDI WTYNAELLVLENERLDFHDSNVKNLYEKVKSOLKNNAKEI GNGCFEFYHKCNNE CMESVKNGTYDPKYSEESKLNREKI DGVKLESMGVYQI LAI YSTVASSLVLLVSLGAI SFWMCSNGSLQ CRI CI

>gi |14587055|gb|AAK70454.1|AF386778_1 hemagglutinin [Influenza A virus (A/Hong Kong/1035/98 (H1N1))]

MKAKLLVLLCTFTATYADTI CI GYHANNSTDTVDTVLEKNVTVTHSVNLLDRHNGKLCLLKGI APLQLG NCSVAGWI LGNPECELLI SKESWSYI VETPNPENGTCYPGYFADYEELREQLSSVSSFERFEI FPKESSW PNHTVTGVSASCSHNGKSSFYRNLWLTCKKGLYPNLSKSYVNNKEKEVLVWGVHHPNSNI GDORAI YHT ENAYVSVSSHYSRRFTPEI AKRPKVRDQEGRI NYYWTLLEPGDTI I FEANGNLI APWYAFALSRGFGSG I I TSNAPMDECDACKQTPQGA I NSSLPFQNVHPVTI GECPKYVRSAKLRMVTGLRNI PSI QSRGLFGAI A GFI EGGWTGMI DGWYGYHHQNEQSGYAADQKSTQNAI NGI TNKVNSI I EKMNTQFTAVGKEFNKLERM ENLNKKVDDGFLDI WTYNAELLVLENERLDFHDSNVKNLYEKVKSOLKNNAKEI GNGCFEFYHKCNNE CMESVKNGTYDPKYSEESKLNREKI DGVKLESMGVYQI LAI YSTVASSLVLLVSLGAI SFWMCSNGSLQ CRI CI

>gi |14587059|gb|AAK70456.1|AF386780_1 hemagglutinin [Influenza A virus (A/Hong Kong/1134/98 (H1N1))]

MKAKLLVLLCTFTATYADTI CI GYHANNSTDTVDTVLEKNVTVTHSVNLLDSDHNGKLCLLKGI APLQLG NCSVAGWI LGNPECELLI PKESWSYI VETPNPENGTCYPGYFADYEELREQLSSVSSFERFEI FPKESSW PNHTVTGVSASCSHNGKSSFYRNLWLTCKKGLYPNLSKSYVNNKEKEVLVWGVHHPNSNI GDORAI YHT ENAYVSVSSHYSRRFTPEI VKRPKVRDQEGRI NYYWTLLEPGDTI I FEANGNLI APWYAFALSRGFGSG I I TSNAPMDECDACKQTPQGA I NSSLPFQNVHPVTI GECPKYVRSAKLRMVTGLRNI PSI QSRGLFGAI A GFI EGGWTGMI DGWYGYHHQNEQSGYAADQKSTQNAI NGI TNKVNSI I EKMNTQFTAVGKEFNKLERM ENLNKKVDDGFLDI WTYNAELLVLENERLDFHDSNVKNLYEKVKSOLKNNAKEI GNGCFEFYHKCNNE CMESVKNGTYDPKYSEESKLNREKI DGVKLESMGVYQI LAI YSTVASSLVLLVSLGAI SFWMCSNGSLQ CRI CI

>gi |117571148|gb|ABK40006.1| hemagglutinin [Influenza A virus (A/New South Wales/24/1999 (H1N1))]

MKAKLLVLLCTFTATYADTI CI GYHANNSTDTVDTVLEKNVTVTHSVNLLDSDHNGKLCLLKGI APLQLG NCSVAGWI LGNPECELLI SKESWSYI VETPNPENGTCYPGYFADYEELREQLSSVSSFERFEI FPKESSW

PNHTVTGVSASCSHNGKSSFYRNLWLTGKNGLYPNLSKSYVNNKEKEVLVWGVHHPNI GDORALYHT
ENAYVSVSSHYSRRFTPEI AKRPKVRDQEGRI NYYWTLLEPGDTI I FEANGNLI APRFAFALSRRGFGSG
I I TSNAPMDECDACKQTPQGA I NSSLPFQNVHPVTI GECPKYVRSAKLRMTGLRNI PSI QSRGLFGAI A
GFI EGGWTGMVDGWYGYHHQNEOGSGYAADQKSTQNAI NGI TNKVNSVI EKMNTQFTAVGKEFNKLERM
ENLNKKVDDGFLDI WTYNAELLVLENERLDFHDSNVKNLYEKVKSOLKNNAKEI GNGCFEFYHKCNDE
CMESVKNGTYDYPKYSEESKLNREKI DGVKLESMGVYQI LAI YSTVASSLVLLVSLGAI SFWMCSNGSLQ
CRI CI

>gi |158830221|gb|ABW81514.1| hemagglutinin [Influenza A virus
(A/Denmark/116/2005(H1N1))]

MKVKLLVLLCTFTATYADTI CI SYHANNSTDTVDTVLEKNVTVTHSVNLLLED SHNGKLC LLKGI APLQLG
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PNHTVTGVSASCSHNGKSSFYRNLWLTGKNGLYPNLSKSYANNKEKEVLVWGVHHPNI GDORALYHT
ENAYVSVSSHYSRRFTPEI AKRPKVRDQEGRI NYYWTLLEPGDTI I FEANGNLI APRFAFALSRRGFGSG
I I TSNAPMDECDACKQTPQGA I NSSLPFQNVHPVTI GECPKYVRSAKLRMTGLRNI PSI QSRGLFGAI A
GFI EGGWTGMVDGWYGYHHQNEOGSGYAADQKSTQNAI NGI TNKVNSVI EKMNTQFTAVGKEFNKLERM
ENLNKKVDDGFLDI WTYNAELLVLENERLDFHDSNVKNLYEKVKSOLKNNAKEI GNGCFEFYHKCNDE
CMESVKNGTYDYPKYSEESKLNREKI DGVKLESMGVYQI LAI YSTVASSLVLLVSLGAI SFWMCSNGSLQ
CRI CI

>gi |158830231|gb|ABW81519.1| hemagglutinin [Influenza A virus
(A/Denmark/33/2005(H1N1))]

MKVKLLVLLCTFTATYADTI CI GYHANNSTDTVDTVLEKNVTVTHSVNLLLED SHNGKLC LLKGI APLQLG
NCSVAGWI LGNPECELLI SKESWSYI VETPNPENGTCYPGYFADYEELREQLSSVSSFERFEI FPKESSW
PNHTVTGVSASCSHNGKSSFYRNLWLTGKNGLYPNLSKSYANNKEKEVLVWGVHHPNI GDORALYHT
ENAYVSVSSHYSRRFTPEI AKRPKVRDQEGRI NYYWTLLEPGDTI I FEANGNLI APRFAFALSRRGFGSG
I I TSNAPMDECDACKQTPQGA I NSSLPFQNVHPVTI GECPKYVRSAKLRMTGLRNI PSI QSRGLFGAI A
GFI EGGWTGMVDGWYGYHHQNEOGSGYAADQKSTQNAI NGI TNKVNSVI EKMNTQFTAVGKEFNKLERM
ENLNKKVDDGFLDI WTYNAELLVLENERLDFHDSNVKNLYEKVKSOLKNNAKEI GNGCFEFYHKCNDE
CMESVKNGTYDYPKYSEESKLNREKI DGVKLESMGVYQI LAI YSTVASSLVLLVSLGAI SFWMCSNGSLQ
CRI CI

>gi |115607765|gb|ABJ16653.1| hemagglutinin [Influenza A virus (A/South
Australia/55/2005(H1N1))]

MKVKLLVLLCTFTATYADTI CI GYHANNSTDTVDTVLEKNVTVTHSVNLLLED SHNGKLC LLKGI APLQLG
NCSVAGWI LGNPECELLI SKESWSYI VETPNPENGTCYPGYFADYEELREQLSSVSSFERFEI FPKESSW
PNHTVTGVSASCSHNGKSSFYRNLWLTGKNGLYPNLSKSYANNKEKEVLVWGVHHPNI GBORALYHT
ENAYVSVSSHYSRRFTPEI AKRPKVRDQEGRI NYYWTLLEPGDTI I FEANGNLI APRFAFALSRRGFGSG
I I TSNAPMDECDACKQTPQGA I NSSLPFQNVHPVTI GECPKYVRSAKLRMTGLRNI PSI QSRGLFGAI A
GFI EGGWTGMVDGWYGYHHQNEOGSGYAADQKSTQNAI NGI TNKVNSVI EKMNTQFTAVGKEFNKLERM
ENLNKKVDDGFLDI WTYNAELLVLENERLDFHDSNVKNLYEKVKSOLKNNAKEI GNGCFEFYHKCNDE
CMESVKNGTYDYPKYSEESKLNREKI DGVKLESMGVYQI LAI YSTVASSLVLLVSLGAI SFWMCSNGSLQ
CRI CI

>gi |115607784|gb|ABJ16664.1| hemagglutinin [Influenza A virus (A/South
Australia/56/2005(H1N1))]

MKVKLLVLLCTFTATYADTI CI GYHANNSTDTVDTVLEKNVTVTHSVNLLLED SHNGKLC LLKGI APLQLG
NCSVAGWI LGNPECELLI SKESWSYI VETPNPENGTCYPGYFADYEELREQLSSVSSFERFEI FPKESSW
PNHTVTGVSASCSHNGKSSFYRNLWLTGKNGLYPNLSKSYANNKEKEVLVWGVHHPNI GDORALYHT
ENAYVSVSSHYSRRFTPEI AKRPKVRDQEGRI NYYWTLLEPGDTI I FEANGNLI APRFAFALSRRGFGSG
I I TSNAPMDECDACKQTPQGA I NSSLPFQNVHPVTI GECPKYVRSAKLRMTGLRNI PSI QSRGLFGAI A
GFI EGGWTGMVDGWYGYHHQNEOGSGYAADQKSTQNAI NGI TNKVNSVI EKMNTQFTAVGKEFNKLERM
ENLNKKVDDGFLDI WTYNAELLVLENERLDFHDSNVKNLYEKVKSOLKNNAKEI GNGCFEFYHKCNDE
CMESVKNGTYDYPKYSEESKLNREKI DGVKLESMGVYQI LAI YSTVASSLVLLVSLGAI SFWMCSNGSLQ
CRI CI

>gi |158830235|gb|ABW81521.1| hemagglutinin [Influenza A virus
(A/Denmark/22/2005(H1N1))]

MKVKLLVLLCTFTATYADTI CI GYHANNSTDTVDTVLEKNVTVTHSVNLLLED SHNGKLC LLKGI APLQLG
NCSVAGWI LGNPECELLI SKESWSYI VETPNPENGTCYPGYFADYEELREQLSSVSSFERFEI FPKESSW
PNHTVTGVSASCSHNGKSSFYRNLWLTGKNGLYPNLSKSYANNKEKEVLVWGVHHPNI GDORALYHT
ENAYVSVSSHYSRRFTPEI AKRPKVRDQEGRI NYYWTLLEPGDTI I FEANGNLI APRFAFALSRRGFGSG
I I SSNAPMDECDACKQTPQGA I NSSLPFQNVHPVTI GECPKYVRSAKLRMTGLRNI PSI QSRGLFGAI A
GFI EGGWTGMVDGWYGYHHQNEOGSGYAADQKSTQNAI NGI TNKVNSVI EKMNTQFTAVGKEFNKLERM
ENLNKKVDDGFLDI WTYNAELLVLENERLDFHDSNVKNLYEKVKSOLKNNAKEI GNGCFEFYHKCNDE
CMESVKNGTYDYPKYSEESKLNREKI DGVKLESMGVYQI LAI YSTVASSLVLLVSLGAI SFWMCSNGSLQ
CRI CI

>gi |158830237|gb|ABW81522.1| hemagglutinin [Influenza A virus
(A/Denmark/79/2005(H1N1))]

MKVKLLVLLCTFTATYADTI CI GYHANNSTDTVDTVLEKNVTVTHSVNLLLED SHNGKLC LLKGI APLQLG
NCSVAGWI LGNPECELLI SKESWSYI VETPNPENGTCYPGYFADYEELREQLSSVSSFERFEI FPKESSW
PNHTVTGVSASCSHNGKSSFYRNLWLTGKNGLYPNLSKSYANNKEKEVLVWGVHHPNI GDORALYHT
ENAYVSVSSHYSRRFTPEI AKRPKVRDQEGRI NYYWTLLEPGDTI I FEANGNLI APRFAFALSRRGFGSG
I I TSNAPMDECDACKQTPQGA I NSSLPFQNVHPVTI GECPKYVRSAKLRMTGLRNI PSI QSRGLFGAI A
GFI EGGWTGMVDGWYGYHHQNEOGSGYAADQKSTQNAI NGI TNKVNSVI EKMNTQFTAVGKEFNKLERM
ENLNKKVDDGFLDI WTYNAELLVLENERLDFHDSNVKNLYEKVKSOLKNNAKEI GNGCFEFYHKCNDE
CMESVKNGTYDYPKYSEESKLNREKI DGVKLESMGVYQI LAI YSTVASSLVLLVSLGAI SFWMCSNGSLQ
CRI CI

>gi |158830241|gb|ABW81524.1| hemagglutinin [Influenza A virus
(A/Denmark/110/2005(H1N1))]

MKVKLLVLLCTFTATYADTI CI GYHANNSTDTI DTVLEKNVTVTHSVNLLLED SHNGKLC LLKGI APLQLG
NCSVAGWI LGNPECELLI SKESWSYI VETPNPENGTCYPGYFADYEELREQLSSVSSFERFEI FPKESSW

PNHTVTGVSASCSHNGKSSFYRNLLWLTGKNGLYPNLSKSYANNKEKEVLVWGVHHPNI GDORALYHT
ENAYVSVSSHYSRRFTPEI AKRPKVRDQEGRI NYYWTLLEPGDTI I FEANGNLI APRFAFALSRRGFGSG
I I TSNAPMDECDACKQTPQGA I NSSLPFQNVHPVTI GECPKYVRSAKLRMATGLRNI PSI QSRGLFGAI A
GFI EGGWTGMVDGWYGYHHQNEOGSGYAADQKSTQNAI NGI TNKVNSVI EKMNTQFTAVGKEFSKLERRM
ENLNKKVDDGFLDI WTYNAELLVLENERLDFHDSNVKNLYEKVKSQKNNAKEI GNGCFEFYHKCNDE
CMESVKNGTYDYPKYSEESKLNREKI DGVKLESMGVYQI LAI YSTVASSLVLLVSLGAI SFWMCSNGSLQ
CRI CI

>gi |158830223|gb|ABW81515.1| hemagglutinin [Influenza A virus
(A/Denmark/11/2005(H1N1))]

MKVKLLVLLCTFTATYADTI CI GYHANNSTDTVDTVLEKNVTVTHSVNLLLED SHNGKLCLLKGI APLQLG
NCSVAGWI LGNPECELLI SKESWSYI VETPNPENGTCYPGYFADYEELREQLSSVSSFERFEI FPKESSW
PNHTVTGVSASCSHNGKSSFYRNLLWLTGKNGLYPNLSKSYANNKEKEVLVWGVHHPNI GDORALYHT
ENAYVSVSSHYSRRFTPEI AKRPKVRDQEGRI NYYWTLLEPGDTI I FEANGNLI APRFAFALSRRGFGSG
I I TSNAPMDECDACKQTPQGA I NSSLPFQNVHPVTI GECPKYVRSAKLRMATGLRNI PSI QSRGLFGAI A
GFI EGGWTGMVDGWYGYHHQNEOGSGYAADQKSTQNAI NGI TNKVNSVI EKMNTQFTAVGKEFSKLERRM
ENLNKKVDDGFLDI WTYNAELLVLENERLDFHDSNVKNLYEKVKSQKNNAKEI GNGCFEFYHKCNDE
CMESVKNGTYDYPKYSEESKLNREKI DGVKLESMGVYQI LAI YSTVASSLVLLVSLGAI SFWMCSNGSLQ
CRI CI

>gi |145278924|gb|ABP49393.1| hemagglutinin [Influenza A virus (A/South
Australia/51/2005(H1N1))]

MKVKLLVLLCTFTATYADTI CI GYHANNSTDTVDTVLEKNVTVTHSVNLLLED SHNGKLCLLKGI APLQLG
NCSVAGWI LGNPECELLI SKESWSYI VETPNPENGTCYPGYFADYEELREQLSSVSSFERFEI FPKESSW
PNHTVTGVSASCSHNGKSSFYRNLLWLTGKNGLYPNLSKSYANNKEKEVLVWGVHHPNI GDORALYHT
ENAYVSVSSHYSRRFTPEI AKRPKVRDQEGRI NYYWTLLEPGDTI I FEANGNLI APRFAFALSRRGFGSG
I I TSNAPMDECDACKQTPQGA I NSSLPFQNVHPVTI GECPKYVRSAKLRMATGLRNI PSI QSRGLFGAI A
GFI EGGWTGMVDGWYGYHHQNEOGSGYAADQKSTQNAI NGI TNKVNSVI EKMNTQFTAVGKEFSKLERRM
ENLNKKVDDGFLDI WTYNAELLVLENERLDFHDSNVKNLYEKVKSQKNNAKEI GNGCFEFYHKCNDE
CMESVKNGTYDYPKYSEESKLNREKI DGVKLESMGVYQI LAI YSTVASSLVLLVSLGAI SFWMCSNGSLQ
CRI CI

>gi |115607822|gb|ABJ16686.1| hemagglutinin [Influenza A virus (A/South
Australia/58/2005(H1N1))]

MKVKLLVLLCTFTATYADTI CI GYHANNSTDTVDTVLEKNVTVTHSVNLLLED SHNGKLCLLKGI APLQLG
NCSVAGWI LGNPECELLI SKESWSYI VETPNPENGTCYPGYFADYEELREQLSSVSSFERFEI FPKESSW
PNHTVTGVSASCSHNGKSSFYRNLLWLTGKNGLYPNLSKSYANNKEKEVLVWGVHHPNI GDORALYHT
ENAYVSVSSHYSRRFTPEI AKRPKVRDQEGRI NYYWTLLEPGDTI I FEANGNLI APRFAFALSRRGFGSG
I I TSNAPMDECDACKQTPQGA I NSSLPFQNVHPVTI GECPKYVRSAKLRMATGLRNI PSI QSRGLFGAI A
GFI EGGWTGMVDGWYGYHHQNEOGSGYAADQKSTQNAI NGI TNKVNSVI EKMNTQFTAVGKEFSKLERRM
ENLNKKVDDGFLDI WTYNAELLVLENERLDFHDSNVKNLYEKVKSQKNNAKEI GNGCFEFYHKCNDE
CMESVKNGTYDYPKYSEESKLNREKI DGVKLESMGVYQI LAI YSTVASSLVLLVSLGAI SFWMCSNGSLQ
CRI CI

>gi |112456302|gb|ABI19015.1| hemagglutinin [Influenza A virus
(A/Iowa/CEI D23/2005(H1N1))]

MKAI I VLLYTFATADADTL CI GYHANNSTDTVDTVLEKNVTVTHSVNLLLENKHGDKLCKLRGI APLHLG
KCN AGWI LGNPECESLFTTSSWSYI VETPNSDNGTCYPGDFI NYEELREHLSVSSVSSFERFEI FPKANSW
PYHDTNKGVTAAQPYAGANSFYRNLI WLVKKGNSYPKLSKSYI NNKKKEVLVI WGI HHPPTSDQDQTLYQ
NADAYVFGSSKYSKRFPKPEI AARPKVRDQAGRMDDYYWTLI EPGDTI TFEATGNLVVPRYAF TMKRGS
GI I VSDAPVHDCNTTCTQPKGAI NTLSPFQNI HPVTI GECPKYVKS TKLRMATGLRNI PSI QSRGLFGAI
AGFI EGGWTGMI DGWYGYHHQNEOGSGYAADQKSTQNAI DGI TNKVNSI I EKMNTQFTAVGKEFSOLEKR
I ESLNKKVDDGFLDI WTYNAELLVLENERLDFHDSNVKNLYEKVRSQKNNAKEI GNGCFEFYHKCDD
TCMESVKNGTYDYPKYSEEA KLNROEI DGVKLESARI YQI LAI YSTVASSLVLLVSLGAVSFWMCSNGSL
QCRI CI

>gi |115607803|gb|ABJ16675.1| hemagglutinin [Influenza A virus (A/South
Australia/57/2005(H1N1))]

MKVKLLVLLCTFTATYADTI CI GYHANNSTDTVDTVLEKNVTVTHSVNLLLED SHNGKLCLLKGI APLQLG
NCSVAGWI LGNPECELLI SKESWSYI VETPNPENGTCYPGYFADYEELREQLSSVSSFERFEI FPKESSW
PNHTVTGVSASCSHNGKSSFYRNLLWLTGKNGLYPNLSKSYANNKEKEVLVWGVHHPNI GDORALYHT
ENAYVSVSSHYSRRFTPEI AKRPKVRDQEGRI NYYWTLLEPGDTI I FEANGNLI APRFAFALSRRGFGSG
I I TSNAPMDECDACKQTPQGA I NSSLPFQNVHPVTI GECPKYVRSAKLRMATGLRNI PSI QSRGLFGAI A
GFI EGGWTGMVDGWYGYHHQNEOGSGYAADQKSTQNAI NGI TNKVNSVI EKMNTQFTAVGKEFSKLERRM
ENLNKKVDDGFLDI WTYNAELLVLENERLDFHDSNVKNLYEKVKSQKNNAKEI GNGCFEFYHKCNDE
CMESVKNGTYDYPKYSEESKLNREKI DGVKLESMGVYQI LAI YSTVASSLVLLVSLGAI SFWMCSNGSLQ
CRI CI

>gi |158830225|gb|ABW81516.1| hemagglutinin [Influenza A virus
(A/Denmark/54/2005(H1N1))]

MKVKLLVLLCTFTATYADTI CI GYHANNSTDTVDTVLEKNVTVTHSVNLLLED SHNGKLCLLKGI APLQLG
NCSVAGWI LGNPECELLI SKESWSYI VETPNPENGTCYPGYFADYEELREQLSSVSSFERFEI FPKESSW
PNHTVTGVSASCSHNGKSSFYRNLLWLTGKNGLYPNLSKSYANNKEKEVLVWGVHHPNI GDORALYHT
ENAYVSVSSHYSRRFTPEI AKRPKVRDQEGRI NYYWTLLEPGDTI I FEANGNLI APRFAFALSRRGFGSG
I I TSNAPMDECDACKQTPQGA I NSSLPFQNVHPVTI GECPKYVRSAKLRMATGLRNI PSI QSRGLFGAI A
GFI EGGWTGMVDGWYGYHHQNEOGSGYAADQKSTQNAI NGI TNKVNSVI EKMNTQFTAVGKEFSKLERRM
ENLNKKVDDGFLDI WTYNAELLVLENERLDFHDSNVKNLYEKVKSQKNNAKEI GNGCFEFYHKCNDE
CMESVKNGTYDYPKYSEESKLNREKI DGVKLESMGVYQI LAI YSTVASSLVLLVSLGAI SFWMCSNGSLQ
CRI CI

>gi |158830227|gb|ABW81517.1| hemagglutinin [Influenza A virus
(A/Denmark/226/2005(H1N1))]

MKVKLLVLLCTFTATYADTI CI GYHANNSTDTVDTVLEKNVTVTHSVNLLLED SHNGKLCLLKGI APLQLG
NCSVAGWI LGNPECELLI SKESWSYI VETPNPENGTCYPGYFADYEELREQLSSVSSFERFEI FPKESSW

PNHVTVTGVSASCSHNGKSSFYRNLWLTGKNGLYPNLSKSYANNKEKEVLVWGVHHPNI GDORALYHT
ENAYVSVSSHYSRRFTPEI AKRPKVRDQEGRI NYYWTLLEPGDTI I FEANGNLI APRFAFALSRRGFGSG
I I TSNAPMDECDACKQTPQGA I NSSLPFQNVHPVTI GECPKYVRSAKLRMATGLRNI PSI QSRGLFGAI A
GFI EGGWQGMVDGWYGYHHQNEQSGSYAADQKSTQNAI NGI TNKVNSVI EKMNTQFVAVGKEFSKLERRM
ENLNKKVDDGFLDI WTYNAELLVLENERLDFHDSNVKNLYEKVKSQKNNAKEI GNGCFEFYHKCNDE
CMESVKNGTYDYPKYSEESKLNREKI DGKLESMGVYQI LAI YSTVASSLVLLVSLGAI SFWMCSNGSLQ
CRI CI

>gi |158830233|gb|ABW81520.1| hemagglutinin [Influenza A virus
(A/Denmark/3/2005(H1N1))]

MKVKLLVLLCTFTATYADTI CI GYHANNSTDTVDTVLEKNVTVTHSVNLLLEDSSHNGKLCLLKGI APLQLG
SCSVAGWI LGNPECELLI SKESWSYI VETPNPENGTCYPGYFADYEELREQLSSVSSFERFEI FPKESSW
PNHTVTGVSASCSHNGKSSFYRNLWLTGKNGLYPNLSKSYANNKEKEVLVWGVHHPNI GDORALYHT
ENAYVSVSSHYSRRFTPEI AKRPKVRDQEGRI NYYWTLLEPGDTI I FEANGNLI APRFAFALSRRGFGSG
I I TSNAPMDECDACKQTPQGA I NSSLPFQNVHPVTI GECPKYVRSAKLRMATGLRNI PSI QSRGLFGAI A
GFI EGGWQGMVDGWYGYHHQNEQSGSYAADQKSTQNAI NGI TNKVNSVI EKMNTQFVAVGKEFSKLERRM
ENLNKKVDDGFLDI WTYNAELLVLENERLDFHDSNVKNLYEKVKSQKNNAKEI GNGCFEFYHKCNDE
CMESVKNGTYDYPKYSEESKLNREKI DGKLESMGVYQI LAI YSTVASSLVLLVSLGAI SFWMCSNGSLQ
CRI CI

H2N2

>gi |26453383|dbj|BAC43764.1| hemagglutinin [Influenza A virus (A/Kayano/57(H2N2))]

MAI I YLI LLFTA VRGDOI CI GYHANNSTEKVDTI LERNVTVTHAKNI LEKTHNGKLCCKLNGI PPLELGDC
SI AGWLLGNPECDRLLI VPEWSYI MEKENPRDGLCYPGSFNDYEELKHLSSVKHFKEVKI LPKDRWTOH
TTTGGSRACAVSNGPSFFRNMVWLTKKGSNYPVAKGSYNNTSGEOMLI I WGVHHPNI DEEQI TLYQNVGT
YVSVGTSTLNKRSTPEI ATRPKVNGLGRMEFSWTLDMWDTI NFESTGNLI APEYGFKI SKRGSSGI MK
TEGTLENCETKQTPGLAI NTTLPFHNVHPLTI GECPKYVVKSEKLVLATGLRNVPOI ESRGLFGAI AGFI
EGGWQGMVDGWYGYHHSNDQSGSYAADKSTQKAFDGI TNKVNSVI EKMNTQFEAVGKEFSNLERRLENL
NKKMEDGFLDVWTYNAELLVLMENERTLDFHDSNVKNLYDKVRMQLRDNVKELGNGCFEFYHKCDDECMN
SVKNGTYDYPKYEEESKLNREKI KGVKLSMGMVYQI LAI YATVAGSLSLAI MMAGI SFWMCSNGSLQFRI
CI

>gi |127057978|dbj|BAF48641.1| haemagglutinin [Influenza A virus
(A/Singapore/1/57(H2N2))]

MAI I YLI LLFTA VRGDOI CI GYHANNSTEKVDTI LERNVTVTHAKDI LEKTHNGKLCCKLNGI PPLELGDC
SI AGWLLGNPECDRLLI VPEWSYI MEKENPRDGLCYPGSFNDYEELKHLSSVKHFKEVKI LPKDRWTOH
TTTGGSRACAVSNGPSFFRNMVWLTKKGSNYPVAKGSYNNTSGEOMLI I WGVHHPNDETEQRTLYQNVGT
YVSVGTSTLNKRSTPEI ATRPKVNGQGGREMEFSWTLDMWDTI NFESTGNLI APEYGFKI SKRGSSGI MK
TEGTLENCETKQTPGLAI NTTLPFHNVHPLTI GECPKYVVKSEKLVLATGLRNVPOI ESRGLFGAI AGFI
EGGWQGMVDGWYGYHHSNDQSGSYAADKSTQKAFDGI TNKVNSVI EKMNTQFEAVGKEFSNLERRLENL
NKKMEDGFLDVWTYNAELLVLMENERTLDFHDSNVKNLYDKVRMQLRDNVKELGNGCFEFYHKCDDECMN
SVKNGTYDYPKYEEESKLNREKI KGVKLSMGMVYQI LAI YATVAGSLSLAI MMAGI SFWMCSNGSLQCRI
CI

>gi |145279038|gb|ABP49459.1| hemagglutinin [Influenza A virus
(A/AI bany/22/1957(H2N2))]

MAI I YLI LLFTA VRGDOI CI GYHANNSTEKVDTI LERNVTVTHAKDI LEKTHNGKLCCKLNGI PPLELGDC
SI AGWLLGNPECDRLLI VPEWSYI MEKENPRDGLCYPGSFNDYEELKHLSSVKHFKEVKI LPKDRWTOH
TTTGGSRACAVSNGPSFFRNMVWLTKKGSNYPVAKGSYNNTSGEOMLI I WGVHHPNDETEQRTLYQNVGT
YVSVGTSTLNKRSTPEI ATRPKVNGQGGREMEFSWTLDMWDTI NFESTGNLI APEYGFKI SKRGSSGI MK
TEGTLENCETKQTPGLAI NTTLPFHNVHPLTI GECPKYVVKSEKLVLATGLRNVPOI ESRGLFGAI AGFI
EGGWQGMVDGWYGYHHSNDQSGSYAADKSTQKAFDGI TNKVNSVI EKMNTQFEAVGKEFSNLERRLENL
NKKMEDGFLDVWTYNAELLVLMENERTLDFHDSNVKNLYDKVRMQLRDNVKELGNGCFEFYHKCDDECMN
SVKNGTYDYPKYEEESKLNREKI KGVKLSMGMVYQI LAI YATVAGSLSLAI MMAGI SFWMCSNGSLQCRI
CI

>gi |146760066|gb|ABQ44460.1| hemagglutinin [Influenza A virus
(A/AI bany/20/1957(H2N2))]

MAI I YLI LLFTA VRGDOI CI GYHANNSTEKVDTI LERNVTVTHAKDI LEKTHNGKLCCKLNGI PPLELGDC
SI AGWLLGNPECDRLLI VPEWSYI MEKENPRDGLCYPGSFNDYEELKHLSSVKHFKEVKI LPKDRWTOH
TTTGGSRACAVSNGPSFFRNMVWLTKKGSNYPVAKGSYNNTSGEOMLI I WGVHHPNDETEQRTLYQNVGT
YVSVGTSTLNKRSTPEI ATRPKVNGLGRMEFSWTLDMWDTI NFESTGNLI APEYGFKI SKRGSSGI MK
TEGTLENCETKQTPGLAI NTTLPFHNVHPLTI GECPKYVVKSEKLVLATGLRNVPOI ESRGLFGAI AGFI
EGGWQGMVDGWYGYHHSNDQSGSYAADKSTQKAFDGI TNKVNSVI EKMNTQFEAVGKEFSNLERRLENL
NKKMEDGFLDVWTYNAELLVLMENERTLDFHDSNVKNLYDKVRMQLRDNVKELGNGCFEFYHKCDDECMN
SVKNGTYDYPKYEEESKLNREKI KGVKLSMGMVYQI LAI YATVAGSLSLAI MMAGI SFWMCSNGSLQCRI
CI

>gi |188504350|gb|ACD56291.1| hemagglutinin [Influenza A virus (A/Ann
Arbor/23/1957(H2N2))]

MAI I YLI LLFTA VRGDOI CI GYHANNSTEKVDTI LERNVTVTHAKDI LEKTHNGKLCCKLNGI PPLELGDC
SI AGWLLGNPECDRLLI VPEWSYI MEKENPRDGLCYPGSFNDYEELKHLSSVKHFKEVKI LPKDRWTOH
TTTGGSRACAVSNGPSFFRNMVWLTKKGSNYPVAKGSYNNTSGEOMLI I WGVHHPNDETEQRTLYQNVGT
YVSVGTSTLNKRSTPEI ATRPKVNGLGRMEFSWTLDMWDTI NFESTGNLI APEYGFKI SKRGSSGI MK
TEGTLENCETKQTPGLAI NTTLPFHNVHPLTI GECPKYVVKSEKLVLATGLRNVPOI ESRGLFGAI AGFI
EGGWQGMVDGWYGYHHSNDQSGSYAADKSTQKAFDGI TNKVNSVI EKMNTQFEAVGKEFSNLERRLENL
NKKMEDGFLDVWTYNAELLVLMENERTLDFHDSNVKNLYDKVRMQLRDNVKELGNGCFEFYHKCDDECMN
SVKNGTYDYPKYEEESKLNREKI KGVKLSMGMVYQI LAI YATVAGSLSLAI MMAGI SFWMCSNGSLQCRI
CI

>gi |189230499|gb|ACD85231.1| hemagglutinin [Influenza A virus (A/Gui yang/1/1957(H2N2))]
 I I YLI LLFTA VRGDI CI GYHANNSTEVDTI LERNVTVTHAKDI LEKTHNGKLCCKLNGI PPLELGDCSI
 AGWLLGNPECDRLLSVPEWSYI MEKENPRDGLCYPGSFNDYEELKHLSSVTHFEKVKI LPRDRWTOHTT
 TGGSRACAVSGNPSFFRNMMVWLTEKGSNYPVAKGSYNNTSGEQMLI I WGVHHPNDETEORTLYQNVGT
 SVGTSTLNKRSTPEI ATRPKVNGLGSRMFEFSWI LLDMMWDTI NFESTGNLI APEYGFKI SKRGSSGI MKTE
 GTLENCETKQCOTPLGAI NTTLPFHNVHPLTI GECPKYVKSEKLVLATGLRNVPOI ESRGLFGAI AGFI EG
 GWQGMVDGWYGYHHSNDQGSYAADKESTQKAFDGI TNKVNSVI EKMNI QFEAVGKEFSNLERRLENL
 NKMEDGFLDVWWTYNAELLVLMENERTLDFHDSNVKNLYDKVRMQLRDNVKELGNGCFEFYHKCDDECMNSV
 KNGTYDYPKYEEESKLNREI KGVKLSMGMVYQI LAI YATVAGSLSLAI MMAGI SFWMCSNGSLOCRI CI

>gi |194352162|gb|ACF54477.1| hemagglutinin [Influenza A virus (A/Singapore/1/1957(H2N2))]
 MAI I YLI LLFTA VRGDI CI GYHANNSTEVDTI LERNVTVTHAKDI LEKTHNGKLCCKLNGI PPLELGDC
 SI AGWLLGNPECDRLLSVPEWSYI MEKENPRDGLCYPGSFNDYEELKHLSSVKHFEKVKI LPKDRWTOH
 TTTGGSRAVSGNPSFFRNMMVWLTKKGSNYPVAKGSYNNTSGEQMLI I WGVHHPNDETEORTLYQNVGT
 YVSVGTSTLNKRSTPDI ATRPKVNGLGSRMFEFSWTLDDMMWDTI NFESTGNLI APEYGFKI SKRGSSGI MK
 TEGTLENCETKQCOTPLGAI NTTLPFHNVHPLTI GECPKYVKSEKLVLATGLRNVPOI ESRGLFGAI AGFI
 EGGWQGMVDGWYGYHHSNDQGSYAADKESTQKAFDGI TNKVNSVI EKMNTQFEAVGKEFSNLERRLENL
 NKKMEDGFLDVWWTYNAELLVLMENERTLDFHDSNVKNLYDKVRMQLRDNVKELGNGCFEFYHKCDDECMN
 SVKNGTYDYPKYEEESKLNREI KGVKLSMGMVYQI LAI YATVAGSLSLAI MMAGI SFWMCSNGSLOCRI
 CI

>gi |194352181|gb|ACF54488.1| hemagglutinin [Influenza A virus (A/Singapore/1-
 MA12/1957(H2N2))]
 MAI I YLI LLFTA VRGDI CI GYHANNSTEVDTI LERNVTVTHAKDI LEKTHNGKLCCKLNGI PPLELGDC
 SI AGWLLGNPECDRLLSVPEWSYI MEKENPRDGLCYPGSFNDYEELKHLSSVKHFEKVKI LPKDRWTOH
 TTTGGSRAVSGNPSFFRNMMVWLTKKGSNYPVAKGSYNNTSGEQMLI I WGVHHPNDETEORTLYQNVGT
 YVSVGTSTLNKRSTPDI ATRPKVNGLGSRMFEFSWTLDDMMWDTI NFESTGNLI APEYGFKI SKRGSSGI MK
 TEGTLENCETKQCOTPLGAI NTTLPFHNVHPLTI GECPKYVKSEKLVLATGLRNVPOI ESRGLFGAI AGFI
 EGGWQGMVDGWYGYHHSNDQGSYAADKESTQKAFDGI TNKVNSVI EKMNTQFEAVGKEFSNLERRLENL
 NKKMEDGFLDVWWTYNAELLVLMENERTLDFHDSNVKNLYDKVRMQLRDNVKELGNGCFEFYHKCDDECMN
 SVKNGTYDYPKYEEESKLNREI KGVKLSMGMVYQI LAI YATVAGSLSLAI MMAGI SFWMCSNGSLOCRI
 CI

>gi |194352200|gb|ACF54499.1| hemagglutinin [Influenza A virus (A/Singapore/1-
 MA12A/1957(H2N2))]
 MAI I YLI LLFTA VRGDI CI GYHANNSTEVDTI LERNVTVTHAKDI LEKTHNGKLCCKLNGI PPLELGDC
 SI AGWLLGNPECDRLLSVPEWSYI MEKENPRDGLCYPGSFNDYEELKHLSSVKHFEKVKI LPKDRWTOH
 TTTGGSRAVSGNPSFFRNMMVWLTKKGSNYPVAKGSYNNTSGEQMLI I WGVHHPNDETEORTLYQNVGT
 YVSVGTSTLNKRSTPDI ATRPKVNGLGSRMFEFSWTLDDMMWDTI NFESTGNLI APEYGFKI SKRGSSGI MK
 TEGTLENCETKQCOTPLGAI NTTLPFHNVHPLTI GECPKYVKSEKLVLATGLRNVPOI ESRGLFGAI AGFI
 EGGWQGMVDGWYGYHHSNDQGSYAADKESTQKAFDGI TNKVNSVI EKMNTQFEAVGKEFSNLERRLENL
 NKKMEDGFLDVWWTYNAELLVLMENERTLDFHDSNVKNLYDKVRMQLRDNVKELGNGCFEFYHKCDDECMN
 SVKNGTYDYPKYEEESKLNREI KGVKLSMGMVYQI LAI YATVAGSLSLAI MMAGI SFWMCSNGSLOCRI
 CI

>gi |194352219|gb|ACF54510.1| hemagglutinin [Influenza A virus (A/Singapore/1-
 MA12B/1957(H2N2))]
 MAI I YLI LLFTA VRGDI CI GYHANNSTEVDTI LERNVTVTHAKDI LEKTHNGKLCCKLNGI PPLELGDC
 SI AGWLLGNPECDRLLSVPEWSYI MEKENPRDGLCYPGSFNDYEELKHLSSVKHFEKVKI LPKDRWTOH
 TTTGGSRAVSGNPSFFRNMMVWLTKKGSNYPVAKGSYNNTSGEQMLI I WGVHHPNDETEORTLYQNVGT
 YVSVGTSTLNKRSTPDI ATRPKVNGLGSRMFEFSWTLDDMMWDTI NFESTGNLI APEYGFKI SKRGSSGI MK
 TEGTLENCETKQCOTPLGAI NTTLPFHNVHPLTI GECPKYVKSEKLVLATGLRNVPOI ESRGLFGAI AGFI
 EGGWQGMVDGWYGYHHSNDQGSYAADKESTQKAFDGI TNKVNSVI EKMNTQFEAVGKEFSNLERRLENL
 NKKMEDGFLDVWWTYNAELLVLMENERTLDFHDSNVKNLYDKVRMQLRDNVKELGNGCFEFYHKCDDECMN
 SVKNGTYDYPKYEEESKLNREI KGVKLSMGMVYQI LAI YATVAGSLSLAI MMAGI SFWMCSNGSLOCRI
 CI

>gi |194352238|gb|ACF54521.1| hemagglutinin [Influenza A virus (A/Singapore/1-
 MA12D/1957(H2N2))]
 MAI I YLI LLFTA VRGDI CI GYHANNSTEVDTI LERNVTVTHAKDI LEKTHNGKLCCKLNGI PPLELGDC
 SI AGWLLGNPECDRLLSVPEWSYI MEKENPRDGLCYPGSFNDYEELKHLSSVKHFEKVKI LPKDRWTOH
 TTTGGSRAVSGNPSFFRNMMVWLTKKGSNYPVAKGSYNNTSGEQMLI I WGVHHPNDETEORTLYQNVGT
 YVSVGTSTLNKRSTPDI ATRPKVNGLGSRMFEFSWTLDDMMWDTI NFESTGNLI APEYGFKI SKRGSSGI MK
 TEGTLENCETKQCOTPLGAI NTTLPFHNVHPLTI GECPKYVKSEKLVLATGLRNVPOI ESRGLFGAI AGFI
 EGGWQGMVDGWYGYHHSNDQGSYAADKESTQKAFDGI TNKVNSVI EKMNTQFEAVGKEFSNLERRLENL
 NKKMEDGFLDVWWTYNAELLVLMENERTLDFHDSNVKNLYDKVRMQLRDNVKELGNGCFEFYHKCDDECMN
 SVKNGTYDYPKYEEESKLNREI KGVKLSMGMVYQI LAI YATVAGSLSLAI MMAGI SFWMCSNGSLOCRI
 CI

>gi |94481522|gb|ABF21270.1| hemagglutinin [Influenza A virus (A/Japan/305/57(H2N2))]
 MAI I YLI LLFTA VRGDI CI GYHANNSTEMVDTI LERNVTVTHAKDI LEKTHNGKLCCKLNGI PPLELGDC
 SI AGWLLGNPECDRLLSVPEWSYI MEKENPRDGLCYPGSFNDYEELKHLSSVKHFEKVKI LPKDRWTOH
 TTTGGSRAVSGNPSFFRNMMVWLTKKGSNYPVAKGSYNNTSGEQMLI I WGVHHPNDETEORTLYQNVGT
 YVSVGTSTLNKRSTPEI ATRPKVNGQGRMEFSWTLDDMMWDTI NFESTGNLI APEYGFKI SKRGSSGI MK
 TEGTLENCETKQCOTPLGAI NTTLPFHNVHPLTI GECPKYVKSEKLVLATGLRNVPOI ESRGLFGAI AGFI
 EGGWQGMVDGWYGYHHSNDQGSYAADKESTQKAFDGI TNKVNSVI EKMNTQFEAVGKEFSNLERRLENL
 NKKMEDGFLDVWWTYNAELLVLMENERTLDFHDSNVKNLYDKVRMQLRDNVKELGNGCFEFYHKCDDECMN
 SVKTGTYPKYEEESKLNREI KGVKLSMGMVYQI LAI YATVAGSLSLAI MMAGI SFWMCSNGSLOCRI
 CI

>gi |324146|gb|AAA43185.1| hemagglutinin precursor [Influenza A virus (A/Japan/305/1957(H2N2))]

MAI I YLI LLFTA VRGDOI CI GYHANNSTEKVDI LERNVTVTHAKDI LEKTHNGKLCCKLNGI PPLELGDC
 SI AGWLLGNPECDRLLSVPEWSYI MEKENPRDGLCYPGSFNDYEELKHLSSVKHFKEVKI LPKDRWTOH
 TTTGGSRAVSGNPSFFRNMMVWLTKKGSNDYPAKGSYNNTSGEOMLI I WGVHHPIDEQEORTLYQNVGT
 YVSVGTSTLNKRSTPEI ATRPKVNGQGRMEFSWTLDMWDTI NFESTGNLI APEYGFKI SKRGSSGI MK
 TEGTLENCETKCOPLGAI NTTLPFHNVHPLTI GECPKYVKSEKLVLATGLRNVPOI ESRGLFGAI AGFI
 EGGWQGMVDGWYGYHHSNDQGSYAADKESTQKAFDGI TNKVN SVI EKMNTQFEAVGKEFSNLERRLENL
 NKKMEDGFLDVWTYNAELLVLMENERTLDFHDSNVKNLYDKVRMQLRDNVVKELGNGCFEFYHKCDECEMN
 SVKNGTYDYPKYEEESKLRNEI KGVKLSMGMVYQI LAI YATVAGSLSLAI MMAGI SFWMCSNGSLQCRI
 CI

>gi |408677|gb|AAA43678.1| hemagglutinin [Influenza A virus (A/Singapore/1/57 (H2N2))]
 MAI I YLI LLFTA VRGDOI CI GYHANNSTEKVDI LERNVTVTHAKDI LEKTHNGKLCCKLNGI PPLELGDC
 SI AGWLLGNPECDRLLSVPEWSYI MEKENPRDGLCYPGSFNDYEELKHLSSVKHFKEVKI LPKDRWTOH
 TTTGGSRAVSGNPSFFRNMMVWLTKKGSNDYPAKGSYNNTSGEOMLI I WGVHHPIDEQEORTLYQNVGT
 YVSVGTSTLNKRSTPEI ATRPKVNGQGRMEFSWTLDMWDTI NFESTGNLI APEYGFKI SKRGSSGI MK
 TEGTLENCETKCOPLGAI NTTLPFHNVHPLTI GECPKYVKSEKLVLATGLRNVPOI ESRGLFGAI AGFI
 EGGWQGMVDGWYGYHHSNDQGSYAADKESTQKAFDGI TNKVN SVI EKMNTQFEAVGKEFSNLERRLENL
 NKKMEDGFLDVWTYNAELLVLMENERTLDFHDSNVKNLYDKVRMQLRDNVVKELGNGCFEFYHKCDECEMN
 SVKNGTYDYPKYEEESKLRNEI KGVKLSMGMVYQI LAI YATVAGSLSLAI MMAGI SFWMCSNGSLQCRI
 CI

>gi |305115|gb|AAA64362.1| hemagglutinin [Influenza A virus (A/Japan/305+/1957(H2N2))]
 MAI I YLI LLFTA VRGDOI CI GYHANNSTEKVDI LERNVTVTHAKDI LEKTHNGKLCCKLNGI PPLELGDC
 SI AGWLLGNPECDRLLSVPEWSYI MEKENPRDGLCYPGSFNDYEELKHLSSVKHFKEVKI LPKDRWTOH
 TTTGGSRAVSGNPSFFRNMMVWLTKKGSNDYPAKGSYNNTSGEOMLI I WGVHHPIDEQEORTLYQNVGT
 YVSVGTSTLNKRSTPEI ATRPKVNGQGRMEFSWTLDMWDTI NFESTGNLI APEYGFKI SKRGSSGI MK
 TEGTLENCETKCOPLGAI NTTLPFHNVHPLTI GECPKYVKSEKLVLATGLRNVPOI ESRGLFGAI AGFI
 EGGWQGMVDGWYGYHHSNDQGSYAADKESTQKAFDGI TNKVN SVI EKMNTQFEAVGKEFSNLERRLENL
 NKKMEDGFLDVWTYNAELLVLMENERTLDFHDSNVKNLYDKVRMQLRDNVVKELGNGCFEFYHKCDECEMN
 SVKNGTYDYPKYEEESKLRNEI KGVKLSMGMVYQI LAI YATVAGSLSLAI MMAGI SFWMCSNGSLQCRI
 CI

>gi |305155|gb|AAA64364.1| hemagglutinin [Influenza A virus (A/Japan/305-/1957(H2N2))]
 MAI I YLI LLFTA VRGDOI CI GYHANNSTEKVDI LERNVTVTHAKDI LEKTHNGKLCCKLNGI PPLELGDC
 SI AGWLLGNPECDRLLSVPEWSYI MEKENPRDGLCYPGSFNDYEELKHLSSVKHFKEVKI LPKDRWTOH
 TTTGGSRAVSGNPSFFRNMMVWLTKKGSNDYPAKGSYNNTSGEOMLI I WGVHHPIDEQEORTLYQNVGT
 YVSVGTSTLNKRSTPEI ATRPKVNGQGRMEFSWTLDMWDTI NFESTGNLI APEYGFKI SKRGSSGI MK
 TEGTLENCETKCOPLGAI NTTLPFHNVHPLTI GECPKYVKSEKLVLATGLRNVPOI ESRGLFGAI AGFI
 EGGWQGMVDGWYGYHHSNDQGSYAADKESTQKAFDGI TNKVN SVI EKMNTQFEAVGKEFSNLERRLENL
 NKKMEDGFLDVWTYNAELLVLMENERTLDFHDSNVKNLYDKVRMQLRDNVVKELGNGCFEFYHKCDECEMN
 SVKNGTYDYPKYEEESKLRNEI KGVKLSMGMVYQI LAI YATVAGSLSLAI MMAGI SFWMCSNGSLQCRI
 CI

>gi |305163|gb|AAA64365.1| hemagglutinin [Influenza A virus (A/RI/5+/1957(H2N2))]
 MAI I YLI LLFTA VRGDOI CI GYHANNSTEKVDI LERNVTVTHAKDI LEKTHNGKLCCKLNGI PPLELGDC
 SI AGWLLGNPECDRLLSVPEWSYI MEKENPRDGLCYPGSFNDYEELKHLSSVKHFKEVKI LPKDRWTOH
 TTTGGSRAVSGNPSFFRNMMVWLTKKGSNDYPAKGSYNNTSGEOMLI I WGVHHPIDEQEORTLYQNVGT
 YVSVGTSTLNKRSTPEI ATRPKVNGQGRMEFSWTLDMWDTI NFESTGNLI APEYGFKI SKRGSSGI MK
 TEGTLENCETKCOPLGAI NTTLPFHNVHPLTI GECPKYVKSEKLVLATGLRNVPOI ESRGLFGAI AGFI
 EGGWQGMVDGWYGYHHSNDQGSYAADKESTQKAFDGI TNKVN SVI EKMNTQFEAVEKEFSNLERRLENL
 NKKMEDGFLDVWTYNAELLVLMENERTLDFHDSNVKNLYDKVRMQLRDNVVKELGNGCFEFYHKCDECEMN
 SVKNGTYDYPKYEEESKLRNEI KGVKLSMGMVYQI LAI YATVAGSLSLAI MMAGI SFWMCSNGSLQCRI
 CI

>gi |305117|gb|AAA64363.1| hemagglutinin [Influenza A virus (A/RI/5-/1957(H2N2))]
 MAI I YLI LLFTA VRGDOI CI GYHANNSTEKVDI LERNVTVTHAKDI LEKTHNGKLCCKLNGI PPLELGDC
 SI AGWLLGNPECDRLLSVPEWSYI MEKENPRDGLCYPGSFNDYEELKHLSSVKHFKEVKI LPKDRWTOH
 TTTGGSRAVSGNPSFFRNMMVWLTKKGSNDYPAKGSYNNTSGEOMLI I WGVHHPIDEQEORTLYQNVGT
 YVSVGTSTLNKRSTPEI ATRPKVNGQGRMEFSWTLDMWDTI NFESTGNLI APEYGFKI SKRGSSGI MK
 TEGTLENCETKCOPLGAI NTTLPFHNVHPLTI GECPKYVKSEKLVLATGLRNVPOI ESRGLFGAI AGFI
 EGGWQGMVDGWYGYHHSNDQGSYAADKESTQKAFDGI TNKVN SVI EKI NTOFEAVEKEFSNLERRLENL
 NKKMEDGFLDVWTYNAELLVLMENERTLDFHDSNVKNLYDKVRMQLRDNVVKELGNGCFEFYHKCDECEMN
 SVKNGTYDYPKYEEESKLRNEI KGVKLSMGMVYQI LAI YATVAGSLSLAI MMAGI SFWMCSNGSLQCRI
 CI

>gi |305171|gb|AAA64366.1| hemagglutinin [Influenza A virus
 (A/Singapore/1/1957(H2N2))]
 MAI I YLI LLFTA VRGDOI CI GYHANNSTEKVDI LERNVTVTHAKDI LEKTHNGKLCCKLNGI PPLELGDC
 SI AGWLLGNPECDRLLSVPEWSYI MEKENPRDGLCYPGSFNDYEELKHLSSVKHFKEVKI LPKDRWTOH
 TTTGGSRAVSGNPSFFRNMMVWLTKKGSNDYPAKGSYNNTSGEOMLI I WGVHHPIDEQEORTLYQNVGT
 YVSVGTSTLNKRSTPEI ATRPKVNGQGRMEFSWTLDMWDTI NFESTGNLI APEYGFKI SKRGSSGI MK
 TEGTLENCETKCOPLGAI NTTLPFHNVHPLTI GECPKYVKSEKLVLATGLRNVPOI ESRGLFGAI AGFI
 EGGWQGMVDGWYGYHHSNDQGSYAADKESTQKAFDGI TNKVN SVI EKMNTQFEAVGKEFSNLERRLENL
 NKKMEDGFLDVWTYNAELLVLMENERTLDFHDSNVKNLYDKVRMQLRDNVVKELGNGCFEFYHKCDECEMN
 SVKNGTYDYPKYEEESKLRNEI KGVKLSMGMVYQI LAI YATVAGSLSLAI MMAGI SFWMCSNGSLQCRI
 CI

>gi |115279062|gb|ABI 84959.1| hemagglutinin [Influenza A virus
 (A/Japan/305/1957(H2N2))]
 MAI I YLI LLFTA VRGDOI CI GYHANNSTEKVDI LERNVTVTHAKDI LEKTHNGKLCCKLNGI PPLELGDC
 SI AGWLLGNPECDRLLSVPEWSYI MEKENPRDGLCYPGSFNDYEELKHLSSVKHFKEVKI LPKDRWTOH
 TTTGGSRAVSGNPSFFRNMMVWLTKKGSNDYPAKGSYNNTSGEOMLI I WGVHHPIDEQEORTLYQNVGT
 YVSVGTSTLNKRSTPEI ATRPKVNGQGRMEFSWTLDMWDTI NFESTGNLI APEYGFKI SKRGSSGI MK
 TEGTLENCETKCOPLGAI NTTLPFHNVHPLTI GECPKYVKSEKLVLATGLRNVPOI ESRGLFGAI AGFI

EGGWQGMVDGWYGYHHSNDQGSYAADKESTQKAFDGI TNKVNSVI EKMNTQFEAVGKEFSNLERRLENL
 NKKMEDGFLDVWTYNAELLVLMENERTLDFHDSNVKNLYDKVRMQLRDNVVKELGNGCFEFYHKCDECEMN
 SVKNGTYDYPKYEEESKLRNEI KGVKLSMGMVYQI LAI YATVAGSLSLAI MMAGI SFWMCSNGSLOCRI
 CI

>gi |133753657|gb|AB038307.1| hemagglutinin [Influenza A virus
 (A/AI bany/26/1957 (H2N2))]

MAI I YLI LLFTA VRGDQI CI GYHANNSTEKVDTI LERNVTVTHAKDI LEKTHNGKLCCKLNGI PPLELGDC
 SI AGWLLGNPECDRLLSVPEWSYI MEKENPRDGLCYPGSFNDYEELKHLSSVKHFKEVKI LPKDRWTOH
 TTTGGSRAVAVSGNPSFFRNMMVWLTKKGSNYPVAKGSYNNTSGEOMLI I WGVHHPNDETEQRTLYQNVGT
 YVSVGTSTLNKRSTPDI ATRPKVNGLGGRMEFSWTLLDMWDTI NFESTGNLI APEYGFKI SKRGSSGI MK
 TEGTLGNCETKCOPLGAI NTTLPFHNVHPLTI GECPKYVKSEKLVLATGLRNVPOI ESRGLFGAI AGFI
 EGGWQGMVDGWYGYHHSNDQGSYAADKESTQKAFDGI TNKVNSVI EKMNTQFEAVGKEFSNLERRLENL
 NKKMEDGFLDVWTYNAELLVLMENERTLDFHDSNVKNLYDKVRMQLRDNVVKELGNGCFEFYHKCDECEMN
 SVKNGTYDYPKYEEESKLRNEI KGVKLSMGMVYQI LAI YATVAGSLSLAI MMAGI SFWMCSNGSLOCRI
 CI

>gi |133752958|gb|AB038098.1| hemagglutinin [Influenza A virus
 (A/AI bany/2/1958 (H2N2))]

MAI I YLI LLFTA VRGDQI CI GYHANNSTEKVDTI LERNVTVTHAKDI LEKTHNGKLCCKLNGI PPLELGDC
 SI AGWLLGNPECDRLLSVPEWSYI MEKENPRDGLCYPGSFNDYEELKHLSSVKHFKEVKI LPKDRWTOH
 TTTGGSRAVAVSGNPSFFRNMMVWLTKKGSNYPVAKGSYNNTSGEOMLI I WGVHHPNDETEQRTLYQNVGT
 YVSVGTSTLNKRSTPDI ATRPKVNGLGGRMEFSWTLLDMWDTI NFESTGNLI APEYGFKI SKRGSSGI MK
 TEGTLGNCETKCOPLGAI NTTLPFHNVHPLTI GECPKYVKSEKLVLATGLRNVPOI ESRGLFGAI AGFI
 EGGWQGMVDGWYGYHHSNDQGSYAADKESTQKAFDGI TNKVNSVI EKMNTQFEAVGKEFSNLERRLENL
 NKKMEDGFLDVWTYNAELLVLMENERTLDFHDSNVKNLYDKVRMQLRDNVVKELGNGCFEFYHKCDECEMN
 SVKNGTYDYPKYEEESKLRNEI KGVKLSMGMVYQI LAI YATVAGSLSLAI MMAGI SFWMCSNGSLOCRI
 CI

>gi |133753638|gb|AB038296.1| hemagglutinin [Influenza A virus
 (A/AI bany/4/1958 (H2N2))]

MVI I YLI LLFTA VRGDQI CI GYHANNSTEKVDTI LERNVTVTHAKDI LEKTHNGKLCCKLNGI PPLELGDC
 SI AGWLLGNPECDRLLSVPEWSYI MEKENPRDGLCYPGSFNDYEELKHLSSVKHFKEVKI LPKDRWTOH
 TTTGGSRAVAVSGNPSFFRNMMVWLTKKGSNYPVAKGSYNNTSGEOMLI I WGVHHPNDETEQRTLYQNVGT
 YVSVGTSTLNKRSTPDI ATRPKVNGLGGRMEFSWTLLDMWDTI NFESTGNLI APEYGFKI SKRGSSGI MK
 TEGTLGNCETKCOPLGAI NTTLPFHNVHPLTI GECPKYVKSEKLVLATGLRNVPOI ESRGLFGAI AGFI
 EGGWQGMVDGWYGYHHSNDQGSYAADKESTQKAFDGI TNKVNSVI EKMNTQFEAVGKEFSNLERRLENL
 NKKMEDGFLDVWTYNAELLVLMENERTLDFHDSNVKNLYDKVRMQLRDNVVKELGNGCFEFYHKCDECEMN
 SVKNGTYDYPKYEEESKLRNEI KGVKLSMGMVYQI LAI YATVAGSLSLAI MMAGI SFWMCSNGSLOCRI
 CI

>gi |134047523|gb|AB052302.1| hemagglutinin [Influenza A virus
 (A/AI bany/3/1958 (H2N2))]

MAI I YLI LLFTA VRGDQI CI GYHANNSTEKVDTI LERNVTVTHAKDI LEKTHNGKLCCKLNGI PPLELGDC
 SI AGWLLGNPECDRLLSVPEWSYI MEKENPRDGLCYPGSFNDYEELKHLSSVKHFKEVKI LPKDRWTOH
 TTTGGSRAVAVSGNPSFFRNMMVWLTKKGSNYPVAKGSYNNTSGEOMLI I WGVHHPNDETEQRTLYQNVGT
 YVSVGTSTLNKRSTPDI ATRPKVNGLGGRMEFSWTLLDMWDTI NFESTGNLI APEYGFKI SKRGSSGI MK
 TEGTLGNCETKCOPLGAI NTTLPFHNVHPLTI GECPKYVKSEKLVLATGLRNVPOI ESRGLFGAI AGFI
 EGGWQGMVDGWYGYHHSNDQGSYAADKESTQKAFDGI TNKVNSVI EKMNTQFEAVGKEFSNLERRLENL
 NKKMEDGFLDVWTYNAELLVLMENERTLDFHDSNVKNLYDKVRMQLRDNVVKELGNGCFEFYHKCDECEMN
 SVKNGTYDYPKYEEESKLRNEI KGVKLSMGMVYQI LAI YATVAGSLSLAI MMAGI SFWMCSNGSLOCRI
 CI

>gi |145279000|gb|ABP49437.1| hemagglutinin [Influenza A virus
 (A/AI bany/24/1958 (H2N2))]

MAI I YLI LLFTA VRGDQI CI GYHANNSTEKVDTI LERNVTVTHAKDI LEKTHNGKLCCKLNGI PPLELGDC
 SI AGWLLGNPECDRLLSVPEWSYI MEKENPRDGLCYPGSFNDYEELKHLSSVKHFKEVKI LPKDRWTOH
 TTTGGSRAVAVSGNPSFFRNMMVWLTKKGSNYPVAKGSYNNTSGEOMLI I WGVHHPNDETEQRTLYQNVGT
 YVSVGTSTLNKRSTPDI ATRPKVNGLGGRMEFSWTLLDMWDTI NFESTGNLI APEYGFKI SKRGSSGI MK
 TEGTLENCEKCOPLGAI NTTLPFHNVHPLTI GECPKYVKSEKLVLATGLRNVPOI ESRGLFGAI AGFI
 EGGWQGMVDGWYGYHHSNDQGSYAADKESTQKAFDGI TNKVNSVI EKMNTQFEAVGKEFSNLERRLENL
 NKKMEDGFLDVWTYNAELLVLMENERTLDFHDSNVKNLYDKVRMQLRDNVVKELGNGCFEFYHKCDECEMN
 SVKNGTYDYPKYEEESKLRNEI KGVKLSMGMVYQI LAI YATVAGSLSLAI MMAGI SFWMCSNGSLOCRI
 CI

>gi |145279057|gb|ABP49470.1| hemagglutinin [Influenza A virus
 (A/AI bany/1/1958 (H2N2))]

MAI I YLI LLFTA VRGDQI CI GYHANNSTEKVDTI LERNVTVTHAKDI LEKTHNGKLCCKLNGI PPLELGDC
 SI AGWLLGNPECDRLLSVPEWSYI MEKENPRDGLCYPGSFNDYEELKHLSSVKHFKEVKI LPKDRWTOH
 TTTGGSRAVAVSGNPSFFRNMMVWLTKKGSNYPVAKGSYNNTSGEOMLI I WGVHHPNDETEQRTLYQNVGT
 YVSVGTSTLNKRSTPDI ATRPKVNGLGGRMEFSWTLLDMWDTI NFESTGNLI APEYGFKI SKRGSSGI MK
 TEGTLGNCETKCOPLGAI NTTLPFHNVHPLTI GECPKYVKSEKLVLATGLRNVPOI ESRGLFGAI AGFI
 EGGWQGMVDGWYGYHHSNDQGSYAADKESTQKAFDGI TNKVNSVI EKMNTQFEAVGKEFSNLERRLENL
 NKKMEDGFLDVWTYNAELLVLMENERTLDFHDSNVKNLYDKVRMQLRDNVVKELGNGCFEFYHKCDECEMN
 SVKNGTYDYPKYEEESKLRNEI KGVKLSMGMVYQI LAI YATVAGSLSLAI MMAGI SFWMCSNGSLOCRI
 CI

>gi |134047408|gb|AB052236.1| hemagglutinin [Influenza A virus
 (A/AI bany/5/1958 (H2N2))]

MAI I YLI LLFTA VRGDQI CI GYHANNSTEKVDTI LERNVTVTHAKDI LEKTHNGKLCCKLNGI PPLELGDC
 SI AGWLLGNPECDRLLSVPEWSYI MEKENPRDGLCYPGSFNDYEELKHLSSVKHFKEVKI LPKDRWTOH
 TTTGGSRAVAVSGNPSFFRNMMVWLTKKGSNYPVAKGSYNNTSGEOMLI I WGVHHPNDETEQRTLYQNVGT
 YVSVGTSTLNKRSTPDI ATRPKVNGLGGRMEFSWTLLDMWDTI NFESTGNLI APEYGFKI SKRGSSGI MK
 TEGTLGNCETKCOPLGAI NTTLPFHNVHPLTI GECPKYVKSEKLVLATGLRNVPOI ESRGLFGAI AGFI

EGGWQGMVDGWYGYHHSNDQGSYAADKESTQKAFDGI TNKVNSVI EKMNTQFEAVGKEFSNLERRLENL
 NKKMEDGFLDVWTYNAELLVLMENERTLDFHDSNVKNLYDKVRMQLRDNVAKELGNGCFEFYHKCDECEMN
 SVKNGTYDYPKYEEESKLRNEI KGVKLSMGMVYQI LAI YATVAGSLSLAI MMAGI SFWMCSNGSLQCRI
 CI
 >gi |408525|gb|AAA43248.1| hemagglutinin [Influenza A virus (A/Krasnodar/101/59
 (H2N2))]
 MAI I YLI LLFTA VRG DQI CI GYHANNSTEKVDTI LERNVTVTHAKDI LEKTHNGKLCCKLNGI PPLELGDC
 SI AGWLLGNPECDRLLSVPEWSYI MEKENPRDGLCYPGSFNDYEELKHLSSVKHFKEVKI LPKDRWTOH
 TTTGGSRACAVSGNPSFFRNMMVWLTQKGSNYPVAKGSYNNTSGEOMLI I WGVHHPNDETEQRTLYQNVGT
 YVSVGTSTLNKRSTPDI ATRPKVNGQGRMEFSWTLDMWDTI NFESTGNLI APEYGFKI SKRGSSGI MK
 TEGTLENCETKCOQPLGAI NTTLPFHNVHPLTI GECPKYVKSEKLVLATGLRNVPOI ESRGLFGAI AGFI
 EGGWQGMVDGWYGYHHSNDQGSYAADKESTQKAFDGI TNKVNSVI EKMNTQFEAVGKEFSNLERRLENL
 NKKMEDGFLDVWTYNAELLVLMENERTLDFHDSNVKNLYDKVRMQLRDNVAKELGNGCFEFYHKCDECEMN
 SVKNGTYDYPKYEEESKLRNEI KGVKLSMGMVYQI LAI YATVAGSLSLAI MMAGI SFWMCSNGSLQCRI
 CI
 >gi |189230461|gb|ACD85209.1| hemagglutinin [Influenza A virus
 (A/Krasnodar/101/1959(H2N2))]
 MAI I YLI LLFTA VRG DQI CI GYHANNSTEKVDTI LERNVTVTHAKDI LEKTHNGKLCCKLNGI PPLELGDC
 SI AGWLLGNPECDRLLSVPEWSYI MEKENPRDGLCYPGSFNDYEELKHLSSVKHFKEVKI LPKDRWTOH
 TTTGGSRACAVSGNPSFFRNMMVWLTQKGSNYPVAKGSYNNTSGEOMLI I WGVHHPNDETEQRTLYQNVGT
 YVSVGTSTLNKRSTPDI ATRPKVNGQGRMEFSWTLDMWDTI NFESTGNLI APEYGFKI SKRGSSGI MK
 TEGTLENCETKCOQPLGAI NTTLPFHNVHPLTI GECPKYVKSEKLVLATGLRNVPOI ESRGLFGAI AGFI
 EGGWQGMVDGWYGYHHSNDQGSYAADKESTQKAFDGI TNKVNSVI EKMNTQFEAVGKEFSNLERRLENL
 NKKMEDGFLDVWTYNAELLVLMENERTLDFHDSNVKNLYDKVRMQLRDNVAKELGNGCFEFYHKCDECEMN
 SVKNGTYDYPKYEEESKLRNEI KGVKLSMGMVYQI LAI YATVAGSLSLAI MMAGI SFWMCSNGSLQCRI
 CI
 >gi |133982551|gb|AB044090.1| hemagglutinin [Influenza A virus
 (A/AI bany/1/1959(H2N2))]
 MAI I YLI LLFTA VRG DQI CI GYHANNSTEKVDTI LERNVTVTHAKDI LEKTHNGKLCCKLNGI PPLELGDC
 SI AGWLLGNPECDRLLRVPEWSYI MEKENPRDGLCYPGSFNDYEELKHLSSVKHFKEVKI LPKDRWTOH
 TTTGGSRACAVSGNPSFFRNMI WLTQKGSNYPVAKGSYNNTSGEOMLI I WGVHHPNDETEQRTLYQNVGT
 YVSVVTSTLNKRSTPKI ATRPKVNGLGRMEFSWTLDMWDTI NFESTGNLI APEYGFKI SKRGSSGI MK
 TEGTLENCETKCOQPLGAI NTTLPFHNVHPLTI GECPKYVKSEKLVLATGLRNVPOI ESRGLFGAI AGFI
 EGGWQGMVDGWYGYHHSNDQGSYAADKESTQKAFDGI TNKVNSVI EKMNTQFEAVGKEFSNLERRLENL
 NKKMEDGFLDVWTYNAELLVLMENERTLDFHDSNVKNLYDKVRMQLRDNVAKELGNGCFEFYHKCDECEMN
 SVKNGTYDYPKYEEESKLRNEI KGVKLSMGMVYQI LAI YATVAGSLSLAI MMAGI SFWMCSNGSLQCRI
 CI
 >gi |146133810|gb|ABQ01355.1| hemagglutinin [Influenza A virus
 (A/AI bany/1/1960(H2N2))]
 MAI I YLI LLFTA VRG DQI CI GYHANNSTEKVDTI LERNVTVTHAKDI LEKTHNGKLCCKLNGI PPLELGDC
 SI AGWLLGNPECDRLLRVPEWSYI MEKENPRDGLCYPGSFNDYEELKHLSSVKHFKEVKI LPKDRWTOH
 TTTGGSRACAVSGNPSFFRNMI WLTQKGSNYPVAKGSYNNTSGEOMLI I WGVHHPNDETEQRTLYQNVGT
 YVSVVTSTLNKRSTPKI ATRPKVNGLGRMEFSWTLDMWDTI NFESTGNLI APEYGFKI SKRGSSGI MK
 TEGTLENCETKCOQPLGAI NTTLPFHNVHPLTI GECPKYVKSEKLVLATGLRNVPOI ESRGLFGAI AGFI
 EGGWQGMVDGWYGYHHSNDQGSYAADKESTQKAFDGI TNKVNSVI EKMNTQFEAVGKEFSNLERRLENL
 NKKMEDGFLDVWTYNAELLVLMENERTLDFHDSNVKNLYDKVRMQLRDNVAKELGNGCFEFYHKCDECEMN
 SVKNGTYDYPKYEEESKLRNEI KGVKLSMGMVYQI LAI YATVAGSLSLAI MMAGI SFWMCSNGSLQCRI
 CI
 >gi |189230480|gb|ACD85220.1| hemagglutinin [Influenza A virus
 (A/Cottbus/1/1964(H2N2))]
 MAI I YLI LLFTA VRG DQI CI GYHANNSTEKVDTI LERNVTVTHAKDI LEKTHNGKLCCKLNGI PPLELGDC
 SI AGWLLGNPECDRLLRVPEWSYI MEKENPKYSLCYPGSFNDYEELKHLSSVKHFKEVKI LPKDRWTOH
 TTTGGSKACAVSGEPSFFRNMMVWLTQKGNYPVAKGSYNNTSGEOMLI I WGVHHPKDEAEORALYQNVGT
 YVSASTSTLNKRSTPEI AARPEVNGLGRMEFSWTLDMWDTI NFESTGNLVAPEYGFKI SKRGSSGI MK
 TEGTLGNCETKCOQPLGAI NTTLPFHNVHPLTI GECPKYVKSEKLVLATGLRNVPOI ESRGLFGAI AGFI
 EGGWQGMVDGWYGYHHSNDQGSYAADKESTQKAFDGI TNKVNSVI EKMNTQFEAVGKEFNLEKRLLENL
 NKKMEDGFLDVWTYNAELLVLMENERTLDFHDSNVKNLYDKVRMQLRDNVAKELGNGCFEFYHKCDECEMN
 SVKNGTYDYPKYEKESKLRNEI KGVKLSMGMVYQI LAI YATVAGSLSLAI MMAGI SFWMCSNGSLQCRI
 CI
 >gi |94481532|gb|ABF21275.1| hemagglutinin [Influenza A virus (A/Tai wan/1964(H2N2))]
 MAI I YLI LLFTA VRG DQI CI GYHANNSTEKVDTI LERNVTVTHAKDI LEKTHNGKLCCKLNGI PPLELGDC
 SI AGWLLGNPECDRLLRVPEWSYI MEKENPRYSLCYPGSFNDYEELKHLSSVKHFKEVKI LPKDRWTOH
 TTTGGSMACAVSGKPSFFRNMMVWLTQKGNYPVAKGSYNNTSGEOMLI I WGVHHPNDEAEORALYQNVGT
 YVSASTSTLNKRSTPEI AARPKVNGLGRMEFSWTLDMWDTI NFESTGNLVAPEYGFKI SKRGSSGI MK
 TEGTLENCETKCOQPLGAI NTTLPFHNVHPLTI GECPKYVKSEKLVLATGLRNVPOI ESRGLFGAI AGFI
 EGGWQGMVDGWYGYHHSNDQGSYAADKESTQKAFDGI TNKVNSVI EKMNTQFEAVGKEFSNLEKRLLENL
 NKKMEDGFLDVWTYNAELLVLMENERTLDFHDSNVKNLYDKVRMQLRDNVAKELGNGCFEFYHKCDECEMN
 SVKNGTYDYPKYEEESKLRNEI KGVKLSMGMVYQI LAI YATVAGSLSLAI MMAGI SFWMCSNGSLQCRI
 CI
 >gi |408515|gb|AAA43090.1| hemagglutinin [Influenza A virus (A/Berlin/3/64 (H2N2))]
 MAI I YLI LLFTA VRG DQI CI GYHANNSTEKVDTI LERNVTVTHAKDI LEKTHNGKLCCKLNGI PPLELGDC
 SI AGWLLGNPECDRLLSVPEWSYI MEKENPRYSLCYPGSFNDYEELKHLSSVKHFKEVKI LPKDRWTOH
 TTTGGSQACAVSGKPSFFRNMMVWLTQKGNYPVAKGSYNNTSGEOMLI I WGVHHPNDEAEORALYQNVGT
 YVSEATSTLNKRSTPEI AARPKVSGLGRMEFSWTLDMWDTI SFESTGNLI APEYGFKI SKRGSSGI MK
 TEGTLENCETKCOQPLGAI NTTLPFHNVHPLTI GECPKYVKSEKLVLATGLRNVPOI ESRGLFGAI AGFI
 EGGWQGMVDGWYGYHHSNDQGSYAADKESTQKAFDGI TNKVNSVI EKMNTQFEAVGKEFNLEKRLLENL
 NKKMEDGFLDVWTYNAELLVLMENERTLDFHDSNVKNLYDKVRMQLRDNVAKELGNGCFEFYHKCDECEMN

SVKNGTYDYPKYEESKLRNREI KGVKLSMGGVYQI LAI YATVAGSLSLAI MMAGI SFWMCSNGSLOCRICI

>gi |189230423|gb|ACD85187.1| hemagglutinin [Influenza A virus (A/Berlin/3/1964 (H2N2))]

MAI I YLI LLFTA VRGDI CI GYHANNSTEKVDTI LERNVTVTHAKDI LEKTHNGKLCCKLNGI PPLELGDC SI AGWLLGNPECDRLLRVPEWSYI MEKENPRYS LCYPGSFNDYEELKHL LSSVKHF EKVKI LPKDRWTOH TTTGGSKACAVSGKPSFFRNMVWLTKKGPYPVAKGSYNNTSGEOMLI I WGVHHPKDEAEQRALYQEVGT YVSASTSTLNKRSTPEI AARPEVNGLSRMEFSWTL LDVWDTI NFESTGNLVAPEYGFKI SKRGSSGI MK TEGTLGNCETKQCOTPLGAI NTTLPFHNVHPLTI GECPKYVKSEKLVLATGLRNVPOI ESRGLFGAI AGFI EGGWQGMVDGWYGYHHSNDQSGYAADKESTQKAFDGI TNKVN SVI EKMNTQFEAVGKEFSNLEKRENL NKKMEDGFLDVWTYNAELLVLMENERTLDFHDSNVKNLYDKVRMQLRDNVKELGNGCFEFYHKCDDCECMN SVKNGTYDYPKYEESKLRNREI KGVKLSMGGVYQI LAI YATVAGSLSLAI MMAGI SFWMCSNGSLOCRICI

>gi |189230442|gb|ACD85198.1| hemagglutinin [Influenza A virus (A/Potsdam/2/1965 (H2N2))]

MAI I YLI LLFTA VRGDI CI GYHANNSTEKVDTI LERNVTVTHAKDI LEKTHNGKLCCKLNGI PPLELGDC SI AGWLLGNPECDRLLRVPEWSYI MEKENPRYS LCYPGSFNDYEELKHL LSSVKHF EKVKI LPKDGWTOH TTTGGSKACAVSGKPSFFRNMVWLTKKGPYPVAKRSYNNTSGEOMLI I WGVHHPDDEAEQRALYQEVGT YVSASTSTLNKRSTPEI AARPEVNGLSRMEFSWTL LDVWDTI NFESTGNLVAPEYGFKI SKRGSSGI MK TEGTLGNCETKQCOTPLGAI NTTLPFHNVHPLTI GECPKYVKSEKLVLATGLRNVPOI ESRGLFGAI AGFI EGGWQGMVDGWYGYHHSNDQSGYAADKESTQKAFDGI TNKVN SVI EKMNTQFEAVGKEFSNLEKRENL NKKMEDGFLDVWTYNAELLVLMENERTLDFHDSNVKNLYDKVRMQLRDNVKELGNGCFEFYHKCDDCECMN SVKNGTYDYPKYEESKLRNREI KGVKLSMGGVYQI LAI YATVAGSLSLAI MMAGI SFWMCSNGSLOCRICI

>gi |188504407|gb|ACD56324.1| hemagglutinin [Influenza A virus (A/Moscow/1019/1965 (H2N2))]

MAI I YLI LLFTA VRGDI CI GYHANNSTEKVDTI LERNVTVTHAKNI LEKTHNGRLCKLNGI PPLELGDC SI AGWLLGNPECDRLLRVPEWSYI MEKENPRNGLCYPGSFNDYEELKHL LSSVKHF EKVRI LPKDRWTOH TTTGSSRACAVSGNPSFFRNMVWLTKKESNYPVAKGSYNNTSGEOMLI I WGVHHPIDEAEQRALYQEVGT YVSASTSTLNKRSTPDI ATRPKVNGLSRMEFSWTL LDVWDTI NFESTGNLI APEYGFKI SKRGSSGI MK TERTLENCETKQCOTPLGAI NTTLPFHNVHPLTI GECPKYVKSEKLVLATGLRNVPOI EPRGLFGAI AGFI EGGWQGMVDGWYGYHHSNDQSGYAADKESTQKAFDGI TNKVN SVI EKMNTQFEAVGKEFSNLEKRENL NKKMEDGFLDVWTYNAELLVLMENERTLDFHDSNVKNLYDKVRMQLRDNVKELGNGCFEFYHKCDDCECMN SVKNGTYDYPKYEESKLRNREI KGVKLSMGGVYQI LAI YATVAGSLSLAI MMAGI SFWMCSNGSLOCRICI

>gi |221326|dbj|BAA02774.1| hemagglutinin [Influenza A virus (A/Izumi/5/65 (H2N2))]

MAI I YLI LLFTA VRGDI CI GYHANNSTEKVDTI LERNVTVTHAKDI LEKTHNGKLCCKLNGI PPLELGDC SI AGWLLGNPECDRLLRVPEWSYI MEKENPRYS LCYPGNFNDYEELKHL LSSVKHF EKVKI LPKDRWTOH TTTGGSKACAVSGKPSFFRNMVWLTKKGPYPVAKGSYNNTSGEOMLI I WGVHHPNDEAEQRALYQEVGT YVSASTSTLNKRSI PEI AARPKVNGLSRMEFSWTL LDVWDTI NFESTGNLVAPEYGFKI SKRGSSGI MK TEGTLGNCETKQCOTPLGAI NTTLPFHNVHPLTI GECPKYVKSEKLVLATGLRNVPOI ESRGLFGAI AGFI EGGWQGMVDGWYGYHHSNDQSGYAADKESTQKAFDGI TNKVN SVI EKMNTQFEAVGKEFSNLEKRENL NKKMEDGFLDVWTYNAELLVLMENERTLDFHDSNVKNLYDKVRMQLRDNVKELGNGCFEFYHKCDDCECMN SVKNGTYDYPKYEESKLRNREI KGVKLSMGGVYQI LAI YATVAGSLSLAI MMAGI SFWMCSNGSLOCRICI

>gi |221324|dbj|BAA02775.1| hemagglutinin [Influenza A virus (A/Izumi/5/65 (R) (H2N2))]

MAI I YLI LLFTA VRGDI CI GYHANNSTEKVDTI LERNVTVTHAKDI LEKTHNGKLCCKLNGI PPLELGDC SI AGWLLGNPECDRLLRVPEWSYI MEKENPRYS LCYPGNFNDYEELKHL LSSVKHF EKVKI LPKDRWTOH TTTGGSKACAVSGKPSFFRNMVWLTKKGPYPVAKGSYNNTSGEOMLI I WGVHHPNDEAEQRALYQEVGT YVSASTSTLNKRSI PEI AARPKVNGLSRMEFSWTL LDVWDTI NFESTGNLVAPEYGFKI SKRGSSGI MK TEGTLGNCETKQCOTPLGAI NTTLPFHNVHPLTI GECPKYVKSEKLVLATGLRNVPOI ESRGLFGAI AGFI EGGWQGMVDGWYGYHHSNDQSGYAADKESTQKAFDGI TNKVN SVI EKMNTQFEAVGKEFSNLEKRENL NKKMEDGFLDVWTYNAELLVLMENERTLDFHDSNVKNLYDKVRMQLRDNVKELGNGCFEFYHKCDDCECMN SVKNGTYDYPKYEESKLRNREI KGVKLSMGGVYQI LAI YATVAGSLSLAI MMAGI SFWMCSNGSLOCRICI

>gi |133755366|gb|AB038701.1| hemagglutinin [Influenza A virus (A/AI bany/6/1967 (H2N2))]

MAI I YFI LLFTA VRGDI CI GYHANNSTEKVDTI LERNVTVTHAKDI LEKTHNGKLCCKLNGI PPLELGDC SI AGWLLGNPECDRLLRVPEWSYI MEKENPRYS LCYPGSFNDYEELKHL LSSVKHF EKVRI LPKDGWTOH TTTGGSKACAVSGKSSFFRNMVWLTKKGPYPVAKRSYNNTSGEOMLI I WGVHHPKDEAEQRALYQKVGTYVSASTSTLNKRSTPEI AARPEVNGLSRMEFSWTL LDVWDTI NFESTGNLVAPEYGFKI SKRGSSGI MK TEGTLGNCETKQCOTPLGAI NTTLPFHNVHPLTI GECPKYVKSEKLVLATGLRNVPOI ESRGLFGAI AGFI EGGWQGMVDGWYGYHHSNDQSGYAADKESTQKAFDGI TNKVN SVI EKMNTQFEAVGKEFSNLEKRENL NKKMEDGFLDVWTYNAELLVLMENERTLDFHDSNVKNLYDKVRMQLRDNVKELGNGCFEFYHKCDDCECMS SVKNGTYDYPKYEESKLRNREI KGVKLSMGGVYQI LAI YATVAGSLSLAI MI AGI SLWMCNSNGSLOCRICI

>gi |133755385|gb|AB038712.1| hemagglutinin [Influenza A virus (A/AI bany/7/1967 (H2N2))]

MAI I YFI LLFTA VRGDI CI GYHANNSTEKVDTI LERNVTVTHAKDI LEKTHNGKLCCKLNGI PPLELGDC SI AGWLLGNPECDRLLRVPEWSYI MEKENPRYS LCYPGSFNDYEELKHL LSSVKHF EKVRI LPKDGWTOH TTSGGSKACAVSGKSSFFRNMVWLTKKGPYPVAKRSYNNTSGEOMLI I WGVHHPKDEAEQRALYQKVGTYVSASTSTLNKRSTPEI AARPEVNGLSRMEFSWTL LDVWDTI NFESTGNLVAPEYGFKI SKRGSSGI MK TEGTLGNCETKQCOTPLGAI NTTLPFHNVHPLTI GECPKYVKSEKLVLATGLRNVPOI ESRGLFGAI AGFI EGGWQGMVDGWYGYHHSNDQSGYAADKESTQKAFDGI TNKVN SVI EKMNTQFEAVGKEFSNLEKRENL NKKMEDGFLDVWTYNAELLVLMENERTLDFHDSNVKNLYDKVRMQLRDNVKELGNGCFEFYHKCDDCECMS SVKNGTYDYPKYEESKLRNREI KGVKLSMGGVYQI LAI YATVAGSLSLAI MI AGI SLWMCNSNGSLOCRICI

>gi |133755404|gb|AB038723.1| hemagglutinin [Influenza A virus (A/AI bany/3/1967(H2N2))]
 MAI I YFI LLFTA VRGDQI CI GYHANNSTEKVDTI LERNVTVTHAKDI LEKTHNGKLCCKLNGI PPLELGDC SI AGWLLGNPECDRLLRVPEWSYI MEKENPRYSLCYPGSFNDYEELKHLSSVKHFKEVRI LPKDGWTOH TTSGGSKACAVSGKSSFFRNMVWLT KKGPNYPVAKRSYNNTSGEOMLI I WGVHHPNDEAEQALYQKVGTT TSGGSKACAVSGKSSFFRNMVWLT KKGPNYPVAKRSYNNTSGEOMLI I WGVHHPNDEAEQALYQKVGTT YVSASTSTLNKRSTPEI AARPEVNGLSRMEFSWTLLDWDWTI NFESTGNLVAPEYGFKI SKRGSSGI MK TEGTLGNCETKQCOTPLGAI NTTLPFHNVHPLTI GECPKYVKSEKLVLATGLRNVPOI ESRGLFGAI AGFI EGGWQGMVDGWYGYHHSNDQGSYAADKESTQKAFDRI TNKVN SVI EKMNTQFEAVGKEFSNLEKRLNENL NKKMEDGFLDVWTYNAELLVLMENERTLDFHDSNVKNLYKVRMQLRDNVVKELGNGCFEFYHKCDDECMN SVKNGTYDYPKYEEESKLRNEI KGVKLSMGMVYQI LAI YATVAGSLSLAI MI AGI SLWMCSNGSLQCRICI

>gi |146760028|gb|AB044438.1| hemagglutinin [Influenza A virus (A/AI bany/4/1967(H2N2))]
 MAI I YFI LLFTA VRGDQI CI GYHANNSTEKVDTI LERNVTVTHAKDI LEKTHNGKLCCKLNGI PPLELGDC SI TGWLLGNPECDRLLRVPEWSYI MEKENPRYSLCYPGSFNDYEELKHLSSVKHFKEVRI LPKDGWTOH TTSGGSKACAVSGKSSFFRNMVWLT KKGPNYPVAKRSYNNTSGEOMLI I WGVHHPNDEAEQALYQKVGTT YVSASTSTLNKRSTPEI AARPEVNGLSRMEFSWTLLDWDWTI NFESTGNLVAPEYGFKI SKRGSSGI MK TEGTLGNCETKQCOTPLGAI NTTLPFHNVHPLTI GECPKYVKSEKLVLATGLRNVPOI ESRGLFGAI AGFI EGGWQGMVDGWYGYHHSNDQGSYAADKESTQKAFDRI TNKVN SVI EKMNTQFEAVGKEFSNLEKRLNENL NKKMEDGFLDVWTYNAELLVLMENERTLDFHDSNVKNLYKVRMQLRDNVVKELGNGCFEFYHKCDDECMN SVKNGTYDYPKYEEESKLRNEI KGVKLSMGMVYQI LAI YATVAGSLSLAI MI AGI SLWMCSNGSLQCRICI

>gi |133982571|gb|AB044101.1| hemagglutinin [Influenza A virus (A/AI bany/8/1967(H2N2))]
 MAI I YLI LLFTA VRGDQI CI GYHANNSTEKVDTI LERNVTVTHAKDI LEKTHNGKLCCKLNGI PPLELGDC SI AGWLLGNPECDRLLRVPEWSYI MEKENPRYSLCYPGSFNDYEELKHLSSVKHFKEVRI LPKDGWTOH TTDGGSKACAVSGKSSFFRNMVWLT KKGPNYPVAKRSYNNTSGEOMLI I WGVHHPNDEAEQALYQKVGTT YVSASTSTLNKRSTPEI AARPEVNGLSRMEFSWTLLDWDWTI SFESTGNLVAPEYGFKI SKRGSSGI MK TEGTLGNCETKQCOTPLGAI NTTLPFHNVHPLTI GECPKYVKSEKLVLATGLRNVPOI ESRGLFGAI AGFI EGGWQGMVDGWYGYHHSNDQGSYAADKESTQKAFDRI TNKVN SVI EKMNTQFEAVGKEFSNLEKRLNENL NKKMEDGFLDVWTYNAELLVLMENERTLDFHDSNVKNLYDKVRMQLRDNVVKELGNGCFEFYHKCDDECMN SVKNGTYDYPKYEEESKLRNEI KGVKLSMGMVYQI LAI YATVAGSLSLAI MI AGI SFWMCSNGSLQCRICI

>gi |133981962|gb|AB044057.1| hemagglutinin [Influenza A virus (A/AI bany/9/1967(H2N2))]
 MAI I YLI LLFTA VRGDQI CI GYHANNSTEKVDTI LERNVTVTHAKDI LEKTHNGKLCCKLNGI PPLELGDC SI AGWLLGNPECDRLLRVPEWSYI MEKENPRYSLCYPGSFNDYEELKHLSSVKHFKEVRI LPKDGWTOH YTDGGSKACAVSGKSSFFRNMVWLT KKGPNYPVAKRSYNNTSGEOMLI I WGVHHPNDEAEQALYQKVGTT YVSASTSTLNKRSTPEI AARPEVNGLSRMEFSWTLLDWDWTI NFESTGNLVAPEYGFKI SKRGSSGI MK TEGTLGNCETKQCOTPLGAI NTTLPFHNVHPLTI GECPKYVKSEKLVLATGLRNVPOI ESRGLFGAI AGFI EGGWQGMVDGWYGYHHSNDQGSYAADKESTQKAFDRI TNKVN SVI EKMNTQFEAVGKEFSNLEKRLNENL NKKMEDGFLDVWTYNAELLVLMENERTLDFHDSNVKNLYDKVRMQLRDNVVKELGNGCFEFYHKCDDECMN SVKNGTYDYPKYEEESKLRNEI KGVKLSMGMVYQI LAI YATVAGSLSLAI MI AGI SFWMCSNGSLQCRICI

>gi |189230518|gb|ACD85242.1| hemagglutinin [Influenza A virus (A/Tashkent/1046/1967(H2N2))]
 MAI I YLI LLFATVRGDQI CI GYHANNSTEKVDTI LERNVTVTHAKDI LEKTHNGKLCCKLNGI PPLELGDC SI AGWLLGNPECDRLLRVPEWSYI MEKENPRYSLCYPGSLNDYEELKHLSSVKHFKEVRI LPKDRWTOH TTTGGSKACAVSGKSSFFRNMVWLT KKGPNYPVAKRSYNNTSGEOMLI I WGVHHPNDEAEQALYQKVGTT YVSASTSTLNKRSTPEI AARPEVNGLSRMEFSWTLLDWDWTI NFESTGNLVAPEYGFKI SKRGSSGI MK TEGTLGNCETKQCOTPLGAI NTTLPFHNVHPLTI GECPKYVKSEKLVLATGLRNVPOI ESRGLFGAI AGFI EGGWQGMVDGWYGYHHSNDQGSYAADKESTQKAFDRI TNKVN SVI EKMNTQFEAVGKEFSNLEKRLNENL NKKMEDGFLDVWTYNAELLVLMENERTLDFHDSNVKNLYDKVRMQLRDNVVKELGNGCFEFYHKCDDECMN SVKNGTYDYPKYEEESKLRNEI KGVKLSMGMVYQI LAI YATVAGSLSLAI MVAGI SFWMCSNGSLQCRICI

>gi |189230537|gb|ACD85253.1| hemagglutinin [Influenza A virus (A/Johannesburg/617/1967(H2N2))]
 MAI I YLI LLFATVRGDQI CI GYHANNSTEKVDTI LERNVTVTHAKDI LEKTHNGKLCCKLNGI PPLELGDC SI AGWLLGNPECDRLLRVPEWSYI MEKENPRYSLCYPGSLNDYEELKHLSSVKHFKEVRI LPKDRWTOH TTTGGSKACAVSGKSSFFRNMVWLT KKGPNYPVAKRSYNNTSGEOMLI I WGVHHPNDEAEQALYQKVGTT YVSASTSTLNKRSTPEI AARPEVNGLSRMEFSWTLLDWDWTI NFESTGNLVAPEYGFKI SKRGSSGI MK TEGTLGNCETKQCOTPLGAI NTTLPFHNVHPLTI GECPKYVKSEKLVLATGLRNVPOI ESRGLFGAI AGFI EGGWQGMVDGWYGYHHSNDQGSYAADKESTQKAFDRI TNKVN SVI EKMNTQFEAVGKEFSNLEKRLNENL NKKMEDGFLDVWTYNAELLVLMENERTLDFHDSNVKNLYDKVRMQLRDNVVKELGNGCFEFYHKCDDECMN SVKNGTYDYPKYEEESKLRNEI KGVKLSMGMVYQI LAI YATVAGSLSLAI MVAGI SFWMCSNGSLQCRICI

>gi |194351979|gb|ACF54389.1| hemagglutinin [Influenza A virus (A/Georgi a/1/1967(H2N2))]
 MAI I YLI LLFATVRGDQI CI GYHANNSTEKVDTI LERNVTVTHAKDI LEKTHNGKLCCKLNGI PPLELGDC SI AGWLLGNPECDRLLRVPEWSYI MEKENPRYSLCYPGSLNDYEELKHLSSVKHFKEVRI LPKDRWTOH TTTGGSKACAVSGKSSFFRNMVWLT KKGPNYPVAKRSYNNTSGEOMLI I WGVHHPNDEAEQALYQKVGTT YVSASTSTLNKRSTPEI AARPEVNGLSRMEFSWTLLDWDWTI NFESTGNLVAPEYGFKI SKRGSSGI MK TEGTLGNCETKQCOTPLGAI NTTLPFHNVHPLTI GECPKYVKSEKLVLATGLRNVPOI ESRGLFGAI AGFI EGGWQGMVDGWYGYHHSNDQGSYAADKESTQKAFDRI TNKVN SVI EKMNTQFEAVGKEFSNLEKRLNENL NKKMEDGFLDVWTYNAELLVLMENERTLDFHDSNVKNLYDKVRMQLRDNVVKELGNGCFEFYHKCDDECMN SVKNGTYDYPKYEEESKLRNEI KGVKLSMGMVYQI LAI YATVAGSLSLAI MVAGI SFWMCSNGSLQCRICI

>gi|408523|gb|AAA43247.1| hemagglutinin [Influenza A virus (A/Korea/426/68 (H2N2))] MAI I YLI LLFTA VRG DQI CI GYHANNSTEKVDTI LERNVTVTHAKDI LEKTHNGKLCCKLNGI PPLELGDC SI AGWLLGNPECDRLLRVP EWSYI MEKENPRYS LCYPGSFNDYEELKHL LSSVKHF EKVKI LPKDRWTOH TTTGGSWACAVSGKPSFFRNMVWL TRKGSNYPVAKGSYNTSGEOMLI I WGVHHPNDEAEQRALYQNVGT YVSVATSTLYKR SI PEI AARPKVNGLGRRMEFSWTL LDMWDTI NFESTGNLVAPEYGFKI SKRGSSGI MK TEGTLENCETK CQTPLGAI NTTLPFHNVHPLTI GECPKYVKSEKLV L ATGLRNVPOI ESRGLFGAI AGFI EGGWQGMVDGWYGYHHSNDQGSYAADK ESTQKAFNGI TNKVN SVI EKMNTQFEAVGKEFSNLEKRL ENL NKKMEDGFLDVWTYNAELLVLMENERTLDFHDSNVKNLYDKVRMQLRDNV KELGNGCFEFYHKCDNECMD SVKNGTYDYPKYEEESKLNRNEI KGVKLSMGMVYQI LAI YATVAGSLSLAI MMAGI SFWMCSNGSLQCR I CI

>gi|408513|gb|AAA43089.1| hemagglutinin [Influenza A virus (A/Berkeley/1/68 (H2N2))] MAI I YLI LLFTA VRG DQI CI GYHANNSTEKVDTI LERNVTVTHAKDI LEKTHNGKLCCKLNGI PPLELGDC SI AGWLLGNPECDRLLRVP EWSYI MEKENPRYS LCYPGSFNDYEELKHL LSSVKHF EKVKI LPKDGWTOH ETTGGSKACAVSGKPSFFRNMVWL TTKGPNYPVAKGSYNTSGEOMLI I WGVHHPNDEAEQRALYQEVGT YGSEATSTLNKRSTPEI AARPKVSGLGRMEFSWTL LDMWDTI SFESTGNLVAPEYGFKI SKRGSSGI MK TEGTLENCETK CQTPLGAI NTTLPFHNVHPLTI GECPKYVKSEKLV L ATGLRNVPOI ESRGLFGAI AGFI EGGWQGMVDGWYGYHHSNDQGSYAADK ESTQKAFDGI TNKVN SVI EKMNTQFEAVGKEFSNLEKRL ENL NKKMEDGFLDVWTYNAELLVLMENERTLDFHDSNVKNLYDKVRMQLRDNV KELGNGCFEFYHKCDNECMD SVKNGTYDYPKYEEESKLNRNEI KGVKLSMGMVYQI LAI YATVAGSLSLAI MI AGI SFWMCSNGSLQCR I CI

>gi|194304556|gb|ACF41691.1| hemagglutinin [Influenza A virus (A/Berkeley/1/1968 (H2N2))] MAI I YLI LLFTA VRG DQI CI GYHANNSTEKVDTI LERNVTVTHAKDI LEKTHNGKLCCKLNGI PPLELGDC SI AGWLLGNPECDRLLRVP EWSYI MEKENPRYS LCYPGSFNDYEELKHL LSSVKHF EKVKI LPKDGWTOH ETDGGSKACAVSGKPSFFRNMVWL TTKGPNYPVAKRSYNTSGEOMLI I WGVHHPNDEAEQRALYQEVGT YVSASTSTLNKRSTPEI AARPKVSGLGRMEFSWTL LDMWDTI SFESTGNLVAPEYGFKI SKRGSSGI MK TEGTLENCETK CQTPLGAI NTTLPFHNVHPLTI GECPKYVKSEKLV L ATGLRNVPOI ESRGLFGAI AGFI EGGWQGMVDGWYGYHHSNDQGSYAADK ESTQKAFDRI TNKVN SVI EKMNTQFEAVGKEFSNLEKRL ENL NKKMEDGFLDVWTYNAELLVLMENERTLDFHDSNVKNLYDKVRMQLRDNV KELGNGCFEFYHKCDNECMD SVKNGTYDYPKYEEESKLNRNEI KGVKLSMGMVYQI LAI YATVAGSLSLAI MI AGI SFWMCSNGSLQCR I CI

>gi|134047427|gb|AB052247.1| hemagglutinin [Influenza A virus (A/AI bany/1/1968 (H2N2))] MAI I YLI LLFTA VRG DQI CI GYHANNSTEKVDTI LERNVTVTHAKDI LEKTHNGKLCCKLNGI PPLELGDC SI AGWLLGNPECDRLLRVP EWSYI MEKENPRYS LCYPGSFNDYEELKHL LSSVKHF EKVKI LPKDGWTOH KTDGGSKACAVSGKPSFFRNMVWL TTKGPNYPVAKRSYNTSGEOMLI I WGVHHPNDEAEQRALYQEVGT YVSASTSTLNKRSTPEI AARPEVSGLGRMEFSWTL LDMWDTI SFESTGNLVAPEYGFKI SKRGSSGI MK TEGTLENCETK CQTPLGAI NTTLPFHNVHPLTI GECPKYVKSEKLV L ATGPRNVPOI ESRGLFGAI AGFI EGGWQGMVDGWYGYHHSNDQGSYAADK ESTQKAFDRI TNKVN SVI EKMNTQFEAVGKEFSNLEKRL ENL NKKMEDGFLDVWTYNAELLVLMENERTLDFHDSNVKNLYDKVRMQLRDNV KELGNGCFEFYHKCDNECMD SVKNGTYDYPKYEEESKLNRNEI KGVKLSMGMVYQI LAI YATVAGSLSLAI MI AGI SFWMCSNGSLQCR I CI

>gi|188504369|gb|ACD56302.1| hemagglutinin [Influenza A virus (A/North Carolina/1/1968 (H2N2))] MAI I YLI LLFTA VRG DQI CI GYHANNSTEKVDTI LERNVTVTHAKDI LEKTHNGKLCCKLNGI PPLELGDC SI AGWLLGNPECDRLLRVP EWSYI MEKENPKYS LCYPGSFNDYEELKHL LSSVKHF EKVKI LPKDRWTOH TTTGGSRACAVSGNPSFFRNMVWL TTKGPNYPVAKGSYNTSGEOMLI I WGVHHPNDEAEQRALYQKVG T YVSASTSTLNKRSTPEI AARPEVNGLGRMEFSWTL LDMWDTI NFESTGNLVAPEYGFKI SKRGSSGI MK TEGTLENCETK CQTPLGAI NTTLPFHNVHPLTI GECPKYVKSEKLV L ATGLRNVPOI ESRGLFGAI AGFI EGGWQGMVDGWYGYHHSNDQGSYAADK ESTQKAFDGI TNKVN SVI EKMNTQFEAVGKEFSNLEKRL ENL NKKMEDGFLDVWTYNAELLVLMENERTLDFHDSNVKNLYDKVRMQLRDNV KELGNGCFEFYHKCDNECMD SVKNGTYDYPKYEEESKLNRNEI KGVKLSMGMVYQI LAI YATVAGSLSLAI MMAGI SFWMCSNGSLQCR I CI

>gi|188504388|gb|ACD56313.1| hemagglutinin [Influenza A virus (A/Korea/426/1968 (H2N2))] MAI I YLI LLFTA VRG DQI CI GYHANNSTEKVDTI LERNVTVTHAKDI LEKTHNGKLCCKLNGI PPLELGDC SI AGWLLGNPECDRLLRVP EWSYI MEKENPRYS LCYPGSFNDYEELKHL LSSVKHF EKVKI LPKDRWTOH TTTGGSMACAVSGKPSFFRNMVWL TTKGPNYPVAGGSYNTSGEOMLI I WGVHHPNDEAEQRALYQKVG T YVSASTSTLYKR SI PEI AARPKVNGLGRRMEFSWTL LDMWDTI NFESTGNLVAPEYGFKI SKRGSSGI MK TEGTLENCETK CQTPLGAI NTTLPFHNVHPLTI GECPKYVKSEKLV L ATGLRNVPOI ESRGLFGAI AGFI EGGWQGMVDGWYGYHHSNDQGSYAADK ESTQKAFDGI TNKVN SVI EKMNTQFEAVGKEFSNLEKRL ENL NKKMEDGFLDVWTYNAELLVLMENERTLDFHDSNVKNLYDKVRMQLRDNV KELGNGCFEFYHKCDNECMD SVKNGTYDYPKYEEESKLNRNEI KGVKLSMGMVYQI LAI YATVAGSLSLAI MMAGI SFWMCSNGSLQCR I CI

>gi|133755423|gb|AB038734.1| hemagglutinin [Influenza A virus (A/AI bany/2/1968 (H2N2))] MAI I YLI LLFTA VRG DQI CI GYHANNSTEKVDTI LERNVTVTHAKDI LEKTHNGKLCCKLNGI PPLELGDC SI AGWLLGNPECDRLLRVP EWSYI MEKENPRYS LCYPGSFNDYEELKHL LSSVKHF EKVKI LPKDGWTOH KTDGGSKACAVSGKPSFFRNMVWL TTKGPNYPVAKRSYNTSGEOMLI I WGVHHPNDEAEQRALYQKVG T YVSASTSTLNKRSTPEI AARPEVSGLGRMEFSWTL LDMWDTI SFESTGNLVAPEYGFKI SKRGSSGI MK TEGTLENCETK CQTPLGAI NTTLPFHNVHPLTI GECPKYVKSEKLV L ATGLRNVPOI ESRGLFGAI AGFI EGGWQGMVDGWYGYHHSNDQGSYAADK ESTQKAFDRI TNKVN SVI EKMNTQFEAVGKEFSNLEKRL ENL NKKMEDGFLDVWTYNAELLVLMENERTLDFHDSNVKNLYDKVRMQLRDNV KELGNGCFEFYHKCDNECMD SVKNGTYDYPKYEEESKLNRNEI KGVKLSMGMVYQI LAI YATVAGSLSLAI MI AGI SFWMCSNGSLQCR I CI

>gi|63054902|gb|AAY28987.1| hemagglutinin [Influenza A virus (A/Canada/720/05 (H2N2))] MAI I YLI LLFTA VRG DQI CI GYHANNSTEKVDTI LERNVTVTHAKDI LEKTHNGKLCCKLNGI PPLELGDC

SI AGWLLGNPECDRLLSVPEWSYI MEKENPRDGLCYPGSFNDYEELKHLSSVKHFVKI LPKDRWTOH
 TTTGGSRAVSGNPSFFRNMVWLTKKGSNYPVAQGSYNNTSGEOMLI I WGVHHPNDETEQRTLYQNVGT
 YVSVGTSTLNKRSTPEI ATRPKVNGOQGRMEFSWTLDDMDDTI NFESTGNLI APEYGFKI SKRGSSGI MK
 TEGTLENCETKCOPLGAI NTTLPFHNVHPLTI GECPKYVKSEKLVLATGLRNVPOI ESRGLFGAI AGFI
 EGGWQGMVDGWYGYHHSNDQGSYAADKSTQKAFDGI TNKVNSVI EKMNTQFEAVGKEFSNLERRLENL
 NKKMEDGFLDVWTYNAELLVLMENERTLDFHDSNVKNLYDKVRMQLRDNVVKELGNGCFEYHKCDDECMN
 SVKNGTYDYPKYEEESKLRNREI KGVKLSMGMVYQI LAI YATVAGSLSLAI MMAGI SFWMCSNGSLOCRI
 CI

H3N2

>gi|85816052|gb|ABC84389.1| hemagglutinin [Influenza A virus (A/Beijing/1/68(H3N2))]
 MKTI I ALSYI FCLALGQDLPGNDNSTATLCLGHHAVPNGTLVKTI TDDQI EVTNATELVQSSSTGKI CNN
 PHRI LDGI DCTLI DALLGDPHCDVFNQNETWDLFVERSKAFSNCYPYDVPDYASLRSLVASSGTLEFI TEG
 FTWTGVTONGGSNACKRGPVSGGFFSRLNWLTKSGSTYPVLNVTMPNNDNFDKLYI WGVHHPSTNOEQTSL
 YVQASGRVTVSTRRSQQT I PNI GSRPWVVRGLSSRI SI YWTI VKPGDVLVI NSNGNLI APRGYFKMRTGK
 SSI MRSDAPI DTCI SECI TPNGSI PNDKPFQNVNKI TYGACPKYVKQNTLKLATGMRNVPEKQTRGLFGA
 I AGFI ENGWEEMI DGWYGFRRHQNSEGTGOAADLKSTQAAI DOI NGKLN RVI EKTNEKFHQI EKEFSEVEG
 RI ODLEKYVEDTKI DLWSYNAELLVALENOHTI DLTDSEMKNLFEKTRRQLRENAEDMNGGCFKI YHKCD
 NACI ESI RNGTHYDHDVYRDEALNRRFOI KGVELKSGYKDWI LWI SFAI SCFLLCVVLLGFI MWACQRGNI
 RCNI CI

>gi|80977928|gb|ABB54514.1| hemagglutinin [Influenza A virus (A/Memphis/1/68(H3N2))]
 MKTI I ALSYI FCLALGQDLPGNDNSTATLCLGHHAVPNGTLVKTI TDDQI EVTNATELVQSSSTGKI CNN
 PHRI LDGI NCTLI DALLGDPHCDVFNQNETWDLFVERSKAFSNCYPYDVPDYASLRSLVASSGTLEFI TEG
 FTWTGVTONGGSNACKRGPVSGGFFSRLNWLTKSGSTYPVLNVTMPNNDNFDKLYI WGVHHPSTNOEQTSL
 YVQASGRVTVSTRRSQQT I PNI GSRPWVVRGLSSRI SI YWTI VKPGDVLVI NSNGNLI APRGYFKMRTGK
 SSI MRSDAPI DTCI SECI TPNGSI PNDKPFQNVNKI TYGACPKYVKQNTLKLATGMRNVPEKQTRGLFGA
 I AGFI ENGWEEMI DGWYGFRRHQNSEGTGOAADLKSTQAAI DOI NGKLN RVI EKTNEKFHQI EKEFSEVEG
 RI ODLEKYVEDTKI DLWSYNAELLVALENOHTI DLTDSEMKNLFEKTRRQLRENAEDMNGGCFKI YHKCD
 NACI ESI RNGTHYDHDVYRDEALNRRFOI KGVELKSGYKDWI LWI SFAI SCFLLCVVLLGFI MWACQRGNI
 RCNI CI

>gi|193805114|gb|ACF22210.1| hemagglutinin [Influenza A virus (A/Hong Kong/1-
 1/1968(H3N2))]

MKTI I ALSYI FCLALGQDLPGNDNSTATLCLGHHAVPNGTLVKTI TDDQI EVTNATELVQSSSTGKI CNN
 PHRI LDGI DCTLI DALLGDPHCDVFNQNETWDLFVERSKAFSNCYPYDVPDYASLRSLVASSGTLEFI TEG
 FTWTGVTONGGSNACKRGPVSGGFFSRLNWLTKSGSTYPVLNVTMPNNDNFDKLYI WGVHHPSTNOEQTSL
 YVQASGRVTVSTRRSQQT I PNI GSRPWVVRGLSSRI SI YWTI VKPGDVLVI NSNGNLI APRGYFKMRTGK
 SSI MRSDAPI DTCI SECI TPNGSI PNDKPFQNVNKI TYGACPKYVKQNTLKLATGMRNVPEKQTRGLFGA
 I AGFI ENGWEEMI DGWYGFRRHQNSEGTGOAADLKSTQAAI DOI NGKLN RVI EKTNEKFHQI EKEFSEVEG
 RI ODLEKYVEDTKI DLWSYNAELLVALENOHTI DLTDSEMKNLFEKTRRQLRENAEDMNGGCFKI YHKCD
 NACI ESI RNGTHYDHDVYRDEALNRRFOI KGVELKSGYKDWI LWI SFAI SCFLLCVVLLGFI MWACQRGNI
 RCNI CI

>gi|193805171|gb|ACF22243.1| hemagglutinin [Influenza A virus (A/Hong Kong/1-
 5/1968(H3N2))]

MKTI I ALSYI FCLALGQDLPGNDNSTATLCLGHHAVPNGTLVKTI TDDQI EVTNATELVQSSSTGKI CNN
 PHRI LDGI DCTLI DALLGDPHCDVFNQNETWDLFVERSKAFSNCYPYDVPDYASLRSLVASSGTLEFI TEG
 FTWTGVTONGGSNACKRGPVSGGFFSRLNWLTKSGSTYPVLNVTMPNNDNFDKLYI WGVHHPSTNOEQTSL
 YVQASGRVTVSTRRSQQT I PNI GSRPWVVRGLSSRI SI YWTI VKPGDVLVI NSNGNLI APRGYFKMRTGK
 SSI MRSDAPI DTCI SECI TPNGSI PNDKPFQNVNKI TYGACPKYVKQNTLKLATGMRNVPEKQTRGLFGA
 I AGFI ENGWEEMI DGWYGFRRHQNSEGTGOAADLKSTQAAI DOI NGKLN RVI EKTNEKFHQI EKEFSEVEG
 RI ODLEKYVEDTKI DLWSYNAELLVALENOHTI DLTDSEMKNLFEKTRRQLRENAEDMNGGCFKI YHKCD
 NACI ESI RNGTHYDHDVYRDEALNRRFOI KGVELKSGYKDWI LWI SFAI SCFLLCVVLLGFI MWACQRGNI
 RCNI CI

>gi|193805209|gb|ACF22265.1| hemagglutinin [Influenza A virus (A/Hong Kong/1-
 7/1968(H3N2))]

MKTI I ALSYI FCLALGQDLPGNDNSTATLCLGHHAVPNGTLVKTI TDDQI EVTNATELVQSSSTGKI CNN
 PHRI LDGI DCTLI DALLGDPHCDVFNQNETWDLFVERSKAFSNCYPYDVPDYASLRSLVASSGTLEFI TEG
 FTWTGVTONGGSNACKRGPVSGGFFSRLNWLTKSGSTYPVLNVTMPNNDNFDKLYI WGVHHPSTNOEQTSL
 YVQASGRVTVSTRRSQQT I PNI GSRPWVVRGLSSRI SI YWTI VKPGDVLVI NSNGNLI APRGYFKMRTGK
 SSI MRSDAPI DTCI SECI TPNGSI PNDKPFQNVNKI TYGACPKYVKQNTLKLATGMRNVPEKQTRGLFGA
 I AGFI ENGWEEMI DGWYGFRRHQNSEGTGOAADLKSTQAAI DOI NGKLN RVI EKTNEKFHQI EKEFSEVEG
 RI ODLEKYVEDTKI DLWSYNAELLVALENOHTI DLTDSEMKNLFEKTRRQLRENAEDMNGGCFKI YHKCD
 NACI ESI RNGTHYDHDVYRDEALNRRFOI KGVELKSGYKDWI LWI SFAI SCFLLCVVLLGFI MWACQRGNI
 RCNI CI

>gi|148628604|gb|ABQ97200.1| hemagglutinin [Influenza A virus (A/Hong Kong/68(H3N2))]

MKTI I ALSYI FCLALGQDLPGNDNSTATLCLGHHAVPNGTLVKTI TDDQI EVTNATELVQSSSTGKI CNN
 PHRI LDGI DCTLI DALLGDPHCDVFNQNETWDLFVERSKAFSNCYPYDVPDYASLRSLVASSGTLEFI TEG
 FTWTGVTONGGSNACKRGPVSGGFFSRLNWLTKSGSTYPVLNVTMPNNDNFDKLYI WGVHHPSTNOEQTSL
 YVQASGRVTVSTRRSQQT I PNI GSRPWVVRGLSSRI SI YWTI VKPGDVLVI NSNGNLI APRGYFKMRTGK
 SSI MRSDAPI DTCI SECI TPNGSI PNDKPFQNVNKI TYGACPKYVKQNTLKLATGMRNVPEKQTRGLFGA
 I AGFI ENGWEEMI DGWYGFRRHQNSEGTGOAADLKSTQAAI DOI NGKLN RVI EKTNEKFHQI EKEFSEVEG
 RI ODLEKYVEDTKI DLWSYNAELLVALENOHTI DLTDSEMKNLFEKTRRQLRENAEDMNGGCFKI YHKCD
 NACI ESI RNGTHYDHDVYRDEALNRRFOI KGVELKSGYKDWI LWI SFAI SCFLLCVVLLGFI MWACQRGNI
 RCNI CI

>gi|194304746|gb|ACF41801.1| hemagglutinin [Influenza A virus (A/Hong Kong/1-11-MA21-
 3/1968(H3N2))]

MKTI I ALSYI FCLALGQDLPGNDNSTATLCLGHHAVPNGTLVKTI TDDQI EVTNATELVQSSSTGKI CNN

PHRI LDGI DCTLI DALLGDPHCDVFNQETWDLFVERSKAFSNCYPYDVPDYASLRSLVASSGTLEFI TEG
 FTWTGVTQNGGSNACKRGPSSGFFSRLNWLTKSGSTYPVLNVTMPNNDNFDKLYI WGVHHPSTNOEQTSL
 YVQASGRVTVSTRRSQQT I PNI GSRPWVWVRLSSRI SI YWTI VKPGDVLVI NSNGNLI APRGYFKMRTGK
 SSI MRSDAPI DTCI SECI TPNGSI PNDKPFQNVNKI TYGACPKYVKQNTLKLATGMRNVPEKQTRGLFGA
 I AGFI ENGWEGMI DGWYGFRHQNSEGTGOAADLKSTQAAI DOI NGKLNRLI EKTNEKFHAI KEFSEVEG
 RI QDLEKYVEDTKI DLWSYNAELLVALENOHTI DLTDSEMKNLFEKTRROLRENAEDMNGGCFKI YHKCD
 NACI ESI RINGTYDHDVYRDEALNNRFOI KGVELKSGYKDWI LWI SFAI SCFLLCVVLLGFI MWACQKGN
 RCNI CI
 >gi |106907813|gb|ABF83447.1| hemagglutinin [Influenza A virus (A/Northern
 Territory/60/1968(H3N2))]
 MKTI I ALSYI FCLALGQDLPGNDNSTATLCLGHHAVPNTLVKTI TDDQI EVTNATELVQSSSTGKI CNN
 PHRI LDGI DCTLI DALLGDPHCDVFNQETWDLFVERSKAFSNCYPYDVPDYASLRSLVASSGTLEFI TEG
 FTWTGVTQNGGSNACKRGPSSGFFSRLNWLTKSGSTYPVLNVTMPNNDNFDKLYI WGVHHPSTNOEQTSL
 YVQASGVTVSTRRSQQT I PNI GSRPWVWVRLSSRI SI YWTI VKPGDVLVI NSNGNLI APRGYFKMRTGK
 SSI MRSDAPI DTCI SECI TPNGSI PNDKPFQNVNKI TYGACPKYVKQNTLKLATGMRNVPEKQTRGLFGA
 I AGFI ENGWEGMI DGWYGFRHQNSEGTGOAADLKSTQAAI DOI NGKLNRLI EKTNEKFHAI KEFSEVEG
 RI QDLEKYVEDTKI DLWSYNAELLVALENOHTI DLTDSEMKNLFEKTRROLRENAEDMNGGCFKI YHKCD
 NACI ESI RINGTYDHDVYRDEALNNRFOI KGVELKSGYKDWI LWI SFAI SCFLLCVVLLGFI MWACQKGN
 RCNI CI
 >gi |145279136|gb|ABP49514.1| hemagglutinin [Influenza A virus
 (A/AI bany/10/1968(H3N2))]
 MKTI I ALSYI FYLALGQDLPGNDNSTATLCLGHHAVPNTLVKTI TNDQI EVTNATELVQSSSTGKI CNN
 PHRI LDGI DCTLI DALLGDPHCDVFNQETWDLFVERSKAFSNCYPYDVPDYASLRSLVASSGTLEFI TEG
 FTWTGVTQNGGSNACKRGPSSGFFSRLNWLTKSGSTYPVLNVTMPNNDNFDKLYI WGVHHPSTNOEQTSL
 YVQASGRVTVSTRRSQQT I PNI GSRPWVWVRLSSRI SI YWTI VKPGDVLVI NSNGNLI APRGYFKMRTGK
 SSI MRSDAPI DTCI SECI TPNGSI PNDKPFQNVNKI TYGACPKYVKQNTLKLATGMRNVPEKQTRGLFGA
 I AGFI ENGWEGMI DGWYGFRHQNSEGTGOAADLKSTQAAI DOI NGKLNRLI EKTNEKFHAI KEFSEVEG
 RI QDLEKYVEDTKI DLWSYNAELLVALENOHTI DLTDSEMKNLFEKTRROLRENAEDMNGGCFKI YHKCD
 NACI ESI RINGTYDHDVYRDEALNNRFOI KGVELKSGYKDWI LWI SFAI SCFLLCVVLLGFI MWACQKGN
 RCNI CI
 >gi |194294011|gb|ACF40100.1| hemagglutinin [Influenza A virus
 (A/Oregon/01/2008(H3N2))]
 MKTI I ALSYI LCLVFAQKFPNGDNSTATLCLGHHAVPNTLVKTI TNDQI EVTNATELVQSSSTGEI CDS
 PHAI LDGENCTLI DALLGDPQCDGFQNKNDLWDLFVERSKAYSNCYPYDVPDYASLRSLVASSGTLEFNNE
 FNWTGVTQNGTSSACI RRSNNSFFSRLNWLTHSKFKYPALNVTMPNNEFDKLYI WGVHHPGTDNDQI FL
 YAQASGRI TVSTKRSQQTVI PNI GSRPRVRNI PSRI SI YWTI VKPGDI LLI NSTGNLI APRGYFKI RSGK
 SSI MRSDAPI GKCNSCI TPNGSI PNDKPFQNVNRI TYGACPRYVKQNTLKLATGMRNVPEKQTRGI FGA
 I AGFI ENGWEGMVDGWYGFRHQNSEGI GOAADLKSTQAAI DOI NGKLNRLI GKTNEKFHAI KEFSEVEG
 RI QDLEKYVEDTKI DLWSYNAELLVALENOHTI DLTDSEMKNLFEKTKKQLRENAEDMNGGCFKI YHKCD
 NACI GSI RINGTYDHDVYRDEALNNRFOI KGVELKSGYKDWI LWI SFAI SCFLLCVVLLGFI MWACQKGN
 RCNI CI
 >gi |194580029|gb|ACF75879.1| hemagglutinin [Influenza A virus
 (A/FI ori da/14/2008(H3N2))]
 MKTI I ALSYI LCLVFAQKLPNGDNSTATLCLGHHAVPNTLVKTI TNDQI EVTNATELVQSSSTGEI CDS
 PHAI LDGENCTLI DALLGDPQCDGFQNKNDLWDLFVERSKAYSNCYPYDVPDYASLRSLVASSGTLEFNNE
 FNWTGVTQNGTSSACI RRSNNSFFSRLNWLTHLKFYKYPALNVTMPNNEFDKLYI WGVHHPGTDNDQI FL
 YAQASGRI TVSTKRSQQTVI PNI GSRPRVRNI PSRI SI YWTI VKPGDI LLI NSTGNLI APRGYFKI RSGK
 SSI MRSDAPI GKCNSCI TPNGSI PNDKPFQNVNRI TYGACPRYVKQNTLKLATGMRNVPEKQTRGI FGA
 I AGFI ENGWEGMVDGWYGFRHQNSEGI GOAADLKSTQAAI DOI NGKLNRLI GKTNEKFHAI KEFSEVEG
 RI QDLEKYVEDTKI DLWSYNAELLVALENOHTI DLTDSEMKNLFEKTKKQLRENAEDMNGGCFKI YHKCD
 NACI GSI RINGTYDHDVYRDEALNNRFOI KGVELKSGYKDWI LWI SFAI SCFLLCVVLLGFI MWACQKGN
 RCNI CI
 >gi |189303163|gb|ACD85638.1| hemagglutinin [Influenza A virus
 (A/Texas/05/2008(H3N2))]
 MKTI I ALSYI LCLVFAQKFPNGDNSTATLCLGHHAVPNTLVKTI TNDQI EVTNATELVQSSSTGEI CDS
 PHAI LDGENCTLI DALLGDPQCDGFQNKNDLWDLFVERSKAYSNCYPYDVPDYASLRSLVASSGTLEFNNE
 FNWTGVTQNGTSSACI RRSNNSFFSRLNWLTHLKFYKYPALNVTMPNNEFDKLYI WGVHHPGTDNDQI FL
 YAQASGRI TVSTKRSQQTVI PNI GSRPRVRNI PSRI SI YWTI VKPGDI LLI NSTGNLI APRGYFKI RSGK
 SSI MRSDAPI GKCNSCI TPNGSI PNDKPFQNVNRI TYGACPRYVKQNTLKLATGMRNVPEKQTRGI FGA
 I AGFI ENGWEGMVDGWYGFRHQNSEGI GOAADLKSTQAAI DOI NGKLNRLI GKTNEKFHAI KEFSEVEG
 RI QDLEKYVEDTKI DLWSYNAELLVALENOHTI DLTDSEMKNLFEKTKKQLRENAEDMNGGCFKI YHKCD
 NACI GSI RINGTYDHDVYRDEALNNRFOI KGVELKSGYKDWI LWI SFAI SCFLLCVVLLGFI MWACQKGN
 RCNI CI
 >gi |194293991|gb|ACF40090.1| hemagglutinin [Influenza A virus
 (A/Washington/04/2008(H3N2))]
 MKTI I ALSYI LCLVFAQKLPNGDNSTATLCLGHHAVPNTLVKTI TNDQI EVTNATELVQSSSTGEI CDS
 PHAI LDGENCTLI DALLGDPQCDGFQNKNDLWDLFVERSKAYSNCYPYDVPDYASLRSLVASSGTLEFNNE
 FNWTGVTQNGTSSACI RRSNNSFFSRLNWLTHLKFYKYPALNVTMPNNEFDKLYI WGVHHPGTDNDQI FL
 YAQASGRI TVSTKRSQQTVI PNI GSRPRVRNI PSRI SI YWTI VKPGDI LLI NSTGNLI APRGYFKI RSGK
 SSI MRSDAPI GKCNSCI TPNGSI PNDKPFQNVNRI TYGACPRYVKQNTLKLATGMRNVPEKQTRGI FGA
 I AGFI ENGWEGMVDGWYGFRHQNSEGI GOAADLKSTQAAI DOI NGKLNRLI GKTNEKFHAI KEFSEVEG
 RI QDLEKYVEDTKI DLWSYNAELLVALENOHTI DLTDSEMKNLFEKTKKQLRENAEDMNGGCFKI YHKCD
 NACI GSI RINGTYDHDVYRDEALNNRFOI KGVELKSGYKDWI LWI SFAI SCFLLCVVLLGFI MWACQKGN
 RCNI CI
 >gi |194294015|gb|ACF40102.1| hemagglutinin [Influenza A virus
 (A/Minnesota/06/2008(H3N2))]
 MKTI I ALSYI LCLVFAQKLPNGDNSTATLCLGHHAVPNTLVKTI TNDQI EVTNATELVQSSSTGEI CDS

PHQI LDGENCTLI DALLGDPQCDGFQNKKWDLFVERSKAYSNCYPYDVPDYASLRSLVASSGTLFNNES
 FNWTGVTONGTSSACI RRSNNSFFSRLNWLTHLKFYKYPALNVTMPNNEQFDKLYI WGVHHPGTDNDQI FL
 YAQASGRI TVSTKRSQQTVI PNI GSRPRVRNI PSRI SI YWTI VKPGDI LLI NSTGNLI APRGYFKI RSGK
 SSI MRSDAPI GKCNSECI TPNGSI PNDKPFQNVNRI TYGACPRYVKQNTLKLATGMRNVPEKQTRGI FGA
 I AGFI ENGWEQMGVWDGWYGRHQNSEGRGOAADLKSTQAAI DOI NGKLNRLI GKTNEKFHAI KEFSEVEG
 RI QDLEKYVEDTKI DLWSYNAELLVALENOHTI DLTSEMKNLFEKTKKQLENAEDMNGGCFKI YHKCD
 NACI GSI RINGTYDHDVYRDEALNNRFOI KGVELKSGYKDWI LWI SFAI SCFLLCVALLGFI MWACQKGN
 RCNI CI
 >gi |194293979|gb|ACF40084.1| hemagglutinin [Influenza A virus (A/New
 Jersey/15/2008(H3N2))]
 MKTI I ALSYI LCLVFAQKLPNGDNSTATLCLGHHAVPNGTI VKTI TNDQI EVTNATELVQSSSTGEI CDS
 PHQI LDGENCTLI DALLGDPQCDGFQNKKWDLFVERSKAYSNCYPYDVPDYASLRSLVASSGTLFNNES
 FNWTGVTONGTSSACI RRSNNSFFSRLNWLTHLKFYKYPALNVTMPNNEQFDKLYI WGVHHPGTDNDQI FL
 YAQASGRI TVSTKRSQQTVI PNI RSRPRVRNI PSRI SI YWTI VKPGDI LLI NSTGNLI APRGYFKI RSGK
 SSI MRSDAPI GKCNSECI TPNGSI PNDKPFQNVNRI TYGACPRYVKQNTLKLATGMRNVPEKQTRGI FGA
 I AGFI ENGWEQMGVWDGWYGRHQNSEGI GOAADLKSTQAAI DOI NGKLNRLI GKTNEKFHAI KEFSEVEG
 RI QDLEKYVEDTKI DLWSYNAELLVALENOHTI DLTSEMKNLFEKTKKQLENAEDMNGGCFKI YHKCD
 NACI GSI RINGTYDHDVYRDEALNNRFOI KGVELKSGYKDWI LWI SFAI SCFLLCVALLGFI MWACQKGN
 RCNI CI
 >gi |193084875|gb|ACF10327.1| hemagglutinin [Influenza A virus
 (A/Texas/06/2008(H3N2))]
 MKTI I ALSYI LCLVFAQKLPNGDNSTATLCLGHHAVPNGTI VKTI TNDQI EVTNATELVQSSSTGEI CDS
 PHQI LDGENCTLI DALLGDPQCDGFQNKKWDLFVERSKAYSNCYPYDVPDYASLRSLVASSGTLFNNES
 FNWTGVTONGTSSACI RRSNNSFFSRLNWLTHLKFYKYPALNVTMPNNEQFDKLYI WGVHHPGTDNDQI FL
 YAQASGRI TVSTKRSQQTVI PNI GSRPRVRNI PSRI SI YWTI VKPGDI LLI NSTGNLI APRGYFKI RSGK
 SSI MRSDAPI GKCNSECI TPNGSI PNDKPFQNVNRI TYGACPRYVKQNTLKLATGMRNVPEKQTRGI FGA
 I AGFI ENGWEQMGVWDGWYGRHQNSEGRGOAADLKSTQAAI DOI NGKLNRLI GKTNEKFHAI KEFSEVEG
 RI QDLEKYVEDTKI DLWSYNAELLVALENOHTI DLTSEMKNLFEKTKKQLENAEDMNGGCFKI YHKCD
 NACI GSI RINGTYDHDVYRDEALNNRFOI KGVELKSGYKDWI LWI SFAI SCFLLCVALLGFI MWACQKGN
 RCNI CI
 >gi |194294019|gb|ACF40104.1| hemagglutinin [Influenza A virus
 (A/Minesota/07/2008(H3N2))]
 MKTI I ALSYI LCLVFAQKLPNGDNSTATLCLGHHAVPNGTI VKTI TNDQI EVTNATELVQSSSTGEI CDS
 PHQI LDGENCTLI DALLGDPQCDGFQNKKWDLFVERSKAYSNCYPYDVPDYASLRSLVASSGTLFNNES
 FNWTGVTONGTSSACI RRSNNSFFSRLNWLTHLKFYKYPALNVTMPNNEQFDKLYI WGVHHPGTDNDQI FL
 YAQASGRI TVSTKRSQQTVI PNI XSRPRVRNI PSRI SI YWTI VKPGDI LLI NSTGNLI APRGYFKI RSGK
 SSI MRSDAPI GKCNSECI TPNGSI PNDKPFQNVNRI TYGACPRYVKQNTLKLATGMRNVPEKQTRGI FGA
 I AGFI ENGWEQMGVWDGWYGRHQNSEGRGOAADLKSTQAAI DOI NGKLNRLI GKTNEKFHAI KEFSEVEG
 XI QDLEKYVEDTKI DLWSYNAELLVALENOHTI DLTSEMKNLFEKTKKQLENAEDMNGGCFKI YHKCD
 NACI GSI RINGTYDHDVYRDEALNNRFOI KGVELKSGYKDWI LWI SFAI SCFLLCVALLGFI MWACQKGN
 RCNI CI
 >gi |193084879|gb|ACF10329.1| hemagglutinin [Influenza A virus (A/Iowa/01/2008(H3N2))]
 MKTI I ALSYI LCLVFAQKLPNGDNSTATLCLGHHAVPNGTI VKTI TNDQI EVTNATELVQSSSTGEI CDS
 PHQI LDGENCTLI DALLGDPQCDGFQNKKWDLFVERSKAYSNCYPYDVPDYASLRSLVASSGTLFNNES
 FNWTGVTONGTSSACI RRSNNSFFSRLNWLTHLKFYKYPALNVTMPNNEQFDKLYI WGVHHPGTDNDQI FL
 YAQASGRI TVSTKRSQQTVI PNI GSRPRVRNI PSRI SI YWTI VKPGDI LLI NSTGNLI APRGYFKI RSGK
 SSI MRSDAPI GKCNSECI TPNGSI PNDKPFQNVNRI TYGACPRYVKQNTLKLATGMRNVPEKQTRGI FGA
 I AGFI ENGWEQMGVWDGWYGRHQNSEGRGOAADLKSTQAAI DOI NGKLNRLI GKTNEKFHAI KEFSEVEG
 RI QDLEKYVEDTKI DLWSYNAELLVALENOHTI DLTSEMKNLFEKTKKQLENAEDMNGGCFKI YHKCD
 NACI GSI RINGTYDHDVYRDEALNNRFOI KGVELKSGYKDWI LWI SFAI SCFLLCVALLGFI MWACQKGN
 RCNI CI
 >gi |194294003|gb|ACF40096.1| hemagglutinin [Influenza A virus
 (A/Illinois/09/2008(H3N2))]
 MKTI I ALSYI LCLVFAQKLPNGDNSTATLCLGHHAVPNGTI VKTI TNDQI EVTNATELVQSSSTGEI CDS
 PHQI LDGENCTLI DALLGDPQCDGFQNKKWDLFVERSKAYSNCYPYDVPDYASLRSLVASSGTLFNNES
 FNWTGVTONGTSSACI RRSNNSFFSRLNWLTHLKFYKYPALNVTMPNNEQFDKLYI WGVHHPGTDNDQI FL
 YAQASGRI TVSTKRSQQTVI PNI GSRPRVRNI PSRI SI YWTI VKPGDI LLI NSTGNLI APRGYFKI RSGK
 SSI MRSDAPI GKCNSECI TPNGSI PNDKPFQNVNRI TYGACPRYVKQNTLKLATGMRNVPEKQTRGI FGA
 I AGFI ENGWEQMGVWDGWYGRHQNSEGRGOAADLKSTQAAI DOI NGKLNRLI GKTNEKFHAI KEFSEVEG
 RI QDLEKYVEDTKI DLWSYNAELLVALENOHTI DLTSEMKNLFEKTKKQLENAEDMNGGCFKI YHKCD
 NACI GSI RINGTYDHDVYRDEALNNRFOI KGVELKSGYKDWI LWI SFAI SCFLLCVALLGFI MWACQKGN
 RCNI CI
 >gi |194294007|gb|ACF40098.1| hemagglutinin [Influenza A virus (A/South
 Carolina/03/2008(H3N2))]
 MKTI I ALSYI LCLVFAQKLPNGDNSTATLCLGHHAVPNGTI VKTI TNDQI EVTNATELVQSSSTGEI CDS
 PHQI LDGENCTLI DALLGDPQCDGFQNKKWDLFVERSKAYSNCYPYDVPDYASLRSLVASSGTLFNNES
 FNWTGVTONGTSSACI RRSNNSFFSRLNWLTHLKFYKYPALNVTMPNNEQFDKLYI WGVHHPGTDNDQI FL
 YAQASGRI TVSTKRSQQTVI PNI GSRPRVRNI PSRI SI YWTI VKPGDI LLI NSTGNLI APRGYFKI RSGK
 SSI MRSDAPI GKCNSECI TPNGSI PNDKPFQNVNRI TYGACPRYVKQNTLKLATGMRNVPEKQTRGI FGA
 I AGFI ENGWEQMGVWDGWYGRHQNSEGRGOAADLKSTQAAI DOI NGKLNRLI GKTNEKFHAI KEFSEVEG
 RI QDLEKYVEDTKI DLWSYNAELLVALENOHTI DLTSEMKNLFEKTKKQLENAEDMNGGCFKI YHKCD
 NACI GSI RINGTYDHDVYRDEALNNRFOI KGVELKSGYKDWI LWI SFAI SCFLLCVALLGFI MWACQKGN
 RCNI CI
 >gi |194293983|gb|ACF40086.1| hemagglutinin [Influenza A virus
 (A/Tennessee/04/2008(H3N2))]
 MKTI I ALSYI LCLVFAQKLPNGDNSTATLCLGHHAVPNGTI VKTI TNDQI EVTNATELVQSSSTGEI CDS
 PHQI LDGENCTLI DALLGDPQCDGFQNKKWDLFVERSKAYSNCYPYDVPDYASLRSLVASSGTLFNNES

FNWTVGTONGTSSACI RRSNNSFFSRLNWLTHSKFKYPALNVTMPNDENFDKLYI WGVHHPGTDNDQI FL YAQASGRI TVSTKRSQQTVI PNI GSRPRVRNI PSRI SI YWTI VKPGDI LLI NSTGNLI APRGYFKI RSGK SSI MRSDAPI GKCNSECI TPNGSI PNDKPFQNVNRI TYGACPRYVKQNTLKLATGMRNVPEKQTRGI FGA I AGFI ENGWEWMVDGWYGFRRHQNSEGI GOAADLKSTQAAI DOI NGKLNRLI GKTNEKFHQI KEFSEVEG RI ODLEKYVEDTKI DLWSYNAELLVALENQHTI DLTDSEMKNLFKTKKQLRENAEDMNGGCFKI YHKCD NACI GSI RNGTHYDHDVYRDEALNNRFOI KGVELKSGYKDWI LWI SFAI SCFLLCI ALLGFI MWACQKGN RCNI CI

>gi |193084883|gb|ACF10331.1| hemagglutinin [Influenza A virus (A/Iowa/02/2008(H3N2))]
MKTII ALSYI LCLVFAQKFPNGDNSTATLCLGHHAVPNGTI VKTI TNDQI EVTNATELVQSSSTGEI CDS PHQI LDGENCTLI DALLGDPQCDGFQNKNDLFFVERSKAYSNCYPYDVPDYASLRSLVASSGTLEFNNEF FNWTVGTONGTSSACI RRSNNSFFSRLNWLTHSKFKYPALNVTMPNNEFDKLYI WGI HHPGTDNDQI FL YAQASGRI TVSTKRSQQTVI PNI GSRPRVRNI PSRI SI YWTI VKPGDI LLI NSTGNLI APRGYFKI RSGK SSI MRSDAPI GKCNSECI TPNGSI PNDKPFQNVNRI TYGACPRYVKQNTLKLATGMRNVPEKQTRGI FGA I AGFI ENGWEWMVDGWYGFRRHQNSEGI GOAADLKSTQAAI DOI NGKLNRLI GKTNEKFHQI KEFSEVEG RI ODLEKYVEDTKI DLWSYNAELLVALENQHTI DLTDSEMKNLFKTKKQLRENAEDMNGGCFKI YHKCD NACI GSI RNGTHYDHDVYRDEALNNRFOI KGVELKSGYKDWI LWI SFAI SCFLLCI ALLGFI MWACQKGN RCNI CI

>gi |194293995|gb|ACF40092.1| hemagglutinin [Influenza A virus (A/New Jersey/14/2008(H3N2))]
MKTII ALSYI LCLVFAQKLPNGDNSTATLCLGHHAVPNGTI VKTI TNDQI EVTNATELVQSSSTGEI CDS PHQI LDGENCTLI DALLGDPQCDGFQNKNDLFFVERSKAYSNCYPYDVPDYASLRSLVASSGTLEFNNEF FNWTVGTONGTSSACI RRSNNSFFSRLNWLTHLKFYKYPALNVTMPNNEFDKLYI WGVHHPGTDNDQI FL YAQASGRI TVSTKRSQQTVI PNI GSRPRVRNI PSRI SI YWTI VKPGDI LLI NSTGNLI APRGYFKI RSGK SSI MRSDAPI GKCNSECI TPNGSI PNDKPFQNVNRI TYGACPRYVKQNTLKLATGMRNVPEKQTRGI FGA I AGFI ENGWEWMVDGWYGFRRHQNSEGI GOAADLKSTQAAI DOI NGKLNRLI GKTNEKFHQI KEFSEVEG RI ODLEKYVEDTKI DLWSYNAELLVALENQHTI DLTDSEMKNLFKTKKQLRENAEDMNGGCFKI YHKCD NACI GSI RNGTHYDHDVYRDEALNNRFOI KGVELKSGYKDWI LWI SFAI SCFLLCVALLGFI MWACQKGN RCNI CI

>gi |194294023|gb|ACF40106.1| hemagglutinin [Influenza A virus (A/New York/09/2008(H3N2))]
MKTII ALSYI LCLVFAQKLPNGDNSTATLCLGHHAVPNGTI VKTI TNDQI EVTNATELVQSSSTGEI CDS PHQI LDGENCTLI DALLGDPQCDGFQNKNDLFFVERSKAYSNCYPYDVPDYASLRSLVASSGTLEFNNEF FNWTVGTONGTSSACI RRSNNSFFSRLNWLTHLKFYKYPALNVTMPNNEFDKLYI WGVHHPGTDNDQI FL YAQASGRI TVSTKRSQQTVI PNI GSRPRVRNI PSRI SI YWTI VKPGDI LLI NSTGNLI APRGYFKI RSGK SSI MRSDAPI GKCNSECI TPNGSI PNDKPFQNVNRI TYGACPRYVKQNTLKLATGMRNVPEKQTRGI FGA I AGFI ENGWEWMVDGWYGFRRHQNSEGI GOAADLKSTQAAI DOI NGKLNRLI GKTNEKFHQI KEFSEVEG RI ODLEKYVEDTKI DLWSYNAELLVALENQHTI DLTDSEMKNLFKTKKQLRENAEDMNGGCFKI YHKCD NACI GSI RNGTHYDHDVYRDEALNNRFOI KGVELKSGYKDWI LWI SFAI SCFLLCVALLGFI MWACQKGN RCNI CI

>gi |193805266|gb|ACF22298.1| hemagglutinin [Influenza A virus (A/Hong Kong/1-12/1968(H3N2))]
MKTII ALSYI FCLALGQDLPGNDSTATLCLGHHAVPNGTLVKTI TDDQI EVTNATELVQSSSTGKI CNN PHRI LDGI DCTLI DALLGDPHCDVFNQETWDLFVERSKAFSNCYPYDVPDYASLRSLVASSGTLEFI TEG FTWTVGTONGGSSNACKRGPSSGFFSRLNWLTKSGSTYPVNLVTMPNNDNFDKLYI WGVHHPSTNOEQTSL YVQASGRVTVSTRRSQQTII PNI GSRPWVVRGLSSRI SI YWTI VKPGDVLVI NSNGNLI APRGYFKMRTGK SSI MRSDAPI DTCI SECI TPNGSI PNDKPFQNVNRI TYGACPKYVKQNTLKLATGMRNVPEKQTRGLFGA I AGFI ENGWEWMI DGWYGFRRHQNSEGTGOAADLKSTQAAI DOI NGKLNRLI EKTNEKFHQI KEFSEVEG RI ODLEKYVEDTKI DLWSYNAELLVALENQHTI DLTDSEMKNLFKTRRQLRENAEDMNGGCFKI YHKCD NACI ESI RNGTHYDHDVYRDEALNNRFOI KGVELKSGYKDWI LWI SFAI SCFLLCVVLLGFI MWACQKGN RCNI CI

>gi |60753|emb|CAA24269.1| haemagglutinin [Influenza A virus (A/Aichi/2/68(H3N2))]
MKTII ALSYI FCLALGQDLPGNDSTATLCLGHHAVPNGTLVKTI TDDQI EVTNATELVQSSSTGKI CNN PHRI LDGI DCTLI DALLGDPHCDVFNQETWDLFVERSKAFSNCYPYDVPDYASLRSLVASSGTLEFI TEG FTWTVGTONGGSSNACKRGPSSGFFSRLNWLTKSGSTYPVNLVTMPNNDNFDKLYI WGI HHPSTNOEQTSL YVQASGRVTVSTRRSQQTII PNI GSRPWVVRGLSSRI SI YWTI VKPGDVLVI NSNGNLI APRGYFKMRTGK SSI MRSDAPI DTCI SECI TPNGSI PNDKPFQNVNRI TYGACPKYVKQNTLKLATGMRNVPEKQTRGLFGA I AGFI ENGWEWMI DGWYGFRRHQNSEGTGOAADLKSTQAAI DOI NGKLNRLI EKTNEKFHQI KEFSEVEG RI ODLEKYVEDTKI DLWSYNAELLVALENQHTI DLTDSEMKNLFKTRRQLRENAEDMNGGCFKI YHKCD NACI ESI RNGTHYDHDVYRDEALNNRFOI KGVELKSGYKDWI LWI SFAI SCFLLCVVLLGFI MWACQKGN RCNI CI

>gi |194304632|gb|ACF41735.1| hemagglutinin [Influenza A virus (A/Hong Kong/1-1-MA-12/1968(H3N2))]
MKTII ALSYI FCLALGQDLPGNDSTATLCLGHHAVPNGTLVKTI TDDQI EVTNATELVQSSSTGKI CNN PHRI LDGI DCTLI DALLGDPHCDVFNQETWDLFVERSKAFSNCYPYDVPDYASLRSLVASSGTLEFI TEG FTWTVGTONGGSSNACKRGPSSGFFSRLNWLTKSGSTYPVNLVTMPNNDNFDKLYI WGVHHPSTNOEQTSL YVQASGRVTVSTRRSQQTII PNI WSRPWVVRGLSSRI SI YWTI VKPGDVLVI NSNGNLI APRGYFKMRTGK SSI MRSDAPI DTCI SECI TPNGSI PNDKPFQNVNRI TYGACPKYVKQNTLKLATGMRNVPEKQTRGLFGA I AGFI ENGWEWMI DGWYGFRRHQNSEGTGOAADLKSTQAAI DOI NGKLNRLI EKTNEKFHQI KEFSEVEG RI ODLEKYVEDTKI DLWSYNAELLVALENQHTI DLTDSEMKNLFKTRRQLRENAEDMNGGCFKI YHKCD NACI ESI RNGTHYDHDVYRDEALNNRFOI KGVELKSGYKDWI LWI SFAI SCFLLCVVLLGFI MWACQKGN RCNI CI

>gi |194304670|gb|ACF41757.1| hemagglutinin [Influenza A virus (A/Hong Kong/1-9-MA21-2/1968(H3N2))]
MKTII ALSYI FCLALGQDLPGNDSTATLCLGHHAVPNGTLVKTI TDDQI EVTNATELVQSSSTGKI CNN PHRI LDGI DCTLI DALLGDPHCDVFNQETWDLFVERSKAFSNCYPYDVPDYASLRSLVASSGTLEFI TEG FTWTVGTONGGSSNACKRGPSSGFFSRLNWLTKSGSTYPVNLVTMPNNDNFDKLYI WGVHHPSTNOEQTSL YVQASGRVTVSTRRSQQTII PNI GSRPWVVRGLSSRI SI YWTI VKPGDVLVI NSNGNLI APRGYFKMRTGK

SSI MRSDAPI DTCI SECI TPNGSI PNDKPFQNVNKI TYGACPKYVKQNTLKLATGMRNVPEKQTRGLFGA
I AGFI ENGWEEMI DGWYGFRRHONSEGTGOAADLKSTQAAI DOI NGKLN RVI EKTNEKFHQI EKEFSEVEG
RI ODLEKYVEDTKI DLWSYNAELLVALENQHTI DLTDSEMKNLFKTRRQLRENAEDMNGGCFKI YHKCD
NACI ESI RNGTHYDHDVYRDEALNNRFOI KGVELKSGYKDWI LWI SFAI SCFLLCVVLLGFI MWACQRGNI
RCNI CI

>gi |194352017|gb|ACF54411.1| hemagglutinin [Influenza A virus (A/Hong Kong/1-
8/1968(H3N2))]

MKTI I ALSYI FCLALGQDLPGNDNSTATLCLGHHAVPNGTLVKTI TDDQI EVTNATELVQSSSTGKI CNN
PHRI LDGI DCTLI DALLGDPHCDVFNQETWDLFVERSKAFSNCYPYDVPDYASLRSLVASSGTLEFI TEG
FTWTGVTONGGSNACKRGP GSGFFSRLNWLTKSGSTYPVLNVTMPNNDNFDKLYI WGVHHPSTNQEQTSL
YVQASGRVTVSTRRSQQT I PNI GSRPWVVRGLSSRI SI YWTI VKPGDVLVI NSNGNLI APRGYFKMRTGK
SSI MRSDAPI DTCI SECI TPNGSI PNDKPFQNVNKI TYGACPKYVKQNTLKLATGMRNVPEKQTRGLFGA
I AGFI ENGWEEMI DGWYGFRRHONSEGTGOAADLKSTQAAI DOI NGKLN RVI EKTNEKFHQI EKEFSEVEG
RI ODLEKYVEDTKI DLWSYNAELLVALENQHTI DLTDSEMKNLFKTRRQLRENAEDMNGGCFKI YHKCD
NACI ESI RNGTHYDHDVYRDEALNNRFOI KGVELKSGYKDWI LWI SFAI SCFLLCVVLLGFI MWACQRGNI
RCNI CI

>gi |194352093|gb|ACF54455.1| hemagglutinin [Influenza A virus (A/Hong Kong/1-8-MA21-
3/1968(H3N2))]

MKTI I ALSYI FCLALGQDLPGNDNSTATLCLGHHAVPNGTLVKTI TDDQI EVTNATELVQSSSTGKI CNN
PHRI LDGI DCTLI DALLGDPHCDVFNQETWDLFVERSKAFSNCYPYDVPDYASLRSLVASSGTLEFI TEG
FTWTGVTONGGSNACKRGP GSGFFSRLNWLTKSGSTYPVLNVTMPNNDNFDKLYI WGVHHPSTNQEQTSL
YVQASGRVTVSTRRSQQT I PNI ESRPWVVRGLSSRI SI YWTI VNP GDVLVI NSNGNLI APRGYFKMRTGK
SSI MRSDAPI DTCI SECI TPNGSI PNDKPFQNVNKI TYGACPKYVKQNTLKLATGMRNVPEKQTRGLFGA
I AGFI ENGWEEMI DGWYGFRRHONSEGTGOAADLKSTQAAI DOI NGKLN RVI EKTNEKFHQI EKEFSEVEG
RI ODLEKYVEDTKI DLWSYNAELLVALENQHTI DLTDSEMKNLFKTRRQLRENAEDMNGGCFKI YHKCD
NACI ESI RNGTHYDHDVYRDEALNNRFOI KGVELKSGYKDWI LWI SFAI SCFLLCVVLLGFI MWACQRGNI
RCNI CI

>gi |14009692|gb|AAK51718.1| hemagglutinin [Influenza A virus (A/Hong
Kong/1/68(H3N2))]

MKTI I ALSYI FCLALGQDLPGNDNSTATLCLGHHAVPNGTLVKTI TDDQI EVTNATELVQSSSTGKI CNN
PHRI LDGI DCTLI DALLGDPHCDVFNQETWDLFVERSKAFSNCYPYDVPDYASLRSLVASSGTLEFI TEG
FTWTGVTONGGSNACKRGP GSGFFSRLNWLTKSGSTYPVLNVTMPNNDNFDKLYI WGVHHPSTNQEQTSL
YVQASGRVTVSTRRSQQT I PNI GSRPWVVRGLSSRI SI YWTI VKPGDVLVI NSNGNLI APRGYFKMRTGK
SSI MRSDAPI DTCI SECI TPNGSI PNDKPFQNVNKI TYGACPKYVKQNTLKLATGMRNVPEKQTRGLFGA
I AGFI ENGWEEMI DGWYGFRRHONSEGTGOAADLKSTQAAI DOI NGKLN RVI EKTNEKFHQI EKEFSEVEG
RI ODLEKYVEDTKI DLWSYNAELLVALENQHTI DLTDSEMKNLFKTRRQLRENAEDMNGGCFKI YHKCD
NACI ESI RNGTHYDHDVYRDEALNNRFOI KGVELKSGYKDWI LWI SFAI SCFLLCVVLLGFI MWACQRGNI
RCNI CI

>gi |125664195|gb|ABN51099.1| hemagglutinin [Influenza A virus
(A/AI bany/11/1968(H3N2))]

MKTI I ALSYI FCLALGQDLPGNDNSTATLCLGHHAVPNGTLVKTI TDDQI EVTNATELVQSSSTGKI CNN
PHRI LDGI DCTLI DALLGDPHCDVFNQETWDLFVERSKAFSNCYPYDVPDYASLRSLVASSGTLEFI TEG
FTWTGVTONGGSNACKRGP GSGFFSRLNWLTKSGSTYPVLNVTMPNNDNFDKLYI WGVHHPSTNQEQTSL
YVQASGRVTVSTRRSQQT I PNI GSRPWVVRGLSSRI SI YWTI VKPGDVLVI NSNGNLI APRGYFKMRTGK
SSI MRSDAPI DTCI SECI TPNGSI PNDKPFQNVNKI TYGACPKYVKQNTLKLATGMRNVPEKQTRGLFGA
I AGFI ENGWEEMI DGWYGFRRHONSEGTGOAADLKSTQAAI DOI NGKLN RVI EKTNEKFHQI EKEFSEVEG
RI ODLEKYVEDTKI DLWSYNAELLVALENQHTI DLTDSEMKNLFKTRRQLRENAEDMNGGCFKI YHKCD
NACI ESI RNGTHYDHDVYRDEALNNRFOI KGVELKSGYKDWI LWI SFAI SCFLLCVVLLGFI MWACQRGNI
RCNI CI

>gi |125664233|gb|ABN51121.1| hemagglutinin [Influenza A virus
(A/AI bany/19/1968(H3N2))]

MKTI I ALSYI FCLALGQDLPGNDNSTATLCLGHHAVPNGTLVKTI TDDQI EVTNATELVQSSSTGKI CNN
PHRI LDGI DCTLI DALLGDPHCDVFNQETWDLFVERSKAFSNCYPYDVPDYASLRSLVASSGTLEFI TEG
FTWTGVTONGGSNACKRGP GSGFFSRLNWLTKSGSTYPVLNVTMPNNDNFDKLYI WGVHHPSTNQEQTSL
YVQASGRVTVSTRRSQQT I PNI GSRPWVVRGLSSRI SI YWTI VKPGDVLVI NSNGNLI APRGYFKMRTGK
SSI MRSDAPI DTCI SECI TPNGSI PNDKPFQNVNKI TYGTCPKYVKQNTLKLATGMRNVPEKQTRGLFGA
I AGFI ENGWEEMI DGWYGFRRHONSEGTGOAADLKSTQAAI DOI NGKLN RVI EKTNEKFHQI EKEFSEVEG
RI ODLEKYVEDTKI DLWSYNAELLVALENQHTI DLTDLEMNKLFKTRRQLRENAEDMNGGCFKI YHKCD
NACI ESI RNGTHYDHDVYRDEALNNRFOI KGVELKSGYKDWI LWI SFAI SCFLLCVVLLGFI MWACQRGNI
RCNI CI

>gi |134047618|gb|AB052357.1| hemagglutinin [Influenza A virus
(A/AI bany/17/1968(H3N2))]

MKTI I ALSYI FCLALGQDLPGNDNSTATLCLGHHAVPNGTLVKTI TDDQI EVTNATELVQSSSTGKI CNN
PHRI LDGI DCTLI DALLGDPHCDVFNQETWDLFVERSKAFSNCYPYDVPDYASLRSLVASSGTLEFI TEG
FTWTGVTONGGSNACKRGP GSGFFSRLNWLTKSGSTYPVLNVTMPNNDNFDKLYI WGVHHPSTNQEQTSL
YVQASGRVTVSTRRSQQT I PNI GSRPWVVRGLSSRI SI YWTI VKPGDVLVI NSNGNLI APRGYFKMRTGK
SSI MRSDAPI DTCI FECI TPNGSI PNDKPFQNVNKI TYGACPKYVKQNTLKLATGMRNVPEKQTRGI FGA
I AGFI ENGWEEMI DGWYGFRRHONSEGTGOAADLKSTQAAI DOI NGKLN RVI EKTNEKFHQI EKEFSEVEG
RI ODLEKYVEDTKI DLWSYNAELLVALENQHTI DLTDSEMKNLFKTRRQLRENAEDMNGGCFKI YHKCD
NACI ESI RNGTHYDHDVYRDEALNNRFOI KGVELKSGYKDWI LWI SFAI SCFLLCVVLLGFI MWACQRGNI
RCNI CI

>gi |148910822|gb|ABR18477.1| hemagglutinin [Influenza A virus (A/AI chi /2/1968(H3N2))]

MKTI I ALSYI FCLALGQDLPGNDNSTATLCLGHHAVPNGTLVKTI TDDQI EVTNATELVQSSSTGKI CNN
PHRI LDGI DCTLI DALLGDPHCDVFNQETWDLFVERSKAFSNCYPYDVPDYASLRSLVASSGTLEFI TEG
FTWTGVTONGGSNACKRGP GSGFFSRLNWLTKSGSTYPVLNVTMPNNDNFDKLYI WGVHHPSTNQEQTSL
YVQASGRVTVSTRRSQQT I PNI GSRPWVVRGLSSRI SI YWTI VKPGDVLVI NSNGNLI APRGYFKMRTGK
SSI MRSDAPI DTCI SECI TPNGSI PNDKPFQNVNKI TYGACPKYVKQNTLKLATGMRNVPEKQTRGLFGA

I AGFI ENGWEEMI DGWYGFRRHONSEGTOAADLKSTQAAI DOI NGKLN RV I EKTNEKFHQI EKEFSEVEG RI ODLEKYVEDTKI DLWSYNAELLVALENOHTI DLTDSEMKNLFEKTRRQLENAEDMGNGCFKI YHKCD NACI ESI RNGTHYDHDVYRDEALNNRFOI KGVELKSGYKDWI LWI SFAI SCFLLCVVLLGFI MWACQRGNI RCNI CI

>gi |148910824|gb|ABR18478.1| hemagglutinin [Influenza A virus (A/Aichi /2/1968(H3N2))]

MKTI I ALSYI FCLALGQDLPNGDNSTATLCLGHHAVPNGTLVKTI TDDQI EVTNATELVQSSSTGKI CNN PHRI LDGI DCTLI DALLGDPHCDVFQNETWDLFVERSKAFSNCYPYDVPDYASLRSLVASSGTLEFI TEG FTWTGVTQNGGSSNACKRGPSSGFFSRLNWLTKSGSTYPVNLVMPNNDNFDKLYI WGVHPHPSTNOEQTSL YVQASGRVTVSTRRSQOTI I PNI GSRPWVVRGLSSRI SI YWTI VKPGDVLVI NSNGNLI APRGYFKMRTGK SSI MRSDAPI DTCI SECI TPNGSI PNDKPFQNVNKI TYGACPKYVKQNTLKLATGMRNVPEKQTRGLFGA I AGFI ENGWEEMI DGWYGFRRHONSEGTOAADLKSTQAAI DOI NGKLN RV I EKTNEKFHQI EKEFSEVEG RI ODLEKYVEDTKI DLWSYNAELLVALENOHTI DLTDSEMKNLFEKTRRQLENAEDMGNGCFKI YHKCD NACI ESI RNGTHYDHDVYRDEALNNRFOI KGVELKSGYKDWI LWI SFAI SCFLLCVVLLGFI MWACQRGNI RCNI CI

>gi |194304651|gb|ACF41746.1| hemagglutinin [Influenza A virus (A/Hong Kong/1-9-MA21-1/1968(H3N2))]

MKTI I ALSYI FCLALGQDLPNGDNSTATLCLGHHAVPNGTLVKTI TDDQI EVTNATELVQSSSTGKI CNN PHRI LDGI DCTLI DALLGDPHCDVFQNETWDLFVERSKAFSNCYPYDVPDYASLRSLVASSGTLEFI TEG FTWTGVTQNGGSSNACKRGPSSGFFSRLNWLTKSGSTYPVNLVMPNNDNFDKLYI WGVHPHPSTNOEQTSL YVQASGRVTVSTRRSQOTI I PNI GSRPWVVRGLSSRI NI YWTI VKPGDVLVI NSNGNLI APRGYFKMRTGK SSI MRSDAPI DTCI SECI TPNGSI PNDKPFQNVNKI TYGACPKYVKQNTLKLATGMRNVPEKQTRGLFGA I AGFI ENGWEEMI DGWYGFRRHONSEGTOAADLKSTQAAI DOI NGKLN RV I EKTNEKFHQI EKEFSEVEG RI ODLEKYVEDTKI DLWSYNAELLVALENOHTI DLTDSEMKNLFEKTRRQLENAEDMGNGCFKI YHKCD NACI ESI RNGTHYDHDVYRDEALNNRFOI KGVELKSGYKDWI LWI SFAI SCFLLCVVLLGFI MWACQRGNI RCNI CI

>gi |194304765|gb|ACF41812.1| hemagglutinin [Influenza A virus (A/Hong Kong/1-12-MA21-1/1968(H3N2))]

MKTI I ALSYI FCLALGQDLPNGDNSTATLCLGHHAVPNGTLVKTI TDDQI EVTNATELVQSSSTGKI CNN PHRI LDGI DCTLI DALLGDPHCDVFQNETWDLFVERSKAFSNCYPYDVPDYASLRSLVASSGTLEFI TEG FTWTGVTQNGGSSNACKRGPSSGFFSRLNWLTKSGSTYPVNLVMPNNDNFDKLYI WGVHPHPSTNOEQTSL YVQASGRVTVSTRRSQOTI I PNI GSRPWVVRGLSSRI SI YWTI VKPGDVLVI NSNGNLI APRGYFKMRTGK SSI MRSDAPI DTCI SECI TPNGSI PNDKPFQNVNKI TYGACPKYVKQNTLKLATGMRNVPEKQTRGLFGA I AGFI ENGWEEMI DGWYGFRRHONSEGTOAADLKSTQAAI DOI NGKLN RV I EKTNEKFHQI EKEFSEVEG RI ODLEKYVEDTKI DLWSYNAELLVALENOHTI DLTDSEMKNLFEKTRRQLENAEDMGNGCFKI YHKCD NACI ESI RNGTHYDHDVYRDEALNNRFOI KGVELKSGYKDWI LWI SFAI SCFLLCVVLLGFI MWACQRGNI RCNI CI

>gi |118420992|dbj|BAF37221.1| hemagglutinin [Influenza A virus (A/Aichi /2/1968(H3N2))]

MKTI I ALSYI FCLAI GQDLPNGDNSTATLCLGHHAVPNGTLVKTI TDDQI EVTNATELVQSSSTGKI CNN PHRI LDGI DCTLI DALLGDPHCDVFQNETWDLFVERSKAFSNCYPYDVPDYASLRSLVASSGTLEFI TEG FTWTGVTQNGGSSNACKRGPSSGFFSRLNWLTKSGSTYPVNLVMPNNDNFDKLYI WGVHPHPSTNOEQTSL YVQASGRVTVSTRRSQOTI I PNI GSRPWVVRGLSSRI SI YWTI VKPGDVLVI NSNGNLI APRGYFKMRTGK SSI MRSDAPI DTCI SECI TPNGSI PNDKPFQNVNKI TYGACPKYVKQNTLKLATGMRNVPEKQTRGLFGA I AGFI ENGWEEMI DGWYGFRRHONSEGTOAADLKSTQAAI DOI NGKLN RV I EKTNEKFHQI EKEFSEVEG RI ODLEKYVEDTKI DLWSYNAELLVALENOHTI DLTDSEMKNLFEKTRRQLENAEDMGNGCFKI YHKCD NACI ESI RNGTHYDHDVYRDEALNNRFOI KGVELKSGYKDWI LWI SFAI SCFLLCVVLLGFI MWACQRGNI RCNI CI

>gi |194352074|gb|ACF54444.1| hemagglutinin [Influenza A virus (A/Hong Kong/1-8-MA21-1/1968(H3N2))]

MKTI I ALSYI FCLALGQDLPNGDNSTATLCLGHHAVPNGTLVKTI TDDQI EVTNATELVQSSSTGKI CNN PHRI LDGI DCTLI DALLGDPHCDVFQNETWDLFVERSKAFSNCYPYDVPDYASLRSLVASSGTLEFI TEG FTWTGVTQNGGSSNACKRGPSSGFFSRLNWLTKSGSTYPVNLVMPNNDNFDKLYI WGVHPHPSTNOEQTSL YVQASGRVTVSTRRSQOTI I PNI GSRPWVVRGLSSRI SI YWTI VKPGDVLVI NSNGNLI APRGYFKMRTGK SSI MRSDAPI DTCI SECI TPNGSI PNDKPFQNVNKI TYGACPKYVKQNTLKLATGMRNVPEKQTRGLFGA I AGFI ENGWEEMI DGWYGFRRHONSEGTOAADLKSTQAAI DOI NGKLN RV I EKTNEKFHQI EKEFSEVEG RI ODLEKYVEDTKI DLWSYNAELLVALENOHTI DLTDSEMKNLFEKTRRQLENAEDMGNGCFKI YHKCD NACI ESI RNGTHYDHDVYRDEALNNRFOI KGVELKSGYKDWI LWI SFAI SCFLLCVVLLGFI MWACQRGNI RCNI CI

>gi |194352112|gb|ACF54466.1| hemagglutinin [Influenza A virus (A/Hong Kong/1-12-MA21-3/1968(H3N2))]

MKTI I ALSYI FCLALGQDLPNGDNSTATLCLGHHAVPNGTLVKTI TDDQI EVTNATELVQSSSTGKI CNN PHRI LDGI DCTLI DALLGDPHCDVFQNETWDLFVERSKAFSNCYPYDVPDYASLRSLVASSGTLEFI TEG FTWTGVTQNGGSSNACKRGPSSGFFSRLNWLTKSGSTYPVNLVMPNNDNFDKLYI WGVHPHPSTNOEQTSL YVQASGRVTVSTRRSQOTI I PNI GSRPWVVRGLSSRI SI YWTI VKPGDVLVI NSNGNLI APRGYFKMRTGK SSI MRSDAPI DTCI SECI TPNGSI PNDKPFQNVNKI TYGACPKYVKQNTLKLATGMRNVPEKQTRGLFGA I AGFI ENGWEEMI DGWYGFRRHONSEGTOAADLKSTQAAI DOI NGKLN RV I EKTNEKFHQI EKEFSEVEG RI ODLEKYVEDTKI DLWSYNAELLVALENOHTI DLTDSEMKNLFEKTRRQLENAEDMGNGCFKI YHKCD NACI ESI RNGTHYDHDVYRDEALNNRFOI KGVELKSGYKDWI LWI SFAI SCFLLCVVLLGFI MWACQRGNI RCNI CI

>gi |126567435|dbj|BAF48361.1| haemagglutinin [Influenza A virus (A/Aichi /2/1968(H3N2))]

MKTI I ALSYI FCLALGQDLPNGDNSTATLCLGHHAVPNGTLVKTI TDDQI EVTNATELVQSSSTGKI CNN PHRI LDGI DCTLI DALLGDPHCDVFQNETWDLFVERSKAFSNCYPYDVPDYASLRSLVASSGTLEFI TEG FTWTGVTQNGGSSNACKRGPSSGFFSRLNWLTKSGSTYPVNLVMPNNDNFDKLYI WGVHPHPSTNOEQTSL YVQASGRVTVSTRRSQOTI I PNI ESRPWVVRGLSSRI SI YWTI VKPGDVLVI NSNGNLI APRGYFKMRTGK SSI MRSDAPI DTCI SECI TPNGSI PNDKPFQNVNKI TYGACPKYVKQNTLKLATGMRNVPEKQTRGLFGA I AGFI ENGWEEMI DGWYGFRRHONSEGTOAADLKSTQAAI DOI NGKLN RV I EKTNEKFHQI EKEFSEVEG

RI ODLEKYVEDTKI DLWSYNAELLVALENOHTI DLTDSEMKNLFEKTRROLRENAEDMGNGCFKI YHKCD
NACI ESI RNGTHYDHDVYRDEALNNRFOI KGVELKSGYKDWI LWI SFAI SCFLLCVALLGFI MWACQKGN
RCNI CI

>gi |189303143|gb|ACD85628.1| hemagglutinin [Influenza A virus
(A/I daho/03/2008(H3N2))]

MKTI I ALSYI LCLVFAQKLPNGDNSTATLCLGHHAVPNGTI VKTI TNDQI EVTNATELVQSSSTGEI CDS
PHQI LDGENCTLI DALLGDPQCDGFQNKKDWL FVERSKAYSNCYPYDVPDYASLRSLVASSGTLEFNNE
FNWTVTQNGTSSACI RRSNNSFFSRLNWLTHLKFYPALNVTMPNNEQFDKLYI WGVHHPGTDNDQI FL
YAQASGRI TVSTKRSQQTVI PNI GSRPRVRDI PSRI SI YWTI VKPGDI LLI NSTGNLI APRGYFKI RSGK
SSI MRSDAPI GKCNSCI TPNGSI PNDKPFQNVNRI TYGACPRYVKQNTLKLATGMRNVPEKQTRGI FGA
I AGFI ENGWEWMVDGWYGFRRHONSEGI GOAADLKSTQAAI DOI NGKLNRLI GKTNEKFHAI KEFSEVEG
RI ODLEKYVEDTKI DLWSYNAELLVALENOHTI DLTDSEMKNLFEKTKKOLRENAEDMGNGCFKI YHKCD
NACI GSI RNGTHYDHDVYRDEALNNRFOI KGVELKSGYKDWI LWI SFAI SCFLLCVALLGFI MWACQKGN
RCNI CI

>gi |189303103|gb|ACD85608.1| hemagglutinin [Influenza A virus
(A/Tennessee/02/2008(H3N2))]

MKTI I ALSYI LCLVFAQKLPNGDNSTATLCLGHHAVPNGTI VKTI TNDQI EVTNATELVQSSSTGEI CDS
PHQI LDGENCTLI DALLGDPQCDGFQNKKDWL FVERSKAYSNCYPYDVPDYASLRSLVASSGTLEFNNE
FNWTVTQNGTSSACI RRSNNSFFSRLNWLTHLKFYPALNVTMPNNEQFDKLYI WGVHHPGTDNDQI FL
YAQASGRI TVSTKRSQQTVI PNI GSRPRVRNI PSRI SI YWTI VKPGDI LLI NSTGNLI APRGYFKI RSGK
SSI MRSDAPI GKCNSCI TPNGSI PNDKPFQNVNRI TYGACPRYVKQNTLKLATGMRNVPEKQTRGI FGA
I AGFI ENGWEWMVDGWYGFRRHONSEGRGOAADLKSTQAAI DOI NGKLNRLI GKTNEKFHAI KEFSEVEG
RI ODLEKYVEDTKI DLWSYNAELLVALENOHTI DLTDSEMKNLFEKTKKOLRENAEDMGNGCFKI YHKCD
NACI GSI RNGTHYDHDVYRDEALNNRFOI KGVELKSGYKDWI LWI SFAI SCFLLCVALLGFI MWACQKGN
RCNI CI

>gi |189303139|gb|ACD85626.1| hemagglutinin [Influenza A virus
(A/Virginia/02/2008(H3N2))]

MKTI I ALSYI LCLVFAQKLPNGDNSTATLCLGHHAVPNGTI VKTI TNDQI EVTNATELVQSSSTGEI CDS
PHQI LDGENCTLI DALLGDPQCDGFQNKKDWL FVERSKAYSNCYPYDVPDYASLRSLVASSGTLEFNNE
FNWTVTQNGTSSACI RRSNNSFFSRLNWLTHLKFYPALNVTMPNNEQFDKLYI WGVHHPGTDNDQI FL
YAQASGRI TVSTKRSQQTVI PNI GSRPRVRNI PSRI SI YWTI VKPGDI LLI NSTGNLI APRGYFKI RSGK
SSI MRSDAPI GKCNSCI TPNGSI PNDKPFQNVNRI TYGACPRYVKQNTLKLATGMRNVPEKQTRGI FGA
I AGFI ENGWEWMVDGWYGFRRHONSEGRGOAADLKSTQAAI DOI NGKLNRLI GKTNEKFHAI KEFSEVEG
RI ODLEKYVEDTKI DLWSYNAELLVALENOHTI DLTDSEMKNLFEKTKKOLRENAEDMGNGCFKI YHKCD
NACI GSI RNGTHYDHDVYRDEALNNRFOI KGVELKSGYKDWI LWI SFAI SCFLLCVALLGFI MWACQKGN
RCNI CI

>gi |194293999|gb|ACF40094.1| hemagglutinin [Influenza A virus
(A/Vermont/02/2008(H3N2))]

MKTI I ALSYI LCLVFAQKLPNGDNSTATLCLGHHAVPNGTI VKTI TNDQI EVTNATELVQSSSTGEI CDS
PHQI LDGENCTLI DALLGDPQCDGFQNKKDWL FVERSKAYSNCYPYDVPDYASLRSLVASSGTLEFNNE
FNWTVTQNGTSSACI RRSNNSFFSRLNWLTHLKFYPALNVTMPNNEQFDKLYI WGVHHPGTDNDQI FL
YAQASGRI TVSTKRSQQTVI PNI GSRPRVRNI PSRI SI YWTI VKPGDI LLI NSTGNLI APRGYFKI RSGK
SSI MRSDAPI GKCNSCI TPNGSI PNDKPFQNVNRI TYGACPRYVKQNTLKLATGMRNVPEKQTRGI FGA
I AGFI ENGWEWMVDGWYGFRRHONSEGI GOAADLKSTQAAI DOI NGKLNRLI GKTNEKFHAI KEFSEVEG
RI ODLEKYVEDTKI DLWSYNAELLVALENOHTI DLTDSEMKNLFEKTKKOLRENAEDMGNGCFKI YHKCD
NACI GSI RNGTHYDHDVYRDEALNNRFOI KGVELKSGYKDWI LWI SFAI SCFLLCVALLGFI MWACQKGN
RCNI CI

>gi |188076381|gb|ACD47217.1| hemagglutinin [Influenza A virus
(A/Wisconsin/07/2008(H3N2))]

MKTI I ALSYI LCLVFAQKLPNGDNSTATLCLGHHAVPNGTI VKTI TNDQI EVTNATELVQSSSTGEI CDS
PHQI LDGENCTLI DALLGDPQCDGFQNKKDWL FVERSKAYSNCYPYDVPDYASLRSLVASSGTLEFNNE
FNWTVTQNGTSSACI RRSNNSFFSRLNWLTHLKFYPALNVTMPNNEQFDKLYI WGVHHPGTDNDQI FL
YAQASGRI TVSTKRSQQTVI PNI GSRPRVRNI PSRI SI YWTI VKPGDI LLI NSTGNLI APRGYFKI RSGK
SSI MRSDAPI GKCNSCI TPNGSI PNDKPFQNI NRI TYGACPRYVKQNTLKLATGMRNVPEKQTRGI FGA
I AGFI ENGWEWMVDGWYGFRRHONSEGRGOAADLKSTQAAI DOI NGKLNRLI GKTNEKFHAI KEFSEVEG
RI ODLEKYVEDTKI DLWSYNAELLVALENOHTI DLTDSEMKNLFEKTKKOLRENAEDMGNGCFKI YHKCD
NACI GSI RNGTHYDHDVYRDEALNNRFOI KGVELKSGYKDWI LWI SFAI SCFLLCVALLGFI MWACQKGN
RCNI CI

>gi |189303151|gb|ACD85632.1| hemagglutinin [Influenza A virus
(A/Wisconsin/10/2008(H3N2))]

MKTI I ALSYI LCLVFAQKLPNGDNSTATLCLGHHAVPNGTI VKTI TNDQI EVTNATELVQSSSTGEI CDS
PHQI LDGENCTLI DALLGDPQCDGFQNKKDWL FVERSKAYSNCYPYDVPDYASLRSLVASSGTLEFNNE
FNWTVTQNGTSSACI RRSNNSFFSRLNWLTHLKFYPALNVTMPNNEQFDKLYI WGVHHPGTDNDQI FL
YAQASGRI TVSTKRSQQTVI PNI GSRPRVRBI PSRI SI YWTI VKPGDI LLI NSTGNLI APRGYFKI RSGK
SSI MRSDAPI GKCNSCI TPNGSI PNDKPFQNVNRI TYGACPRYVKQNTLKLATGMRNVPEKQTRGI FGA
I AGFI ENGWEWMVDGWYGFRRHONSEGRGOAADLKSTQAAI DOI NGKLNRLI GKTNEKFHAI KEFSEVEG
RI ODLEKYVEDTKI DLWSYNAELLVALENOHTI DLTDSEMKNLFEKTKKOLRENAEDMGNGCFKI YHKCD
NACI GSI RNGTHYDHDVYRDEALNNRFOI KGVELKSGYKDWI LWI SFAI SCFLLCVALLGFI MWACQKGN
RCNI CI

>gi |194293953|gb|ACF40071.1| hemagglutinin [Influenza A virus
(A/Memphis/28/2008(H3N2))]

MKTI I ALSYI LCLVFAQKLPNGDNSTATLCLGHHAVPNGTI VKTI TNDQI EVTNATELVQSSSTGEI CDS
PHQI LDGENCTLI DALLGDPQCDGFQNKKDWL FVERSKAYSNCYPYDVPDYASLRSLVASSGTLEFNNE
FNWTVTQNGTSSACI RRSNNSFFSRLNWLTHLKFYPALNVTMPNNEQFDKLYI WGVHHPGTDNDQI FL
YAQASGRI TVSTKRSQQTVI PNI GSRPRVRNI PSRI SI YWTI VKPGDI LLI NSTGNLI APRGYFKI RSGK
SSI MRSDAPI GKCNSCI TPNGSI PNDKPFQNVNRI TYGACPRYVKQNTLKLATGMRNVPEKQTRGI FGA
I AGFI ENGWEWMVDGWYGFRRHONSEGRGOAADLKSTQAAI DOI NGKLNRLI GKTNEKFHAI KEFSEVEG

RI ODLEKYVEDTKI DLWSYNAELLVALENOHTI DLTDSEMKNLFEKTKKOLRENAEDMGNGCFKI YHKCD
NACI GSI RNGTHYDHDVYRDEALNNRFOI KGVELKSGYKDWI LWI SFAI SCFLLCVALLGFI MWACQKGN
RCNI CI

>gi |194293949|gb|ACF40069.1| hemagglutinin [Influenza A virus
(A/FI ori da/10/2008(H3N2))]

MKTI I ALSYI LCLVFAKFPNGDNSTATLCLGHHAVPNGTI VKTI TNDQI EVTNATELVQSSSTGEI CDS
PHQI LDGENCTLI DALLGDPQCDGFQNKNDLWDLFVERSKAYSNCYPYDVPDYASLRSLVASSGTLEFNES
FNWGTGTONGTSSACI RRSNNSFFSRLNWLTHSKFKYPALNVTMPNNEFDKLYI WGVHHPGTDNDQI FL
YAQASGRI TVSTKRSQQTVI PNI GSRPRVRNI PSRI SI YWTI VKPGDI I LI NSTGNLI APRGYFKI RSGK
SSI MRSDAPI GKCNSECI TPNGSI PNDKPFQNVNRI TYGACPRYVKQNTLKLATGMRNVPEKQTRGI FGA
I AGFI ENGWEGMVDGWYGFRRHONSEGI GOAADLKSTQAAI DOI NGKLNRLI GKTNEKFHAI KEFSEVEG
RI ODLEKYVEDTKI DLWSYNAELLVALENOHTI DLTDSEMKNLFEKTKKOLRENAEDMGNGCFKI YHKCD
NACI GSI RNGTHYDHDVYRDEALNNRFOI KGVELKSGYKDWI LWI SFAI SCFLLCI ALLGFI MWACQKGN
RCNI CI

>gi |188076407|gb|ACD47230.1| hemagglutinin [Influenza A virus
(A/Vi rgi ni a/01/2008(H3N2))]

MKTI I ALSYI LCLVFAKFPNGDNSTATLCLGHHAVPNGTI VKTI TNDQI EVTNATELVQSSSTGEI CDS
PHQI LDGENCTLI DALLGDPQCDGFQNKNDLWDLFVERSKAYSNCYPYDVPDYASLRSLVASSGTLEFNES
FNWGTGTONGTSSACI RRSNNSFFSRLNWLTHSKFKYPALNVTMPNNEFDKLYI WGVHHPGTDNDQI FL
YAQASGRI TVSTKRSQQTVI PNI GSRPRVRNI PSRI SI YWTI VKPGDI I LI NSTGNLI APRGYFKI RSGK
SSI MRSDAPI GKCNSECI TPNGSI PNDKPFQNVNRI TYGACPRYVKQNTLKLATGMRNVPEKQTRGI FGA
I AGFI ENGWEGMVDGWYGFRRHONSEGI GOAADLKSTQAAI DOI NGKLNRLI GKTNEKFHAI KEFSEVEG
RI ODLEKYVEDTKI DLWSYNAELLVALENOHTI DLTDSEMKNLFEKTKKOLRENAEDMGNGCFKI YHKCD
NACI GSI RNGTHYDHDVYRDEALNNRFOI KGVELKSGYKDWI LWI SFAI SCFLLCI ALLGFI MWACQKGN
RCNI CI

>gi |189303115|gb|ACD85614.1| hemagglutinin [Influenza A virus
(A/FI ori da/07/2008(H3N2))]

MKTI I ALSSI LCLVFAQKLPNGDNSTATLCLGHHAVPNGTI VKTI ANDQI EVTNATELVQSSSTGEI CDS
PHQI LDGENCTLI DALLGDPQCDGFQNKNDLWDLFVERSKAYSNCYPYDVPDYASLRSLVASSGTLEFNES
FNWGTGTONGTSSACI RRSNNSFFSRLNWLTHLKFYPALNVTMPNNEFDKLYI WGVHHPGTDNDQI FL
YAQASGRI TVSTKRSQQTVI PNI GSRPRVRNI PSRI SI YWTI VKPGDI I LI NSTGNLI APRGYFKI RSGK
SSI MRSDAPI GKCNSECI TPNGSI PNDKPFQNVNRI TYGACPRYVKQNTLKLATGMRNVPEKQTRGI FGA
I AGFI ENGWEGMVDGWYGFRRHONSEGI GOAADLKSTQAAI DOI NGKLNRLI GKTNEKFHAI KEFSEVEG
RI ODLEKYVEDTKI DLWSYNAELLVALENOHTI DLTDSEMKNLFEKTKKOLRENAEDMGNGCFKI YHKCD
NACI GSI RNGTHYDHDVYRDEALNNRFOI KGVELKSGYKDWI LWI SFAI SCFLLCVALLGFI MWACQKGN
RCNI CI

>gi |194293957|gb|ACF40073.1| hemagglutinin [Influenza A virus
(A/Georgi a/07/2008(H3N2))]

MKTI I ALSYI LCLVFAQKLPNGDNSTATLCLGHHAVPNGTI VKTI TNDQI EVTNATELVQSSSTGEI CDS
PHQI LDGENCTLI DALLGDPQCDGFQNKNDLWDLFVERSKAYSNCYPYDVPDYASLRSLVASSGTLEFNES
FNWGTGTONGTSSACI RRSNNSFFSRLNWLTHLKFYPALNVTMPNNEFDKLYI WGVHHPGTDNDQI FL
YAQASGRI TVSTKRSQQTVI PNI GSRPRVRNI PSRI SI YWTI VKPGDI I LI NSTGNLI APRGYFKI RSGK
SSI MRSDAPI GKCNSECI TPNGSI PNDKPFQNVNRI TYGACPRYVKQNTLKLATGMRNVPEKQTRGI FGA
I AGFI ENGWEGMVDGWYGFRRHONSEGRGOAADLKSTQAAI DOI NGKLNRLI GKTNEKFHAI KEFSEVEG
RI ODLEKYVEDTKI DLWSYNAELLVALENOHTI DLTDSEMKNLFEKTKKOLRENAEDMGNGCFKI YHKCD
NACI GSI RNGTHYDHDVYRDEALNNRFOI KGVELKSGYKDWI LWI SFAI SCFLLCVALLGFI MWACQKGN
RCNI CI

>gi |188076387|gb|ACD47220.1| hemagglutinin [Influenza A virus
(A/Wi sconsi n/08/2008(H3N2))]

MKTI I ALSYI LCLVFAQKLPNGDNSTATLCLGHHAVPNGTI VKTI TNDQI EVTNATELVQSSSTGEI CDS
PHQI LDGENCTLI DALLGDPQCDGFQNKNDLWDLFVERSKAYSNCYPYDVPDYASLRSLVASSGTLEFNES
FNWGTGTONGTSSACI RRSNNSFFSRLNWLTHLKFYPALNVTMPNNEFDKLYI WGVHHPGTDNDQI FL
YAQASGRI TVSTKRSQQTVI PNI GSRPRVRNI PSRI SI YWTI VKPGDI I LI NSTGNLI APRGYFKI RSGK
SSI MRSDAPI GKCNSECI TPNGSI PNDKPFQNVNRI TYGACPRYVKQNTLKLATGMRNVPEKQTRGI FGA
I AGFI ENGWEGMVDGWYGFRRHONSEGRGOAADLKSTQAAI DOI NGKLNRLI GKTNEKFHAI KEFSEVEG
RI ODLEKYVEDTKI DLWSYNAELLVALENOHTI DLTDSEMKNLFEKTKKOLRENAEDMGNGCFKI YHKCD
NACI GSI RNGTHYDHDVYRDEALNNRFOI KGVELKSGYKDWI LWI SFAI SCFLLCVALLGFI MWACQKGN
RCNI CI

>gi |193084867|gb|ACF10323.1| hemagglutinin [Influenza A virus (A/North
Carol i na/01/2008(H3N2))]

MKTI I ALSYI LCLVFAQKLPNGDNSTATLCLGHHAVPNGTI VKTI TNDQI EVTNATELVQSSSTGEI CDS
PHQI LDGENCTLI DALLGDPQCDGFQNKNDLWDLFVERSKAYSNCYPYDVPDYASLRSLVASSGTLEFNES
FNWGTGTONGTSSACI RRSNNSFFSRLNWLTHLKFYPALNVTMPNNEFDKLYI WGVHHPGTDNDQI FL
YAQASGRI TVSTKRSQQTVI PNI GSRPRVRNI PSRI SI YWTI VKPGDI I LI NSTGNLI APRGYFKI RSGK
SSI MRSDAPI GKCNSECI TPNGSI PNDKPFQNVNRI TYGACPRYVKQNTLKLATGMRNVPEKQTRGI FGA
I AGFI ENGWEGMVDGWYGFRRHONSEGRGOAADLKSTQAAI DOI NGKLNRLI GKTNEKFHAI KEFSEVEG
RI ODLEKYVEDTKI DLWSYNAELLVALENOHTI DLTDSEMKNLFEKTKKOLRENAEDMGNGCFKI YHKCD
NACI GSI RNGTHYDHDVYRDEALNNRFOI KGVELKSGYKDWI LWI SFAI SCFLLCVALLGFI MWACQKGN
RCNI CI

>gi |193084863|gb|ACF10321.1| hemagglutinin [Influenza A virus (A/New
York/06/2008(H3N2))]

MKTI I ALSYI LCLVFAQKLPNGDNSTATLCLGHHAVPNGTI VKTI TNDQI EVTNATELVQSSSTGEI CDS
PHQI LDGENCTLI DALLGDPQCDGFQNKNDLWDLFVERSKAYSNCYPYDVPDYASLRSLVASSGTLEFNES
FNWGTGTONGTSSACI RRSNNSFFSRLNWLTHLKFYPALNVTMPNNEFDKLYI WGVHHPGTDNDQI FL
YAQASGRI TVSTKRSQQTVI PNI GSRLRVRDI PSRI SI YWTI VKPGDI I LI NSTGNLI APRGYFKI RSGK
SSI MRSDAPI GKCNSECI TPNGSI PNDKPFQNVNRI TYGACPRYVKQNTLKLATGMRNVPEKQTRGI FGA
I AGFI ENGWEGMVDGWYGFRRHONSEGTGOAADLKSTQAAI DOI NGKLNRLI GKTNEKFHAI KEFSEVEG

RI ODLEKYVEDTKI DLWSYNAELLVALENOHTI DLTDSEMKNLFEKTKKOLRENAEDMNGGCFKI YHKCD NACI GSI RNGTHYDHDVYRDEALNNRFOI KGVELKSGYKDWI LWI SFAI SCFLLCVALLGFI MWACQKGN RCNI CI

>gi |189303147|gb|ACD85630.1| hemagglutinin [Influenza A virus (A/Oklahoma/01/2008(H3N2))]

MKTI I ALSYI LCLVFAQKLPNGDNSTATLCLGHHAVPNGTI VKTI TNDQI EVTNATELVQSSSTGEI CDS PHQI LDGENCTLI DALLGDPQCDGFGONKNWDLFVERSKAYSNCYPYDVPDYASLRSLVASSGTLEFNNE FNWTVGTONGTSSACI RRSNNSFFSRLNWLTHSKFKYPALNVTMPNNEFDKLYI WGVHHPGTDNDQI FL YAQASGRI TVSTKRSQQTVI PNI GSRPRVRDI PSRI SI YWTI VKPGDI LLI NSTGNLI APRGYFKI RSGK SSI MRSDAPI GKCNSCI TPNGSI PNDKPFQNVNRI TYGACPRYVKQNTLKLATGMRNVPEKQTRGI FGA I AGFI ENGWEGMVDGWYGFRRHONSEGI GOAADLKSTQAAI DOI NGKLNRLI GKTNEKFHAI KEFSEVEG RI ODLEKYVEDTKI DLWSYNAELLVALENOHTI DLTDSEMKNLFEKTKKOLRENAEDMNGGCFKI YHKCD NACI GSI RNGTHYDHDVYRDEALNNRFOI KGVELKSGYKDWI LWI SFAI SCFLLCI ALLGFI MWACQKGN RCNI CI

>gi |189303155|gb|ACD85634.1| hemagglutinin [Influenza A virus (A/Missouri/01/2008(H3N2))]

MKTI I ALSYI LCLVFAQKLPNGDNSTATLCLGHHAVPNGTI VKTI TNDQI EVTNATELVQSSSTGEI CDS PHQI LDGENCTLI DALLGDPQCDGFGONKNWDLFVERSKAYSNCYPYDVPDYASLRSLVASSGTLEFNNE FNWTVGTONGTSSACI RRSNNSFFSRLNWLTHLKFYKYPALNVTMPNNEFDKLYI WGVHHPGTDNDQI FL YAQASGRI TVSTKRSQQTVI PNI GSRPRVRNI PSRI SI YWTI VKPGDI LLI NSTGNLI APRGYFKI RSGK SSI MRSDAPI GKCNSCI TPNGSI PNDKPFQNVNRI TYGACPRYVKQNTLKLATGMRNVPEKQTRGI FGA I AGFI ENGWEGMVDGWYGFRRHONSEGRGOAADLKSTQAAI DOI NGKLNRLI GKTNEKFHAI KEFSEVEG RI ODLEKYVEDTKI DLWSYNAELLVALENOHTI DLTDSEMKNLFEKTKKOLRENAEDMNGGCFKI YHKCD NACI GSI RNGTHYDHDVYRDEALNNRFOI KGVELKSGYKDWI LWI SFAI SCFLLCVALLGFI MWACQKGN RCNI CI

>gi |194293961|gb|ACF40075.1| hemagglutinin [Influenza A virus (A/Indiana/05/2008(H3N2))]

MKTI I ALSYI LCLVFAQKLPNGDNSTATLCLGHHAVPNGTI VKTI TNDQI EVTNATELVQSSSTGEI CDS PHQI LDGENCTLI DALLGDPQCDGFGONKNWDLFVERSKAYSNCYPYDVPDYASLRSLVASSGTLEFNNE FNWTVGTONGTSSACI RRSNNSFFSRLNWLTHSKFKYPALNVTMPNNEFDKLYI WGVHHPGTDNDQI FL YAQASGRI TVSTKRSQQTVI PNI GSRPRVRNI PSRI SI YWTI VKPGDI LLI NSTGNLI APRGYFKI RSGK SSI MRSDAPI GKCNSCI TPNGSI PNDKPFQNVNRI TYGACPRYVKQNTLKLATGMRNVPEKQTRGI FGA I AGFI ENGWEGMVDGWYGFRRHONSEGI GOAADLKSTQAAI DOI NGKLNRLI GKTNEKFHAI KEFSEVEG RI ODLEKYVEDTKI DLWSYNAELLVALENOHTI DLTDSEMKNLFEKTKKOLRENAEDMNGGCFKI YHKCD NACI GSI RNGTHYDHDVYRDEALNNRFOI KGVELKSGYKDWI LWI SFAI SCFLLCI ALLGFI MWACQKGN RCNI CI

>gi |189303159|gb|ACD85636.1| hemagglutinin [Influenza A virus (A/Georgia/04/2008(H3N2))]

MKTI I ALSYI LCLVFAQKLPNGDNSTATLCLGHHAVPNGTI VKTI TNDQI EVTNATELVQSSSTGEI CDS PHQI LDGENCTLI DALLGDPQCDGFGONKNWDLFVERSKAYSNCYPYDVPDYASLRSLVASSGTLEFNNE FNWTVGTONGTSSACI RRSNNSFFSRLNWLTHSKFKYPALNVTMPNNEFDKLYI WGVHHPGTDNDQI FL YAQASGRI TVSTKRSQQTVI PNI GSRPRVRNI PSRI SI YWTI VKPGDI LLI NSTGNLI APRGYFKI RSGK SSI MRSDAPI GKCNSCI TPNGSI PNDKPFQNVNRI TYGACPRYVKQNTLKLATGMRNVPEKQTRGI FGA I AGFI ENGWEGMVDGWYGFRRHONSEGI GOAADLKSTQAAI DOI NGKLNRLI GKTNEKFHAI KEFSEVEG RI ODLEKYVEDTKI DLWSYNAELLVALENOHTI DLTDSEMKNLFEKTKKOLRENAEDMNGGCFKI YHKCD NACI GSI RNGTHYDHDVYRDEALNNRFOI KGVELKSGYKDWI LWI SFAI SCFLLCVALLGFI MWACQKGN RCNI CI

>gi |194293971|gb|ACF40080.1| hemagglutinin [Influenza A virus (A/Arkansas/05/2008(H3N2))]

MKTI I ALSYI LCLVFAQKLPNGDNSTATLCLGHHAVPNGTI VKTI TNDQI EVTNATELVQSSSTGEI CDS PHQI LDGENCTLI DALLGDPQCDGFGONKNWDLFVERSKAYSNCYPYDVPDYASLRSLVASSGTLEFNNE FNWTVGTONGTSSACI RRSNNSFFSRLNWLTHLKFYKYPALNVTMPNNEFDKLYI WGVHHPGTDNDQI FL YAQASGRI TVSTKRSQQTVI PNI GSRPRVRDI PSRI SI YWTI VKPGDI LLI NSTGNLI APRGYFKI RSGK SSI MRSDAPI GKCNSCI TPNGSI PNDKPFQNVNRI TYGACPRYVKQNTLKLATGMRNVPEKQTRGI FGA I AGFI ENGWEGMVDGWYGFRRHONSEGRGOAADLKSTQAAI DOI NGKLNRLI GKTNEKFHAI KEFSEVEG RI ODLEKYVEDTKI DLWSYNAELLVALENOHTI DLTDSEMKNLFEKTKKOLRENAEDMNGGCFKI YHKCD NACI GSI RNGTHYDHDVYRDEALNNRFOI KGVELKSGYKDWI LWI SFAI SCFLLCVALLGFI MWACQKGN RCNI CI

>gi |194293975|gb|ACF40082.1| hemagglutinin [Influenza A virus (A/Washington/03/2008(H3N2))]

MKTI I ALSYI LCLVFAQKLPNGDNSTATLCLGHHAVPNGTI VKTI TNDQI EVTNATELVQSSSTGEI CDS PHQI LDGENCTLI DALLGDPQCDGFGONKNWDLFVERXKAYSNCYPYDVPDYASLRSLVASSGTLEFNNE FNWTVGTONGTSSACI RRSNNSFFSRLNWLTHLKFYKYPALNVTMPNNEFDKLYI WGVHHPGTDNDQI FL YAQASGRI TVSTKRSQQTVI PNI GSRPRVRNI PSRI SI YWTI VKPGDI LLI NSTGNLI APRGYFKI RSGK SSI MRSDAPI GKCNSCI TPNGSI PNDKPFQNVNRI TYGACPRYVKQNTLKLATGMRNVPEKQTRGI FGA I AGFI ENGWEGMVDGWYGFRRHONSEGRGOAADLKSTQAAI DOI NGKLNRLI GKTNEKFHAI KEFSEVEG RI ODLEKYVEDTKI DLWSYNAELLVALENOHTI DLTDSEMKNLFEKTKKOLRENAEDMNGGCFKI YHKCD NACI GSI RNGTHYDHDVYRDEALNNRFOI KGVELKSGYKDWI LWI SFAI SCFLLCVALLGFI MWACQKGN RCNI CI

>gi |90571879|gb|ABD94932.1| hemagglutinin [Influenza A virus (A/New York/600/1996(H3N2))]

MKTI I ALSYI LCLVFAQKLPNGDNSTATLCLGHHAVPNGTLVKTI TNDQI EVTNATELVQSSSTGRI CDS PHQI LDGKNCTLI DALLGDPHCDGFGONKEWDLFVERSTAYSNCYPYDVPDYASLRSLVASSGTLEFTKEG FNWTVGVAQDGTSYACKRGSVKSFFSRLNWLHKLEYKYPALNVTMPNNDKFDKLYI WGVHHPSTDSQDQSL YVQASGRVTVSTKRSQQTVI PNI GSRPWVRGVSSRI SI YWTI VKPGDI LLI NSTGNLI APRGYFKI RSGK SSI MRSDAPI DNCNSCI TPNGSI SNDKPFQNVNRI TYGACPRYVKQNTLKLATGMRNVPEKQTRGI FGA I AGFI ENGWEGMVDGWYGFRRHONSEGTGOAADLKSTQAAI DOI NGKLNRLI EKTNEKFHAI KEFSEVEG

RI ODLEKYVEDTKI DLWSYNAELLVALENOHTI DLTDSEMKNLFFERTRKOLRENAEDMGNGCFKI YHKCD NACI GSI RNGTHYDHDVYRDEALNNRFOI KGVELKSGYKDWI LWI SFAI SCFLLCVVLLGFI MWACQKGN RCNI CI

>gi |109675432|gb|ABG37142.1| hemagglutinin [Influenza A virus (A/New York/577/1996(H3N2))]
MKTII ALSYI LCLVFAQKLPNGDNSTATLCLGHHAVPNGTLVKTI TNDQI EVTNATELVQSSSTGRI CDS PHRI LDGKNCTLI DALLGDPHCDGFONKEWDLFVERSKAYSNCYPYDVPDYASLRSLVASSGTLEFNNEF FNTWGVAQNGTSYACKRRSVKSFSSRLNWLHKLEYKYPALNVTMPNNDKFDKLYI WGVHPSTSDSDQTSL YVQASGRVTVSTKRSQQTVI PNI GSRPWVRGVSSRI SI YWTI VKPGDI LLI NSTGNLI APRGYFKI RSGK SSI MRSDAPI DNCNSECI TPNGSI PNDKPFQNVNRI TYGACPRYVKQNTLKLATGMRNVPEKQTRGI FGA I AGFI ENGWEGMVDGWYGFRRHONSEGTOAADLKSTQAAI NOI NGKLNRLI EKTNEKFHAI KEFSEVEG RI ODLEKYVEDTKI DLWSYNAELLVALENOHTI DLTDSEMKNLFFERTRKOLRENAEDMGNGCFKI YHKCD NACI GSI RNGTHYDHDVYRDEALNNRFOI KGVELKSGYKDWI LWI SFAI SCFLLCVVLLGFI MWACQKGN RCNI CI

>gi |91126541|gb|ABE13323.1| hemagglutinin [Influenza A virus (A/New York/578/1996(H3N2))]
MKTII ALSYI LCLVFAQKLPNGDNSTATLCLGHHAVPNGTLVKTI TNDQI EVTNATELVQSSSTGRI CDS PHRI LDGKNCTLI DALLGDPHCDGFONKEWDLFVERSKAYSNCYPYDVPDYASLRSLVASSGTLEFNNEF FNTWGVAQNGTSYACKRRSVKSFSSRLNWLHKLEYKYPALNVTMPNNDKFDKLYI WGVHPSTSDSDQTSL YVQASGRVTVSTKRSQQTVI PNI GSRPWVRGVSSRI SI YWTI VKPGDI LLI NSTGNLI APRGYFKI RSGK SSI MRSDAPI DNCNSECI TPNGSI PNDKPFQNVNRI TYGACPRYVKQNTLKLATGMRNVPEKQTRGI FGA I AGFI ENGWEGMVDGWYGFRRHONSEGTOAADLKSTQAAI NOI NGKLNRLI EKTNEKFHAI KEFSEVEG RI ODLEKYVEDTKI DLWSYNAELLVALENOHTI DLTDSEMKNLFFERTRKOLRENAEDMGNGCFKI YHKCD NACI GSI RNGTHYDHDVYRDEALNNRFOI KGVELKSGYKDWI LWI SFAI SCFLLCVVLLGFI MWACQKGN RCNI CI

>gi |89784791|gb|ABD77884.1| hemagglutinin [Influenza A virus (A/New York/588/1996(H3N2))]
MKTII ALSYI LCLVFAQKLPNGDNSTATLCLGHHAVPNGTLVKTI TNDQI EVTNATELVQSSSTGRI CDS PHRI LDGKNCTLI DALLGDPHCDGFONKEWDLFVERSKAYSNCYPYDVPDYASLRSLVASSGTLEFNNEF FNTWGVAQNGTSYACKRRSVKSFSSRLNWLHKLEYKYPALNVTMPNNDKFDKLYI WGVHPSTSDSDQTSL YVQASGRVTVSTKRSQQTVI PNI GSRPWVRGVSSRI SI YWTI VKPGDI LLI NSTGNLI APRGYFKI RSGK SSI MRSDAPI DNCNSECI TPNGSI PNDKPFQNVNRI TYGACPRYVKQNTLKLATGMRNVPEKQTRGI FGA I AGFI ENGWEGMVDGWYGFRRHONSEGTOAADLKSTQAAI NOI NGKLNRLI EKTNEKFHAI KEFSEVEG RI ODLEKYVEDTKI DLWSYNAELLVALENOHTI DLTDSEMKNLFFERTRKOLRENAEDMGNGCFKI YHKCD NACI GSI RNGTHYDHDVYRDEALNNRFOI KGVELKSGYKDWI LWI SFAI SCFLLCVVLLGFI MWACQKGN RCNI CI

>gi |89789541|gb|ABD78115.1| hemagglutinin [Influenza A virus (A/New York/584/1996(H3N2))]
MKTII ALSYI LCLVFAQKLPNGDNSTATLCLGHHAVPNGTLVKTI TNDQI EVTNATELVQSSSTGRI CDS PHRI LDGKNCTLI DALLGDPHCDGFONKEWDLFVERSKAYSNCYPYDVPDYASLRSLVASSGTLEFTNEG FNTWGVAQDGTSYACKRGSVKSFSSRLNWLHKLEYKYPALNVTMPNNDKFDKLYI WGVHPSTSDSDQTSL YVQASGRVTVSTKRSQQTVI PNI GSRPWVRGVSSRI SI YWTI VKPGDI LLI NSTGNLI APRGYFKI RSGK SSI MRSDAPI GNCNSECI TPNGSI PNDKPFQNVNRI TYGACPRYVKQNTLKLATGMRNVPEKQTRGI FGA I AGFI ENGWEGMVDGWYGFRRHONSEGTOAADLKSTQAAI NOI NGKLNRLI EKTNEKFHAI KEFSEVEG RI ODLEKYVEDTKI DLWSYNAELLVALENOHTI DLTDSEMKNLFFERTRKOLRENAEDMGNGCFKI YHKCD NACI GSI RNGTHYDHDVYRNEALNNRFOI KGVELKSGYKDWI LWI SFAI SCFLLCVVLLGFI MWACQKGN RCNI CI

>gi |14030469|gb|AAK52911.1|AF363503_1 hemagglutinin [Influenza A virus (A/Paris/906/97(H3N2))]
MKTII ALSYI LCLVFAQKLPNGDNSTATLCLGHHAVPNGTLVKTI TNDQI EVTNATELVQSSSTGRI CDS PHQI LDGKNCTLI DALLGDPHCDGFONKEWDLFVERSTAYSNCYPYDVPDYASLRSLVASSGTLEFTKEG FNTWGVAQDGTSYACKRGSVKSFSSRLNWLHKLEYKYPALNVTMPNNDKFDKLYI WGVHPSTSDSDQTSL YVQASGRVTVSTKRSQQTVI PNI GSRPWVRGVSSRI SI YWTI VKPGDI LLI NSTGNLI APRGYFKI RSGK SSI MRSDAPI DNCNSECI TPNGSI PNDKPFQNVNRI TYGACPRYVKQNTLKLATGMRNVPEKQTRGI FGA I AGFI ENGWEGMVDGWYGFRRHONSEGTOAADLKSTQAAI NOI NGKLNRLI EKTNEKFHAI KEFSEVEG RI ODLEKYVEDTKI DLWSYNAELLVALENOHTI DLTDSEMKNLFFERTRKOLRENAEDMGNGCFKI YHKCD NACI GSI RNGTHYDHDVYRDEALNNRFOI KGVELKSGYKDWI LWI SFAI SCFLLCVVLLGFI MWACQKGN RCNI CI

>gi |14030467|gb|AAK52910.1|AF363502_1 hemagglutinin [Influenza A virus (A/Paris/896/97(H3N2))]
MKTII ALSYI LCLVFAQKLPNGDNSTATLCLGHHAVPNGTLVKTI TNDQI EVTNATELVQSSSTGRI CDS PHQI LDGKNCTLI DALLGDPHCDGFONKEWDLFVERSTAYSNCYPYDVPDYASLRSLVASSGTLEFTKEG FNTWGVAQDGTSYACKRGSVKSFSSRLNWLHKLEYKYPALNVTMPNNDKFDKLYI WGVHPSTSDSDQTSL YVQASGRVTVSTKRSQQTVI PNI GSRPWVRGVSSRI SI YWTI VKPGDI LLI NSTGNLI APRGYFKI RSGK SSI MRSDAPI DNCNSECI TPNGSI PNDKPFQNVNRI TYGACPRYVKQNTLKLATGMRNVPEKQTRGI FGA I AGFI ENGWEGMVDGWYGFRRHONSEGTOAADLKSTQAAI NOI NGKLNRLI EKTNEKFHAI KEFSEVEG RI ODLEKYVEDTKI DLWSYNAELLVALENOHTI DLTDSEMKNLFFERTRKOLRENAEDMGNGCFKI YHKCD NACI GSI RNGTHYDHDVYRDEALNNRFOI KGVELKSGYKDWI LWI SFAI SCFLLCVVLLGFI MWACQKGN RCNI CI

>gi |14030471|gb|AAK52912.1|AF363504_1 hemagglutinin [Influenza A virus (A/Paris/908/97(H3N2))]
MKTII ALSYI LCLVFAQKLPNGDNSTATLCLGHHAVPNGTLVKTI TNDQI EVTNATELVQSSSTGRI CDS PHRI LDGKNCTLI DALLGDPHCDGFONKEWDLFVERTKAYSNCYPYDVPDYASLRSLVASSGTLEFTNEG FNTWGVAQNGTSYACKRGSVKSFSSRLNWLHKLEYKYPALNVTMPNNDKFDKLYI WGVHPSTSDSDQTSL YVQASGRVTVSTKRSQQTVI PNI GSRPWVRGVSSRI SI YWTI VKPGDI LLI NSTGNLI APRGYFKI RSGK SSI MRSDAPI GNCNSECI TPNGSI PNDKPFQNVNRI TYGACPRYVKQNTLKLATGMRNVPEKQTRGI FGA I AGFI ENGWEGMVDGWYGFRRHONSEGTOAADLKSTQAAI NOI NGKLNRLI EKTNEKFHAI KEFSEVEG

RI ODLEKYVEDTKI DLWSYNAELLVALENOHTI DLTDSEMKNLFFERTRKOLRENAEDMNGGCFKI YHKCD NACI GSI RNGTHYDHDVYRDEALNNRFOI KGVELKSGYKDWI LWI SFAI SCFLLCVVLLGFI MWACQKGN RCNI CI

>gi |89938645|gb|ABD79167.1| hemagglutinin [Influenza A virus (A/New York/579/1997(H3N2))]

MKTI I ALSYI LCLVFAQKLPNGDNSTATLCLGHHAVPNGTLVKTI TNDQI EVTNATELVQSSSTGRI CDS PHQI LDGKNCTLI DALLGDPHCDGFONKEWDLFVERSTAYSNCYPYDVPDYASLRSLVASSGTLEFTKEG FNWTGVAQDGTSYACKRGSVKSFFSRLNWLHKLEYKYPALNVTMPNNDKFDKLYI WGVHHPSTSDSDQTSL YVQASGRVTVSTKRSQQTVI PNI GSRPWVRGVSSRI SI YWTI VKPGDI LLI NSTGNLI APRGYFKI RSGK SSI MRSDAPI DNCNSECI TPNGSI PNDKPFQNVNRI TYGACPRYVKQNTLKLATGMRNVPEKQTRGI FGA I AGFI ENGWEWMVDGWYGFRRHONSEGTOAADLKSTQAAI NOI NGKLNRLI EKTNEKFHAI KEFSEVEG RI ODLEKYVEDTKI DLWSYNAELLVALENOHTI DLTDSEMKNLFFERTRKOLRENAEDMNGGCFKI YHKCD NACI GSI RNGTHYDHDVYRDEALNNRFOI KGVELKSGYKDWI LWI SFAI SCFLLCVVLLGFI MWACQKGN RCNI CI

>gi |89923293|gb|ABD79134.1| hemagglutinin [Influenza A virus (A/New York/564/1997(H3N2))]

MKTI I ALSYI LCLVFAQKLPNGDNSTATLCLGHHAVPNGTLVKTI TNDQI EVTNATELVQSSSTGRI CDS PHQI LDGKNCTLI DALLGDPHCDGFONKEWDLFVERSTAYSNCYPYDVPDYASLRSLVASSGTLEFTKEG FNWTGVAQDGTSYACKRGSVKSFFSRLNWLHKLEYKYPALNVTMPNNDKFDKLYI WGVHHPSTSDSDQTSL YVQASGRVTVSTKRSQQTVI PNI GSRPWVRGVSSRI SI YWTI VKPGDI LLI NSTGNLI APRGYFKI RSGK SSI MRSDAPI DNCNSECI TPNGSI PNDKPFQNVNRI TYGACPRYVKQNTLKLATGMRNVPEKQTRGI FGA I AGFI ENGWEWMVDGWYGFRRHONSEGTOAADLKSTQAAI NOI NGKLNRLI EKTNEKFHAI KEFSEVEG RI ODLEKYVEDTKI DLWSYNAELLVALENOHTI DLTDSEMKNLFFERTRKOLRENAEDMNGGCFKI YHKCD NACI GSI RNGTHYDHDVYRDEALNNRFOI KGVELKSGYKDWI LWI SFAI SCFLLCVVLLGFI MWACQKGN RCNI CI

>gi |194268899|gb|ACF36373.1| hemagglutinin [Influenza A virus (A/Hong Kong/4245/1997(H3N2))]

MKTI I ALSYI LCMVFAQKLPNGDNSTATLCLGHHAVPNGTLVKTI TNDQI EVTNATELVQSSSTGRI CDS PHRI LDGKNCTLI DALLGDPHCDGFONKEWDLFVERSKAYSNCYPYDVPDYASLRSLVASSGTLEFTFNES FNWTGVAQDGTSYACKRGSVKSFFSRLNWLHKLEYKYPALNVTMPNNDKFDKLYI WGVHHPSTSDSDQTSL YVQASGRVTVSTKRSQQTVI PNI GSRPWVRGVSSRI SI YWTI VKPGDI LLI NSTGNLI APRGYFKI RSGK SSI MRSDAPI DNCNSECI TPNGSI PNDKPFQNVNRI TYGACPRYVKQNTLKLATGMRNVPEKQTRGI FGA I AGFI ENGWEWMVDGWYGFRRHONSEGTOAADLKSTQAAI NOI NGKLNRLI EKTNEKFHAI KEFSEVEG RI ODLEKYVEDTKI DLWSYNAELLVALENOHTI DLTDSEMKNLFFERTRKOLRENAEDMNGGCFKI YHKCD NACI GSI RNGTHYDHDVYRDEALNNRFOI KGVELKSGYKDWI LWI SFAI SCFLLCVVLLGFI MWACQKGN RCNI CI

>gi |194268907|gb|ACF36377.1| hemagglutinin [Influenza A virus (A/Hong Kong/4391/1997(H3N2))]

MKTI I ALSYI LCLVFAQKLPNGDNSTATLCLGHHAVPNGTLVKTI TNDQI EVTNATELVQSSSTGRI CDS PHRI LDGKNCTLI DALLGDPHCDGFONKEWDLFVERSTAYSNCYPYDVPDYASLRSLVASSGTLEFTNEG FNWTGVAQDGTSYACKRGSVKSFFSRLNWLHKLEYKYPALNVTMPNNDKFDKLYI WGI HHPSTSDSDQTSL YVHASGRVTVSTKRSQQTVI PNI GSRPWVRGVSSRI SI YWTI VKPGDI LLI NSTGNLI APRGYFKI RSGK SSI MRSDAPI DNCNSECI TPNGSI PNDKPFQNVNRI TYGACPRYVKQNTLKLATGMRNVPEKQTRGI FGA I AGFI ENGWEWMVDGWYGFRRHONSEGTOAADLKSTQAAI NOI NGKLNRLI EKTNEKFHAI KEFSEVEG RI ODLEKYVEDTKI DLWSYNAELLVALENOHTI DLTDSEMKNLFFERTRKOLRENAEDMNGGCFKI YHKCD NACI GSI RNGTHYDHDVYRDEALNNRFOI KGVELKSGYKDWI LWI SFAI SCFLLCVVLLGFI MWACQKGN RCNI CI

>gi |194268913|gb|ACF36380.1| hemagglutinin [Influenza A virus (A/Hong Kong/4542/1997(H3N2))]

MKTI I ALSYI LCLVFAQKLPNGDNSTATLCLGHHAVPNGTLVKTI TNDQI EVTNATELVQSSSTGRI CDS PHRI LDGKNCTLI DALLGDPHCDGFONKEWDLFVERSTAYSNCYPYDVPDYASLRSLVASSGTLEFTNEG FNWTGVAQDGTSYACKRGSVKSFFSRLNWLHKLEYKYPALNVTMPNNDKFDKLYI WGVHHPSTSDSDQTSL YVHASGRVTVSTKRSQQTVI PNI GSRPWVRGVSSRI SI YWTI VKPGDI LLI NSTGNLI APRGYFKI RSGK SSI MRSDAPI DNCNSECI TPNGSI PNDKPFQNVNRI TYGACPRYVKQNTLKLATGMRNVPEKQTRGI FGA I AGFI ENGWEWMVDGWYGFRRHONSEGTOAADLKSTQAAI NOI NGKLNRLI EKTNEKFHAI KEFSEVEG RI ODLEKYVEDTKI DLWSYNAELLVALENOHTI DLTDSEMKNLFFERTRKOLRENAEDMNGGCFKI YHKCD NACI GSI RNGTHYDHDVYRDEALNNRFOI KGVELKSGYKDWI LWI SFAI SCFLLCVVLLGFI MWACQKGN RCNI CI

>gi |194268911|gb|ACF36379.1| hemagglutinin [Influenza A virus (A/Hong Kong/4529/1997(H3N2))]

MKTI I ALSYI LCLVFAQKLPNGDNSTATLCLGHHAVPNGTLVKTI TNDQI EVTNATELVQSSSTGRI CDN PHRI LDGKNCTLI DALLGDPHCDGFONKEWDLFVERSTAYSNCYPYDVPDYASLRSLVASSGTLEFTNEG FNWTGVAQDGTSYACKRGSVKSFFSRLNWLHKLEYKYPALNVTMPNNDKFDKLYI WGVHHPSTSDSDQTSL YVHASGRVTVSTKRSQQTVI PNI GSRPWVRGVSSRI SI YWTI VKPGDI LLI NSTGNLI APRGYFKI RSGK SSI MRSDAPI DNCNSECI TPNGSI PNDKPFQNVNRI TYGACPRYVKQNTLKLATGMRNVPEKQTRGI FGA I AGFI ENGWEWMVDGWYGFRRHONSEGTOAADLKSTQAAI NOI NGKLNRLI EKTNEKFHAI KEFSEVEG RI ODLEKYVEDTKI DLWSYNAELLVALENOHTI DLTDSEMKNLFFERTRKOLRENAEDMNGGCFKI YHKCD NACI GSI RNGTHYDHDVYRDEALNNRFOI KGVELKSGYKDWI LWI SFAI SCFLLCVVLLGFI MWACQKGN RCNI CI

>gi |194268915|gb|ACF36381.1| hemagglutinin [Influenza A virus (A/Hong Kong/4622/1997(H3N2))]

MKTI I ALSYI LCLVFAQKLPNGDNSTATLCLGHHAVPNGTLVKTI TNDQI EVTNATELVQSSSTGRI CDN PHRI LDGKNCTLI DALLGDPHCDGFONKEWDLFVERSTAYSNCYPYDVPDYASLRSLVASSGTLEFTNEG FNWTGVAQDGTSYACKRGSVKSFFSRLNWLHKLEYKYPALNVTMPNNDKFDKLYI WGVHHPSTSDSDQTSL YVHASGRVTVSTKRSQQTVI PNI GSRPWVRGVSSRI SI YWTI VKPGDI LLI NSTGNLI APRGYFKI RSGK SSI MRSDAPI DNCNSECI TPNGSI PNDKPFQNVNRI TYGACPRYVKQNTLKLATGMRNVPEKQTRGI FGA I AGFI ENGWEWMVDGWYGFRRHONSEGTOAADLKSTQAAI NOI NGKLNRLI EKTNEKFHAI KEFSEVEG

RI ODLEKYVEDTKI DLWSYNAELLVALENOHTI DLTDSEMKNLFFERTRKOLRENAEDMNGGCFKI YHKCD
NACI GSI RNGTHYDHDVYRDEALNNRFOI KGVELKSGYKDWI LWI SFAI SCFLLCVVLLGFI MWACQKGN
RCNI CI

>gi |194268917|gb|ACF36382.1| hemagglutinin [Influenza A virus (A/Hong
Kong/CUHK4803/1997(H3N2))]

MKTI I ALSYI LCLVFAQKLPNGDNSTATLCLGHHAVPNGTLVKTI TNDQI EVTNATELVQSSSTGRI CDS
PHRI LDGKNCTLI DALLGDPHCDGFONKEWDLFVERSTAYSNCYPYDVPDYASLRSLVASSGTLEFTNEG
FNWTVGVAQDGTSYACKRRSVKSFSSRLNWLHKLEYKYPALNVTMPNNDKFDKLYI WGVHPSTSDSDQTS
YVHASGRVTVSTKRSQQTVI PNI GSRPWVWVGVSSRI SI YWTI VKPGDI LLI NSTGNLI APRGYFKI RSGK
SSI MRSDAPI DNCNSECI TPNGSI PNDKPFQNVNRI TYGACPRYVKQNTLKLATGMRNVPEKQTRGI FGA
I AGFI ENGWEWMVDGWYGFRRHONSEGTOAADLKSTQAAI NOI NGKLNRLI EKTNEKFHAI KEFSEVEG
RI ODLEKYVEDTKI DLWSYNAELLVALENOHTI DLTDSEMKNLFFERTRKOLRENAEDMNGGCFKI YHKCD
NACI GSI RNGTHYDHDVYRDEALNNRFOI KGVELKSGYKDWI LWI SFAI SCFLLCVVLLGFI MWACQKGN
RCNI CI

>gi |194268561|gb|ACF36204.1| hemagglutinin [Influenza A virus (A/Hong
Kong/CUHK12160/1997(H3N2))]

MKTI I ALSYI LCLVFAQKLPNGDNSTATLCLGHHAVPNGTLVKTI TNDQI EVTNATELVQSSSTGRI CDS
PHRI LDGKNCTLI DALLGDPHCDGFONKEWDLFVERSKAYSNCYPYDVPDYASLRSLVASSGTLEFTNNE
FNWTVGVAQDGTSYACKRRSVKSFSSRLNWLHKLEYKYPALNVTMPNNDKFDKLYI WGVHPSTSDSDQTS
YAQASGRVTVSTKRSQQTVI PNI GSRPWVWVGVSSRI SI YWTI VKPGDI LLI NSTGNLI APRGYFKI RSGK
SSI MRSDAPI GKCNSECI TPNGSI PNDKPFQNVNRI TYGACPRYVKQNTLKLATGMRNVPEKQTRGI FGA
I AGFI ENGWEWMVDGWYGFRRHONSEGTOAADLKSTQAAI NOI NGKLNRLI EKTNEKFHAI KEFSEVEG
RI ODLEKYVEDTKI DLWSYNAELLVALENOHTI DLTDSEMKNLFFERTRKOLRENAEDMNGGCFKI YHKCD
NACI GSI RNGTHYDHDVYRDEALNNRFOI KGVELKSGYKDWI LWI SFAI SCFLLCVVLLGFI MWACQKGN
RCNI CI

>gi |194268575|gb|ACF36211.1| hemagglutinin [Influenza A virus (A/Hong
Kong/CUHK12566/1997(H3N2))]

MKTI I ALSYI LCLVFAQKLPNGDNSTATLCLGHHAVPNGTLVNTI TNDQI EVTNATELVQSSSTGRI CDS
PHRI LDGKNCTLI DALLGDPHCDGFONKEWDLFVERSTAYSNCYPYDVPDYASLRSLVASSGTLEFTNEG
FNWTVGVAQDGTSYACKRRSVKSFSSRLNWLHKLEYKYPALNVTMPNNDKFDKLYI WGVHPSTSDSDQTS
YVHASGRVTVSTKRSQQTVI PNI GSRPWVWVGVSSRI SI YWTI VKPGDI LLI NSTGNLI APRGYFKI RSGK
SSI MRSDAPI DNCNSECI TPNGSI PNDKPFQNVNRI TYGACPRYVKQNTLKLATGMRNVPEKQTRGI FGA
I AGFI ENGWEWMVDGWYGFRRHONSEGTOAADLKSTQAAI NOI NGKLNRLI EKTNEKFHAI KEFSEVEG
RI ODLEKYVEDTKI DLWSYNAELLVALENOHTI DLTDSEMKNLFFERTRKOLRENAEDMNGGCFKI YHKCD
NACI GSI RNGTHYDHDVYRDEALNNRFOI KGVELKSGYKDWI LWI SFAI SCFLLCVVLLGFI MWACQKGN
RCNI CI

>gi |194268573|gb|ACF36210.1| hemagglutinin [Influenza A virus (A/Hong
Kong/CUHK12563/1997(H3N2))]

MKTI I ALSYI LCLVFAQKLPNGDNSTATLCLGHHAVPNGTLVKTI TNDQI EVTNATELVQSSSTGRI CDS
PHRI LDGKNCTLI DALLGDPHCDGFONKEWDLFVERSTAYSNCYPYDVPDYASLRSLVASSGTLEFTNEG
FNWTVGVAQDGTSYACKRRSVKSFSSRLNWLHKLEYKYPALNVTMPNNDKFDKLYI WGVHPSTSDSDQTS
YVHASGRVTVSTKRSQQTVI PNI GSRPWVWVGVSSRI SI YWTI VKPGDI LLI NSTGNLI APRGYFKI RSGK
SSI MRSDAPI DNCNSECI TPNGSI PNDKPFQNVNRI TYGACPRYVKQNTLKLATGMRNVPEKQTRGI FGA
I AGFI ENGWEWMVDGWYGFRRHONSEGTOAADLKSTQAAI NOI NGKLNRLI EKTNEKFHAI KEFSEVEG
RI ODLEKYVEDTKI DLWSYNAELLVALENOHTI DLTDSEMKNLFFERTRKOLRENAEDMNGGCFKI YHKCD
NACI GSI RNGTHYDHDVYRDEALNNRFOI KGVELKSGYKDWI LWI SFAI SCFLLCVVLLGFI MWACQKGN
RCNI CI

>gi |194268581|gb|ACF36214.1| hemagglutinin [Influenza A virus (A/Hong
Kong/CUHK12626/1997(H3N2))]

MKTI I ALSYI LCLVFAQKLPNGDNSTATLCLGHHAVPNGTLVKTI TNDQI EVTNATELVQSSSTGRI CDS
PHRI LDGKNCTLI DALLGDPHCDGFONKEWDLFVERSTAYSNCYPYDVPDYASLRSLVASSGTLEFTNEG
FNWTVGVAQDGTSYACKRRSVKSFSSRLNWLHKLEYKYPALNVTMPNNDKFDKLYI WGVHPSTSDSDQTS
YVHASGRVTVSTKRSQQTVI PNI GSRPWVWVGVSSRI SI YWTI VKPGDI LLI NSTGNLI APRGYFKI RSGK
SSI MRSDAPI DNCNSECI TPNGSI PNDKPFQNVNRI TYGACPRYVKQNTLKLATGMRNVPEKQTRGI FGA
I AGFI ENGWEWMVDGWYGFRRHONSEGTOAADLKSTQAAI NOI NGKLNRLI EKTNEKFHAI KEFSEVEG
RI ODLEKYVEDTKI DLWSYNAELLVALENOHTI DLTDSEMKNLFFERTRKOLRENAEDMNGGCFKI YHKCD
NACI GSI RNGTHYDHDVYRDEALNNRFOI KGVELKSGYKDWI LWI SFAI SCFLLCVVLLGFI MWACQKGN
RCNI CI

>gi |14486408|gb|AAK62042.1| hemagglutinin [Influenza A virus (A/Hong
Kong/1180/99(H3N2))]

MKTI I ALSYI LCLVFAQKLPNGDNSTATLCLGHHAVPNGTLVKTI TNDQI EVTNATELVQSSSTGRI CDS
PHRI LDGENCTLI DALLGDPHCDGFONKEWDLFVERSKAYSNCYPYDVPDYASLRSLVASSGTLEFTNNE
FNWTVGVAQDGTSSACKRRSI KSFSSRLNWLHQLKYRYPALNVTMPNNDKFDKLYI WGVHPSTSDSDQTS
YAQASGRVTVSTKRSQQTVI PNI GSRPWVWVGVSSRI SI YWTI VKPGDI LLI NSTGNLI APRGYFKI RSGK
SSI MRSDAPI GKCNSECI TPNGSI PNDKPFQNVNRI TYGACPRYVKQNTLKLATGMRNVPEKQTRGI FGA
I AGFI ENGWEWMVDGWYGFRRHONSEGTOAADLKSTQAAI NOI NGKLNRLI EKTNEKFHAI KEFSEVEG
RI ODLEKYVEDTKI DLWSYNAELLVALENOHTI DLTDSEMKNLFFERTRKOLRENAEDMNGGCFKI YHKCD
NACI GSI RNGTHYDHDVYRDEALNNRFOI KGVELKSGYKDWI LWI SFAI SCFLLCVVLLGFI MWACQKGN
RCNI CI

>gi |46981871|gb|AAT08002.1| hemagglutinin [Influenza A virus (A/Moscow/10/99(H3N2))]

MKTI I ALSYI LCLVFAQKLPNGDNSTATLCLGHHAVPNGTLVKTI TNDQI EVTNATELVQSSSTGRI CDS
PHRI LDGENCTLI DALLGDPHCDGFONKEWDLFVERSKAYSNCYPYDVPDYASLRSLVASSGTLEFTNNE
FNWTVGVAQDGTSSACKRRSI KSFSSRLNWLHQLKYRYPALNVTMPNNDKFDKLYI WGVHPSTSDSDQTS
YTOASGRVTVSTKRSQQTVI PNI GSRPWVWVGVSSRI SI YWTI VKPGDI LLI NSTGNLI APRGYFKI RSGK
SSI MRSDAPI GKCNSECI TPNGSI PNDKPFQNVNRI TYGACPRYVKQNTLKLATGMRNVPEKQTRGI FGA
I AGFI ENGWEWMVDGWYGFRRHONSEGTOAADLKSTQAAI NOI NGKLNRLI EKTNEKFHAI KEFSEVEG
RI ODLEKYVEDTKI DLWSYNAELLVALENOHTI DLTDSEMKNLFFERTRKOLRENAEDMNGGCFKI YHKCD

NACI GSI RNGTHYDHDVYRDEALNNRFOI KGVELKSGYKDWI LWI SFAI SCFLLCVVLLGFI MWACQKGN
RCNI CI
>gi |115607670|gb|ABJ16598.1| hemagglutinin [Influenza A virus (A/New South
Wales/17/1999(H3N2))]
MKTI I ALSYI LCLVFAQKLPNGDNSTATLCLGHHAVPNGTLVKTI TNDQI EVTNATELVQSSSTGRI CNS
PHQI LDGENCTLI DALLGDPHCDGFONKEWDLFVERSKAYSNCYPYDVPDYASLRSLVASSGTLEFNES
FNWTVGVAQNGTSSACKRRSI KSFSSRLNWLHQLKYKYPALNVTMPNNEKFDKLYI WGVHPSTDSQI SL
YAQASGRVTVSTKRSQOTVI PNI GSRPWVRGVSSRI SI YWTI VKPGDI LLI NSTGNLI APRGYFKI RSGK
SSI MRSDAPI GKCNSCI TPNGSI PNDKPFQNVNRI TYGACPRYVKQNTLKLATGMRNVPEKQTRGI FGA
I AGFI ENGWEQMDGWYGFRRHONSEGTGOAADLKSTQAAI NOI NGKLNRLI EKTNEKFHAI KEFSEVEG
RI ODLEKYVEDTKI DLWSYNAELLVALENOHTI DLTDSEMKNLFERTKQOLRENAEDMNGGCFKI YHKCD
NACI GSI RNGTHYDHDVYRDEALNNRFOI KGVELKSGYKDWI LWI SFAI SCFLLCVVLLGFI MWACQKGN
RCNI CI
>gi |115521598|gb|ABJ09250.1| hemagglutinin [Influenza A virus (A/New South
Wales/2/1999(H3N2))]
MKTI I ALSYI LCLVFAQKLPNGDNSTATLCLGHHAVPNGTLVKTI TNDQI EVTNATELVQSSSTGRI CNS
PHQI LDGENCTLI DALLGDPHCDGFONKEWDLFVERSKAYSNCYPYDVPDYASLRSLVASSGTLEFNES
FNWTVGVAQNGTSSACKRRSI KSFSSRLNWLHQLKYKYPALNVTMPNNEKFDKLYI WGI HHPSTDSQI SL
YAQASGRVTVSTKRSQOTVI PNI GSRPWVRGVSSRI SI YWTI VKPGDI LLI NSTGNLI APRGYFKI RSGK
SSI MRSDAPI GKCNSCI TPNGSI PNDKPFQNVNRI TYGACPRYVKQNTLKLATGMRNVPEKQTRGI FGA
I AGFI ENGWEQMDGWYGFRRHONSEGTGOAADLKSTQAAI NOI NGKLNRLI EKTNEKFHAI KEFSEVEG
RI ODLEKYVEDTKI DLWSYNAELLVALENOHTI DLTDSEMKNLFERTKQOLRENAEDMNGGCFKI YHKCD
NACI GSI RNGTHYDHDVYRDEALNNRFOI KGVELKSGYKDWI LWI SFAI SCFLLCVVLLGFI MWACQKGN
RCNI CI
>gi |115521636|gb|ABJ09272.1| hemagglutinin [Influenza A virus (A/New South
Wales/6/1999(H3N2))]
MKTI I ALSYI LCLVFAQKLPNGDNSTATLCLGHHAVPNGTLVKTI TNDQI EVTNATELVQSSSTGRI CNS
PHQI LDGENCTLI DALLGDPHCDGFONKEWDLFVERSKAYSNCYPYDVPDYASLRSLVASSGTLEFNES
FNWTVGVAQNGTSSACKRRSI KSFSSRLNWLHQLKYKYPALNVTMPNNEKFDKLYI WGVHPSTDSQI SL
YAQASGRVTVSTKRSQOTVI PNI GSRPWVRGVSSRI SI YWTI VKPGDI LLI NSTGNLI APRGYFKI RSGK
SSI MRSDAPI GKCNSCI TPNGSI PNDKPFQNVNRI TYGACPRYVKQNTLKLATGMRNVPEKQTRGI FGA
I AGFI ENGWEQMDGWYGFRRHONSEGTGOAADLKSTQAAI NOI NGKLNRLI EKTNEKFHAI KEFSEVEG
RI ODLEKYVEDTKI DLWSYNAELLVALENOHTI DLTDSEMKNLFERTKQOLRENAEDMNGGCFKI YHKCD
NACI GSI RNGTHYDHDVYRDEALNNRFOI KGVELKSGYKDWI LWI SFAI SCFLLCVVLLGFI MWACQKGN
RCNI CI
>gi |92090508|gb|ABE73114.1| hemagglutinin [Influenza A virus
(A/Panama/2007/1999(H3N2))]
MKTI I ALSYI LCLVFAQKLPNGDNSTATLCLGHAVSNGTLVKTI TNDQI EVTNATELVQSSSTGRI CNS
PHQI LDGENCTLI DALLGDPHCDGFONKEWDLFVERSKAYSNCYPYDVPDYASLRSLVASSGTLEFNES
FNWTVGVAQNGTSSACKRRSNNSSFFSRLNWLHQLKYKYPALNVTMPNNEKFDKLYI WGVHPSTDSQI SI
YAQASGRVTVSTKRSQOTVI PNI GSI PWVRGVSSRI SI YWTI VKPGDI LLI NSTGNLI APRGYFKI RSGK
SSI MRSDAPI GKCNSCI TPNGSI PNDKPFQNVNRI TYGACPRYVKQNTLKLATGMRNVPEKQTRGI FGA
I AGFI ENGWEQMDGWYGFRRHONSEGTGOAADLKSTQAAI NOI NGKLNRLI EKTNEKFHAI KEFSEVEG
RI ODLEKYVEDTKI DLWSYNAELLVALENOHTI DLTDSEMKNLFERTKQOLRENAEDMNGGCFKI YHKCD
NACI GSI RNGTHYDHDVYRDEALNNRFOI KGVELKSGYKDWI LWI SFAI SCFLLCVVLLGFI MWACQKGN
RCNI CI
>gi |92090510|gb|ABE73115.1| hemagglutinin [Influenza A virus (A/Moscow/10/99(H3N2))]
MKTI I ALSYI LCLVFAQKLPNGDNSTATLCLGHAVSNGTLVKTI TNDQI EVTNATELVQSSSTGRI CNS
PHQI LDGENCTLI DALLGDPHCDGFONKEWDLFVERSKAYSNCYPYDVPDYASLRSLVASSGTLEFNES
FNWTVGVAQNGTSSACKRRSI KSFSSRLNWLHQLNRYPALNVTMPNNDKFDKLYI WGVHPSTDSVQTSV
YVQASGRVTVSTKRSQOTVI PNI GSRPWVRGVSSRI SI YWTI VKPGDI LLI NSTGNLI APRGYFKI RSGK
SSI MRSDAPI GKCNSCI TPNGSI PNDKPFQNVNRI TYGACPRYVKQNTLKLATGMRNVPEKQTRGI FGA
I AGFI ENGWEQMDGWYGFRRHONSEGTGOAADLKSTQAAI NOI NGKLNRLI EKTNEKFHAI KEFSEVEG
RI ODLEKYVEDTKI DLWSYNAELLVALENOHTI DLTDSEMKNLFERTKQOLRENAEDMNGGCFKI YHKCD
NACI GSI RNGTHYDHDVYRDEALNNRFOI KGVELKSGYKDWI LWI SFAI SCFLLCVVLLGFI MWACQKGN
RCNI CI
>gi |94481528|gb|ABF21273.1| hemagglutinin [Influenza A virus
(A/Panama/2007/1999(H3N2))]
MKTI I ALSYI LCLVFAQKLPNGDNSTATLCLGHAVSNGTLVKTI TNDQI EVTNATELVQSSSTGRI CNS
PHQI LDGENCTLI DALLGDPHCDGFONKEWDLFVERSKAYSNCYPYDVPDYASLRSLVASSGTLEFNES
FNWTVGVAQNGTSSACKRRSNNSSFFSRLNWLHQLKYKYPALNVTMPNNEKFDKLYI WGVHPSTDSQI SI
YAQASGRVTVSTKRSQOTVI PNI GSSPWVRGVSSRI SI YWTI VKPGDI LLI NSTGNLI APRGYFKI RSGK
SSI MRSDAPI GKCNSCI TPNGSI PNDKPFQNVNRI TYGACPRYVKQNTLKLATGMRNVPEKQTRGI FGA
I AGFI ENGWEQMDGWYGFRRHONSEGTGOAADLKSTQAAI NOI NGKLNRLI EKTNEKFHAI KEFSEVEG
RI ODLEKYVEDTKI DLWSYNAELLVALENOHTI DLTDSEMKNLFERTKQOLRENAEDMNGGCFKI YHKCD
NACI GSI RNGTHYDHDVYRDEALNNRFOI KGVELKSGYKDWI LWI SFAI SCFLLCVVLLGFI MWACQKGN
RCNI CI
>gi |14275704|emb|CAC40044.1| haemagglutinin [Influenza A virus (A/Hong
Kong/1774/99(H3N2))]
MKTI I ALSYI FCMVLGQDLPKGNNTATLCLGHAVPNGTLVKTI TDDQVEVTNATELVONLSMGKI CSN
PHRI LDGANCTLI DALLGDPHCDGFONKEWDLFERSKAFSNCYPYDVEHASLRSLI ASSGTLEFNES
FNWTVGTVONGSSNACKRGPDSFFSRLNWLKSGNTYPMNLNVTMPNSDGFDKLYI WGVHPSTDREQI NL
YVQASGKI TVSTKRSQOTI I PNVGSRPWVRLSSRI SI YWTI VKPGDI LI I SSSGNLI APRGYFKVHTGK
SSI MRSDAPI ETCSSCI TPNGSI PNDKPFQNVNRI TYGACPRYVKQNTLKLATGMRNI PEKQTRGI FGA
I AGFI ENGWEQMDGWYGFRRHONSEGTGOAADLKSTQAAI NOI NGKLNRLI EKTNEKFHAI KEFSEVEG
RI ODLEKYVEDTKI DLWSYNAELLVALENOHTI DLTDSEMKNLFERTKQOLRENAEDMNGGCLKI YHKCD
NSCI DSI RNGTHYDHDVYRDEALNNRFOI KSVELKTGYKDWI LWI SFAI SCFLLCVVLLGFI MWACQKGN

RCNI C

>gi |194352295|gb|ACF54554.1| hemagglutinin [Influenza A virus (A/Panama/2007/1999(H3N2))]
 MKTI I ALSYI LCLVFAQKLPNGDNSTATLCLGHHA VSNGLTVKTI TNDQI EVTNATELVQSSSTGRI CDS
 PHQI LDGENCTLI DALLGDPHCDGFONKEWDLFVERS KAYSNCYPYDVPDYASLRSLVASSGTLFNNES
 FNWTGVAQNGTSSACKRRSNKSFSSRLNWLHQLKYKYPALNVTMPNNEKFDKLYI WGVHHPSTDSQI SI
 YAQASGRVTVSTKRSQQTVI PNI GSSPWVRGVSSRI SI YWTI VKPGDI LLI NSTGNLI APRGYFKI RSGK
 SSI MRSDAPI GKCNSECI TPNGSI PNDKPFQNVNRI TYGACPRYVKQNTLKLATGMRNVPEKQTRGI FGA
 I AGFI ENGWEGMVDGWYGFRRHQNSEGTGOAADLKSTQAAI NQI NGKLNRLI EKTNEKFHQI EKEFSEVEG
 RI ODLEKYVEDTKI DLWSYNAELLVALENOHTI DLTDSEMNKLFERTKKQLRENAEDMNGGCFKI YHKCD
 NACI GSI RNGTYDHDVYRDEALNRRFOI KGVLEKSGYKDWI LWI SFAI SCFLLCVVLLGFI MWACQKGN
 RCNI CI

H5N1

>gi |3421260|gb|AAC32100.1| hemagglutinin subtype H5 [Influenza A virus (A/Hong Kong/482/97(H5N1))]

MEKI VLLLATVSLVKSQDI CI GYHANNSTEQVDTI MEKNVTVTHAQDI LERTHNGKLCDLNGVKPLI LRD
 CSVAGWLLGNPMCMDEFI NVPEWSYI VEKASPANDLCYPGNFNDYEELKHLLSRI NHFEKI QI I PKSSWSN
 HDASSGVSSACPYLGRSSFFRN VVWLI KKN SAYPTI KRSYNNTNOEDLLVWGI HHPNDAAEQTKLYQNP
 TTYI SVGTSTLNQRLVPEI ATRPKVNGQSGRMEFFWTI LKPNDAI NFESNGNFI APEYAYKI VKKGDSTI
 MKSELEYGNCNTKQCTPMGAI NSSMPFHNI HPLTI GECPKYVKS NRLVLATGLRNTPQRERRRKRGLFG
 AI AGFI EGGWQGMVDGWYGYHHSNEQSGYAADKESTQKAI DGVTKVNSI I NKMNTOFEAVGREFNLE
 RRI ENLNKMKMEDGFLD VWTYNAELLVLMENERTLDFHDSNVKNLYDKVRLQLRDN AKELGNGCFEFYHKC
 DNECMESVRNGTYDYPQYSEEARLNREEI SGVKLESMGTYQI LSI YSTVASSLALAI MVAGLSLWMCNSG
 SLOCRI CI

>gi |54402287|gb|AAV34704.1| hemagglutinin [Influenza A virus (A/Thailand/4(SP-528)/2004(H5N1))]

MEKI VLLFAI VSLVKSQDI CI GYHANNSTEQVDTI MEKNVTVTHAQDI LEKTHNGKLCDLGDKVPLI LRD
 CSVAGWLLGNPMCMDEFI NVPEWSYI VEKANPVNDLCYPGDFNDYEELKHLLSRI NHFEKI QI I PKSSWSS
 HEASLGVSACPYQKSSFFRN VVWLI KKNSTYPTI KRSYNNTNOEDLLVWGI HHPNDAAEQTKLYQNP
 TTYI SVGTSTLNQRLVPR I ATRSKVNGQSGRMEFFWTI LKPNDAI NFESNGNFI APEYAYKI VKKGDSTI
 MKSELEYGNCNTKQCTPMGAI NSSMPFHNI HPLTI GECPKYVKS NRLVLATGLRNSPQRERRRKRGLFG
 AI AGFI EGGWQGMVDGWYGYHHSNEQSGYAADKESTQKAI DGVTKVNSI I DKMNTOFEAVGREFNLE
 RRI ENLNKMKMEDGFLD VWTYNAELLVLMENERTLDFHDSNVKNLYDKVRLQLRDN AKELGNGCFEFYHKC
 DNECMESVRNGTYDYPQYSEEARLKREEI SGVKLESI GI YQI LSI YSTVASSLALAI MVAGLSLWMCNSG
 SLOCRI CI

>gi |58618438|gb|AAW80717.1| hemagglutinin HA [Influenza A virus (A/Viet Nam/1203/2004(H5N1))]

MEKI VLLFAI VSLVKSQDI CI GYHANNSTEQVDTI MEKNVTVTHAQDI LEKTHNGKLCDLGDKVPLI LRD
 CSVAGWLLGNPMCMDEFI NVPEWSYI VEKANPVNDLCYPGDFNDYEELKHLLSRI NHFEKI QI I PKSSWSS
 HEASLGVSACPYQKSSFFRN VVWLI KKNSTYPTI KRSYNNTNOEDLLVWGI HHPNDAAEQTKLYQNP
 TTYI SVGTSTLNQRLVPR I ATRSKVNGQSGRMEFFWTI LKPNDAI NFESNGNFI APEYAYKI VKKGDSTI
 MKSELEYGNCNTKQCTPMGAI NSSMPFHNI HPLTI GECPKYVKS NRLVLATGLRNSPQRERRRKRGLFG
 AI AGFI EGGWQGMVDGWYGYHHSNEQSGYAADKESTQKAI DGVTKVNSI I DKMNTOFEAVGREFNLE
 RRI ENLNKMKMEDGFLD VWTYNAELLVLMENERTLDFHDSNVKNLYDKVRLQLRDN AKELGNGCFEFYHKC
 DNECMESVRNGTYDYPQYSEEARLKREEI SGVKLESI GI YQI LSI YSTVASSLALAI MVAGLSLWMCNSG
 SLOCRI CI

>gi |113494676|gb|ABI 36040.1| hemagglutinin [Influenza A virus (A/Indonesia/CDC184/2005(H5N1))]

DQI CI GYHANNSTEQVDTI MEKNVTVTHAQDI LEKTHNGKLCDLGDKVPLI LRDCSVAGWLLGNPMCMDEF
 I NVPEWSYI VEKANPTNDLCYPGSFNDYEELKHLLSRI NHFEKI QI I PKSSWSDHEASSGVSSACPYLGS
 PSFFRN VVWLI KKNSTYPTI KRSYNNTNOEDLLVWGI HHPNDGAEQTRLYQNP TTYI SI GTSTLNQRLV
 PKI ATRSKVNGQSGRMEFFWTI LKPNDAI NFESNGNFI APEYAYKI VKKGD SAI MKSELEYGNCNTKQCT
 PMGAI NSSMPFHNI HPLTI GECPKYVKS NRLVLATGLRNSPQRESRRKRGLFGAI AGFI EGGWQGMVDG
 WYGYHHSNEQSGYAADKESTQRAI DGVTKVNSI I DKMNTOFEAVGREFNLE RRI ENLNKMKMEDGFLD
 VWTYNAELLVLMENERTLDFHDSNVKNLYDKVRLQLRDN AKELGNGCFEFYHKCDNECMESI RNGTYNYP
 QYSEEARLKREEI SGVKLESI GTYQI LSI YSTVASSLALAI MMAGLSLWMCNSG SLOCRI CI

>gi |113494698|gb|ABI 36044.1| hemagglutinin [Influenza A virus (A/Indonesia/CDC292N/2005(H5N1))]

DQI CI GYHANNSTEQVDTI MEKNVTVTHAQDI LEKTHNGKLCDLGDKVPLI LRDCSVAGWLLGNPMCMDEF
 I NVPEWSYI VEKANPTNDLCYPGSFNDYEELKHLLSRI NHFEKI QI I PKSSWSDHEASSGVSSACPYLGS
 PSFFRN VVWLI KKNSTYPTI KRSYNNTNOEDLLVWGI HHPNDAAEQTRLYQNP TTYI SI GTSTLNQRLV
 PKI ATRSKVNGQSGRMEFFWTI LNPNDAI NFESNGNFI APEYAYKI VKKGD SAI MKSELEYGNCNTKQCT
 PMGAI NSSMPFHNI HPLTI GECPKYVKS NRLVLATGLRNSPQRESRRKRGLFGAI AGFI EGGWQGMVDG
 WYGYHHSNEQSGYAADKESTQKAI DGVTKVNSI I DKMNTOFEAVGREFNLE RRI ENLNKMKMEDGFLD
 VWTYNAELLVLMENERTLDFHDSNVKNLYDKVRLQLRDN AKELGNGCFEFYHKCDNECMESI RNGTYNYP
 QYSEEARLKREEI SGVKLESI GTYQI LSI YSTVASSLALAI MMAGLSLWMCNSG SLOCRI CI

>gi |113494703|gb|ABI 36045.1| hemagglutinin [Influenza A virus (A/Indonesia/CDC292T/2005(H5N1))]

DQI CI GYHANNSTEQVDTI MEKNVTVTHAQDI LEKTHNGKLCDLGDKVPLI LRDCSVAGWLLGNPMCMDEF
 I NVPEWSYI VEKANPTNDLCYPGSFNDYEELKHLLSRI NHFEKI QI I PKSSWSDHEASSGVSSACPYLGS
 PSFFRN VVWLI KKNSTYPTI KRSYNNTNOEDLLVWGI HHPNDAAEQTRLYQNP TTYI SI GTSTLNQRLV
 PKI ATRSKVNGQSGRMEFFWTI LNPNDAI NFESNGNFI APEYAYKI VKKGD SAI MKSELEYGNCNTKQCT
 PMGAI NSSMPFHNI HPLTI GECPKYVKS NRLVLATGLRNSPQRESRRKRGLFGAI AGFI EGGWQGMVDG
 WYGYHHSNEQSGYAADKESTQKAI DGVTKVNSI I DKMNTOFEAVGREFNLE RRI ENLNKMKMEDGFLD
 VWTYNAELLVLMENERTLDFHDSNVKNLYDKVRLQLRDN AKELGNGCFEFYHKCDNECMESI RNGTYNYP

QYSEEARLKREEI SGVKLESI GTYQI LSI YSTVASSLALAI MMAGLSLWMCNSGSLQCRI CI
 >gi |113494709|gb|ABI 36046. 1| hemagglutinin [Influenza A virus
 (A/Indonesia/326N/2006(H5N1))]
 DOI CI GYHANNSTEQVDTI MEKNVTVTHAQDI LEKTHNGKLCDLGDKVPLI LRDCSVAGWLLGNPMCEFI
 I NVPEWSYI VEKANPTNDLCYPGSFNDYEELKHLLSRI NHFEKI QI I PKSSWSDEASSGVSSACPYLGS
 PSFFRNVVWLI KKNSTYPTI KKSNNNTNOEDLLVWGI HHPNDAAEQTRLYQNPTTYI SI GTSTLNQRLV
 PKI ATRSKVNGQSGRMEFFWTI LNPNDI NFESNGNFI APEYAYKI VKKGDSAI MKSELEYGNCNTKCO
 PMGAI NSSMPFHNI HPLTI GECPKYVKSRLVATGLRNSPQRESRRKRGLFGAI AGFI EGGWQGMVDG
 WYGYHHSNEQGSYAADKESTQKAI DGVTKVNSI I DKMNTQFEAVGREFFNNLERRI ENLNKKMEDGFLD
 VWTYNAELLVLMENERTLDFHDSNVKNLYDKVRLQLRDNAKELGNGCFEFYHKCDNECMESI RINGTYNYP
 QYSEEARLKREEI SGVKLESI GTYQI LSI YSTVASSLALAI MMAGLSLWMCNSGSLQCRI CI
 >gi |113494718|gb|ABI 36047. 1| hemagglutinin [Influenza A virus
 (A/Indonesia/326N2/2006(H5N1))]
 DOI CI GYHANNSTEQVDTI MEKNVTVTHAQDI LEKTHNGKLCDLGDKVPLI LRDCSVAGWLLGNPMCEFI
 I NVPEWSYI VEKANPTNDLCYPGSFNDYEELKHLLSRI NHFEKI QI I PKSSWSDEASSGVSSACPYLGS
 PSFFRNVVWLI KKNSTYPTI KKSNNNTNOEDLLVWGI HHPNDAAEQTRLYQNPTTYI SI GTSTLNQRLV
 PKI ATRSKVNGQSGRMEFFWTI LNPNDI NFESNGNFI APEYAYKI VKKGDSAI MKSELEYGNCNTKCO
 PMGAI NSSMPFHNI HPLTI GECPKYVKSRLVATGLRNSPQRESRRKRGLFGAI AGFI EGGWQGMVDG
 WYGYHHSNEQGSYAADKESTQKAI DGVTKVNSI I DKMNTQFEAVGREFFNNLERRI ENLNKKMEDGFLD
 VWTYNAELLVLMENERTLDFHDSNVKNLYDKVRLQLRDNAKELGNGCFEFYHKCDNECMESI RINGTYNYP
 QYSEEARLKREEI SGVKLESI GTYQI LSI YSTVASSLALAI MMAGLSLWMCNSGSLQCRI CI
 >gi |113494735|gb|ABI 36049. 1| hemagglutinin [Influenza A virus
 (A/Indonesia/326T/2006(H5N1))]
 DOI CI GYHANNSTEQVDTI MEKNVTVTHAQDI LEKTHNGKLCDLGDKVPLI LRDCSVAGWLLGNPMCEFI
 I NVPEWSYI VEKANPTNDLCYPGSFNDYEELKHLLSRI NHFEKI QI I PKSSWSDEASSGVSSACPYLGS
 PSFFRNVVWLI KKNSTYPTI KKSNNNTNOEDLLVWGI HHPNDAAEQTRLYQNPTTYI SI GTSTLNQRLV
 PKI ATRSKVNGQSGRMEFFWTI LNPNDI NFESNGNFI APEYAYKI VKKGDSAI MKSELEYGNCNTKCO
 PMGAI NSSMPFHNI HPLTI GECPKYVKSRLVATGLRNSPQRESRRKRGLFGAI AGFI EGGWQGMVDG
 WYGYHHSNEQGSYAADKESTQKAI DGVTKVNSI I DKMNTQFEAVGREFFNNLERRI ENLNKKMEDGFLD
 VWTYNAELLVLMENERTLDFHDSNVKNLYDKVRLQLRDNAKELGNGCFEFYHKCDNECMESI RINGTYNYP
 QYSEEARLKREEI SGVKLESI GTYQI LSI YSTVASSLALAI MMAGLSLWMCNSGSLQCRI CI
 >gi |113495235|gb|ABI 36056. 1| hemagglutinin [Influenza A virus
 (A/Indonesia/370T/2006(H5N1))]
 DOI CI GYHANNSTEQVDTI MEKNVTVTHAQDI LEKTHNGKLCDLGDKVPLI LRDCSVAGWLLGNPMCEFI
 I NVPEWSYI VEKANPTNDLCYPGSFNDYEELKHLLSRI NHFEKI QI I PKSSWSDEASSGVSSACPYLGS
 PSFFRNVVWLI KKNSTYPTI KKSNNNTNOEDLLVWGI HHPNDAAEQTRLYQNPTTYI SI GTSTLNQRLV
 PKI ATRSKVNGQSGRMEFFWTI LNPNDI NFESNGNFI APEYAYKI VKKGDSAI MKSELEYGNCNTKCO
 PMGAI NSSMPFHNI HPLTI GECPKYVKSRLVATGLRNSPQRESRRKRGLFGAI AGFI EGGWQGMVDG
 WYGYHHSNEQGSYAADKESTQKAI DGVTKVNSI I DKMNTQFEAVGREFFNNLERRI ENLNKKMEDGFLD
 VWTYNAELLVLMENERTLDFHDSNVKNLYDKVRLQLRDNAKELGNGCFEFYHKCDNECMESI RINGTYNYP
 QYSEEARLKREEI SGVKLESI GTYQI LSI YSTVASSLALAI MMAGLSLWMCNSGSLQCRI CI
 >gi |113495243|gb|ABI 36057. 1| hemagglutinin [Influenza A virus
 (A/Indonesia/390/2006(H5N1))]
 DOI CI GYHANNSTEQVDTI MEKNVTVTHAQDI LEKTHNGKLCDLGDKVPLI LRDCSVAGWLLGNPMCEFI
 I NVPEWSYI VEKANPTNDLCYPGSFNDYEELKHLLSRI NHFEKI QI I PKSSWSDEASSGVSSACPYLGS
 PSFFRNVVWLI KKNSTYPTI KKSNNNTNOEDLLVWGI HHPNDAAEQTRLYQNPTTYI SI GTSTLNQRLV
 PKI ATRSKVNGQSGRMEFFWTI LNPNDI NFESNGNFI APEYAYKI VKKGDSAI MKSELEYGNCNTKCO
 PMGAI NSSMPFHNI HPLTI GECPKYVKSRLVATGLRNSPQRESRRKRGLFGAI AGFI EGGWQGMVDG
 WYGYHHSNEQGSYAADKESTQKAI DGVTKVNSI I DKMNTQFEAVGREFFNNLERRI ENLNKKMEDGFLD
 VWTYNAELLVLMENERTLDFHDSNVKNLYDKVRLQLRDNAKELGNGCFEFYHKCDNECMESI RINGTYNYP
 QYSEEARLKREEI SGVKLESI GTYQI LSI YSTVASSLALAI MMAGLSLWMCNSGSLQCRI CI
 >gi |124098875|gb|ABM90456. 1| hemagglutinin [Influenza A virus
 (A/Indonesia/1031T2/2007(H5N1))]
 DOI CI GYHANNSTEQVDTI MEKNVTVTHAQDI LEKTHNGKLCDLGDKVPLI LRDCSVAGWLLGNPMCEFI
 I NVPEWSYI VEKANPTNDLCYPGSFNDYEELKHLLSRI NHFEKI QI I PKSSWSDEASSGVSSACPYLGS
 PSFFRNVVWLI KKNSTYPTI KKSNNNTNOEDLLVWGI HHPNDAAEQTRLYQNPTTYI SI GTSTLNQRLV
 PKI ATRSKVNGQSGRMEFFWTI LNPNDI NFESNGNFI APEYAYKI VKKGDSAI MKSELEYGNCNTKCO
 PMGAI NSSMPFHNI HPLTI GECPKYVKSRLVATGLRNSPQRESRRKRGLFGAI AGFI EGGWQGMVDG
 WYGYHHSNEQGSYAADKESTQKAI DGVTKVNSI I DKMNTQFEAVGREFFNNLERRI ENLNKKMEDGFLD
 VWTYNAELLVLMENERTLDFHDSNVKNLYDKVRLQLRDNAKELGNGCFEFYHKCDNECMESI RINGTYNYP
 QYSEEARLKREEI SGVKLESI GTYQI LSI YSTVASSLALAI MMAGLSLWMCNSGSLQCRI CI
 >gi |118864330|gb|ABI 49415. 2| hemagglutinin [Influenza A virus
 (A/Indonesia/759/2006(H5N1))]
 MEKI VLLLAI VSLVKSQDI CI GYHANNSTEQVDTI MEKNVTVTHAQDI LEKTHNGKLCDLGDKVPLI LRDCSVAGWLLGNPMCEFI
 I NVPEWSYI VEKANPTNDLCYPGSFNDYEELKHLLSRI NHFEKI QI I PKSSWSDEASSGVSSACPYLGS
 PSFFRNVVWLI KKNSTYPTI KKSNNNTNOEDLLVWGI HHPNDAAEQTRLYQNPTTYI SI GTSTLNQRLV
 PKI ATRSKVNGQSGRMEFFWTI LNPNDI NFESNGNFI APEYAYKI VKKGDSAI MKSELEYGNCNTKCO
 PMGAI NSSMPFHNI HPLTI GECPKYVKSRLVATGLRNSPQRESRRKRGLFGAI AGFI EGGWQGMVDG
 WYGYHHSNEQGSYAADKESTQKAI DGVTKVNSI I DKMNTQFEAVGREFFNNLERRI ENLNKKMEDGFLD
 VWTYNAELLVLMENERTLDFHDSNVKNLYDKVRLQLRDNAKELGNGCFEFYHKCDNECMESI RINGTYNYP
 QYSEEARLKREEI SGVKLESI GTYQI LSI YSTVASSLALAI MMAGLSLWMCNSGSLQCRI CI
 >gi |118864126|gb|ABL31744. 1| hemagglutinin [Influenza A virus
 (A/Indonesia/835/2006(H5N1))]
 MEKI VLLLAI VSLVKSQDI CI GYHANNSTEQVDTI MEKNVTVTHAQDI LEKTHNGKLCDLGDKVPLI LRDCSVAGWLLGNPMCEFI
 I NVPEWSYI VEKANPTNDLCYPGSFNDYEELKHLLSRI NHFEKI QI I PKSSWSDEASSGVSSACPYLGS
 PSFFRNVVWLI KKNSTYPTI KKSNNNTNOEDLLVWGI HHPNDAAEQTRLYQNPTTYI SI GTSTLNQRLV
 PKI ATRSKVNGQSGRMEFFWTI LNPNDI NFESNGNFI APEYAYKI VKKGDSAI MKSELEYGNCNTKCO
 PMGAI NSSMPFHNI HPLTI GECPKYVKSRLVATGLRNSPQRESRRKRGLFGAI AGFI EGGWQGMVDG
 WYGYHHSNEQGSYAADKESTQKAI DGVTKVNSI I DKMNTQFEAVGREFFNNLERRI ENLNKKMEDGFLD
 VWTYNAELLVLMENERTLDFHDSNVKNLYDKVRLQLRDNAKELGNGCFEFYHKCDNECMESI RINGTYNYP
 QYSEEARLKREEI SGVKLESI GTYQI LSI YSTVASSLALAI MMAGLSLWMCNSGSLQCRI CI

TTYI SI GTSTLNQRLVPKI ATRSKVNGQSGRMEFFWTI LKPNDAI NFESNGNFI APEYAYKI VKKGDSDAI
MKSELEYGNCNTKCQTPMGAI NSSMPFHNI HPLTI GECPKYVKS NRLVLATGLRNSPORESRRKKRGLFGAI
AGFI EGGWQGMVDGWYGYHHSNEQSGYAADKESTOKAI DGVTNKVNSI I DKMNTQFEAVGREFNNLE
RRI ENLNKMKMEDGFLDVWYTNAELLVLMENERLDFHDSNVKNLYDKVRLQLRDNAKELGNGCFEFYHKC
DNECMESI RNGTHYNYPOYSEEARLKREEI SGVKLESI GTYQI LSI YSTVASSLALAI MI AGLSLWMCNSG
SLQCRI CI

>gi |157103062|gb|ABV23940.1| hemagglutinin [Influenza A virus
(A/Iraq/756/2006(H5N1))]

DOI CI GYHANNSTEQVDTI MEKNVTVTHAQDI LEKTHNGKLCDLGDKVPLI LRDCSVAGWLLGNPMCD
LNVPEWSYI VEKI NPANDLCYPGNFNDYEELKHLLSRI NHFEKI QI I PKSSWSDHEASSGVSSACYPQGR
SSFFRNWVWLI KKNSTYPTI KRSYNNNTNOEDLLVWGI HHPNDAAEQTRLYRNPTTYI SVGTSTLNQRLV
PKI ATRSKVNGQSGRMEFFWTI LKPNDAI NFESNGNFI APENAYKI VKKGDSTI MKSELEYGNCNTKCQ
PI GAI NSSMPFHNI HPLTI GECPKYVKS NRLVLATGLRNSPOGERRRKRGLFGAI AGFI EGGWQGMVDG
WYGYHHSNEQSGYAADKESTOKAI DGVTNKVNSI I DKMNTQFEAVGREFNNLERRI ENLNKMKMEDGFLD
VWYTNAELLVLMENERLDFHDSNVKNLYDKVRLQLRDNAKELGNGCFEFYHRCNECMESVRNGTYDYP
QYSEEARLKREEI SGVKLESI GTYQI LSI YSTVASSLALAI MVAGLSLWMCNSGSLQCRI CI

>gi |159144911|gb|ABW90130.1| hemagglutinin [Influenza A virus (A/Viet
Nam/1203/2004(H5N1))]

MEKI VLLFAI VSLVKSQDI CI GYHANNSTEQVDTI MEKNVTVTHAQDI LEKTHNGKLCDLGDKVPLI LRD
CSVAGWLLGNPMCDDEFI NVPEWSYI VEKANPVNDLCYPGDFNDYEELKHLLSRI NHFEKI QI I PKSSWSS
HEASLGVSACYPQGRKSSFFRNWVWLI KKNSTYPTI KRSYNNNTNOEDLLVWGI HHPNDAAEQTKLYQNP
TTYI SVGTSTLNQRLVPRI ATRSKVNGQSGRMEFFWTI LKPNDAI NFESNGNFI APEYAYKI VKKGDSTI
MKSELEYGNCNTKCQTPMGAI NSSMPFHNI HPLTI GECPKYVKS NRLVLATGLRNSPORETRGLFGAI AG
FI EGGWQGMVDGWYGYHHSNEQSGYAADKESTOKAI DGVTNKVNSI I DKMNTQFEAVGREFNNLERRI E
NLNKKMEDGFLDVWYTNAELLVLMENERLDFHDSNVKNLYDKVRLQLRDNAKELGNGCFEFYHKCDNEC
MESVRNGTYDYPQYSEEARLKREEI SGVKLESI GI YQI LSI YSTVASSLALAI MVAGLSLWMCNSGSLQ
CRI CI

>gi |159144913|gb|ABW90131.1| hemagglutinin [Influenza A virus (A/Viet
Nam/1203/2004(H5N1))]

MEKI VLLFAI VSLVKSQDI CI GYHANNSTEQVDTI MEKNVTVTHAQDI LEKTHNGKLCDLGDKVPLI LRD
CSVAGWLLGNPMCDDEFI NVPEWSYI VEKANPVNDLCYPGDFNDYEELKHLLSRI NHFEKI QI I PKSSWSS
HEASLGVSACYPQGRKSSFFRNWVWLI EKNSTYPTI KRSYNNNTNOEDLLVWGI HHPNDAAEQTKLYQNP
TTYI SVGTSTLNQRLVPRI ATRSKVNGQSGRMEFFWTI LKPNDAI NFESNGNFI APEYAYKI VKKGDSTI
MKSELEYGNCNTKCQTPMGAI NSSMPFHNI HPLTI GECPKYVKS NRLVLATGLRNSPORETRGLFGAI AG
FI EGGWQGMVDGWYGYHHSNEQSGYAADKESTOKAI DGVTNKVNSI I DKMNTQFEAVGREFNNLERRI E
NLNKKMEDGFLDVWYTNAELLVLMENERLDFHDSNVKNLYDKVRLQLRDNAKELGNGCFEFYHKCDNEC
MESVRNGTYDYPQYSEEARLKREEI SGVKLESI GI YQI LSI YSTVASSLALAI MVAGLSLWMCNSGSLQ
CRI CI

>gi |159144915|gb|ABW90132.1| hemagglutinin [Influenza A virus (A/Viet
Nam/1203/2004(H5N1))]

MEKI VLLFAI VSLVKSQDI CI GYHANNSTEQVDTI MEKNVTVTHAQDI LEKTHNGKLCDLGDKVPLI LRD
CSVAGWLLGNPMCDDEFI NVPEWSYI VEKANPVNDLCYPGDFNDYEELKHLLSRI NHFEKI QI I PKSSWSS
HEASLGVSACYPQGRKSSFFRNWVWLI KKNSTYPTI KRSYNNNTNOEDLLVWGI HHPNDAAEQTKLYQNP
TTYI SVGTSTLNQRLVPRI ATRSKVNGQSGRMEFFWTI LKPNDAI NFESNGNFI APEYAYKI VKKGDSTI
MKSELEYGNCNTKCQTPMGAI NSSMPFHNI HPLTI GECPKYVKS NRLVLATGLRNSPORETRGLFGAI AG
FI EGGWQGMVDGWYGYHHSNEQSGYAADKESTOKAI DGVTNKVNSI I DKMNTQFEAVGREFNNLERRI E
NLNKKMEDGFLDVWYTNAELLVLMENERLDFHDSNVKNLYDKVRLQLRDNAKELGNGCFEFYHKCDNEC
MESVRNGTYDYPQYSEEARLKREEI SGVKLESI GI YQI LSI YSTVASSLALAI MVAGLSLWMCNSGSLQ
CRI CI

>gi |159144917|gb|ABW90133.1| hemagglutinin [Influenza A virus (A/Viet
Nam/1203/2004(H5N1))]

MEKI VLLFAI VSLVKSQDI CI GYHANNSTEQVDTI MEKNVTVTHAQDI LEKTHNGKLCDLGDKVPLI LRD
CSVAGWLLGNPMCDDEFI NVPEWSYI VEKANPVNDLCYPGDFNDYEELKHLLSRI NHFEKI QI I PKSSWSS
HEASLGVSACYPQGRKSSFFRNWVWLI KKNSTYPTI KRSYNNNTNOEDLLVWGI HHPNDAAEQTKLYQNP
TTYI SVGTSTLNQRLVPRI ATRSKVNGQSGRMEFFWTI LKPNDAI NFESNGNFI APEYAYKI VKKGDSTI
MKSELEYGNCNTKCQTPMGAI NSSMPFHNI HPLTI GECPKYVKS NRLVLATGLRNSPORETRGLFGAI AG
FI EGGWQGMVDGWYGYHHSNEQSGYAADKESTOKAI DGVTNKVNSI I DKMNTQFEAVGREFNNLERRI E
NLNKKMEDGFLDVWYTNAELLVLMENERLDFHDSNVKNLYDKVRLQLRDNAKELGNGCFEFYHKCDNEC
MESVRNGTYDYPQYSEEARLKREEI SGVKLESI GI YQI LSI YSTVASSLALAI MVAGLSLWMCNSGSLQ
CRI CI

>gi |159144923|gb|ABW90136.1| hemagglutinin [Influenza A virus (A/Viet
Nam/1203/2004(H5N1))]

MEKI VLLFAI VSLVKSQDI CI GYHANNSTEQVDTI MEKNVTVTHAQDI LEKTHNGKLCDLGDKVPLI LRD
CSVAGWLLGNPMCDDEFI NVPEWSYI VEKANPVNDLCYPGDFNDYEELKHLLSRI NHFEKI QI I PKSSWSS
HEASLGVSACYPQGRKSSFFRNWVWLI KKNSTYPTI KRSYNNNTNOEDLLVWGI HHPNDAAEQTKLYQNP
TTYI SVGTSTLNQRLVPRI ATRSKVNGQSGRMEFFWTI LKPNDAI NFESNGNFI APEYAYKI VKKGDSTI
MKSELEYGNCNTKCQTPMGAI NSSMPFHNI HPLTI GECPKYVKS NRLVLATGLRNSPORETRGLFGAI AG
FI EGGWQGMVDGWYGYHHSNEQSGYAADKESTOKAI DGVTNKVNSI I DKMNTQFEAVGREFNNLERRI E
NLNKKMEDGFLDVWYTNAELLVLMENERLDFHDSNVKNLYDKVRLQLRDNAKELGNGCFEFYHKCDNEC
MESVRNGTYDYPQYSEEARLKREEI SGVKLESI GI YQI LSI YSTVASSLALAI MVAGLSLWMCNSGSLQ
CRI CI

>gi |159144925|gb|ABW90137.1| hemagglutinin [Influenza A virus (A/Viet
Nam/1203/2004(H5N1))]

MEKI VLLFAI VSLVKSQDI CI GYHANNSTEQVDTI MEKNVTVTHAQDI LEKTHNGKLCDLGDKVPLI LRD
CSVAGWLLGNPMCDDEFI NVPEWSYI VEKANPVNDLCYPGDFNDYEELKHLLSRI NHFEKI QI I PKSSWSS
HEASLGVSACYPQGRKSSFFRNWVWLI KKNSTYPTI KRSYNNNTNOEDLLVWGI HHPNDAAEQTKLYQNP
TTYI SVGTSTLNQRLVPRI ATRSKVNGQSGRMEFFWTI LKPNDAI NFESNGNFI APEYAYKI VKKGDSTI

MKSELEYGNCNTKCQTPMGA I NSSMPFHNI HPLTI GECPKYVKS NRLVLATGLRNSPQRETRGLFGAI AG FI EGGWQGMVDGWYGYHHSNEQSGYAADKESTQKAI DGVTNKVNSI I DKMNTQFEAVGREFNLERRI E NLNKKMEDGFLDVWYTNAELLVLMENERTLDFHDSNVKNLYDKVRLQLRDNNAKELGNGCFEFYHKCDNEC MESVRNGTYDYPQYSEEARLKREEI SGVKLESI GI YQI LSI YSTVASSLALAI MVAGLSLWMCNSNGSLOCR I CI

>gi |50296053|gb|AAT73274.1| hemagglutinin [Influenza A virus (A/Viet Nam/1203/2004 (H5N1))]

MEKI VLLFAI VSLVKSDQI CI GYHANNSTEQVDTI MEKNVTVTHAQDI LEKTHNGKLCDLGDKVPLI LRD CSVAGWLLGNPMCMDEFI NVPEWSYI VEKANPVNDLCYPGDFNDYEELKHLRSRI NHFEKI QI I PKSSWSS HEASLGVSACPYQKSSFFRNWVWLI KKNSTYPTI KRSYNNTNOEDLLVWGI HHPNDAAEQTKLYQNP TTYI SVGTSTLNQRLVPR I ATRSKVNGQSGRMEFFWTI LKPNDAI NFESNGNFI APEYAYKI VKKGDSTI MKSELEYGNCNTKCQTPMGA I NSSMPFHNI HPLTI GECPKYVKS NRLVLATGLRNSPQRETRRRRKRGLFG AI AGFI EGGWQGMVDGWYGYHHSNEQSGYAADKESTQKAI DGVTNKVNSI I DKMNTQFEAVGREFNLER RRI ENLNKKMEDGFLDVWYTNAELLVLMENERTLDFHDSNVKNLYDKVRLQLRDNNAKELGNGCFEFYHKC DNECMESVRNGTYDYPQYSEEARLKREEI SGVKLESI GI YQI LSI YSTVASSLALAI MVAGLSLWMCNSNG SLOCR

>gi |50296057|gb|AAT73276.1| hemagglutinin [Influenza A virus (A/Viet Nam/3062/2004 (H5N1))]

MEKI VLLFAI VSLVKSDQI CI GYHANNSTEQVDTI MEKNVTVTHAQDI LEKTHNGKLCDLGDKVPLI LRD CSVAGWLLGNPMCMDEFI NVPEWSYI VEKANPVNDLCYPGDFNDYEELKHLRSRI NHFEKI QI I PKSSWSS HEASLGVSACPYQKSSFFRNWVWLI KKNSTYPTI KRSYNNTNOEDLLVWGI HHPNDAAEQTKLYQNP TTYI SVGTSTLNQRLVPR I ATRSKVNGQSGRMEFFWTI LKPNDAI NFESNGNFI APEYAYKI VKKGDSTI MKSELEYGNCNTKCQTPMGA I NSSMPFHNI HPLTI GECPKYVKS NRLVLATGLRNSPQRETRRRRKRGLFG AI AGFI EGGWQGMVDGWYGYHHSNEQSGYAADKESTQKAI DGVTNKVNSI I DKMNTQFEAVGREFNLER RRI ENLNKKMEDGFLDVWYTNAELLVLMENERTLDFHDSNVKNLYDKVRLQLRDNNAKELGNGCFEFYHKC DNECMESVRNGTYDYPQYSEEARLKREEI SGVKLESI GI YQI LSI YSTVASSLALAI MVAGLSLWMCNSNG S

>gi |148767765|gb|ABR10842.1| hemagglutinin [Influenza A virus (A/China/2006 (H5N1))]

MEKI VLLFAI VSLVKSDQI CI GYHANNSTEQVDTI MEKNVTVTHAQDI LEKTHNGKLCDLGDKVPLI LRD CSVAGWLLGNPMCMDEFI NVPEWSYI VEKANPVNDLCYPGDFNDYEELKHLRSRI NHFEKI QI I PKSSWSD HEASLGVSACPYQKSSFFRNWVWLI KKNSTYPTI KRSYNNTNOEDLLVWGI HHPNDAAEQTKLYQNP TTYI SVGTSTLNQRLVPR I ATRSKVNGQSGRMEFFWTI LKPNDAI NFESNGNFI APEYAYKI VKKGDSTI LKSEVEYGNCTKCQTPMGA I NSSMPFHNI HPLTI GECPKYVKS NRLVLATGLRNSPQRETRRRRKRGLFG AI AGFI EGGWQGMVDGWYGYHHSNEQSGYAADKESTQKAI DGVTNKVNSI I DKMNTQFEAVGREFNLER RI ENLNKKMEDGFLDVWYTNAELLVLMENERTLDFHDSNVKNLYDKVRLQLRDNNAKELGNGCFEFYHKC DNECMESVRNGTYDYPQYSEEARLKREEI SGVKLESI GI YQI LSI YSTVASSLALAI MVAGLSLWMCNSNG SLOCR I CI

>gi |158604874|gb|ABW74708.1| hemagglutinin [Influenza A virus (A/Indonesia/TLL008/2006 (H5N1))]

MEKI VLLFAI VSLVKSDQI CI GYHANNSTEQVDTI MEKNVTVTHAQDI LEKTHNGKLCDLGDKVPLI LRD CSVAGWLLGNPMCMDEFI NVPEWSYI VEKANPVNDLCYPGDFNDYEELKHLRSRI NHFEKI QI I PKSSWSD HEASLGVSACPYQKSSFFRNWVWLI KKNSTYPTI KRSYNNTNOEDLLVWGI HHPNDAAEQTKLYQNP TTYI SVGTSTLNQRLVPR I ATRSKVNGQSGRMEFFWTI LKPNDAI NFESNGNFI APEYAYKI VKKGDSTI LKSEVEYGNCTKCQTPMGA I NSSMPFHNI HPLTI GECPKYVKS NRLVLATGLRNSPQRETRRRRKRGLFG AI AGFI EGGWQGMVDGWYGYHHSNEQSGYAADKESTQKAI DGVTNKVNSI I DKMNTQFEAVGREFNLER RRI ENLNKKMEDGFLDVWYTNAELLVLMENERTLDFHDSNVKNLYDKVRLQLRDNNAKELGNGCFEFYHKC DNECMESVRNGTYDYPQYSEEARLKREEI SGVKLESI GI YQI LSI YSTVASSLALAI MVAGLSLWMCNSNG SLOCR I CI

>gi |4457129|gb|AAD21155.1| hemagglutinin [Influenza A virus (A/Hong Kong/516/97 (H5N1))]

DOI CI GYHANNSTEQVDTI MEKNVTVTHAQDI LERTHNGKLCDLNGVKPLI LRDCSVAGWLLGNPMCMDEF I NVPEWSYI VEKASPANDLCYPGDFNDYEELKHLRSRI NHFEKI QI I PKSSWSNHDASSGVSSACPYLGR SSFFRNWVWLI KKNSTYPTI KRSYNNTNOEDLLVWGI HHPNDAAEQTKLYQNP TTYI SVGTSTLNQRLV PEI ATRPKVNGQSGRMEFFWTI LKPNDAI NFESNGNFI APEYAYKI VKKGDSTI MKSELEYGNCNTKCQ TP MGA I NSSMPFHNI HPLTI GECPKYVKS NRLVLATGLRNTPQRETRRRRKRGLFGAI AGFI EGGWQGMVDG WYGYHHSNEQSGYAADKESTQKAI DGVTNKVNSI I NKMNTQFEAVGREFNLERRI ENFNKKMEDGFLD VWYTNAELLVLMENERTLDFHDSNVKNLYDKVRLQLRDNNAKELGNGCFEFYHKCDNECMESVRNGTYDYP QYSEEARLNREEI SGVKLESMGTIYQI LSI YSTVASSLALAI MVAGLSLWMCNSNGSLOCR I CI

>gi |4457134|gb|AAD21160.1| hemagglutinin [Influenza A virus (A/Hong Kong/542/97 (H5N1))]

DOI CI GYHANNSTEQVDTI MEKNVTVTHAQDI LERTHNGKLCDLNGVKPLI LRDCSVAGWLLGNPMCMDEF I NVPEWSYI VEKASPANDLCYPGDFNDYEELKHLRSRI NHFEKI QI I PKSSWSNHDASSGVSSACPYLGR SSFFRNWVWLI KKNSTYPTI KRSYNNTNOEDLLVWGI HHPNDAAEQTKLYQNP TTYI SVGTSTLNQRLV PEI ATRPKVNGQSGRMEFFWTI LKPNDAI NFESNGNFI APEYAYKI VKKGDSTI MKSELEYGNCNTKCQ TP MGA I NSSMPFHNI HPLTI GECPKYVKS NRLVLATGLRNTPQRETRRRRKRGLFGAI AGFI EGGWQGMVDG WYGYHHSNEQSGYAADKESTQKAI DGVTNKVNSI I NKMNTQFEAVGREFNLERRI ENLNKKMEDGFLD VWYTNAELLVLMENERTLDFHDSNVKNLYDKVRLQLRDNNAKELGNGCFEFYHKCDNECMESVRNGTYDYP QYSEEARLNREEI SGVKLESMGTIYQI LSI YSTVASSLALAI MVAGLSLWMCNSNGSLOCR I CI

>gi |4457136|gb|AAD21162.1| hemagglutinin [Influenza A virus (A/Hong Kong/532/1997 (H5N1))]

DOI CI GYHANNSTEQVDTI MEKNVTVTHAQDI LERTHNGKLCDLNGVKPLI LRDCSVAGWLLGNPMCMDEF I NVPEWSYI VEKASPANDLCYPGDFNDYEELKHLRSRI NHFEKI QI I PKSSWSNHDASSGVSSACPYLGR SSFFRNWVWLI KKNSTYPTI KRSYNNTNOEDLLVWGI HHPNDAAEQTKLYQNP TTYI SVGTSTLNQRLV PEI ATRPKVNGQSGRMEFFWTI LKPNDAI NFESNGNFI APEYAYKI VKKGDSTI MKSELEYGNCNTKCQ TP MGA I NSSMPFHNI HPLTI GECPKYVKS NRLVLATGLRNTPQRETRRRRKRGLFGAI AGFI EGGWQGMVDG WYGYHHSNEQSGYAADKESTQKAI DGVTNKVNSI I NKMNTQFEAVGREFNLERRI ENLNKKMEDGFLD VWYTNAELLVLMENERTLDFHDSNVKNLYDKVRLQLRDNNAKELGNGCFEFYHKCDNECMESVRNGTYDYP

QYSEEARLNREEI SGVKLESMGTYOI LSI YSTVASSLALAI MVAGLSLWMCNSGSLQCRICI
 >gi |4457138|gb|AAD21164.1| hemagglutinin [Influenza A virus (A/Hong Kong/514/97 (H5N1))]
 DQI CI GYHANNSTEQVDTI MEKNVTVTHAQDI LERTHNGKLCDLNGVKPLI LRDCSVAGWLLGNPMCMDEFI
 I NVPEWSYI VEKASPANDLCYPGNFNDYEELKHLLSRI NHFEKI QI I PKSSWSNHDASSGLSSACPYLGR
 SSFFRNWVWLI KKNSSYPTI KRSYNNNOEDLLVLWGI HHPNDAAEQTKLYQNPTTYI SVGTSTLNQRLV
 PEI ATRPKVNGQSGRMEFFWTI LKPNDAI NFESNGNFI APEYAYKI VKKGDSTI MKSELEYGNCNTKCCOT
 PMGAI NSSMPFHNI HPLTI GECPKYVKSRLVATGLRNTPHRERRRRKRGLFGAI ARFI EGGWQGMVDG
 WYGYHHSNEQSGYAADOESTQKAI DGVTKVNSI I NKMNTOFEAVGREFNLERRI ENLNKMKMEDGFLD
 VWTYNAELLVLMENERTLDFHDSNVKNLYDKVRLQLRDNAKELGNGCFEFYHKCDNECMESVKNGTIDYP
 QYSEEARLNREEI SGVKLESMGTYOI LSI YSTVASSLALAI MVAGLSLWMCNSGSLLCRI CI
 >gi |8307803|gb|AAF74330.1|AF084280_1 hemagglutinin [Influenza A Virus (A/Hong Kong/483/97 (H5N1))]
 MEKI VLLLATVSLVKSQDI CI GYHANNSTEQVDTI MEKNVTVTHAQDI LERTHNGKLCDLNGVKPLI LRD
 CSVAGWLLGNPMCMDEFI NVPEWSYI VEKASPANDLCYPGNFNDYEELKHLLSRI NHFEKI QI I PKSSWSN
 HDASSGVSSACPYLGRSSFFRNWVWLI KKNSTYPTI KRSYNNNOEDLLVLWGI HHPNDAAEQTKLYQNP
 TTYI SVGTSTLNQRLVPEI ATRPKVNGQSGRI EFFWTI LKPNDAI NFESNGNFI APEYAYKI VKKGDSTI
 MKSELEYGNCNTKCCOTPMGAI NSSMPFHNI HPLTI GECPKYVKSRLVATGLRNPQRERRRRKRGLFG
 AI AGFI EGGWQGMVDGWYGYHHSNEQSGYAADOESTQKAI DGVTKVNSI I NKMNTOFEAVGREFNLE
 RRI ENLNKMKMEDGFLDVTYNAELLVLMENERTLDFHDSNVKNLYDKVRLQLRDNAKELGNGCFEFYHK
 DNECMESVKNGTIDYPQYSEEARLNREEI SGVKLESMGTYOI LSI YSTVASSLALAI MVAGLSLW
 >gi |8307805|gb|AAF74331.1|AF084281_1 hemagglutinin [Influenza A virus (A/Hong Kong/486/97 (H5N1))]
 MEKI VLLLATVSLVKSQDI CI GYHANNSTEQVDTI MEKNVTVTHAQDI LERTHNGKLCDLNGVKPLI LRD
 CSVAGWLLGNPMCMDEFI NVPEWSYI VEKASPANDLCYPGNFNDYEELKHLLSRI NHFEKI QI I PKSSWSN
 HDASSGVSSACPYLGRSSFFRNWVWLI KKNSTYPTI KRSYNNNOEDLLVLWGI HHPNDAAEQTKLYQNP
 TTYI SVGTSTLNQRLVPEI ATRPKVNGQSGRI EFFWTI LKPNDAI NFESNGNFI APEYAYKI VKKGDSTI
 MKSELEYGNCNTKCCOTPMGAI NSSMPFHNI HPLTI GECPKYVKSRLVATGLRNPQRERRRRKRGLFG
 AI AGFI EGGWQGMVDGWYGYHHSNEQSGYAADKESTQKAI DGVTKVNSI I NKMNTOFEAVGREFNLE
 RRI ENLNKMKMEDGFLDVTYNAELLVLMENERTLDFHDSNVKNLYDKVRLQLRDNAKELGNGCFEFYHK
 DNECMESVKNGTIDYPQYSEEARLNREEI SGVKLESMGTYOI LSI YSTVASSLALAI MVAGLSLW
 >gi |4457132|gb|AAD21158.1| hemagglutinin [Influenza A virus (A/HongKong/97/98(H5N1))]
 DOI CI GYHANNSTEQVDTI MEKNVTVTHAQDI LERTHNGKLCDLNGVKPLI LRDCSVAGWLLGNPMCMDEFI
 I NVPEWSYI VEKASPANDLCYPGNFNDYEELKHLLSRI NHFEKI QI I PKSSWSNHDASSGVSSACPYLGR
 SSFFRNWVWLI KKNSTYPTI KRSYNNNOEDLLVLWGI HHPNDAAEQTKLYQNPTTYI SVGTSTLNQRLV
 PEI ATRPKVNGQSGRMEFFWTI LKPNDAI NFESNGNFI APEYAYKI VKKGDSTI MKSELEYGNCNTKCCOT
 PMGAI NSSMPFHNI HPLTI GECPKYVKSRLVATGLRNTPHRERRRRKRGLFGAI AGFI EGGWQGMVDG
 WYGYHHSNEQSGYAADOESTQKAI DGVTKVNSI I NKMNTOFEAVGREFNLERRI ENLNKMKMEDGFLD
 VWTYNAELLVLMENERTLDFHDSNVKNLYDKVRLQLRDNAKELGNGCFEFYHKCDNECMESVKNGTIDYP
 QYSEEARLNREEI SGVKLESMGTYOI LSI YSTVASSLALAI MVAGLSLWMCNSGSLQCRICI
 >gi |71013498|dbj|BAE07201.1| hemagglutinin [Influenza A virus (A/Hong Kong/213/03 (H5N1))]
 MEKI VLLFAI VSLVKSQDI CI GYHANNSTEQVDTI MEKNVTVTHAQDI LEKTHNGKLCDLGDKVPLI LRD
 CSVAGWLLGNPMCMDEFI NVPEWSYI VEKANPANDLCYPGDFNDYEELKHLLSRI NHFEKI QI I PKSSWS
 HEASLGVSSACPYQKSSFFRNWVWLI KKNSTYPTI KRSYNNNOEDLLVLWGI HHPNDAAEQTKLYQNP
 TTYI SVGTSTLNQRLVPEI ATRSKVNGQNGRMEFFWTI LKPNDAI NFESNGNFI APEYAYKI VKKGDSTI
 MKSELEYGNCNTKCCOTPMGAI NSSMPFHNI HPLTI GECPKYVKSRLVATGLRNPQRERRRRKRGLFG
 AI AGFI EGGWQGMVDGWYGYHHSNEQSGYAADKESTQKAI DGVTKVNSI I DKMNTOFEAVGREFNLE
 RRI ENLNKMKMEDGFLDVTYNAELLVLMENERTLDFHDSNVKNLYDKVRLQLRDNAKELGNGCFEFYHK
 DNECMESVRNGTYDYPQYSEEARLKREEI SGVKLESI GTYOI LSI YSTVASSLALAI MVAGLSLWMCNSG
 SLQCRICI
 >gi |145284462|gb|ABP51975.1| hemagglutinin [Influenza A virus (A/Hong Kong/213/2003 (H5N1))]
 MEKI VLLFAI VSLVKSQDI CI GYHANNSTEQVDTI MEKNVTVTHAQDI LEKTHNGKLCDLGDKVPLI LRD
 CSVAGWLLGNPMCMDEFI NVPEWSYI VEKANPANDLCYPGDFNDYEELKHLLSRI NHFEKI QI I PKSSWS
 HEASLGVSSACPYQKSSFFRNWVWLI KKNSTYPTI KRSYNNNOEDLLVLWGI HHPNDAAEQTKLYQNP
 TTYI SVGTSTLNQRLVPEI ATRSKVNGQNGRMEFFWTI LKPNDAI NFESNGNFI APEYAYKI VKKGDSTI
 MKSELEYGNCNTKCCOTPMGAI NSSMPFHNI HPLTI GECPKYVKSRLVATGLRNPQRERRRRKRGLFG
 AI AGFI EGGWQGMVDGWYGYHHSNEQSGYAADKESTQKAI DGVTKVNSI I DKMNTOFEAVGREFNLE
 RRI ENLNKMKMEDGFLDVTYNAELLVLMENERTLDFHDSNVKNLYDKVRLQLRDNAKELGNGCFEFYHK
 DNECMESVRNGTYDYPQYSEEARLKREEI SGVKLESI GTYOI LSI YSTVASSLALAI MVAGLSLWMCNSG
 SLQCRICI
 >gi |148340806|gb|ABQ58979.1| hemagglutinin [Influenza A virus (A/Beijing/01/2003 (H5N1))]
 MEKI VLLLA I SLVKSQDI CI GSHANNSTEQVDTI MEKNVTVTHAQDI LEKTHNGKLCDLGDKVPLI LRD
 CSVAGWLLGNPMCMDEFI NVPEWSYI VEKASPANDLCYPGDFNDYEELKHLLSRI NHFEKI QI I PKSSWSN
 HEASSGVSSACPYLGRPSFFRNWVWLI KKNSTYPTI KRSYNNNOEDLLVLWGI HHPNDAAEQI KLYQNP
 TTYI SVGTSTLNQRLVPEI ATRSKVNGQSGRMEFFWAI LKPNDAI NFESNGNFI APEYAYKI VKKGDSTI
 MKSELEYGNCNTKCCOTPMGAI NSSMPFHNI HPLTI GECPKYVKSRLVATGLRNPQRERRRRKRGLFG
 AI AGFI EGGWQGMVDGWYGYHHSNEQSGYAADKESTQKAI DGVTKVNSI I DKMNTOFEAVGREFNLE
 RRI ENLNKMKMEDGFLDVTYNAELLVLMENERTLDFHDSNVKNLYDKVRLQLRDNAKELGNGCFEFYHK
 DNECMESVKNGTIDYPQYSEEARLNREEI SGVKLESMGTYOI LSI YSTVASSLALAI MVAGLSLWMCNSG
 SLQCRICI
 >gi |145284448|gb|ABP51968.1| hemagglutinin [Influenza A virus (A/Prachinburi/76231/2004 (H5N1))]
 MEKI VLLFAI VSLVKSQDI CI GYHANNSTEQVDTI MEKNVTVTHAQDI LEKTHNGKLCDLGDKVPLI LRD
 CSVAGWLLGNPMCMDEFI NVPEWSYI VEKANPANDLCYPGDFNDYEELKHLLSRI NHFEKI QI I PKSSWS

HEASLGVSSACPYQKGSSFFRNVVWLI KKNSTYPTI KRSYNNTOEDLLVWLG I HHPNDAAEQTKLYQNP
 TTYI SVGTSTLNQRLVPR I ATRSKVNGQSGRMEFFWT I LKPNDAI NFESNGNFI APEYAYKI VKKGDSTI
 MKSELEYGNCNTKCQTPMGA I NSSMPFHNI HPLTI GECPKYVKS NRLLVATGLRNSPQRERRRKRGLFG
 AI AGFI EGGWQGMVDGWYGYHHSNEQSGYAADKESTOKAI DGVTNKVNSI I DKMNTQFEAVGREFNNLE
 RRI ENLNKMKMEDGFLDVWYTNAELLVLMENERTLDFHDSNVKNLYDKVRLQLRDN AKELGNGCFEFYHKC
 DNECMESVRNGTYDYPQYSEEARLKREEI SGVKLESI GI YQI LSI YSTVASSLALAI MVAGLSLWMCNSNG
 SLOCRICI

>gi |159895958|gb|ABX10515.1| hemagglutinin [Influenza A virus
 (A/Thailand/16/2004(H5N1))]

MEKI VLLFAI VSLVKSDQI CI GYHANNSTEQVDTI MEKNVTVTHAQDI LEKTHNGKLCDLGDKVPLI LRD
 CSVAGWLLGNPMDDEFI NVPEWSYI VEKANPVNDLCYPGDFNDYEELKHLLSRI NHFEKI QI I PKSSWSS
 HEASLGVSSACPYQKGSSFFRNVVWLI KKNSTYPTI KRSYNNTOEDLLVWLG I HHPNDAAEQTKLYQNP
 TTYI SVGTSTLNQRLVPR I ATRSKVNGQSGRMEFFWT I LKPNDAI NFESNGNFI APEYAYKI VKKGDSTI
 MKSELEYGNCNTKCQTPMGA I NSSMPFHNI HPLTI GECPKYVKS NRLLVATGLRNSPQRERRRKRGLFG
 AI AGFI EGGWQGMVDGWYGYHHSNEQSGYAADKESTOKAI DGVTNKVNSI I DKMNTQFEAVGREFNNLE
 RRI ENLNKMKMEDGFLDVWYTNAELLVLMENERTLDFHDSNVKNLYDKVRLQLRDN AKELGNGCFEFYHKC
 DNECMESVRNGTYDYPQYSEEARLKREEI SGVKLESI GI YQI LSI YSTVASSLALAI MVAGLSLWMCNSNG
 SLOCRICI

>gi |118722729|gb|ABL10088.1| hemagglutinin [Influenza A virus (A/Thailand/1(KAN-
 1A)/2004(H5N1))]

MEKI VLLFAI VSLVKSDQI CI GYHANNSTEQVDTI MEKNVTVTHAQDI LEKTHNGKLCDLGDKVPLI LRD
 CSVAGWLLGNPMDDEFI NVPEWSYI VEKANPVNDLCYPGDFNDYEELKHLLSRI NHFEKI QI I PKSSWSS
 HEASLGVSSACPYQKGSSFFRNVVWLI KKNSTYPTI KRSYNNTOEDLLVWLG I HHPNDAAEQTKLYQNP
 TTYI SVGTSTLNQRLVPR I ATRSEVNGQSGRMEFFWT I LKPNDAI NFESNGNFVAPEYAYKI VKKGDSTI
 MKSELEYGNCNTKCQTPMGA I NSSMPFHNI HPLTI GECPKYVKS NRLLVATGLRNSPQRERRRKRGLFG
 AI AGFI EGGWQGMVDGWYGYHHSNEQSGYAANKESTOKAI DGVTNKVNSI I DKMNTQFEAVGREFNNLE
 RRI ENLNKMKMEDGFLDVWYTNAELLVLMENERTLDFHDSNVKNLYDKVRLQLRDN AKELGNGCFEFYHKC
 DNECMESVRNGTYDYPQYSEEARLKREEI SGVKLESI GI YQI LSI YSTVASSLALAI MVAGLSLWMCNSNG
 SLOCRICI

>gi |156992239|gb|ABU99108.1| hemagglutinin [Influenza A virus
 (A/Vietnam/1196/2004(H5N1))]

MEKI VLLFAI VSLVKSDQI CI GYHANNSTEQVDTI MEKNVTVTHAQDI LEKTHNGKLCDLGDKVPLI LRD
 CSVAGWLLGNPMDDEFI NVPEWSYI VEKANPVNDLCYPGDFNDYEELKHLLSRI NHFEKI QI I PKSSWSS
 HEASLGVSSACPYQKGSSFFRNVVWLI KKNSTYPTI KRSYNNTOEDLLVWLG I HHPNDAAEQTKLYQNP
 TTYI SVGTSTLNQRLVPR I ATRSKVNGQSGRMEFFWT I LKPNDAI NFESNGNFI APEYAYKI VKKGDSTI
 MKSELEYGNCNTKCQTPMGA I NSSMPFHNI HPLTI GECPKYVKS NRLLVATGLRNSPQRERRRKRGLFG
 AI AGFI EGGWQGMVDGWYGYHHSNEQSGYAADKESTOKAI DGVTNKVNSI I DKMNTQFEAVGREFNNLE
 RRI ENLNKMKMEDGFLDVWYTNAELLVLMENERTLDFHDSNVKNLYDKVRLQLRDN AKELGNGCFEFYHKC
 DNECMESVRNGTYDYPQYSEEARLKREEI SGVKLESI GI YQI LSI YSTVASSLALAI MVAGLSLWMCNSNG
 SLOCRICI

>gi |159144901|gb|ABW90125.1| hemagglutinin [Influenza A virus (A/Viet
 Nam/1203/2004(H5N1))]

MEKI VLLFAI VSLVKSDQI CI GYHANNSTEQVDTI MEKNVTVTHAQDI LEKTHNGKLCDLGDKVPLI LRD
 CSVAGWLLGNPMDDEFI NVPEWSYI VEKANPVNDLCYPGDFNDYEELKHLLSRI NHFEKI QI I PKSYWSS
 HEASLGVSSACPYQKGSSFFRNVVWLI KKNSTYPTI KRSYNNTOEDLLVWLG I HHPNDAAEQTKLYQNP
 TTYI SVGTSTLNQRLVPR I ATRSKVNGQSGRMEFFWT I LKPNDAI NFESNGNFI APEYAYKI VKKGDSTI
 MKSELEYGNCNTKCQTPMGA I NSSMPFHNI HPLTI GECPKYVKS NRLLVATGLRNSPQRETRGLFGAI AG
 FI EGGWQGMVDGWYGYHHSNEQSGYAADKESTOKAI DGVTNKVNSI I DKMNTQFEAVGREFNNLE
 RRI ENLNKMKMEDGFLDVWYTNAELLVLMENERTLDFHDSNVKNLYDKVRLQLRDN AKELGNGCFEFYHKC
 DNECMESVRNGTYDYPQYSEEARLKREEI SGVKLESI GI YQI LSI YSTVASSLALAI MVAGLSLWMCNSNG
 SLOCRICI

>gi |159144907|gb|ABW90128.1| hemagglutinin [Influenza A virus (A/Viet
 Nam/1203/2004(H5N1))]

MEKI VLLFAI VSLVKSDQI CI GYHANNSTEQVDTI MEKNVTVTHAQDI LEKTHNGKLCDLGDKVPLI LRD
 CSVAGWLLGNPMDDEFI NVPEWSYI VEKANPVNDLCYPGDFNDYEELKHLLSRI NHFEKI QI I PKSSWSS
 HEASLGVSSACPYQKGSSFFRNVVWLI EKNSTYPTI KRSYNNTOEDLLVWLG I HHPNDAAEQTKLYQNP
 TTYI SVGTSTLNQRLVPR I ATRSKVNGQSGRMEFFWT I LKPNDAI NFESNGNFI APEYAYKI VKKGDSTI
 MKSELEYGNCNTKCQTPMGA I NSSMPFHNI HPLTI GECPKYVKS NRLLVATGLRNSPQRETRGLFGAI AG
 FI EGGWQGMVDGWYGYHHSNEQSGYAADKESTOKAI DGVTNKVNSI I DKMNTQFEAVGREFNNLE
 RRI ENLNKMKMEDGFLDVWYTNAELLVLMENERTLDFHDSNVKNLYDKVRLQLRDN AKELGNGCFEFYHKC
 DNECMESVRNGTYDYPQYSEEARLKREEI SGVKLESI GI YQI LSI YSTVASSLALAI MVAGLSLWMCNSNG
 SLOCRICI

>gi |145284464|gb|ABP51976.1| hemagglutinin [Influenza A virus (A/Viet
 Nam/1194/2004(H5N1))]

MEKI VLLFAI VSLVKSDQI CI GYHANNSTEQVDTI MEKNVTVTHAQDI LEKTHNGKLCDLGDKVPLI LRD
 CSVAGWLLGNPMDDEFI NVPEWSYI VEKANPVNDLCYPGDFNDYEELKHLLSRI NHFEKI QI I PKSSWSS
 HEASLGVSSACPYQKGSSFFRNVVWLI KKNSTYPTI KRSYNNTOEDLLVWLG I HHPNDAAEQTKLYQNP
 TTYI SVGTSTLNQRLVPR I ATRSKVNGQSGRMEFFWT I LKPNDAI NFESNGNFI APEYAYKI VKKGDSTI
 MKSELEYGNCNTKCQTPMGA I NSSMPFHNI HPLTI GECPKYVKS NRLLVATGLRNSPQRERRRKRGLFG
 AI AGFI EGGWQGMVDGWYGYHHSNEQSGYAADKESTOKAI DGVTNKVNSI I DKMNTQFEAVGREFNNLE
 RRI ENLNKMKMEDGFLDVWYTNAELLVLMENERTLDFHDSNVKNLYDKVRLQLRDN AKELGNGCFEFYHKC
 DNECMESVRNGTYDYPQYSEEARLKREEI SGVKLESI GI YQI LSI YSTVASSLALAI MVAGLSLWMCNSNG
 SLOCRICI

>gi |118864224|gb|ABL31766.1| hemagglutinin [Influenza A virus
 (A/Indonesia/CDC836T/2006(H5N1))]

MEKI VLLFAI VSFVKSDQI CI GYHANNSTEQVDTI MEKNVTVTHAQDI LEKTHNGKLCDLGDKVPLI LRD
 CSVAGWLLGNPMDDEFI NVPEWSYI VEKANPTNDLCYPGDFNDYEELKHLLSRI NHFEKI QI I PKSSWSD

HEASSGVSSACPYLGGSPSFFRNVVWLI KKNSTYPTI KKSNNNTNOEDLLVWLG I HHPNDAAEQTRLYQNP
 TTYI SI GTSTLNQRVLPKI ATRSKVNGQSGRMEFFWAI LKPNDAI NFESNGNFI APEYAYKI VKKGD
 SA I MKSELEYGNCNTKCQTPMGA I NSSMPFHNI HPLTI GECPKYVKSRLVATGLRNSPQRESRRK
 RGLFG AI AGFI EGGWQGMVDGWYGYHHSNEQSGYAADKESTQKAI DGVTKVNSI I DKMNTQF
 EAVGREFNLE RRI ENLNKMKMEDGFLDVWYTNAELLVLMENERTLDFHDSNVKNLYDKVRLQ
 LRDNAKELGNGCFEFYHKC DNECMESI RNGTHYNYPOYSEEARLKREEI SGVKLESI GTYQI
 LSI YSTVASSLALAI MI AGLSLWMCNSG SLOCRICI

>gi |118864183|gb|ABL31755.1| hemagglutinin [Influenza A virus
 (A/Indonesia/2006(H5N1))]

MEKI VLLLAI VSLVKSQDI CI GYHANNSTEQVDTI MEKNVTVTHAQDI LEKTHNGKLC
 DLDGVKPLI LRD CSVAGWLLGNPMCMDEFI NVPEWSYI VEKANPTNDLCYPGSFNDYEELKHLLSRI
 NHFEKI QI I PKSSWSD HEASSGVSSACPYLGGSPSFFRNVVWLI KKNSTYPTI KKSNNNT
 NOEDLLVWLG I HHPNDAAEQTRLYQNP TTYI SI GTSTLNQRVLPKI ATRSKVNGQSGR
 MEFFWAI LKPNDAI NFESNGNFI APEYAYKI VKKGD SA I MKSELEYGNCNTKCQTPMGA
 I NSSMPFHNI HPLTI GECPKYVKSRLVATGLRNSPQRESRRK RGLFG AI AGFI EGGWQGM
 VDGWYGYHHSNEQSGYAADKESTQKAI DGVTKVNSI I DKMNTQF EAVGREFNLE RRI
 ENLNKMKMEDGFLDVWYTNAELLVLMENERTLDFHDSNVKNLYDKVRLQ LRDNAKELGNGCF
 EFYHKC DNECMESI RNGTHYNYPOYSEEARLKREEI SGVKLESI GTYQI LSI YSTVASSL
 ALAI MI AGLSLWMCNSG SLOCRICI

>gi |118864380|gb|ABL31780.1| hemagglutinin [Influenza A virus
 (A/Indonesia/2006(H5N1))]

MEKI VLLLSI VSLVKSQDI CI GYHANNSTEQVDTI MEKNVTVTHAQDI LEKTHNGKLC
 DLDGVKPLI LRD CSVAGWLLGNPMCMDEFI NVPEWSYI VEKANPTNDLCYPGSFNDYEELKHLLSRI
 NHFEKI QI I PKSSWSD HEASSGVSSACPYLGGSPSFFRNVVWLI KKNSTYPTI KKSNNNT
 NOEDLLVWLG I HHPNDAAEQTRLYQNP TTYI SI GTSTLNQRVLPKI ATRSKVNGQSGR
 MEFFWAI LKPNDAI NFESNGNFI APEYAYKI VKKGD SA I MKSELEYGNCNTKCQTPMGA
 I NSSMPFHNI HPLTI GECPKYVKSRLVATGLRNSPQRESRRK RGLFG AI AGFI EGGWQGM
 VDGWYGYHHSNEQSGYAADKESTQKAI DGVTKVNSI I DKMNTQF EAVGREFNLE RRI
 ENLNKMKMEDGFLDVWYTNAELLVLMENERTLDFHDSNVKNLYDKVRLQ LRDNAKELGNGCF
 EFYHKC DNECMESI RNGTHYNYPOYSEEARLKREEI SGVKLESI GTYQI LSI YSTVASSL
 ALAI MI AGLSLWMCNSG SLOCRICI

>gi |118574870|gb|ABL07008.1| hemagglutinin [Influenza A virus
 (A/Indonesia/2006(H5N1))]

MEKI VLLLSI VSLVKSQDI CI GYHANNSTEQVDTI MEKNVTVTHAQDI LEKTHNGKLC
 DLDGVKPLI LRD CSVAGWLLGNPMCMDEFI NVPEWSYI VEKANPTNDLCYPGSFNDYEELKHLLSRI
 NHFEKI QI I PKSSWSD HEASSGVSSACPYLGGSPSFFRNVVWLT KKNSTYPTI KKSNNNT
 NOEDLLVWLG I HHPNDAAEQTRLYQNP TTYI SI GTSTLNQRVLPKI ATRSKVNGQSGR
 MEFFWAI LKPNDAI NFESNGNFI APEYAYKI VKKGD SA I MKSELEYGNCNTKCQTPMGA
 I NSSMPFHNI HPLTI GECPKYVKSRLVATGLRNSPQRESRRK RGLFG AI AGFI EGGWQGM
 VDGWYGYHHSNEQSGYAADKESTQKAI DGVTKVNSI I DKMNTQF EAVGREFNLE RRI
 ENLNKMKMEDGFLDVWYTNAELLVLMENERTLDFHDSNVKNLYDKVRLQ LRDNAKELGNGCF
 EFYHKC DNECMESI RNGTHYNYPOYSEEARLKREEI SGVKLESI GTYQI LSI YSTVASSL
 ALAI MI AGLSLWMCNSG SLOCRICI

>gi |118574889|gb|ABL07019.1| hemagglutinin [Influenza A virus
 (A/Indonesia/2006(H5N1))]

MEKI VLLLSI VSLVKSQDI CI GYHANNSTEQVDTI MEKNVTVTHAQDI LEKTHNGKLC
 DLDGVKPLI LRD CSVAGWLLGNPMCMDEFI NVPEWSYI VEKANPTNDLCYPGSFNDYEELKHLLSRI
 NHFEKI QI I PKSSWSD HEASSGVSSACPYLGGSPSFFRNVVWLT KKNSTYPTI KKSNNNT
 NOEDLLVWLG I HHPNDAAEQTRLYQNP TTYI SI GTSTLNQRVLPKI ATRSKVNGQSGR
 MEFFWAI LKPNDAI NFESNGNFI APEYAYKI VKKGD SA I MKSELEYGNCNTKCQTPMGA
 I NSSMPFHNI HPLTI GECPKYVKSRLVATGLRNSPQRESRRK RGLFG AI AGFI EGGWQGM
 VDGWYGYHHSNEQSGYAADKESTQKAI DGVTKVNSI I DKMNTQF EAVGREFNLE RRI
 ENLNKMKMEDGFLDVWYTNAELLVLMENERTLDFHDSNVKNLYDKVRLQ LRDNAKELGNGCF
 EFYHKC DNECMESI RNGTHYNYPOYSEEARLKREEI SGVKLESI GTYQI LSI YSTVASSL
 ALAI MI AGLSLWMCNSG SLOCRICI

>gi |118574908|gb|ABL07030.1| hemagglutinin [Influenza A virus
 (A/Indonesia/2006(H5N1))]

MEKI VLLLAI VSLVKSQDI CI GYHANNSTEQVDTI MEKNVTVTHAQDI LEKTHNGKLC
 DLDGVKPLI LRD CSVAGWLLGNPMCMDEFI NVPEWSYI VEKANPTNDLCYPGSFNDYEELKHLLSRI
 NHFEKI QI I PKSSWSD HEASSGVSSACPYLGGSPSFFRNVVWLI KKNSTYPTI KKSNNNT
 NOEDLLVWLG I HHPNDAAEQTRLYQNP TTYI SI GTSTLNQRVLPKI ATRSKVNGQSGR
 MEFFWAI LKPNDAI NFESNGNFI APEYAYKI VKKGD SA I MKSELEYGNCNTKCQTPMGA
 I NSSMPFHNI HPLTI GECPKYVKSRLVATGLRNSPQRESRRK RGLFG AI AGFI EGGWQGM
 VDGWYGYHHSNEQSGYAADKESTQKAI DGVTKVNSI I DKMNTQF EAVGREFNLE RRI
 ENLNKMKMEDGFLDVWYTNAELLVLMENERTLDFHDSNVKNLYDKVRLQ LRDNAKELGNGCF
 EFYHKC DNECMESI RNGTHYNYPOYSEEARLKREEI SGVKLESI GTYQI LSI YSTVASSL
 ALAI MI AGLSLWMCNSG SLOCRICI

>gi |145843656|gb|ABP96845.1| hemagglutinin [Influenza A virus (A/Egypt/1394-
 NAMRU3/2007 (H5N1))]

MEKI VLLLAI VSLVKSQDI CI GYHANNSTEQVDTI MEKNVTVTHAQDI LEKTHNGKLC
 NLDGVKPLI LRD CSVAGWLLGNPMCMDEFI NVPEWSYI VEKI NPANDLCYPGNFNDYEELKHLLSRI
 NHFEKI QI I PKSSWSD HEASGVSSACPYOGRSSFFRNVVWLT KRDNAYPTI KRSYNNNT
 NOEDLLVWLG I HHPNDAAEQTRLYQNP TYI SVGTSTLNQRVLPKI ATRSKVNGQXGR
 MEFFWAI LKSNDAI NFESNGNFI APENAYKI VKKGDSTI M KSELEYGNCNTKCQTP
 I GAI NSSMPFHNI HPLTI GECPKYVKSRLVATGLRNSPQRESRRK RGLFGA I AGFI
 EGGWQGMVDGWYGYHHSNEQSGYAADKESTQKAI DGVTKVNSI I DKMNTQF EAVGREFNLE
 RRI ENLNKMKMEDGFLDVWYTNAELLVLMENERTLDFHDSNVKNLYDKVRLQ LRDNAKELG
 NGCFEFYHRC DNECMESVRNGTYDYPQYSEEARLKREEI SGVKLESI GTYQI LSI YSTVASSL
 ALAI MVAGLSLWMCNSGS LQCRICI

>gi |145843658|gb|ABP96846.1| hemagglutinin [Influenza A virus (A/Egypt/1604-
 NAMRU3/2007 (H5N1))]

MEKI VLLLAI VSLVKSQDI CI GYHANNSTEQVDTI MEKNVTVTHAQDI LEKTHNGKLC
 DLDGVKPLI LRD CSVAGWLLGNPMCMDEFI NVPEWSYI VEKI NPANDLCYPGNFNDYEELKHLLSRI
 NHFEKI QI I PKSSWSD

HEASSGVSSACPYQGRSSFFRNVVWLI KKDNEYPTI KRSYNNTOEDLLVWGI HHPNDAAEQTRLYQNP
 TTYI SVGTSTLNQRLVPKI ATRSKVNGQSGRI EFFWTI LKSNDAI NFESNGNFI APENAYKI VKKGDSTI
 MKSELEYGNCNTKCQTP I GAI NSSMPFHNI HPLTI GECPKYVKS NRLLVATGLRNSPOGERRRRKRGLFG
 AI AGFI EGGWQGMVDGWYGYHHSNEQSGYAADKESTOKAI DGVTKVNSI I DKMNTQFEAVGREFNLE
 RRI ENLNKMKMEDGFLDVTYNAELLVLMENERTLDFHDSNVKNLYDKVRLQLRD NAKELGNGCFEFYHRC
 DNECMESVRNGTYDYPQYSEEARLKREEI SGVKLESI GTYQI LSI YSTVASSLALAI MVAGFLWMCNSG
 SLOCRI CI
 >gi |145843660|gb|ABP96847.1| hemagglutinin [Influenza A virus (A/Egypt/1731-
 NAMRU3/2007 (H5N1))]
 MEKI VLLLA I VSLVKSDQI CI GYHANNSTEQVDTI MEKNVTVTHAQDI LEKTHNGKLCDLGDKVPLI LRD
 CSVAGWLLGNPMCDEFNLVPEWSYI VEKI NPANDLCYPGNFNDYEEELKHLLSRI NHFEKI QI I PKSSWSD
 HEASSGVSSACPYQGRSSFFRNVVWLI KKDNEYPTI KRSYNNTOEDLLI LWGI HHPNDAAEQTRLYQNP
 TTYI SVGTSTLNQRLVPKI ATRSKVNGQSGRMEFFWTI LKSNDAI NFESNGNFI APENAYKI VKKGDSTI
 MKSELEYGNCNTKCQTP I GAI NSSMPFHNI HPLTI GECPKYVKS NRLLVATGLRNSPOGERRRRKRGLFG
 AI AGFI EGGWQGMVDGWYGYHHSNEQSGYAADKESTOKAI DGVTKVNSI I DKMNTQFEAVGREFNLE
 RRI ENLNKMKMEDGFLDVTYNAELLVLMENERTLDFHDSNVKNLYDKVRLQLRD NAKELGNGCFEFYHRC
 DNECMESVRNGTYDYPQYSEEARLKREEI SGVKLESI GTYQI LSI YSTVAGSLALAI MVAGFLWMCNSG
 SLOCRI CI
 >gi |145843662|gb|ABP96848.1| hemagglutinin [Influenza A virus (A/Egypt/1902-
 NAMRU3/2007 (H5N1))]
 MEKI VLLLA I VNLVKSDQI CI GYHANNSTEQVDTI MEKNVTVTHAQDI LEKTHNGKLCDLGDKVPLI LRD
 CSVAGWLLGNPMCDEFNLVPEWSYI VEKI NPANDLCYPGTFNDYEEELKHLLSRI NHFEKI QI I PKSSWSD
 HEASSGVSSACPYQGRSSFFRNVVWLI KKNNA YPTI KI SYNNTOEDLLVWGI HHPNDAAEQTRLYQNP
 TTYI SVGTSTLNQRLVPKI ATRSKVNGQSGRMEFFWTI LKSNDAI NFESNGNFI APENAYKI VKKGDSTI
 MKSELEYGNCNTKCQTP I GAI NSSMPFHNI HPLTI GECPKYVKS NRLLVATGLRNSPOGERRRRKRGLFG
 AI AGFI EGGWQGMVDGWYGYHHSNEQSGYAADKESTOKAI DGVTKVNSI I DKMNTQFEAVGREFNLE
 RRI ENLNKMKMEDGFLDVTYNAELLVLMENERTLDFHDSNVKNLYDKVRLQLRD NAKELGNGCFEFYHRC
 DNECMESVRNGTYDYPQYSEEARLKREEI SGVKLESI GTYQI LSI YSTVASSLALAI MVAGFLWMCNSG
 SLOCRI CI
 >gi |145843664|gb|ABP96849.1| hemagglutinin [Influenza A virus (A/Egypt/2256-
 NAMRU3/2007 (H5N1))]
 MEKI VLLLA I VSLVKSDQI CI GYHANNSTEQVDTI MEKNVTVTHAQDI LEKTHNGKLCDLGDKVPLI LRD
 CSVAGWLLGNPMCDEFNLVPEWSYI VEKI NPANDLCYPGNFNDYEEELKHLLSRI NHFEKI QI I PKSSWSD
 HEASSGVSSACPYQGRSSFFRNVVWLI KKDNEYPTI KRSYNNTOEDLLVWGI HHPNDAAEQTRLYQNP
 TTYI SVGTSTLNQRLVPKI ATRSKVNGQSGRMEFFWTI LKSNDAI NFESNGNFI APENAYKI VKKGDSTI
 MKSELEYGNCNTKCQTP I GAI NSSMPFHNI HPLTI GECPKYVKS NRLLVATGLRNSPOGERRRRKRGLFG
 AI AGFI EGGWQGMVDGWYGYHHSNEQSGYAADKESTOKAI DGVTKVNSI I DKMNTQFEAVGREFNLE
 RRI ENLNKMKMEDGFLDVTYNAELLVLMENERTLDFHDSNVKNLYDKVRLQLRD NAKELGNGCFEFYHRC
 DNECI ESRVNGTYDYPQYSEEARLKREEI SGVKLESI GTYQI LSI YSTVASSLALAI MVAGFLWMCNSG
 SLOCRI CI
 >gi |145843668|gb|ABP96851.1| hemagglutinin [Influenza A virus (A/Egypt/2331-
 NAMRU3/2007 (H5N1))]
 MEKI VLLLA I VSLVKSDQI CI GYHANNSTEQVDTI MEKNVTVTHAQDI LEKTHNGKLCDLGDKVPLI LRD
 CSVAGWLLGNPMCDEFNLVPEWSYI VEKI NPANDLCYPGDFNDYEEELKHLLSRI NHFEKI QI I PKSSWSD
 YEASSGVSSACPYQGRSSFFRNVVWLI KKNNA YPTI KRSYNNTOEDLLVWGI HHPNDAAEQI RLYQNP
 TTYI SVGTSTLNQRLVPKI ATRSKVNGQSGRMEFFWTI LKSNDAI NFESNGNFI APEYAYKI VKKGDSTI
 MKSELEYGNCNTKCQTP I GAI NSSMPFHNI HPLTI GECPKYVKS NRLLVATGLRNSPOGERRRRKRGLFG
 AI AGFI EGGWQGMVDGWYGYHHSNEQSGYAADKESTOKAI DGVTKVNSI I DKMNTQFEAVGREFNLE
 RRI ENLNKMKMEDGFLDVTYNAELLVLMENERTLDFHDSNVKNLYDKVRLQLRD NAKELGNGCFEFYHRC
 DNECMESVRNGTYDYPQYSEEARLKREEI SGVKLESI GI YQI LSI YSTVASSLALAI MVAGFLWMCNSG
 SLOCRI CI
 >gi |182382596|gb|ACB87573.1| hemagglutinin [Influenza A virus
 (A/Ji angsu/1/2007 (H5N1))]
 MEKI VLLLA I VSLVKSDQI CI GYHANNSTEQVDTI MEKNVTVTHAQDI LEKTHNGKLCDLGDKVPLI LRD
 CSVAGWLLGNPMCDEFI NVPEWSYI VEKANPANDLCYPGNFNDYEEELKHLLSRI NHFEKI QI I PKSSWSD
 HEASSGVSSACPYQGTSPFFRNVVWLI KKNNA YPTI KRSYNNTOENL LI LWGI HHSNDAAEQI KLYQNP
 TTYI SVGTSTLNQRLVPKI ATRSKVNGQSGRMDFFWTI LKPNDAI NFESNGNFI APEYAYKI VKEGDSAI
 MKSEVEYGNCNTKCQTP I GAI NSSMPFHNI HPLTI GECPKYVKS NRLLVATGLRNSPLRERRRRKRGLFGA
 I AGFI EGGWQGMVDGWYGYHHSNEQSGYAADKESTOKAI DGVTKVNSI I DKMNTQFEAVGREFNLER
 RI ENLNKMKMEDGFLDVTYNAELLVLMENERTLDFHDSNVKNLYDRVRLQLRD NAKELGNGCFEFYHKCD
 NECMESVRNGTYDYPQYSEEARLKREEI SGVKLESMGT YQI LSI YSTVASSLALAI MVAGFLWMCNSG
 LQCRI CI
 >gi |145843666|gb|ABP96850.1| hemagglutinin [Influenza A virus (A/Egypt/2321-
 NAMRU3/2007 (H5N1))]
 MEKI VLLLA I VSLVKSDQI CI GYHANNSTEQVDTI MEKNVTVTHAQDI LEKTHNGKLCDLGDKVPLI LRD
 CSVAGWLLGNPMCDEFNLVPEWSYI VEKI NPANDLCYPGDFNDYEEELKHLLSRI NHFEKI QI I PKSSWSD
 YEASSGVSSACPYQGRSSFFRNVVWLI KKNNA YPTI KRSYNNTOEDLLVWGI HHPNDAAEQI RLYQNP
 TTYI SVGTSTLNQRLVPKI ATRSKVNGQSGRMEFFWTI LKSNDAI NFESNGNFI APEYAYKI VKKGDSTI
 MKSELEYGNCNTKCQTP I GAI NSSMPFHNI HPLTI GECPKYVKS NRLLVATGLRNSPOGERRRRKRGLFG
 AI AGFI EGGWQGMVDGWYGYHHSNEQSGYAADKESTOKAI DGVTKVNSI I NKMNTQFEAVGREFNLE
 RRI ENLNKMKMEDGFLDVTYNAELLVLMENERTLDFHDSNVKNLYDKVRLQLRD NAKELGNGCFEFYHRC
 DNECMESVRNGTYDYPQYSEEARLKREEI SGVKLESI GI YQI LSI YSTVASSLALAI MVAGFLWMCNSG
 SLOCRI CI
 >gi |145843670|gb|ABP96852.1| hemagglutinin [Influenza A virus (A/Egypt/2616-
 NAMRU3/2007 (H5N1))]
 MEKI VLLLA I VSLVKSDQI CI GYHANNSTEQVDTI MEKNVTVTHAQDI LEKTHNGKLCDLGDKVPLI LRD
 CSVAGWLLGNPMCDEFNLVPEWSYI VEKI NPANDLCYPGDFNDYEEELKHLLSRI NHFEKI QI I PKSSWSD

YEASSGVSSACPYQGRSSFFRNVVWLI KKNAYPTI KRSYNNTOEDLLVLWGI HHPNDAAEQI RLYQNP
 TTYI SI GTSTLNQRLVPKI ATRSKVNGQSGRMEFFWTI LKSNDAI NFESNGNFI APEYAYKI VKKGDSTI
 MKSELEYGNCNTKCQTPAI GAI NSSMPFHNI HPLTI GECPKYVKSRLVATGLRNSPQGERRRRKRGLFG
 AI AGFI EGGWQGMVDGWYGYHHSNEQSGYAADKESTQKAI DGVTKVNSI I NKMNTQFEAVGREFNLE
 RRI ENLNKMKMEDGFLDVWTYNAELLVLMENERTLDFHDSNVKNLYDKVRLQLRDRAKELGNGCFEYHRC
 DNECMESVRNGTYDYPQYSEEARLKREEI SGVKLESMGI YQI LSI YSTVASSLALAI MVAGLFLWMCNSG
 SLOCRI CI

>gi |145843674|gb|ABP96854.1| hemagglutinin [Influenza A virus (A/Egypt/2621-
 NAMRU3/2007 (H5N1))]

MEKI VLLFAI VSLVKSDQI CI GYHANNSTEQVDTI MEKNVTVTHAQDI LEKTHNGKLCNLDGVKPLI LRD
 CSVAGWLLGNPMCDFEFLNPEWSYI VEKIPVNDLCYPGDFNDYEELKHLLSRI NHFEKI QI I PKSSWSS
 HEASGVSSACPYQGRSSFFRNVVWLI KKNAYPTI KRSYNNTOEDLLVLWGI HHPNDAAEQRLYQNP
 TYI SVGTSTLNQRLVPKI ATRSKVNGQSGRMEFFWTI LKSNDAI NFESNGNFI APENAYKI VKKGDSTI M
 KSELEYGNCNTKCQTPAI GAI NSSMPFHNI HPLTI GECPKYVKSRLVATGLRNSPQGERRRRKRGLFG
 I AGFI EGGWQGMVDGWYGYHHSNEQSGYAADKESTQKAI DGVTKVNSI I DKMNTQFEAVGREFNLE
 RI ENLNKMKMEDGFLDVWTYNAELLVLMENERTLDFHDSNVKNLYDKVRLQLRDRAKELGNGCFEYHRC
 DNECMESVRNGTYDYPQYSEEARLKREEI SGVKLESI GYQI LSI YSTVASSLALAI MVAGLFLWMCNSG
 SLOCRI CI

>gi |46578416|gb|AAS89004.2| hemagglutinin [Influenza A virus (A/Thailand/3(SP-
 83)/2004 (H5N1))]

MEKI VLLFAI VSLVKSDQI CI GYHANNSTEQVDTI MEKNVTVTHAQDI LEKTHNGKLCNLDGVKPLI LRD
 CSVAGWLLGNPMCDFEFLNPEWSYI VEKIPVNDLCYPGDFNDYEELKHLLSRI NHFEKI QI I PKSSWSS
 HEASGVSSACPYQGRSSFFRNVVWLI KKNAYPTI KRSYNNTOEDLLVLWGI HHPNDAAEQRLYQNP
 TTYI SVGTSTLNQRLVPKI ATRSKVNGQSGRMEFFWTI LKSNDAI NFESNGNFI APEYAYKI VKKGDSTI
 MKSELEYGNCNTKCQTPMGA I NSSMPFHNI HPLTI GECPKYVKSRLVATGLRNSPQGERRRRKRGLFG
 AI AGFI EGGWQGMVDGWYGYHHSNEQSGYAADKESTQKAI DGVTKVNSI I DKMNTQFEAVGREFNLE
 RRI ENLNKMKMEDGFLDVWTYNAELLVLMENERTLDFHDSNVKNLYDKVRLQLRDRAKELGNGCFEYHRC
 DNECMESVRNGTYDYPQYSEEARLKREEI SGVKLESI GI YQI LSI YSTVASSLALAI MVAGLSLWMCNSG
 SLOCRI CI

>gi |93008393|gb|ABE97627.1| hemagglutinin [Influenza A virus
 (A/Vietnam/CL20/2004 (H5N1))]

MEKI VLLFAI VSLVKSDQI CI GYHANNSTEQVDTI MEKNVTVTHAQDI LEKTHNGKLCNLDGVKPLI LRD
 CSVAGWLLGNPMCDFEFLNPEWSYI VEKIPVNDLCYPGDFNDYEELKHLLSRI NHFEKI QI I PKSSWSS
 HEASGVSSACPYQGRSSFFRNVVWLI KKNAYPTI KRSYNNTOEDLLVWGI HHPNDAAEQRLYQNP
 TTYI SVGTSTLNQRLVPKI ATRSKVNGQSGRMEFFWTI LKPNDAI NFESNGNFI APEYAYKI VKKGDSTI
 MKSELEYGNCNTKCQTPMGA I NSSMPFHNI HPLTI GECPKYVKSRLVATGLRNSPQGERRRRKRGLFG
 AI AGFI EGGWQGMVDGWYGYHHSNEQSGYAADKESTQKAI DGVTKVNSI I DKMNTQFEAVGREFNLE
 RRI ENLNKMKMEDGFLDVWTYNAELLVLMENERTLDFHDSNVKNLYDKVRLQLRDRAKELGNGCFEYHRC
 DNECMESVRNGTYDYPQYSEEARLKREEI SGVKLESI GI YQI LSI YSTVASSLALAI MVAGLSLWMCNSG
 SLOCRI CI

>gi |145284466|gb|ABP51977.1| hemagglutinin [Influenza A virus (A/Viet
 Nam/1203/2004 (H5N1))]

MEKI VLLFAI VSLVKSDQI CI GYHANNSTEQVDTI MEKNVTVTHAQDI LEKTHNGKLCNLDGVKPLI LRD
 CSVAGWLLGNPMCDFEFLNPEWSYI VEKIPVNDLCYPGDFNDYEELKHLLSRI NHFEKI QI I PKSSWSS
 HEASGVSSACPYQGRSSFFRNVVWLI KKNAYPTI KRSYNNTOEDLLVLWGI HHPNDAAEQRLYQNP
 TTYI SVGTSTLNQRLVPKI ATRSKVNGQSGRMEFFWTI LKPNDAI NFESNGNFI APEYAYKI VKKGDSTI
 MKSELEYGNCNTKCQTPMGA I NSSMPFHNI HPLTI GECPKYVKSRLVATGLRNSPQGERRRRKRGLFG
 AI AGFI EGGWQGMVDGWYGYHHSNEQSGYAADKESTQKAI DGVTKVNSI I DKMNTQFEAVGREFNLE
 RRI ENLNKMKMEDGFLDVWTYNAELLVLMENERTLDFHDSNVKNLYDKVRLQLRDRAKELGNGCFEYHRC
 DNECMESVRNGTYDYPQYSEEARLKREEI SGVKLESI GI YQI LSI YSTVASSLALAI MVAGLSLWMCNSG
 SLOCRI CI

>gi |145284468|gb|ABP51978.1| hemagglutinin [Influenza A virus (A/Viet
 Nam/1204/2004 (H5N1))]

MEKI VLLFAI VSLVKSDQI CI GYHANNSTEQVDTI MEKNVTVTHAQDI LEKTHNGKLCNLDGVKPLI LRD
 CSVAGWLLGNPMCDFEFLNPEWSYI VEKIPVNDLCYPGDFNDYEELKHLLSRI NHFEKI QI I PKSSWSS
 HEASGVSSACPYQGRSSFFRNVVWLI KKNAYPTI KRSYNNTOEDLLVLWGI HHPNDAAEQRLYQNP
 TTYI SVGTSTLNQRLVPKI ATRSKVNGQSGRMEFFWTI LKPNDAI NFESNGNFI APEYAYKI VKKGDSTI
 MKSELEYGNCNTKCQTPMGA I NSSMPFHNI HPLTI GECPKYVKSRLVATGLRNSPQGERRRRKRGLFG
 AI AGFI EGGWQGMVDGWYGYHHSNEQSGYAADKESTQKAI DGVTKVNSI I DKMNTQFEAVGREFNLE
 RRI ENLNKMKMEDGFLDVWTYNAELLVLMENERTLDFHDSNVKNLYDKVRLQLRDRAKELGNGCFEYHRC
 DNECMESVRNGTYDYPQYSEEARLKREEI SGVKLESI GI YQI LSI YSTVASSLALAI MVAGLSLWMCNSG
 SLOCRI CI

>gi |145284482|gb|ABP51985.1| hemagglutinin [Influenza A virus
 (A/Thailand/Kan353/2004 (H5N1))]

MEKI VLLFAI VSLVKSDQI CI GYHANNSTEQVDTI MEKNVTVTHAQDI LEKTHNGKLCNLDGVKPLI LRD
 CSVAGWLLGNPMCDFEFLNPEWSYI VEKIPVNDLCYPGDFNDYEELKHLLSRI NHFEKI QI I PKSSWSS
 HEASGVSSACPYQGRSSFFRNVVWLI KKNAYPTI KRSYNNTOEDLLVLWGI HHPNDAAEQRLYQNP
 TTYI SVGTSTLNQRLVPKI ATRSKVNGQSGRMEFFWTI LKPNDAI NFESNGNFI APEYAYKI VKKGDSTI
 MKSELEYGNCNTKCQTPMGA I NSSMPFHNI HPLTI GECPKYVKSRLVATGLRNSPQGERRRRKRGLFG
 AI AGFI EGGWQGMVDGWYGYHHSNEQSGYAADKESTQKAI DGVTKVNSI I DKMNTQFEAVGREFNLE
 RRI ENLNKMKMEDGFLDVWTYNAELLVLMENERTLDFHDSNVKNLYDKVRLQLRDRAKELGNGCFEYHRC
 DNECMESVRNGTYDYPQYSEEARLKREEI SGVKLESI GI YQI LSI YSTVASSLALAI MVAGLSLWMCNSG
 SLOCRI CI

>gi |159144905|gb|ABW90127.1| hemagglutinin [Influenza A virus (A/Viet
 Nam/1203/2004 (H5N1))]

MEKI VLLFAI VSLVKSDQI CI GYHANNSTEQVDTI MEKNVTVTHAQDI LEKTHNGKLCNLDGVKPLI LRD
 CSVAGWLLGNPMCDFEFLNPEWSYI VEKIPVNDLCYPGDFNDYEELKHLLSRI NHFEKI QI I PKSSWSS

HEASLGVSSACPYQGESSFFRNVVWLI KKNSTYPTI KRSYNNTOEDLLVLWGI HHPNDAAEQTKLYQNP
 TTYI SVGTSTLNQRLVPRI ATRSKVNGQSGRMEFFWTI LKPNDAI NFESNGNFI APEYAYKI VKKGDSTI
 MKSELEYGNCNTKCQTPMGAI NSSMPFHNI HPLTI GECPKYVKS NRLVLATGLRNSPQRETRGLFGAI AG
 FI EGGWQGMVDGWYGYHHSNEQSGYAADKESTOKAI DGVTKVNSI I DKMNTQFEAVGREFFNNLERRI E
 NLNKKMEDGFLDVWYTNAELLVLMENERLDFHDSNVKNLYDKVRLQRLDNAKELGNGCFEFYHKCDNEC
 MESVRNGTYDYPQYSEEARLKREEI SGVKLESI GI YQI LSI YSTVASSLALAI MVAGLSLWMCNSGSLQC
 RI CI

>gi |159144909|gb|ABW90129.1| hemagglutinin [Influenza A virus (A/Viet
 Nam/1203/2004(H5N1))]

MEKI VLLFAI VSLVKSQDI CI GYHANNSTEQVDTI MEKNVTVTHAQDI LEKTHNGKLCDLGDKVPLI LRD
 CSVAGWLLGNPMDDEFI NVPEWSYI VEKANPVNDLCYPGDFNDYEELKHLLSRI NHFEKI QI I PKSSWSS
 HEASLGVSSACPYQKSSFFRNVVWLI KKNSTYPTI KRSYNNTOEDLLVLWGI HHPNDAAEQTKLYQNP
 TTYI SVGTSTLNQRLVPRI ATRSKVNGQSGRMEFFWTI LKPNDAI NFESNGNFI APEYAYKI VKKGDSTI
 MKSELEYGNCNTKCQTPMGAI NSSMPFHNI HPLTI GECPKYVKS NRLVLATGLRNSPQRETRGLFGAI AG
 FI EGGWQGMVDGWYGYHHSNEQSGYAADKESTOKAI DGVTKVNSI I DKMNTQFEAVGREFFNNLERRI E
 NLNKKMEDGFLDVWYTNAELLVLMENERLDFHDSNVKNLYDKVRLQRLDNAKELGNGCFEFYHKCDNEC
 MESVRNGTYDYPQYSEEARLKREEI SGVKLESI GI YQI LSI YSTVASSLALAI MVAGLSLWMCNSGSLQC
 RI CI

>gi |159144921|gb|ABW90135.1| hemagglutinin [Influenza A virus (A/Viet
 Nam/1203/2004(H5N1))]

MEKI VLLFAI VSLVKSQDI CI GYHANNSTEQVDTI MEKNVTVTHAQDI LEKTHNGKLCDLGDKVPLI LRD
 CSVAGWLLGNPMDDEFI NVPEWSYI VEKANPVNDLCYPGDFNDYEELKHLLSRI NHFEKI QI I PKSSWSS
 HEASLGVSSACPYQKSSFFRNVVWLI KKNSTYPTI KRSYNNTOEDLLVLWGI HHPNDAAEQTKLYQNP
 TTYI SVGTSTLNQRLVPRI ATRSKVNGQSGRMEFFWTI LKPNDAI NFESNGNFI APEYAYKI VKKGDSTI
 MKSELEYGNCNTKCQTPMGAI NSSMPFHNI HPLTI GECPKYVKS NRLVLATGLRNSPQRETRGLFGAI AG
 FI EGGWQGMVDGWYGYHHSNEQSGYAADKESTOKAI DGVTKVNSI I DKMNTQFEAVGREFFNNLERRI E
 NLNKKMEDGFLDVWYTNAELLVLMENERLDFHDSNVKNLYDKVRLQRLDNAKELGNGCFEFYHKCDNEC
 MESVRNGTYDYPQYSEEARLKREEI SGVKLESI GI YQI LSI YSTVASSLALAI MVAGLSLWMCNSGSLQC
 RI CI

>gi |126361918|gb|AB010181.1| hemagglutinin [Influenza A virus (A/Viet
 Nam/JP178/2004(H5N1))]

MEKI VLLFAI VSLVKSQDI CI GYHANNSTEQVDTI MEKNVTVTHAQDI LEKTHNGKLCDLGDKVPLI LRD
 CSVAGWLLGNPMDDEFI NVPEWSYI VEKANPVNDLCYPGDFNDYEELKHLLSRI NHFEKI QI I PKSSWSS
 HEASLGVSSACPYQKSSFFRNVVWLI KKNSTYPTI KRSYNNTOEDLLVMWGI HHPNDAAEQTKLYQNP
 TTYI SVGTSTLNQRLVPRI ATRSKVNGQSGRMEFFWTI LKPNDAI NFESNGNFI APEYAYKI VKKGDSTI
 MKSELEYGNCNTKCQTPMGAI NSSMPFHNI HPLTI GECPKYVKS NRLVLATGLRNSPQRETRGLFGAI AG
 FI EGGWQGMVDGWYGYHHSNEQSGYAADKESTOKAI DGVTKVNSI I DKMNTQFEAVGREFFNNLE
 RRI ENLNKKMEDGFLDVWYTNAELLVLMENERLDFHDSNVKNLYDKVRLQRLDNAKELGNGCFEFYHKC
 DNECMESVRNGTYDYPQYSEEARLKREEI SGVKLESI GI YQI LSI YSTVASSLALAI MVAGLSLWMCNSG
 SLQCRVCI

>gi |126361922|gb|AB010183.1| hemagglutinin [Influenza A virus (A/Viet
 Nam/JP4207/2005(H5N1))]

MEKI VLLFAI VSLVKSQDI CI GYHANNSTEQVDTI MEKNVTVTHAQDI LEKTHNGKLCDLGDKVPLI LRD
 CSVAGWLLGNPMDDEFI NVPEWSYI VEKANPVNDLCYPGDFNDYEELKHLLSRI NHFEKI QI I PKSSWSS
 HEASLGVSSACPYQKSSFFRNVVWLI KKNSTYPTI KRSYNNTOEDLLVMWGI HHPNDAAEQTKLYQNP
 TTYI SVGTSTLNQRLVPRI ATRSKVNGQSGRI EFFWTI LKPNDAI NFESNGNFI APEYAYKI VKKGDSTI
 MKSELEYGNCNTKCQTPMGAI NSSMPFHNI HPLTI GECPKYVKS NRLVLATGLRNSPQRETRGLFGAI AG
 FI EGGWQGMVDGWYGYHHSNEQSGYAADKESTOKAI DGVTKVNSI I DKMNTQFEAVGREFFNNLE
 RRI ENLNKKMEDGFLDVWYTNAELLVLMENERLDFHDSNVKNLYDKVRLQRLDNAKELGNGCFEFYHKC
 DNECMESVRNGTYDYPQYSEEARLKREEI SGVKLESI GI YQI LSI YSTVASSLALAI MVAGLSLWMCNSG
 SLQCRI CI

>gi |157955881|gb|ABW06367.1| hemagglutinin [Influenza A virus
 (A/Indonesia/7/2005(H5N1))]

MEKI MLLLAI VSLVKSQDI CI GYHANNSTEQVDTI MEKNVTVTHAQDI LEKTHNGKLCDLGDKVPLI LRD
 CSVAGWLLGNPMDDEFI NVPEWSYI VEKANPTNDLCYPGDFNDYEELKHLLSRI NHFEKI QI I PKSSWSD
 HEASSGVSSACPYLGSSFFRNVVWLI KKNSTYPTI KRSYNNTOEDLLVLWGI HHPNDAAEQTRLYQNP
 TTYI SI GTSTLNQRLVPKI ATRSKVNGQSGRMEFFWTI LKPNDAI NFESNGNFI APEYAYKI VKKGDSTI
 MKSELEYGNCNTKCQTPMGAI NSSMPFHNI HPLTI GECPKYVKS NRLVLATGLRNSPQRESRRKRRGLFG
 AI AGFI EGGWQGMVDGWYGYHHSNEQSGYAADKESTOKAI DGVTKVNSI I DKMNTQFEAVGREFFNNLE
 RRI ENLNKKMEDGFLDVWYTNAELLVLMENERLDFHDSNVKNLYDKVRLQRLDNAKELGNGCFEFYHKC
 DNECI ESI RNGTYNYPQYSEEARLKREEI SGVKLESI GTYQI LSI YSTVASSLALAI MMAGLSLWMCNSG
 SLOCRICI

>gi |93008405|gb|ABE97633.1| hemagglutinin [Influenza A virus
 (A/Vietnam/CL119/2005(H5N1))]

MEKI VLLFAI VSLVKSQDI CI GYHANNSTEQVDTI MEKNVTVTHAQDI LEKTHNGKLCDLGDKVPLI LKD
 CSVAGWLLGNPMDDEFI NVPEWSYI VEKANPVNDLCYPGDFNDYEELKHLLSRI NHFEKI QI I PKSSWSS
 HEASLGVSSACPYQGRSSFFRNVVWLI KKNSTYPTI KRSYNNTOEDLLVMWGI HHPNDAAEQTRLYQNP
 TTYI SVGTSTLNQRLVPRI ATRSKVNGQSGRMEFFWTI LKPNDAI NFESNGNFI APEYAYKI VKKGDSTI
 MKSELEYGNCNTKCQTPMGAI NSSMPFHNI HPLTI GECPKYVKS NRLVLATGLRNSPQRETRGLFGAI AG
 FI EGGWQGMVDGWYGYHHSNEQSGYAADKESTOKAI DGVTKVNSI I DKMNTQFEAVGREFFNNLE
 RRI ENLNKKMEDGFLDVWYTNAELLVLMENERLDFHDSNVKNLYDKVRLQRLDNAKELGNGCFEFYHKC
 DNECMESVRNGTYDYPQYSEEARLKREEI SGVKLESI GI YQI LSI YSTVASSLALAI MVAGLSLWMCNSG
 SLQC

>gi |126361924|gb|AB010184.1| hemagglutinin [Influenza A virus (A/Viet
 Nam/JP14/2005(H5N1))]

MEKI VLLFAI VSLVKSQDI CI GYHANNSTEQVDTI MEKNVTVTHAQDI LEKTHNGKLCDLGDKVPLI LRD
 CSVAGWLLGNPMDDEFI NVPEWSYI VEKANPVNDLCYPGDFNDYEELKHLLSRI NHFEKI QI I PKSSWSS

HEASLGVSAACPYQKSSFFRNWVWLI KKNSTYPTI KRSYNNTOEDLLVMWGI HHPNDAAEQTKLYQNP
 TTYI SVGTSTLNQRLVPR I ATRSKVNGQSGRMEFFWTI LKPNDAI NFESNGNFI APEYAYKI VKKGDSTI
 MKSELEYGNCNTKCQTPMGA I NSSMPLHNI HPLTI GECPKYVKS NRLLVATGLRNSPQRERRRKRGLFG
 AI AGFI EGGWQGMVDGWYGYHHSNEQSGYAADKESTQKAI DGVTKVNSI I DKMNTQFEAVGREFNLE
 RRI ENLNKMKMEDGFLDVWWTYNAELLVLMENERTLDFHDSNVKNLYDKVRLQLRD NAKELGNGCFEFYHKC
 DNECMESVRNGTYDYPQYSEEARLKREEI SGVKLESI GI YQI LSI YSTVASSLALAI MVAGLSLWMCNSG
 SLOCRI CI

>gi |78096576|dbj|BAE46949.1| hemagglutinin [Influenza A virus
 (A/Hanoi/30408/2005(H5N1))]

MEKI VLLFAI VSLVKSQDI CI GYHANNSTEQVDTI MEKNVTVTHAQDI LEKTHNGKLCDLGDKVPLI LRD
 CSVAGWLLGNPMDDEFI NVPEWSYI VEKANPVNDLCYPGDFNDYEELKHLLSRI NHFEKI QI I PKSSWLS
 HEASLGVSACPYQKSSFFRNWVWLI KKNSTYPTI KRSYNNTOEDLLVWGI HHPNDAAEQTKLYQNP
 TTYI SVGTSTLNQRLVPR I ATRSKVNGQSGRMEFFWTI LKPNDAI NFESNGNFI APEYAYKI VKKGDSTI
 MKSELEYGNCNTKCQTPMGA I NSSMPFHNI HPLTI GECPKYVKS NRLLVATGLRNSPQRERRRKRGLFG
 AI AGFI EGGWQGMVDGWYGYHHSNEQSGYAADKESTQKAI DGVTKVNSI I DKMNTQFEAVGREFNLE
 RI ENLNKMKMEDGFLDVWWTYNAELLVLMENERTLDFHDSNVKNLYDKVRLQLRD NAKELGNGCFEFYHKC
 DNECMESVRNGTYDYPQYSEEARLKREEI SGVKLESI GI YQI LSI YSTVASSLALAI MVAGLSLWMCNSG
 SLOCRI CI

>gi |85680918|gb|ABC72655.1| hemagglutinin [Influenza A virus
 (A/Thailand/676/2005(H5N1))]

MEKI VLLFAI VSLVKSQDI CI GYHANNSTEQVDTI MEKNVTVTHAQDI LEKTHNGKLCDLGDKVPLI LRD
 CSVAGWLLGNPMDDEFI NVPEWSYI VEKANPVNDLCYPGDFNDYEELKHLLSRI NHFEKI QI I PKSSWSS
 HEASVGVSSVCPYQKSSFFRNWVWLI KKNSTYPTI KRSYNNTOEDLLVWGI HHPNDAAEQTKLYQNP
 TTYI SVGTSTLNQRLVPR I ATRSKVNGQSGRMEFFWTI LKPNDAI NFESNGNFI APEYAYKI VKKGDSTI
 MKSELEYGNCNTKCQTPMGA I NSSMPFHNI HPLTI GECPKYVKS NRLLVATGLRNSPQRERRRKRGLFG
 AI AGFI EGGWQGMVDGWYGYHHSNEQSGYAADKESTQKAI DGVTKVNSI I DKMNTQFEAVGREFNLE
 RI ENLNKMKMEDGFLDVWWTYNAELLVLMENERTLDFHDSNVKNLYDKVRLQLRD NAKELGNGCFEFYHKC
 DNECMESVRNGTYDYPQYSEEARLKREEI SGVKLESI GI YQI LSI YSTVASSLALAI MVAGLSLWMCNSG
 SLOCRI CI

>gi |87137941|gb|ABD28182.1| hemagglutinin [Influenza A virus
 (A/Guangxi/1/2005(H5N1))]

MEKI VLLFAI VSLVKSQDI CI GYHANNSTEQVDTI MEKNVTVTHAQDI LEKTHNGKLCDLGDKVPLI LRD
 CSVAGWLLGNPMDDEFI NVPEWSYI VEKANPVNDLCYPGDFNDYEELKHLLSRI NHFEKI QI I PKSSWSD
 HEASSGSSACPYQGTSPFFRNWVWLI KKNSTYPTI KRSYNNTOEDLLVWGI HHSNDAAEQTKLYQNP
 TTYI SVGTSTLNQRLVPR I ATRSKVNGQSGRMEFFWTI LKPNDAI NFESNGNFI APEYAYKI VKKGDSTI
 MKSELEYGNCNTKCQTPMGA I NSSMPFHNI HPLTI GECPKYVKS NRLLVATGLRNSPQRERRRKRGLFG
 AI AGFI EGGWQGMVDGWYGYHHSNEQSGYAADKESTQKAI DGVTKVNSI I DKMNTQFEAVGREFNLE
 RI ENLNKMKMEDGFLDVWWTYNAELLVLMENERTLDFHDSNVKNLYDKVRLQLRD NAKELGNGCFEFYHKC
 DNECMESVRNGTYDYPQYSEEARLKREEI SGVKLESI GYQI LSI YSTVASSLALAI MVAGLSLWMCNSG
 SLOCRI CI

>gi |116295112|gb|ABJ98529.1| hemagglutinin [Influenza A virus
 (A/Thailand/RPNP/2005(H5N1))]

LKVSQDI CI GYHANNSTERVDTI REKNVTVTHAQDI LEKTHNGKLCDLGDKVPLI LRD
 CSVAGWLLGNPMDDEFI NVPEWSYI VEKANPVNDLCYPGDFNDYEELKHLLSRI NHFEKI QI I PKSSWSS
 HEASVGVSSVCPYQKSSFFRNWVWLI KKNSTYPTI KRSYNNTOEDLLVWGI HHPNDAAEQTKLYQNP
 TTYI SVGTSTLNQRLVPR I ATRSKVNGQSGRMEFFWTI LKPNDAI NFESNGNFI APEYAYKI VKKGDSTI
 MKSELEYGNCNTKCQTPMGA I NSSMPFHNI HPLTI GECPKYVKS NRLLVATGLRNSPQRERRRKRGLFG
 AI AGFI EGGWQGMVDGWYGYHHSNEQSGYAADKESTQKAI DGVTKVNSI I DKMNTQFEAVGREFNLE
 RI ENLNKMKMEDGFLDVWWTYNAELLVLMENERTLDFHDSNVKNLYDKVRLQLRD NAKELGNGCFEFYHKC
 DNECMESVRNGTYDYPQYSEEARLKREEI SGVKLESI GI YQI LSI YSTVASSLALAI MVAGLSLWMCNSG
 SLOCRI CI

>gi |116295116|gb|ABJ98531.1| hemagglutinin [Influenza A virus
 (A/Thailand/HA20/2005(H5N1))]

MEKI VLLFAI VSLVKSQDI CI GYHANNSTEQVDTI MEKNVTVTHAQDI LEKTHNGKLCDLGDKVPLI LRD
 CSVAGWLLGNPMDDEFI NVPEWSYI VEKANPVNDLCYPGDFNDYEELKHLLSRI NHFEKI QI I PKSSWSS
 HEASLGVSACPYQKSSFFRNWVWLI KKTSTYPTI KRSYNNTOEDLLVWGI HHPNDAAEQTRLYQNP
 TTYI SVGTSTLNQRLVPR I ATRSKVNGQSGRMEFFWTI LKPNDAI NFESNGNFI APEYAYKI VKKGDSTI
 MKSELEYGNCNTKCQTPMGA I NSSMPFHNI HPLTI GECPKYVKS NRLLVATGLRNSPQRERRRKRGLFG
 AI AGFI EGGWQGMVDGWYGYHHSNEQSGYAADKESTQKAI DGVTKVNSI I DKMNTQFEAVGREFNLE
 RRI ENLNKMKMEDGFLDVWWTYNAELLVLMENERTLDFHDSNVKNLYDKVRLQLRD NAKELGNGCFEFYHKC
 DNECMESVRNGTYDYPQYSEEARLKREEI SGVKLESI GI YQI LSI YSTVASSLALAI MVAGLSLWMCNSG
 SL

>gi |113494436|gb|ABI36012.1| hemagglutinin [Influenza A virus
 (A/Indonesia/CDC7/2005(H5N1))]

DQI CI GYHANNSTEQVDTI MEKNVTVTHAQDI LEKTHNGKLCDLGDKVPLI LRD
 CSVAGWLLGNPMDDEFI NVPEWSYI VEKANPVNDLCYPGDFNDYEELKHLLSRI NHFEKI QI I PKSSWSD
 HEASVGVSSVCPYQKSSFFRNWVWLI KKNSTYPTI KRSYNNTOEDLLVWGI HHPNDAAEQTRLYQNP
 TTYI SVGTSTLNQRLVPR I ATRSKVNGQSGRMEFFWTI LKPNDAI NFESNGNFI APEYAYKI VKKGDSTI
 MKSELEYGNCNTKCQTPMGA I NSSMPFHNI HPLTI GECPKYVKS NRLLVATGLRNSPQRERRRKRGLFG
 AI AGFI EGGWQGMVDGWYGYHHSNEQSGYAADKESTQKAI DGVTKVNSI I DKMNTQFEAVGREFNLE
 RRI ENLNKMKMEDGFLDVWWTYNAELLVLMENERTLDFHDSNVKNLYDKVRLQLRD NAKELGNGCFEFYHKC
 DNECMESVRNGTYDYPQYSEEARLKREEI SGVKLESI GYQI LSI YSTVASSLALAI MVAGLSLWMCNSG
 SLOCRI CI

>gi |157955845|gb|ABW06347.1| hemagglutinin [Influenza A virus
 (A/Indonesia/160H/2005(H5N1))]

MEKI MLLAI VSLVKSQDI CI GYHANNSTEQVDTI MEKNVTVTHAQDI LEKTHNGKLCDLGDKVPLI LRD
 CSVAGWLLGNPMDDEFI NVPEWSYI VEKANPVNDLCYPGDFNDYEELKHLLSRI NHFEKI QI I PKSSWSD
 HEASVGVSSVCPYQKSSFFRNWVWLI KKNSTYPTI KRSYNNTOEDLLVWGI HHPNDGAEQTRLYQNP
 TTYI SVGTSTLNQRLVPR I ATRSKVNGQSGRMEFFWTI LKPNDAI NFESNGNFI APEYAYKI VKKGDSTI

MKSELEYGNCNTKCQTPMGAI NSSMPFHNI HPLTI GECPKYVKS NRLVLATGLRNSPQRESRRKKRGLFG
AI AGFI EGGWQGMVDGWYGYHHSNEQSGYAADKESTQRAI DGVTNKVN SI I DKMNTQFEAVGREFNLE
RRI ENLNKMKMEDGFLDVTYNAELLVLMENERTLDFHDSNVKNLYDKVRLQLRD NAKELGNGCFEFYHKC
DNECMESI RNGTHYNYPOYSEEARKREEI SGVKLESI GTYQI LSI YSTVASSLALAI MMAGLSLWMC SNG
SLOCRI CI K

>gi |157955864|gb|ABW06358.1| hemagglutinin [Influenza A virus
(A/Indonesia/175H/2005(H5N1))]

MEKI VLLLAI VSLVKSQI CI GYHANNSTEQVDTI MEKNVTVTHAQDI LEKTHNGKLCDL DGVKPLI LRD
CSVAGWLLGNPM CDEFI NVPEWSYI VEKANPTNGLCYPGSFNDYEELKHLLSRI NHFEKI QI I PKSSWSD
HEASSGVSSACPYLGS PFFRN VVWLI KKNSTYPTI KKSNNNTNOEDLLVWGI HHPNDAAEQTRLYQNP
TTYI SI GTSTLNQRLV PKI ATRSKVNGQSGRMEFFWTI LKPNDAI NFESNGNFI APEYAYKI VKKGD SAI
MKSELEYGNCNTKCQTPMGAI NSSMPFHNI HPLTI GECPKYVKS NRLVLATGLRNSPQRESRRKKRGLFG
AI AGFI EGGWQGMVDGWYGYHHSNEQSGYAADKESTQKAI DGVTNKVN SI I DKMNTQFEAVGREFNLE
RRI ENLNKMKMEDGFLDVTYNAELLVLMENERTLDFHDSNVKNLYDKVRLQLRD NAKELGNGCFEFYHKC
DNECMESI RNGTHYNYPOYSEEARKREEI SGVKLESI GTYQI LSI YSTVASSLALAI MMAGLSLWMC SNG
SLOCRI CI K

>gi |113494681|gb|ABI36041.1| hemagglutinin [Influenza A virus
(A/Indonesia/194P/2005(H5N1))]

DQI CI GYHANNSTEQVDTI MEKNVTVTHAQDI LEKTHNGKLCDL DGVKPLI LRD CSVAGWLLGNPM CDEFI
I NVPEWSYI VEKANPTNGLCYPGSFNDYEELKHLLSRI NHFEKI QI I PKSSWSDHEASSGVSSACPYLGS
PSFFRN VVWLI KKNSTYPTI KKSNNNTNOEDLLVWGI HHPNDAAEQTRLYQNP TTYI SI GTSTLNQRLV
PKI ATRSKVNGQSGRMEFFWTI LKPNDAI NFESNGNFI APEYAYKI VKKGD SAI MKSELEYGNCNTKCQ
TPMGAI NSSMPFHNI HPLTI GECPKYVKS NRLVLATGLRNSPQRESRRKKRGLFGAI AGFI EGGWQGMVDG
WYGYHHSNEQSGYAADKESTQKAI DGVTNKVN SI I DKMNTQFEAVGREFNLE RRI ENLNKMKMEDGFLD
VWTYNAELLVLMENERTLDFHDSNVKNLYDKVRLQLRD NAKELGNGCFEFYHKC DNECMESI RNGTHYNYP
QYSEEARLKREEI SGVKLESI GTYQI LSI YSTVASSLALAI MMAGLSLWMC SNGSLOCRI CI

>gi |157955826|gb|ABW06336.1| hemagglutinin [Influenza A virus
(A/Indonesia/195H/2005(H5N1))]

MEKI VLLLAI VSLVKSQI CI GYHANNSTEQVDTI MEKNVTVTHAQDI LEKTHNGKLCDL DGVKPLI LRD
CSVAGWLLGNPM CDEFI NVPEWSYI VEKANPTNGLCYPGSFNDYEELKHLLSRI NHFEKI QI I PKSSWSD
HEASSGVSSACPYLGS PFFRN VVWLI KKNSTYPTI KKSNNNTNOEDLLVWGI HHPNDVAEQTRLYQNP
ATYI SI GTSTLNQRLV PKI ATRSKVNGQSGRMEFFWTI LKPNDAI NFESNGNFI APEYAYKI VKKGD SAI
MKSELEYGNCNTKCQTPMGAI NSSMPFHNI HPLTI GECPKYVKS NRLVLATGLRNSPQRESRRKKRGLFG
AI AGFI EGGWQGMVDGWYGYHHSNEQSGYAADKESTQKAI DGVTNKVN SI I DKMNTQFEAVGREFNLE
RRI ENLNKMKMEDGFLDVTYNAELLVLMENERTLDFHDSNVKNLYDKVRLQLRD NAKELGNGCFEFYHKC
DNECMESI RNGTHYNYPOYSEEARKREEI SGVKLESI GTYQI LSI YSTVASSLALAI MMAGLSLWMC SNG
SLOCR

>gi |113494687|gb|ABI36042.1| hemagglutinin [Influenza A virus
(A/Indonesia/287E/2005(H5N1))]

DQI CI GYHANNSTEQVDTI MEKNVTVTHAQDI LEKTHNGKLCDL DGVKPLI LRD CSVAGWLLGNPM CDEFI
I NVPEWSYI VEKANPTNGLCYPGSFNDYEELKHLLSRI NHFEKI QI I PKSSWSDHEASSGVSSACPYLGS
PSFFRN VVWLI KKNSTYPTI KKSNNNTNOEDLLVWGI HHPNDAAEQTRLYQNP TTYI SI GTSTLNQRLV
PKI ATRSKVNGQSGRMEFFWTI LNPNDAI NFESNGNFI APEYAYKI VKKGD SAI MKSELEYGNCNTKCQ
TPMGAI NSSMPFHNI HPLTI GECPKYVKS NRLVLAKGLRNSPQRESRRKKRGLFGAI AGFI EGGWQGMVDG
WYGYHHSNEQSGYAADKESTQKAI DGVTNKVN SI I DKMNTQFEAVGREFNLE RRI ENLNKMKMEDGFLD
VWTYNAELLVLMENERTLDFHDSNVKNLYDKVRLQLRD NAKELGNGCFEFYHKC DNECMESI RNGTHYNYP
QYSEEARLKREEI SGVKLESI GTYQI LSI YSTVASSLALAI MMAGLSLWMC SNGSLOCRI CI

Neurami ni dase

H1N1

>gi |8572181|gb|AAF77042.1|AF250362_1 neurami ni dase [influenza A virus
(A/duck/Alberta/35/76(H1N1))]

MNPNQKI I TI GSI CMAI GI I SLMLQI GNI I SI VVSHSI QTGSQNH PETCNQSVI TYENNTWVNQTYI NI S
NTNLI AEQAVVSVTLAGNSSLCP I GGWAI YSKDNGI RI GSKGDV FVI REPFI SC SHLE CRTFFLTQ GALL
NDKHSNGTVKDRSPYRTLMSCPVGEAPSPYNSRFESVAWSASACHDGI SWLTI GI SGPDNGAVAVLKYNG
I I TDTI KSWRNNI LRTQSEACI NGSCFTI MTDGSPNGOASYKI FK I EKGKVVKSVELNAPNYHYECS
CYPDAGEVMCVRDNWHGSRNPVVSFNQNL EYQI GYI CSGVFGDNPRPNDGTGSCGPVSSNGAYGVKGF S
FKYNGVWVI GRKTSSRS GFEMI WDPNGWTE TDNSFSVKQDI VAI TDW S GSGS FVQHP ELTGLDCMRP
CFWVELI RGRPKENTI WTS GSSI SFCGVNSDVTGWSWPDGAELPFTI DK

>gi |78095594|gb|ABB19417.1| neurami ni dase [influenza A virus (A/mal Iard
duck/ALB/65/1976(H1N1))]

MNPNQKI I TI GSI CMAI GI I SLMLQI GNI I SI VVSHSI QTGSQNH PETCNQSVI TYENNTWVNQTYI NI S
NTNLI AEQAVVSVTLAGNSSLCP I GGWAI YSKDNGI RI GSKGDV FVI REPFI SC SHLE CRTFFLTQ GALL
NDKHSNGTVKDRSPYRTLMSCPVGEAPSPYNSRFESVAWSASACHDGI SWLTI GI SGPDNGAVAVLKYNG
I I TDTI KSWRNNI LRTQSEACI NGSCFTI MTDGSPNGOASYKI FK I EKGKVVKSVELNAPNYHYECS
CYPDAGEVMCVRDNWHGSRNPVVSFNQNL EYQI GYI CSGVFGDNPRPNDGTGSCGPVSSNGAYGVKGF S
FKYNGVWVI GRKTSSRS GFEMI WDPNGWTE TDNSFSVKQDI VAI TDW S GSGS FVQHP ELTGLDCMRP

CFWVELI RGRPKENTI WTSGSSI SFCGVNSDVTGWSWPDGAELPFTI DK
>gi |78097953|gb|ABB20505.1| neurami ni dase [Influenza A virus (A/mallard
duck/ALB/35/1976(H1N1))]
MNPNQKI I TI GSI CMAI GI I SLMLQI GNI I SI WVSHSI QTGSONHPETCNQSVI TYENNTWVNOQTYI NI S
NTNLI AEQAVSVTLGNSLCP I GGWAI YSKDNGI RI GSKGDV FVI REPFI SCSHLECR TFFLTQ GALL
NDKHSNGTVKDRSPYRTLMSCPVGEAPSPYNSRFESVAWSASACHDGI SWLTI GI SGPDNGAVAVLK YNG
I I TDTI KSWRNNI LRTQSEECACI NGSCFTI MTDGPSNGOASYKI FKI EKGKVVKSVELNAPNYHYEECS
CYPDAGEVMCVC RDNNHGSNRPWVWVFNQNL EYQI GYI CSGVFGDNPRPNDGTGSCG PVSSNGAYGVKGF S
FKYGN G VVI GR TKSTSSRSGFEMI WDPNGWTE TDNSF SVKQDI VAI TDWSGYSGSFVQHP ELTGLDCMRP
CFWVELI RGRPKENTI WTSGSSI SFCGVNSDVTGWSWPDGAELPFTI DK
>gi |113531187|dbj|BAF03628.1| neurami ni dase [Influenza A virus
(A/duck/Mi yagi /66/77(H1N1))]
MNPNQKI I TI GSI CMVVG I SLI LQI GNI I SI WVSHSI QTGNQNPETCNQSI I TYENNTWVNOQTYI NI S
NTNFAAEQAVASVALAGNSLCP I SGWAI YSKDNGI RI GSRGDV FVI REPFI SCSHLECR TFFLTQ GALL
NDKHSNGTVKDRSPYRTLMSCPVGEAPSPYNSRFESVAWSASACHDGI SWLTI GI SGPDNGAVAVLK YNG
I I TDTI KSWRNNI LRTQSEECACMNGSCFTVMTDGPSNGOASYKI FKI EKGKVVKSVELNAPNYHYEECS
CYPDAGEI TCVC RDNNHGSNRPWVWVFNQNL EYQI GYI CSGVFGDNPRPNDGTGSCG PVSSNGAYGVKGF S
FKYGN G VVI GR TKSTSSRSGFEMI WDPNGWTE TDSSFSMKQDI VAI TDWSGYSGSFVQHP ELTGLDCMRP
CFWVELI RGRPKENTI WTSGSSI SFCGVNSDVTGWSWPDGAELPFTI DK
>gi |37955297|gb|AA062048.1| neurami ni dase [Influenza A virus
(A/duck/Mi yagi /9/77(H1N1))]
MNPNQKI I TI GSI CMVVG I SLI LQI GNI I SI WVSHSI QTGNQNPETCNQSI I TYENNTWVNOQTYI NI S
NTNFAAEQAVASVALAGNSLCP I SGWAI YSKDNGI RI GSRGDV FVI REPFI SCSHLECR TFFLTQ GALL
NDKHSNGTVKDRSPYRTLMSCPVGEAPSPYNSRFESVAWSASACHDGI SWLTI GI SGPDNGAVAVLK YNG
I I TDTI KSWRNNI LRTQSEECACMNGSCFTVMTDGPSNGOASYKI FKI EKGKVVKSVELNAPNYHYEECS
CYPDAGEI TCVC RDNNHGSNRPWVWVFNQNL EYQI GYI CSGVFGDNPRPNDGTGSCG PVSSNGAYGVKGF S
FKYGN G VVI GR TKSTSSRSGFEMI WDPNGWTE TDSSFSMKQDI VAI TDWSGYSGSFVQHP ELTGLDCMRP
CFWVELI RGRPKENTI WTSGSSI SFCGVNSDVTGWSWPDGAELPFTI DK
>gi |78095767|gb|ABB19521.1| neurami ni dase [Influenza A virus (A/mallard
duck/ALB/46/1977(H1N1))]
MNPNQKI I TI GSI CMAI GI I SLMLQI GNI I SI WVSHSI QTGNQNPETCNQSI I TYENNTWVNOQTYI NI S
NTNLI AEQAVASVTLGNSLCP I SGWAI YSKDNGI RI GSKGDV FVI REPFI SCSHLECR TFFLTQ GALL
NDKHSNGTVKDRSPYRTLMSCP I GEAPSPYNSRFESVAWSASACHDGI SWLTI GI SGPDNGAVAVLK YNG
I I TDTI KSWRNNI LRTQSEECACI NGSCFTI MTDGPSNGOASYKI FKI EKGKVVKSVELNAPNHHEECS
CYPDAGEI MCVC RDNNHGSNRPWVWVFNQNL EYQI GYI CSGVFGDNPRPNDGTGSCG PVSSNGAYGVKGF S
FKYGN G VVI GR TKSTSSRSGFEMI WDPNGWTE TDSSFSVKQDI VAI TDWSGYSGSFVQHP ELTGLDCMRP
CFWVELI RGRPKENTI WTSGSSI SFCGVNSDVTGWSWPDGAELPFTI DK
>gi |78096022|gb|ABB19670.1| neurami ni dase [Influenza A virus (A/mallard
duck/ALB/127/1977(H1N1))]
MNPNQKI I TI GSI CMAI GI I SLMLQI GNI I SI WVSHSI QTGGQNPETCNQSVI TYENNTWVNOQTYI NI S
NTNLI AEQAVSVTLGNSLCP I SGWAI YSKDNGI RI GSKGDV FVI REPFI SCSHLECR TFFLTQ GALL
NDKHSNGTVKDRSPYRTLMSCPVGEAPSPYNSRFESVAWSASACHDGI SWLTI GI SGPDNGAVAVLK YNG
MI TDTI KSWRNNI LRTQSEECACI NGSCFTI MTDGPSNGOASYKI FKI EKGKVVKSVELNAPNYHYEECS
CYPDAGEVMCVC RDNNHGSNRPWVWVFNQNL EYQI GYI CSGVFGDNPRPNDGTGSCG PVSSNGAYGVKGF S
FKYGN G VVI GR TKSTSSRSGFEMI WDPNGWTE TDNSF SVKQDI VAI TDWSGYSGSFVQHP ELTGLDCI RP
CFWVELI RGRPKENTI WTSGSSI SFCGVNSDVTGWSWPDGAELPFTI DK
>gi |78095786|gb|ABB19532.1| neurami ni dase [Influenza A virus (A/pintail
duck/ALB/219/1977(H1N1))]
MNPNQKI I TI GSI CMAI GI I SLMLQI GNI I SI WVSHSI QTGGQNPETCNQSVI TYENNTWVNOQTYI NI S
NTNLI AEQAVASVTLGNSLCP I SGWAI YSKDNGI RI GSKGDV FVI REPFI SCSHLECR TFFLTQ GALL
NDKHSNGTVKDRSPYRTLMSCPVGEAPSPYNSRFESVAWSASACHDGI SWLTI GI SGPDNGAVAVLK YNG
I I TDTI KSWRNNI LRTQSEECACI NGSCFTI MTDGPSNGOASYKI FKI EKGKVVKSVELNAPNYHYEECS
CYPDAGEVMCVC RDNNHGSNRPWVWVFNQNL EYQI GYI CSGVFGDNPRPNDGTGSCG PVSSNGAYGVKGF S
FKYGN G VVI GR TKSTSSRSGFEMI WDPNGWTE TDNSF SVKQDI VAI TDWSGYSGSFVQHP ELTGLDCMRP
CFWVELI RGRPKENTI WTSGSSI SFCGVNSDVTGWSWPDGAELPFTI DK
>gi |78095805|gb|ABB19543.1| neurami ni dase [Influenza A virus (A/pintail
duck/ALB/238/1979(H1N1))]
MNPNQKI I TI GSI CMAI GI I SLVLQI GNI I SI WVSHSI QTGSONHPETCNQSVI TYENNTWVNOQTYI NI S
NTNLI AEQAVAPVTLGNSLCP I SGWAI YSKDNGI RI GSKGDV FVI REPFI SCSHLECR TFFLTQ GALL
NDKHSNGTVKDRSPYRTLMSCPVGEAPSPYNSRFESVAWSASACHDGI SWLTI GI SGPDNGAVAVLK YNG
MI TDTI KSWRNNI LRTQSEECACI NGSCFTI MTDGPSNGOASYKI FKI EKGKVVKSVELNAPNYHYEECS
CYPDAGEVMCVC RDNNHGSNRPWVWVFNQNL EYQI GYI CSGVFGDNPRPNDGTGSCG PVSSNGAYGVKGF S
FKYGN G VVI GR TKSTSSRSGFEMI WDPNGWTE TDNSF SVKQDI VAI TDWSGYSGSFVQHP ELTGLDCMRP
CFWVELI RGRPKENTI WTSGSSI SFCGVNSDVTGWSWPDGAELPFTI DK
>gi |78095824|gb|ABB19554.1| neurami ni dase [Influenza A virus (A/mallard
duck/ALB/965/1979(H1N1))]
MNPNQKI I TI GSI CMAI GI I SLVLQI GNI I SI WVSHSI QTGSONHPETCNQSVI TYENNTWVNOQTYI NI S
NTNLI AEQAVAPVTLGNSLCP I SGWAI YSKDNGI RI GSKGDV FVI REPFI SCSHLECR TFFLTQ GALL
NDKHSNGTVKDRSPYRTLMSCPVGEAPSPYNSRFESVAWSASACHDGI SWLTI GI SGPDNGAVAVLK YNG
I I TDTI KSWRNNI LRTQSEECACI NGSCFTI MTDGPSNGOASYKI FKI EKGKVVKSVELNAPNYHYEECS
CYPDAGEVMCVC RDNNHGSNRPWVWVFNQNL EYQI GYI CSGVFGDNPRPNDGTGSCG PVSSNGAYGVKGF S
FKYGN G VVI GR TKSTSSRSGFEMI WDPNGWTE TDNSF SVKQDI VAI TDWSGYSGSFVQHP ELTGLDCMRP
CFWVELI RGRPKENTI WTSGSSI SFCGVNSDVTGWSWPDGAELPFTI DK
>gi |78097742|gb|ABB20381.1| neurami ni dase [Influenza A virus
(A/duck/AUS/749/1980(H1N1))]
MNPNQKI I TI GSTCMVI GI I SLI LQI GNI I SI WVSHSI QTGNQNPETCNQSVI TYENK TWVNOQTYVNI S
NTNLVI ERDVI SVALLGNSLCP I SGWAI YSKDNGI RI GSKGDV FVI REPFI SCSHLECR TFFLTQ GALL

NDKHSNGTVKDRSPYRTLMSCPVGEAPSPYNSRFESVAWSASACHDGI SWLTVGI SGPDPNGAVAVLKYN
 I I TDTVKSWRNNI LRTQSEECACI NGSCFTI MTDGSPNGOASYKI FKI EKGKVVKSVELNAPNYHYEES
 CYPDASEI MCVCRDNWHGSRNPWVSFNQNLLEYQI GYI CSGVFGDNPRPNDGTGSCGPVSSNGAYGVKGF
 FKYGNGVWI GRKTSTSSRSGFEMI WDPNGWTE TDSSFSVKQDI VAI TDWSGYSGSFVQHPPELTGLDCI RP
 CFWVELI RGRPKENTI WTSGSSI SFCGVNSDTVGWSWPDGAELPFTI DK
 >gi |189312997|gb|ACD88519.1| neurami ni dase [Influenza A virus
 (A/turkey/KS/4880/1980(H1N1))]
 MNTNQRI I TI GTI CLI VGI VSLLOI GNI VSLWI SHSI QTGEKNHPEVCNQSVI TYENNTWVNQTYNI S
 NTNLI AEGQVAPVTI LAGNSSLCP I SGWAI YSKDNGI RI GSKGDFVI REPFI SCSHLECRFTFFLTQGALL
 NDRHSNGTVRDRSPYRTLMSCP I GEAPSPYNSRFESVAWSASACHDGMWLT I GI SGPDPNGAVAVLKYN
 I I TDTI KSWRNKI LRTQSEECVCI NGSCFTI MTDGSPNGOASYKI FKMEKGI I KSI ELDAPNYHYEES
 CYPDTGKVVVCRDNWHGSRNPWVSFNQNLLEYQI GYI CSGVFGDNPRPNDGTGSCGPVSSNGAYGVKGF
 FRYGNGVWI GRKTSI SSRSGFEMI WDPNGWTE TDSSFSMKQDI I ALTDWSGYSGSFVQHPPELTGMNCI RP
 CFWVELI RGQPKENTI WTSGSSI SFCGVNSDTVGWSWPDGADLPFTI DK
 >gi |18103339|gb|ABB21775.1| neurami ni dase [Influenza A virus
 (A/pi geon/MN/1407/1981(H1N1))]
 MNPNQKI I TI GSI CMAI GI I SLVLOI GNI I SI WVSHSI QTGSQNHPEVCNQSVI TYENNTWVNQTYNI S
 NTNLI AEGQVAPVTI LAGNSSLCP I SGWAI YSKDNGI RI GSKGDFVI REPFI SCSHLECRFTFFLTQGALL
 NDKHSNGTVKDRSPYRTLMSCPVGEAPSPYNSRFESVAWSASACHDGI SWLTI GI SGPDPNGAVAVLKYN
 I I TDTI KSWRNKI LRTQSEECACI NGSCFTI MTDGSPNGOASYKI FKI EKGKVVKSVELNAPNYHYEES
 CYPDASEVMCVCRDNWHGSRNPWVSFNQNLLEYQI GYI CSGVFGDNPRPNDGTGSCGPVSSNGAYGVKGF
 FKYGNGVWI GRKTSTSSRSGFEMI WDPNGWTE TDNSFSVKQDI VAI TDWSGYSGSFVQHPPELTGLDCMRP
 CFWVELI RGRPKENTI WTSGSSI SFCGVNSDTVGWSWPDGAELPFTI DK
 >gi |115278678|gb|ABI 84736.1| neurami ni dase [Influenza A virus (A/mallard
 duck/Tennessee/11464/1985(H1N1))]
 MNPNQKI I TI GSI CMVI GI I SLALOI GNI I SI WVSHSI QTGSQNHPEVCNQSVI TYENNTWVNQTYNI S
 NTNLI AEGQVAPVTI LAGNSSLCP I SGWAI YSKDNGI RI GSKGDFVI REPFI SCSNLECRFTFFLTQGALL
 NDKHSNGTVKDRSPYRTLMSCPVGEAPSPYNSRFESVAWSASACHDGI SWLTI GI SGPDPNGAVAVLKYN
 I I TDTI KSWRNKI LRTQSEECACI NGSCFTI MTDGSPNGOASYKI FKI EKGKVVKSVELNAPNYHYEES
 CYPDASEVMCVCRDNWHGSRNPWVSFNQNLLEYQI GYI CSGVFGDNPRPNDGTGSCGPVSSNGAYGVKGF
 FKYGNGVWI GRKTSTSSRSGFEMI WDPNGWTE TDNSFSVKQDI I AI TDWSGYSGSFVQHPPELTGLDCMRP
 CFWVELI RGRPKENTI WTSGSSI SFCGVNSDTVGWSWPDGAELPFTI DK
 >gi |85721773|gb|AAF77038.1|AF250358_1 neurami ni dase [Influenza A virus
 (A/Duck/Ohio/175/86 (H1N1))]
 MNPNQKI I TI GSI CMAI GI I SLVLOI GNI I SI WVSHSI QTGSQNHPEVCNQSVI TYENNTWVNQTYNI S
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 I I TDTI KSWRNKI LRTQSEECACI NGSCFTI MTDGSPNGOASYKI FKI EKGKVVKSVELNAPNYHYEES
 CYPDASEVMCVCRDNWHGSRNPWVSFNQNLLEYQI GYI CSGVFGDNPRPNDGTGSCGPVSSNGAYGVKGF
 FKYGNGVWI GRKTSTSSRSGFEMI WDPNGWTE TDNSFSVKQDI VAI TDWSGYSGSFVQHPPELTGLDCMRP
 CFWVELI RGRPKENTI WTSGSSI SFCGVNSDTVGWSWPDGAELPFTI DK
 >gi |85721773|gb|AAF77039.1|AF250359_1 neurami ni dase [Influenza A virus
 (A/Duck/Ohio/30/86 (H1N1))]
 MNPNQKI I TI GSI CMAI GI I SLVLOI GNI I SI WVSHSI QTGSQNHPEVCNQSVI TYENNTWVNQTYNI S
 NTNLI AEGQVAPVTI LAGNSSLCP I SGWAI YSKDNGI RI GSKGDFVI REPFI SCSHLECRFTFFLTQGALL
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 I I TDTI KSWRNKI LRTQSEECACI NGSCFTI MTDGSPNGOASYKI FKI EKGKVVKSVELNAPNYHYEES
 CYPDASEVMCVCRDNWHGSRNPWVSFNQNLLEYQI GYI CSGVFGDNPRPNDGTGSCGPVSSNGAYGVKGF
 FKYGNGVWI GRKTSTSSRSGFEMI WDPNGWTE TDNSFSVKQDI VAI TDWSGYSGSFVQHPPELTGLDCMRP
 CFWVELI RGRPKENTI WTSGSSI SFCGVNSDTVGWSWPDGAELPFTI DK
 >gi |85721773|gb|AAF77040.1|AF250360_1 neurami ni dase [Influenza A virus
 (A/Duck/Ohio/194/86 (H1N1))]
 MNPNQKI I TI GSI CMAI GMI SLVLOI GNI I SI WVSHSI QTGSQNHPEVCNQSVI TYENNTWVNQTYNI S
 NI NLVAEQVAPVTI LAGNSSLCP I SGWAI YSKDNGI RI GSKGDFVI REPFI SCSHLECRFTFFLTQGALL
 NDKHSNGTVKDRSPYRTLMSCPVGEAPSPYNSRFESVAWSASACHDGI SWLTI GI SGPDPNGAVAVLKYN
 I I TDTI KSWRNKI LRTQSEECACI NGSCFTI MTDGSPNGOASYKI FKI EKGKVI KVELNAPNYHYEES
 CYPDASEVMCVCRDNWHGSRNPWVSFNQNLLEYQI GYI CSGVFGDNPRPNDGTGSCGPVSSNGAYGVKGF
 FKYGNGVWI GRKTSTSSRSGFEMI WDPNGWTE TDNSFSVKQDI VAI TDWSGYSGSFVQHPPELTGLDCMRP
 CFWVELI RGRPKENTI WTSGSSI SFCGVNSDTVGWSWPDGAELPFTI DK
 >gi |156777931|gb|ABU95361.1| neurami ni dase [Influenza A virus (A/bl ue-wi nged
 teal /LA/B228/1986(H1N1))]
 MNPNQKI I TI GSI CMAI GI I SLVLOI GNI I SI WVSHSI QTGSQNHPEVCNQSVI TYENNTWVNQTYNI S
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 I I TDTI KSWRNKI LRTQSEECACI NGSCFTI MTDGSPNGOASYKI FKI EKGKVI KVELNAPNYHYEES
 CYPDASEVMCVCRDNWHGSRNPWVSFNQNLLEYQI GYI CSGVFGDNPRPNDGTGSCGPVSSNGAYGVKGF
 FKYGNGVWI GRKTSTSSRSGFEMI WDPNGWTE TDNSFSVKQDI VAI TDWSGYSGSFVQHPPELTGLDCMRP
 CFWVELI RGRPKENTI WTSGSSI SFCGVNSDTVGWSWPDGAELPFTI DK
 >gi |193877823|gb|ACF25582.1| neurami ni dase [Influenza A virus
 (A/turkey/SD/7034/1986(H1N1))]
 MNPNQKI I TI GSI CMAI GI I SLVLOI GNI I SI WI SHSI QTGSQNHPEVCNQSVI TYENNTWVNQTYNI S
 NTNLI AEGQVAPVTI LAGNSSLCP I SGWAI YSKDNGI RI GSKGDFVI REPFI SCSHLECRFTFFLTQGALL
 NDKHSNGTVKDRSPYRTLMSCPVGEAPSTYNSRFESVAWSASACHDGI SWLTI GI SGPDPNGAVAVLKYN
 I I TDTI KSWRNKI LRTQSEECACI NGSCFTI MTDGSPNGOASYKI FKI EKGKVI KVELNAPNYHYEES
 CYPDASEVMCVCRDNWHGSRNPWVSFNQNLLEYQI GYI CSGVFGDNPRPNDGTGSCGPVSSNGAYGVKGF
 FKYGNGVWI GRKTSTSSRSGFEMI WDPNGWTE TDNNFSVKQDI VAI TDWSGYSGSFVQHPPELTGLDCMRP
 CFWVELI RGRPKENTI WTSGSSI SFCGVNSDTVGWSWPDGAELPFTI DK

>gi |193877620|gb|ACF25464.1| neurami ni dase [Influenza A virus (A/blue-winged teal /LA/B228/1986(H1N1))]
MNPNQKI I TI GSI CMAI GI I SLVLIQI GNI I SI VVSHSI QTGSQNHPEPCNQSVI TYENNTWVNQTYI NI S
NTNLI AEQVAAPVTLAGNSSLCP I SGWAI YSKDNGI RI GSKGDV FVI REPFI SCSHLECR TFFLTQ GALL
NDKHSNGTVKDRSPYRTLMSCPVGEAPSPYNSRFESVAWSASACHDGI SWLTVGI SGPDNGAVAVLKYNG
I I TDTI KSWRNNI LRTQESECACI NGSCFTI MTDGSPNGOASYKI FK I EKGKVI KSVELNAPNYHYEECS
CYPDASEVMCVC RDNWHGSNRPWVVSFNQNL DYQI GYI CSGVFGDNPRPNDGTGSCGPVSSNGAYGVKGF S
FKYNGVWVI GRKTSSRSRGFEMI WDPNGWTE TDNSFSVKODI VAI TDWSGYSGSFVQHP ELTGLDCMRP
CFWVELI RGRPKENTI WTSGSSI SFCGVNSD TVGWSWPDGAELPFTI DK
>gi |156777939|gb|ABU95365.1| neurami ni dase [Influenza A virus (A/green-winged teal /LA/213GW/1987(H1N1))]
MNPNQKI I TI GSI CMAI GI I SLVLIQI GNI I SI VVSHSI QTGSQNHPEPCNQSVI TYENNTWVNQTYI NI S
NTNLI AEQVAAPVTLAGNSSLCP I SGWAI YSKDNGI RI GSKGDV FVI REPFI SCSHLECR TFFLTQ GALL
NDKHSNGTVKDRSPYRTLMSCPVGEAPSPYNSRFESVAWSASACHDGI SWLTI GI SGPDNGAVAVLKYNG
I I TDTI KSWRNNI LRTQESECACMNGSCFTI MTDGSPNGOASYKI FK I EKGKVI KSVELNAPNYHYEECS
CYPDASEVMCVC RDNWHGSNRPWVVSFNQNL EYQI GYI CSGVFGDNPRPNDGTGSCGPVSSNGAYGVKGF S
FKYNGVWVI GRKTSSRSRGFEMI WDPNGWTE TDNSFSVKODI VAI TDWSGYSGSFVQHP ELTGLDCMRP
CFWVELI RGRPKENTI WTSGSSI SFCGVNSD TVGWSWPDGAELPFTI DK
>gi |193877878|gb|ACF25613.1| neurami ni dase [Influenza A virus (A/turkey/MO/21939/1987(H1N1))]
MNTNQR I I TI GTI CLI VGI VSLLLQI GNI VSLWI SHSI QTGEKNHPEI CNQNV I TYENNTWVNQTYVNI S
NTNI AAGQGVTSI I LAGNSSLCP I SGWAI YSKDNSI RI GSKGDI FVI REPFI SCSHLECR TFFLTQ GALL
NDRHSNGTVKDRSPYRTLMSCP I GEAPSPYNSRFESVAWSASACHDGMGLTI GI SGPDNGAVAVLKYNG
I I TDTI KSWRNNI LRTQESECACI NGSCFTI MTDGSPNGOASYKI FK I EKGKVI KSVELNAPNYHYEECS
CYPDTGKVV CVC RDNWHASNRPWVVSFNQNL DYQI GYI CSGVFGDNPRPNDGTGKNGC GPVLSNGANGVKGF S
FRYNGVWVI GRKTSI SSRSRGFEMI WDPNGWTE TDSSFSMKODI I ASTDWSGYSGSFVQHP ELTGMDCI RP
CFWVELI RGRPKENTI WTSGSSI SFCGVNSETASWSWPDGADLPFTI DK
>gi |39840720|emb|CAC95054.1| neurami ni dase [Influenza A virus (A/turkey/France/87075/87(H1N1))]
MNPNQKI I TI GSI CMTI GI ASLMLQI GNI I SI VVSHSI QI QNQNOPETPCNQSVI TYENNTWVNQTYVNI S
NTNFVAEQAVVSKLAGNSSLCP I SGWAI YSKDNGVRI GSKGDV FVI REPFI SCSHLECR TFFLTQ GALL
NDKHSNGTI KDRSPYRTLMSCPVGEVPSYNSKRFESVAWSASACHDGI SWLTI GI SGPDNGAVAVLKYNG
I I TDTI KSWRNNI LRTQESECACMNGSCFTVMTDGPNGOASYKI FK I EKGKVI KSVELNAPNYHYEECS
CYPDSGEI TCVC RDNWHASNRPWVVSFNQNL EYQI GYI CSGI FGDSRPNDGTGSCGPVSSKANGVKGF S
FKYNGVWVI GRKTSSRSRGFEMI WDPNGWTE TDSSFSVKODI VGI TDWSGYSGSFVQHP ELTGLDCMRP
CFWVELI RGRPKENTI WTSGSSI SFCGVNSD TVGWSWPDGAELPFTI DK
>gi |110733283|gb|ABG88215.1| neurami ni dase [Influenza A virus (A/green-winged teal /Ohi o/430/1987(H1N1))]
MNPNQKI I TI GSI CMAI GI I SLVLIQI GNI I SI VVSHSI QTGSQNHPEPCNQSVI TYENNTWVNQTYI NI S
NTNLI TEQTAVPVTLAGNSSLCP I SGWAI YSKDNGI RI GSKGDV FVI REPFI SCSHLECR TFFLTQ GALL
NDKHSNGTVKDRSPYRTLMSCPVGEAPSPYNSRFESVAWSASACHDGI SWLTI GI SGPDNGAVAVLKYNG
I I TDTI KSWRNNI LRTQESECACI NGSCFTI MTDGSPNGOASYKI FK I EKGKVI KSVELNAPNYHYEECS
CYPDASEVMCVC RDNWHGSNRPWVVSFNQNL DYQI GYI CSGVFGDNPRPNDGTGSCGPVSSNGAYGVKGF S
FKYNGVWVI GRKTSSRSRGFEMI WDPNGWTE TDNSFSVKODI VAI TDWSGYSGSFVQHP ELTGLDCMRP
CFWVELI RGRPKENTI WTSGSSI SFCGVNSD TVGWSWPDGAELPFTI DK
>gi |189313201|gb|ACD88706.1| neurami ni dase [Influenza A virus (A/turkey/NC/19762/1988(H1N1))]
MNTNQR I I TI GTVCLI VGI VSLLLQI GNI VSLWI SHSI QTGEKNHSEI CSQNV I TYENNTWVNQTYVNI S
NTNI ADGQGVTSI I LAGNSSLCP I SGWAI YSKDNSI RI GSKGDI FVI REPFI SCSHLECR TFFLTQ GALL
NDRHSNGTVKDRSPYRTLMSCP I GEAPSPYNSRFESVAWSASACHDGMGLTI GI SGPDNGAVAVLKYNG
I I TDTI KSWRNNI LRTQESECACI NGSCFTI MTDGSPNGOASYKI FK I EKGKVI KSVELNAPNYHYEECS
CYPDTGKVV CVC RDNWHASNRPWVVSFNQNL DYQI GYI CSGVFGDNPRPNDGTGKNGC GPVLSNGANGVKGF S
FRYNGVWVI GRKTSI SSRSRGFEMI WDPNGWTE TDSSFSI KODI I ALTDWSGYSGSFVQHP ELTGMNCI RP
CFWVELI RGRPKENTI WTSGSSI SFCGVNSETASWSWPDGADLPFTI DK
>gi |78095921|gb|ABB19610.1| neurami ni dase [Influenza A virus (A/mallard duck/ALB/322/1988(H1N1))]
MNPNQKI I TI GSI CMAI GI I SLVLIQI GNI I SI VVSHSI QTGSQNHPEPCNQSVI TYENNTWVNQTYI NI S
NTNLI AEQTAAPVTLAGNSSLCP I SGWAI YSKDNGI RI GSKGDV FVI REPFI SCSHLECR TFFLTQ GALL
NDKHSNGTVKDRSPYRTLMSCPVGEAPSPYNSRFESVAWSASACHDGI SWLTI GI SGPDNGAVAVLKYNG
I I TDTI KSWRNNI LRTQESECACI NGSCFTI MTDGSPNGOASYKI FK I EKGKVI KSVELNAPNYHYEECS
CYPDASEVMCVC RDNWHGSNRPWVVSFNQNL DYQI GYI CSGVFGDNPRPNDGTGSCGPVSSNGAYGVKGF S
FKYNGVWVI GRKTSSRSRGFEMI WDPNGWTE TDNSFSMKODI VAI TDWSGYSGSFVQHP ELTGLDCMRP
CFWVELI RGRPKENTI WTSGSSI SFCGVNSD TVGWSWPDGAELPFTI DK
>gi |193877860|gb|ACF25603.1| neurami ni dase [Influenza A virus (A/turkey/IA/10271-3/1990(H1N1))]
MNTNQR I I TI GTVCM I VGI VSLLLQI GNI VSLWI SHSI QTGEKNHSEI CSQNV I TYENNTWVNQTYVNI S
NTNI ADGQGVTSI I LAGNSPLCP I SGWAI YSKDNSI RI GSKGDI FVI REPFI SCSHLECR TFFLTQ GALL
NDRHSNGTI KDRSPYRTLMSCP I GEAPSPYNSRFESVAWSASACHDGI GWLTI GI SGPDNGAVAVLKYNG
I I TDTI KSWRNNI LRTQESECACI NGSCFTI MTDGSPNGOASYKI FK I EKGKVI KSVELNAPNYHYEECS
CYPDTSKVV CVC RDNWHASNRPW I SFDQNL DYQI GYI CSGVFGDNPRPNDGTGKNGC GPVLSNGANGVKGF S
FRYNGVWVI GRKTSI SSRSRGFEMI WDPNGWTE TDSSFSI KODI I ALTDWSGYSGSFVQHP ELTGMNCI RP
CFWVELI RGRPKENTI WTSGSSI SFCGVNSETASWSWPDGADLPFTI DK
>gi |110733264|gb|ABG88204.1| neurami ni dase [Influenza A virus (A/mallard/Ohi o/171/1990(H1N1))]
MNPNQKI I TI GSI CMAI GI I SLVLIQI GNI I SI VVSHSI QTGGQNHPEPCNQSVI TYENNTWVNQTYI NI S
NTNLI AEQTAAPVTLAGNSSLCP I SGWAI YSKDNGI RI GSKGDV FVI REPFI SCSHLECR TFFLTQ GALL
NDKHSNGTVKDRSPYRTLMSCPVGEAPSPYNSRFESVAWSASACHDGI SWLTI GI SGPDNGAVAVLKYNG

I I TDTI KSWRNNI LRTQESECACI NGSCFTI MTDGPSNGOASYKI FKI EKGKVI KSVELNAPNYHYEECS
 CYPDASEVMCVCARDNWHGSRNPWVWVFNQNLQDI GYI CSGVFGDNPRPNDGTGSCGVPVSSNGAYGVKGF
 FKYGNVWI GRTKSTSSRSGFEMI WDPNGWTE DNSFSVKQDI VAI TDWSGYSGSFVQHPPELTGLDCMRP
 CFWVELI RGRPKENTI WTSGSSI SFCGVNSDTVGWSWPDGAELPFTI DK
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 (A/mal I ard/AI berta/99/91 (H1N1))]
 MNPNQI I TI GSI CMAI GI I SLVLI GNI I SI WVSHLI OTGSONHPETCNQSVI TYENNTWVNOQYI NI S
 NTNLI AEQAAPVTLAGNSSLCP I SGWAI YSKDNGI RI GSKGDV FVI REPFI SCSHLECRFFLTQ GALL
 NDKHSNGTVKDRSPYRTLMSCPVGEAPSPYNSRFESVAWSASACHDGI SWLTI GI SGPDNGAVAVLK YNG
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 FKYGNVWI GRTKSTSSRSGFEMI WDPNGWTE DNSFSVKQDI VAI TDWSGYSGSFVQHPPELTGLDCMRP
 CFWVELI RGRPKENTI WTSGSSI SFCGVNSDTVGWSWPDGAELPFTI DK
 >gi |189313182|gb|ACD88695.1| neurami ni dase [Influenza A virus
 (A/chi cken/PA/35154/1991 (H1N1))]
 MNTNQI I TI GTI CLI VGI VSLLLQI GNI VSLWI SHSI QTGEKNHPEVCNQS VI TYENNTWVNOQYI NI S
 NTNLI AAGQGVPTI I LAGNSSLCP I SGWAI YSKDNGI RI GSKGDI FVMREPFI SCSHLECRFFLTQ GALL
 NDRHSNGTVKDRSPYRTLMSCPVGEAPSPYNSRFESVAWSASACHDGI SWLTI GI SGPDNGAVAVLK YNG
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 CYPDTGKVVVCARDNWHASNRPWVWVFNQNLQDI GYI CSGVFGDNPRPNDGTGKNGCGPVL SNGANGVKG
 FRYGNVWI GRTKSTSSRSGFEMI WDPNGWTE DNSFSVKQDI I ALTDWSGYSGSFVQHPPELTGMNCI RP
 CFWVELI RGQPKESTI WTSGSSI SFCGVNSDTASWSWPDGADLPFTI DK
 >gi |193877842|gb|ACF25593.1| neurami ni dase [Influenza A virus (A/turkey/I A/21089-
 3/1992 (H1N1))]
 MNTNQI I TI GTVCLI VGI VSLLLQI GNI VSLWI SHSI QTGEKNHSEI CNQNI I TYENNTWVNOQYI NI S
 NTNLI ADGQGVPTI I LAGNSSLCP I GGWAI YSKDNGI RI GSKGDI FVI REPFI SCSHLECRFFLTQ GALL
 NDRHSNGTVKDRSPYRTLMSCPVGEAPSPYNSRFESVAWSASACHDGI SWLTI GI SGPDNGAVAVLK YNG
 I I TDTI KSWRNNI LRTQESECACI NGSCFTI MTDGPSNGOASYKI FKI EKGKVI KSVELNAPNYHYEECS
 CYPDTGKVVVCARDNWHASNRPWVWVFNQNLQDI GYI CSGVFGDNPRPNDGTGKNGCGPVL SNGANGVKG
 FRYGNVWI GRTKSTSSRSGFEMI WDPNGWTE DNSFSVKQDI I ALTDWSGYSGSFVQHPPELTGMNCI RP
 CFWVELI RGQPKESTI WTSGSSI SFCGVNSDTASWSWPDGADLPFTI DK
 >gi |115278019|gb|ABI 84398.1| neurami ni dase [Influenza A virus (A/b/ue-wi nged
 teal /AI berta/141/1992 (H1N1))]
 MNPNQI I TI GSI CMAI GI I SLVLI GNI I SI WVSHSI OTGGONHPETCNQSVI TYENNTWVNOQYI NI S
 NTNLI AEQTAAPVTLAGNSSLCP I SGWAI YSKDNGI RI GSKGDV FVI REPFI SCSHLECRFFLTQ GALL
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 I I TDTI KSWRNNI LRTQESECACI NGSCFTI MTDGPSNGOASYKI FKI EKGKVI KSVELNAPNYHYEECS
 CYPDASEVMCVCARDNWHGSRNPWVWVFNQNLQDI GYI CSGVFGDNPRPNDGTGSCGVPVSSNGAYGVKGF
 FKYGNVWI GRTKSTSSRSGFEMI WDPNGWTE DNSFSVKQDI VAI TDWSGYSGSFVQHPPELTGLDCMRP
 CFWVELI RGRPKENTI WTSGSSI SFCGVNSDTVGWSWPDGAELPFTI DK
 >gi |8572179|gb|AAF77041.1|AF250361_1 neurami ni dase [Influenza A virus
 (A/Duck/Oh i o/118C/93 (H1N1))]
 MNPNQI I TI GSV CMAI GI I SLVLI GNI I SI WVSHSI OTGSONRPETCNQSVI TYENNTWVNOQYI NI S
 NTNLI AEQTAAPVTLAGNSSLCP I SGWAI YSKDNGI RI GSKGDV FVI REPFI SCSHLECRFFLTQ GALL
 NDKHSNGTVKDRSPYRTLMSCPVGEAPSPYNSRFESVAWSASACHDGI SWLTI GI SGPDNGAVAVLK YNG
 I I TDTI KSWRNNI LRTQESECACI NGSCFTI MTDGPSNGOASYKI FKI EKGKVI KSVELNAPNYHYEECS
 CYPDASEVMCVCARDNWHGSRNPWVWVFNQNLQDI GYI CSGVFGDNPRPNDGTGSCGVPVSSNGAYGVKGF
 FKYGNVWI GRTKSTSSRSGFEMI WDPNGWTE DNSFSVKQDI VAI TDWSGYSGSFVQHPPELTGLDCMRP
 CFWVELI RGRPKENTI WTSGSSI SFCGVNSDTVGWSWPDGAELPFTI DK
 >gi |156777943|gb|ABU95367.1| neurami ni dase [Influenza A virus
 (A/quai l /I N/38685/1993 (H1N1))]
 MNPNQI I TI GSV CMAI GI I SLVLI GNI I SI WVSHSI OTGSONRPETCNQSVI TYENNTWVNOQYI NI S
 NTNLI AEQTAAPVTLAGNSSLCP I SGWAI YSKDNGI RI GSKGDV FVI REPFI SCSHLECRFFLTQ GALL
 NDKHSNGTVKDRSPYRTLMSCPVGEAPSPYNSRFESVAWSASACHDGI SWLTI GI SGPDNGAVAVLK YNG
 I I TDTI KSWRNNI LRTQESECACI NGSCFTI MTDGPSNGOASYKI FKI EKGKVI KSVELNAPNYHYEECS
 CYPDASEVMCVCARDNWHGSRNPWVWVFNQNLQDI GYI CSGVFGDNPRPNDGTGSCGVPVSSNGAYGVKGF
 FKYGNVWI GRTKSTSSRSGFEMI WDPNGWTE DNSFSVKQDI VAI TDWSGYSGSFVQHPPELTGLDCMRP
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 >gi |189313163|gb|ACD88684.1| neurami ni dase [Influenza A virus
 (A/quai l /I N/38685/1993 (H1N1))]
 MNPNQI I TI GSV CMAI GI I SLVLI GNI I SI WVSHSI OTGSONRPETCNQSVI TYENNTWVNOQYI NI S
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 NDKHSNGTVKDRSPYRTLMSCPVGEAPSPYNSRFESVAWSASACHDGI SWLTI GI SGPDNGAVAVLK YNG
 I I TDTI KSWRNNI LRTQESECACI NGSCFTI MTDGPSNGOASYKI FKI EKGKVI KSVELNAPNYHYEECS
 CYPDASEVMCVCARDNWHGSRNPWVWVFNQNLQDI GYI CSGVFGDNPRPNDGTGSCGVPVSSNGAYGVKGF
 FKYGNVWI GRTKSTSSRSGFEMI WDPNGWTE DNSFSVKQDI VAI TDWSGYSGSFVQHPPELTGLDCMRP
 CFWVELI RGRPKENTI WTSGSSI SFCGVNSDTVGWSWPDGAELPFTI DK
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 (A/mal I ard/Oh i o/118/1993 (H1N1))]
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 NDKHSNGTVKDRSPYRTLMSCPVGEAPSPYNSRFESVAWSASACHDGI SWLTI GI SGPDNGAVAVLK YNG
 I I TDTI KSWRNNI LRTQESECACI NGSCFTI MTDGPSNGOASYKI FKI EKGKVI KSVELNAPNYHYEECS
 CYPDASEVMCVCARDNWHGSRNPWVWVFNQNLQDI GYI CSGVFGDNPRPNDGTGSCGVPVSSNGAYGVKGF
 FKYGNVWI GRTKSTSSRSGFEMI WDPNGWTE DNSFSVKQDI VAI TDWSGYSGSFVQHPPELTGLDCMRP
 CFWVELI RGRPKENTI WTSGSSI SFCGVNSDTVGWSWPDGAELPFTI DK

>gi |115289126|gb|ABI92184.1| neurami ni dase [Influenza A virus (A/duck/Ohi o/95/1993(H1N1))]
MNPNQKI I TI GSVCMAI GI I SLVLQI GNI I SI VVSHSI QTGSQNRPETCNQSVI TYENNTWVNQTYI NI S
NTNLI AEKTAAPVTLAGNSSLCP I SGWAI YSKDNGI RI GSKGDV FVI REPFI SCSHLECR TFFLTQ GALL
NDKHSNGTVKDRSPYR TLMSCP VGEAPSPYNSRFESVAWSASACHDGI SWLTI GI SGP DNGAVAVLKYNG
I I TDTI KSWRNNI LRTQESECACI NGSCFTI MTDGSPNGOASYKI FK I EKGKVI KSVELNAPNYHYEECS
CYPDASEVMCVC RDNWHG SNRPWVSFNQNL DYQI GYI CSGVFGDNPRPNDGTGSCGPVSSNGAYGVKGF S
FKYGNVWVI GR TKSTSSRS GFEMI WDPNGWTE TDNSFSVKQDI VAI TDW S GYSGSFVQHP ELTGLDCMRP
CFWVELI RGRPKENTI WTS GSSI SFCGVNSDTVGWSWPDGAELPFTI DK

>gi |156777935|gb|ABU95363.1| neurami ni dase [Influenza A virus (A/duck/NY/13152-13/1994(H1N1))]
MNPNQKI I TI GSVCMVI GI I SLVLQI GNI I SI VVSHSI QTGSQNRPETCNQSVI TYENNTWVNQTYI NI S
NTNLI TEQTAAPVTLAGNSSLCP I SGWAI YSKDNGI RI GSKGDV FVI REPFI SCSHLECR TFFLTQ GALL
NDKHSNGTVKDRSPYR TLMSCSVGEAPSPYNSRFESVAWSASACHDGI SWLTI GI SGP DNGAVAVLKYNG
I I TDTI KSWRNNI LRTQESECACI NGSCFTI MTDGSPNGOASYKI FK I EKGKVI KSVELNAPNYHYEECS
CYPDASEVMCVC RDNWHG SNRPWVSFNQNL DYQI GYI CSGVFGDNPRPNDGTGSCGPVSSNGAYGVKGF S
FKYGNVWVI GR TKSTSSRS GFEMI WDPNGWTE TDNSFSVKQDI VAI TDW S GYSGSFVQHP ELTGLDCMRP
CFWVELI RGRPKENTI WTS GSSI SFCGVNSDTVGWSWPDGAELPFTI DK

>gi |154152623|gb|ABS70430.1| neurami ni dase [Influenza A virus (A/duck/NY/13152-13/1994(H1N1))]
MNPNQKI I TI GSVCMVI GI I SLVLQI GNI I SI VVSHSI QTGSQNRPETCNQSVI TYENNTWVNQTYI NI S
NTNLI TEQTAAPVTLAGNSSLCP I SGWAI YSKDNGI RI GSKGDV FVI REPFI SCSHLECR TFFLTQ GALL
NDKHSNGTVKDRSPYR TLMSCSVGEAPSPYNSRFESVAWSASACHDGI SWLTI GI SGP DNGAVAVLKYNG
I I TDTI KSWRNNI LRTQESECACI NGSCFTI MTDGSPNGOASYKI FK I EKGKVI KSVELNAPNYHYEECS
CYPDASEVMCVC RDNWHG SNRPWVSFNQNL DYQI GYI CSGVFGDNPRPNDGTGSCGPVSSNGAYGVKGF S
FKYGNVWVI GR TKSTSSRS GFEMI WDPNGWTE TDNSFSVKQDI VAI TDW S GYSGSFVQHP ELTGLDCMRP
CFWVELI RGRPKENTI WTS GSSI SFCGVNSDTVGWSWPDGAELPFTI DK

>gi |154154393|gb|ABS70441.1| neurami ni dase [Influenza A virus (A/duck/NJ/7717-70/1995(H1N1))]
MNPNQKI I TI GSI CMAI GI I SLVLQI GNI I SI VVSHSI QTGSQSHPETCNQSVI TYENNTWVNQTYI NI S
NTNLVAEQTVAPVTLAGNSSLCP I SGWAI YSKDNGI RI GSKGDV FVI REPFI SCSHLECR TFFLTQ GALL
NDKHSNGTVKDRSPYR TLMSCP VGEAPSPYNSRFESVAWSASACHDGI SWLTI GI SGP DNGAVAVLKYNG
I I TDTI KSWRNNI LRTQESECACI NGSCFTI MTDGSPNGOASYKI FK I EKGKVVKSVELNAPNYHYEECS
CYPDASEVMCVC RDNWHG SNRPWVSFNQNL EYQI GYI CSGVFGDNPRPNDGTGSCGPVSSNGAYGVKGF S
FKYGNVWVI GR TKSTSSRS GFEMI WDPNGWTE TDNSFSVKQDI VAI TDW S GYSGSFVQHP ELTGLDCMRP
CFWVELI RGRPKENTI WTS GSSI SFCGVNSDTVGWSWPDGAELPFTI DK

>gi |156777933|gb|ABU95362.1| neurami ni dase [Influenza A virus (A/duck/NJ/7717-70/1995(H1N1))]
MNPNQKI I TI GSI CMAI GI I SLVLQI GNI I SI RVSHSI QTGSQSHPETCNQSVI TYENNTWVNQTYI NI S
NTNLVAEQTVAPVTLAGNSSLCP I SGWAI YSKDNGI RI GSKGDV FVI REPFI SCSHLECR TFFLTQ GALL
NDKHSNGTVKDRSPYR TLMSCP VGEAPSPYNSRFESVAWSASACHDGI SWLTI GI SGP DNGAVAVLKYNG
I I TDTI KSWRNNI LRTQESECACI NGSCFTI MTDGSPNGOASYKI FK I EKGKVVKSVELNAPNYHYEECS
CYPDASEVMCVC RDNWHG SNRPWVSFNQNL EYQI GYI CSGVFGDNPRPNDGTGSCGPVSSNGAYGVKGF S
FKYGNVWVI GR TKSTSSRS GFEMI WDPNGWTE TDNSFSVKQDI VAI TDW S GYSGSFVQHP ELTGLDCMRP
CFWVELI RGRPKENTI WTS GSSI SFCGVNSDTVGWSWPDGAELPFTI DK

>gi |156777937|gb|ABU95364.1| neurami ni dase [Influenza A virus (A/duck/NY/15024-21/1996(H1N1))]
MNPNQKI I TI GSI CMAI GI I SLVLQI GNI I SI VVSHSI QTGSQSHPETCNQSVI TYENNTWVNQTYI NI S
NTNLVAEQTVAPVTLAGNSSLCP I SGWAI YSKDNGI RI GSKGDV FVI REPFI SCSHLECR TFFLTQ GALL
NDKHSNGTVKDRSPYR TLMSCP VGEAPSPYNSRFESVAWSASACHDGI SWLTI GI SGP DNGAVAVLKYNG
I I TDTI KSWRNNI LRTQESECACI NGSCFTI MTDGSPNGOASYKI FK I EKGKVVKSVELNAPNYHYEECS
CYPDASEVMCVC RDNWHG SNRPWVSFNQNL EYQI GYI CSGVFGDNPRPNDGTGSCGPVSSNGAYGVKGF S
FKYGNVWVI GR TKSTSSRS GFEMI WDPNGWTE TDNSFSVKQDI VAI TDW S GYSGSFVQHP ELTGLDCMRP
CFWVELI RGRPKENTI WTS GSSI SFCGVNSDTVGWSWPDGAELPFTI DK

>gi |113531191|dbj|BAF03630.1| neurami ni dase [Influenza A virus (A/duck/Hokkai do/55/96(H1N1))]
MNPNQKI I TI GSI CMVI GI I VSLMLQI GNI I SI VVSHSI QTGNQHOPEPCNQSI I TYENNTWVNQTYVNI S
NTNFLT EQAVT SVTLAGNSSLCP I SGWAI YSKDNGI RI GSKGDV CVI REPFI SCSHLECR TFFLTQ GALL
NDKHSNGTVKDRSPYR TLMSCP VGEAPSPYNSRFESVAWSASACHDGI SWLTI GI SGP DNGAVAVLKYNG
I I TDTI KSWRNNI LRTQESECACVNGSCFTVMTD GSPNGOASYKI FK I EKGKVVKSVELNAPNYHYEECS
CYPDSGEI TCVC RDNWHG SNRPWVSFNQNL EYQI GYI CSGVFGDNPRPNDGTGSCGPVSSNGAYGVKGF S
FKYGNVWVI GR TKSTSSRS GFEMI WDPNGWTE TDSSFSVKQDI VAI TDW S GYSGSFVQHP ELTGLNLCMRP
CFWVELI RGRPKENTI WTS GSSI SFCGVNSDTVGWSWPDGAELPFTI DK

>gi |78095855|gb|ABB19572.1| neurami ni dase [Influenza A virus (A/mal I ard/AI berta/267/1996(H1N1))]
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NDKHSNGTVKDRSPYR TLMSCP VGEAPSPYNSRFESVAWSASACHDGI SWLTI GI SGP DNGAVAVLKYNG
I I TDTI KSWRNNI LRTQESECACI NGSCFTI MTDGSPNGOASYKI FK I EKGKVVKSVELNAPNYHYEECS
CYPDASEVMCVC RDNWHG SNRPWVSFDQNL EYQI GYI CSGVFGDNPRPNDGTGSCGPVSSNGAYGVKGF S
FKYGNVWVI GR TKSTSSRS GFEMI WDPNGWTE TDNSFSVKQDI VAI TDW S GYSGSFVQHP ELTGLDCMRP
CFWVELI RGRPKENTI WTS GSSI SFCGVNSDTVGWSWPDGAELPFTI DK

>gi |49357281|gb|AAT65399.1| neurami ni dase [Influenza A virus (A/mal I ard/AI berta/211/98(H1N1))]
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I I TDTI KSWRNNI LRTQESECACI NGSCFTI MTDGPSNGOASYKI FKI EKGKVVKSVELNAPNYHYEECS
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 FKYGNVWVI GRTKSTSSRSGFEMI WDPNGWTE DNSFSVKQDI VAI TDWSGYSGSFVQHPPELTGLDCMRP
 CFWVELI RGRPKENTI WTSGSSI SFCGVNSDTVGWSWPDGAELPFTI DK
 >gi |193876870|gb|ACF25034.1| neurami ni dase [Influenza A vi rus (A/chicken/NY/21665-
 73/1998(H1N1))]
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 NDRHSNGTVKDRSPYRTLMSCPVGEAPSPYNSRFESVAWSASACHDGMGLTI GI SGPDNGAVAVLKYNIG
 I I TDTI KSWRNNI LRTQESECACI NGSCFTI MTDGPSNGOASYKI FKI EKGKVVKSVELNAPNYHYEECS
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 FRYGNVWVI GRTKSTSSRSGFEMI WDPNGWTE DSSFSI QDI I SLTDWSGYSGSFVQHPPELTGMNCI RP
 CFWVELI RGPKESTI WTSGSSI SFCGVNSDTVGWSWPDGADLPFTI DK
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 (A/malIard/ALB/201/1998(H1N1))]
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 I I TDTI KSWRNNI LRTQESECACI NGSCFTI MTDGPSNGOASYKI FKI EKGKVVKSVELNAPNYHYEECS
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 FRYGNVWVI GRTKSTSSRSGFEMI WDPNGWTE DNSFSVKQDI VAI TDWSGYSGSFVQHPPELTGLDCMRP
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 >gi |119365220|gb|ABL67069.1| neurami ni dase [Influenza A vi rus
 (A/pitai/Ohi o/25/1999(H1N1))]
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 NDKHSNGTVKDRSPYRTLMSCPVGEAPSPYNSRFESVAWSASACHDGI SWLTI GI SGPDNGAVAVLKYNIG
 I I TDTI KSWRNNI LRTQESECACI NGSCFTI MTDGPSNGOASYKI FKI EKGKVVKSVELNAPNYHYEECS
 CYPDASEVMCVCARDNWHGSRNPWVSFNQNLLEYQI GYI CSGVFGDNPRPNDGTGSCGVPVSSNGAYGVKGF
 FRYGNVWVI GRTKSTSSRSGFEMI WDPNGWTE DNSFSVKQDI VAI TDWSGYSGSFVQHPPELTGLDCMRP
 CFWVELI RGRPKENTI WTSGSSI SFCGVNSDTVGWSWPDGAELPFTI DK
 >gi |119365220|gb|ABL67069.1| neurami ni dase [Influenza A vi rus
 (A/pitai/Ohi o/25/1999(H1N1))]
 MNPNQKI I TI GSI CMVI GI I SMLLQI GNI I SI WWSHSI QTGSRNHPETCNQSVI TYENNTWVNTQYNI S
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 I I TDTI KSWRNNI LRTQESECACI NGSCFTI MTDGPSNGOASYKI FKI EKGKVVKSVELNAPNYHYEECS
 CYPDASEVMCVCARDNWHGSRNPWVSFNQNLLEYQI GYI CSGVFGDNPRPNDGTGSCGVPVSSNGAYGVKGF
 FRYGNVWVI GRTKSTSSRSGFEMI WDPNGWTE DNSFSVKQDI VAI TDWSGYSGSFVQHPPELTGLDCMRP
 CFWVELI RGRPKENTI WTSGSSI SFCGVNSDTVGWSWPDGAELPFTI DK
 >gi |110733359|gb|ABG88259.1| neurami ni dase [Influenza A vi rus
 (A/malIard/Ohi o/56/1999(H1N1))]
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 I I TDTI KSWRNNI LRTQESECACI NGSCFTI MTDGPSNGOASYKI FKI EKGKVVKSVELNAPNYHYEECS
 CYPDASEVMCVCARDNWHGSRNPWVSFNQNLLEYQI GYI CSGVFGDNPRPNDGTGSCGVPVSSNGAYGVKGF
 FRYGNVWVI GRTKSTSSRSGFEMI WDPNGWTE DNSFSVKQDI VAI TDWSGYSGSFVQHPPELTGLDCMRP
 CFWVELI RGRPKENTI WTSGSSI SFCGVNSDTVGWSWPDGAELPFTI DK
 >gi |116069871|gb|ABJ53430.1| neurami ni dase [Influenza A vi rus
 (A/malIard/Ohi o/66/1999(H1N1))]
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 I I TDTI KSWRNNI LRTQESECACI NGSCFTI MTDGPSNGOASYKI FKI EKGKVVKSVELNAPNYHYEECS
 CYPDASEVMCVCARDNWHGSRNPWVSFNQNLLEYQI GYI CSGVFGDNPRPNDGTGSCGVPVSSNGAYGVKGF
 FRYGNVWVI GRTKSTSSRSGFEMI WDPNGWTE DNSFSVKQDI VAI TDWSGYSGSFVQHPPELTGLDCMRP
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 (A/malIard/Ohi o/66/1999(H1N1))]
 MNPNQKI I TI GSI CMVI GI I SMLLQI GNI I SI WWSHSI QTGSRNHPETCNQSVI TYENNTWVNTQYNI S
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 I I TDTI KSWRNNI LRTQESECACI NGSCFTI MTDGPSNGOASYKI FKI EKGKVVKSVELNAPNYHYEECS
 CYPDASEVMCVCARDNWHGSRNPWVSFNQNLLEYQI GYI CSGVFGDNPRPNDGTGSCGVPVSSNGAYGVKGF
 FRYGNVWVI GRTKSTSSRSGFEMI WDPNGWTE DNSFSVKQDI VAI TDWSGYSGSFVQHPPELTGLDCMRP
 CFWVELI RGRPKENTI WTSGSSI SFCGVNSDTVGWSWPDGAELPFTI DK
 >gi |119365201|gb|ABL67058.1| neurami ni dase [Influenza A vi rus (A/green-winged
 teal/Ohi o/72/1999(H1N1))]
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 I I TDTI KSWRNNI LRTQESECACI NGSCFTI MTDGPSNGOASYKI FKI EKGKVVKSVELNAPNYHYEECS
 CYPDASEVMCVCARDNWHGSRNPWVSFNQNLLEYQI GYI CSGVFGDNPRPNDGTGSCGVPVSSNGAYGVKGF
 FRYGNVWVI GRTKSTSSRSGFEMI WDPNGWTE DNSFSVKQDI VAI TDWSGYSGSFVQHPPELTGLDCMRP
 CFWVELI RGRPKENTI WTSGSSI SFCGVNSDTVGWSWPDGAELPFTI DK
 >gi |27466288|gb|AAN85704.1| neurami ni dase [Influenza A vi rus (A/Quail/Nanchang/12-
 340/2000(H1N1))]
 MNPNQKI I TI GSI CMVI GI I SMLLQI GNI I SI WWSHSI QTGSRNHPETCNQSVI TYENNTWVNTQYNI S
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 NDKHSNGTVKDRSPYRTLMSCPVGEAPSPYNSRFESVAWSASACHDGMGLTI GI SGPDNGAVAVLKYNIG
 I I TDTI KSWRNNI LRTQESECACI NGSCFTI MTDGPSNGOASYKI FKI EKGKVVKSVELNAPNYHYEECS
 CYPDASEVMCVCARDNWHGSRNPWVSFNQNLLEYQI GYI CSGVFGDNPRPNDGTGSCGVPVSSNGAYGVKGF
 FRYGNVWVI GRTKSTSSRSGFEMI WDPNGWTE DNSFSVKQDI VAI TDWSGYSGSFVQHPPELTGLDCMRP
 CFWVELI RGRPKENTI WTSGSSI SFCGVNSDTVGWSWPDGAELPFTI DK
 >gi |78097232|gb|ABB20164.1| neurami ni dase [Influenza A vi rus (A/Quail/Nanchang/12-
 340/2000(H1N1))]
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 I I TDTI KSWRNNI LRTQESECACI NGSCFTI MTDGPSNGOASYKI FKI EKGKVVKSVELNAPNYHYEECS
 CYPDASEVMCVCARDNWHGSRNPWVSFNQNLLEYQI GYI CSGVFGDNPRPNDGTGSCGVPVSSNGAYGVKGF
 FRYGNVWVI GRTKSTSSRSGFEMI WDPNGWTE DNSFSVKQDI VAI TDWSGYSGSFVQHPPELTGLDCMRP
 CFWVELI RGRPKENTI WTSGSSI SFCGVNSDTVGWSWPDGAELPFTI DK

>gi |93204701|emb|CAG27352.1| neurami ni dase [Influenza A virus (A/Pekin Duck/France/M-2060/01 (H1N1))]
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NDKHSNGTI KDRSPYRTLMSCP VGEAPSPYNSRFESVAWSASACHDGI SWLTI GI SGPDNGAVAVLKYNG
I I TDTI KSWRNNI LRTQSEACVNGSCFTVMTDGP SNGOASYKI FK I EKGKVVKSVELNAPNYHYEECS
CYPDAGEI I CVCRDNWHG SNRPWV SFNQNL EYQI GYI CSGVFGDNPRPNDGTGSCGPVSSNGAYGVKGF S
FKYGNVWVI GR TKSPSSRS GFEMI WDPNGWTE TDSSFSVKQDI VAI TDWSGYSGSFVQHP ELTGLDCMRP
CFWVELI RGRPKENTI WTS GSSI SFCGVNSDTVGWSWPDGAELPFTI DK

>gi |93204703|emb|CAG27353.1| neurami ni dase [Influenza A virus (A/Mallard/France/D-691/02 (H1N1))]
MNPNQKI I TI GSI CMVI GI ASLMLQI GNI I SI VVSHSI QTENQHOPEPCNQSI I TYENNTWVNQTYI NI S
NTNLPTEQAVASMTLAGNSSLCP I SGWAI YSKDNGI RI GSKGDV FVI REPFI SCSNLECR TFFLTQ GALL
NDKHSNGTVKDRSPYRTLMSCP VGEAPSPYNSRFESVAWSASACHDGI SWLTI GI SGPDNGAVAVLKYNG
I I TDTI KSWRNNI LRTQSEACVNGSCFTVMTDGP SNGOASYKI FK I EKGKVVKSVELNAPNYHYEECS
CYPDASEI I CVCRDNWHG SNRPWV SFNQNL EYQI GYI CSGVFGDNPRPNDGTGSCGPVSSNGAYGVKGF S
FKYGNVWVI GR TKSTSSRS GFEMI WDPNGWTE TDSSFSVKQDI VAI TDWSGYSGSFVQHP ELTGLDCMRP
CFWVELI RGRPKENTI WTS GSSI SFCGVNSDTVGWSWPDGAELPFTI DK

>gi |93204705|emb|CAG27354.1| neurami ni dase [Influenza A virus (A/Mallard/France/D-710/02 (H1N1))]
MNPNQKI I TI GSI CMVI GI ASLMLQI GNI I SI VVSHSI QTENQHOPEPCNQSI I TYENNTWVNQTYI NI S
NTNLPTEQAVASMTLAGNSSLCP I SGWAI YSKDNGI RI GSKGDV FVI REPFI SCSNLECR TFFLTQ GALL
NDKHSNGTVKDRSPYRTLMSCP VGEAPSPYNSRFESVAWSASACHDGI SWLTI GI SGPDNGAVAVLKYNG
I I TDTI KSWRNNI LRTQSEACVNGSCFTVMTDGP SNGOASYKI FK I EKGKVVKSVELNAPNYHYEECS
CYPDASEI I CVCRDNWHG SNRPWV SFNQNL EYQI GYI CSGVFGDNPRPNDGTGSCGPVSSNGAYGVKGF S
FKYGNVWVI GR TKSTSSRS GFEMI WDPNGWTE TDSSFSVKQDI VAI TDWSGYSGSFVQHP ELTGLDCMRP
CFWVELI RGRPKENTI WTS GSSI SFCGVNSDTVGWSWPDGAELPFTI DK

>gi |156777941|gb|ABU95366.1| neurami ni dase [Influenza A virus (A/mallard/MD/321/2002(H1N1))]
MNPNQKI I TI GSI CMAI GI I SLVLQI GNI I SI VVSHSI QTGGQNHPEPCNQSVI TYENNTWVNQTYI NI S
NTNLI AEQAVAVPTLAGNSSLCL I SGWAI YSKDNGI RI GSKGDV FVFSRE PFI SCSHLECR TFFLTQ GALL
NDKHSNGTVKDRSPYRTLMSCP VGEAPSPYNSRFESVAWSASACHDGI SWLTI GI SGPDNGAVAVLKYNG
I I TDTI KSWRNNI LRTQSEACACI NGSCFTI MTDGP SNGOASYKI FK I EKGKVVKSVELNAPNYHYEECS
CYPDASEVMCVC RDNWHG SNRPWV SFNQNL EYQI GYI CSGVFGDNPRPNDGTGSCGPVSSNGAYGVKGF S
FKYGNVWVI GR TKSTSSRS GFEMI WDPNGWTE TDNSFSVKQDI VAI TDWSGYSGSFVQHP ELTGLDCMRP
CFWVELI RGRPKENTI WTS GSSI SFCGVNSDTVGWSWPDGAELPFTI DK

>gi |159156228|gb|ABW94126.1| neurami ni dase [Influenza A virus (A/mallard/MD/02-163/2002(H1N1))]
MNPNQKI I TI GSI CMAI GVI SLVLQI GNI I SI VVSHSI QTGNQNHPEI CNQSVI TYENNTWVNQTYI NI S
NTNLI AEQAVAVPTLAGNSSLCP I SGWAI YSKDNGI RI GSKGDV FVI REPFI SCSHLECR TFFLTQ GALL
NDKHSNGTVKDRSPYRTLMSCP VGEAPSPYNSRFESVAWSASACHDGI SWLTI GI SGPDNGAVAVLKYNG
I I TDTI KSWRNNI LRTQSEACACI NGSCFTI MTDGP SNGOASYKI FK I EKGKVVKSVELNAPNYHYEECS
CYPDASEVMCVC RDNWHG SNRPWV SFNQNL EYQI GYI CSGVFGDNPRPNDGTGSCGPVSSNGAYGVKGF S
FKYGNVWVI GR TKSTSSRS GFEMI WDPNGWTE TDNSFSVKQDI VAI TDWSGYSGSFVQHP ELTGLDCMRP
CFWVELI RGRPKENTI WTS GSSI SFCGVNSDTVGWSWPDGAELPFTI DK

>gi |159156232|gb|ABW94128.1| neurami ni dase [Influenza A virus (A/mallard/MD/02-358/2002(H1N1))]
MNPNQKI I TI GSI CMAI GVI SLVLQI GNI I SI VVSHSI QTGNQNHPEI CNQSVI TYENNTWVNQTYI NI S
NTNLI AEQAVAVPTLAGNSSLCP I SGWAI YSKDNGI RI GSKGDV FVI REPFI SCSHLECR TFFLTQ GALL
NDKHSNGTVKDRSPYRTLMSCP VGEAPSPYNSRFESVAWSASACHDGI SWLTI GI SGPDNGAVAVLKYNG
I I TDTI KSWRNNI LRTQSEACACI NGSCFTI MTDGP SNGOASYKI FK I EKGKVVKSVELNAPNYHYEECS
CYPDASEVMCVC RDNWHG SNRPWV SFNQNL EYQI GYI CSGVFGDNPRPNDGTGSCGPVSSNGAYGVKGF S
FKYGNVWVI GR TKSTSSRS GFEMI WDPNGWTE TDNSFSVKQDI VAI TDWSGYSGSFVQHP ELTGLDCMRP
CFWVELI RGRPKENTI WTS GSSI SFCGVNSDTVGWSWPDGAELPFTI DK

>gi |156777945|gb|ABU95368.1| neurami ni dase [Influenza A virus (A/mallard/MD/163/2002(H1N1))]
MNPNQKI I TI GSI CMAI GVI SLVLQI GNI I SI VVSHSI QTGNQNHPEI CNQSVI TYENNTWVNQTYI NI S
NTNLI AEQAVAVPTLAGNSSLCP I SGWAI YSKDNGI RI GSKGDV FVI REPFI SCSHLECR TFFLTQ GALL
NDKHSNGTVKDRSPYRTLMSCP VGEAPSPYNSRFESVAWSASACHDGI SWLTI GI SGPDNGAVAVLKYNG
I I TDTI KSWRNNI LRTQSEACACI NGSCFTI MTDGP SNGOASYKI FK I EKGKVVKSVELNAPNYHYEECS
CYPDASEVMCVC RDNWHG SNRPWV SFNQNL EYQI GYI CSGVFGDNPRPNDGTGSCGPVSSNGAYGVKGF S
FKYGNVWVI GR TKSTSSRS GFEMI WDPNGWTE TDNSFSVKQDI VAI TDWSGYSGSFVQHP ELTGLDCMRP
CFWVELI RGRPKENTI WTS GSSI SFCGVNSDTVGWSWPDGAELPFTI DK

>gi |156777947|gb|ABU95369.1| neurami ni dase [Influenza A virus (A/mallard/MD/168/2002(H1N1))]
MNPNQKI I TI GSI CMAI GVI SLVLQI GNI I SI VVSHSI QTGNQNHPEI CNQSVI TYENNTWVNQTYI NI S
NTNLI AEQAVAVPTLAGNSSLCP I SGWAI YSKDNGI RI GSKGDV FVI REPFI SCSHLECR TFFLTQ GALL
NDKHSNGTVKDRSPYRTLMSCP VGEAPSPYNSRFESVAWSASACHDGI SWLTI GI SGPDNGAVAVLKYNG
I I TDTI KSWRNNI LRTQSEACACI NGSCFTI MTDGP SNGOASYKI FK I EKGKVVKSVELNAPNYHYEECS
CYPDASEVMCVC RDNWHG SNRPWV SFNQNL EYQI GYI CSGVFGDNPRPNDGTGSCGPVSSNGAYGVKGF S
FKYGNVWVI GR TKSTSSRS GFEMI WDPNGWTE TDNSFSVKQDI VAI TDWSGYSGSFVQHP ELTGLDCMRP
CFWVELI RGRPKENTI WTS GSSI SFCGVNSDTVGWSWPDGAELPFTI DK

>gi |156777949|gb|ABU95370.1| neurami ni dase [Influenza A virus (A/mallard/MD/170/2002(H1N1))]
MNPNQKI I TI GSI CMAI GVI SLVLQI GNI I SI VVSHSI QTGNQNHPEI CNQSVI TYENNTWVNQTYI NI S
NTNLI AEQAVAVPTLAGNSSLCP I SGWAI YSKDNGI RI GSKGDV FVI REPFI SCSHLECR TFFLTQ GALL
NDKHSNGTVKDRSPYRTLMSCP VGEAPSPYNSRFESVAWSASACHDGI SWLTI GI SGPDNGAVAVLKYNG

I I TDTI KSWRNNI LRTQESECACI NGSCFTI MTDGPSNGOASYKI FKVEKGGVVKSVELNAPNYHYEECS
 CYPDASEVMCVCARDNWHGSRNPWVWVFNQNLQYQI GYI CSGVFGDNPRPNDGTGSCGVPVSSNGAYGVKGFCS
 FKYGNGVWI GRTKSTSSRSGFEMI WDPNGWTE TDNSFSAKQDI VAI TDWSGYSGSFVQHPPELTGLDCMRP
 CFWVELI RGRPKENTI WTSGSSI SFCGVNSDVTGWSWPDGAELPFTI DK
 >gi |156777951|gb|ABU95371.1| neurami ni dase [Influenza A vi rus
 (A/mal |ard/MD/181/2002(H1N1))]
 MNPNQKI I TI GSI CMAI GVI SLVLI GNI I SI WVSHSI QTGNQNHPEI CNQSVI TYENNTWVNOQYI NI S
 NTNLI AEQAVAPATLAGNSSLCP I SGWAI YSKDNGI RI GSKGDVFI REFFI SCSHLECRFFLTQGALL
 NDKHSNGTVKDRSPYRTLMSCPVGEAPSPYNSRFESVAWSASACHDGI SWLTI GI SGPDNGAVAVLKYNIG
 I I TDTI KSWRNNI LRTQESECACI NGSCFTI MTDGPSNGOASYKI FKVEKGGVVKSVELNAPNYHYEECS
 CYPDASEVMCVCARDNWHGSRNPWVWVFNQNLQYQI GYI CSGVFGDNPRPNDGTGSCGVPVSSNGAYGVKGFCS
 FKYGNGVWI GRTKSTSSRSGFEMI WDPNGWTE TDNSFSAKQDI VAI TDWSGYSGSFVQHPPELTGLDCMRP
 CFWVELI RGRPKENTI WTSGSSI SFCGVNSDVTGWSWPDGAELPFTI DK
 >gi |156777953|gb|ABU95372.1| neurami ni dase [Influenza A vi rus
 (A/mal |ard/MD/307/2002(H1N1))]
 MNPNQKI I TI GSI CMAI GI I SLVLI GNI I SI WVSHSI QTGGQNHPEI CNQSVI TYENNTWVNOQYI NI S
 NTNLI AEQAVAPVTLAGNSSLCLI SGWAI YSKDNGI RI GSKGDVFI REFFI SCSHLECRFFLTQGALL
 NDKHSNGTVKDRSPYRTLMSCPVGEAPSPYNSRFESVAWSASACHDGI SWLTI GI SGPDNGAVAVLKYNIG
 I I TDTI KSWRNNI LRTQESECACI NGSCFTI MTDGPSNGOASYKI FKVEKGGVVKSVELNAPNYHYEECS
 CYPDASEVMCVCARDNWHGSRNPWVWVFNQNLQYQI GYI CSGVFGDNPRPNDGTGSCGVPVSSNGAYGVKGFCS
 FKYGNGVWI GRTKSTSSRSGFEMI WDPNGWTE TDNSFSAKQDI VAI TDWSGYSGSFVQHPPELTGLDCMRP
 CFWVELI RGRPKENTI WTSGSSI SFCGVNSDVTGWSWPDGAELPFTI DK
 >gi |156777955|gb|ABU95373.1| neurami ni dase [Influenza A vi rus
 (A/mal |ard/MD/322/2002(H1N1))]
 MNPNQKI I TI GSI CMAI GI I SLVLI GNI I SI WVSHSI QTGGQNHPEI CNQSVI TYENNTWVNOQYI NI S
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 I I TDTI KSWRNNI LRTQESECACI NGSCFTI MTDGPSNGOASYKI FKVEKGGVVKSVELNAPNYHYEECS
 CYPDASEVMCVCARDNWHGSRNPWVWVFNQNLQYQI GYI CSGVFGDNPRPNDGTGSCGVPVSSNGAYGVKGFCS
 FKYGNGVWI GRTKSTSSRSGFEMI WDPNGWTE TDNSFSAKQDI VAI TDWSGYSGSFVQHPPELTGLDCMRP
 CFWVELI RGRPKENTI WTSGSSI SFCGVNSDVTGWSWPDGAELPFTI DK
 >gi |156777957|gb|ABU95374.1| neurami ni dase [Influenza A vi rus
 (A/mal |ard/MD/334/2002(H1N1))]
 MNPNQKI I TI GSI CMAI GI I SLVLI GNI I SI WVSHSI QTGGQNHPEI CNQSVI TYENNTWVNOQYI NI S
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 NDKHSNGTVKDRSPYRTLMSCPVGEAPSPYNSRFESVAWSASACHDGI SWLTI GI SGPDNGAVAVLKYNIG
 I I TDTI KSWRNNI LRTQESECACI NGSCFTI MTDGPSNGOASYKI FKVEKGGVVKSVELNAPNYHYEECS
 CYPDASEVMCVCARDNWHGSRNPWVWVFNQNLQYQI GYI CSGVFGDNPRPNDGTGSCGVPVSSNGAYGVKGFCS
 FKYGNGVWI GRTKSTSSRSGFEMI WDPNGWTE TDNSFSAKQDI VAI TDWSGYSGSFVQHPPELTGLDCMRP
 CFWVELI RGRPKENTI WTSGSSI SFCGVNSDVTGWSWPDGAELPFTI DK
 >gi |156777959|gb|ABU95375.1| neurami ni dase [Influenza A vi rus
 (A/mal |ard/MD/352/2002(H1N1))]
 MNPNQKI I TI GSI CMAI GVI SLVLI GNI I SI WVSHSI QTGNQNHPEI CNQSVI TYENNTWVNOQYI NI S
 NTNLI AEQAVAPVTLAGNSSLCP I SGWAI YSKDNGI RI GSKGDVFI REFFI SCSHLECRFFLTQGALL
 NDKHSNGTVKDRSPYRTLMSCPVGEAPSPYNSRFESVAWSASACHDGI SWLTI GI SGPDNGAVAVLKYNIG
 I I TDTI KSWRNNI LRTQESECACI NGSCFTI MTDGPSNGOASYKI FKVEKGGVVKSVELNAPNYHYEECS
 CYPDASEVMCVCARDNWHGSRNPWVWVFNQNLQYQI GYI CSGVFGDNPRPNDGTGSCGVPVSSNGAYGVKGFCS
 FKYGNGVWI GRTKSTSSRSGFEMI WDPNGWTE TDNSFSAKQDI VAI TDWSGYSGSFVQHPPELTGLDCMRP
 CFWVELI RGRPKENTI WTSGSSI SFCGVNSDVTGWSWPDGAELPFTI DK
 >gi |156777961|gb|ABU95376.1| neurami ni dase [Influenza A vi rus
 (A/mal |ard/MD/369/2002(H1N1))]
 MNPNQKI I TI GSI CMAI GVI SLVLI GNI I SI WVSHSI QTGNQNHPEI CNQSVI TYENNTWVNOQYI NI S
 NTNLI AEQAVAPATLAGNSSLCP I SGWAI YSKDNGI RI GSKGDVFI REFFI SCSHLECRFFLTQGALL
 NDKHSNGTVKDRSPYRTLMSCPVGEAPSPYNSRFESVAWSASACHDGI SWLTI GI SGPDNGAVAVLKYNIG
 I I TDTI KSWRNNI LRTQESECACI NGSCFTI MTDGPSNGOASYKI FKVEKGGVVKSVELNAPNYHYEECS
 CYPDASEVMCVCARDNWHGSRNPWVWVFNQNLQYQI GYI CSGVFGDNPRPNDGTGSCGVPVSSNGAYGVKGFCS
 FKYGNGVWI GRTKSTSSRSGFEMI WDPNGWTE TDNSFSAKQDI VAI TDWSGYSGSFVQHPPELTGLDCMRP
 CFWVELI RGRPKENTI WTSGSSI SFCGVNSDVTGWSWPDGAELPFTI DK
 >gi |156777963|gb|ABU95377.1| neurami ni dase [Influenza A vi rus
 (A/mal |ard/MD/382/2002(H1N1))]
 MNPNQKI I TI GSI CMAI GVI SLVLI GNI I SI WVSHSI QTGNQNHPEI CNQSVI TYENNTWVNOQYI NI S
 NTNLI AEQAVAPVTLAGNSSLCP I SGWAI YSKDNGI RI GSKGDVFI REFFI SCSHLECRFFLTQGALL
 NDKHSNGTVKDRSPYRTLMSCPVGEAPSPYNSRFESVAWSASACHDGI SWLTI GI SGPDNGAVAVLKYNIG
 I I TDTI KSWRNNI LRTQESECACI NGSCFTI MTDGPSNGOASYKI FKVEKGGVVKSVELNAPNYHYEECS
 CYPDASEVMCVCARDNWHGSRNPWVWVFNQNLQYQI GYI CSGVFGDNPRPNDGTGSCGVPVSSNGAYGVKGFCS
 FKYGNGVWI GRTKSTSSRSGFEMI WDPNGWTE TDNSFSAKQDI VAI TDWSGYSGSFVQHPPELTGLDCMRP
 CFWVELI RGRPKENTI WTSGSSI SFCGVNSDVTGWSWPDGAELPFTI DK
 >gi |156777965|gb|ABU95378.1| neurami ni dase [Influenza A vi rus
 (A/mal |ard/MD/390/2002(H1N1))]
 MNPNQKI I TI GSI CMAI GVI SLVLI GNI I SI WVSHSI QTGNQNHPEI CNQSVI TYENNTWVNOQYI NI S
 NTNLI AEQAVAPATLAGNSSLCP I SGWAI YSKDNGI RI GSKGDVFI REFFI SCSHLECRFFLTQGALL
 NDKHSNGTVKDRSPYRTLMSCPVGEAPSPYNSRFESVAWSASACHDGI SWLTI GI SGPDNGAVAVLKYNIG
 I I TDTI KSWRNNI LRTQESECACI NGSCFTI MTDGPSNGOASYKI FKVEKGGVVKSVELNAPNYHYEECS
 CYPDASEVMCVCARDNWHGSRNPWVWVFNQNLQYQI GYI CSGVFGDNPRPNDGTGSCGVPVSSNGAYGVKGFCS
 FKYGNGVWI GRTKSTSSRSGFEMI WDPNGWTE TDNSFSAKQDI VAI TDWSGYSGSFVQHPPELTGLDCMRP
 CFWVELI RGRPKENTI WTSGSSI SFCGVNSDVTGWSWPDGAELPFTI DK

>gi |156777967|gb|ABU95379.1| neurami ni dase [Influenza A vi rus
(A/mal |ard/MD/403/2002(H1N1))]
MNPNQKI I TI GSI CMAI GVI SLVLQI GNI I SI WVSHSI QTGNQNHPEI CNQSVI TYENNTWVNQTYI NI S
NTNLI AEQAVAPVTLAGNSSLCP I SGWAI YSKDNGI RI GSKGDV FVI REPFI SCSHLECRTFFLTQGALL
NDKHSNGTVKDRSPYRTLMSCPVGEAPSPYNSRFESVAWSASACHDGI SWLTI GI SGPDNGAVAVLKYNG
I I TDTI KSWRNNI LRTQESECACI NGSCFTI MTDGSPNGOASYKI FKVEKGVVKSVELNAPNYHYEECS
CYPDASEVMCVCARDNWHGNSRNPWVSFNQNL EYQI GYI CSGVFGDNPRPNDGTGSCGPVSSNGAYGVKGF S
FKYGNVWVI GRKTSSRSRGFEMI WDPNGWTE TDNSFSAKODI VAI TDWSGYSGSFVQHP ETLGLDCMRP
CFWVELI RGRPKENTI WTSGSSI SFCGVNSDTVGWSWPDGAELPFTI DK

>gi |156777969|gb|ABU95380.1| neurami ni dase [Influenza A vi rus
(A/mal |ard/MD/304/2002(H1N1))]
MNPNQKI I TI GSI CMAI GI I SLVLQI GNI I SI WVSHSI QTGGQNHPEI CNQSVI TYENNTWVNQTYI NI S
NTNLI AEQAVAPVTLAGNSSLCL I SGWAI YSKDNGI RI GSKGDV FVI REPFI SCSHLECRTFFLTQGALL
NDKHSNGTVKDRSPYRTLMSCPVGEAPSPYNSRFESVAWSASACHDGI SWLTI GI SGPDNGAVAVLKYNG
I I TDTI KSWRNNI LRTQESECACI NGSCFTI MTDGSPNGOASYKI FKVEKGVVKSVELNAPNYHYEECS
CYPDASEVMCVCARDNWHGNSRNPWVSFNQNL EYQI GYI CSGVFGDNPRPNDGTGSCGPVSSNGAYGVKGF S
FKYGNVWVI GRKTSSRSRGFEMI WDPNGWTE TDNSFSAKODI VAI TDWSGYSGSFVQHP ETLGLDCMRP
CFWVELI RGRPKENTI WTSGSSI SFCGVNSDTVGWSWPDGAELPFTI DK

>gi |156777971|gb|ABU95381.1| neurami ni dase [Influenza A vi rus
(A/mal |ard/MD/350/2002(H1N1))]
MNPNQKI I TI GSI CMAI GVI SLVLQI GNI I SI WVSHSI QTGNQNHPEI CNQSVI TYENNTWVNQTYI NI S
NTNLI AEQAVAPVTLAGNSSLCP I SGWAI YSKDNGI RI GSKGDV FVI REPFI SCSHLECRTFFLTQGALL
NDKHSNGTVKDRSPYRTLMSCPVGEAPSPYNSRFESVAWSASACHDGI SWLTI GI SGPDNGAVAVLKYNG
I I TDTI KSWRNNI LRTQESECACI NGSCFTI MTDGSPNGOASYKI FKVEKGVVKSVELNAPNYHYEECS
CYPDASEVMCVCARDNWHGNSRNPWVSFNQNL EYQI GYI CSGVFGDNPRPNDGTGSCGPVSSNGAYGVKGF S
FKYGNVWVI GRKTSSRSRGFEMI WDPNGWTE TDNSFSAKODI VAI TDWSGYSGSFVQHP ETLGLDCMRP
CFWVELI RGRPKENTI WTSGSSI SFCGVNSDTVGWSWPDGAELPFTI DK

>gi |154152413|gb|ABS70308.1| neurami ni dase [Influenza A vi rus
(A/mal |ard/MD/161/2002(H1N1))]
MNPNQKI I TI GSI CMAI GVI SLVLQI GNI I SI WVSHSI QTGNQNHPEI CNQSVI TYENNTWVNQTYI NI S
NTNLI AEQAVAPVTLAGNSSLCP I SGWAI YSKDNGI RI GSKGDV FVI REPFI SCSHLECRTFFLTQGALL
NDKHSNGTVKDRSPYRTLMSCPVGEAPSPYNSRFESVAWSASACHDGI SWLTI GI SGPDNGAVAVLKYNG
I I TDTI KSWRNNI LRTQESECACI NGSCFTI MTDGSPNGOASYKI FKVEKGVVKSVELNAPNYHYEECS
CYPDASEVMCVCARDNWHGNSRNPWVSFNQNL EYQI GYI CSGVFGDNPRPNDGTGSCGPVSSNGAYGVKGF S
FKYGNVWVI GRKTSSRSRGFEMI WDPNGWTE TDNSFSAKODI VAI TDWSGYSGSFVQHP ETLGLDCMRP
CFWVELI RGRPKENTI WTSGSSI SFCGVNSDTVGWSWPDGAELPFTI DK

>gi |154152449|gb|ABS70329.1| neurami ni dase [Influenza A vi rus
(A/mal |ard/MD/168/2002(H1N1))]
MNPNQKI I TI GSI CMAI GVI SLVLQI GNI I SI WVSHSI QTGNQNHPEI CNQSVI TYENNTWVNQTYI NI S
NTNLI AEQAVAPVTLAGNSSLCP I SGWAI YSKDNGI RI GSKGDV FVI REPFI SCSHLECRTFFLTQGALL
NDKHSNGTVKDRSPYRTLMSCPVGEAPSPYNSRFESVAWSASACHDGI SWLTI GI SGPDNGAVAVLKYNG
I I TDTI KSWRNNI LRTQESECACI NGSCFTI MTDGSPNGOASYKI FKVEKGVVKSVELNAPNYHYEECS
CYPDASEVMCVCARDNWHGNSRNPWVSFNQNL EYQI GYI CSGVFGDNPRPNDGTGSCGPVSSNGAYGVKGF S
FKYGNVWVI GRKTSSRSRGFEMI WDPNGWTE TDNSFSAKODI VAI TDWSGYSGSFVQHP ETLGLDCMRP
CFWVELI RGRPKENTI WTSGSSI SFCGVNSDTVGWSWPDGAELPFTI DK

>gi |154152468|gb|ABS70340.1| neurami ni dase [Influenza A vi rus
(A/mal |ard/MD/170/2002(H1N1))]
MNPNQKI I TI GSI CMAI GVI SLVLQI GNI I SI WVSHSI QTGNQNHPEI CNQSVI TYENNTWVNQTYI NI S
NTNLI AEQAVAPVTLAGNSSLCP I SGWAI YSKDNGI RI GSKGDV FVI REPFI SCSHLECRTFFLTQGALL
NDKHSNGTVKDRSPYRTLMSCPVGEAPSPYNSRFESVAWSASACHDGI SWLTI GI SGPDNGAVAVLKYNG
I I TDTI KSWRNNI LRTQESECACI NGSCFTI MTDGSPNGOASYKI FKVEKGVVKSVELNAPNYHYEECS
CYPDASEVMCVCARDNWHGNSRNPWVSFNQNL EYQI GYI CSGVFGDNPRPNDGTGSCGPVSSNGAYGVKGF S
FKYGNVWVI GRKTSSRSRGFEMI WDPNGWTE TDNSFSAKODI VAI TDWSGYSGSFVQHP ETLGLDCMRP
CFWVELI RGRPKENTI WTSGSSI SFCGVNSDTVGWSWPDGAELPFTI DK

>gi |154152485|gb|ABS70350.1| neurami ni dase [Influenza A vi rus
(A/mal |ard/MD/352/2002(H1N1))]
MNPNQKI I TI GSI CMAI GVI SLVLQI GNI I SI WVSHSI QTGNQNHPEI CNQSVI TYENNTWVNQTYI NI S
NTNLI AEQAVAPVTLAGNSSLCP I SGWAI YSKDNGI RI GSKGDV FVI REPFI SCSHLECRTFFLTQGALL
NDKHSNGTVKDRSPYRTLMSCPVGEAPSPYNSRFESVAWSASACHDGI SWLTI GI SGPDNGAVAVLKYNG
I I TDTI KSWRNNI LRTQESECACI NGSCFTI MTDGSPNGOASYKI FKVEKGVVKSVELNAPNYHYEECS
CYPDASEVMCVCARDNWHGNSRNPWVSFNQNL EYQI GYI CSGVFGDNPRPNDGTGSCGPVSSNGAYGVKGF S
FKYGNVWVI GRKTSSRSRGFEMI WDPNGWTE TDNSFSAKODI VAI TDWSGYSGSFVQHP ETLGLDCMRP
CFWVELI RGRPKENTI WTSGSSI SFCGVNSDTVGWSWPDGAELPFTI DK

>gi |154152519|gb|ABS70370.1| neurami ni dase [Influenza A vi rus
(A/mal |ard/MD/369/2002(H1N1))]
MNPNQKI I TI GSI CMAI GVI SLVLQI GNI I SI WVSHSI QTGNQNHPEI CNQSVI TYENNTWVNQTYI NI S
NTNLI AEQAVAPATLAGNSSLCP I SGWAI YSKDNGI RI GSKGDV FVI REPFI SCSHLECRTFFLTQGALL
NDKHSNGTVKDRSPYRTLMSCPVGEAPSPYNSRFESVAWSASACHDGI SWLTI GI SGPDNGAVAVLKYNG
I I TDTI KSWRNNI LRTQESECACI NGSCFTI MTDGSPNGOASYKI FKVEKGVVKSVELNAPNYHYEECS
CYPDASEVMCVCARDNWHGNSRNPWVSFNQNL EYQI GYI CSGVFGDNPRPNDGTGSCGPVSSNGAYGVKGF S
FKYGNVWVI GRKTSSRSRGFEMI WDPNGWTE TDNSFSAKODI VAI TDWSGYSGSFVQHP ETLGLDCMRP
CFWVELI RGRPKENTI WTSGSSI SFCGVNSDTVGWSWPDGAELPFTI DK

>gi |154152538|gb|ABS70381.1| neurami ni dase [Influenza A vi rus
(A/mal |ard/MD/382/2002(H1N1))]
MNPNQKI I TI GSI CMAI GVI SLVLQI GNI I SI WVSHSI QTGNQNHPEI CNQSVI TYENNTWVNQTYI NI S
NTNLI AEQAVAPVTLAGNSSLCP I SGWAI YSKDNGI RI GSKGDV FVI REPFI SCSHLECRTFFLTQGALL
NDKHSNGTVKDRSPYRTLMSCPVGEAPSPYNSRFESVAWSASACHDGI SWLTI GI SGPDNGAVAVLKYNG

I I TDTI KSWRNNI LRTQESECACI NGSCFTI MTDGPSNGOASYKI FKVEKGGVVKSVELNAPNYHYEECS
 CYPDASEVMCVCARDNWHGSRNPWVWVFNQNLQYQI GYI CSGVFGDNPRPNDGTGSCGVPVSSNGAYGVKGF
 FKYGNGVWI GRTKSTSSRSGFEMI WDPNGWTE DNSFSAKQDI VAI TDWSGYSGSFVQHPPELTGLDCMRP
 CFWVELI RGRPKENTI WTSGSSI SFCGVNSDVTGWSWPDGAELPFTI DK
 >gi |154152557|gb|ABS70392.1| neurami ni dase [Influenza A virus
 (A/mal |ard/MD/390/2002(H1N1))]
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 NDKHSNGTVKDRSPYRTLMSCPVGEAPSPYNSRFESVAWSASACHDGI SWLTI GI SGPNGAVAVLKYN
 I I TDTI KSWRNNI LRTQESECACI NGSCFTI MTDGPSNGOASYKI FKVEKGGVVKSVELNAPNYHYEECS
 CYPDASEVMCVCARDNWHGSRNPWVWVFNQNLQYQI GYI CSGVFGDNPRPNDGTGSCGVPVSSNGAYGVKGF
 FKYGNGVWI GRTKSTSSRSGFEMI WDPNGWTE DNSFSAKQDI VAI TDWSGYSGSFVQHPPELTGLDCMRP
 CFWVELI RGRPKENTI WTSGSSI SFCGVNSDVTGWSWPDGAELPFTI DK
 >gi |154152576|gb|ABS70403.1| neurami ni dase [Influenza A virus
 (A/mal |ard/MD/403/2002(H1N1))]
 MNPNQKI I TI GSI CMAI GVI SLVLI GNI I SI WVSHSI QTGNQNHPEI CNQSVI TYENNTWVNTQYI NI S
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 NDKHSNGTVKDRSPYRTLMSCPVGEAPSPYNSRFESVAWSASACHDGI SWLTI GI SGPNGAVAVLKYN
 I I TDTI KSWRNNI LRTQESECACI NGSCFTI MTDGPSNGOASYKI FKVEKGGVVKSVELNAPNYHYEECS
 CYPDASEVMCVCARDNWHGSRNPWVWVFNQNLQYQI GYI CSGVFGDNPRPNDGTGSCGVPVSSNGAYGVKGF
 FKYGNGVWI GRTKSTSSRSGFEMI WDPNGWTE DNSFSAKQDI VAI TDWSGYSGSFVQHPPELTGLDCMRP
 CFWVELI RGRPKENTI WTSGSSI SFCGVNSDVTGWSWPDGAELPFTI DK
 >gi |154152595|gb|ABS70414.1| neurami ni dase [Influenza A virus
 (A/mal |ard/MD/406/2002(H1N1))]
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 NDKHSNGTVKDRSPYRTLMSCPVGEAPSPYNSRFESVAWSASACHDGI SWLTI GI SGPNGAVAVLKYN
 I I TDTI KSWRNNI LRTQESECACI NGSCFTI MTDGPSNGOASYKI FKVEKGGVVKSVELNAPNYHYEECS
 CYPDASEVMCVCARDNWHGSRNPWVWVFNQNLQYQI GYI CSGVFGDNPRPNDGTGSCGVPVSSNGAYGVKGF
 FKYGNGVWI GRTKSTSSRSGFEMI WDPNGWTE DNSFSAKQDI VAI TDWSGYSGSFVQHPPELTGLDCMRP
 CFWVELI RGRPKENTI WTSGSSI SFCGVNSDVTGWSWPDGAELPFTI DK
 >gi |193877090|gb|ACF25157.1| neurami ni dase [Influenza A virus (A/mal |ard/MD/02-
 181/2002(H1N1))]
 MNPNQKI I TI GSI CMAI GVI SLVLI GNI I SI WVSHSI QTGNQNHPEI CNQSVI TYENNTWVNTQYI NI S
 NTNLI AEQAVAPVTLAGNSSLCP I SGWAI YSKDNGI RI GSKGDVFI REPFI SCSHLECRFFLTQGALL
 NDKHSNGTVKDRSPYRTLMSCPVGEAPSPYNSRFESVAWSASACHDGI SWLTI GI SGPNGAVAVLKYN
 I I TDTI KSWRNNI LRTQESECACI NGSCFTI MTDGPSNGOASYKI FKVEKGGVVKSVELNAPNYHYEECS
 CYPDASEVMCVCARDNWHGSRNPWVWVFNQNLQYQI GYI CSGVFGDNPRPNDGTGSCGVPVSSNGAYGVKGF
 FKYGNGVWI GRTKSTSSRSGFEMI WDPNGWTE DNSFSAKQDI VAI TDWSGYSGSFVQHPPELTGLDCMRP
 CFWVELI RGRPKENTI WTSGSSI SFCGVNSDVTGWSWPDGAELPFTI DK
 >gi |193877071|gb|ACF25146.1| neurami ni dase [Influenza A virus (A/mal |ard/MD/02-
 184/2002(H1N1))]
 MNPNQKI I TI GSI CMAI GVI SLVLI GNI I SI WVSHSI QTGNQNHPEI CNQSVI TYENNTWVNTQYI NI S
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 NDKHSNGTVKDRSPYRTLMSCPVGEAPSPYNSRFESVAWSASACHDGI SWLTI GI SGPNGAVAVLKYN
 I I TDTI KSWRNNI LRTQESECACI NGSCFTI MTDGPSNGOASYKI FKVEKGGVVKSVELNAPNYHYEECS
 CYPDASEVMCVCARDNWHGSRNPWVWVFNQNLQYQI GYI CSGVFGDNPRPNDGTGSCGVPVSSNGAYGVKGF
 FKYGNGVWI GRTKSTSSRSGFEMI WDPNGWTE DNSFSAKQDI VAI TDWSGYSGSFVQHPPELTGLDCMRP
 CFWVELI RGRPKENTI WTSGSSI SFCGVNSDVTGWSWPDGAELPFTI DK
 >gi |193877052|gb|ACF25135.1| neurami ni dase [Influenza A virus (A/mal |ard/MD/02-
 359/2002(H1N1))]
 MNPNQKI I TI GSI CMAI GVI SLVLI GNI I SI WVSHSI QTGNQNHPEI CNQSVI TYENNTWVNTQYI NI S
 NTNLI AEQAVAPVTLAGNSSLCP I SGWAI YSKDNGI RI GSKGDVFI REPFI SCSHLECRFFLTQGALL
 NDKHSNGTVKDRSPYRTLMSCPVGEAPSPYNSRFESVAWSASACHDGI SWLTI GI SGPNGAVAVLKYN
 I I TDTI KSWRNNI LRTQESECACI NGSCFTI MTDGPSNGOASYKI FKVEKGGVVKSVELNAPNYHYEECS
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 FKYGNGVWI GRTKSTSSRSGFEMI WDPNGWTE DNSFSAKQDI VAI TDWSGYSGSFVQHPPELTGLDCMRP
 CFWVELI RGRPKENTI WTSGSSI SFCGVNSDVTGWSWPDGAELPFTI DK
 >gi |193877033|gb|ACF25124.1| neurami ni dase [Influenza A virus (A/mal |ard/MD/02-
 375/2002(H1N1))]
 MNPNQKI I TI GSI CMAI GVI SLVLI GNI I SI WVSHSI QTGNQNHPEI CNQSVI TYENNTWVNTQYI NI S
 NTNLI AEQAVAPVTLAGNSSLCP I SGWAI YSKDNGI RI GSKGDVFI REPFI SCSHLECRFFLTQGALL
 NDKHSNGTVKDRSPYRTLMSCPVGEAPSPYNSRFESVAWSASACHDGI SWLTI GI SGPNGAVAVLKYN
 I I TDTI KSWRNNI LRTQESECACI NGSCFTI MTDGPSNGOASYKI FKVEKGGVVKSVELNAPNYHYEECS
 CYPDASEVMCVCARDNWHGSRNPWVWVFNQNLQYQI GYI CSGVFGDNPRPNDGTGSCGVPVSSNGAYGVKGF
 FKYGNGVWI GRTKSTSSRSGFEMI WDPNGWTE DNSFSAKQDI VAI TDWSGYSGSFVQHPPELTGLDCMRP
 CFWVELI RGRPKENTI WTSGSSI SFCGVNSDVTGWSWPDGAELPFTI DK
 >gi |189220496|gb|ACD85146.1| neurami ni dase [Influenza A virus
 (A/mal |ard/Maryl and/350/2002(H1N1))]
 MNPNQKI I TI GSI CMAI GVI SLVLI GNI I SI WVSHSI QTGNQNHPEI CNQSVI TYENNTWVNTQYI NI S
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 NDKHSNGTVKDRSPYRTLMSCPVGEAPSPYNSRFESVAWSASACHDGI SWLTI GI SGPNGAVAVLKYN
 I I TDTI KSWRNNI LRTQESECACI NGSCFTI MTDGPSNGOASYKI FKVEKGGVVKSVELNAPNYHYEECS
 CYPDASEVMCVCARDNWHGSRNPWVWVFNQNLQYQI GYI CSGVFGDNPRPNDGTGSCGVPVSSNGAYGVKGF
 FKYGNGVWI GRTKSTSSRSGFEMI WDPNGWTE DNSFSAKQDI VAI TDWSGYSGSFVQHPPELTGLDCMRP
 CFWVELI RGRPKENTI WTSGSSI SFCGVNSDVTGWSWPDGAELPFTI DK

>gi |78095957|gb|ABB19631.1| neurami ni dase [Influenza A virus (A/pintai I duck/AI berta/210/2002(H1N1))]
MNPNQKI I TI GSI CMAI GI I SLVLIQI GNI I SI VVSHSI QTGSQNHPEPCNQSVI TYENNTWVNOQTYI NI S
NTNLI AEQAVAPVTLAGNSSLCPI SGWAI YSKDNGI RI GSKGDV FVI REPFI SCSHLECRTEFFLTQGALL
NDKHSNGTVKDRSPYRTLMSCPVGEAPSPYNSRFESVAWSASACHDGI SWLTI GI SGPDNGAVAVLKYNG
I I TDTI KSWRNNI LRTQSEECACI NGSCFTI MTDGSPNGOASYKI FKIEGKVVKSVELNAPNYHYEECS
CYPDASEVMCVCRDNDWHGNSRNPWVSFNQDLEYQI GYI CSGVFGDNPRPNDGTGSCGPVSSNGAYGVKGF
FKYGNVWI GRKTSSRSRGFEMI WDPNGWTE TDNSFSVKQDI VAI TDWSGYSGSFVQHPTEGLDCMRP
CFWVELI RGRPKENTI WTSGSSI SFCGVNSDTVGWSWPDGAELPFTI DK
>gi |167859464|gb|ACA04691.1| neurami ni dase [Influenza A virus (A/duck/Eastern
Chi na/103/2003(H1N1))]
MNPNQKI I TI GSI CMVI GI VSLMLQI GNI I SI VVSHSI QTGNQYOPEPCNQSI I TYENNTWVNOQTYVNI S
NTNFLAEQAVTSVTLAGNSSLCPI SGWAI YSKDNGI RI GSKGDV FVI REPFI SCSHLECRTEFFLTQGALL
NDKHSNGTVKDRSPYRTLMSCPVGEAPSPYNSRFESVAWSASACHDGI SWLTI GI SGPDNGAVAVLKYNG
I I TDTI KSWRNNI LRTQSEECACVNGSCFTVMTDGPNGOASYKI FKIEGKVVKSVELSAPNYHYEECS
CYPDAGEI MCVCRDNWHGNSRNPWVSFNQDLEYQI GYI CSGVFGDNPRPNDGTGSCGPMSNGAYGVKGF
FKYGNVWI GRKTSSRSRGFEMI WDPNGWTE TDSSFSVKQDI VAI TDWSGYSGSFVQHPTEGLDCMRP
CFWVELI RGRPKENTI WTSGSSI SFCGVNSDTVGWSWPDGAELPFTI DK
>gi |167859468|gb|ACA04693.1| neurami ni dase [Influenza A virus (A/duck/Eastern
Chi na/152/2003(H1N1))]
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NDKHSNGTVKDRSPYRTLMSCPVGEAPSPYNSRFESVAWSASACHDGI SWLTI GI SGPDNGAVAVLKYNG
I I TDTI KSWRNNI LRTQSEECACVNGSCFTVMTDGPNGOASYKI FKIEGKVVKSVELSAPNYHYEECS
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SFYGNVWI GRKTSSRSRGFEMI WDPNGWTE TDSSFSVKQDI VAI TDWSGYSGSFVQHPTEGLDCMRP
PCFWVELI RGRPKENTI WTSRSSI SFCGVNSDTVGWSWPDGAELPFTI DK
>gi |195958017|gb|ACG59855.1| neurami ni dase [Influenza A virus
(A/mal I ard/MD/11/2003(H1N1))]
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NDKHSNGTVKDRSPYRTLMSCPVGEAPSPYNSRFESVAWSASACHDGI SWLTI GI SGPDNGAVAVLKYNG
I I TDTI KSWRNNI LRTQSEECACI NGSCFTI MTDGSPNGOASYKI FKIEGKVVKSVELNAPNYHYEECS
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FKYGNVWI GRKTSSRSRGFEMI WDPNGWTE TDNSFSVKQDI VAI TDWSGYSGSFVQHPTEGLDCMRP
CFWVELI RGRPKENTI WTSGSSI SFCGVNSDTVGWSWPDGAELPFTI DK
>gi |195958000|gb|ACG59845.1| neurami ni dase [Influenza A virus
(A/mal I ard/MD/199/2003(H1N1))]
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NTNLI AEQAVAPVALAGNSSLCPI NGWAI YSKDNGI RI GSKGDV FVI REPFI SCSHLECRTEFFLTQGALL
NDKHSNGTVKDRSPYRTLMSCPVGEAPSPYNSRFESVAWSASACHDGI SWLTI GI SGPDNGAVAVLKYNG
I I TDTI KSWRNNI LRTQSEECACI NGSCFTI MTDGSPNGOASYKI FKIEGKVVKSVELNAPNYHYEECS
CYPDASEVMCVCRDNDWHGNSRNPWVSFNQDLEYQI GYI CSGI FGDNPRPNDGTGSCGPVSSNGAYGVKGF
FKYGNVWI GRKTSSRSRGFEMI WDPNGWTE TDNSFSVKQDI VAI TDWSGYSGSFVQHPTEGLDCMRP
CFWVELI RGRPKENTI WTSGSSI SFCGVNSDTVGWSWPDGAELPFTI DK
>gi |167859136|gb|ACA04511.1| neurami ni dase [Influenza A virus (A/muscovy duck/New
York/21211-5/2005(H1N1))]
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NDKHSNGTVKDRSPYRTLMSCPVGEAPSPYNSRFESVAWSASACHDGI SWLTI GI SGPDNGAVAVLKYND
I I TDTI KSWRNDI LRTQSEECACI NGSCFTI MTDGSPNGOASYKI FKIEGKVVKSVELNAPNYHYEECS
CYPDASEVMCVCRDNDWHGNSRNPWVSFNQDLEYQI GYI CSGVFGDNPRPNDGTGSCGPVSSNGAYGVKGF
FKYGNVWI GRKTSSRSRGFEMI WDPNGWTE TDNSFSVKQDI VAI TDWSGYSGSFVQHPTEGLDCMRP
CFWVELI RGRPKENTI WTSGSSI SFCGVNSDTVGWSWPDGAELPFTI DK

H2N2
>gi |116013110|dbj|BAF34378.1| neurami ni dase [Influenza A virus
(A/duck/Hokkai do/95/01(H2N2))]
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TTI EKEI CPEVLEYRNVSKPQCOI TGFAPFSKDNSI RLSAGGDI WVTREPYVSCGPKCYQFALGQGTLL
DNKHSNGTI HDRTPHRTLLMNLGVPFHLGKQVCI AWSSSSCHDGHKAWLHVCTGDDRNATASFI YNGM
LVDSI GSWSONI LRTQSEECVCI NGI CTVMVMTDGSASGRADTRI LFI REGKI VHI SPLSGSAQHI EECS
YPRYPDVRVCRDNDWHGNSRNPVI DI NMVDYSI DSSYVCSGLVGDTPRNDSSSSNCRDPNNERNRGNPVK
GWAFFDNGNDVVMGRTI SKDSRSGYETFRVI GGWATANSKSQVDRQVI VDNNNWSGYSGI FSVEGKSCVNR
CFYVELI RGRPQETRVWWTNSI VVFCGTSGTGTGSIWPDGANI NFMP
>gi |78097446|gb|ABB20232.1| neurami ni dase [Influenza A virus (A/duck/Hong
Kong/319/1978(H2N2))]
MNPNQKI I TI GSVSLTI ATI CFLMQI AI LATTVTLHFQKNECNSPAI NQVTPCEPI I I ERNTEI VYLN
TTI EKEI CPEI AEYRNWSKPQCOI TGFAPFSKDNSI RLSAGGDI WVTREPYVSCDPGPKCYQFALGQGTLL
DNKHSNGTI HDRI PHRTLLMNLGVPFHLGKQVCI AWSSSSCHDGRWLHVCTGDDKNATASFI YDGK
LADSI GSWSONI LRTQSEECVCI NGCTVMVMTDGSASGRADTRI LFI KEGKI VHI SPLSGSAQHI EECS
YPQYDPVRCVCRDNWHGNSRNPVI DI NMADYSI DSSYVCSGLVGDTPRNDSSSSNCRDPNNERNRGNPVK
GWAFFDNGNDVVMGRTI SKDSRLGYETFKVI GGWSTPNSKSQVNRQI I VDNNNWSGYSGI FSVESKSCVNR
CFYVELI RGRPQETRVWWTNSI VVFCGTSGTGTGSIWPDGANI NFMP
>gi |115278697|gb|ABI 84747.1| neurami ni dase [Influenza A virus (A/chi cken/New
York/13828-3/1995(H2N2))]
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QI TGFAPFSKDNSI RLSAGGDI WVTREPYVSCDTSKCYQFALGQGTLLDNKHSNGTI HDRI PHRTLLMNE
 LGVPFHLGKQVCI AWSSSSCHDGKAWLHVCVTGDDRNATASFI YDGMVLVDSI GSWSONI LRTQSEECVCI
 I NGTCTVVMTDGSASGKADTRI LFI KEGKVHII SPLSGSAQHI EECSCYPRYPNVRCVCRDNWKGSRPVI
 I DI NI AEYSI DSSYVCSGLVGDTPRNDSSSSSNCRPNNERGNPGVKWAFDDGNDVMMGRTI SKDSRS
 GYETFRVI GGWATADSKSQTNRQVI VDNNNWSGYSI FSVENKGC I NRCFYVELI RGRPOETRVWVWTSNS
 I VVFCGTSGYGTGSWPDGADI NFMPI
 >gi |115278716|gb|ABI84758.1| neurami ni dase [Influenza A virus (A/guinea fowl/New
 York/20221-11/1995(H2N2))]
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 TI I EKEI CSKVVDYRSWSKQPCQI TGFAPFSKDNSI RLSAGGDI WI TREPYPVSCDTSKCYQFALGQGTLL
 DNKHSNGTI HDRI PHRTLLMNELGVPFHLGKQVCI AWSSSSCHDGKAWLHVCVTGDDRNATASFI YNGM
 LVDSI GSWSONI LRTQSEECVCI NGTCTVVMTDGSASGKADTRI LFI KEGKI I HI SPLSGSAQHI EECSC
 YPRYPNVRCVCRDNWKGSRPVI DI NMADYSI DSSYVCSGLVGDTPRNDSSSSSNCRDPNNERGNPGVK
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 >gi |68164871|gb|AA87411.1| neurami ni dase [Influenza A virus (A/mallard/Postdam/178-
 4/83(H2N2))]
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 TTI EREI CPEAVEYRNWSKQPCQI TGFAPFSKDNSI RLSAGGDI WVTREPYVSCDTSKCYQFALGQGTLL
 DNKHSNGTI HDRI PHRTLLMNELGVPFHLGKQVCI AWSSSSCHDGRAWLHVCVTGDDRNATASFI YDGR
 LVDSI GSWSONI LRTQSEECVCI NGTCTVVMTDGSASGKADTRI LFI KEGKI I HI SPLSGSAQHI EECSC
 YPRYPNVRCVCRDNWKGSRPVI DI NMADYSI DSSYVCSGLVGDTPRNDSSSSSNCRDPNNERGNPGVK
 GWAFDSDGDDVMMGRTI SKDSRSGYETFKVI GGWSTANSKSQVNRQVI VDNNNWSGYSI FSVGKSCI NR
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 >gi |68164892|gb|AA87423.1| neurami ni dase [Influenza A virus (A/mallard/Postdam/178-
 4/83(H2N2))]
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 TTI EREI CPEAVEYRNWSKQPCQI TGFAPFSKDNSI RLSAGGDI WVTREPYVSCDTSKCYQFALGQGTLL
 DNKHSNGTI HDRI PHRTLLMNELGVPFHLGKQVCI AWSSSSCHDGRAWLHVCVTGDDRNATASFI YDGR
 LVDSI GSWSONI LRTQSEECVCI NGTCTVVMTDGSASGKADTRI LFI KEGKI I HI SPLSGSAQHI EECSC
 YPRYPNVRCVCRDNWKGSRPVI DI NMADYSI DSSYVCSGLVGDTPRNDSSSSSNCRDPNNERGNPGVK
 GWAFDSDGDDVMMGRTI SKDSRSGYETFKVI GGWSTANSKSQVNRQVI VDNNNWSGYSI FSVGKSCI NR
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 >gi |189313144|gb|ACD88673.1| neurami ni dase [Influenza A virus (A/chicken/PA/298101-
 4/2004(H2N2))]
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 TTI EREI CPEVPEYRNWSKQPCQI TGFAPFSKDNSI RLSAGGDI WVTREPYVSCDTSKCYQFALGQGTLL
 NNKHSNGTI HDRI PHRTLLMNELGVPFHLGKQVCI AWSSSSCHDGKAWLHVCVTGDDRNATASFI YDGM
 LVDSI GSWSONI LRTQSEECVCI NGTCTVVMTDGSASGRADTRI LFI KEGKI I HI SPLSGSAQHI EECSC
 YPRYPNVRCVCRDNWKGSRPVI DI NMADYSI DSSYVCSGLVGDTPRNDSSSSSNCRDPNNERGNPGVK
 GWAFDNGDNDVMMGRTI SKDSRSGYETFRVI GGWTTANSKSQVNRQVI VDNNNWSGYSI FSVGKGC I NR
 CFYVELI RGRPOETRVWVWTSNSI VVFCGTSGYGTGSWPDGANI DFMPV

H3N2
 >gi |119371724|emb|CAE00566.1| neurami ni dase [Influenza A virus
 (A/turkey/England/69(H3N2))]
 MNPNOI I TI GSVSLTI ATVCFLMOI AI LATTVTLHFQKQNECSI PANNOQVVPCEPI I I ERNI TEI VYLNN
 TTI EREI CPEVVKYRNWSKQPCQI TGFAPFSKDNSI RLSAGGDI WVTREPYVSCDTSKCYQFALGQGTLL
 DNKHSNGTI HDRI PHRTLLMSELGI PFHLGKQVCI AWSSSSCHDGKAWLHVCVTGDDRNATASFI YDGR
 LVDSI RSWSONI LRTQSEECVCI NGTCTVVMTDGSASGRADTRI LFI KEGKI I HVSPLSGSAQHI EECSC
 YPRYPNVRCVCRDNWKGSRPVI DI NMADYSI DSSYVCSGLVGDTPRNDSSSSSNCRDPNNERGNPGVK
 GWAFDNGDDI WMMGRTI SKDSRSGYETFRVI GGWSTPNKSKQVNRQVI VDNKWSGYSI FSVGKSCI NR
 CFYVELI RGRPOETRVWVWTSNSI VVFCGTSGYGTGSWPDGANI NFMPI
 >gi |82654670|gb|ABB88259.1| neurami ni dase [Influenza A virus (A/duck/Hong
 Kong/7/1975(H3N2))]
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 DNKHSNGTI HDRI PHRTLLMNELGVPFHLGKQVCI AWSSSSCHDGRAWLHVCVTGDDRNATASFI YDGR
 LVDSI GSWSONI LRTQSEECVCI NGTCTVVMTDGSASGRADTKI LFI KEGKI I HI SPLSGSAQHI EECSC
 YPRYPNVRCVCRDNWKGSRPVI DI NMADYSI DSSYVCSGLVGDTPRNDSSSSSNCRDPNNERGNPGVK
 GWAFDNGDDVMMGRTI SKDSRSGYETFKVI GGWSTPNKSKQVNRQVI VDNNNWSGYSI FSVGKSCI NR
 CFYVELI RGRPOETRVWVWTSNSI VVFCGTSGYGTGSWPDGADI NFMPI
 >gi |418073|dbj|BAA04720.1| neurami ni dase [Influenza A virus (A/duck/Hong
 Kong/24/76(H3N2))]
 MOI AI LATTVTLHFQKQNECSIPANOI VPEPI I I ERNI TEI VYLNN TTI EREI CPEVVKYRNWSKQPCQI
 I TGFAPFSKDNSI RLSAGGDI WVTREPYVSCDTSKCYQFALGQGTLLDNKHSNGTI HDRI PHRTLLMNE
 LGVPFHLGKQVCI AWSSSSCHDGRAWLHVCVTGDDRNATASFI YDGR LVDSI GSWSONI LRTQSEECVCI
 NGTCTVVMTDGSASGRADTKI LFI KEGKI I HI SPLSGSAQHI EECSCYPRYPNVRCVCRDNWKGSRPVI
 I DI NMADYSI DSSYVCSGLVGDTPRNDSSSSSNCRDPNNERGNPGVKWAFDDGNDVMMGRTI SKDSRS
 GYETFKGI GGWSTANSKSQVNRQVI VDNNNWSGYSI FSVGKSCI I RCFYVELI RGRPOETRVWVWTSNSI
 VVFCGTSGYGTGSWPTGANI NFMPI
 >gi |82652548|gb|ABB87380.1| neurami ni dase [Influenza A virus (A/pintail
 duck/ALB/86/1976(H3N2))]
 MNPNOI I TI GSVSLTI ATVCFLMOI AI LATTVTLHFQKQNECSI PANNOI VPEPI I I ERNI TEI VYLNN
 TTI EREI CPEVVEYRNWSKQPCQI TGFAPFSKDNSI RLSAGGDI WVTREPYVSCDTSKCYQFALGQGTLL
 DNKHSNGTI HDRI PHRTLLMNELGVPFHLGKQVCI AWSSSSCHDGKAWLHVCVTGDDRNATASFI YDGM
 LVDSI GSWSONI LRTQSEECVCI NGTCTVVMTDGSASGRADTRI LFI REGKI I HI SPLSGSAQHI EECSC

YPRYPNVRVCVRDNWKGSNRPVI DI NMADYSI DSSYVCSGLVGDTPRNDSSASSNSCRDPNNERGNPGVK
 GWAFDNGNDVVMGRTI SKDSRSYG YETFRVI GGWTTANSKSTQNRQVI VDNMNSGSGY FSVESKSCI NR
 CFYVELI RGRPQETRVWVTSNSI VVFCGTSYGTGSWPDGANI NFMPPI
 >gi |116235393|dbj |BAF34925.1| neurami ni dase [Influenza A virus
 (A/duck/Hokkai do/5/1977(H3N2))]
 MNPNOKI I TI GSVSLTI ATVCFLMQI AI LATTVTLHFKQNECSI PSYNQVVPCEPI I I ERNI TEI VYLNN
 TTI EKEI CPEVVEYRNWSKQPCQI TGFAPFSKDNSI RLSAGGDI VWTREPYVSCDPSKCYQFALGQGTTL
 DNKHSNGTI HDRI PHRTLLMNELGVPFHLGKQVCI AWSSSSCHDGKAWLHVCTGDDRNATASFI YDGM
 LVDSI GSWSONI LRTQSEECVCI NGTCTVMTDGSASGRADTRI LFI REGKI VHI SPLSGSAQHI EECS
 YPRYPNVRVCVRDNWKGSNRPVI DI NMADYSI DSSYVCSGLVGDTPRNDSSASSNSCRDPNNERGNPGVK
 GWAFDNGNDVVMGRTI SKDSRSYG YETFRVI GGWATANSKSTQNRQVI VDNMNSGSGY FSVESKSCI NR
 CFYVELI RGRPQETRVWVTSNSI VVFCGTSYGTGSWPDGANI NFMPPI
 >gi |418075|dbj |BAA04721.1| neurami ni dase [Influenza A virus (A/duck/Hong
 Kong/245/77(H3N2))]
 MQI AI LATTVTLHFKQHECNPPAI NQVTPCEPI I I ERNI TEI VYLNTTI EREVCPVI ADYRNWSKQPCQ
 I TGFAPFSKDNSI RLSAGGDI VWTREPYVSCDPSKCYQFALGQGTTL DNKHSNGTI HDRI PHRTLLMNEL
 GVPFHLGKQVCI AWSSSSCHDGRWLHVCTGDDRNATASFI YDGLRDSI GSWSONI LRTQSEECVCI
 NGTCTVMTDGSASGRADTRI LFI REGKI VHI SPLSGSAQHI EECSYPRFPNVRVCVRDNWKGSNRPVI I
 DI NMADYSI DSSYLCSGLVGDTPRNDSSASSNSCRDPNNERGNPGVKWAFDNGDDVVMGRTI SKDSRS
 YETFKVI GGWSTPNSKSTQNRQVI VDNMNSGSGY FSVESGSCI I RCFYVELI RRRPQETRVWVTSNSL
 VVFWGTSYGTGSWPDGANI NFMPPI
 >gi |189312959|gb |ACD88497.1| neurami ni dase [Influenza A virus
 (A/duck/NY/6874/1978(H3N2))]
 MNPNOKI I TI GSVSLTI ATVCFLMQI AI LATTVTLHFKQNECSI PANNQVVPCEPI I I ERNI TEI VYLNN
 TTI EKEI CPEVVEYRSWSKQPCQI TGFAPFSKDNSI RLSAGGDI WI TREPYVSCDPNKCYQFALGQGTTL
 DNKHSNGTI HDRI PHRTLLMNELGVPFHLGKQVCI AWSSSSCHDGKAWLHI CVTGDDRNATASFI YDGL
 LVDSI GSWSONI LRTQSEECVCI NGTCTVMTDGSASGRADTRI LFI REGKI VHI SPLSGSAQHI EECS
 YPRYPNVRVCVRDNWKGSNRPVI DI NMADYSI DSSYVCSGLVGDTPRNDSSASSNSCRDPNNERGNPGVK
 GWAFDNGNDVVMGRTI SKDSRSYG YETFRVI GGWATANSKSTQNRQVI VDNMNSGSGY FSVESKSCI NR
 CFYVELI RGRPQETRVWVTSNSI VVFCGTSYGTGSWPDGANI NFMPPI
 >gi |134044270|gb |AB051832.1| neurami ni dase [Influenza A virus
 (A/mal Iard/Ohi o/48/1986(H3N2))]
 MNPNOKI I TI GSVSLTI ATVCFLMQI AI LATTVTLHFKQNECSI PANNQVVPCEPI I I ERNI TEI VYLNN
 TTI EKEI CPKAVDYRNWSKQPCQI TGFAPFSKDNSI RLSAGGDI VWTREPYVSCDTSKCYQFALGQGTTL
 DNKHSNGTI HDRI PHRTLLMNELGVPFHLGKQVCI AWSSSSCHDGKAWLHVCTGDDRNATASFI YDGM
 LVDSI GSWSONI LRTQSEECVCI NGTCTVMTDGSASGRADTRI LFI KEGKI VHI SPLSGSAQHI EECS
 YPRYPNVRVCVRDNWKGSNRPVI DI NMADYSI DSSYVCSGLVGDTPRNDSSASSNSCRDPNNERGNPGVK
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 CFYVELI RGRPQETRVWVTSNSI VVFCGTSYGTGSWPDGANI NFMPPI
 >gi |78096130|gb |ABB19734.1| neurami ni dase [Influenza A virus (A/mal Iard
 duck/ALB/144/1987(H3N2))]
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 DNKHSNGTI HDRI PHRTLLMNELGVPFHLGKQVCI AWSSSSCHDGKAWLHVCTGDDRNATASFI YDGM
 LVDSI GSWSONI LRTQSEECVCI NGTCTVMTDGSASGRADTRI LFI KEGKI VHI SPLSGSAQHI EECS
 YPRYPNVRVCVRDNWKGSNRPVI DI NMADYSI DSSYVCSGLVGDTPRNDSSASSNSCRDPNNERGNPGVK
 GWAFDNGDDVVMGRTI SKDSRSYG YETFRVI GGWATANSKSTQNRQVI VDNMNSGSGY FSVENKSCI NR
 CFYVELI RGRPQETRVWVTSNSI VVFCGTSYGTGSWPDGANI NFMPPI
 >gi |118314107|gb |ABK80017.1| neurami ni dase [Influenza A virus
 (A/mal Iard/Ohi o/424/1988(H3N2))]
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 TTI EKEI CPEVVEYRNWSKQPCQI TGFAPFSKDNSI RLSAGGDI VWTREPYVSCDPSKCYQFALGQGTTL
 DNKHSNGTI HDRI PHRTLLMNELGVPFHLGKQVCI AWSSSSCHDGKAWLHVCTGDDRNATASFI YDGM
 LVDSI GSWSONI LRTQSEECVCI NGTCTVMTDGSASGRADTRI LFI REGKI VHI SPLSGSAQHI EECS
 YPRYPNVRVCVRDNWKGSNRPVI DI NMADYSI DSSYVCSGLVGDTPRNDSSASSNSCKDPNNERGNPGVK
 GWAFDNGNDVVMGRTI SKDSRSYG YETFRVI GGWATANSKSTQNRQVI VDNMNSGSGY FSVESKSCI NR
 CFYVELI RGRPQETRVWVTSNSI VVFCGTSYGTGSWPDGANI NFMPPI
 >gi |193877768|gb |ACF25550.1| neurami ni dase [Influenza A virus (A/gui nea fowl /NJ/8848-
 18/1998(H3N2))]
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 TVI EKEI CPKAI DYRNWSKQPCQI TGFAPFSKDNSI RLSAGGDI VWTREPYVSCDTSKCYQFALGQGTTL
 DNKHSNGTI HDRI PHRTLLMNELGVPFHLGKQVCI AWSSSSCHDGKAWLHVCTGDDRNATASFI YDGM
 LVDSI GSWSONI LRTQSEECVCI NGTCTVMTDGSASGRADTRI LFI KEGKI VHI SPLSGSAQHI EECS
 YPRYPNVRVCVRDNWKGSNRPVI DI NMADYSI DSSYVCSGLVGDTPRNDSSASSNSCRDPNNERGNPGVK
 GWAFDDGNDVVMGRTI SKDSRSYG YETFRVI GGWATANSKSTQNRQVI VDNMNSGSGY FSVENKSCI NR
 CFYVELI RGRPQETRVWVTSNSI VVFCGTSYGTGSWPDGANI NFMPPI
 >gi |193877785|gb |ACF25560.1| neurami ni dase [Influenza A virus (A/chi cken/NY/11602-
 12/1998(H3N2))]
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 TVI EKEI CPKTVDYRNWSKQPCQI TGFAPFSKDNSI RLSAGGDI VWTREPYVSCDTSKCYQFALGQGTTL
 DNKHSNGTI HDRI PHRTLLMNELGVPFHLGKQVCI AWSSSSCHDGKAWLHVCTGDDRNATASFI YDGI
 LVDSI GSWSONI LRTQSEECVCI NGTCTVMTDGSASGRADTRI LFI KEGKI VHI SPLSGSAQHI EECS
 YPRYPNVRVCVRDNWKGSNRPVI DI NMADYSI DSSYVCSGLVGDTPRNDSSASSNSCRDPNNERGNPGVK
 GWAFDDGNDVVMGRTI SKDSRSYG YETFRVI GGWATANSKSTQNRQVI VDNMNSGSGY FSVENKSCI NR
 CFYVELI RGRPQETRVWVTSNSI VVFCGTSYGTGSWPDGANI NFMPPI
 >gi |193876809|gb |ACF25000.1| neurami ni dase [Influenza A virus
 (A/mal Iard/MN/290/1999(H3N2))]

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>gi|193877204|gb|ACF25223.1|neurami ni dase [Influenza A vi rus (A/mal lard/MN/380/1999(H3N2))]
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>gi|193876825|gb|ACF25009.1|neurami ni dase [Influenza A vi rus (A/mal lard/MN/68/1999(H3N2))]
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>gi|119502416|gb|ABL75566.1|neurami ni dase [Influenza A vi rus (A/bl ue-wi nged teal /Ohi o/31/1999(H3N2))]
MNPNQKI I TI GSVSLTI ATACFLMQI AI LATTVTLHFKONECSTPANNQAVPCEPI I I ERNI TEI VYLNN TI LEKEI CPKAVDYRNWSKPOCOI TGFAPFSKDNSI RLSAGGDI WI TREPVVSCDTSKCYQFALGQGTLL DNKHSNGTI HDRI PHRTLLMNLGVPFHLGKQVCI AWSSSSCHDGKAWLHI CVTGDDRNATASFY YDGM LI DSI GWSQNI LRTQSEECVCI NGCTVVMVDGSASGKADTRI LFI EEGKVHI SPLSGSAQHI EECSC YPRYPNVRVCVRDNWKGNSRPVI DI NMADYSVDSNYVCSGLVGDTPRNDSSSSNSNCRDPNNERGNPGVK GWAFFDDGNDVVMGRTI SKDSRSGYETFRVI GGWSTANSKSOI NRQVI VDNNNWSGYSGI FSVENKSCI NR CFYVELI RGRPQETRVWVWTSNSI VVFCGTSYGTGSGWPDGANI NFMPI
>gi|93204711|emb|CAG27357.1|neruami ni dase [Influenza A vi rus (A/duck/Ontari o/05/00 (H3N2))]
MNPNQKI I TI GSVSLTI ATICFLMQI AI LVTTVTLHFKQYECDPANNQAMPCEPI I I ERNI TEI VYLNT TTI EKEVCPKLVYRNWSKPOCKI TGFAPFSKDNSI RLSAGGDI WVTREPVVSCDPGKCYQFALGQGTLL DNKHSNDTI HDRTPHRTLLMNLGVPFHLGTRQVCI AWSSSSCHDGKAWLHVCVTGYDKNATASFI YDGM LVDSI GWSQNI LRTQSEECVCI NGCTVVMVDGSASGRADTKI LFI EEGKI VHTSPLSGSAQHVEECSC YPRYPGVRCI CRDNWKGNSRPVVI NVKDYSI NSSYVCSGLVGDTPRNDSSSSNSNCRDPNNEKGTGKGVK GWAFFDDGNDVVMGRTI SEDSRSGYETFRVI GGWSTPNSKLOI NRQVI VDSNDRSGYSGI FSVEGKSCI NR CFYVELI RGREQETRVWVWTSNSI VVFCGTSYGTGSGWPDGADI NI MPI
>gi|78097273|gb|ABB20188.1|neurami ni dase [Influenza A vi rus (A/chi cken/Nanchang/3-120/2001(H3N2))]
MNPNQKI I AI GSVSLTI ATICFLMQI AI LATTMTLHFKOI GCSNPSNNOVVPCEPI I I EKNI VHLNSTTI EKEI CPKVVEYRNWSKPOCOI TGFAPFSKDNSI RLSAGGDI WVTREPVVSCGLGKCYQFALGQGTLLKNE HSNGTTHDRI PHRTLLMNLGVPFHLGTRQVCI AWSSSSCHDGKAWLHVCVTGDDKNATASFI YDGM LVDSI GWSQNI LRTQSEECVCI NGCTVVMVDGSASGRADTRI LFI REGKI VHI SPLSGSAQHVEECSCYPR YPEVRCVRDNWKGNSRPVLI NMADYSI ESSYVCSGLVGDTPRNDSSSSNSNCRDPNNERGAPGVKGIWA FDNNDI WMGRTI KEDSRSGYETFRVVGWTTANSKSOI NRQVI VDSNDRSGYSGI FSVEGKSCI NR CFYVELI RGRPQETRVWVWTSNSI VVFCGTSYGTGSGWPDGANI NFMPI
>gi|167859368|gb|ACA04643.1|neurami ni dase [Influenza A vi rus (A/duck/Eastern Chi na/36/2002(H3N2))]
MNPNQKI I TI GSVSLTI ATICFLMQI AI LATTI TLHFKONECSI PSNNQVVPCEPI I I ERNI TEMVYLNN TTI EKEI CPKAVDYRNWSKPOCOI TGFAPFSKDNSI RLSAGGDI WVTREPVVSCDTSKCYQFALGQGTLL DNKHSNGTI HDRI PHRTLLMNLGVPFHLGTRQVCI AWSSSSCHDGKAWLHVCVTGDDRNATASFI YDGM LVDSI GWSQNI LRTQSEECVCI NGCTVVMVDGSASGRADTRI LFI KEGKI VHI SPLSGSAQHI EECSC YPRYPNVRVCVRDNWKGNSRPVI DI NMADYSI DSSYVCSGLVGDTPRYDDSSSSNSNCRDPNNERGNPGVK GWAFFDDGNDVVMGRTI SKDSRSGYETFRVI GGWTTANSKSOI NRQVI VDNNNWSGYSGI FSVEGKSCI NR CFYVELI RGRPQETRVWVWTSNSI VVFCGTSYGTGSGWPDGANI NFMPI
>gi|113901312|gb|ABI 48009.1|neurami ni dase [Influenza A vi rus (A/bl ue-wi nged teal /Ohi o/908/2002(H3N2))]
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>gi|58429315|gb|AAW78084.1|neurami ni dase [Influenza A vi rus (A/dove/Korea/S11/03(H3N2))]
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GWAFDNENDVMMGRTI SKDSRSGYETFVKVI GGWTTANSKQVNRQVI VDNNNWSGYSI FSVEGKSCVNR
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 >gi |167859408|gb|ACA04663.1| neurami ni dase [Influenza A virus (A/duck/Eastern
 Chi na/848/2003(H3N2))]
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 DNKHSNGTI HDRI PHRTLLMNLGVPFHLGKQVCI AWSSSSCHDGRWLHVCTGDDRNATASFI YDGM
 LVDSI GSWSONI LRTQSECEVCI NGCTVVMTDGSASGRADTRI LFKVKEGKI VHI SPLSGSAQHI ECESC
 YPSYDPVRCVCRDNWKGSNRPI I DI NMADYSI GSSYVCSGLVGDTPRNDSSSNCRDPNNERNRGNPGVK
 GWAFDYGNDVMMGRTI SKDSRSGYETFVRI GGWTMANSKQVNRQVI VDNNSWSGYSI FSVEGKSCI NR
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 >gi |167859440|gb|ACA04679.1| neurami ni dase [Influenza A virus (A/duck/Eastern
 Chi na/855/2003(H3N2))]
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 DNKHSNGTI HDRI PHRTLLMNLGVPFHLGKQVCI AWSSSSCHDGRWLHVCTGDDRNATASFI YDGM
 LVDSI GSWSONI LRTHSECEVCI NGCTVVMTDGSASGRADTRI LFKVKEGKI VHI SPLSGSAQHI ECESC
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 Chi na/857/2003(H3N2))]
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 DNKHSNGTI HDRI PHRTLLMNLGVPFHLGKQVCI AWSSSSCHDGRWLHVCTGDDRNATASFI YDGM
 LVDSI GSWSONI LRTHSECEVCI NGCTVVMTDGSASGRADTRI LFKVKEGKI VHI SPLSGSAQHI ECESC
 YPSYDPVRCVCRDNWKGSNRPI I DI NMADYSI GSSYVCSGLVGDTPRNDSSSNCRDPNNERNRGNPGVK
 GWAFDYGNDVMMGRTI SKDSRSGYETFVRI GGWTMANSKQVNRQVI VDNNSWSGYSI FSVEGKSCI NR
 CFYVELI RGRPQETRVWWTNSI VVFCGTSGTYGTGSWPDGANI NFMPI
 >gi |58429307|gb|AAW78080.1| neurami ni dase [Influenza A virus
 (A/duck/Korea/S7/03(H3N2))]
 MNPNQI I TI GSVSLTI ATVCFLMQI AI LATTVTLHFKONGCSI PSNNQVVPCEPI I VERNI TEVYVYLN
 TTI KEKELCPKVLLEYRDWSKPQCCI TGFAPFSKDNSI RLSAGGDI WVSREPYVSCSPDKCYQFALGQGTTL
 DNEHSNGTI HDRI PHRTLLMNLGVPFHLGKQVCI AWSSSSCHDGRWLHVCTGDDRNATASFI YDGM
 LVDSI GSWSONI LRTQSECEVCI NGCTVVMTDGSASGRADTRI LFI REGKI VHI SPLSGSAQHI ECESC
 YPRYPDVRCVCRDNWKGSNRPI I DI NMADYSI DSSYVCSGLVGDTPRNDSSSNCRDPNNERNRGNPGVK
 GWAFDNENDVMMGRTI SKDSRSGYETFVKVI GGWTTANSKQVNRQVI VDNNNWSGYSI FSVEGKSCVNR
 CFYVELI RGRPQETRVWWTNSI VAFCGTSGTYGTGSWPDGANI NFMPI
 >gi |167859406|gb|ACA04662.1| neurami ni dase [Influenza A virus (A/duck/Eastern
 Chi na/838/2003(H3N2))]
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 TTI EKELCPKVLLEYRDWSKPQCCI TGFAPFSKDNSI RLSAGGDI WVTREPYVSCSPDKCYQFALGQGTTL
 DNKHSNGTI HDRI PHRTLLMNLGVPFHLGKQVCI AWSSSSCHDGRWLHVCTGDDRNATASFI YDGM
 LVDSI GSWSONI LRTQSECEVCI NGCTVVMTDGSASGRADTRI LFKVKEGKI VHI SPLSGSAQHI ECESC
 YPSYDPVRCVCRDNWKGSNRPI I DI NMADYSI GSSYVCSGLVGDTPRNDSSSNCRDPNNERNRGNPGVK
 GWAFDYGNDVMMGRTI SKDSRSGYETFVRI GGWTMANSKQVNRQVI VDNNSWSGYSI FSVEGKSCI NR
 CFYVELI RGRPQETRVWWTNSI VVFCGTSGTYGTGSWPDGANI NFMP
 >gi |167859438|gb|ACA04678.1| neurami ni dase [Influenza A virus (A/duck/Eastern
 Chi na/770/2003(H3N2))]
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 TTI EKELCPKVLLEYRDWSKPQCCI TGFAPFSKDNSI RLSAGGDI WVTREPYVSCSPDKCYQFALGQGTTL
 DNKHSNGTI HDRI PHRTLLMNLGVPFHLGKQVCI AWSSSSCHDGRWLHVCTGDDRNATASFI YDGM
 LVDSI GSWSONI LRTHSECEVCI NGCTVVMTDGSASGRADTRI LFKVKEGKI VHI SPLSGSAQHI ECESC
 YPSYDPVRCVCRDNWKGSNRPI I DI NMADYSI GSSYVCSGLVGDTPRNDSSSNCRDPNNERNRGNPGVK
 GWAFDYGNDVMMGRTI SKDSRSGYETFVRI GGWTMANSKQVNRQVI VDNNSWSGYSI FSVEGKSCI NR
 CFYVELI RGRPQETRVWWTNSI VVFCGTSGTYGTGSWPDGANI NFMPI
 >gi |167859442|gb|ACA04680.1| neurami ni dase [Influenza A virus (A/duck/Eastern
 Chi na/875/2003(H3N2))]
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 DNKHSNGTI HDRI PHRTLLMNLGVPFHLGKQVCI AWSSSSCHDGRWLHVCTGDDRNATASFI YDGI
 LVDSI GSWSONI LRTHSECEVCTNGCTVVMTDGSASGRADTRI LFKVKEGKI VHI SPLSGSAQHI ECESC
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 GWAFDYGNDVMMGRTI SKDSRSGYETFVRI GGWTMANSKQVNRQVI VDNNSWSGYSI FSVEGKSCI NR
 CFYVELI RGRPQETRVWWTNSI VVFCGTSGTYGTGSWPDGANI NFMPI
 >gi |167859478|gb|ACA04698.1| neurami ni dase [Influenza A virus (A/duck/Eastern
 Chi na/866/2003(H3N2))]
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 TTI EKELCPKVLLEYRDWSKPQCCI TGFAPFSKDNSI RLSAGRDI WVTREPYVSCSPDKCYQFALGQGTTL
 DNKHSNGTI HDRI PHRTLLMNLGVPFHLGKQVCI AWSSSSCHDGRWLHVCTGDDRNATASFI YDGM
 LVDSI GSWSONI LRTQSECEVCI NGCTVVMTDGKCI REGLI LEYFVKEGKI VHI SPLSGSAQHI ECESC
 CYPSPDVRCVCRDNWKGSNRPI I DI NMADYSI GSSYVCSGLVGDTPRNDSSSNCRDPNNERNRGNPGV
 KGWAFDYGNDVMMGRTI SKDSRSGYETFVRI GGWTMANSKQVNRQVI VDNNSWSGYSI FSVEGKSCI N
 RCFYVELI RGRPQETRVWWTNSI VVFCGTSGTYGTGSWPDGANI NFMPI
 >gi |167859500|gb|ACA04709.1| neurami ni dase [Influenza A virus (A/duck/Eastern
 Chi na/852/2003(H3N2))]
 MNPNQI I TI GSVSLTI ATI CFLMQI AI LATTVTLHFKONECSI PSNNQVVPCEPI I VERNI TEI VYLN

TTI EKELCPKVLEYRDWSKQCCQI TGFAPFSKDNSI RLSAGGDI WVTREPYVSCSPDKCYQFALGQGTTL
DNKHSNGTI HDRI PHRTLLMNLGVPFHLGKQVCI AWSSSSCHDGRAWLHVCTGDDRNATASFI YDGM
LVDSI GSWSONI LRTQSEECVCI NGTCTVVMTDGSASGRADTRI LFKVKEGKI VHI SPLSGSAQHI EECS
FPSYPDVRVCVRDNWKGSRPVI I DI NMADYSI GSSYVCSGLVGDTPRNDSSSSSNCRDPNNERGNPGVK
GWAFDYGNDVVMGRTI SKDSRSGYETFRVI GGWTMANSKSQVNRQVI VDNNSWGSYSGI FSVEGKSCI NR
CFYVELI RGRPQETRVVWTSNSI VVFCGTSGYGTGSWPDGANI NFMPPI
>gi |167859430|gb|ACA04674.1| neurami ni dase [Influenza A virus (A/duck/Eastern
Chi na/160/2003(H3N2))]
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TTI EKELCPKALYRDWSKQCCQI TGFAPFSKDNSI RLSAGGDI WVTREPYVSCSPDKCYQFALGQGTTL
DNKHSNGTI HDRI PHRTLLMNLGVPFHLGKQVCI AWSSSSCHDGRAWLHVCTGDDRNATASFI YDGM
LVDSI GSWSONI LRTQSEECVCI NGTCTVVMTDGSASGRADTRI LFKVKEGKI VHI SPLSGSAQHI EECS
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GWAFDYGNDVVMGRTI SKDSRSGYETFRVI GGWTMANSKSQVNRQVI VDNNSWGSYSGI FSVEGKSCNCR
CFYVELI RGRPQETRVVWTSNSI VVFCGTSGYGTGSWPDGANI NFMPPI
>gi |58429305|gb|AAW78079.1| neurami ni dase [Influenza A virus
(A/chi cken/Korea/S6/03(H3N2))]
MNPNOKI I TI GSVSLTI ATICFLMQI AI LATTVTLHFQKQNCESI PSNNQVVPCEPTI I ERNI TEVYLLN
TTVEKEI CPGMPYRNVWSKQCCQI TGFAPFSKDNSI RLSAGGDI WVTREPYVSCSPDKCYQFALGQGTTL
DNKHSNGTI HDRI PHRTLLMNLGVPFHLGKQVCI AWSSSSCHDGRAWLHVCTGDDRNATASFI YDGM
LVDSI GSWSONI LRTQSEECVCI NGTCTVVMTDGSASGRADTRI LFKVKEGKI VHI SPLSGSAQHI EECS
YPRYPDVRVCVRDNWKGSRPVI I DI NMADYSI GSSYVCSGLVGDTPRNDSSSSSNCRDPNNERGNPGVK
GWAFDYGNDVVMGRTI SKDSRSGYETFRVI GGWTMANSKSQVNRQVI VDNNSWGSYSGI FSVEGKSCVNR
CFYVELI RGRPQETRVVWTSNSI VVFCGTSGYGTGSWPDGANI NFMPPI
>gi |58429309|gb|AAW78081.1| neurami ni dase [Influenza A virus
(A/duck/Korea/S8/03(H3N2))]
MNPNOKI I TI GSVSLTI ATICFLMQI AI LATTVTLHFQKQNCESI PSNNQVVPCEPTI I ERNI TEVYLLN
TTVEKEI CPGMPYRNVWSKQCCQI TGFAPFSKDNSI RLSAGGDI WVTREPYVSCSPDKCYQFALGQGTTL
DNEHSNGTI HDRI PHRTLLMNLGVPFHLGKQVCI AWSSSSCHDGRAWLHVCTGDDRNATASFI YDGM
LVDSI GSWSONI LRTQSEECVCI NGTCTVVMTDGSASGRADTRI LFKVKEGKI VHI SPLSGSAQHI EECS
YPRYPDVRVCVRDNWKGSRPVI I DI NMADYSI GSSYVCSGLVGDTPRNDSSSSSNCRDPNNERGNPGVK
GWAFDYGNDVVMGRTI SKDSRSGYETFRVI GGWTMANSKSQVNRQVI VDNNSWGSYSGI FSVEGKSCVNR
CFYVELI RGRPQETRVVWTSNSI VVFCGTSGYGTGSWPDGANI NFMPPI
>gi |167859444|gb|ACA04681.1| neurami ni dase [Influenza A virus (A/duck/Eastern
Chi na/901/2003(H3N2))]
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TTI EKELCPKVLEYRDWSKQCCQI TGFAPFSKDI SI RLSAGGDI WVTREPYVSCSPDKCYQFALGQGTTL
DNKHSNGTI HDRI PHRTLLMNLGVPFHLGKQVCI AWSSSSCHDGRAWLHVCTGDDRNATASFI YDGM
LVDSI GSWSONI LRTQSEECVCI NGTCTVVMTDGSASGRADTRI LFKVKEGKI VHI SPLSGSAQHI EECS
YPSYPDVRVCVRDNWKGSRPVI I DI NMADYSI GSSYVCSGLVGDTPRNDSSSSSNCRDPNNERGNPGVK
GWAFDYGNDVVMGRTI SKDSRSGYETFRVI GGWTMANSKSQVNRQVI VDNNSWGSYSGI FSVEGKSCI NR
CFYVELI RGRPQETRVVWTSNSI VVFCGTSGYGTGSWPDGANI NFMPPI
>gi |84626340|gb|ABC59711.1| neurami ni dase [Influenza A virus
(A/turkey/Ohi o/313053/04(H3N2))]
MNPNOKI I TI GSVSLTI ATICFLMQI AI LVTTVTLHFQKQNCESI PSNNQVVPCEPTI I ERNTEI VYLLN
TTI EKELCPKALYRNVWSKQCCQI TGFAPFSKDNSI RLSAGGDI WVTREPYVSCSPDKCYQFALGQGTTL
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LVDSI GSWSONI LRTQSEECVCI NGTCTVVMTDGSASGRADTRI LFKVKEGKI VHI SPLSGSAQHI EECS
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GWAFDYGNDVVMGRTI SKDSRSGYETFRVI GGWTMANSKSQVNRQVI VDNNSWGSYSGI FSVEGKSCI NR
CFYVELI RGRPQETRVVWTSNSI VVFCGTSGYGTGSWPDGANI NFMPPI
>gi |167996870|gb|ACA14285.1| neurami ni dase [Influenza A virus
(A/duck/Korea/LPM01/2004(H3N2))]
MNPNOKI I TI GSVSLTI ATICFLMQI AI LVTTVTLHFQKQNCESI PSNNQI VPCEPI I I ERNI TEI VYLLN
TTI EKELCPKALYRNVWSKQCCQI TGFAPFSKDNSI RLSAGGDI WVTREPYVSCSPDKCYQFALGQGTTL
DNKHSNGTI HDRI PHRTLLMNLGVPFHLGKQVCI AWSSSSCHDGRAWLHVCTGDDRNATASFI YDGM
LVDSI GSWSONI LRTQSEECVCI NGTCTVVMTDGSASGRADTRI LFKVKEGKI VHI SPLSGSAQHI EECS
YPRYPDVRVCVRDNWKGSRPVI I DI NMADYSI GSSYVCSGLVGDTPRNDSSSSSNCRDPNNERGNPGVK
GWAFDYGNDVVMGRTI SKDSRSGYETFRVI GGWTMANSKSQVNRQVI VDNNSWGSYSGI FSVEKSCVNR
CFYVELI RGRPQETRVVWTSNSI VVFCGTSGYGTGSWPDGANI NFMPPI
>gi |167859456|gb|ACA04687.1| neurami ni dase [Influenza A virus (A/duck/Eastern
Chi na/6/2004(H3N2))]
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TTI EKELCPKVLEYRDWSKQCCQI AGFAPFSKDNSI RLSAGGDI WVTREPYVSCSPDKCYQFALGQGTTL
DNKHSNGTI HDRI PHRTLLMNLGVPFHLGKQVCI AWSSSSCHDGRAWLHVCTGDDRNATASFI YDGM
LVDSI GSWSONI LRTQSEECVCI NGTCTVVMTDGSASGRADTRI LFKVKEGKI VHI SPLSGSAQHI EECS
YPRYPDVRVCVRDNWKGSRPVI I DI NMADYSI GSSYVCSGLVGDTPRNDSSSSSNCRDPNNERGNPGVK
GWAFDYGNDVVMGRTI SKDSRSGYETFRVI GGWTMANSKSQVNRQVI VDNNSWGSYSGI FSVEGKSCVNR
CFYVELI RGRPQETRVVWTSNSI VVFCGTSGYGTGSWPDGANI NFMPPI
>gi |146454452|gb|ABQ41890.1| neurami ni dase [Influenza A virus
(A/turkey/I I I i noi s/2004(H3N2))]
MNPNOKI I TI GSVSLTI ATICFLMQI AI LVTTVTLHFQKQNCESI PSNNQVVPCEPTI I ERNTEI VYLLN
TTI EKELCPKALYRNVWSKQCCQI TGFAPFSKDNSI RLSAGGDI WVTREPYVSCSPDKCYQFALGQGTTL
NNGHSNDTVHTRTPYRLLMNLGVPFHLGTRQVCI AWSSSSCHDGRAWLHVCTGDDRNATASFI YDGM
LVDSI GSWSONI LRTQSEECVCI NGTCTVVMTDGSASGRADTRI LFKVKEGKI VHI SPLSGSAQHI EECS
YPRYPDVRVCVRDNWKGSRPVI I DI NMADYSI GSSYVCSGLVGDTPRNDSSSSSNCRDPNNERGNPGVK
GWAFDYGNDVVMGRTI SKDSRSGYETFRVI GGWTMANSKSQVNRQVI VDNNSWGSYSGI FSVEGKSCI NR

CFYVELI RGRKEETKVVWTSNSI VVFCGTSYGTGSGWPDGADI NLMPI
 >gi |167996851|gb|ACA14276.1| neurami ni dase [Influenza A virus (A/aquatic
 bird/Korea/CN-2/2004(H3N2))]
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 DNKHSNGTI HDRI PHRTLLMNLGVPFHLGKQVCI AWSSSSCHDGKAWLHVCVTGDDRNATASFI YNGM
 LVDSI GWSQNI LRTQSEECVCI NGTCTVVMTDGSASGKADTRI LFI REGKI VHI SPLSGSAQHI EECSC
 YPRYPDVRCVCRDNWKGNSRPVI DI NMADYSI DSSYVCSGLVGDTPRNDSSSSSNCRDPNNERGNPGVK
 GWAFFDNENDVVMGRTI SKDSRSGYETFKVI GGWTTANSKSOVNRQVI VDNNNWSGYSGI FSVEKSCVNR
 CFYVELI RGRPQETRVWVWTSNSI VVFCGTSYGTGSGWPDGADI NLMPI
 >gi |189313125|gb|ACD88662.1| neurami ni dase [Influenza A virus
 (A/turkey/OH/313053/2004(H3N2))]
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 TTI EKEI CPKLAEYRNWWSKQPCNI TGFAPFSKDNSI RLSAGGDI WVTREPYVSCDPPDKCYQFALGQGTTL
 NNGHSNDTVHDRTPYRTRLLMNLGVPFHLGTRQVCI AWSSSSCHDGKAWLHVCVTGDDRNATASFI YNGM
 LVDSI GWSKNI LRTQSEECVCI NGTCTVVMTDGSASGKADTKI LFI EEGKI VHI STLSGSAQHVVEECS
 YPRYPGVRCVCRDNWKGNSRPI VDI NVKDYSI VSSYVCSGLVGDTPRKNDSFSSSHCLDPNNEEGGHGVK
 GWAFFDNENDVVMGRTI SEKLSRSGYETFKVI EGWSPKNSKLTQNRQVI VERGNRSGYSGI FSVEKSCVNR
 CFYVELI RGRKEETKVVWTSNSI VVFCGTSYGTGSGWPDGADI NLMPI
 >gi |167996872|gb|ACA14286.1| neurami ni dase [Influenza A virus
 (A/chi cken/Korea/LPM03/2004(H3N2))]
 MNPNSQKI I TI GAVSLTI ATICFLMQI AI LTTTTLHFKONECSI PSNNQI VPCEPI I I ERNI TEI VYLN
 TTI EKEI YPRVLEYRNWWSKQPCQI TGFAPFSKDNSI RLSAGGDI WVTREPYVSCDPSKCYQFALGQGTTL
 DNKHSNGTI HDRI PHRTLLMNLGVPFHLGKQVCI AWSSSSCHDGKAWLHVCVTGDDRNATASFI YNGM
 LVDSI VWSQNI LRTQSEECVCI NGTCTVVMTDGSASGRADTRI LFI REGKI I HI SPLSGSAQHI EECSC
 YPRYPNVRCVCRDNWKGNSRPI DI NMADYSI GSSYVCSGLVGDTPRNDSSSSSNCKDPNNERGNPGVK
 GWAFFDNENDVVMGRTI SKDSRSGYETFRVI GGWTTANSKSOVNRQVI VDNNNWSGYSGI FSVEKSCVNR
 CFYVELI RGRPQETRVWVWTSNSI VVFCGTSYGTGSGWPDGANI NFMP
 >gi |167996874|gb|ACA14287.1| neurami ni dase [Influenza A virus
 (A/duck/Korea/LPM09/2004(H3N2))]
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 TTI EKEI YPRVLEYRNWWSKQPCQI TGFAPFSKDNSI RLSAGGDI WVTREPYVSCDPSKCYQFALGQGTTL
 DNKHSNGTI HDRI PHRTLLMNLGVPFHLGKQVCI AWSSSSCHDGKAWLHVCVTGDDRNATASFI YNGM
 LVDSI VWSQNI LRTQSEECVCI NGTCTVVMTDGSASGRADTRI LFI REGKI I HI SPLSGSAQHI EECSC
 YPRYPNVRCVCRDNWKGNSRPI DI NMADYSI GSSYVCSGLVGDTPRNDSSSSSNCKDPNNERGNPGVK
 GWAFFDNENDVVMGRTI SKDSRSGYETFRVI GGWTTANSKSOVNRQVI VDNNNWSGYSGI FSVEKSCVNR
 CFYVELI RGRPQETRVWVWTSNSI VVFCGTSYGTGSGWPDGANI NFMP
 >gi |167996876|gb|ACA14288.1| neurami ni dase [Influenza A virus
 (A/chi cken/Korea/LPM17/2004(H3N2))]
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 DNKHSNGTI HDRI PHRTLLMNLGVPFHLGKQVCI AWSSSSCHDGKAWLHVCVTGDDRNATASFI YNGM
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 (A/duck/Korea/LPM18/2004(H3N2))]
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 DNKHSNGTI HDRI PHRTLLMNLGVPFHLGKQVCI AWSSSSCHDGKAWLHVCVTGDDRNATASFI YNGM
 LVDSI VWSQNI LRTQSEECVCI NGTCTVVMTDGSASGRADTRI LFI REGKI I HI SPLSGSAQHI EECSC
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 CFYVELI RGRPQETRVWVWTSNSI VVFCGTSYGTGSGWPDGANI NFMP
 >gi |167996888|gb|ACA14294.1| neurami ni dase [Influenza A virus
 (A/duck/Korea/LPM39/2005(H3N2))]
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 TTI EKEI HPRVLEYRNWWSKQPCQI TGFAPFSKDNSI RLSAGGDI WVTREPYVSCDPSKCYQFALGQGTTL
 DNKHSNGTI HDRI PHRTLLMNLGVPFHLGKQVCI AWSSSSCHDGKAWLHVCVTGDDRNATASFI YNGM
 LIDSI VWSQNI LRTQSEECVCI NGTCTVVMTDGSASGRADTRVLF I REGKI I HI SPLSGSAQHI EECSC
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 (A/chi cken/Korea/LPM43/2005(H3N2))]
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 TTI EKEI YPRVLEYRNWWSKQPCQI TGFAPFSKDNSI RLSAGGDI WVTREPYVSCDPSKCYQFALGQGTTL
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 duck/ALB/627/1979(H3N2))]
 MNPNQKI I TI GSVALTI ATVCLLMQI AI LATTVTLHFKONECSI PVNNQVVPCEPI I I ERNI TEI VYLN
 TTI EKEI CPKVVDRNWSKQPCQI TGFAPFSKDNSI RLSAGGDI WVTREPYVSCDPSKCYQFALGQGTTL

DNKHSNGTI HDRI PHRTLLMNLGVPFHLGKQVCI AWSSSSCHDGKAWLHVCTGDDRNATASFI YDGM
 LVDSI GSWSONI LRTQSECEVCI NGCTVVMTDGSASGKADTRI LFI KEGKI VHI SPLSGSAQHI EECSC
 YPRYPDVRCVCRDNWKGSRNPVI DI NMEDYSI DSSYVCSGLVGDTPRNDSSSSNCRDPNNERGNPGVK
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 >gi |167996855|gb|ACA14278.1| neurami ni dase [Infl uenza A virus (A/aquati c
 bi rd/Korea/KN-2/2005(H3N2))]
 MNPNQI I TI GSVSLTI ATVCFLMQI AI LATTVTLHFKONECSI PSNNQVVPCEPI I I ERNI TEI VYLNN
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 DNKHSNGTI HDRTPHRTLLMNLGVPFHLGKQVCI AWSSSSCHDGKAWLHVCTGDDRNATASFI YNGM
 LVDSI GSWSONI LRTQSECEVCI NGCTVVMTDGSASGRADTRI LFI REGKI VHI SPLSGSAQHI EECSC
 YPRYPDVRCVCRDNWKGSRNPVI DI NMVDYSI DSSYVCSGLVGDTPRNDSSSSNCRDPNNERGNPGVK
 GWAFDNGNDVVMGRTI SKDSRSGYETFRVI GGWATANSKQVNRQVI VDNNNWSGYSI FSVEKSCVNR
 CFYVELI RGRPQETRVWWTNSI VVFCGTSYGTGSGWPDGANI NFMPI
 >gi |194404624|gb|ABF17977.1| neurami ni dase [Infl uenza A virus
 (A/turkey/Ontari o/31232/2005(H3N2))]
 MNPNQI I TI GSVSLI I ATI CFLMQI AI LVTTVTLHFKOHCNNSPNNQVMLCEPTI I ERNTTEI VYLTN
 TTI EKEI CPKLAEYRNWSKPQCCI TGFAPFSKDNSI RLSAGGDI WVTREPYVSCGSPKCYQFALGQGTTL
 NNGHSNDTVHDRTPYRLLMNLGVPFHLGTRQVCI AWSSSSCHDGKAWLHVCI TGDDKNATASFI YNGR
 LVDSI GSWKNI LRTQSECEVCI NGCTVVMTDGSASGKADTKI LFI EEGKI VHI STLSGSAQHVEECSC
 YPRYPDVRCVCRDNWKGSRNPVI VDI NVKDYSI VSSYVCSGLVGDTPRNDSSSSHCLDPNNEEGNGPVK
 GWAFDDGNDVVMGRTI SEKLRSGYETFKVI EGWSKPNKSLQTNROVI VERGNRSGYSI FSVEKSCVNR
 CFYVELI RGRKEETKVWWTNSI VVFCGTSYGTGSGWPDGADI NLMP
 >gi |138393046|gb|AB076949.1| neurami ni dase [Infl uenza A virus
 (A/mal i ard/Maryl and/615/2005(H3N2))]
 MNPNQI I TI SSVSLTI ATVCFLMQI AI LATTVTLHFKONECSI PSNNQVVPCEPI I I EKNI TEI VYLN
 S TTI EKEI CPELPEYRNWSKPQCCI TGFAPFSKDNSI RLSAGGDI WVTREPYVSCGSPKCYQFALGQGTTL
 NNKHSNGTI HDRI PHRTLLMNLGVPFHLGKQVCI AWSSSSCHDGKAWLHVCTGDDRNATASFI YDGM
 LVDSI GSWSONI LRTQSECEVCI NGCTVVMTDGSASGRADTRI LFI KEGKI I HI SPLSGSAQHI EECSC
 YPRYPDVRCVCRDNWKGSRNPVI I DI NMADYSI DSSYI CSGLVGDTPRNDSSSSNCRDPNNERGNPGVK
 GWAFDNGNDVVMGRTI SKDSRSGYETFRVI GGWTTANSKQVNRQVI VDNNNWSGYSI FSVEKSCVNR
 CFYVELI RGRPQETRVWWTNSI VVFCGTSYGTGSGWPDGANI NFMPI
 >gi |167996892|gb|ACA14296.1| neurami ni dase [Infl uenza A virus
 (A/chi cken/Korea/LPM44/2005(H3N2))]
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 N TI I EKEI YPRVLEAYRNWSKPQCCI TGFAPFSKDNSI RLSAGGDI WVTREPYVSCDPSKCYQFALGQGTTL
 DNKHSNGTI HDRI PHRTLLMNLGVPFHLGKQVCI AWSSSSCHDGKAWLHVCTGDDRNATASFI YNGM
 LI DSI VSWSONI LRTQSECEVCI NGCTVVMTDGSASGRADTRVLF I REGKI I HI SPLSGSAQHI EECSC
 YPRYPDVRCVCRDNWKGSRNPVI I DI NMADYSI GSSYVCSGLVGDTPRNDSSSSNCRDPNNERGNPGVK
 GWAFDDNDVVMGRTI SKDSRSGYETFRVI GGWTTANSKQVNRQVI VDNNNWSGYSI FSVEKSCVNR
 CFYVELI RGRPQETRVWWTNSI VVFCGTSYGTGSGWPDGANI NFMPI
 >gi |167996894|gb|ACA14297.1| neurami ni dase [Infl uenza A virus
 (A/duck/Korea/LPM56/2005(H3N2))]
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 DNKHSNGTI HDRI PHRTLLMNLGVPFHLGKQVCI AWSSSSCHDGKAWLHVCTGDDRNATASFI YNGM
 LI DSI VSWSONI LRTQSECEVCI NGCTVVMTDGSASGRADTRVLF I REGKI I HI SPLSGSAQHI EECSC
 YPRYPDVRCVCRDNWKGSRNPVI I DI NMADYSI GSSYVCSGLVGDTPRNDSSSSNCRDPNNERGNPGVK
 GWAFDDNDVVMGRTI SKDSRSGYETFRVI GGWTTANSKQVNRQVI VDNNNWSGYSI FSVEKSCVNR
 CFYVELI RGRPQETRVWWTNSI VVFCGTSYGTGSGWPDGANI NFMPI
 >gi |134048055|gb|AB052569.1| neurami ni dase [Infl uenza A virus
 (A/mal i ard/Maryl and/681/2005(H3N2))]
 MNPNQI I TI SSVSLTI ATVCFLMQI AI LATTVTLHFKONECSI PSNNQVVPCEPI I I EKNI TEI VYLN
 S TTI EKEI CPELPEYRNWSKPQCCI TGFAPFSKDNSI RLSAGGDI WVTREPYVSCGSPKCYQFALGQGTTL
 NNKHSNGTI HDRI PHRTLLMNLGVPFHLGKQVCI AWSSSSCHDGKAWLHVCTGDDRNATASFI YDGM
 LVDSI GSWSONI LRTQSECEVCI NGCTVVMTDGSASGRADTRI LFI KEGKI I HI SPLSGSAQHI EECSC
 YPRYPDVRCVCRDNWKGSRNPVI I DI NMADYSI DSSYI CSGLVGDTPRNDSSSSNCRDPNNERGNPGVK
 GWAFDNGNDVVMGRTI SKDSRSGYETFRVI GGWTTANSKQVNRQVI VDNNNWSGYSI FSVEKSCVNR
 CFYVELI RGRPQETRVWWTNSI VVFCGTSYGTGSGWPDGANI NFMPI
 >gi |134048093|gb|AB052591.1| neurami ni dase [Infl uenza A virus
 (A/mal i ard/Maryl and/631/2005(H3N2))]
 MNPNQI I TI SSVSLTI ATVCFLMQI AI LATTVTLHFKONECSI PSNNQVVPCEPI I I EKNI TEI VYLN
 S TTI EKEI CPELPEYRNWSKPQCCI TGFAPFSKDNSI RLSAGGDI WVTREPYVSCGSPKCYQFALGQGTTL
 NNKHSNGTI HDRI PHRTLLMNLGVPFHLGKQVCI AWSSSSCHDGKAWLHVCTGDDRNATASFI YDGM
 LVDSI GSWSONI LRTQSECEVCI NGCTVVMTDGSASGRADTRI LFI KEGKI I HI SPLSGSAQHI EECSC
 YPRYPDVRCVCRDNWKGSRNPVI I DI NMADYSI DSSYI CSGLVGDTPRNDSSSSNCRDPNNERGNPGVK
 GWAFDNGNDVVMGRTI SKDSRSGYETFRVI GGWTTANSKQVNRQVI VDNNNWSGYSI FSVEKSCVNR
 CFYVELI RGRPQETRVWWTNSI VVFCGTSYGTGSGWPDGANI NFMPI
 >gi |167996882|gb|ACA14291.1| neurami ni dase [Infl uenza A virus
 (A/duck/Korea/LPM23/2005(H3N2))]
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 N TI I EKEI YPRVLEAYRNWSKPQCCI TGFAPFSKDNSI RLSAGGDI WVTREPYVSCDPSKCYQFALGQGTTL
 DNKHSNGTI HDRI PHRTLLMNLGVPFHLGKQVCI AWSSSSCHDGKAWLHVCTGDDRNATASFI YNGM
 LI DSI VSWSONI LRTQSECEVCI NGCTVVMTDGSASGRADTRVLF I REGKI I HI SPLSGSAQHI EECSC
 YPRYPDVRCVCRDNWKGSRNPVI I DI NMADYSI GSSYVCSGLVGDTPRNDSSSSNCRDPNNERGNPGVK
 GWAFDDNDVVMGRTI SKDSRSGYETFRVI GGWTTANSKQVNRQVI VDNNNWSGYSI FSVEKSCVNR
 CFYVELI RGRPQETRVWWTNSI VVFCGTSYGTGSGWPDGANI NFMPI

>gi |167996896|gb|ACA14298.1| neurami ni dase [Influenza A virus (A/chi cken/Korea/LPM61/2005(H3N2))]
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TTI I EKEI HPRVLEYRNVSKPQCQI TGFAPFSKDNSI RLSAGGDI WVTREPYVSCDPKCYQFALGQGTTL
DNKHSNGTI HDRI PHRTLLMNLGVPFHLGKQVCI AWSSSSCHDGKAWLHVCTGDDRNATASFI YNGM
LIDSI VSWSONI LRTQSEECVCI NGTCTVMTDGSASGRADTRVLI REGKI I HI SPLSGSAQHI EECS
YPRYPNVRCVCRDNWKGSRPVI DI NMADYSI GSSYVCSGLVGDTPRNDSSSSSNCKDPNNEKGNPGVK
GWAFDNENDVVMGRTI SKDSRSGYETFRVI GGWTTANSKSQVNRQVI VDNNNWSGYSI FSVESKSCVNR
CFYVELI RGRPQETRVVWTSNSI VVFCGTSGYGTGSWPDGANI NFMP
>gi |138393241|gb|AB076960.1| neurami ni dase [Influenza A virus (A/mal I ard/Maryl and/710/2005(H3N2))]
MNPNOKI I TI SSVSLTI ATVCFLMQI AI LATTVTLHFKQNECSI PSNNQVVPCEPI I I EKNI TEI VYLNS
TTI EKEI CPELPEYRNVSKPQCQI TGFAPFSKDNSI RLSAGGDI WVTREPYVSCGPKCYQFALGQGTTL
NNKHSNGTI HDRI PHRTLLMNLGVPFHLGKQVCI AWSSSSCHDGKAWLHVCTGDDRNATASFI YDGM
LVDSI GSWSONI LRTQSEECVCI NGTCTVMTDGSASGRADTRVLI LFI REGKI I HI SPLSGSAQHI EECS
YPRYPDVRCVCRDNWKGSRPVI DI NMADYSI DSSYI CGLVGDTPRNDSSSSSNCRDPNNERGNPGVK
GWAFDNGNDVVMGRTI SKDSRSGYETFRVI GGWTTANSKSQVNRQVI VDNNNWSGYSI FSVGKSCI NR
CFYVELI RGRPQETRVVWTSNSI VVFCGTSGYGTGSWPDGANI NFMP
>gi |167859528|gb|ACA04723.1| neurami ni dase [Influenza A virus (A/duck/Eastern
Chi na/03/2005(H3N2))]
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TTI EKELCPKI SEYRDWSKPQCQI TGFAPFSKDNSI RLSAGGDI WVTREPYVSCDPKCYQFALGQGTTL
DNKHSNGTI HDRI PHRTLLMNLGVPFHLGKQVCI AWSSSSCHDGKAWLHVCTGDDRNATASFI YDGM
LVDSI GSWSONI LRTQSEECVCI NGTCTVMTDGSASGRADTRVLI LFI REGKI I HI SPLSGSAQHI EECS
YPRYPDVRCVCRDNWKGSRPVI DI NMADYSI GSSYVCSGLVGDTPRNDSSSSSNCRDPNNERGNPGVK
GWAFDNGNDVVMGRTI SKDSRSGYETFRVI GGWTTANSKSQVNRQVI VDNNNWSGYSI FSVGKSCI NR
CFYVELI RGRPQETRVVWTSNSI VVFCGTSGYGTGSWPDGANI NFMP
>gi |193877761|gb|ACF25546.1| neurami ni dase [Influenza A virus (A/turkey/MN/366767/2005(H3N2))]
MNPNOKI I TI GSVSLTI TATI CFLMQI ATLVTTLHFKQNECSI PSNNQVVPCEPI I I ERNTTEI VYLNN
TTI EKEI CPKLAERYNVSKPQCQI TGFAPFSKDNSI RLSAGGDI WVTREPYVSCDPKCYQFALGQGTTL
NNGHSNDTVHTRTPYRLLMNLGVPFHLGTRQVCI AWSSSSCHDGKAWLHVCI TGDDKNATASFI YNGR
LVDSI GSWSONI LRTQSEECVCI NGTCTVMTDGSASGRADTRVLI LFI REGKI I HI SPLSGSAQHI EECS
YPRYPGVRCVCRDNWKGSRPVI VDI NVKDYSI VSSYVCSGLVGDTPRKNDSFSSSHCLDPNNEEGGHGK
GWAFDDGNDVVMGRTI SEKLRSGYETFKVI EGWSRPNKSLQTNROVI VERGNRSGYSI FSVGKSCI NR
CFYVELI RGRPQETRVVWTSNSI VVFCGTSGYGTGSWPDGANI NFMP
>gi |134048074|gb|AB052580.1| neurami ni dase [Influenza A virus (A/mal I ard/Maryl and/691/2005(H3N2))]
MNPNOKI I TI SSVSLTI ATVCFLMQI AI LATTVTLHFKQNECSI PSNNQVVPCEPI I I EKNI TEI VYLNS
TTI EKEI CPELPEYRNVSKPQCQI TGFAPFSKDNSI RLSAGGDI WVTREPYVSCGPKCYQFALGQGTTL
NNKHSNGTI HDRI PHRTLLMNLGVPFHLGKQVCI AWSSSSCHDGKAWLHVCTGDDRNATASFI YDGM
LVDSI GSWSONI LRTQSEECVCI NGTCTVMTDGSASGRADTRVLI LFI REGKI I HI SPLSGSAQHI EECS
YPRYPDVRCVCRDNWKGSRPVI DI NMADYSI DSSYI CGLVGDTPRNDSSSSSNCRDPNNERGNPGVK
GWAFDNGNDVVMGRTI SKDSRSGYETFRVI GGWTTANSKSQVNRQVI VDNNNWSGYSI FSVGKSCI NR
CFYVELI RGRPQETRVVWTSNSI VVFCGTSGYGTGSWPDGANI NFMP
>gi |189313106|gb|ACD88651.1| neurami ni dase [Influenza A virus (A/turkey/NC/353568/2005(H3N2))]
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TTI EKEI CPKLAERYNVSKPQCQI TGFAPFSKDNSI RLSAGGDI WVTREPYVSCDPKCYQFALGQGTTL
NNGHSNDTVHTRTPYRLLMNLGVPFHLGTRQVCI AWSSSSCHDGKAWLHVCI TGDDKNATASFI YNGR
LVDSI GSWSONI LRTQSEECVCI NGTCTVMTDGSASGRADTRVLI LFI REGKI I HI SPLSGSAQHI EECS
YPRYPGVRCVCRDNWKGSRPVI VDI NVKDYSI VSSYVCSGLVGDTPRKNDSFSSSHCLDPNNEEGGHGK
GWAFDDGNDVVMGRTI SEKLRSGYETFKVI EGWSKPNKSLQTNROVI VERGNRSGYSI FSVGKSCI NR
CFYVELI RGRPQETRVVWTSNSI VVFCGTSGYGTGSWPDGANI NFMP
>gi |167996880|gb|ACA14290.1| neurami ni dase [Influenza A virus (A/duck/Korea/LPM22/2005(H3N2))]
MNPNOKI I TI GAVSLTI ATI CFLMQI AI LTTTTLHFKQNECSI PSNNQI VPCEPI I I ERNI TEI VYLNN
TTI I EKEI YPRVLEYRNVSKPQCQI TGFAPFSKDNSI RLSAGGDI WVTREPYVSCDPKCYQFALGQGTTL
DNKHSNGTI HDRI PHRTLLMNLGVPFHLGKQVCI AWSSSSCHDGKAWLHVCTGDDRNATASFI YNGM
LIDSI VSWSONI LRTQSEECVCI NGTCTVMTDGSASGRADTRVLI REGKI I HI SPLSGSAQHI EECS
YPRYPNVRCVCRDNWKGSRPVI DI NMADYSI GSSYVCSGLVGDTPRNDSSSSSNCKDPNNEKGNPGVK
GWAFDNENDVVMGRTI SKDSRSGYETFRVI GGWTTANSKSQVNRQVI VDNNNWSGYSI FSVESKSCVNR
CFYVELI RGRPQETRVVWTSNSI VVFCGTSGYGTGSWPDGANI NFMP
>gi |155016310|gb|ABS89401.1| neurami ni dase [Influenza A virus (A/mal I ard. Maryl and/708/2005(H3N2))]
MNPNOKI I TI SSVSLTI ATVCFLMQI AI LATTVTLHFKQNECSI PSNNQVVPCEPI I I EKNI TEI VHLNS
TTI EKEI CPELPEYRNVSKPQCQI TGFAPFSKDNSI RLSAGGDI WVTREPYVSCGPKCYQFALGQGTTL
NNKHSNGTI HDRI PHRTLLMNLGVPFHLGKQVCI AWSSSSCHDGKAWLHVCTGDDRNATASFI YDGM
LVDSI GSWSONI LRTQSEECVCI NGTCTVMTDGSASGRADTRVLI LFI REGKI I HI SPLSGSAQHI EECS
YPRYPDVRCVCRDNWKGSRPVI DI NMADYSI DSSYI CGLVGDTPRNDSSSSSNCRDPNNERGNPGVK
GWAFDNGNDVVMGRTI SKDSRSGYETFRVI GGWTTANSKSQVNRQVI VDNNNWSGYSI FSVGKSCI NR
CFYVELI RGRPQETRVVWTSNSI VVFCGTSGYGTGSWPDGANI NFMP
>gi |149930114|gb|ABR37487.1| neurami ni dase [Influenza A virus (A/mal I ard/Maryl and/712/2005(H3N2))]
MNPNOKI I TI SSVSLTI ATVCFLMQI AI LATTVTLHFKQNECSI PSNNQVVPCEPI I I EKNI TEI VYLNS
TTI EKEI CPELPEYRNVSKPQCQI TGFAPFSKDNSI RLSAGGDI WVTREPYVSCGPKCYQFALGQGTTL
NNKHSNGTI HDRI PHRTLLMNLGVPFHLGKQVCI AWSSSSCHDGKAWLHVCTGDDRNATASFI YDGM

LVDSI GSWSONI LRTQSEECVCI NGTCTVVMTDGSASGRADTRI LFI KEGKI I HI SPLSGSAQHI EECSC
 YPRYPDVRVCVRDNWKGNSRPI I DI NMADYSI DSSYI CSGLVGDTPRNDDSSSSSNCRDPNNERGNPGVK
 GWAFDNGNDVVMGRTI SKDSRSGYETFRVI GGWTTANSKSOVNRQVI VDNNNWSGYSYGI FSVEGKSCI NR
 CFYVELI RGRPQETRVWVWTSNSI VVFCGTSYGTGSGWPDGANI NFMPPI
 >gi |167996898|gb|ACA14299.1| neurami ni dase [Influenza A virus
 (A/duck/Korea/LPM66/2006(H3N2))]
 MNPNQKI I TI GAVSLTI ATI CFLMQI AI LTTTTLHFKONECSI PSNNQI VPCEPI I I ERNI TEI VYLLN
 TI I EKEI HPRVLEYRNWWSKPOCOI TGFAPFSKDNSI RLSAGGDI WVTREPYVSCDPKCYQFALGQGTTL
 DNKHSNGTI HDRI PHRTLLMNLGVPFHLGKQVCI AWSSSSCHDGKAWLHVCVTGDDRNATASFI YNGM
 LI DSI VSWSONI LRTQSEECVCI NGTCTVVMTDGSASGRADTRVLFVKEGKI I HI SPLSGSAQHI EECSC
 YPRYPNVRVCVRDNWKGNSRPI I DI NMADYSI GSSYVCSGLVGDTPRNDSSSSSNCKDPNNERGNPGVK
 GWAFDNGNDVVMGRTI SKDSRSGYETFRVI GGWTTANSKSOVNRQVI VDNNNWSGYSYGI FSVEGKSCVNR
 CFYVELI RGRPQETRVWVWTSNSI VVFCGTSYGTGSGWPDGANI NFMPPI
 >gi |167996906|gb|ACA14303.1| neurami ni dase [Influenza A virus
 (A/duck/Korea/LPM91/2006(H3N2))]
 MNPNQKI I TI GAVSLTI ATI CFLMQI AI LTTTTLHFKONECSI PSNNQI VPCEPI I I EKNI TEI VYLLN
 TI I EKEI CPRVQYRNWWSKPOCOI TGFAPFSKDNSI RLSAGGDI WVTREPYVSCDPKCYQFALGQGTTL
 DNKHSNGTI HDRI PHRTLLMNLGVPFHLGKQVCI AWSSSSCHDGKAWLHVCVTGDDRNATASFI YNGM
 LVDSI VSWSONI LRTQSEECVCI NGTCTVVMTDGSASGRADTRI LFI REGKI I HVSPLSGSAQHI EECSC
 YPRYPNVRVCVRDNWKGNSRPI I DI NMADYSI GSSYVCSGLVGDTPRNDSSSSSNCKDPNNERGNPGVK
 GWAFDNGNDVVMGRTI SKDSRSGYETFRVI GGWTTANSKSOVNRQVI VDNNNWSGYSYGI FSVEGKSCVNR
 CFYVELI RGRPQETRVWVWTSNSI VVFCGTSYGTGSGWPDGANI NFMPPI
 >gi |167859450|gb|ACA04684.1| neurami ni dase [Influenza A virus (A/duck/Eastern
 Chi na/142/2006(H3N2))]
 MNPNQKI I TI GAVSLTI ATI CFLMQI AI LATTVTLHFKONECSI PSNNQVVPCEPI I I VERNI TEI VYLLN
 TTI EKELCPKVSEYRDWSKPOCOI TGFAPFSKDNSI RLSAGGDI WVTREPYVSCDPKCYQFALGQGTTL
 DNKHSNGTI HDRI PHRTLLMNLGVPFHLGKQVCI AWSSSSCHDGKAWLHVCVTGDDRNATASFI YNGM
 LVDSI GSWSONI LRTQSEECVCI NGTCTVVMTDGSASGRADTRI LFI VKEGKI VHI SPLSGSAQHI EECSC
 YPRYPDVRVCVRDNWKGNSRPI I DI NMADYSI GSSYVCSGLVGDTPRNDSSSSSNCKDPNNERGNPGVK
 GWAFDNGNDVVMGRTI SKDSRSGYETFRVI GGWTTANSKSOVNRQVI VDNNNWSGYSYGI FSVEGKSCI NR
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 Chi na/35/2006(H3N2))]
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 TTI EKELCPKVSEYRDWSKPOCOI AGFAPFSKDNSI RLSAGGDI WVTREPYVSCDPKCYQFALGQGTTL
 NNKHSNGTI HDRI PHRTLLMNLGVPFHLGKQVCI AWSSSSCHVGKAWLHVCVTGDDRNATASFI YNGM
 LVDSI GSWSONI LRTQSEECVCI NGTCTVVMTDGSASGRADTRI LFI VKEGKI VHI SPLSGSAQHI EECSC
 YPRYPDVRVCVRDNWKGNSRPI I DI NMADYSI GSSYVCSGLVGDTPRNDSSSSSNCKDPNNERGNPGVK
 GWAFDNGNDVVMGRTI SKDSRSGYETFRVI GGWTTANSKSOVNRQVI VDNNNWSGYSYGI FSVEGKSCI NR
 CFYVELI RRRPQEARVWVWTSNSI VVFCGTSYGTGSGWPDGANI NFMPPI
 >gi |167859510|gb|ACA04714.1| neurami ni dase [Influenza A virus (A/duck/Eastern
 Chi na/23/2006(H3N2))]
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 TTI EKELCPKI SEYRDWSKPOCOI TGFAPFSKDNSI RLSAGGDI WVTREPYVSCDPKCYQFALGQGTTL
 DNKHSNGTI HDRI PHRTLLMNLGVPFHLGKQVCI AWSSSSCHDGKAWLHVCVTGDDRNATASFI YNGM
 LVDSI GSWSONI LRTQSEECVCI NGTCTVVMTDGSASGRADTRI LFI VKEGKI VHI SPLSGSAQHI EECSC
 YPRYPDVRVCVRDNWKGNSRPI I DI NMADYSI GSSYVCSGLVGDTPRNDSSSSSNCKDPNNERGNPGVK
 GWAFDNGNDVVMGRTI SKDSRSGYETFRVI GGWTTANSKSOVNRQVI VDNNNWSGYSYGI FSVEGKSCI NR
 CFYVELI RGRPQEARVWVWTSNSI VVFCGTSYGTGSGWPDGANI NFMPPI
 >gi |167859514|gb|ACA04716.1| neurami ni dase [Influenza A virus (A/duck/Eastern
 Chi na/42/2006(H3N2))]
 MNPNQKI I TI GAVSLTI ATI CFLMQI AI LATTVTLHFKONECSI PSNNQVVPCEPI I I ERNI TEI VYLLN
 TTI EKELCPKI SEYRDWSKPOCOI TGFAPFSKDNSI RLSAGGDI WVTREPYVSCDPKCYQFALGQGTTL
 DNKHSNGTI HDRI PHRTLLMNLGVPFHLGKQVCI AWSSSSCHDGKAWLHVCVTGDDRNATASFI YNGM
 LVDSI GSWSONI LRTQSEECVCI NGTCTVVMTDGSASGRADTRI LFI VKEGKI VHI SPLSGSAQHI EECSC
 YPRYPDVRVCVRDNWKGNSRPI I DI NMADYSI GSSYVCSGLVGDTPRNDSSSSSNCKDPNNERGNPGVK
 GWAFDNGNDVVMGRTI SKDSRSGYETFRVI GGRTMANSKSOVNRQVI VDNNNWSGYSYGI FSVEGKSCI NR
 CFYVELI RGRPQEARVWVWTSNSI VVFCGTSYGTGSGWPDGANI NFMPPI
 >gi |167859504|gb|ACA04711.1| neurami ni dase [Influenza A virus (A/duck/Eastern
 Chi na/02/2006(H3N2))]
 MNPNQKI I TI GAVSLTI ATI CFLMQI AI LATTVTLHFKONECSI PSNNQVVPCEPI I I ERNI TEI VYLLN
 TTI EKELCPKI SEYRDWSKPOCOI TGFAPFSKDNSI RLSAGGDI WVTREPYVSCDPKCYQFALGQGTTL
 DNKHSNGTI HDRI PHRTLLMNLGVPFHLGKQVCI AWSSSSCHDGKAWLHVCVTGDDRNATASFI YNGM
 LVDSI GSWSONI LRTQSEECVCI NGTCTVVMTDGSASGRADTRI LFI VKEGKI VHI SPLSGSAQHI EECSC
 YPRYPDVRVCVRDNWKGNSRPI I DI NMADYSI GSSYVCSGLVGDTPRNDSSSSSNCKDPNNERGNPGVK
 GWAFDNGNDVVMGRTI SKDSRSGYETFRVI GGWTTANSKSOVNRQVI VDNNNWSGYSYGI FSVEGRSCI NR
 CFYVELI RGRPQEARVWVWTSNSI VVFCGTSYGTGSGWPDGANI NFMPPI
 >gi |167859512|gb|ACA04715.1| neurami ni dase [Influenza A virus (A/duck/Eastern
 Chi na/31/2006(H3N2))]
 MNPNQKI I TI GAVSLTI ATI CFLMQI AI LATTVTLHFKONECSI PSNNQVVPCEPI I I VERNI TEI VYLLN
 TTI EKELCPKI SEYRDWSKPOCOI TGFAPFSKDNSI RLSAGGDI WVTREPYVSCDPKCYQFALGQGTTL
 DNKHSNGTI HDRI PHRTLLMNLGVPFHLGKQVCI AWSSSSCHDGKAWLHVCVTGDDRNATASFI YNGM
 LVDSI GSWSONI LRTQSEECVCI NGTCTVVMTDGSASGRADTRI LFI VKEGKI VHI SPLSGSAQHI EECSC
 YPRYPDVRVCVRDNWKGNSRPI I DI NMADYSI GSSYVCSGLVGDTPRNDSSSSSNCKDPNNERGNPGVK
 GWAFDNGNDVVMGRTI SKDSRSGYETFRVI GGWTTANSKSOVNRQVI VDNNNWSGYSYGI FSVEGKSCI NR
 CFYVELI RGRPQEARVWVWTSNSI VVFCGTSYGTGSGWPDGANI NFMPPI

>gi |167859516|gb|ACA04717.1| neurami ni dase [Influenza A virus (A/duck/Eastern Chi na/53/2006(H3N2))]
MNPNOKI I TI GSVSLTI ATI CFLMQI AI LATTVTLHFQNECSI PSNNQVVPCEPI I VERNI TEI VYLLN
TTI EKELCPKI SEYRDWSKPQCCI TGFAPFSKDNSI RLSAGGDI WVTREPYVSCSPDKCYQFALGQGTTL
DNKHSNGTI HDRI PHRTLLMNLGVPFHLGKQVCI AWSSSSYHDGKAWLHVCVTGDDRNAAASFI YGGM
LVDSI GSWSONI LRTQSEECVCI NGTCTVVMTDGSASGRADTRI LFKVKEGKI VHI SPLSGSAQHI EECS
YLRYPDVRCVCRDNWKGSRPI I DI NMADYSI GSSYVCSGLVGDTPRNDSSSSNSNCRDPNNERGNPGVK
GWAFDYGNDVVMGRTI SKDSRSGYETFRVI GGWTI ANSKSQVNROVI VDNNSWGSYSGI FSVEGKSCI NR
CFYVELI RGRPQEARVWVTSNSI VVFCGTSPTYGTGSWPDGANI NFMP I

>gi |167859518|gb|ACA04718.1| neurami ni dase [Influenza A virus (A/duck/Eastern Chi na/60/2006(H3N2))]
MNPNOKI I TI GSVSLTI ATI CFLMQI AI LATTVTLHFQNECSI PSNNQVVPCEPI I VERNI TEI VYLLN
TTI EKELCPKI SEYRDWSKPQCCI TGFAPFSKDNSI RLSAGGDI WVTREPYVSCSPDKCYQFALGQGTTL
DNKHSNGTI HDRI PHRTLLMNLGVPFHLGKQVCI AWSSSSCHDGKAWLHVCVTGDDRNATASFI YGGM
LVDSI GSWSONI LRTQSEECVCI NGTCTVVMTDGSASGRADTRI LFKVKEGKI VHI SPLSGSAQHI EECS
YLRYPDVRCVCRDNWKGSRPI I DI NMADYSI GSSYVCSGLVGDTPRNDSSSSNSNCRDPNNERGNPGVK
GWAFDYGNDVVMGRTI SKDSRSGYETFRVI GGWTI ANSKSQVNROVI VDNNSWGSYSGI FSVEGKSCI NR
CFYVELI RGRPQEARVWVTSNSI VVFCGTSPTYGTGSWPDGANI NFMP I

>gi |167859520|gb|ACA04719.1| neurami ni dase [Influenza A virus (A/duck/Eastern Chi na/63/2006(H3N2))]
MNPNOKI I TI GSVSLTI ATI CFLMQI AI LATTVTLHFQNECSI PSNNQVVPCEPI I I ERNI TEI VYLLN
TTI EKELCPKVSEYRDWSKPQCCI TGFAPFSKDNSI RLSAGGDI WVTREPYVSCSPDKCYQFALGQGTTL
DNKHSNGTI HDRI PHRTLLMNLGVPFHLGKQVCI AWSSSSCHDGKAWLHVCVTGDDRNATASFI YGGM
LVDSI GSWSONI LRTQSEECVCI NGTCTVVMTDGSASGRADTRI LFKVKEGKI VHI SPLSGSAQHI EECS
YLRYPDVRCVCRDNWKGSRPI I DI NMADYSI GSSYVCSGLVGDTPRNDSSSSNSNCRDPNNERGNPGVK
GWAFDYGNDVVMGRTI SKDSRSGYETFRVI GGWTMANSKQVNROVI VDNNSWGSYSGI FSVEGKSCI NR
CFYVELI RGRPQEARVWVTSNSI VVFCGTSPTYGTGSWPDGANI NFMP I

>gi |167996900|gb|ACA14300.1| neurami ni dase [Influenza A virus (A/chi cken/Korea/LPM67/2006(H3N2))]
MNPNOKI I TI GAVSLTI ATI CFLMQI AI LTTTTLHFQNECSI PSNNQI VPCEPI I I ERNI TEI VYLLN
TTI I EKEI HPRVLEARNWSKPQCCI TGFAPFSKDNSI RLSAGGDI WVTREPYVSCSPDKCYQFALGQGTTL
DNKHSNGTI HDRI PHRTLLMNLGVPFHLGKQVCI AWSSSSCHDGKAWLHVCVTGDDRNATASFI YNGM
LI DSI VSGSONI LRTQSEECVCI NGTCTVVMTDGSXSGRADXRVLFXEKGKI I XI SPLSGSAQHI EECS
YLRYPDVRCVCRDNWKGSRPI I DI NMADYSI GSSYVCSGLVGDTPRNDSSSSNSNCRDPNNERGNPGVK
GWAFDNDVVMGRTI XKDSRSGYETFRVI GGWTANSKQVNROVI VDNNSWGSYSGI FSVESKSCVNR
CFYVELI RGRPQEARVWVTSNSI VVFCGTSPTYGTGSWPDGANI NFMP I

>gi |167996904|gb|ACA14302.1| neurami ni dase [Influenza A virus (A/chi cken/Korea/LPM88/2006(H3N2))]
MNPNOKI I TI GAVSLTI ATI CFLMQI AI LTTTTLHFQNECSI PSNNQI VPCEPI I I ERNI TEI VYLLN
TTI I EKEI HPRVLEARNWSKPQCCI TGFAPFSKDNSI RLSAGGDI WVTREPYVSCSPDKCYQFALGQGTTL
DNKHSNGTI HDRI PHRTLLMNLGVPFHLGKQVCI AWSSSSCHDGKAWLHVCVTGDDRNATASFI YNGM
LI DSI VSGSONI LRTQSEECVCI NGTCTVVMTDGSASGRADTRVLF I REGKI I HI SPLSGSAQHI EECS
YLRYPDVRCVCRDNWKGSRPI I DI NMADYSI GSSYVCSGLVGDTPRNDSSSSNSNCRDPNNERGNPGVK
GWAFDNDVVMGRTI SKDSRSGYETFRVI GGWTANSKQVNROVI VDNNSWGSYSGI FSVESKSCVNR
CFYVELI RGRPQEARVWVTSNSI VVFCGTSPTYGTGSWPDGANI NFMP I

>gi |167996908|gb|ACA14304.1| neurami ni dase [Influenza A virus (A/duck/Korea/LPM92/2006(H3N2))]
MNPNOKI I TI GAVSLTI ATI CFLMQI AI LTTTTLHFQNECSI PSNNQI VPCEPI I I EKNI TEI VYLLN
TTI I EKEI CPRVQYARNWSKPQCCI TGFAPFSKDNSI RLSAGGDI WVTREPYVSCSPDKCYQFALGQGTTL
DNKHSNGTI HDRI PHRTLLMNLGVPFHLGKQVCI AWSSSSCHDGKAWLHVCVTGDDRNATASFI YNGM
LVDSI VSWSONI LRTQSEECVCI NGTCTVVMTDGSASGRADTRI LFKVKEGKI I HI SPLSGSAQHI EECS
YLRYPDVRCVCRDNWKGSRPI I DI NMADYSI GSSYVCSGLVGDTPRNDSSSSNSNCRDPNNERGNPGVK
GWAFDNDVVMGRTI SKDSRSGYETFRVI GGWTANSKQVNROVI VDNNSWGSYSGI FSVEGKSCVNR
CFYVELI RGRPQEARVWVTSNSI VVFCGTSPTYGTGSWPDGANI NFMP I

>gi |167859508|gb|ACA04713.1| neurami ni dase [Influenza A virus (A/duck/Eastern Chi na/21/2006(H3N2))]
MNPNOKI I TTGVSLLTI ATI CFLMQI AI LATTVTLHFQNECSI PSNNQVVPCEPI I I ERNI TEI VYLLN
TTI EKELCPKVSEYRDWSKPQCCI TGFAPFSKDNSI RLSAGGDI WVTREPYVSCSPDKCYQFALGQGTTL
DNKHSNGTI HDRI PHRTLLMNLGVPFHLGKQVCI AWSSSSCHDGKAWLHVCVTGDDRNATASFI YGGM
LVDSI GSWSONI LRTQSEECVCI NGTCTVVMTDGSASGRADTRI LFKVKEGKI VHI SPLSGSAQHI EECS
YLRYPDVRCVCRDNWKGSRPI I DI NMADYSI GSSYVCSGLVGDTPRNDSSSSNSNCRDPNNERGNPGVK
GWAFDYGNDVVMGRTI SKDSRSGYETFRVI GGWTMANSKQVNROVI VDNNSWGSYSGI FSVEGKSCI NR
CFYVELI RGRPQEARVWVTSNSI VVFCGTSPTYGTGSWPDGANI NFMP I

>gi |167859506|gb|ACA04712.1| neurami ni dase [Influenza A virus (A/duck/Eastern Chi na/04/2006(H3N2))]
MNPNOKI I TI GSVSLTI ATI CFLMQI AI LATTVTLHFQNECSI PSNNQVVPCEPI I VERNI TEI VYLLN
TTI EKELCPKI SEYRDWSKPQCCI TGFAPFSKDNSI RLSAGGDI WVTREPYVSCSPDKCYQFALGQGTTL
DNKHSNGTI HDRI PHRTLLMNLGVPFHLGKQVCI AWSSSSCHDGKAWLHVCVTGDDRNATASFI YGGM
LVDSI GSWSONI LRTQSEECVCI NGTCTVVMTDGSASGRADTRI LFKVKEGKI VHI SPLSGSAQHI EECS
YLRYPDVRCVCRDNWKGSRPI I DI NMADYSI GSSYVCSGLVGDTPRNDSSSSNSNCRDPNNERGNPGVK
GWAFDYGNDVVMGRTI SKDSRSGYETFRVI GGWTI ANSKSQVNROVI VDNNSWGSYSGI FSVEGKSCI NR
CFYVELI RGRPQEARVWVTSNSI VVFCGTSPTYGTGSWPDGANI NFMP I

>gi |167859534|gb|ACA04726.1| neurami ni dase [Influenza A virus (A/duck/Eastern Chi na/62/2006(H3N2))]
MNPNOKI I TI GSVSLTI ATI CFLMQI AI LATTVTLHFQNECSI PSSNQVVPCEPI I VERNI TEI VYLLN
TTI EKELCPKVSEYRDWSKPQCCI TGFAPFSKDNSI RLSAGGDI WVTREPYVSCSPDKCYQFALGQGTAL
DNKHSNGTI HDRI PHRTLLMNLGVPFHLGKQVCI AWSSSSCHDGKAWLHVCVTGDDRNATASFI YGGM

LVDSI GSWSONI PRTOESECVC I NGTCTVVM TDGSASGRADTRI LFKVKEGKI VHI SPLSGSAQHI EECSC YPRYPDVRVCVRDNWKGSRNP I DI NMADYSI GSSYVCSGLVGDTPRNDSSSSSNCRDPNNERGNPGVK GWAFDYGNDVVMGRTI SKDSRSYETFRVI SKWTMANSKSOVNRHVI VDNNSWGSYSGI FSVEGKSCI NR CFYVELI RGRPQEARVWVTSNSI VVFCGTSYGTGSGWPDGANI NFMP I

>gi |167996902|gb|ACA14301.1| neurami ni dase [Influenza A virus (A/duck/Korea/LPM86/2006(H3N2))]
MNPNQI I TI GAVSLTI AT I CFLMQI AI LTTT VTLHFKONECSI PSNNQI VPCEPI I I EKNI TEI VYLNNT I I EKEI CPRVQYRNWWSKPOCOI TGFAPFSKDNSI RLSAGGDI WVTREPYVSCDPSKCYQFALGQGTLL DNKHSNGTI HDRI PHRTLLMNLGVPFHLGKQVCI AWSSSSCHDGKAWLHVCVTGDDRNATASFI YNGM LVDSI VSWSONI LRTQESECVC I NGTCTVVM TDGSASGRADTRI LFI REGKI I HVSPLSGSAQHI EECSC YPRYPNVRVCVRDNWKGSRNPVI DI NMADYSI GSSYVCSGLVGDTPRNDSSSSSNCKDPNNERGNPGVK GWAFDNGNDVVMGRTI SKDSRSYETFRVI GGWATANSKSOVNRQVI VDNNSWGSYSGI FSVEGKSCVNR CFYVELI RGRPQETRVWVTSNSI VVFCGTSYGTGSGWPDGANI NFMP I

>gi |167996853|gb|ACA14277.1| neurami ni dase [Influenza A virus (A/aquatic bird/Korea/JN-2/2006(H3N2))]
MNPNQI I AI GS VSLTI AT V CFLMQI AI LATT VTLHFKONECNI PSNNQVVPCEPI I I ERNI TEVVYLNNT TTI EKEI CPVVLEYRNWWSKPOCOI TGFAPFSKDNSI RLSAGGDI WVTREPYVSCDPSKCYQFALGQGTLL DNKHSNGTI HDRI PHRTLLMNLGVPFHLGKQVCI AWSSSSCHDGKAWLHVCVTGDDRNATASFI YNGM LVDSI GSWSRNI LRTQESECVC I NGTCTVVM TDGSASGRADTRI LFI REGKI VHI SPLSGSAQHI EECSC YPRYPDVRVCVRDNWKGSRNPVI DI NMADYSI DSSYVCSGLVGDTPRNDSSSSSNCRDPNNERGNPGVK GWAFDNGNDVVMGRTI SKDSRSYETFRVI GGWTTANSKLVNRQVI VDNNSWGSYSGI FSVEGKSCVNR CFYVELI RGRPQETRVWVTSNSI VV F

H5N1

>gi |39840718|emb|CAC95053.1| neurami ni dase [Influenza A virus (A/chicken/Scotland/59(H5N1))]
MNPNQI I TI GSI CMI VGI I SLI LQI GNI I SI VVSHSI QTGNQNOPEI CNQSI I TYENNTWVNQTYVNI S NTNFLVTEQALAPVALAGNSSLCP I SGWAI YSKDNGI RI GSKGDV FVI REPFI SCSHLECRTEFFLTQGALL NDKHSNGTVKDRSPYRTLMSCPI GESPSYNSRFESVAWSASACHDGI GWLTI GI SGPDNGAVAVLK YNG I I TDTI KSWRNNI LRTQESECACMNGSCFTI MTDGSPNGOASYKI FK I EKGKVVKSVELNAPNYHYEECS CYPDAGEI MCVCRDNW HGSNRPWVVSFNQNL EYQI GYI CSGVFGDNPRPNDGAGSCGPVSPNGAYGVKGF S FKYGNGVWI GRKTSTSSRS GFEMI WDPNGWTE TDSSFSVKODI VAI TDWSGYSGSFVQHP ELTGLDCMRP CFWVELI RGRPKENTI WTS GSSI SFCGVNSDTVGSWPDGAELPFTI DK

>gi |115279319|gb|ABI85109.1| neurami ni dase [Influenza A virus (A/chicken/Scotland/1959(H5N1))]
MNPNQI I TI GSI CMI VGI I SLI LQI GNI I SI VVSHSI QTGNQNOPEI CNQSI I TYENNTWVNQTYVNI S NTNFLVTEQALAPVALAGNSSLCP I SGWAI YSKDNGI RI GSKGDV FVI REPFI SCSHLECRTEFFLTQGALL NDKHSNGTVKDRSPYRTLMSCPI GESPSYNSRFESVAWSASACHDGI GWLTI GI SGPDNGAVAVLK YNG I I TDTI KSWRNNI LRTQESECACMNGSCFTI MTDGSPNGOASYKI FK I EKGKVVKSVELNAPNYHYEECS CYPDAGEI MCVCRDNW HGSNRPWVVSFNQNL EYQI GYI CSGVFGDNPRPNDGAGSCGPVSPNGAYGVKGF S FKYGNGVWI GRKTSTSSRS GFEMI WDPNGWTE TDSSFSVKODI VAI TDWSGYSGSFVQHP ELTGLDCMRP CFWVELI RGRPKENTI WTS GSSI SFCGVNSDTVGSWPDGAELPFTI DK

>gi |5805285|gb|AAD51926.1|AF144304_1 neurami ni dase [influenza A virus (A/Goose/Guangdong/1/96(H5N1))]
MNPNQI I TI GSI CMVVG I I SLMLOI GNI I SI VVSHSI QTGNQHOAEPNCQSI I TYENNTWVNQTYVNI S NTNFLTEKAVASVTLAGNSSLCP I SGWAVHSDNGI RI GSKGDV FVI REPFI SCSHLECRTEFFLTQGALL NDKHSNGTVKDRSPHRTLMSCPVGEAPSPYNSRFESVAWSASACHDGT SWLTI GI SGPDNGAVAVLK YNG I I TDTI KSWRNNI LRTQESECACVNGSCFTVMTDGPNGOASYKI FK I EKGKVVKSVELNAPNYHYEECS CYPDAGEI TCVC RDNW HGSNRPWVVSFNQNL EYQI GYI CSGVFGDNPRPNDGTGSCGPVSPNGAYGVKGF S FKYGNGVWI GRKTSTNSRS GFEMI WDPNGWTE TDSSFSVKODI VAI TDWSGYSGSFVQHP ELTGLDCI RP CFWVELI RGRPKENTI WTS GSSI SFCGVNSDTVGSWPDGAELPFTI DK

>gi |3335405|gb|AAC32079.1| neurami ni dase subtype 1 [Influenza A virus (A/Chicken/Hong Kong/220/97 (H5N1))]
MNPNQI I TI GSI CMVVG I I SLMLOI GNI I SI VVSHSI I QTWHPNOPEPCNQSI N FYTEQAAA SVTLAGNS SLCP I SGWAI YSKDNSI RI GSKGDV FVI REPFI SCSHLECRTEFFLTQGALL NDKHSNGTVKDRSPYRTLM SCPVGEAPSPYKSRFESVAWSASACHDGI SWLTI GI SGPDNGAVAVLK YNG I I TDTI KSWRNNI LRTQES ECACVNGSCFTVMTDGPNEQASYKI FK I EKGKVVKSVELNAPNYHYEECS CYPDAGEI TCVC RDNW HGS NRPWVVSFNQNL EYQI GYI CSGVFGDSPRPNDGTGSCGPVSLNGAYGVKGF S FKYGNGVWI GRKTSTSSRS GFEMI WDPNGWTE TDSSFSVKODI I AI TDWSGYSGSFI QHP ELTGLNCRMPCFWVELI RGRPKENTI WTS GSSI SFCGVNSDTVGSWPDGAELPFTI DK

>gi |13676827|gb|AAK38299.1|AF364335_1 neurami ni dase [Influenza A virus (A/goose/Guangdong/3/1997(H5N1))]
MNPNQI I TI GSI CMVI GI VSLMLQI GNI I SI VVSHSI QTGNQHOAEPNCQSI I TYENNTWVNQTYVNI S NTNFLTEKAVASVTLAGNSSLCP I SGWAVHSDNGI RI GSKGDV FVI REPFI SCSHLECRTEFFLTQGALL NDKHSNGTVKDRGRPHRTLMSCPVGEAPSPYNSRFESVAWSASACHDGT SWLTI GI SGPDNGAVAVLK YNG I I TDTI KSWRNNI LRTQESECACVNGSCFTVMTDGPNGOASYKI FK I EKGKVVKSVELNAPNYHYEECS CYPDAGEI TCVC RDNW HGSNRPWVVSFNQNL EYQI GYI CSGVFGDNPRPNDGTGSCGPVSPNGAYGVKGF S FKYGNGVWI GRKTSTNSRS GFEMI WDPNGWTE TDSSFSVKODI VAI TDWSGYSGSFVQHP ELTGLDCI RP CFWVELI RGRPKENTI WTS GSSI SFCGVNSDTVGSWPDGAELPFTI DK

>gi |115343552|gb|ABI94755.1| neurami ni dase [Influenza A virus (A/chicken/Hubei/wh/1997(H5N1))]
MNPNQI TTI GSI CMVLI VSLMLQMGNI I SI VVSHSFQTGNQHOAEPNCQSI I TYENNTWVNQTYVNI S NTNFLTEKAVASVTLAGNSSLCP I SGWAVYKSDNGI RI GSKGDV FVI REPFI SCSHLECRTEFFLTQGALL NDKHSNGTVKDRSPHRTLMSCPVGEAPSPYNSRFESVAWSASACHDGT SWLTI GI SGPDNRAVAVLK YNG I I TDTI KSWRNNI LRTQESECACVNGSCFTVMTDGPNGOASYKI FK I EKGKVVKSVELDAPNYHYEECS CYPDAGEI TCVC RDNW HGSNRPWVVSFNQNL EYQI GYI CSGVFGDNPRPNDGTGSCGPVSPNGAYGVKGF S FKYGNGVWI GRKTSI NSRS GFEMI WDPNGWTE TDSSFSVKODI VAI TDWSGYSGSFVQHP ELTGLDCI RP

CFWVELI RGRPKESTI WTSGSSI SFCGVNSDTVGRSWSGDAELPFTI DK
 >gi |115382792|gb|ABI 96720.1| neurami ni dase [Influenza A vi rus
 (A/chi cken/Hubei /wj /1997 (H5N1))]
 MNPNQKI I TI GSI CMVI GI VSLMLQI GSI SI WWSHSI QTGSQROAEPI SNTKFLAEKAVASVTLAGNSS
 LCPI SGWAVHSDKNSI RI GSKGDVFI REPFI SCSHLECRFFLTQGALLNDKHSNGTVKDRSPHRTLMS
 CPVGEAPSPYNSRFESVAWSASACHDGT SWLTI GI SGPDNGAVAVLKYNIGI I TDTI KSWRNNI LRTQESE
 CACVNGSCFTVMTDGPNSGOASYKI FKMKGKVVKSVELDAPNYHYEECS CYPDAGEI TCVCARDNWHGSGN
 RPWVSFNQNLQYI GYI CSGVFGDNPRPNDGTGSCGVPSPGAYGVKGFSSFKYNGVWI GRKSTNSRSRSG
 FEMI WDPNGWTGTDSSFSVKQDI VAI TDWSSGSGSFVQHPPEMTGLDCI RPCFWVELI RGRPKESTI WTSG
 SSI SFCGVNSDTVGRSWSGDAELPFTI DK
 >gi |115382815|gb|ABI 96733.1| neurami ni dase [Influenza A vi rus
 (A/chi cken/Hubei /wk /1997 (H5N1))]
 MNPNQKI I TI GSI CMVI GI VSLMLQI GSI SI WWSHSI QTGNQHOAEPI SNTNLLTEKAVASVTLAGNSS
 LCPI RGWAVHSDKNGI RI GSKGDVFI REPFI SCSHLECRFFLTQGALLNDKHSNGTVKDRSPHRTLMS
 CPMGEAPSPYNSRFESVAWSASACHDGT SWLTI GI SGPDNGAVAVLKYNMGI I TDTI KSWRNNI LRTQESE
 CACVNGSCFTVMTDGPNSGOASYKI FKMKGKVVKSVELDAPNYHYEECS CYPDAGEI TCVCARDNWHGSGN
 RPWVSFNQNLQYI GYI CSGVFGDNPRPNDGTGSCGVPSPGAYGVKGFSSFKYNGVWI GRKSTNSRSRSG
 FEMI WDPNGWTGTDSSFSVKQDI VAI TDWSSGSGSFVQHPPEMTGLDCI RPCFWVELI RGRPKESTI WTSG
 SSI SFCGVNSDTVGRSWSGDAELPFTI DK
 >gi |115382833|gb|ABI 96742.1| neurami ni dase [Influenza A vi rus
 (A/chi cken/Hubei /wl /1997 (H5N1))]
 MNPNQKI TTI GSI CMVI GI VSLMLQI GSI SI WWSHSI QTGNQHOAEPCPSI I TYENNTWVNTQYVNI S
 NTNFLAEKAVASVTLAGNSSLCPI SGWAVYKSDNGI RI GSKGDVFI REPFI SCSHLECRFFLTQGALL
 NDKHSNGTVKDRSPHRTLMSCPVGEAPSPYNSRFESVAWSASACHDGT SWLTI GI SGPDNGAVAVLKYNIGI
 I I TDTI KSWRNNI LRTQESE CACVNGSCFTVMTDGPNSGOASYKI FKI EKGKVVKSVELDAPNYHYEECS
 CYPDAGEI TCVCARDNWHGSGNRPWVSFNQNLQYI GYI CSGVFGDNPRPNDGTGSCGVPSPGAYGVKGFSS
 FKYNGVWI GRKSTNSRSRSGFEMI WDPNGWTGTDSSFSVKQDI VAI TDWSSGSGSFVQHPPEMTGLDCI RP
 CFWVELI RGPKESTI WTSGSSI SFCGVNSDTVGRSWSGDAELPFTI DK
 >gi |9863879|gb|AAG01196.1|AF216714_1 neurami ni dase 1 [Influenza A vi rus
 (A/Environment/Hong Kong/437-6/99 (H5N1))]
 MNPNQKI TTI GSI CMVI GI VSLMLQI GSI SI WWSHSI QTGNQHOAEPCNQSI I TYENNTWVNTQYVNI S
 NTNFLAEKAVASVTLAGNSSLCPI SGWAVYKSDNGI RI GSKGDVFI REPFI SCSHLECRFFLTQGALL
 NDKHSNGTVKDRSPHRTLMSCPVGEAPSPYNSRFESVAWSASACHDGT SWLTI GI SGPDNGAVAVLKYNIGI
 I I TDTI KSWRNNI LRTQESE CACVNGSCFTVMTDGPNSGOASYKI FKI EKGKVVKSVELDAPNYHYEECS
 CYPDAGEI TCVCARDNWHGSGNRPWVSFNQNLQYI GYI CSGVFGDNPRPNDGTGSCGVPSPGAYGVKGFSS
 FKYNGVWI GRKSTNSRSRSGFEMI WDPNGWTGTDSSFSVKQDI VAI TDWSSGSGSFVQHPPEMTGLDCI RP
 CFWVELI RGRPKESTI WTSGSSI SFCGVNSDTVGRSWSGDAELPFTI DK
 >gi |9863898|gb|AAG01206.1|AF216722_1 neurami ni dase [Influenza A vi rus
 (A/Environment/Hong Kong/437-8/99 (H5N1))]
 MNPNQKI I TI GSI CMVI GI VSLMLQI GSI SI WWSHSI QTGNQHOAEPCNQSI I TYENNTWVNTQYVNI S
 NTNFLAEKAVASVTLAGNSSLCPI SGWAVYKSDNGI RI GSKGDVFI REPFI SCSHLECRFFLTQGALL
 NDKHSNGTVKDRSPHRTLMSCPVGEAPSPYNSRFESVAWSASACHDGT SWLTI GI SGPDNGAVAVLKYNIGI
 I I TDTI KSWRNNI LRTQESE CACVNGSCFTVMTDGPNSGOASYKI FKI EKGKVVKSVELDAPNYHYEECS
 CYPDAGEI TCVCARDNWHGSGNRPWVSFNQNLQYI GYI CSGVFGDNPRPNDGTGSCGVPSPGAYGVKGFSS
 FKYNGVWI GRKSTNSRSRSGFEMI WDPNGWTGTDSSFSVKQDI VAI TDWSSGSGSFVQHPPEMTGLDCI RP
 CFWVELI RGRPKESTI WTSGSSI SFCGVNSDTVGRSWSGDAELPFTI DK
 >gi |9863916|gb|AAG01216.1|AF216730_1 neurami ni dase 1 [Influenza A vi rus
 (A/Environment/Hong Kong/437-8/99 (H5N1))]
 MNPNQKI TTI GSI CMVI GI VSLMLQI GSI SI WWSHSI QTGNQHOAEPCNQSI I TYENNTWVNTQYVNI S
 NTNFLAEKAVASVTLAGNSSLCPI SGWAVYKSDNGI RI GSKGDVFI REPFI SCSHLECRFFLTQGALL
 NDKHSNGTVKDRSPHRTLMSCPVGEAPSPYNSRFESVAWSASACHDGT SWLTI GI SGPDNGAVAVLKYNIGI
 I I TDTI KSWRNNI LRTQESE CACVNGSCFTVMTDGPNSGOASYKI FKI EKGKVVKSVELDAPNYHYEECS
 CYPDAGEI TCVCARDNWHGSGNRPWVSFNQNLQYI GYI CSGVFGDNPRPNDGTGSCGVPSPGAYGVKGFSS
 FKYNGVWI GRKSTNSRSRSGFEMI WDPNGWTGTDSSFSVKQDI VAI TDWSSGSGSFVQHPPEMTGLDCI RP
 CFWVELI RGRPKESTI WTSGSSI SFCGVNSDTVGRSWSGDAELPFTI DK
 >gi |9863934|gb|AAG01226.1|AF216738_1 neurami ni dase 1 [Influenza A vi rus
 (A/Environment/Hong Kong/437-10/99 (H5N1))]
 MNPNQKI TTI GSI CMVI GI VSLMLQI GSI SI WWSHSI QTGNQHOAEPCNQSI I TYENNTWVNTQYVNI S
 NTNFLAEKAVASVTLAGNSSLCPI SGWAVYKSDNGI RI GSKGDVFI REPFI SCSHLECRFFLTQGALL
 NDKHSNGTVKDRSPHRTLMSCPVGEAPSPYNSRFESVAWSASACHDGT SWLTI GI SGPDNGAVAVLKYNIGI
 I I TDTI KSWRNNI LRTQESE CACVNGSCFTVMTDGPNSGOASYKI FKI EKGKVVKSVELDAPNYHYEECS
 CYPDAGEI TCVCARDNWHGSGNRPWVSFNQNLQYI GYI CSGVFGDNPRPNDGTGSCGVPSPGAYGVKGFSS
 FKYNGVWI GRKSTNSRSRSGFEMI WDPNGWTGTDSSFSVKQDI VAI TDWSSGSGSFVQHPPEMTGLDCI RP
 CFWVELI RGRPKESTI WTSGSSI SFCGVNSDTVGRSWSGDAELPFTI DK
 >gi |47156371|gb|AAT12073.1| neurami ni dase [Influenza A vi rus
 (A/duck/Guangxi /07/1999 (H5N1))]
 MNPNQKI I TI GSI CMVI GMVSLVLI GSI SI WWSHSI QTRNOHOAEPCNQSI I TYENNTWVNTQYVNI S
 NTNFLAEKAVASVTLAGNSSLCPI SGWAVYKSDNGI RI GSKGDVFI REPFI SCQLECRFFLTQGALL
 NDKHSNGTVKDRSPHRTLMSCPVGEAPSPYNSRFESVAWSASACHDGT SWLTI GI SGPDNGAVAVLKYNIGI
 I I TDTI KSWRNNI LRTQESE CACVNGSCFTVMTDGPNSGOASYKI FKI EKGKVVKSVELDAPNYHYEECS
 CYPDAGEI TCVCARDNWHGSGNRPWVSFNQNLQYI GYI CSGVFGDNPRPNDGTGSCGVPSPGAYGVKGFSS
 FKYNGVWI GRKSTNSRSRSGFEMI WDPNGWTGTDSSFSVKQDI VAI TDWSSGSGSFVQHPPEMTGLDCI RP
 CFWVELI RGRPKESTI WTSGSSI SFCGVNSDTVGRSWSGDAELPFTI DK
 >gi |47156359|gb|AAT12067.1| neurami ni dase [Influenza A vi rus
 (A/duck/Fuji an/19/2000 (H5N1))]
 MNPNQKI I TI GSI CMVI GI VSLMLQI GSI SI WWSHSI QTGNQHOAEPI SNTNFLAEKAVASVTLAGNSS
 LCPI SGWAVHSDKNGI RI GSKGDVFI REPFI SCSHLECRFFLTQGALLNDKHSNGTVKDRSPHRTLMS

CPVGEAPSPYNSRFESVAWSASACHDGTSWLTI GI SGPDNGAVAVLKYNIGI I TDTI KSWRNNI LRTQESE
CACVNGSCFTVMTDGPSSNGOASYKI FKMEKGVVKSVELDAPNYHYEECSYCPDAGEI TCVCARDNWHGNS
RPWVSFNONLEYQI GYI CSGVFGDNPDPNDGTGSCGPVSPNGAYGVKGFSEFKYNGNVWI GRTKSTNSRSG
FEMI WDPNGWTGTDSSFSVKQDI VAI TDWSGYSGSFVQHPPEMTGLDCI RPCFWVELI RGRPKESTI WTSG
SSI SFCGVNSDVTGWSWPDGAELPFTI DK
>gi |168203842|gb|ACA21690.1| neurami ni dase [Influenza A virus (A/starling/Rostov-on-
Don/39/2007(H5N1))]
MNPNQKI I TI GSI CMVI GI VSLMLOI GNMI SI WVSHSI OTGNQROVEPI SNTKFLTEKAVASLTLAGNSS
LCPI SGWAVYSKDNSI RI GSRGDVFI REPFVSCSHLECRFTFFLTQGALLNDKHSNGTVKDRSPHRTLMS
CPVGEAPSPYNSRFESVAWSASACHDGTSWLTI GI SGPDNGAVAVLKYNIGI I TDTI KSWRNNI LRTQESE
CACVNGSCFTVMTDGPSSNGOASYKI FKMEKGVVKSVELDAPNYHYEECSYCPDAGEI TCVCARDNWHGNS
RPWVSFNONLEYQI GYI CSGVFGDNPDPNDGTGSCGPVSPNGAYGVKGFSEFKYNGNVWI GRTKSTNSRSG
FEMI WDPNGWTGTDSSFSVKQDI VAI TDWSGYSGSFVQHPPEMTGLDCI RPCFWVELI RGRPKESTI WTSG
SSI SFCGVNSDVTGWSWPDGAELPFTI DK
>gi |175362936|gb|ACB72445.1| neurami ni dase [Influenza A virus
(A/chi cken/Israael/1055/2008(H5N1))]
MNPNQKI I TI GSI CMVI GI VSLMLOI GNMI SI WVSHSI OTGNQCOAEPI SNTKFLTEKAVASVTLAGNSS
LCPI SGWAVYSKDNSI RI GSRGDVFI REPFVSCSHLECRFTFFLTQGALLNDKHSNGTVKDRSPHRTLMS
CPVGEAPSPYNSRFESVAWSASACHDGT SWLTI GI SGPDNGAVAVLKYNIGI I TDTI KSWRNNI LRTQESE
CACVNGSCFTVMTDGPSSNGOASYKI FKMEKGVVKSVELDAPNYHYEECSYCPDAGEI TCVCARDNWHGNS
RPWVSFNONLEYQI GYI CSGVFGDNPDPNDGTGSCGPVSPNGAYGVKGFSEFKYNGNVWI GRTKSTNSRSG
FEMI WDPNGWTGTDSSFSVKQDI VAI TDWSGYSGSFVQHPPEMTGLDCI RPCFWVELI RGRPKESTI WTSG
SSI SFCGVNSDVTGWSWPDGAELPFTI DK
>gi |193345879|gb|ACF17960.1| neurami ni dase [Influenza A virus (A/chi cken/Thailand/NS-
339/2008(H5N1))]
MNPNKKI I TI GSI CMVTGMVSLMLOI GNLI SI WVSHSI HTGNQOAEPI SNTNFLTAKAVASVTLAGNSS
LCPI NGWAVYSKDNSI RI GSKGDVFI REPFVSCSHLECRFTFFLTQGSLLNDKHSNGTVKDRSPHRTLMS
CPVGEAPSPYNSRFESVAWSASACHDGT SWLTI GI SGPDSGAVAVLKYNIGI I TDTI KSWRNNI LRTQESE
CACVNGSCFTVMTDGPSSNGOASHKI FKMDKGVVKSVELDAPDYHYEECSYCPDAGEI TCVCARDNWHGNS
RPWVSFNONLEYQI GYI CSGVFGDTPRNDGTGSCGPVSSNGTYGVKGFSEFKYNGNVWI GRTKSTNSRSG
FEMI WDPNGWTETDSSFSVKQDI VAI TDWSGYSGSFVQHPPEMTGLDCI RPCFWVELI RGRPKESTI WTSG
SSI SFCGVNSDVTGWSWPDGAELPFTI DK
>gi |193345897|gb|ACF17970.1| neurami ni dase [Influenza A virus (A/chi cken/Thailand/PC-
340/2008(H5N1))]
MNPNKKI I TI GSI CMVTGMVSLMLOI GNLI SI WVSHSI HTGNQOAEPI SNTNFLTAKAVASVTLAGNSS
LCPI NGWAVYSKDNSI RI GSKGDVFI REPFVSCSHLECRFTFFLTQGSLLNDKHSNGTVKDRSPHRTLMS
CPVGEAPSPYNSRFESVAWSASACHDGT SWLTI GI SGPDSGAVAVLKYNIGI I TDTI KSWRNNI LRTQESE
CACVNGSCFTVMTDGPSSNGOASHKI FKMDKGVVKSVELDAPDYHYEECSYCPDAGEI TCVCARDNWHGNS
RPWVSFNONLEYQI GYI CSGVFGDTPRNDGTGSCGPVSSNGTYGVKGFSEFKYNGNVWI GRTKSTNSRSG
FEMI WDPNGWTETDSSFSVKQDI VAI TDWSGYSGSFVQHPPEMTGLDCI RPCFWVELI RGRPKESTI WTSG
SSI SFCGVNSDVTGWSWPDGAELPFTI DK
>gi |193299706|gb|ACF17941.1| neurami ni dase [Influenza A virus (A/chi cken/Thailand/NS-
341/2008(H5N1))]
NKKI I TI GSI CMVTGMVSLMLOI GNLI SI WVSHSI HTGNQOAEPI SNTNFLTAKAVASVTLAGNSS
LCPI NGWAVYSKDNSI RI GSKGDVFI REPFVSCSHLECRFTFFLTQGSLLNDKHSNGTVKDRSPHRTLMS
GEAPSPYNSRFESVAWSASACHDGT SWLTI GI SGPDI GAVAVLKYNIGI I TDTI KSWRNNI LRTQESAC
VNGSCFTVMTDGPSSNGOASHKI FKMDKGVVKSVELDAPDYHYEECSYCPDAGEI TCVCARDNWHGNS
VSNRPFVFNONLEYQI GYI CSGVFGDTPRNDGTGSCGPVSSNGTYGVKGFSEFKYNGNVWI GRTKSTNSRSG
FEMI WDPNGWTETDSSFSVKQDI VAI TDWSGYSGSFVQHPPEMTGLDCI RPCFWVELI RGRPKESTI WTSG
SSI SFCGVNSDVTGWSWPDGAELPFTI DK
>gi |193299724|gb|ACF17951.1| neurami ni dase [Influenza A virus (A/chi cken/Thailand/NS-
342/2008(H5N1))]
MNPNKKI I TI GSI CMVTGMVSLMLOI GNLI SI WVSHSI HTGNQOAEPI SNTNFLTAKAVASVTLAGNSS
LCPI NGWAVYSKDNSI RI GSKGDVFI REPFVSCSHLECRFTFFLTQGSLLNDKHSNGTVKDRSPHRTLMS
CPVGEAPSPYNSRFESVAWSASACHDGT SWLTI GI SGPDSGAVAVLKYNIGI I TDTI KSWRNNI LRTQESE
CACVNGSCFTVMTDGPSSNGOASHKI FKMDKGVVKSVELDAPDYHYEECSYCPDAGEI TCVCARDNWHGNS
RPWVSFNONLEYQI GYI CSGVFGDTPRNDGTGSCGPVSSNGTYGVKGFSEFKYNGNVWI GRTKSTNSRSG
FEMI WDPNGWTETDSSFSVKQDI VAI TDWSGYSGSFVQHPPEMTGLDCI RPCFWVELI RGRPKESTI WTSG
SSI SFCGVNSDVTGWSWPDGAELPFTI DK
>gi |190195509|gb|ACE73618.1| neurami ni dase [Influenza A virus (A/duck/Thailand/ICRC-
V629/2008(H5N1))]
MNPNKKI I TI GSI CMVTGMVSLMLOI GNLI SI WVSHSI HTGNQOAEPI SNTNFLTAKAVASVTLVGNSS
LCPI TGWAVYSKDNSI RI GSKGDVFI REPFVSCSHLECRFTFFLTQGSLLNDKHSNGTVKDRSPHRTLMS
CPVGEAPSPYNSRFESVAWSASACHDGT SWLTI GI SGPDSGAVAVLKYNIGI I TDTI KSWRNNI LRTQESE
CACVNGSCFTVMTDGPSSNGOASHKI FKMDKGVVKSVELDAPDYHYEECSYCPDAGEI TCVCARDNWHGNS
RPWVSFNONLEYQI GYI CSGVFGDTPRNDGTGSCGPVSSNGTYGVKGFSEFKYNGNVWI GRTKSTNSRSG
FEMI WDPNGWTETDSSFSVKQDI VAI TDWSGYSGSFVQHPPEMTGLDCI RPCFWVELI RGRPKESTI WTSG
SSI SFCGVNSDVTGWSWPDGAELPFTI DK
>gi |190195523|gb|ACE73624.1| neurami ni dase [Influenza A virus (A/Kalij
pheasant/Thailand/vsmu-1/2008(H5N1))]
MNPNKKI I TI GSI CMVTGMVSLMLOI GNLI SI WVSHSI HTGNQOAEPI SNTNFLTAKAVASVTLVGNSS
LCPI TGWAVYSKDNSI RI GSKGDVFI REPFVSCSHLECRFTFFLTQGSLLNDKHSNGTVKDRSPHRTLMS
CPVGEAPSPYNSRFESVAWSASACHDGT SWLTI GI SGPDSGAVAVLKYNIGI I TDTI KSWRNNI LRTQESE
CACVNGSCFTVMTDGPSSNGOASHKI FKMDKGVVKSVELDAPNYHYEECSYCPDAGEI TCVCARDNWHGNS
RPWVSFNONLEYQI GYI CSGVFGDNPDPNDGTGSCGPVSSNGAYGVKGFSEFKYNGNVWI GRTKSTNSRSG
FEMI WDPNGWTETDSSFSVKQDI VAI TDWSGYSGSFVQHPPEMTGLDCI RPCFWVELI RGRPKESTI WTSG
SSI SFCGVNSDVTGWSWPDGAELPFTI DK

>gi |190195374|gb|ACE73594.1| neurami ni dase [Influenza A vi rus (A/chi cken/Thailand/1/2008(H5N1))]
MNPNNKI I TI GSI CMVTGMVSLMLQI GNLI SI WWSHSI HTGNQQAEP I SNTNFLT EKAVASV KLAGNSS
LCPI NGWAVYSKDNSI RI GSKGDV FVI REPFI SCSHLEC RTFFLTQ G SLLNDKHSNGTVKDRSPHRTLMS
CPVGEAPSPYNSRFESVAWSASACHDGT SWLTI GI SGPDSGAVAVLK YNGI I TDTI KSWRNNI LRTQESE
CACVNGSCFTVMTDGP SNGQASHKI FKMDKGGV VVKSVELDAPNYHYEECSY PDAGEI TCVC RDNWHG SN
RPWVSFNONLEYRI GYI CSGVFGDTPRPNDGTG SCGPVSSNGTYGVKGF SFKYNGVWI GR TKSTNSRSG
FEMI WDPNGWTE TDS SFSVKODI VAI TDWSGYSGSFVQHP EMTGLDCI RPCFWVELI RGRPKETHNL DCL
GSRHI FLWCKI VTTVGWSWPDGAELPFTI DK

>gi |189046951|dbj |BAG34612.1| neurami ni dase [Influenza A vi rus (A/chi cken/Laos/1/2008(H5N1))]
MNPNNKI I TI GSI CMVI GI VSLMLQI GNMI SI WWSHSI QTGNQHOAEP I RNANFLT ENAVASV TLAGNSS
LCPV RGVAVH SKDNSI RI GSKGDV FVI REPFI SCSHLEC RTFFLTQ GALLNDKHSNGTVKDRSPHRTLMS
CPVGEAPSPYNSRFESVAWSASACHDGT SWLTI GI SGPDNGAVAVLK YNGI I TDTI KSWRNNI LRTQESE
CACVNGSCFTVMTDGP SNGQASYKI FKMEKGGV VVKSVELNAPNYHYEECSY PDAGEI TCVC RDNWHG SN
RPWVSFNONLEYQI GYI CSGVFGDNPRPNDGTG SCGPVSPNGAYGI KGF SFKYNGVWI GR TKSTNSRSG
FEMI WDPNGWTE TDS SFSVKODI VAI TDWSGYSGSFVQHP EMTGLDCI RPCFWVELI RGRPKETI WTSG
SSI SFCGVNSDTV SWSWPDGAELPFTI DK

>gi |188035688|dbj |BAG32241.1| neurami ni dase [Influenza A vi rus (A/whooper swan/Hokkai do/1/2008(H5N1))]
MNPNNKI I TI GSVCM I GI VSLMLQI GNMI SI WWSHSI QTGNQHOAEP I RNTNFLT ENAVASV TLAGNSS
LCPV RGVAVH SKDNSI RI GSKGDV FVI REPFI SCSHLEC RTFFLTQ GALLNDKHSNGTVKDRSPHRTLMS
CPVGEAPSPYNSRFESVAWSASACHDGT SWLTI GI SGPDNGAVAVLK YNGI I TDTI KSWRNNI LRTQESE
CACVNGSCFTVMTDGP SNGQASYKI FK EKGKVVKSVELNAPNYHYEECSY PDAGEI I CVCRDNWHG SN
RPWI SFNONLEYQI GYI CSGVFGDNPRPNDGTG SCGPMSPN GAYGI KGF SFKYNGVWI GR TKSTNSRSG
FEMI WDPNGWTE TDS SFSVKODI VAI TDWSGYSGSFVQHP EMTGLDCI RPCFWVELI RGRPKETI WTSG
SSI SFCGVNSDTV SWSWPDGAELPFTI DK

>gi |195536909|dbj |BAG68177.1| neurami ni dase [Influenza A vi rus (A/whooper swan/Aki ta/2008(H5N1))]
MNPNNKI I TI GSVCM I GI VSLMLQI GNMI SI WWSHSI QTGNQHOAEP I RNTNFLT ENAVASV TLAGNSS
LCPV RGVAVH SKDNSI RI GSKGDV FVI REPFI SCSHLEC RTFFLTQ GALLNDKHSNGTVKDRSPHRTLMS
CPVGEAPSPYNSRFESVAWSASACHDGT SWLTI GI SGPDNGAVAVLK YNGI I TDTI KSWRNNI LRTQESE
CACVNGSCFTVMTDGP SNGQASYKI FK EKGKVVKSVELNAPNYHYEECSY PDAGEI I CVCRDNWHG SN
RPWI SFNONLEYQI GYI CSGVFGDNPRPNDGTG SCGPMSPN GAYGI KGF SFKYNGVWI GR TKSTNSRSG
FEMI WDPNGWTE TDS SFSVKODI VAI TDWSGYSGSFVQHP EMTGLDCI RPCFWVELI RGRPKETI WTSG
SSI SFCGVNSDTV SWSWPDGAELPFTI DK

>gi |188572140|gb|ACD65005.1| neurami ni dase [Influenza A vi rus (A/chi cken/Egypt/1709-6/2008(H5N1))]
MNPNNKI I TI GSI CMVI GI VSLMLQI GNMI SI WWSHSI QTGNQQAEP I SNTKFLTEKAVASV TLAGNSS
LCPI SGWAVYSKDNSI RI GSRGDV FVI REPFI SCSHLEC RTFFLTQ GALLNDKHSNGTVKDRSPHRTLMS
CPVGEAPSPYNSRFESVAWSASACHDGI SWLTI GI SGPDNGAVAVLK YNGI I TDTI KSWRNNI LRTQESE
CACVNGSCFTVMTDGP SSGQASYKI FKMEKGGV VVKSVELDAPNYHYEECSY PDAGEI TCVC RDNWHG SN
RPWVSFNONLEYQI GYI CSGVFGDNPRPNDGTG SCGPVSPNGAYGVKGF SFKYNGVWI GR TKSTNSRSG
FEMI WDPNGWTE TDS SFSVKODI VAI TDWSGYSGSFVQHP EMTGLDCI RPCFWVELI RGRPKETI WTSG
SSI SFCGVNSDTV SWSWPDGAELPFTI DK

>gi |188572138|gb|ACD65004.1| neurami ni dase [Influenza A vi rus (A/chi cken/Egypt/1709-5/2008(H5N1))]
MNPNNKI I TI GSI CMVI GI VSLMLQI GNMI SI WWSHSI QTRNQCQAEP I SNTKFLTEKAVASV TLAGNSS
LCPI SGWAVYSKDNSI RI GSRGDV FVI REPFI SCSHLEC RTFFLTQ GALLNDKHSNGTVKDRSPHRTLMS
CPVGEAPSPYNSRFESVAWSASACHDGI SWLTI GI SGPDNGAVAVLK YNGI I TDTI KSWRNNI LRTQESE
CACVNGSCFTVMTDGP SSGQASYKI FKMEKGGV VVKSVELDAPNYHYEECSY PDAGEI TCVC RDNWHG SN
RPWVSFNONLEYQI GYI CSGVFGDNPRPNDGTG SCGPVSPNGAYGVKGF SFKYNGVWI GR TKSTNSRSG
FEMI WDPNGWTE TDS SFSVKODI VAI TDWSGYSGSFVQHP EMTGLDCI RPCFWVELI RGRPKETI WTSG
SSI SFCGVNSDTV SWSWPDGAELPFTI DK

>gi |188526737|gb|ACD62245.1| neurami ni dase [Influenza A vi rus (A/chi cken/Pri morje/1/2008(H5N1))]
MNPNNKI I TI GSVCM I GI VSLMLQI GNMI SI WWSHSI QTGNQHOAEP I RNTNFLT ENAVASV TLAGNSS
LCPV RGVAVH SKDNSI RI GSKGDV FVI REPFI SCSHLEC RTFFLTQ GALLNDKHSNGTVKDRSPHRTLMS
CPVGEAPSPYNSRFESVAWSASACHDGT SWLTI GI SGPDNGAVAVLK YNGI I TDTI KSWRNNI LRTQESE
CACVNGSCFTVMTDGP SNGQASYKI FK EKGKVVKSVELNAPNYHYEECSY PDAGEI I CVCRDNWHG SN
RPWI SFNONLEYQI GYI CSGVFGDNPRPNDGTG SCGPMSPN GAYGI KGF SFKYNGVWI GR TKSTNSRSG
FEMI WDPNGWTE TDS SFSVKODI VAI TDWSGYSGSFVQHP EMTGLDCI RPCFWVELI RGRPKETI WTSG
SSI SFCGVNSDTV SWSWPDGAELPFTI DK

>gi |47156363|gb|AAT12069.1| neurami ni dase [Influenza A vi rus (A/duck/Guangdong/07/2000(H5N1))]
MNPNNKI I TI GSI CMVI GI VSLMLQI GNI I SI WWSHSI QTGNQHOAEP CNQSI I TYENNTWVNQTYVNI G
NTNFLT EKAVASV TLAGNSS LCPI SGWAVYSKDNGI RI GSKGDV FVI REPFI SCSHLEC RTFFLTQ GALL
NDKHSNGTVKDRSPYRTLMS CPVGEAPSPYNSRFESVAWSASACHDGT SWLTI GI SGPDNGAVAVLK YNG
I I TDTI KSWRNNI LRTQESE CACVNGSCFTVMTDGP SNGQASYKI FK EKGKVVKSVELNAPNYHYEECS
YPDAGEI TCVC RDNWHG SNRPWVSFNONLEYKI GYI CSGVFGDNPRPNDGTG SCGPVSPNGAYGVKGF S
FKYNGVWI GR TKSTNSRSG FEMI WDPNGWTE TDS SFSVKODI VAI TDWSGYSGSFVQHP EMTGLDCI RP
CFWVELI RGRPKETI WTSG SSI SFCGVNSDTV GWSWPDGAELPFTI DK

>gi |47156365|gb|AAT12070.1| neurami ni dase [Influenza A vi rus (A/duck/Guangdong/12/2000(H5N1))]
MNPNNKI I TI GSI CMVI GI VSLMLQI GNI I SI WWSHSI QTGNQHOAEP I SNTNFLT EKAVASI TLAGNSS
LCPI SGWAVYSKDNGI RI GSKGDV FV VREPFI SCSHLEC RTFFLTQ GALLNDKHSNGTVKDRSPHRTLMS
CPVGEAPFPYNSRFESVAWSASACHDGT SWLTI GI SGPDNGAVAVLK YNGI I TDTI KSWRNNI LRTQESE

CACVNGSCFTVMTDGPNSGOASYKI FKMEKGGVVKSVELDAPNYHYEECSYCPDAGEI TCVCRDNWHGSRN
 RPWVSNQNLWEYQI GYI CSGVFGDNPRPNDGTGSCGVPSPNGAYGVKGFSSFKYNGVWVI GRKSTNSRSRG
 FEMI WDPNGWTGDSSFSVKQDI VAI TDWSGYSGSFVQHPLELTGLDCI RPCFWVELI RGRPKESTI WTSG
 SSI SFCGVNSDVTGWSWPDGAELPFTI DK

>gi |47156391|gb|AAT12083.1| neurami ni dase [Infl uenza A vi rus

(A/duck/Zhej i ang/11/2000(H5N1))

MNPNQKI I TI GSI CMVI GI VSLMLQI GNI I SI WVSHSI QTGNQHOAEPNI SNTNFLTTEKAVASVTLAGNSS
 LCPI SGWAVHSDNGI RI GSKGDVFI REPI SCSHLECRFFLTQGALLNDKHSNGTVKDRSPHRTLMS
 CPVGEAPSPYNSRFESVAWSASACHDGTSLWTI GI SGPDNGAVAVLKYNIGI I TDTI KSWRNNI LRTQESE
 CACVNGSCFTVMTDGPNSGOASYKI FKMEKGGVVKSVELDAPNYHYEECSYCPDAGEI TCVCRDNWHGSRN
 RPWVSNQNLWEYQI GYI CSGVFGDNPRPNDGTGSCGVPSPNGAYGVKGFSSFKYNGVWVI GRKSTNSRSRG
 FEMI WDPNGWTGDSSFSVKQDI VAI TDWSGYSGSFVQHPLELTGLDCI RPCFWVELI RGRPKESTI WTSG
 SSI SFCGVNSDVTGWSWPDGAELPFTI DK

>gi |47156393|gb|AAT12084.1| neurami ni dase [Infl uenza A vi rus

(A/duck/Zhej i ang/52/2000(H5N1))

MNPNQKI TTI GSI CMVI GI VSLMLQI GNI I SI WVSHSI QTGNQHOAEPNCQSI I TYENNTWVNTQYVNI S
 NTNFLTTEKAVASVTLAGNSSLCPI SGWAVYSDNGI RI GSKGDVFI REPI SCSHLECRFFLTQGALL
 NDKHSNGTVKDRSPYRRTLMSCPVGEAPSPYNSRFESVAWSASACHDGTSLWTI GI SGPDNGAVAVLKYNIGI
 I I TDTI KSWRNNI LRTQESEACVNGSCFTVMTDGPNSGOASYKI FRI EKGKVVKSVELNAPNYHYEECS
 CYPDAGEI TCVCRDNWHGSRNRPWVSNQNLWEYQI GYI CSGI FGDNPRPNDGTGSCGVPSPNGAYGI KGFS
 FKYNGVWVI GRKSTNSRSRGFEMI WDPNGWTGDSSFSVKQDI VAI TDWSGYSGSFVQHPLELTGLDCI RP
 CFWVELI RGRPKESTI WTSGSSI SFCGVNSDVTGWSWPDGAELPFTI DK

>gi |47156369|gb|AAT12072.1| neurami ni dase [Infl uenza A vi rus

(A/duck/Guangdong/40/2000(H5N1))

MNPNQKI MTI GSI CMVI GMVSLMLQI GNI I SI WVSHSI QTGNQHOAEPNCQSI I TYENNTWVNTQYVNI S
 NTNFLTTEKAVASVTLAGNSSLCPI SGWAVYSDNGI RI GSKGDVFI REPI SCSHLECRFFLTQGALL
 NDKHSNGTVKDRSPYRRTLMSCPVGEAPSPYNSRFESVAWSASACHDGTSLWTI GI SGPDNGAVAVLKYNIGI
 I I TDTI KSWRNNI LRTQESEACVNGSCFTVMTDGPNSGOASYKI FKI EKGKVVKSVELNAPNYHYEECS
 CYPDAGEI TCVCRDNWHGSRNRPWVSNQNLWEYQI GYI CSGVFGDNPRPNDGTGSCGVPSSNGAYGVKGFSS
 FKYNGVWVI GRKSTNSRSRGFEMI WDPNGWTGDSSFSVKQDI VAI SDWSGYSGSFVQHPLELTGLDCI RP
 CFWVELI RGRPKESAI WTSGSSI SFCGVNSDVTGWSWPDGAELPFTI

>gi |18092174|gb|AAL59146.1|AF398421_1 neurami ni dase [Infl uenza A vi rus (A/Goose/Hong

Kong/385.3/2000(H5N1))

MNPNQKI I TI GSI CMVI GTVSLMLQI GNI I SI WVSHSI QTGNQHOAEPNCQSI I TYENNTWVNTQYVNI S
 NTNFLTTEKAVASVTLAGNSSLCPI SGWAVYSDNGI RI GSKGDVFI REPI SCSHLECRFFLTQGALL
 NDKHSNGTVKDRSPYRRTLMSCPVGEAPSPYNSRFESVAWSASACHDGTSLWTI GI SGPDNGAVAVLKYNIGI
 I I TDTI KSWRNNI LRTQESEACVNGSCFTVMTDGPNSGOASYKI FKI EKGKVVKSVELNAPNYHYEECS
 CYPDAGEI TCVCRDNWHGSRNRPWVSNQNLWEYQI GYI CSGVFGDNPRPNDGTGSCGVPSPNGAYGVKGFSS
 FKYNGVWVI GRKSTNSRSRGFEMI WDPNGWTGDSSFSVKQDI VAI TDWSGYSGSFVQHPLELTGLDCI KP
 CFWVELI RGRPKESTI WTSGSSI SFCGVNSDVTGWSWPDGAELPFTI DK

>gi |18092176|gb|AAL59147.1|AF398422_1 neurami ni dase [Infl uenza A vi rus (A/Goose/Hong

Kong/385.5/2000(H5N1))

MNPNQKI I TI GSI CMVI GTVSLMLQI GNI I SI WVTHSI QTGNQHOAEPNCQSI I TYENNTWVNTQYVNI S
 NTNFLTTEKAVASVTLAGNSSLCPI SGWAVYSDNGLRI GSKGDVFI REPI SCSHLECRFFLTQGALL
 NDKHSNGTVKDRSPYRRTLMSCPVGEAPSPYNSRFESVAWSASACHDGTSLWTI GI SGPDNGAVAVLKYNIGI
 I I TDTI KSWRNNI LRTQESEACVNGSCFTVMTDGPNSGOASYKI FKI EKGKVVKSVELNAPNYHYEECS
 CYPDAGEI TCVCRDNWHGSRNRPWVSNQNLWEYQI GYI CSGVFGDNPRPNDGTGSCGVPSPNGAYGVKGFSS
 FKYNGVWVI GRKSTNSRSRGFEMI WDPNGWTGDSSFSVKQDI VAI TDWSGYSGSFVQHPLELTGLDCI RP
 CFWVELI RGRPKESTI WTSGSSI SFCGVNSDVTGWSWPDGAELPFTI DK

>gi |21326683|gb|AAL75844.1| neurami ni dase N1 [Infl uenza A vi rus (A/Goose/Hong

Kong/3014.5/2000(H5N1))

MNSNQKI I TI GSI CMVI GI VSLMLQI GNI I SI WI SHSI QTGNQHOAEPNCQSI I TYENNTWVNTQYI NI S
 NTNFLTTEKAVASVTLAGNSSLCPI SGWAVYSDNGI RI GSKGDVFI REPI SCSHLECRFFLTQGALL
 NDKHSNGTVKDRSPYRRTLMSCPVGEAPSPYNSRFESVAWSASACHDGTSLWTI GI SGPDNGAVAVLKYNIGI
 I I TDTI KSWRNNI LRTQESEACVNGSCFTVMTDGPNSGOASYKI FKI EKGKVVKSVELNAPNYHYEECS
 CYPDAGEI TCVCRDNWHGSRNRPWVSNQNLWEYQI GYI CSGVFGDNPRPNDGTGSCGVPSPNGAYGI KGFS
 FKYNGVWVI GRKSTNSRSRGFEMI WDPNGWTGDSSFSVKQDI VAI TDWSGYSGSFVQHPLELTGLDCI RP
 CFWVELI RGRPKESTI WTSGSSI SFCGVNSDVTGWSWPDGAELPFTI DK

>gi |19697776|gb|AAL31389.1| neurami ni dase [Infl uenza A vi rus (A/Goose/Hong

Kong/ww26/2000(H5N1))

MNPNQKI I TI GSI CMVI GI VSLMLQI GNI I SI WVSHSI QTGNQHOAEPNCQSI I TYENNTWVNTQYVNI S
 NTNFLTTEKAVASVTLAGNSSLCPI SGWAVYSDNSI RI GSKGDVFI REPI SCSHLECRFFLTQGALL
 NDKHSNGTVKDRSPYRRTLMSCPVGEAPSPYNSRFESVAWSASACHDGTSLWTI GI SGPDNGAVAVLKYNIGI
 I I TDTI KSWRNNI LRTQESEACVNGSCFTVMTDGPNSGOASYKI FKI EKGKVVKSVELNAPNYHYEECS
 CYPDAGEI TCVCRDNWHGSRNRPWVSNQNLWEYQI GYI CSGVFGDNPRPNDGTGSCGVPSPNGAYGVKGFSS
 FKYNGVWVI GRKSTNSRSRGFEMI WDPNGWTGDSSFSVKQDI VAI TDWSGYSGSFVQHPLELTGLDCI RP
 CFWVELI RGRPKESTI WTSGSSI SFCGVNSDVTGWSWPDGAELPFTI DK

>gi |19697778|gb|AAL31390.1| neurami ni dase [Infl uenza A vi rus (A/Goose/Hong

Kong/ww28/2000(H5N1))

MNPNQKI I TI GSI CMVI GI VSLMLQI GNI I SI WVSHSI QTGNQHOAEPNCQSI I TYENNTWGNQYVNI S
 NTNLLTEKAVASVTLAGNPSLCPI SGWAVYSDNSI RI GSKGDVFI REPI SCSHLECRFFLTQGALL
 NDKHSNGTVKDRSPYRRTLMSCPVGEAPSPYNSRFESVAWSASACHDGTSLWTI GI SGPDNGAVAVLKYNIGI
 I I TDTI KSWRNNI LRTQESEACVNGSCFTVMTDGPNSGOASYKI FKI EKGKVVKSVELNAPNYHYEECS
 CYPDAGEI TCVCRDNWHGSRNRPWVSNQNLWEYQI GYI CSGVFGDNPRPNDGTGSCGVPSPNGAYGVKGFSS
 FKYNGVWVI GRKSTNSRSRGFEMI WDPNGWTGDSSFSVKQDI VAI TDWSGYSGSFVQHPLELTGLDCI RP
 CFWVELI RGRPKESTI WTSGSSI SFCGVNSDVTGWSWPDGAELPFTI DK

>gi |19697780|gb|AAL31391.1| neurami ni dase [Influenza A vi rus (A/Duck/Hong Kong/ww381/2000(H5N1))]
MNPNQKI I TI GSI CMVI GI VSLMLQI GNI I SI VVSHSI QTGNQHOAEPNCQSI I TYENNTWVNQTYVNI S
NTNFLTTEKAVASVTLAGNSSLCP I SGWAVYSKDNGI RI GSKGDV FVI REPFI SCSHLECR TFFLTQ GALL
NDKHSNGTVKDRSPYRTLMSCPVGEAPSPYNSRFESVAWSASACHDGT SWLTI GI SGPDSGAVAVLKYNG
I I TDTI KSWRNNI LRTQSEACACVNGSCFTVMTDGP SNGOASYKI FK I EKGKVVKSVELNAPNYHYEECS
CYPDAGEI TCVC RDNWHG SNRPWV SFNQNL EYKI GYI CSGVFGDNPRPNDGTGSCGPVSPNGAYGVKGF S
FKYGNVWVI GR TKTNSRSGFEMI WDPNGWTGTDSSFSVKQDI VAI TDW S GYSGSFVQHP ELTGLDCI RP
CFWVELI RGPKESTI WTS GSSI SFCGVNSDTV GWSWPDGAELPFTI DK

>gi |19697782|gb|AAL31392.1| neurami ni dase [Influenza A vi rus (A/Duck/Hong Kong/ww382/2000(H5N1))]
MNPNQKI I TI GSI CMVI GI VSLMLQI GNI I SI VVSHSI QTGNQHOAEPNCQSI I TYENNTWVNQTYVNI S
NTNFLTENAVASVTLAGNSSLCP I SGWAVYSKDNGI RI GSKGDV FVI REPFI SCSHLECR TFFLTQ GALL
NDKHSNGTVKDRSPYRTLMSCPVGEAPSPYNSRFESVAWSASACHDGT SWLTI GI SGPDSGAVAVLKYNG
I I TDTI KSWRNNI LRTQSEACACVNGSCFTVMTDGP SNGOASYKI FK I EKGKVVKSVELNAPNYHYEECS
CYPDAGEI TCVC RDNWHG SNRPWV SFNQNL EYKI GYI CSGVFGDNPRPNDGTGSCGPVSPNGAYGVKGF S
FKYGNVWVI GR TKTNSRSGFEMI WDPNGWTGTDSSFSVKQDI VAI TDW S GYSGSFVQHP ELTGLDCI RP
CFWVELI RGPKESTI WTS GSSI SFCGVNSDTV GWSWPDGAELPFTI DK

>gi |19697784|gb|AAL31393.1| neurami ni dase [Influenza A vi rus (A/Duck/Hong Kong/ww461/2000(H5N1))]
MNPNQKI I TI GSI CMVI GI VSLMLQI GNI I SI VVSHSI QTGNQHOAEPNCQSI I TYENNTWVNQTYVNI S
NTNFLTTEKAVASVTLAGNSSLCP I SGWAVYSKDNGI RI GSKGDV FVI REPFI SCSHLECR TFFLTQ GALL
NDKHSNGTVKDRSPYRTLMSCPVGEAPSPYNSRFESVAWSASACHDGT SWLTI GI SGPDSGAVAVLKYNG
I I TDTI KSWRNNI LRTQSEACACVNGSCFTVMTDGP SNGOASYKI FK I EKGKVVKSVELNAPNYHYEECS
CYPDAGEI TCVC RDNWHG SNRPWV SFNQNL EYKI GYI CSGVFGDNPRPNDGTGSCGPVSPNGAYGVKGF S
FKYGNVWVI GR TKTNSRSGFEMI WDPNGWTGTDSSFSVKQDI VAI TDW S GYSGSFVQHP ELTGLDCI RP
CFWVELI RGPKESTI WTS GSSI SFCGVNSDTV GWSWPDGAELPFTI DK

>gi |19697786|gb|AAL31394.1| neurami ni dase [Influenza A vi rus (A/Duck/Hong Kong/ww487/2000(H5N1))]
MNPNQKI I TI GSI CMVI GI VSLMLQI GNI I SI VVSHSI QTGNQHOAEPNCQSI I TYENNTWVNQTYVNI S
NTNFLTTEKAVASVTLAGNSSLCP I SGWAVYSKDNGI RI GSKGDV FVI REPFI SCSHLECR TFFLTQ GALL
NDKHSNGTVKDRSPYRTLMSCPVGEAPSPYNSRFESVAWSASACHDGT SWLTI GI SGPDSGAVAVLKYNG
I I TDTI KSWRNNI LRTQSEACACVNGSCFTVMTDGP SNGOASYKI FK I EKGKVVKSVELNAPNYHYEECS
CYPDAGEI TCVC RDNWHG SNRPWV SFNQNL EYKI GYI CSGVFGDNPRPNDGTGSCGPVSPNGAYGVKGF S
FKYGNVWVI GR TKTNSRSGFEMI WDPNGWTGTDSSFSVKQDI VAI TDW S GYSGSFVQHP ELTGLDCI RP
CFWVELI RGPKESTI WTS GSSI SFCGVNSDTV GWSWPDGAELPFTI DK

>gi |19697788|gb|AAL31395.1| neurami ni dase [Influenza A vi rus (A/Goose/Hong Kong/ww491/2000(H5N1))]
MNPNQKI I TI GSI CMVI GI VSLMLQI GNI I SI VVSHSI QTGNQHOAEPNCQSI I TYENNTWVNQTYVNI S
NTNFLTTEKAVASVTLAGNSSLCP I SGWAVYSKDNGI RI GSKGDV FVI REPFI SCSHLECR TFFLTQ GALL
NDKHSNGTVKDRSPYRTLMSCPVGEAPSPYNSRFESVAWSASACHDGT SWLTI GI SGPDSGAVAVLKYNG
I I TDTI KSWRNNI LRTQSEACACVNGSCFTVMTDGP SNGOASYKI FK I EKGKVVKSVELNAPNYHYEECS
CYPDAGEI TCVC RDNWHG SNRPWV SFNQNL EYKI GYI CSGVFGDNPRPNDGTGSCGPVSPNGAYGVKGF S
FKYGNVWVI GR TKTNSRSGFEMI WDPNGWTGTDSSFSVKQDI VAI TDW S GYSGSFVQHP ELTGLDCI RP
CFWVELI RGPKESTI WTS GSSI SFCGVNSDTV GWSWPDGAELPFTI DK

>gi |19697790|gb|AAL31396.1| neurami ni dase [Influenza A vi rus (A/Duck/Hong Kong/2986.1/2000(H5N1))]
MNPNQKI I TI GSI CMVI GI VSLMLQI GNI I SI VVSHSI QTGNQHOAEPNCQSI I TYENNTWVNQTYVNI S
NTNFLTTEKAVASVTLAGNSSLCP I SGWAVYSKDNGI RI GSKGDV FVI REPFI SCSHLECR TFFLTQ GALL
NDKHSNGTVKDRSPYRTLMSCPVGEAPSPYNSRFESVAWSASACHDGT SWLTI GI SGPDSGAVAVLKYNG
I I TDTI KSWRNNI LRTQSEACACVNGSCFTVMTDGP SNGOASYKI FK I EKGKVVKSVELNAPNYHYEECS
CYPDAGEI TCVC RDNWHG SNRPWV SFNQNL EYKI GYI CSGVFGDNPRPNDGTGSCGPVSPNGAYGI KGF S
FKYGNVWVI GR TKTNSRSGFEMI WDPNGWTGTDSSFSVKQDI VAI TDW S GYSGSFVQHP ELTGLDCI RP
CFWVELI RGRPK ESTI WTS GSSI SFCGVNSDTV GWSWPDGAELPFTI DK

>gi |19697792|gb|AAL31397.1| neurami ni dase [Influenza A vi rus (A/Goose/Hong Kong/3014.8/2000(H5N1))]
MNPNQKI I TI GSI CMVI GI VSLMLQI GNI I SI WJ SHSI QTGNQHOAEPNCQSI I TYENNTWVNQTYVNI S
NTNFLTTEKAVASVTLAGNSSLCP I SGWAVYSKDNGI RI GSKGDV FVI REPFI SCSHLECR TFFLTQ GALL
NDKHSNGTVKDRSPYRTLMSCPVGEAPSPYNSRFESVAWSASACHDGT SWLTI GI SGPDSGAVAVLKYNG
I I TDTI KSWRNNI LRTQSEACACVNGSCFTVMTDGP SNGOASYKI FK I EKGKVVKSVELNAPNYHYEECS
CYPDAGEI TCVC RDNWHG SNRPWV SFNQNL EYKI GYI CSGVFGDNPRPNDGTGSCGPVSPNGAYGI KGF S
FKYGNVWVI GR TKTNSRSGFEMI WDPNGWTGTDSSFSVKQDI VAI TDW S GYSGSFVQHP ELTGLDCI RP
CFWVELI RGRPK ESTI WTS GSSI SFCGVNSDTV GWSWPDGAELPFTI DK

>gi |76786309|gb|ABA54916.1| neurami ni dase [Influenza A vi rus (A/Goose/Huadong/1/2000(H5N1))]
MNPNQKI I TTGSI CMVI GMVSLMLQI GNI I SI VVSHSI QTGTQHRAEPNCRSI I NYENNTWVNQTYVNI S
NTNFLTTEKAVASVRLVGNSSLCP I SGWAVYSKDNSI RI GSKGDV FVI REPFI SCSHLECR TFFLTQ GALL
NDKHSNGTVKDRSPYRTLMSCPVGEAPSPYNSRFESVAWSASACHDGT SWLTI GI SGPDSGAVAVLKYNG
I I TDTI KSWRNNI LRAQSEACACVNGSCFTVMTDGP SNGOASYKI FK I EKGKVVKSVELNAPNYHYEECS
CYPDAGEI TCVC RDNWHG SNRPWV SFNQNL EYKI GYI CSGVFGDNPRPNDGTGSCGPVSPNGAYGVKGF S
FKYGNVWVI GR TKTNSRSGFEMI WDPNGWTGTDSSFSVKQDI VAI TDW S GYSGSFVQHP ELTGLDCI RP
CFWVELI RGRPK ESTI WTS GSSI SFCGVNSDTV GWSWPDGAELPFTI DK

>gi |169124083|gb|ACA47419.1| neurami ni dase [Influenza A vi rus (A/chi cken/Shantou/904/2001(H5N1))]
MNPNQKI I TI GSI CMVI GI VSLMLQI GNI I SI WASHSI QTGNQHOAEPNCQSI I TYENNTWVNQTYVNI S
NTNFLTTEKAVASVTLAGNSSLCP I SGWAVYSKDNGI RI GSKGDV FVI REPFI SCSHLECR TFFLTQ GALL
NDKHSNGTVKDRSPYRTLMSCPVGEAPSPYNSRFESVAWSASACHDGT SWLTI GI SGPDSGAVAVLKYNG

I I TDTI KSWRNNI LRTQESECACVNGSCFTVMTDGPNSGOASYKI FKI EKGKVVKSVELNAPNYHYEECS
 CYPDAGEI TCVCARDNWHGSRNPWVWVFNQNLQYI GYI CSGVFGDNPRPNDGTGSCGVPSPNGAYGI KGFS
 FKYGNGVWI GRKSTNSRSGFEMI WDPNGWTGTDNSFVSKQDVAI TDWSGYSGSFVQHPPELTGLDCI RP
 CFVWELI RGRPKESTI WTSGSSI SFCGVNSDVTGWSWPDGAE

>gi |169124102|gb|ACA47430.1| neurami ni dase [Influenza A vi rus
 (A/duck/Shantou/1101/2001(H5N1))]
 MNPNQKI I TI GSI CMVI GI VSLMLQI GNI I SI WI SHSI QTGNQHOAEPNCQSI I TYENNTWVNOYVNI S
 NTNFLTEKAVASVTLAGNSSLCPI SGWAVYSKDNGI RI GSKGDV FVI RE PFI SC SHLEC RTFFLTQ GALL
 NDKHSNGTVKDRSPYRTLMSCPVGEAPSPYNSRFESVAWSASACHDGT SWLTI GI SGP DNGAVAVLKYNG
 I I TDTI KSWRNNI LRTQESECACVNGSCFTVMTDGPNSGOASYKI FKI EKGKVVKSVELNAPNYHYEECS
 CYPDAGEI I CVCRDNWHGSRNPWVWVFNQNLQYI GYI CSGVFGDNPRPNDGTGSCGPMNLNGAYGI KGFS
 FKYGNGVWI GRKSTNSRSGFEMI WDPNGWTGTDNSFVSKQDI VAI TDWSGYSGSFVQHPPELTGLDCI RP
 CFVWELI RGRPKESTI WTSGSSI SFCGVN

>gi |194719730|emb|CAQ58532.1| neurami ni dase [Influenza A vi rus
 (A/chi cken/Ni geri a/OG11/2007(H5N1))]
 MNPNQKI I TI GSI CMVI GI VSLMLQI GNMI SI WWSHSI QTGNQROAEP I SNTKFLTEKAVASVTLAGNSS
 LCPI SGWAVYSKD NSI RI GSRGDV FVI RE PFI SC SHLEC RTFFLTQ GALLNDKHSNGTVKDRSPHRTLMS
 CPVGEAPSPYNSRFESVAWSASACHDGT SWLTI GI SGP DNGAVAVLKYNGI I TDTI KSWRNNI LRTQESE
 CACANGSCFTVMTDGPNSGOASYKI FKMEKGGKVVKSVELDAPNYHYEECS CYPDAGEI TCVCARDNWHGSRN
 RPWVWVFNQNLQYI GYI CSGVFGDNPRPNDGTGSCGVPSPNGAYGVKGF SFKYNGVWI GRKSTNSRSG
 FEMI WDPNGWTGTDSSFSVKQDI VAI TDWSGYSGSFVQHPPELTGLDCI RPFVWELI RGRPKESTI WTSG
 SSI SFCGVNSDVTVSWWPDGAELPFTI D

>gi |194719732|emb|CAQ58533.1| neurami ni dase [Influenza A vi rus
 (A/chi cken/Ni geri a/OY014/2007(H5N1))]
 KI I TI GSI CMVI GI VSLMLQI GNMI SI WWSHSI QTGNQROAEP I SNTKFLTEKAVASVTLAGNSSLCPI S
 GWAVYSKD NSI RI GSRGDV FVI RE PFI SC SHLEC RTFFLTQ GALLNDKHSNGTVKDRSPHRTLMSCPVGE
 APSPYNSRFESVAWSASACHDGT SWLTI GI SGP DNGAVAVLKYNGI I TDTI KSWRNNI LRTQESEACV N
 SSCFTVMTDGPNSGOASYKI FKMEKGGKVVKSVELDAPNYHYEECS CYPDAGEI MCVCRDNWHGSRNPWVW
 FNQNLQYI GYI CSGVFGDNPRPNDGTGSCGVPSPNGAYGVKGF SFKYNGVWI GRKSTNSRSGFEMI W
 DPNGWTGTDSSFSVKQDI VAI TDWSGYSGSFVQHPPELTGLDCI RPFVWELI RGRPKESTI WTSGSSI SF
 CGVNSDVTVSWWPDGAELPFTI DK

>gi |194719734|emb|CAQ58534.1| neurami ni dase [Influenza A vi rus
 (A/chi cken/Ni geri a/EKI 15/2007(H5N1))]
 I I TI GSI CMVI GI VSLMLQI GNMI SI WWSHSI QTGSQROAEP I SNTKFLTEKAGASVTLAGNSSLCPI SG
 WAVYSKD NSI RI GSRGDV FVI RE PFI SC SHLEC RTFFLTQ GALLNDKHSNGTVKDRSPHRTLMSCPVGEA
 PSPYNSRFESVAWSASACHDGT SWLTI GI SGP DNGAVAVLKYNGI I TDTI KSWRNNI LRTQESECACVNG
 SCFTVMTDGPNSGOASYKI FKMEKGGKVVKSVELDAPNYHYEECS CYPDAGEI TCVCARDNWHGSRNPWVW
 FNQNLQYI GYI CSGVFGDNPRPNDGTGSCGVPSPNGAYGVKGF SFKYNGVWI GRKTSI NSRSGFEMI W
 DPNGWTGTDSSFSVKQDI VAI TDWSGYSGSFVQHPPELTGLDCI RPFVWELI RGRPKESTI WTSGSSI SFC
 GVNSDVTVSWWPDGAELPFTI DK

>gi |190195352|gb|ACE73583.1| neurami ni dase [Influenza A vi rus
 (A/chi cken/Thai I and/I CRC-195/2007(H5N1))]
 MNPNKKI I TI GSI CMVTGMVSLMLQI GNLI SI WWSHSI HTGNQQAEP I SNTNFLTEKAVASVTLAGNSS
 LCPI NGWAVYSKD NSI RI GSKGDV FVI RE PFI SC SHLEC RTFFLTQ GALLNDKHSNGTVKDRSPHRTLMS
 CPVGEAPSPYNSRFESVAWSASACHDGT SWLTI GI SGP DNGAVAVLKYNGI I TDTI KSWRNNI LRTQESE
 CACVNGSCFTVMTDGPNSGOASYKI FKMDKGGKVVKSVELDAPDYHYEECS CYPDAGEI TCVCARDNWHGSRN
 RPWVWVFNQNLQYI GYI CSGVFGDTPRPNDGTGSCGVPSSNGTYGVKGF SFKYNGVWI GRKSTNSRSG
 FEMI WDPNGWTGTDSSFSVKQDI VAI TDWSGYSGSFVQHPPELTGLDCI RPFVWELI RGRPKESTI WTSG
 SSI SFCGVNSDVTGWSWPDGAELPFTI DK

>gi |183238978|gb|ACC61060.1| neurami ni dase [Influenza A vi rus (A/turkey/Saudi
 Arabi a/6732-6/2007(H5N1))]
 MNPNQKI I TI GSI CMVI GI VSLMLQI GNMI SI WWSHSI QTGNQROAEP I SNTKFLTEKAVASVTLAGNSS
 LCPI SGWAVYSKD NSI RI GSRGDV FVI RE PFI SC SHLEC RTFFLTQ GALLNDKHSNGTVKDRSPHRTLMS
 CPVGEAPSPYNSRFESVAWSASACHDGT SWLTI GI SGP DNGAVAVLKYNGI I TDTI KSWRNNI LRTQESE
 CACVNGSCFTVMTDGPNSGOASYKI FKI EKGKVI KVELDAPNYHYEECS CYPDAGEI TCVCARDNWHGSRN
 RPWVWVFNQNLQYI GYI CSGVFGDNPRPNDGTGSCGVPSPNGAYGVKGF SFKYNGVWI GRKTSANSRSG
 FEMI WDPNGWTGTDSSFSVKQDI VAI TDWSGYSGSFVQHPPELTGLDCI RPFVWELI RGRPKESTI WTSG
 SSI SFCGVNSDVTGWSWPDGAELPFTI DK

>gi |156994170|gb|ABU99152.1| neurami ni dase [Influenza A vi rus
 (A/Chi cken/I ndonesi a/Magel ang1631-57/2007(H5N1))]
 MNPNQKI I TI GSI CMVI GVVSLMLQI GNMI SI WWSHSI QTGNQHOAESTSNTNPLTEKAVASVTLAGNSS
 LCPI RGWAI HSKD NSI RI GSKGDV FVI RE PFI SC SHLEC RTFFLTQ GALLNDKHSNGTVKDRSPHRTLMS
 CPVGEAPSPYNSRFESVAWSASACHDGT SWLTI GI SGP DNGAVAVLKYNGI I TDTI KSWRNNI LRTQESE
 CACVNGSCFTVMTDGPNSGOASYKI FKMEKGGKVVKSVELDAPNYHYEECS CYPDAGEI TCVCARDNWHGSRN
 RPWVWVFNQNLQYI GYI CSGVFGDNPRPNDGTGSCGPMSPNGAYGVKGF AFKYNGVWI GRKTSI NSRSG
 FEMI WDPNGWTGTDSSFSVKQDI VAI TDWSGYSGSFVQHPPELTGLDCI RPFVWELI RGRPKESTI WTSG
 SSI SFCGVNSDVTVSWWPDGA

>gi |156994172|gb|ABU99153.1| neurami ni dase [Influenza A vi rus
 (A/Swan/I ndonesi a/Magel ang1631-57/2007(H5N1))]
 MNPNQKI I TI GSI CMVI GI VSLMLQI GNMI SI WWSHSI QKGNQHOAESI SNTNPLTEKAVASVTLAGNSS
 LCPI RGWAVHSDKDNVRI GSKGDV FVI RE PFI SC SHLEC RTFFLTQ GALLNDKHSNGTVKDRSPHRTLMS
 CPVGEAPSPYNSRFESVAWSASACHDGT SWLTI GI SGP DNEAVAVLKYNGI I TDTI KSWRNNI LRTQESE
 CACVNGSCFTVMTDGPNSGOASYKI FKMEKGGKVVKSVELDAPNYHYEECS CYPDAGEI TCVCARDNWHGSRN
 RPWVWVFNQNLQYI GYI CSGVFGDNPRPNDGTGSCGPMSPNGAYGVKGF SFKYNGVWI GRKSTNSRSG
 FEMI WDPNGWTGTDSSFSVKQDI VAI TDWSGYSGSFVQHPPELTGLDCI RPFVWELI RGRPKESTI WTSG
 SSI SFCGVNSDVTVSWWPDGA

>gi |156992255|gb|ABU99117.1| neurami ni dase [Influenza A vi rus (A/Chi cken/I ndonesi a/Soppeng1631-71/2007(H5N1))]
MNPNQKI I TI GSI CMVI GI VSLMLQI GNMI SI WVSHSI QKGNQHOAESI SNTNPLTEKAVASVTLAGNSS
LCPI RGWAVVHSDKNSI RI GSRGDFVFI REPFI SCSHLECRTEFFLTQGALLNDKHSNGTVKDRSPHRTLMS
CPVGEAPSPYNSRFESVAWSASACHDGTSWLTI GI SGPDXAVAVLKYNGI I TDTI KSWRNNI LRTQESE
CACVNGSCFTVMTDGPSSGQASYKI FKMEKGGKVVKSVELDAPNYHYEECSYDPAGEI TCVCRDNWHGNS
RPWVFSFNQONLEYQI GYI CSGVFGDNPRPNDGTGSCGPMSPNGAYGVKGF SFKYNGVWI GRKSTNSRSG
FEMI WDPNGWTGTDSSFSVKQDI VAI TDWSGYSGSFVQHPTELGLDCI RPCFWVELI RGRPKESTI WTSG
SSI SFCGVNSDTVSWSPDGAELP

>gi |129910655|gb|AB031431.1| neurami ni dase [Influenza A vi rus (A/chi cken/Moscow/2/2007(H5N1))]
MNPNQKI I TI GSI CMVI GI VSLMLQI GNMI SI WVSHSI QTGNQCOAEPI SNTKFLTEKAVASVTLAGNSS
LCPI SGWAVVYKDNSI RI GSRGDFVFI REPFI SCSHLECRTEFFLTQGALLNDKHSNGTVKDRSPHRTLMS
CPVGEAPSPYNSRFESVAWSASACHDGTSWLTI GI SGPDXAVAVLKYNGI I TDTI KSWRNNI LRTQESE
CACVNGSCFTVMTDGPSSGQASYKI FKMEKGGKVVKSVELDAPNYHYEECSYDPAGEI TCVCRDNWHGNS
RPWVFSFNQONLEYQI GYI CSGVFGDNPRPNDGTGSCGVPSPNGAYGVKGF SFKYNGVWI GRKSTNSRSG
FEMI WDPNGWTGTDSSFSVKQDI VAI TDWSGYSGSFVQHPTELGLDCI RPCFWVELI RGRPKESTI WTSG
SSI SFCGVNSDTVSWSPDGAELPFTI DK

>gi |188572132|gb|ACD65001.1| neurami ni dase [Influenza A vi rus (A/chi cken/Egypt/1709-1VI R08/2007(H5N1))]
MNPNQKI I TI GSI CMVI GI VSLMLQI GNMI SI WVSHSI QTGNQCOAEPI SNTKFLTEKAVASVTLAGNSS
LCPI SGWAVVYKDNSI RI GSRGDFVFI REPFI SCSHLECRTEFFLTQGALLNDKHSNGTVKDRSPHRTLMS
CPVGEAPSPYNSRFESVAWSASACHDGTSWLTI GI SGPDXAVAVLKYNGI I TDTI KSWRNNI LRTQESE
CACVNGSCFTVMTDGPSSGQASYKI FKMEKGGKVVKSVELDAPNYHYEECSYDPAGEI TCVCRDNWHGNS
RPWVFSFNQONLEYQI GYI CSGVFGDNPRPNDGTGSCGVPSPNGAYGVKGF SFKYNGVWI GRKSTNSRSG
FEMI WDPNGWTGTDSSFSVKQDI VAI TDWSGYSGSFVQHPTELGLDCI RPCFWVELI RGRPKESTI WTSG
SSI SFCGVNSDTVSWSPDGAELP

>gi |156994174|gb|ABU99154.1| neurami ni dase [Influenza A vi rus (A/Chi cken/I ndonesi a/Semerang1631-62/2007(H5N1))]
MNPNQKI I TI GSI CMVI GI VSLMLQI GNMI SI WVSHSI QTGNQHOSES I SNTNPLAEKAVASVTLAGNSS
LCPI RGWAVVHSDKNSI RI GSRGDFVFI REPFI SCSHLECRTEFFLTQGALLNDKHSNGTVKDRSPHRTLMS
CPVGEAPSPYNSRFESVAWSASACHDGTSWLTI GI SGPDXAVAVLKYNGI I TDTI KSWRNNI LRTQESE
CACVNGSCFTVMTDGPSSGQASYKI FKMEKGGKVVKSVELDAPNYHYEECSYDPAGEI TCVCRDNWHGNS
RPWVFSFNQONLEYQI GYI CSGVFGDNPRPNDGTGSCGPMFPNGAYGI KGF SFKYNGVWI GRKSTNSRSG
FEMI WDPNGWTGTDSSFSVKQDI VAI TDWSGYSGSFVQHPTELGLDCI RPCFWVELI RGRPKESTI WTSG
SSI SFCGVNSDTVSWSPDGA

>gi |188572134|gb|ACD65002.1| neurami ni dase [Influenza A vi rus (A/duck/Egypt/1709-3VI R08/2007(H5N1))]
MNPNQKI I TI GSI CMVI GI VSLMLQI GNMI SI WVSHPI QTGNQCOAEPI SNTKFLI EKAVASVTLVGNSS
LCPI SGWAVVYKDNSI RI GSRGDFVFI REPFI SCSHLECRTEFFLTQGALLNDKHSNGTVKDRSPHRTLMS
CPVGEAPSPYNSRFESVAWSASACHDGTSWLTI GI SGPDXAVAVLKYNGI I TDTI KSWRNNI LRTQESE
CACVNGSCFTVMTDGPSSGQASYKI FKMEKGGKVVKSVELDAPNYHYEECSYDPAGEI TCVCRDNWHGNS
RPWVFSFNQONLEYQI GYI CSGVFGDNPRPNDGTGSCGVPSPNGAYGVKGF SFKYNGVWI GRKSTNSRSG
FEMI WDPNGWTGTDSSFSVKQDI VAI TDWSGYSGSFVQHPTELGLDCI RPCFWVELI RGRPKESTI WTSG
SSI SFCGVNSDTVSWSPDGAELP

>gi |188572136|gb|ACD65003.1| neurami ni dase [Influenza A vi rus (A/chi cken/Egypt/1709-4VI R08/2007(H5N1))]
MNPNQKI I TI GSI CMVI GI VSLMLQI GNMI SI WVSHPI QTGNQCOAEPI SNTKFLI EKAVASVTLVGNSS
LCPI SGWAVVYKDNSI RI GSRGDFVFI REPFI SCSHLECRTEFFLTQGALLNDKHSNGTVKDRSPHRTLMS
CPVGEAPSPYNSRFESVAWSASACHDGTSWLTI GI SGPDXAVAVLKYNGI I TDTI KSWRNNI LRTQESE
CACVNGSCFTVMTDGPSSGQASYKI FKMEKGGKVVKSVELDAPNYHYEECSYDPAGEI TCVCRDNWHGNS
RPWVFSFNQONLEYQI GYI CSGVFGDNPRPNDGTGSCGVPSPNGAYGVKGF SFKYNGVWI GRKSTNSRSG
FEMI WDPNGWTGTDSSFSVKQDI VAI TDWSGYSGSFVQHPTELGLDCI RPCFWVELI RGRPKESTI WTSG
SSI SFCGVNSDTVSWSPDGAELPFTI D

>gi |168805416|gb|ACA28785.1| neurami ni dase [Influenza A vi rus (A/turkey/Czech Republ i c/10309-3/07(H5N1))]
NOKI I TI GSI CMVI GI VSLMLQI GNMI SI WVSHSI LTRNQRQAEPI SNTKFLTEKAVASVTLAGNSSLCP
I SGWAVVYKDNSI RI GSRGDFVFI REPFI SCSHLECRTEFFLTQGALLNDKHSNGTVKDRSPHRTLMS
CPVGEAPSPYNSRFESVAWSASACHDGTSWLTI GI SGPDXAVAVLKYNGI I TDTI KSWRNNI LRTQESE
CACVNGSCFTVMTDGPSSGQASYKI FKMEKGGKVVKSVELDAPNYHYEECSYDPAGEI TCVCRDNWHGNS
RPWVFSFNQONLEYQI GYI CSGVFGDNPRPNDGTGSCGVPVSLNGAYGVKGF SFKYNGVWI GRKSTNSRSG
FEMI WDPNGWTGTDSSFSVKQDI VAI TDWSGYSGSFVQHPTELGLDCI RPCFWVELI RGRPEESTI WTSGSSI
SFCGVNSDTVSWSPDGAELP

>gi |157678115|gb|ABV60443.1| neurami ni dase [Influenza A vi rus (A/chi cken/Krasnodar/300/07(H5N1))]
MNPNQKI I TI GSI CMVI GI VSLMLQI GNMI SI WVSHSI LTRNQRQAEPI SNTKFLTEKAVASVTLAGNSS
LCPI SGWAVVYKDNSI RI GSRGDFVFI REPFI SCSHLECRTEFFLTQGALLNDKHSNGTVKDRSPHRTLMS
CPVGEAPSPYNSRFESVAWSASACHDGTSWLTI GI SGPDXAVAVLKYNGI I TDTI KSWRNNI LRTQESE
CACVNGSCFTVMTDGPSSGQASYKI FKMEKGGKVVKSVELDAPNYHYEECSYDPAGEI TCVCRDNWHGNS
RPWVFSFNQONLEYQI GYI CSGVFGDNPRPNDGTGSCGVPVSLNGAYGVKGF SFKYNGVWI GRKSTNSRSG
FEMI WDPNGWTGTDSSFSVKQDI VAI TDWSGYSGSFVQHPTELGLDCI RPCFWVELI RGRPEESTI WTSG
SSI SFCGVNSDTVSWSPDGAELPFTI DK

>gi |161019236|gb|ABX56048.1| neurami ni dase [Influenza A vi rus (A/Cygnus cygnus/Krasnodar/329/07(H5N1))]
MNPNQKI I TI GSI CMVI GI VSLMLQI GNMI SI WGSHSI LTRNQRQAEPI SNTKFLTEKAVASVTLAGNSS
LCPI SGWAVVYKDNSI RI GSRGDFVFI REPFI SCSHLECRTEFFLTQGALLNDKHSNGTVKDRSPHRTLMS
CPVGEAPSPYNSRFESVAWSASACHDGTSWLTI GI SGPDXAVAVLKYNGI I TDTI KSWKNNI LRTQESE

CACVNGSCFTVMTDGPNSGQASYKI FKMEKGGKVVKSVELDAPNYHYEECSYCPDAGEI TCVCRDNWHGNSN
 RPWVSNFNQLEIYQI GYI CSGVFGDNPRPNDGTGSCGVPVSLNGAYGVKGFSSFKYNGVWI GRKTSTNSRSRSG
 FEMI WDPNGWTGTDSSFSVKQDI VAI TDWSGYSGSFVQHPLETLGLDCI RPCFWVELI RGRPKESTI WTSRSG
 SSI SFCGVNSDVTVSWSPDGAELPFTI DK
 >gi |166798264|gb|ABY89677.1| neurami ni dase [Influenza A virus (A/chicken/Rostov-on-
 Don/35/2007(H5N1))]
 MNPNQKI I TI GSI CMVI GI VSLMLQI GNMI SI WVSHSI QTGNQROVEPI SNTKFLTEKAVASVTLAGNSS
 LCPI SGWAVYSKDNGI RI GSRGDV FVI REPFVSCSHLECRTFFLTQGALLNDKHSNGTVKDRSPHRTLMS
 CPVGEAPSPYNSRFESVAWSASACHDGT SWLTI GI SGPDNGAVAVLK YNGI I TDTI KSWRNNI LRTQESE
 CACVNGSCFTVMTDGPNSGQASYKI FKMEKGGKVVKSVELDAPNYHYEECSYCPDAGEI TCVCRDNWHGNSN
 RPWVSNFNQLEIYQI GYI CSGVFGDNPRPNDGTGSCGVPVSPNGAYGVKGFSSFKYNGVWI GRKTSTNSRSRSG
 FEMI WDPNGWTGTDSSFSVKQDI VAI TDWSGYSGSFVQHPLETLGLDCI RPCFWVELI RGRPKESTI WTSRSG
 SSI SFCGVNSDVTVSWSPDGAELPFTI DK
 >gi |168445541|gb|ACA23996.1| neurami ni dase [Influenza A virus (A/pigeon/Rostov-on-
 Don/6/2007(H5N1))]
 MNPNQKI I TI GSI CMVI GI VSLMLQI GNMI SI WVSHSI QTGNQROVEPI SNTKFLTEKAVASVTLAGNSS
 LCPI SGWAVYSKDNGI RI GSRGDV FVI REPFVSCSHLECRTFFLTQGALLNDKHSNGTVKDRSPHRTLMS
 CPVGEAPSPYNSRFESVAWSASACHDGT SWLTI GI SGPDNGAVAVLK YNGI I TDTI KSWRNNI LRTQESE
 CACVNGSCFTVMTDGPNSGQASYKI FKMEKGGKVVKSVELDAPNYHYEECSYCPDAGEI TCVCRDNWHGNSN
 RPWVSNFNQLEIYQI GYI CSGVFGDNPRPNDGTGSCGVPVSPNGAYGVKGFSSFKYNGVWI GRKTSTNSRSRSG
 FEMI WDPNGWTGTDSSFSVKQDI VAI TDWSGYSGSFVQHPLETLGLDCI RPCFWVELI RGRPKESTI WTSRSG
 SSI SFCGVNSDVTVSWSPDGAELPFTI DK
 >gi |190683270|gb|ACE81948.1| neurami ni dase [Influenza A virus (A/rook/Rostov-on-
 Don/26/2007(H5N1))]
 MNPNQKI I TI GSI CMVI GI VSLMLQI GNMI SI WVSHSI QTGNQROVEPI SNTKFLTEKAVASVTLAGNSS
 LCPI SGWAVYSKDNGI RI GSRGDV FVI REPFVSCSHLECRTFFLTQGALLNDKHSNGTVKDRSPHRTLMS
 CPVGEAPSPYNSRFESVAWSASACHDGT SWLTI GI SGPDNGAVAVLK YNGI I TDTI KSWRNNI LRTQESE
 CACVNGSCFTVMTDGPNSGQASYKI FKMEKGGKVVKSVELDAPNYHYEECSYCPDAGEI TCVCRDNWHGNSN
 RPWVSNFNQLEIYQI GYI CSGVFGDNPRPNDGTGSCGVPVSPNGAYGVKGFSSFKYNGVWI GRKTSTNSRSRSG
 FEMI WDPNGWTGTDSSFSVKQDI VAI TDWSGYSGSFVQHPLETLGLDCI RPCFWVELI RGRPKESTI WTSRSG
 SSI SFCGVNSDVTVSWSPDGAELPFTI DK
 >gi |168445523|gb|ACA23986.1| neurami ni dase [Influenza A virus (A/muscovy duck/Rostov-
 on-Don/51/2007(H5N1))]
 MNPNQKI I TI GSI CMVI GI VSLMLQI GNMI SI WVSHSI QTGNQROVEPI SNTKFLTEKAVASVTLAGNSS
 LCPI SGWAVYSKDNGI RI GSRGDV FVI REPFVSCSHLECRTFFLTQGALLNDKHSNGTVKDRSPHRTLMS
 CPVGEAPSPYNSRFESVAWSASACHDGT SWLTI GI SGPDNGAVAVLK YNGI I TDTI KSWRNNI LRTQESE
 CACVNGSCFTVMTDGPNSGQASYKI FKMEKGGKVVKSVELDAPNYHYEECSYCPDAGEI TCVCRDNWHGNSN
 RPWVSNFNQLEIYQI GYI CSGVFGDNPRPNDGTGSCGVPVSPNGAYGVKGFSSFKYNGVWI GRKTSTNSRSRSG
 FEMI WDPNGWTGTDSSFSVKQDI VAI TDWSGYSGSFVQHPLETLGLDCI RPCFWVELI RGRPKESTI WTSRSG
 SSI SFCGVNSDVTVSWSPDGAELPFTI DK
 >gi |115396994|gb|ABI 97324.1| neurami ni dase [Influenza A virus
 (A/chicken/Jilin/hg/2002(H5N1))]
 MNPNQKI I TI GSI CMVI GI VSLMLQI GNMI SI WVSHSI QTGNQROVEPI SNTKFLTEKAVASVTLAGNSS
 LCPI SGWAVYSKDNGI RI GSKGDV FVI REPFV SCSHLECRTFFLTQGALLNDKHSNGTVKDRSPHRTLMS
 CPVGEAPSPYNSRFESVAWSASACHDGT SWLTI GI SGPDNGAVAVLK YNGI I TDTI KSWRNNI LRTQESE
 CACVNGSCFTVMTDGPNSGQASYKI FKMEKGGKVVKSVELDAPNYHYEECSYCPDAGEI TCVCRDNWHGNSN
 RPWVSNFNQLEIYQI GYI CSGVFGDNPRPNDGTGSCGVPVSPNGAYGVKGFSSFKYNGVWI GRKTSTNSRSRSG
 FEMI WDPNGWTGTDSSFSVKQDI VAI TDWSGYSGSFVQHPLETLGLDCI RPCFWVELI RGRPKESTI WTSRSG
 SSI SFCGVNSDVTVSWSPDGAELPFTI DK
 >gi |115397015|gb|ABI 97336.1| neurami ni dase [Influenza A virus
 (A/chicken/Jilin/hh/2002(H5N1))]
 MNPNQKI I TI GSI CMVI GI VSLMLQI GNMI SI WVSHSI QTGNQROVEPI SNTKFLTEKAVASVTLAGNSS
 LCPI SGWAVYSKDNGI RI GSKGDV FVI REPFV SCSHLECRTFFLTQGALLNDKHSNGTVKDRSPHRTLMS
 CPVGEAPSPYNSRFESVAWSASACHDGT SWLTI GI SGPDNGAVAVLK YNGI I TDTI KSWRNNI LRTQESE
 CACVNGSCFTVMTDGPNSGQASYKI FKMEKGGKVVKSVELDAPNYHYEECSYCPDAGEI TCVCRDNWHGNSN
 RPWVSNFNQLEIYQI GYI CSGVFGDNPRPNDGTGSCGVPVSPNGAYGVKGFSSFKYNGVWI GRKTSTNSRSRSG
 FEMI WDPNGWTGTDSSFSVKQDI VAI TDWSGYSGSFVQHPLETLGLDCI RPCFWVELI RGRPKESTI WTSRSG
 SSI SFCGVNSDVTVSWSPDGAELPFTI DK
 >gi |115502993|gb|ABI 98930.1| neurami ni dase [Influenza A virus
 (A/chicken/Jilin/hf/2002(H5N1))]
 MNPNQKI I TI GSI CMVI GI VSLMLQI GNMI SI WVSHSI QTGNQROVEPI SNTKFLTEKAVASVTLAGNSS
 LCPI SGWAVYSKDNGI RI GSKGDV FVI REPFV SCSHLECRTFFLTQGALLNDKHSNGTVKDRSPHRTLMS
 CPVGEAPSPYNSRFESVAWSASACHDGT SWLTI GI SGPDNGAVAVLK YNGI I TDTI KSWRNNI LRTQESE
 CACVNGSCFTVMTDGPNSGQASYKI FKMEKGGKVVKSVELDAPNYHYEECSYCPDAGEI TCVCRDNWHGNSN
 RPWVSNFNQLEIYQI GYI CSGVFGDNPRPNDGTGSCGVPVSPNGAYGVKGFSSFKYNGVWI GRKTSTNSRSRSG
 FEMI WDPNGWTGTDSSFSVKQDI VAI TDWSGYSGSFVQHPLETLGLDCI RPCFWVELI RGRPKESTI WTSRSG
 SSI SFCGVNSDVTVSWSPDGAELPFTI DK
 >gi |115343524|gb|ABI 94742.1| neurami ni dase [Influenza A virus
 (A/chicken/Hubei/wf/2002(H5N1))]
 MNPNQKI I TI GSI CMVI GI VSLMLQI GNMI SI WVSHSI QTGNQROVEPI SNTKFLTEKAVASVTLAGNSS
 LCPI SGWAVYSKDNGI RI GSKGDV FVI REPFV SCSHLECRTFFLTQGALLNDKHSNGTVKDRSPHRTLMS
 CPVGEAPSPYNSRFESVAWSASACHDGT SWLTI GI SGPDNGAVAVLK YNGI I TDTI KSWRNNI LRTQESE
 CACVNGSCFTVMTDGPNSGQASYKI FKMEKGGKVVKSVELDAPNYHYEECSYCPDAGEI TCVCRDNWHGNSN
 RPWVSNFNQLEIYQI GYI CSGVFGDNPRPNDGTGSCGVPVSPNGAYGVKGFSSFKYNGVWI GRKTSTNSRSRSG
 FEMI WDPNGWTGTDSSFSVKQDI VAI TDWSGYSGSFVQHPLETLGLDCI RPCFWVELI RGRPKESTI WTSRSG
 SSI SFCGVNSDVTVSWSPDGAELPFTI DK

>gi |115343537|gb|ABI 94748.1| neurami ni dase [Influenza A vi rus
(A/duck/Hubei /wg/2002(H5N1))]
MNPNQKI I TI GSI CMVI GI VSLMLQI GNI I SI WWSHSI QTGNQHOAEPI SNTNFLTEKAVASVTLAGNSS
LCPI SGWAVHSDKDNGI RI GSKGDV FVI REPFI SCSHLECRTFFLTQGALLNDKHSNGTVKDRSPHRTLMS
CPVGEAPSPYNSRFESVAWSASACHDGT SWLTI GI SGPDNGAVAVLK YNGI I TDTI KSWRNNI LRTQESE
CACVNGSCFTVMTDGP SNGQASYKI FRI EKGKVVKS AELNAPNYHYEECSY PDAGEI TCVC RDNWHG SN
RPWV SFNQNLEYQI GYI CSGVFGDNPRPNDGTGSCGPVSPNGAYGI KGF SFKYNGVWI GR TKSTNSRSG
FEMI WDPNGWTGTD SNFSVRQDI VAI TDWSGYSGSFVQHP ELTGLDCI RPCFWVELI RGRPK ESTI WTS G
SSI SFCGVNSDTVGWSPDGAELPFTI DK

>gi |115382884|gb|ABI 96768.1| neurami ni dase [Influenza A vi rus
(A/chi cken/Ji angsu/cz1/2002(H5N1))]
MNPNQKI TTI GSI CMVI GI VSLMLQI GNI I SI WWSHSI QTGNQHOAEPCNQSI I TYENNTWVNQTYVNI S
NTKFLAEKAVASVTLAGNSSLCPI SGWAVHSDKDNGI RI GSKGDV FVI REPFI SCSHLECRTFFLTQGALL
NDKHSNGTVKDRSPHRTLMSCPVGEAPSPYNSRFESVAWSASACHDGT SWLTI GI SGPDNGAVAVLK YNG
I I TDTI KSWRNNI LRTQESECACVNGSCFTVMTDGP SNGQASYKI FRI EKGKVVKS AELNAPNYHYEECS
CYPDAGEI TCVC RDNWHG SNRPWV SFNQNLEYQI GYI CSGVFGDNPRPNDGTGSCGPVSPNGAYGI KGF S
FKYNGVWI GR TKSTNSRSGFEMI WDPNGWTGTD SNFSVKQDI VAI TDWSGYSGSFVQHP ELTGLDCI RP
CFWVELI RGRPK ESTI WTS GSSI SFCGVNSDTVGWSPDGAELPFTI DK

>gi |47156379|gb|AAT12077.1| neurami ni dase [Influenza A vi rus
(A/duck/Guangxi /53/2002(H5N1))]
MNPNQKI TI GSI CMAI GTVSLMLQI GNI I SI WWSHSI QTENQHOAEPI SNTNFLTEKAVASVTLAGNSS
LCPI SGWAVHSDKDNGI RI GSKGDV FVI REPFI SCSHLECRTFFLTQGALLNDKHSNGTVKDRSPHRTLMS
CPVGEAPSPYNSRFESVAWSASACHDGT SWLTI GI SGPDNGAVAVLK YNGI I TDTI KSWRNNI LRTQESE
CACVNGSCFTVMTDGP SNGQASYKI FRI EKGKVVKS AELNAPNYHYEECSY PDAGEI TCVC RDNWHG SN
RPWV SFNQNLEYQI GYI CSGVFGDNPRPNDGTGSCGPVSPNGAYG VKGF SFKYNGVWI GR TKSTNSRSG
FEMI WDPNGWTGTD SSVSVKQDI VAI TDWSGYSGSFVQHP ELTGLDCI RPCFWVELI RERPK ESTTWTSG
SSI SFCGVNSDTVGWSPDGAELPFTI DK

>gi |47156367|gb|AAT12071.1| neurami ni dase [Influenza A vi rus
(A/duck/Guangdong/22/2002(H5N1))]
MNPNQKI I TI GSI CMAI GI VSLMLQI GNI I PI WWSHSI QTGNQHOAEPCNQSI I TYENNTWVNQTYVNI N
NTNFLTEKAVASVTLAGNSSLCPI SGWAVYSKDNGI RI GSKGDV FVI REPFI SCSHLECRTFFLTQEALL
NDKHSNGTVKDRSPYRTLMSCPVGEAPSPYNSRFESVAWSASACHDGT SWLTI GI SGPDNGAVAVLK YNG
I I TDTI KSWRNNI LRTQESECACVNGSCFTVMTDGP SNGQASYKI FRI EKGKVVKS AELNAPNYHYEECS
CYLDAGEI TCVC RDNWHG SNRPWV SFNQNLEYQI GYI CSGVFGDNPRPNDGTGSCGPVSPNGAHGI KGF S
FKYNGVWI GR TKSTNSRSGFEMI WDPNGWTGTD SNFSVKQDI VAI TDWSGYSGSFVQHP ELTGLDCI RP
CFWVELI RGRPK ESTI WTS GSSI SFCGVNSDTVGWSPDGAELPFTI DK

>gi |47156353|gb|AAT12064.1| neurami ni dase [Influenza A vi rus
(A/duck/Fuj i an/01/2002(H5N1))]
MNPNQKI I TI GSI CMVI GI VSLMLQI GNI I SI WWSHSI QTENQHOAEPI SNTNFLTEKAVASVTLAGNSS
LCPI SGWAVHSDKDNGI RI GSKGDV FVI REPFI SCSHLECRTFFLTQGALLNDKHSNGTVKDRSPHRTLMS
CPVGEAPSPYNSRFESVAWSASACHDGT SWLTI GI SGPDNGAVAVLK YNGI I TDTI KSWRNNI LRTQESE
CACVNGSCFTVMTDGP SNGQASYKI FRI EKGKVVKS AELNAPNYHYEECSY PDAGEI TCVC RDNWHG SN
RPWV SFNQNLEYQI GYI CSGVFGDNPRPNDGTGSCGPVSPNGAYG VKGF SFKYNGVWI GR TKSTNSRSG
FEMI WDPNGWTGTD SSVSVKQDI VAI TDWSGYSGSFVQHP ELTGLDCI RPCFWVELI RGRPK ESTI WTS G
SSI SFCGVNSDTVGWSPDGAELPFTI DK

>gi |47156355|gb|AAT12065.1| neurami ni dase [Influenza A vi rus
(A/duck/Fuj i an/13/2002(H5N1))]
MNPNQKI I TI GSI CMVI GI VSLMLQI GNI I SI WWSHSI QTENQHOAEPI SNTNFLTEKAVASVTLAGNSS
LCPI SGWAVHSDKDNGI RI GSKGDV FVI REPFI SCSHLECRTFFLTQGALLNDKHSNGTVKDRSPHRTLMS
CPVGEAPSPYNSRFESVAWSASACHDGT SWLTI GI SGPDNGAVAVLK YNGI I TDTI KSWRNNI LRTQESE
CACVNGSCFTVMTDGP SNGQASYKI FRI EKGKVVKS AELNAPNYHYEECSY PDAGEI TCVC RDNWHG SN
RPWV SFNQNLEYQI GYI CSGVFGDNPRPNDGTGSCGPVSPNGAYG VKGF SFKYNGVWI GR TKSTNSRSG
FEMI WDPNGWTGTD SSVSVKQDI VAI TDWSGYSGSFVQHP ELTGLDCI RPCFWVELI RGRPK ESTI WTS G
SSI SFCGVNSDTVGWSPDGAELPFTI DK

>gi |115382759|gb|ABI 96702.1| neurami ni dase [Influenza A vi rus
(A/chi cken/Henan/wu/2004(H5N1))]
MNPNQKI I TI GSI CMVI GI VSLMLQI GNI I SI WWSHSI QTGNQHOAEPI SNTNFLTEKAVASVTLAGNSS
LCPI SGWAVHSDKDNGI RI GSKGDV FVI REPFI SCSHLECRTFFLTQGALLNDKHSNGTVKDRSPHRTLMS
CPVGEAPSPYNSRFESVAWSASACHDGT SWLTI GI SGPDNGAVAVLK YNGI I TDTI KSWRNNI LRTQESE
CACVNGSCFTVMTDGP SNGQASYKI FRI EKGKVVKS AELNAPNYHYEECSY PDAGEI TCVC RDNWHG SN
RPWV SFNQNLEYQI GYI CSGVFGDNPRPNDGTGSCGPVSPNGAYG VKGF SFKYNGVWI GR TKSTNSRSG
FEMI WDPNGWTGTD SSVSVKQDI VAI TDWSGYSGSFVQHP ELTGLDCI RPCFWVELI RGRPK ESTI WTS G
SSI SFCGVNSDTVGWSPDGAELPFTI DK

>gi |110287941|gb|ABG65734.1| neurami ni dase [Influenza A vi rus
(A/goose/Huadong/220/2004(H5N1))]
MNPNQKI I TI GSI CMVI GI VSLMLQI GNI I SI WWSHSI QEGNQHOAEPI SNI NFI TEKAVASVTLAGNSS
LCPI SGWAVHSDKDNGI RI GSKGDV FVI REPFI SCSHLECRTFFLTQGALLNDKHSNGTVKDRSPHRTLMS
CPVGEAPSPYNSRFESVAWSASACHDGI SWLTI GI SGPDNGAVAVLK YNGI I TDTI KSWRNNI LRTQESE
CACVNGSCFTVMTDGP SNGQASYKI FRI EKGKVVKS AELNAPNYHYEECSY PDAGEI TCVC RDNWHG SN
RPWV SFNQNLEYQI GYI CSGVFGDNPRPNDGTGSCGPVSPNGAYG VKGF SFKYNGVWI GR TKSTNSRSG
FEMI WDPNGWTGTD SSVSVKQDI VAI TDWSGYSGSFVQHP ELTGLDCI RPCFWVELI RGRPK ESTI WTS G
SSI SFCGVNSDTVGWSPDGAELPFTI DK

>gi |111433453|gb|ABH09780.1| neurami ni dase [Influenza A vi rus
(A/chi cken/Vi etnam/486A/2004(H5N1))]
MNPNQKI I TI GSI CMVTGI VSLMLQVGNMI SI WWSHSI HTGNQHOAEPI SNTNFLTEKAVASVTLAGNSS
LCPI NGWAVYSKDNGI RI GSKGDV FVI REPFI SCSHLECRTFFLTQGALLNDKHSNGTVKDRSPHRTLMS
CPVGEAPSPYNSRFESVAWSASACHDGT SWLTI GI SGPDNGAVAVLK YNGI I TDTI KSWRNNI LRTQESE

CACVNGSCFTVMTDGPNSGOASHKI FKMEKGGKVVKSVELDAPNYHYEECSYCPDAGEI TCVCARDNWHGNS
 RPWVFNQNLKQI GYI CSGVFGDNPRNDGTGSCGPVSSNGAYGVKGFSSFKYNGVWI GRKSTNSRSR
 FEMI WDPNGWTE TDSSFSVKQDI VAI TDWSGYSGSFVQHPGLTGLDCI RPCFWVELI RGRPKESTI WTS
 SSI SFCGVNSDVTGWSWPDGAELPSP

>gi |119368927|gb|ABL67772.1| neurami ni dase [Influenza A virus (A/open-billed
 stork/Nakhonsawan/BBD0104F/2004(H5N1))]
 MNPNKKI I TI GSI CMVTGMVSLMLQI GNLI SI WVSHSI HTGNOHKAPEI SNTNFLTTEKAVASV
 KLAGNSS LCPI NGWAVYSKDNSI RI GSKGDV FVI RE PFI SCSHLECR TFFLTQ GALLNDKHSNGT
 VKDRSPHRT LMS CPVGEAPSPYNSRFESVAWSASACHDGT SWLTI GI SGPDNGAVAVLK YNGI I TDTI
 KSWRNNI LRTQESE CACVNGSCFTVMTDGPNSGOASHKI FKMEKGGKVVKSVELDAPNYHYEECSYCPDAGEI
 TCVCARDNWHGNS RPWVFNQNLKQI GYI CSGVFGDNPRNDGTGSCGPVSSNGAYGVKGFSSFKYNGVWI
 GRKSTNSRSR FEMI WDPNGWTE TDSSFSVKQDI VAI TDWSGYSGSFVQHPGLTGLDCI RPCFWVELI
 RGRPKESTI WTS SSI SFCGVNSDVTGWSWPDGAELPFTI DK

>gi |119368946|gb|ABL67783.1| neurami ni dase [Influenza A virus (A/open-billed
 stork/Nakhonsawan/BBD0404F/2004(H5N1))]
 MNPNKKI I TI GSI CMVTGMVSLMLQI GNLI SI WVSHSI HTGNOHKAPEI SNTNFLTTEKAVASV
 KLAGNSS LCPI NGWAVYSKDNSI RI GSKGDV FVI RE PFI SCSHLECR TFFLTQ GALLNDKHSNGT
 VKDRSPHRT LMS CPVGEAPSPYNSRFESVAWSASACHDGT SWLTI GI SGPDNGAVAVLK YNGI I TDTI
 KSWRNNI LRTQESE CACVNGSCFTVMTDGPNSGOASHKI FKMEKGGKVVKSVELDAPNYHYEECSYCPDAGEI
 TCVCARDNWHGNS RPWVFNQNLKQI GYI CSGVFGDNPRNDGTGSCGPVSSNGAYGVKGFSSFKYNGVWI
 GRKSTNSRSR FEMI WDPNGWTE TDSSFSVKQDI VAI TDWSGYSGSFVQHPGLTGLDCI RPCFWVELI
 RGRPKESTI WTS SSI SFCGVNSDVTGWSWPDGAELPFTI DK

>gi |119368969|gb|ABL67796.1| neurami ni dase [Influenza A virus (A/open-billed
 stork/Suphanburi /TSD0912F/2004(H5N1))]
 MNPNKKI I TI GSI CMVTGMVSLMLQI GNLI SI WVSHSI HTGNOHKAPEI SNTNFLTTEKAVASV
 KLAGNSS LCPI NGWAVYSKDNSI RI GSKGDV FVI RE PFI SCSHLECR TFFLTQ GALLNDKHSNGT
 VKDRSPHRT LMS CPVGEAPSPYNSRFESVAWSASACHDGT SWLTI GI SGPDNGAVAVLK YNGI I TDTI
 KSWRNNI LRTQESE CACVNGSCFTVMTDGPNSGOASHKI FKMEKGGKVVKSVELDAPNYHYEECSYCPDAGEI
 TCVCARDNWHGNS RPWVFNQNLKQI GYI CSGVFGDNPRNDGTGSCGPVSSNGAYGVKGFSSFKYNGVWI
 GRKSTNSRSR FEMI WDPNGWTE TDSSFSVKQDI VAI TDWSGYSGSFVQHPGLTGLDCI RPCFWVELI
 RGRPKESTI WTS SSI SFCGVNSDVTGWSWPDGAELPFTI DK

>gi |132653825|gb|AB034194.1| neurami ni dase [Influenza A virus (A/open-billed
 stork/Bangkok/LBD0111F/04(H5N1))]
 QKQEFKMNPNKKI I TI GSI CMVTGMVSLMLQI GNLI SI WVSHSI HTGNOHKAPEI SNTNFLTTEKAVASV
 KLAGNSS LCPI NGWAVYSKDNSI RI GSKGDV FVI RE PFI SCSHLECR NFFLTQ GALLNDKHSNGT
 VKDRSPHRT LMS HRTLMSCPVGEAPSPYNSRFESVAWSASACHDGT SWLTI GI SGPDNGAVAVLK YNGI I
 TDTI KSWRNNI L RTQESE CACVNGSCFTVMTDGPNSGOASHKI FKMEKGGKVVKSVELDAPNYHYEECSYCPDAGEI
 TCVCARDNWHGNS RPWVFNQNLKQI GYI CSGVFGDNPRNDGTGSCGPVSSNGAYGVKGFSSFKYNGVWI
 GRKSTNSRSR FEMI WDPNGWTE TDSSFSVKQDI VAI TDWSGYSGSFVQHPGLTGLDCI RPCFWVELI
 RGRPKESTI WTS SSI SFCGVNSDVTGWSWPDGAELPFTI DK

>gi |132653827|gb|AB034195.1| neurami ni dase [Influenza A virus (A/open-billed
 stork/Bangkok/LBD0511F/04(H5N1))]
 QKQEFKMNPNKKI I TI GSI CMVTGMVSLMLQI GNLI SI WVSHSI HTGNOHKAPEI SNTNFLTTEKAVASV
 KLAGNSS LCPI NGWAVYSKDNSI RI GSKGDV FVI RE PFI SCSHLECR TFFLTQ GALLNDKHSNGT
 VKDRSPHRT LMS HRTLMSCPVGEAPSPYNSRFESVAWSASACHDGT SWLTI GI SGPDNGAVAVLK YNGI I
 TDTI KSWRNNI L RTQESE CACVNGSCFTVMTDGPNSGOASHKI FKMEKGGKVVKSVELDAPNYHYEECSYCPDAGEI
 TCVCARDNWHGNS RPWVFNQNLKQI GYI CSGVFGDNPRNDGTGSCGPVSSNGAYGVKGFSSFKYNGVWI
 GRKSTNSRSR FEMI WDPNGWTE TDSSFSVKQDI VAI TDWSGYSGSFVQHPGLTGLDCI RPCFWVELI
 RGRPKESTI WTS SSI SFCGVNSDVTGWSWPDGAELPFTI DK

>gi |50296137|gb|AAT73316.1| neurami ni dase [Influenza A virus
 (A/Dk/Indonesia/MS/2004(H5N1))]
 MNPNQKI I TI GSI CMVI GI VSLMLQI GNMI SI WVSHSI QTGNOHQSESI SNTNPLTEKAVASV
 TLAGNSS LCPI NGWAVHSKDNSI RI GSKGDV FVI RE PFI SCSHLECR TFFLTQ GALLNDKHSNGT
 VKDRSPHRT LMS CPVGEAPSPYNSRFESVAWSASACHDGT SWLTI GI SGPDNGAVAVLK YNGI I TDTI
 KSWRNNI LRTQESE CACVNGSCFTVMTDGPNSGOASYKI FKMEKGGKVVKSVELDAPNYHYEECSYCPDAGEI
 TCVCARDNWHGNS RPWVFNQNLKQI GYI CSGVFGDNPRNDGTGSCGPVSSNGAYGVKGFSSFKYNGVWI
 GRKSTNSRSR FEMI WDPNGWTE TDSSFSVKQDI VAI TDWSGYSGSFVQHPGLTGLDCI RPCFWVELI
 RGRPKESTI WTS SSI SFCGVNSDVTGWSWPDGAELPFTI DK

>gi |48431280|gb|AAS89184.2| neurami ni dase [Influenza A virus (A/chicken/Nakorn-
 Patom/Thai Land/CU-2/2004(H5N1))]
 TI GSI CMVTGMVSLMLQI GNLI SI WVSHSI HTGNOHKAPEI SNTNFLTTEKAVASV KLAGNSS LCPI NGWA
 VYSKDNSI RI GSKGDV FVI RE PFI SCSHLECR TFFLTQ GALLNDKHSNGT VKDRSPHRT LMS CPVGEAP
 SPYNSRFESVAWSASACHDGT SWLTI GI SGPDNGAVAVLK YNGI I TDTI KSWRNNI LRTQESE CACVNGSC
 FTVMTDGPNSGOASHKI FKMEKGGKVVKSVELDAPNYHYEECSYCPDAGEI TCVCARDNWHGNS RPWVFNQ
 NLEYQI GYI CSGVFGDNPRNDGTGSCGPVSSNGAYGVKGFSSFKYNGVWI GRKSTNSRSR FEMI WDPN
 GWTE TDSSFSVKQDI VAI TDWSGYSGSFVQHPGLTGLDCI RPCFWVELI RGRPKESTI WTS SSI SFCGV
 NSDVTGWSWPDGAELPFTI DK

>gi |71277737|gb|AAZ30016.1| neurami ni dase [Influenza A virus (A/sparrow/Phang-
 Nga/Thai Land/CU-203/04(H5N1))]
 MNPNKKI I TI GSI CMVTGMVSLMLQI GNLI SI WVSHSI HTGNOHKAPEI SNTNFLTTEKAVASI
 KLAGNSS LCPI NGWAVYSKDNSI RI GSKGDV FVI RE PFI SCSHLECR TFFLTQ GALLNDKHSNGT
 VKDRSPHRT LMS CPVGEAPSPYNSRFESVAWSASACHDGT SWLTI GI SGPDNGAVAVLK YNGI I TDTI
 KSWRNNI LRTQESE CACVNGSCFTVMTDGPNSGOASHKI FKMEKGGKVVKSVELDAPNYHYEECSYCPDAGEI
 TCVCARDNWHGNS RPWVFNQNLKQI GYI CSGVFGDNPRNDGTGSCGPVSSNGAYGVKGFSSFKYNGVWI
 GRKSTNSRSR FEMI WDPNGWTE TDSSFSVKQDI VAI TDWSGYSGSFVQHPGLTGLDCI RPCFWVELI
 RGRPKESTI WTS SSI SFCGVNSDVTGWSWPDGAELPFTI D

>gi |71277739|gb|AAZ30017.1| neurami ni dase [Influenza A virus (A/Mynas/Ranong/Thai Land/CU-209/04(H5N1))]
MNPNQKI I TI GSI CMVTGI VSLMLQVGNMI SI WWSHSI HTGNQHQAEPI SNTNFLTEKAVASVLAGNS
LCPI NGWAVYSKDNSI RI GSKGDV FVI REPFI SCSHLECRTEFFLTQGALLNDKHSNGTVKDRSPHRTLMS
CPVGEAPSPYNSRFESVAWSASACHDGT SWLTI GI SGPDNGAVAVLK YNGI I TDTI KSWRNNI LRTQESE
CACVNGSCFTVMTDGP SNGQASHKI FKMEKGGVVKSVELDAPNYHYEECSYDPAGEI TCVCRDNWHGNS
RPWVSFNONLEYQI GYI CSGVFGDNPRPNDGTGSCGPVSSNGAYGVKGF SFKYNGVWI GRKSTNSRSG
FEMI WDPNGWTE TDSSFSVKQDI VAI TDWSGYSGSFVQHP ELTGLDCI RPCFWVELI RGRPKESTI WTS
SSI SFCGVNSDTVGWSPDGAELPFTI DK

>gi |72398577|gb|AAZ72706.1| neurami ndase [Influenza A virus (A/chicken/Viet Nam/TN-025/2004(H5N1))]
MNPNQKI I TI GSI CMVTGI VSLMLQVGNMI SI WWSHSI HTGNQHQAEPI SNTNFLTEKAVASVLAGNS
LCPI NGWAVYSKDNSI RI GSKGDV FVI REPFI SCSHLECRTEFFLTQGALLNDKHSNGTVKDRSPHRTLMS
CPVGEAPSPYNSRFESVAWSASACHDGT SWLTI GI SGPDNGAVAVLK YNGI I TDTI KSWRNNI LRTQESE
CACVNGSCFTVMTDGP SNGQASHKI FKMEKGGVVKSVELDAPNYHYEECSYDPAGEI TCVCRDNWHGNS
RPWVSFNONLEYQI GYI CSGVFGDNPRPNDGTGSCGPVSSNGAYGVKGF SFKYNGVWI GRKSTNSRSG
FEMI WDPNGWTE TDSSFSVKQDI VAI TDWSGYSGSFVQHP ELTGLDCI RPCFWVELI RGRPKESTI WTS
SSI SFCGVNSDTVGWSPDGAELPFTI DK

>gi |72398579|gb|AAZ72707.1| neurami ndase [Influenza A virus (A/chicken/Viet Nam/VL-008/2004(H5N1))]
MNPNQKI I TI GSI CMVTGI VSLMLQVGNMI SI WWSHSI HTGNQHQAEPI SNTNFLTEKAVASVLAGNS
LCPI NGWAVYSKDNSI RI GSKGDV FVI REPFI SCSHLECRTEFFLTQGALLNDKHSNGTVKDRSPHRTLMS
CPVGEAPSPYNSRFESVAWSASACHDGT SWLTI GI SGPDNGAVAVLK YNGI I TDTI KSWRNNI LRTQESE
CACVNGSCFTVMTDGP SNGQASHKI FKMEKGGVVKSVELDAPNYHYEECSYDPAGEI TCVCRDNWHGNS
RPWVSFNONLEYQI GYI CSGVFGDNPRPNDGTGSCGPVSSNGAYGVKGF SFKYNGVWI GRKSTNSRSG
FEMI WDPNGWTE TDSSFSVKQDI VAI TDWSGYSGSFVQHP ELTGLDCI RPCFWVELI RGRPKESTI WTS
SSI SFCGVNSDTVGWSPDGAELPFTI DK

>gi |72398581|gb|AAZ72708.1| neurami ndase [Influenza A virus (A/chicken/Viet Nam/AG-010/2004(H5N1))]
MNPNQKI I TI GSI CMVTGI VSLMLQVGNMI SI WWSHSI HTGNQHQAEPI SNTNFLTEKAVASVLAGNS
LCPI NGWAVYSKDNSI RI GSKGDV FVI REPFI SCSHLECRTEFFLTQGALLNDKHSNGTVKDRSPHRTLMS
CPVGEAPSPYNSRFESVAWSASACHDGT SWLTI GI SGPDNGAVAVLK YNGI I TDTI KSWRNNI LRTQESE
CACVNGSCFTVMTDGP SNGQASHKI FKMEKGGVVKSVELDAPNYHYEECSYDPAGEI TCVCRDNWHGNS
RPWVSFNONLEYQI GYI CSGVFGDNPRPNDGTGSCGPVSSNGAYGVKGF SFKYNGVWI GRKSTNSRSG
FEMI WDPNGWTE TDSSFSVKQDI VAI TDWSGYSGSFVQHP ELTGLDCI RPCFWVELI RGRPKESTI WTS
SSI SFCGVNSDTVGWSPDGAELPFTI DK

>gi |72398583|gb|AAZ72709.1| neurami ndase [Influenza A virus (A/chicken/Viet Nam/DT-015/2004(H5N1))]
MNPNQKI I TI GSI CMVTGI VSLMLQVGNMI SI WWSHSI HTGNQHQAEPI SNTNFLTEKAVASVLAGNS
LCPI NGWAVYSKDNSI RI GSKGDV FVI REPFI SCSHLECRTEFFLTQGALLNDKHSNGTVKDRSPHRTLMS
CPVGEAPSPYNSRFESVAWSASACHDGT SWLTI GI SGPDNGAVAVLK YNGI I TDTI KSWRNNI LRTQESE
CACVNGSCFTVMTDGP SNGQASHKI FKMEKGGVVKSVELDAPNYHYEECSYDPAGEI TCVCRDNWHGNS
RPWVSFNONLEYQI GYI CSGVFGDNPRPNDGTGSCGPVSSNGAYGVKGF SFKYNGVWI GRKSTNSRSG
FEMI WDPNGWTE TDSSFSVKQDI VAI TDWSGYSGSFVQHP ELTGLDCI RPCFWVELI RGRPKESTI WTS
SSI SFCGVNSDTVGWSPDGAELPFTI DK

>gi |72398585|gb|AAZ72710.1| neurami ndase [Influenza A virus (A/chicken/Viet Nam/CT-018/2004(H5N1))]
MNPNQKI I TI GSI CMVTGI VNLMLQVGNMI SI WWSHSI HTGNQHQAEPI SNTNFLTEKAVASVLAGNS
LCPI NGWAVYSKDNSI RI GSKGDV FVI REPFI SCSHLECRTEFFLTQGALLNDKHSNGTVKDRSPHRTLMS
CPVGEAPSPYNSRFESVAWSASACHDGT SWLTI GI SGPDNGAVAVLK YNGI I TDTI KSWRNNI LRTQESE
CACVNGSCFTVMTDGP SNGQASHKI FKMEKGGVVKSVELDAPNYHYEECSYDPAGEI TCVCRDNWHGNS
RPWVSFNONLEYQI GYI CSGVFGDNPRPNDGTGSCGPVSSNGAYGVKGF SFKYNGVWI GRKSTNSRSG
FEMI WDPNGWTE TDSSFSVKQDI VAI TDWSGYSGSFVQHP ELTGLDCI RPCFWVELI RGRPKESTI WTS
SSI SFCGVNSDTVGWSPDGAELPFTI DK

>gi |72398587|gb|AAZ72711.1| neurami ndase [Influenza A virus (A/chicken/Viet Nam/TG-023/2004(H5N1))]
MNPNQKI I TI GSI CMVTGI VNLMLQVGNMI SI WWSHSI HTGNQHQAEPI SNTNFLTEKAVASVLAGNS
LCPI NGWAVYSKDNSI RI GSKGDV FVI REPFI SCSHLECRTEFFLTQGALLNDKHSNGTVKDRSPHRTLMS
CPVGEAPSPYNSRFESVAWSASACHDGT SWLTI GI SGPDNGAVAVLK YNGI I TDTI KSWRNNI LRTQESE
CACVNGSCFTVMTDGP SNGQASHKI FKMEKGGVVKSVELDAPNYHYEECSYDPAGEI TCVCRDNWHGNS
RPWVSFNONLEYQI GYI CSGVFGDNPRPNDGTGSCGPVSSNGAYGVKGF SFKYNGVWI GRKSTNSRSG
FEMI WDPNGWTE TDSSFSVKQDI VAI TDWSGYSGSFVQHP ELTGLDCI RPCFWVELI RGRPKESTI WTS
SSI SFCGVNSDTVGWSPDGAELPFTI DK

>gi |72398589|gb|AAZ72712.1| neurami ndase [Influenza A virus (A/chicken/Viet Nam/LA-024/2004(H5N1))]
MNPNQKI I TI GSI CMVTGI VSLMLQVGNMI SI WWSHSI HTGNQHQAEPI SNTNFLTEKAVASVLAGNS
LCPI NGWAVYSKDNSI RI GSKGDV FVI REPFI SCSHLECRTEFFLTQGALLNDKHSNGTVKDRSPHRTLMS
CPVGEAPSPYNSRFESVAWSASACHDGT SWLTI GI SGPDNGAVAVLK YNGI I TDTI KSWRNNI LRTQESE
CACVNGSCFTVMTDGP SNGQASHKI FKMEKGGVVKSVELDAPNYHYEECSYDPAGEI TCVCRDNWHGNS
RPWVSFNONLEYQI GYI CSGVFGDNPRPNDGTGSCGPVSSNGAYGVKGF SFKYNGVWI GRKSTNSRSG
FEMI WDPNGWTE TDSSFSVKQDI VAI TDWSGYSGSFVQHP ELTGLDCI RPCFWVELI RGRPKESTI WTS
SSI SFCGVNSDTVGWSPDGAELPFTI DK

>gi |72398591|gb|AAZ72713.1| neurami ndase [Influenza A virus (A/chicken/Viet Nam/HCM-022/2004(H5N1))]
MNPNQKI I TI GSI CMVTGI VNLMLQVGNMI SI WWSHSI HTGNQHQAEPI SNTNFLTEKAVASVLAGNS
LCPI NGWAVYSKDNSI RI GSKGDV FVI REPFI SCSHLECRTEFFLTQGALLNDKHSNGTVKDRSPHRTLMS
CPVGEAPSPYNSRFESVAWSASACHDGT SWLTI GI SGPDNGAVAVLK YNGI I TDTI KSWRNNI LRTQESE

CACVNGSCFTVMTDGPNSGOASHKI FKMEKGGVVKSVELDAPNYHYEECSYCPDAGEI TCVCRDNWHGNSN
 RPWVFNQNLLEYQI GYI CSGVFGDNPRPNDGTGSCGVPSSNGAYGVKGFYKYGNGVWI GRKTKSTNSRSG
 FEMI WDPNGWTE TDSSFSVKQDI VAI TDWSGYSGSFVQHPPELTGLDCI RPCFWVELI RGRPKESTI WTSG
 SSI SFCGVNSDVTGWSWPDGAELPFTI DK
 >gi |8572169|gb|AAF77036.1|AF250356_1 neurami ni dase [Influenza A virus
 (A/Brevig_Mi ssi on/1/18(H1N1))]
 MNPNQKI I TI GSI CMVVG I SLI LOI GNI I SI WSHSI QTGNQNHPTCNQSI I TYENNTWVNOQTVNI S
 NTNVAAGQDATSVI LTGNSSLCPI SGWAI YSKDNGI RI GSKGDVFI REFFI SCSHLECRFFLTOGALL
 NDKHNSGTVKDRSPYR TLMSCPVGEAPSPYNSRFESVAWSASACHDGMGWLTI GI SGPDDGAVAVLKYN
 I I TDTI KSWRNNI LRTQESEACVNGSCFTI MTDGPNNGOASYKI LKI EKGKVTCSI ELNAPNYHYEECS
 CYPDTGKVMCVCRDNWHGNSRNPWVWFDQNLDYQI GYI CSGVFGDNPRPNDGTGSCGVPSSNGANGI KGFS
 FRYDNGVWI GRKTKSTSSRSGFEMI WDPNGWTE TDSSFSVRQDI VAI TDWSGYSGSFVQHPPELTGLDCMRP
 CFWVELI RGQPKENTI WTSGSSI SFCGVNSDVTGWSWPDGAELPFSI DK
 >gi |94960376|gb|ABF47958.1| neurami ni dase [Influenza A virus (A/WSN/1933 TS61(H1N1))]
 MNPNQKI I TI GSI CMVVG I SLI LOI GNI I SI WSHSI QTGNQNHPTI CNQSI TYKVVAGQDSTSVI LT
 GNSSLCPI RGWAI HSKDNGI RI GSKGDVFI REFFI SCSHLECRFFLTOGALLNDKHSRGTFFKDRSPYR
 ALMSCPVEAPSPYNSRFESVAWSASACHDGMGWLTI GI SGPDDGAVAVLKYN I TETI KSWRNNI LRT
 QESECTVNGSCFTI MTDGPNNGOASYKI FKI EKGKVTCSI ELNAPNSHYEECSYCPDTGKVMCVCRDNW
 HGSNRPWVWFDQNLDYKI GYI CSGVFGDNPRPKDGTGSCGVPVADGANGVKGFSYKYGNGVWI GRKTKSDS
 SRHGFEMI WDPNGWTE TDSRFSMRQDVVAMTDRSGYSGSFVQHPPELTGLDCMRPCFWVELI RGLPEEADI
 WTSGSI I SFCGVNSDVTGWSWPDGAELPFTI DK
 >gi |194352376|gb|ACF54601.1| neurami ni dase [Influenza A virus (A/WSN/1933(H1N1))]
 MNPNQKI I TI GSI CMVVG I SLI LOI GNI I SI WSHSI QTGNQNHPTI CNQSI TYKVVAGQDSTSVI LT
 GNSSLCPI RGWAI HSKDNGI RI GSKGDVFI REFFI SCSHLECRFFLTOGALLNDKHSRGTFFKDRSPYR
 ALMSCPVEAPSPYNSRFESVAWSASACHDGMGWLTI GI SGPDDGAVAVLKYN I TETI KSWRNNI LRT
 QESECTVNGSCFTI MTDGPNNGOASYKI FKI EKGKVTCSI ELNAPNSHYEECSYCPDTGKVMCVCRDNW
 HGSNRPWVWFDQNLDYKI GYI CSGVFGDNPRPKDGTGSCGVPVADGANGVKGFSYKYGNGVWI GRKTKSDS
 SRHGFEMI WDPNGWTE TDSRFSMRQDVVAMTDRSGYSGSFVQHPPELTGLDCMRPCFWVELI RGLPEEADI
 WTSGSI I SFCGVNSDVTGWSWPDGAELPFTI DK
 >gi |324482|gb|AAA43397.1| neurami ni dase [Influenza A virus (A/WSN/1933(H1N1))]
 MNPNQKI I TI GSI CMVVG I SLI LOI GNI I SI WSHSI QTGNQNHPTI CNQSI TYKVVAGQDSTSVI LT
 GNSSLCPI RGWAI HSKDNGI RI GSKGDVFI REFFI SCSHLECRFFLTOGALLNDKHSRGTFFKDRSPYR
 ALMSCPVEAPSPYNSRFESVAWSASACHDGMGWLTI GI SGPDDGAVAVLKYN I TETI KSWRNNI LRT
 QESECTVNGSCFTI MTDGPNNGOASYKI FKI EKGKVTCSI ELNAPNSHYEECSYCPDTGKVMCVCRDNW
 HGSNRPWVWFDQNLDYKI GYI CSGVFGDNPRPKDGTGSCGVPVADGANGVKGFSYKYGNGVWI GRKTKSDS
 SRHGFEMI WDPNGWTE TDSRFSMRQDVVAMTDRSGYSGSFVQHPPELTGLDCMRPCFWVELI RGLPEEADI
 WTSGSI I SFCGVNSDVTGWSWPDGAELPFTI DK
 >gi |414309|gb|AAA91326.1| neurami ni dase [Influenza A virus (A/NWS/1933(H1N1))]
 MNPNQKI I TI GSI CMVVG I SLI LOI GNI I SI WSHSI QTGNQNHPTI CNQSI I THKVVAGQDSTSVI LT
 GNSSLCPI RGWAI HSKDNGI RI GSKGDVFI REFFI SCSHLECRFFLTOGALLNDKHSYGTGSKDRSPYR
 ALMSCPVEAPSPYNSRFESVAWSASACHDGMGWLTI GI SGPDDGAVAVLKYN I TETI KSWRNNI LRT
 QESECTVNGSCFTI MTDGPNNGOASYKI FKI EKGKVTCSI ELNAPNSHYEECSYCPDTGKVMCVCRDNW
 HGSNRPWVWFDQNLDYQI GYI CSGVFGDNPRPKDGTGSCGVPVADGANGVKGFSYRYGNGVWI GRKTKSDS
 SRHGFEMI WDPNGWTE TDSRFSVRQDVVAMTDRSGYSGSFVQHPPELTGLDCMRPCFWVELI RGQPEEETI
 WTSGSI I SFCGVNSDVTGWSWPDGAELPFTI DK
 >gi |414311|gb|AAA91327.1| neurami ni dase [Influenza A virus (A/WS/1933(H1N1))]
 MNPNQKI I TI GSI CMVVG I SLI LOI GNI I SI WSHSI QTGNQNHPTI CNQSI I TYNVAVAGQDSTSVI LT
 GNSSLCPI RGWAI HSKDNGI RI GSKGDVFI REFFI SCSHLECRFFLTOGALLNDKHSNGTVKDRSPYR
 ALMSCPVEAPSPYNSRFESVAWSASACHDGMGWLTI GI SGPDDGAVAVLKYN I TETI KSWRNNI LRT
 QESECTVNGSCFTI MTDGPNNGOASYKI FKI EKGKVTCSI ELNAPNSHYEECSYCPDTGKVMCVCRDNW
 HGSNRPWVWFDQNLDYQI GYI CSGVFGDNPRPKDGTGSCGVPVADGANGVKGFSYRYGNGVWI GRKTKSDS
 SRHGFEMI WDPNGWTE TDSRFSVRQDVVAMTDRSGYSGSFVQHPPELTGLDCMRPCFWVELI RGRPEEETI
 WTSGSI I SFCGVNSDVTGWSWPDGAELPFTI DK
 >gi |94481608|gb|ABF21334.1| neurami ni dase [Influenza A virus (A/Wilson-
 Smith/1933(H1N1))]
 MNPNQKI I TI GSI CMVVG I SLI LOI GNI I SI WSHSI QTGNQNHPTI CNQSI TYKVVAGQDSTSVI LT
 GNSSLCPI RGWAI HSKDNGI RI GSKGDVFI REFFI SCSHLECRFFLTOGALLNDKHSKGTGKDRSPYR
 ALMSCPVEAPSPYNSRFESVAWSASACHDGMGWLTI GI SGPDDGAVAVLKYN I TETI KSWRNNI LRT
 QESECTVNGSCFTI MTDGPNNGOASYKI FKI EKGKVTCSI ELNAPNSHYEECSYCPDTGKVMCVCRDNW
 HGSNRPWVWFDQNLDYKI GYI CSGVFGDNPRPKDGTGSCGVPVADGANGVKGFSYRYGNGVWI GRKTKSDS
 SRHGFEMI WDPNGWTE TDSRFSVRQDVVAMTDRSGYSGSFVQHPPELTGLDCMRPCFWVELI RGRPEEETI
 WTSGSI I SFCGVNSDVTGWSWPDGAELPFTI DK
 >gi |89782161|gb|ABD77799.1| neurami ni dase [Influenza A virus (A/Wilson-
 Smith/33(H1N1))]
 MNPNQKI I TI GSI CMVVG I SLI LOI GNI I SI WSHSI QTGNQNHPTI CNQSI I TYNVAVAGQDSTSVI LT
 GNSSLCPI RGWAI HSKDNGI RI GSKGDVFI REFFI SCSHLECRFFLTOGALLNDKHSNGTVKDRSPYR
 ALMSCPVEAPSPYNSRFESVAWSASACHDGMGWLTI GI SGPDDGAVAVLKYN I TETI KSWRNNI LRT
 QESECTVNGSCFTI MTDGPNNGOASYKI FKI EKGKVTCSI ELNAPNSHYEECSYCPDTGKVMCVCRDNW
 HGSNRPWVWFDQNLDYQI GYI CSGVFGDNPRPKDGTGSCGVPVADGANGVKGFSYRYGNGVWI GRKTKSDS
 SRHGFEMI WDPNGWTE TDSRFSVRQDVVAMTDRSGYSGSFVQHPPELTGLDCMRPCFWVELI RGRPEEETI
 WTSGSI I SFCGVNSDVTGWSWPDGAELPFTI DK
 >gi |414313|gb|AAA91328.1| neurami ni dase [Influenza A virus (A/WSN/1933(H1N1))]
 MNPNQKI I TI GSI CMVVG I SLI LOI GNI I SI WSHSI QTGNQNHPTI CNQSI TYKVVAGQDSTSVI LT
 GNSSLCPI RGWAI HSKDNGI RI GSKGDVFI REFFI SCSHLECRFFLTOGALLNDKHSRGTFFKDRSPYR
 ALMSCPVEAPSPYNSRFESVAWSASACHDGMGWLTI GI SGPDDGAVAVLKYN I TETI KSWRNNI LRT
 QESECTVNGSCFTI MTDGPNNGOASYKI FKI EKGKVTCSI ELNAPNSHYEECSYCPDTGKVMCVCRDNW
 HGSNRPWVWFDQNLDYKI GYI CSGVFGDNPRPKDGTGSCGVPVADGANGVKGFSYKYGNGVWI GRKTKSDS

SRHGFEMI WDPNGWTETDSRFSMRQDVVAMTDRSGYSGSFVQHPPELTGLDCMRPCFWVELI RGLPEEDAI
 WTSGSI | SFCGVNGDVTVDWSWPDGAELPFTI DK
 >gi | 324508 | gb | AAA43412. 1 | neurami ni dase [Influenza A virus (A/Puerto
 Rico/8/1934(Cambri dge) (H1N1))]
 MNPNQI | TI GSI CLVVGLI SLI LOI GNI | SI WI SHSI QTGSQNTGI CNQNI | TYKNSTWVKDTTSVIL
 TGNSSLCP | RGWAI YSKDNSI RI GSKGDVFI REFFI SCSHLECRFTFLTOGALLNDRHSNGTVKDRSPY
 RALMSPVGEAPSPYNSRFESVAWSASACHDGMGLTI GI SGPDNGAVAVLKYNIGI | TETI KSWRKKI LR
 TOESECACVNGSCFTI MTDGSPDGLASYKI FKI EKGKVTKSI ELNAPNSHYEECSYPTDGKVMCVCRDN
 WHGSRPWVWVFDONLDYQI GYI CSGVFGDNPRPEDGTGSCGPVYVDGANGVKGFYSYRYNGVWI GRTKSH
 SSRHGFEMI WDPNGWTETDSKFSVRQDVVAMTDRSGYSGSFVQHPPELTGLDCI RPCFWVELI RGRPKEKT
 I WTSASSI SFCGVNSDVTVDWSWPDGAELPFTI DK
 >gi | 21693173 | gb | AAM75160. 1 | AF389120_1 neurami ni dase NA [Influenza A virus (A/Puerto
 Rico/8/34/Mount Si nai (H1N1))]
 MNPNQI | TI GSI CLVVGLI SLI LOI GNI | SI WI SHSI QTGSQNTGI CNQNI | TYKNSTWVKDTTSVIL
 TGNSSLCP | RGWAI YSKDNSI RI GSKGDVFI REFFI SCSHLECRFTFLTOGALLNDRHSNGTVKDRSPY
 RALMSPVGEAPSPYNSRFESVAWSASACHDGMGLTI GI SGPDNGAVAVLKYNIGI | TETI KSWRKKI LR
 TOESECACVNGSCFTI MTDGSPDGLASYKI FKI EKGKVTKSI ELNAPNSHYEECSYPTDGKVMCVCRDN
 WHGSRPWVWVFDONLDYQI GYI CSGVFGDNPRPEDGTGSCGPVYVDGANGVKGFYSYRYNGVWI GRTKSH
 SSRHGFEMI WDPNGWTETDSKFSVRQDVVAMTDRSGYSGSFVQHPPELTGLDCMRPCFWVELI RGRPKEKT
 I WTSASSI SFCGVNSDVTVDWSWPDGAELPFTI DK
 >gi | 194304808 | gb | ACF41837. 1 | neurami ni dase [Influenza A virus (A/Puerto
 Rico/8/34(H1N1))]
 MNPNQI | TI GSI CLVVGLI SLI LOI GNI | SI WI SHSI QTGSQNTGI CNQNI | TYKNSTWVKDTTSVIL
 TGNSSLCP | RGWAI YSKDNSI RI GSKGDVFI REFFI SCSHLECRFTFLTOGALLNDRHSNGTVKDRSPY
 RALMSPVGEAPSPYNSRFESVAWSASACHDGMGLTI GI SGPDNGAVAVLKYNIGI | TETI KSWRKKI LR
 TOESECACVNGSCFTI MTDGSPDGLASYKI FKI EKGKVTKSI ELNAPNSHYEECSYPTDGKVMCVCRDN
 WHGSRPWVWVFDONLDYQI GYI CSGVFGDNPRPEDGTGSCGPVYVDGANGVKGFYSYRYNGVWI GRTKSH
 SSRHGFEMI WDPNGWTETDSKFSVRQDVVAMTDRSGYSGSFVQHPPELTGLDCMRPCFWVELI RGRPKEKT
 I WTSASSI SFCGVNSDVTVDWSWPDGAELPFTI DK
 >gi | 126599291 | gb | AB021711. 1 | neurami ni dase [Influenza A virus (A/Puerto
 Rico/8/34(H1N1))]
 MNPNQI | TI GSI CLVVGLI SLI LOI GNI | SI WI SHSI QTGSQNTGI CNQNI | TYKNSTWVKDTTSVIL
 TGNSSLCP | RGWAI YSKDNSI RI GSKGDVFI REFFI SCSHLECRFTFLTOGALLNDRHSNGTVKDRSPY
 RALMSPVGEAPSPYNSRFESVAWSASACHDGMGLTI GI SGPDNGAVAVLKYNIGI | TETI KSWRKKI LR
 TOESECACVNGSCFTI MTDGSPDGLASYKI FKI EKGKVTKSI ELNAPNSHYEECSYPTDGKVMCVCRDN
 WHGSRPWVWVFDONLDYQI GYI CSGVFGDNPRPEDGTGSCGPVYVDGANGVKGFYSYRYNGVWI GRTKSH
 SSRHGFEMI WDPNGWTETDSKFSVRQDVVAMTDRSGYSGSFVQHPPELTGLDCMRPCFWVELI RGRPKEKT
 I WTSASSI SFCGVNSDVTVDWSWPDGAELPFTI DK
 >gi | 89779326 | gb | ABD77678. 1 | neurami ni dase [Influenza A virus (A/Puerto
 Rico/8/34(H1N1))]
 MNPNQI | TI GSI CLVVGLI SLI LOI GNI | SI WI SHSI QTGSQNTGI CNQNI | TYKNSTWVKDTTSVIL
 TGNSSLCP | RGWAI YSKDNSI RI GSKGDVFI REFFI SCSHLECRFTFLTOGALLNDRHSNGTVKDRSPY
 RALMSPVGEAPSPYNSRFESVAWSASACHDGMGLTI GI SGPDNGAVAVLKYNIGI | TETI KSWRKKI LR
 TOESECACVNGSCFTI MTDGSPDGLASYKI FKI EKGKVTKSI ELNAPNSHYEECSYPTDGKVMCVCRDN
 WHGSRPWVWVFDONLDYQI GYI CSGVFGDNPRPEDGTGSCGPVYVDGANGVKGFYSYRYNGVWI GRTKSH
 SSRHGFEMI WDPNGWTETDSKFSVRQDVVAMTDRSGYSGSFVQHPPELTGLDCMRPCFWVELI RGRPKEKT
 I WTSASSI SFCGVNSDVTVDWSWPDGAELPFTI DK
 >gi | 125976186 | gb | ABN59415. 1 | neurami ni dase [Influenza A virus (A/Alaska/1935(H1N1))]
 MNPNQI | TI GSI CLVVGLI SLI LOI GNI | SI WI SHSI QTGSQNTGI CNQNI | TYKNSTWVKDTTSVIL
 TGNSSLCP | RGWAI YSKDNSI RI GSKGDVFI REFFI SCSHLECRFTFLTOGALLNDRHSNGTVKDRSPY
 RALMSPVGEAPSPYNSRFESVAWSASACHDGMGLTI GI SGPDNGAVAVLKYNIGI | TETI KSWRKKI LR
 TOESECACVNGSCFTI MTDGSPDGLASYKI FKI EKGKVTKSI ELNAPNSHYEECSYPTDGKVMCVCRDN
 WHGSRPWVWVFDONLDYQI GYI CSGVFGDNPRPEDGTGSCGPVYVDGANGVKGFYSYRYNGVWI GRTKSH
 SSRHGFEMI WDPNGWTETDSKFSVRQDVVAMTDRSGYSGSFVQHPPELTGLDCMRPCFWVELI RGRPKEKT
 I WTSASSI SFCGVNSDVTVDWSWPDGAELPFTI DK
 >gi | 194294067 | gb | ACF40128. 1 | neurami ni dase [Influenza A virus (A/New
 Jersey/13/2008(H1N1))]
 MNPNQI | TI GSI SI AI GI | SLMLQI GNI | SI WASHSI QTGSQNTGI CNQNI | TYENSTWVNHHTYVNI N
 NTNNAVAGEDKTSVTLAGNSSLCSI SGWAI YTKDNSI RI GSKGDVFI REFFI SCSHLECRFTFLTOGALL
 NDKHSNGTVKDRSPYRALSPLGEAPSPYNSKFEVAVWSASACHDGMGLTI GI SGPDNGAVAVLKYNIGI
 I | TGTI KSWKKQI LRTQSECVCMNGSCFTI MTDGSPNKAASYKI FKI EKGKVTKSI ELNAPNFHYEECS
 CYPDTGI VMCVCRDNWHGSRPWVWVWVFNQNLDYQI GYI CSGVFGDNPRPEDGEGSCNPVTVVDGANGVKGF
 YKYDNGVWI GRTKSNRLRKGFEI WDPNGWTNTDSDFSVKQDVVAI TDWSGYSGSFVQHPPELTGLDCI RP
 CFVVELVRGLPRENTTI WTSGSI | SFCGVNSDTANWSWPDGAELPFTI DK
 >gi | 189303430 | gb | ACD85790. 1 | neurami ni dase [Influenza A virus
 (A/Indiana/04/2008(H1N1))]
 MNPNQI | TI GSI SI AI GI | SLMLQI GNI | SI WASHSI QTGSQNTGI CNQNI | TYENSTWVNHHTYVNI N
 NTNNAVAGEDKTSVTLAGNSSLCSI SGWAI YTKDNSI RI GSKGDVFI REFFI SCSHLECRFTFLTOGALL
 NDKHSNGTVKDRSPYRALSPLGEAPSPYNSKFEVAVWSASACHDGMGLTI GI SGPDNGAVAVLKYNIGI
 I | TGTI KSWKKQI LRTQSECVCMNGSCFTI MTDGSPNKAASYKI FKI EKGKVTKSI ELNAPNFHYEECS
 CYPDTGI VMCVCRDNWHGSRPWVWVWVFNQNLDYQI GYI CSGVFGDNPRPEDGEGSCNPVTVVDGANGVKGF
 YKYDNGVWI GRTKSNRLRKGFEI WDPNGWTNTDSDFSVKQDVVAI TDWSGYSGSFVQHPPELTGLDCI RP
 CFVVELVRGLPRENTTI WTSGSI | SFCGVNSDTANWSWPDGAELPFTI DK
 >gi | 189303428 | gb | ACD85789. 1 | neurami ni dase [Influenza A virus
 (A/Oklahoma/03/2008(H1N1))]
 MNPNQI | TI GSI SI AI GI | SLMLQI GNI | SI WASHSI QTGSQNTGI CNQNI | TYENSTWVNHHTYVNI N
 NTNNAVAGEDKTSVTLAGNSSLCSI SGWAI YTKDNSI RI GSKGDVFI REFFI SCSHLECRFTFLTOGALL

NDKHSNGTVKDRSPYRALMSCPLGEAPSPYNSKFEVAVSASACHDGMWLT I GI SGPDNGAVAVLKYN
 I I TGTI KSWKKQI LRTQSEECVMNGSCFTI MTDGSPNKAASYKI FKI EKGKVTKSI ELNAPNFHYE
 EECSCYPDTGI VMCVCRDNWHGSRNPWVSFNQNLDYQI GYI CSGVFGDNPRPEDGEGSCNPVTV
 DGANGVKGFYSKYDNGVWI GRTKSNRLRKGFEI WDPNGWNTDSDFSVKQDVVAI TDW
 SGYSGSFVQHPPELTGLDCI RP
 CFWVELVRGLPRENTTI WTSGSSI SFCGVNSDTANWSWPDGAELPFTI DK
 >gi |189303442|gb|ACD85796.1| neurami ni dase [Influenza A virus
 (A/Illinois/06/2008(H1N1))]
 MNPNQKI I TI GSI SI AI GI I SLMLQI GNI I SI WASHSI QTGSONNTGI CNQRI I TYENSTW
 VNHHTYVNI N
 NTNNAVAGEDKTSVTLAGNSSLCSI SGWAI YTKDNSI RI GSKGDVFI REPFI SCSHLECR
 TFFLTQGALL
 NDKHSNGTVKDRSPYRALMSCPLGEAPSPYNSKFEVAVSASACHDGMWLT I GI SGPDNGAVAVLK
 YNG I I TGTI KSWKKQI LRTQSEECVMNGSCFTI MTDGSPNKAASYKI FKI EKGKVTKSI ELN
 APNFHYE
 EECSCYPDTGI VMCVCRDNWHGSRNPWVSFNQNLDYQI GYI CSGVFGDNPRPEDGEGSCNPVTV
 DGANGVKGFYSKYDNGVWI GRTKSNRLRKGFEI WDPNGWNTDSDFSVKQDVVAI TDW
 SGYSGSFVQHPPELTGLDCI RP
 CFWVELVRGLPRENTTI WTSGSSI SFCGVNSDTANWSWPDGAELPFTI DK
 >gi |193084915|gb|ACF10347.1| neurami ni dase [Influenza A virus (A/Ohio/02/2008(H1N1))]
 MNPNQKI I TI GSI SI AI GI I SLMLQI GNI I SI WASHSI QTGSONNTGI CNQRI I TYENSTW
 VNHHTYVNI N
 NTNNAVAGEDKTSVTLAGNSSLCSI SGWAI YTKDNSI RI GSKGDVFI REPFI SCSHLECR
 TFFLTQGALL
 NDKHSNGTVKDRSPYRALMSCPLGEAPSPYNSKFEVAVSASACHDGMWLT I GI SGPDNGAVAVLK
 YNG I I TGTI KSWKKQI LRTQSEECVMNGSCFTI MTDGSPNKAASYKI FKI EKGKVTKSI ELN
 APNFHYE
 EECSCYPDTGI VMCVCRDNWHGSRNPWVSFNQNLDYQI GYI CSGVFGDNPRPEDGEGSCNPVTV
 DGANGVKGFYSKYDNGVWI GRTKSNRLRKGFEI WDPNGWNTDSDFSVKQDVVAI TDW
 SGYSGSFVQHPPELTGLDCI RP
 CFWVELVRGLPRENTTI WTSGSSI SFCGVNSDTANWSWPDGAELPFTI DK
 >gi |193084909|gb|ACF10344.1| neurami ni dase [Influenza A virus
 (A/Tennessee/03/2008(H1N1))]
 MNPNQKI I TI GSI SI AI GI I SLMLQI GNI I SI WASHSI QTGSONNTGI CNQRI I TYENSTW
 VNHHTYVNI N
 NTNNAVAGEDKTSVTLAGNSSLCSI SGWAI YTKDNSI RI GSKGDVFI REPFI SCSHLECR
 TFFLTQGALL
 NDKHSNGTVKDRSPYRALMSCPLGEAPSPYNSKFEVAVSASACHDGMWLT I GI SGPDNGAVAVLK
 YNG I I TGTI KSWKKQI LRTQSEECVMNGSCFTI MTDGSPNKAASYKI FKI EKGKVTKSI ELN
 APNFHYE
 EECSCYPDTGI VMCVCRDNWHGSRNPWVSFNQNLDYQI GYI CSGVFGDNPRPEDGEGSCNPVTV
 DGANGVKGFYSKYDNGVWI GRTKSNRLRKGFEI WDPNGWNTDSDFSVKQDVVAI TDW
 SGYSGSFVQHPPELTGLDCI RP
 CFWVELVRGLPRENTTI WTSGSSI SFCGVNSDTANWSWPDGAELPFTI DK
 >gi |194294071|gb|ACF40130.1| neurami ni dase [Influenza A virus (A/South
 Carolina/01/2008(H1N1))]
 MNPNQKI I TI GSI SI AI GI I SLMLQI GNI I SI WASHSI QTGSONNTGI CNQRI I TYENSTW
 VNHHTYVNI N
 NTNNAVAGEDKTSVTLAGNSSLCSI SGWAI YTKDNSI RI GSKGDVFI REPFI SCSHLECR
 TFFLTQGALL
 NDKHSNGTVKDRSPYRALMSCPLGEAPSPYNSKFEVAVSASACHDGMWLT I GI SGPDNGAVAVLK
 YNG I I TGTI KSWKKQI LRTQSEECVMNGSCFTI MTDGSPNKAASYKI FKI EKGKVTKSI ELN
 APNFHYE
 EECSCYPDTGI VMCVCRDNWHGSRNPWVSFNQNLDYQI GYI CSGVFGDNPRPEDGEGSCNPVTV
 DGANGVKGFYSKYDNGVWI GRTKSNRLRKGFEI WDPNGWNTDSDFSVKQDVVAI TDW
 SGYSGSFVQHPPELTGLDCI RP
 CFWVELVRGLPRENTTI WTSGSSI SFCGVNSDTANWSWPDGAELPFTI DK
 >gi |195661089|gb|ACG50711.1| neurami ni dase [Influenza A virus
 (A/Johannesburg/14/2008(H1N1))]
 MNPNQKI I TI GSI SI AI GI I SLMLQI GNI I SI WASHSI QTGSONNTGI CNQRI I TYENSTW
 VNHHTYVNI N
 NTNNAVAGEDKTSVTLAGNSSLCSI SGWAI YTKDNSI RI GSKGDVFI REPFI SCSHLECR
 TFFLTQGALL
 NDKHSNGTVKDRSPYRALMSCPLGEAPSPYNSKFEVAVSASACHDGMWLT I GI SGPDNGAVAVLK
 YNG I I TGTI KSWKKQI LRTQSEECVMNGSCFTI MTDGSPNKAASYKI FKI EKGKVTKSI ELN
 APNFHYE
 EECSCYPDTGI VMCVCRDNWHGSRNPWVSFNQNLDYQI GYI CSGVFGDNPRPEDGEGSCNPVTV
 DGANGVKGFYSKYDNGVWI GRTKSNRLRKGFEI WDPNGWNTDSDFSVKQDVVAI TDW
 SGYSGSFVQHPPELTGLDCI RP
 CFWVELVRGLPRENTTI WTSGSSI SFCGVNSDTANWSWPDGAELPFTI DK
 >gi |195661083|gb|ACG50708.1| neurami ni dase [Influenza A virus
 (A/Johannesburg/12/2008(H1N1))]
 QKI I TI GSI SI AI GI I SLMLQI GNI I SI WASHSI QTGSONNTGI CNQRI I TYENSTW
 VNHHTYVNI NNTKV
 VAGEDKTSVTLAGNSSLCSI SGWAI YTKDNSI RI GSKGDVFI REPFI SCSHLECR
 TFFLTQGALLNDKH
 SNGTVKDRSPYRALMSCPLGEAPSPYNSKFEVAVSASACHDGMWLT I GI SGPDNGAVAVLK
 YNG I I TGTI KSWKKQI LRTQSEECVMNGSCFTI MTDGSPNKAASYKI FKI EKGKVTKSI ELN
 APNFHYE
 EECSCYPDTGI VMCVCRDNWHGSRNPWVSFNQNLDYQI GYI CSGVFGDNPRPEDGEGSCNPVTV
 DGANGVKGFYSKYDNGVWI GRTKSNRLRKGFEI WDPNGWNTDSDFSVKQDVVAI TDW
 SGYSGSFVQHPPELTGLDCI RP
 CFWVELVRGLPRENTTI WTSGSSI SFCGVNSDTANWSWPDGAELPFTI DK
 >gi |195661085|gb|ACG50709.1| neurami ni dase [Influenza A virus
 (A/CapeTown/26/2008(H1N1))]
 QKI I TI GSI SI AI GI I SLLLQI GNI I SI WASHSI QTGSONNTGI CNQRI I TYENSTW
 VNHHTYVNI NNTNV
 VAGEDKTSVTLAGNSSLCSI SGWAI YTKDNSI RI GSKGDVFI REPFI SCSHLECR
 TFFLTQGALLNDKH
 SNGTVKDRSPYRALMSCPLGEAPSPYNSKFEVAVSASACHDGMWLT I GI SGPDNGAVAVLK
 YNG I I TGTI KSWKKQI LRTQSEECVMNGSCFTI MTDGSPNKAASYKI FKI EKGKVTKSI ELN
 APNFHYE
 EECSCYPDTGI VMCVCRDNWHGSRNPWVSFNQNLDYQI GYI CSGVFGDNPRPEDGEGSCNPVTV
 DGANGVKGFYSKYDNGVWI GRTKSNRLRKGFEI WDPNGWNTDSDFSVKQDVVAI TDW
 SGYSGSFVQHPPELTGLDCI RP
 CFWVELVRGLPRENTTI WTSGSSI SFCGVNSDTANWSWPDGAELPFTI DK
 >gi |195661087|gb|ACG50710.1| neurami ni dase [Influenza A virus
 (A/Johannesburg/21/2008(H1N1))]
 MNPNQKI I TI GSI SI AI GI I SLLLQI GNI I SI WASHSI QTGSONNTGI CNQRI I TYENSTW
 VNHHTYVNI N
 NTNNAVAGEDKTSVTLAGNSSLCSI SGWAI YTKDNSI RI GSKGDVFI REPFI SCSHLECR
 TFFLTQGALL
 NDKHSNGTVKDRSPYRALMSCPLGEAPSPYNSKFEVAVSASACHDGMWLT I GI SGPDNGAVAVLK
 YNG I I TGTI KSWKKQI LRTQSEECVMNGSCFTI MTDGSPNKAASYKI FKI EKGKVTKSI ELN
 APNFHYE
 EECSCYPDTGI VMCVCRDNWHGSRNPWVSFNQNLDYQI GYI CSGVFGDNPRPEDGEGSCNPVTV
 DGANGVKGFYSKYDNGVWI GRTKSNRLRKGFEI WDPNGWNTDSDFSVKQDVVAI TDW
 SGYSGSFVQHPPELTGLDCI RP
 CFWVELVRGLPRENTTI WTSGSSI SFCGVNSDTANWSWPDRAELPFTI DK

>gi |195661091|gb|ACG50712.1| neurami ni dase [Influenza A vi rus (A/Johannesburg/33/2008(H1N1))]
MNPNQI I TI GSI STAI GI I SMLQI GNI I SI WASHSI QTGSQNTGI CNQRI I TYENSTWVNHTYVNI N
NTKVVAGEDKTSVTLAGNSSLCSI SGWAI YTKDNSI RI GSKGDV FVI REPFI SCSHLECRTEFFLTQGALL
NDKHSNGTVKDRSPYRALMSPCLGEAPSPYNSKFESVAWSASACHDGMGWLTI GI SGPDNGAVAVLKYN
I I TGTI KSWKKQI LRTQSECEVCVMNGSCFTI MTDGSPNKAASYKI FKI EKGKVTKSI ELNAPNFYEECS
CYPDTGI VMCVCRDNWHGSRNPWVSFNQNLDYQI GYI CSGVFGDNPRPEDGEGSCNPVTVDGANGVKGFS
YKYGNGVWI GRKTSNRLRKG FEMI WDPNGWTNTDSDFSVKQDVVAI TDWSGYSGSFVQHPTEGLDCI RP
CFWVELVRGLPRENTTI WTSGSSI SFCGVNSDTANWSWPDGAELPFTI DK

>gi |195661093|gb|ACG50713.1| neurami ni dase [Influenza A vi rus (A/Johannesburg/35/2008(H1N1))]
MNPNQI I TI GSI STAI GI I SMLQI GNI I SI WASHSI QTGSQNTGI CNQRI I TYENSTWVNHTYVNI N
NTKVVAGEDKTSVTLAGNSSLCSI SGWAI YTKDNSI RI GSKGDV FVI REPFI SCSHLECRTEFFLTQGALL
NDKHSNGTVKDRSPYRALMSPCLGEAPSPYNSKFESVAWSASACHDGMGWLTI GI SGPDNGAVAVLKYN
I I TGTI KSWKKQI LRTQSECEVCVMNGSCFTI MTDGSPNKAASYKI FKI EKGKVTKSI ELNAPNFYEECS
CYPDTGI VI CVCRDNWHGSRNPWVSFNQNLDYQI GYI CSGVFGDNPRPEDGEGSCNPVTVDGANGVKGFS
YKYGNGVWI GRKTSNRLRKG FEMI WDPNGWTNTDSDFSVKQDVVAI TDWSGYSGSFVQHPTEGLDCI RP
CFWVELVRGLPRENTTI WTSGSSI SFCGVNSDTANWSWPDGAELPFTI DK

>gi |195661095|gb|ACG50714.1| neurami ni dase [Influenza A vi rus (A/Johannesburg/36/2008(H1N1))]
MNPNQI I TI GSI STAI GI I SMLQI GNI I SI WASHSI QTGSQNTGI CNQRI I TYENSTWVNHTYVNI N
NTN VVAGEDKTSVTLAGNSSLCSI SGWAI YTKDNSI RI GSKGDV FVI REPFI SCSHLECRTEFFLTQGALL
NDKHSNGTVKDRSPYRALMSPCLGEAPSPYNSKFESVAWSASACHDGMGWLTI GI SGPDNGAVAVLKYN
I I TGTI KSWKKQI LRTQSECEVCVMNGSCFTI MTDGSPNKAASYKI FKI EKGKVTKSI ELNAPNFYEECS
CYPDTGI VMCVCRDNWHGSRNPWVSFNQNLDYQI GYI CSGVFGDNPRPEDGEGSCNPVTVDGANGVKGFS
YKYGNGVWI GRKTSNRLRKG FEMI WDPNGWTNTDSDFSVKQDVVAI TDWSGYSGSFVQHPTEGLDCI RP
CFWVELVRGLPRENTTI WTSGSSI SFCGVNSDTANWSWPDGAELPFTI DK

>gi |195661097|gb|ACG50715.1| neurami ni dase [Influenza A vi rus (A/Johannesburg/45/2008(H1N1))]
MNPNQI I TI GSI STAI GI I SMLQI GNI I SI WASHSI QTGSQNTGI CNQRI I TYENSTWVNHTYVNI N
NTN VVAGEDKTSVTLAGNSSLCSI SGWAI YTKDNSI RI GSKGDV FVI REPFI SCSHLECRTEFFLTQGALL
NDKHSNGTVKDRSPYRALMSPCLGEAPSPYNSKFESVAWSASACHDGMGWLTI GI SGPDNGAVAVLKYN
I I TGTI KSWKKQI LRTQSECEVCVMNGSCFTI MTDGSPNKAASYKI FKI EKGKVTKSI ELNAPNFYEECS
CYPDTGI VMCVCRDNWHGSRNPWVSFNQNLDYQI GYI CSGVFGDNPRPEDGEGSCNPVTVDGANGVKGFS
YKYGNGVWI GRKTSNRLRKG FEMI WDPNGWTNTDSDFSVKQDVVAI TDWSGYSGSFVQHPTEGLDCI RP
CFWVELVRGLPRENTTI WTSGSSI SFCGVNSDTANWSWPDGAELPFTI DK

>gi |89148082|gb|ABD62784.1| neurami ni dase [Influenza A vi rus (A/Mel bourne/35(H1N1))]
MNPNQI I TI GSI CMVVG I SLI LQI GNI I SI WI SHSI QAGSSTWVNQTYVNI SNTN VVAGPDATSVI LT
GNSSLCP I RGWAI YSKDNGI RI GSKGDI FVI REPFI SCSHLECRTEFFLTQGALLNDKHSNGTVKDRSPYR
ALMSCP VGEAPSPYNSRFESVAWSASACHDGMGWLTI GI SGPDNGAVAVLKYN I TETI KSWRKKI LRT
QSECEACVNGSCFTI MTDGSPDGASYKI FKI EKGKVTKSI ELDAPNSHYEECSYCPDTGKVMCVRDNW
HGSNRPWVSFDQNLDYQI GYI CSGVFGDSPRPKDG TGSCGVPVVDGANGVKGFYRYGNGVWI GRKTSKS
SRHGFEMI WDPNGWTE TDSRFSVRQDVVAMTDWSGYSGSFVQHPTEGLDCMRPCFWVELI RGOPKEKI
WTSGSSI SFCGVNSDTVDWSWPDGAELPFTI DK

>gi |133754194|gb|AB038387.1| neurami ni dase [Influenza A vi rus (A/Phi la/1935(H1N1))]
MNPNQI I TI GSI CMVVG I SLI LQI GNI I SI WI SHSI QTGSQNTGI CNQSI I TYKNSTWVNQTYVNI S
NTN VVAGQDTTSVI LTGNSSLCP I RGWAI YSKDNGI RI GSKGDV FVI REPFI SCSHLECRTEFFLTQGALL
NDKHSNGTVKDRSPYRALMSPVGEAPSPYNSRFESVAWSASACHDGMGWLTI GI SGPDNEAVAVLKYN
I I TETI KSWRKKI LRTQSECEACVNGSCFTI MTDGSPDGLASYKI FKI EKGKVTKSI ELNAPNSHYEECS
CYPDTGKVMCVRDNWHGSRNPWVSFDQNLDYQI GYI CSGVFGDNPRPKDGTGSCGVPVVDGANGVKGFS
YRYGNGVWI GRKTSNRRHGFEMI WDPNGWTE TDSKFSVRQDVVAMTDWSGYSGSFVQHPTEGLDCMRP
CFWVELI RGOPKEKI WTSGSSI SFCGVNSDTVDWSWPDGAELPFTI DK

>gi |133754137|gb|AB038354.1| neurami ni dase [Influenza A vi rus (A/Henry/1936(H1N1))]
MNPNQI I TI GSI CMVVG I SLI LQI GNI I SI WI SHSI QTGSQNTGI CNQSI I TYKNSTWVNQTYVNI S
NTN VVAGQDTTSVI LTGNSSLCP I RGWAI YSKDNSI RI GSKGDV FVI REPFI SCSHLECRTEFFLTQGALL
NDRHSNGTVKDRSPYRALMSPVGEAPSPYNSRFESVAWSASACHDGMGWLTI GI SGPDNGAVAVLKYN
I I TETI KSWRKKI LRTQSECEACVNGSCFTI MTDGSPNGLASYKI FKI EKGKVTKSI ELNAPNSHYEECS
CYPDTGKVMCVRDNWHGSRNPWVSFDQNLDYQI GYI CSGVFGDNPRPKDGTGSCGVPVVDGANGVKGFS
YRYGNGVWI GRKTSNRRHGFEMI WDPNGWTE TDSKFSVRQDVVAMTDWSGYSGSFVQHPTEGLDCMRP
CFWVELI RGRPKENTI WTSGSSI SFCGVNSDTVDWSWPDGAELPFTI DK

>gi |112787551|gb|ABI 20829.1| neurami ni dase [Influenza A vi rus (A/Hi ckox/1940(H1N1))]
MNPNQI I TI GSI CMVVG I SLI LQI GNI VSI WI SHSI QTGNQNTGTGNCQSI I TYKNSTWVNQTYVNI S
NTN VVAGKDTTSVI LAGNSSLCP I RGWAI YSKDNGVRI GSKGDV FVI REPFI SCSHLECRTEFFLTQGALL
NDKHSNGTVKDRSPYRALMSPVGEAPSPYNSRFESVAWSASACHDGMGWLTI GI SGPDDGAVAVLKYN
I I TETI KSWRKEI LRTQSECEVCVNGSCFTI MTDGSPGGPASYKI FKI EKGKVTKSI ELDAPNSHYEECS
CYPDTGKVMCVRDNWHGSRNPWVSFDQNLDYQMGYI CSGVFGDNPRPKDGTGSCGVPVVDGANGVKGFS
YRYGNGVWI GRKTSNRRHGFEMI WDPNGWTE TDSNFFMKQDVVAVTDWSGYSGSFVQHPTEGLDCMRP
CFWVELI RGRPKENTI WTSGSSI SFCGVNSDTVDWSWPDGAELPFTI DK

>gi |89152219|gb|ABD62845.1| neurami ni dase [Influenza A vi rus (A/Bel /1942(H1N1))]
MNPNQI I TI GSI CMVVG I SLI LQI GNI I SI WI SHSI QTGSQNTGI CNQSI I TYKNSTWVNQTYVNI S
NTN VVAGKDTTSMI LAGNSSLCP I RGWAI YSKDNGI RI GSKGDV FVI REPFI SCSHLECRTEFFLTQGALL
NDKHSNGTVKDRSPYRALMSPVGEAPSPYNSRFESVAWSASACHDGMGWLTI GI SGPDDGAVAVLKYN
I I TETI KSWKKKI LRTQSECEVCVNGSCFTI MTDGSPDGASYKI FKI EKGKVTKSI ELDAPNSHYEECS
CYPDTGKVMCVRDNWHGSRNPWVSFDQNLDYQI GYI CSGVFGDNPRPKDGTGSCGVPVVDGANGVKGFS
YRYGNGVWI GRKTSNRRHGFEMI WDPNGWTE TDSFFVKQDVVAMTDWSGYSGSFVQHPTEGLDCMRP
CFWVELI RGRPKENTI WTSGSSI SFCGVNSDTVDWSWPDGAELPFTI DK

>gi |8572187|gb|AAF77045.1|AF250365_1 neurami ni dase [Influenza A virus (A/Wei ss/43(H1N1))]
MNPNQI I TI GSI CMVVG I SLI LQI GNI I SI WI SHSI QTGSQNHGTI CNQSI I TYKNSTWVNQTYVNI S
NTNVVAGKGTTSVI LAGNSSLCP I RGWAI YSKDNGI RI GSKGDV FVI REPFI SCSHLECR TFFLTQ GALL
NDKHSNGTVKDRSPYRALMSPVGEAPSPYNSRFESVAWSASACHDGMGWLTI GI SGPDD EAVAVLKYNG
I I TETI KSWRKKI LRTQSEECV VNGSCFTI MTDGSPDGPASYKI FKI EKGKVT KSI ELDAPNSHYEECS
CYPDTGKVMCVC RDNNHGSNRPWV SFDONLDYQI GYI CSGVFGDNPRPKDGKSGCPVYVDGANGVKGFS
YRYGNGVWI GR TKS DSSRQGFEMI WDPNGWTE TDSNFFVKQDI VAMTDW S GSGSFVQHP ELTGLDCMRP
CFWVELI RGRPK EKI WTS GSSI SFCGVNSDTVDW S WPDGAELPFTI DK

>gi |133754175|gb|AB038376.1| neurami ni dase [Influenza A virus (A/Iowa/1943(H1N1))]
MNPNQI I TI GSI CMVVG I SLI LQI GNI I SI WI SHSI QTGSQNHGTI CNQSI I TYKNSTWVNQTYVNI S
NTNVVAGKGTTSVI LAGNSSLCP I RGWAI YSKDNGVRI GSKGDV FVI REPFI SCSHLECR TFFLTQ GALL
NDKHSNGTVKDRSPYRALMSPVGEAPSPYNSRFESVAWSASACHDGMGWLTI GI SGPDDGAVAVLKYNG
I I TETI KSWRKEI LRTQSEECACV VNGSCFTI MTDGSPGGPASYKI FKI EKGKVT KSI ELDAPNSHYEECS
CYPDTGKVMCVC RDNNHGSNRPWV SFDONLDYQMGYI CSGVFGDNPRPKDGKGNCGPVYVDGANGVKGFS
YRYGNGVWI GR TKS NSSRQGFEMI WDPNGWTE TDSNFFVKQDVAVT DWSGYS GSGSFVQHP ELTGLDCMRP
CFWVELI RGRPK EKI WTS GSSI SFCGVNSDTVDW S WPDGAELPFTI DK

>gi |21724202|gb|AAM75501.1| neurami ni dase [Influenza A virus (A/Marton/43(H1N1))]
MNPNQI I TI GSI CMVVG I SLI LQI GNI I SI WI SHSI QTGSQNHGTI CNQSI I TYKNSTWVNQTYVNI S
NTNVVAGKGTTSVI LAGNSSLCP I RGWAI YSKDNGVRI GSKGDV FVI REPFI SCSHLECR TFFLTQ GALL
NDKHSNGTVKDRSPYRALMSPVGEAPSPYNSRFESVAWSASACHDGMGWLTI GI SGPDDGAVAVLKYNG
I I TETI KSWRKEI LRTQSEECACV VNGSCFTI MTDGSPGGPASYKI FKI EKGKVT KSI ELDAPNSHYEECS
CYPDTGKVMCVC RDNNHGSNRPWV SFDONLDYQMGYI CSGVFGDNPRPKDGKGNCGPVYVDGANGVKGFS
YRYGNGVWI GR TKS NSSRQGFEMI WDPNGWTE TDSNFFVKQDVAVT DWSGYS GSGSFVQHP ELTGLDCMRP
CFWVELI RGRPK EKI WTS GSSI SFCGVNSDTVDW S WPDGAELPFTI DK

>gi |21717610|gb|AAM76692.1|AF494252_1 neurami ni dase [Influenza A virus (A/Wei ss/43(H1N1))]
MNPNQI I TI GSI CMVVG I SLI LQI GNI I SI WI SHSI QTGSQNHGTI CNQSI I TYKNSTWVNQTYVNI S
NTNVVAGKGTTSVI LAGNSSLCP I RGWAI YSKDNGI RI GSKGDV FVI REPFI SCSHLECR TFFLTQ GALL
NDKHSNGTVKDRSPYRALMSPVGEAPSPYNSRFESVAWSASACHDGMGWLTI GI SGPDD EAVAVLKYNG
I I TETI KSWRKKI LRTQSEECV VNGSCFTI MTDGSPDGPASYKI FKI EKGKVT KSI ELDAPNSHYEECS
CYPDTGKVMCVC RDNNHGSNRPWV SFDONLDYQI GYI CSGVFGDNPRPKDGKSGCPVYVDGANGVKGFS
YRYGNGVWI GR TKS NSSRQGFEMI WDPNGWTE TDSNFFVKQDI VAMTDW S GSGSFVQHP ELTGLDCMRP
CFWVELI RGRPK EKI WTS GSSI SFCGVNSDTVDW S WPDGAELPFTI DK

>gi |133752887|gb|AB038057.1| neurami ni dase [Influenza A virus (A/AA/Marton/1943(H1N1))]
MNPNQI I TI GSI CMVVG I SLI LQI GNI I SI WI SHSI QTGSQNHGTI CNQSI I TYKNSTWVNQTYVNI S
NTNVVAGKGTTSVI LAGNSSLCP I RGWAI YSKDNGVRI GSKGDV FVI REPFI SCSHLECR TFFLTQ GALL
NDKHSNGTVKDRSPYRALMSPVGEAPSPYNSRFESVAWSASACHDGMGWLTI GI SGPDDGAVAVLKYNG
I I TETI KSWRKEI LRTQSEECACV VNGSCFTI MTDGSPGGPASYKI FKI EKGKVT KSI ELDAPNSHYEECS
CYPDTGKVMCVC RDNNHGSNRPWV SFDONLDYQMGYI CSGVFGDNPRPKDGKGNCGPVYVDGANGVKGFS
YRYGNGVWI GR TKS NSSRQGFEMI WDPNGWTE TDSNFFVKQDVAVT DWSGYS GSGSFVQHP ELTGLDCMRP
CFWVELI RGRPK EKI WTS GSSI SFCGVNSDTVDW S WPDGAELPFTI DK

>gi |89903061|gb|ABD79104.1| neurami ni dase [Influenza A virus (A/Wei ss/43(H1N1))]
MNPNQI I TI GSI CMVVG I SLI LQI GNI I SI WI SHSI QTGSQNHGTI CNQSI I TYKNSTWVNQTYVNI S
NTNVVAGKGTTSVI LAGNSSLCP I RGWAI YSKDNGI RI GSKGDV FVI REPFI SCSHLECR TFFLTQ GALL
NDKHSNGTVKDRSPYRALMSPVGEAPSPYNSRFESVAWSASACHDGMGWLTI GI SGPDD EAVAVLKYNG
I I TETI KSWRKKI LRTQSEECV VNGSCFTI MTDGSPDGPASYKI FKI EKGKVT KSI ELDAPNSHYEECS
CYPDTGKVMCVC RDNNHGSNRPWV SFDONLDYQI GYI CSGVFGDNPRPKDGKSGCPVYVDGANGVKGFS
YRYGNGVWI GR TKS DSSRQGFEMI WDPNGWTE TDSNFFVKQDI VAMTDW S GSGSFVQHP ELTGLDCMRP
CFWVELI RGRPK EKI WTS GSSI SFCGVNSDTVDW S WPDGAELPFTI DK

>gi |145278815|gb|ABP49330.1| neurami ni dase [Influenza A virus (A/AA/Huston/1945(H1N1))]
MNPNQI I TI GSI CMVVG I SLI LQI GNI I SI WI SHSI QTGSQNHGTI CNQSI I TYKNSTWVNQTYVNI S
NTNVVAGKGTTPVI LAGNSSLCP I RGWAI YSKDNGI RI GSKGDV FVI REPFI SCSHLECR TFFLTQ GALL
NDKHSNGTVKDRSPYRALMSPVGEAPSPYNSRFESVAWSASACHDGMGWLTI GI SGPDD EAVAVLKYNG
I I TETI KSWRKKI LRTQSEECV VNGSCFTI MTDGSPDGPASYKI FKI EKGKVT KSI ELDAPNSHYEECS
CYPDTGKVMCVC RDNNHGSNRPWV SFDONLDYQI GYI CSGVFGDNPRPKDGKSGCPVYVDGANGVKGFS
YRYGNGVWI GR I KSNSSRQGFEMI WDPNGWTE TDSNFFVKQDVAVT DWSGYS GSGSFVQHP ELTGLDCMRP
CFWVELI RGRPK EKI WTS GSSI SFCGVNSDTVDW S WPDGAELPFTI DK

>gi |89903080|gb|ABD79115.1| neurami ni dase [Influenza A virus (A/Cam/46(H1N1))]
MNPNQI I TI GSI CMVVG I SLI LQI GNI VSI WI SHSI TGTCNRSI YVNI SNTNVVAGKGTTSVI LAGN
SLCP I RGWAI YSKDNGVRI GSKGDV FVI REPFI SCSHLECR TFFLTQ GALLNDKHSNGTVKDRSPYR TLM
SCPVGEAPSPYNSRFESVAWSASACHDGMGWLTI GI SGPDDGAVAVLKYNGI I TGTI KSWRKEI LRTQES
ECV VNGSCFTI MTDGSPGGPASYKI FKI EKGKVT KSI ELDAPNSHYEECS CYPDT SKVMCVC RDNNHGS
NRPWV SFDONLDYQMGYI CSGVFGDNPRPKDGKSGCPVYVDGANGVKGFSYRYGNGVWI GR TKS SSSRQ
GFEMI WDPNGWTE TDSNFFVKQDVAVT DWSGYS GSGSFVQHP ELTGLDCMRPCFWVELI RGRPKENTI WTS
GSSI SFCGVNSDTVDW S WPDGAELPFTI DK

>gi |4583795|emb|CAB40419.1| neurami ni dase [Influenza A virus (A/Fort Monmouth/1/47-
MA(H1N1))]
MNPNQI I TI GSI CMVVG I SLI LQI GNI VSI WI SHSI QTGNQNHGTI CNQSI I TYKNSTWVNQTYVNVV
AGKDTTSVI LAGNSSLCP I RGWAI YSKDNGVRI GSKGDV FVI REPFI SCSHLECR TFFLTQ GALLNDKHS
NGTVKDRSPYRALMSPVGEAPSPYNSRFESVAWSASACHDGMGWLTI GI SGPDDGAVAVLKYNGI I TET
I KSWRKEI LRTQSEECV VNGSCFTI MTDGSPGGPASYKI FKI EKGKVT KSI ELDAPNSHYEECS CYPDT
SKVMCVC RDNNHGSNRPWV SFDONLDYQMGYI CSGVFGDNPRPKDGKSGCPVYVDGANGVKGFSYRYGNG
VWI GR TKS NSSRQGFEMI WDPNGWTE TDSNFFTKQDVAVT DWSGYS GSGSFVQHP ELTGLDCMRPCFWVE
LI RGRPKENTI WTS GSSI SFCGVNSDTVDW S WPDGAELPFTI DK

>gi |89782392|gb|ABD77810.1| neurami ni dase [Influenza A virus (A/FortMonmouth/1/47(H1N1))]
MNPNQKI I TI GSI CMVVG I SLI LQI GNI VSI WI SHSI QTGNQNHGTGCDQSI I TYKNSTWVNQTYVNI S
NTNVVAGKDTTSMI LAGNSSLCP I RGWAI YSKDNGVRI GSKGDV FVI REPFI SCSHLECR TFFLTQ GALL
NDKHSNGTVKDRSPYRALM SCVPGEAPSPYNSRFESVAWSASACHDGMGWLTI GI SGPDDGAVAVLK YNG
I I TETI KSWRKEI LRTQSEECV CVNGSCFTI MTDGPGSGGPASYKI FKI EKGKVT KSI ELDAPNSHYEECS
CYPDTGKVMCVC RDNNHGSNRPWVW SFDONLDYQMGYI CSGVFGDNPRPKDGK GSCGPVYVDGANGVKGF S
YRYGNGVWI GR TKSNSRRKGFEMI WDPNGWTE TDSNFFTKQDVAVT DWSGYSGSFVQHP ELTGLDCMRP
CFWVELI RGRPKENTI WTS GSSI SFCGVNSDTVDWSPDGAELPFTI DK

>gi |8572171|gb|AAF77037.1|AF250357_1 neurami ni dase [Influenza A virus (A/FM/1/47(H1N1))]
MNPNQKI I TI GSI CMVVG I SLI LQI GNI VSI WI SHSI QTGNQNHGTGCDQSI I TYKNSTWVNQTYVNVV
AGKDTTSMI LAGNSSLCP I RGWAI YSKDNGVRI GSKGDV FVI REPFI SCSHLECR TFFLTQ GALLNDKHS
NGTVKDRSPYRALM SCVPGEAPSPYNSRFESVAWSASACHDGMGWLTI GI SGPDDGAVAVLK YNGI I TET
I KSWRKEI LRTQSEECV CVNGSCFTI MTDGPGSGGPASYKI FKI EKGKVT KSI ELDAPNSHYEECS
CYPDTGKVMCVC RDNNHGSNRPWVW SFDONLDYQMGYI CSGVFGDNPRPKDGK GSCGPVYVDGANGVKGF S
YRYGNGVWI GR TKSNSRRKGFEMI WDPNGWTE TDSNFFTKQDVAVT DWSGYSGSFVQHP ELTGLDCMRP
CFWVELI RGRPKENTI WTS GSSI SFCGVNSDTVDWSPDGAELPFTI DK

>gi |21724204|gb|AAM75502.1| neurami ni dase [Influenza A virus (A/Rhodes/47(H1N1))]
MNPNQKI I TI GSI CMVVG I SLI LQI GNI VSI WI SHSI QTGNQNHGTGCDQSI I TYKNSTWVNQTYVNI S
NTNVVAGKDTTSMI LAGNSSLCP I RGWAI YSKDNGVRI GSKGDV FVI REPFI SCSHLECR TFFLTQ GALL
NDKHSNGTVKDRSPYRALM SCVPGEAPSPYNSRFESVAWSASACHDGMGWLTI GI SGPDDGAVAVLK YNG
I I TETI KSWRKEI LRTQSEECV CVNGSCFTI MTDGPGSGGPASYKI FKI EKGKVT KSI ELDAPNSHYEECS
CYPDTGKVMCVC RDNNHGSNRPWVW SFDONLDYQMGYI CSGVFGDNPRPKDGK GSCGPVYVDGANGVKGF S
YRYGNGVWI GR TKSNSRRKGFEMI WDPNGWTE TDSNFFTKQDVAVT DWSGYSGSFVQHP ELTGLDCMRP
CFWVELI RGRPKENTI WTS GSSI SFCGVNSDTVDWSPDGAELPFTI DK

>gi |21717612|gb|AAM76693.1|AF494253_1 neurami ni dase [Influenza A virus (A/FortMonmouth/1/47(H1N1))]
MNPNQKI I TI GSI CMVVG I SLI LQI GNI VSI WI SHSI QTGNQNHGTGCDQSI I TYKNSTWVNQTYVNI S
NTNVVAGKDTTSMI LAGNSSLCP I RGWAI YSKDNGVRI GSKGDV FVI REPFI SCSHLECR TFFLTQ GALL
NDKHSNGTVKDRSPYRALM SCVPGEAPSPYNSRFESVAWSASACHDGMGWLTI GI SGPDDGAVAVLK YNG
I I TETI KSWRKEI LRTQSEECV CVNGSCFTI MTDGPGSGGPASYKI FKI EKGKVT KSI ELDAPNSHYEECS
CYPDTGKVMCVC RDNNHGSNRPWVW SFDONLDYQMGYI CSGVFGDNPRPKDGK GSCGPVYVDGANGVKGF S
YRYGNGVWI GR TKSNSRRKGFEMI WDPNGWTE TDSNFFTKQDVAVT DWSGYSGSFVQHP ELTGLDCMRP
CFWVELI RGRPKENTI WTS GSSI SFCGVNSDTVDWSPDGAELPFTI DK

>gi |125976167|gb|ABN59404.1| neurami ni dase [Influenza A virus (A/AI bany/4835/1948(H1N1))]
MNPNQKI I TI GSI CMAI GI I SLI LQI GNI I SI WVSHSI QTGSONHTGI CNQRI I TYENNTWVNQTYVNI S
NTNVVAGKDTTSMI LAGNSSLCP I RGWAI YSKDNGVRI GSKGDV FVI REPFI SCSHLECR TFFLTQ GALL
NDKHSNGTVKDRSPYRALM SCVPGEAPSPYNSRFESVAWSASACHDGMGWLTI GI SGPDDGAVAVLK YNG
I I TETI KSWRKEI LRTQSEECV CVNGSCFTI MTDGPGSDGPASYRI FKI EKGK T KSI ELDAPNSHYEECS
CYPDTGKVMCVC RDNNHGSNRPWVW SFDONLDYQI GYI CSGVFGDNPRPKDGK GSCGPVYVDGANGVKGF S
YRYGNGVWI GR TKSNSRRKGFEMI WDPNGWTE TDSNFFTKQDVAVT DWSGYSGSFVQHP ELTGLDCMRP
CFWVELI RGRPREKTTI WTS GSSI SFCGVNSDTVDWSPDGAELPFTI DK

>gi |125976224|gb|ABN59437.1| neurami ni dase [Influenza A virus (A/Roma/1949(H1N1))]
MNPNQKI I TI GSI CMAI GI I SLI LQI GNI I SI WVSHSI QTGSONHTGI CNQRI I TYENNTWVNQTYVNI S
NTNVVAGKDTTSMI LAGNSSLCP I RGWAI YSKDNGVRI GSKGDV FVI REPFI SCSHLECR TFFLTQ GALL
NDKHSNGTVKDRSPYRALM SCVPGEAPSPYNSRFESVAWSASACHDGMGWLTI GI SGPDDGAVAVLK YNG
I I TETI KSWRKEI LRTQSEECV CVNGSCFTI MTDGPGSDGPASYRI FKI EKGK T KSI ELDAPNSHYEECS
CYPDTGKVMCVC RDNNHGSNRPWVW SFDONLDYQI GYI CSGVFGDNPRPKDGK GSCGPVYVDGANGVKGF S
YRYGNGVWI GR TKSNSRRKGFEMI WDPNGWTE TDSNFFTKQDVAVT DWSGYSGSFVQHP ELTGLDCMRP
CFWVELI RGRPREKTTI WTS GSSI SFCGVNSDTVDWSPDGAELPFTI DK

>gi |170181723|gb|ACB11776.1| neurami ni dase [Influenza A virus (A/New Jersey/05/2008(H1N1))]
MNPNQKI I TI GSI SI AI GI I SLMLQI GNI I SI WASHSI QTGSONNTGI CNQRI I TYENSTWVNHTYVNI N
NTNVVAGEDKTSVTLAGNSSLCSI SGWAI YTKDNGVRI GSKGDV FVI REPFI SCSHLECR TFFLTQ GALL
NDKHSNGTVKDRSPYRALM SCPLGEAPSPYNSK FESVAWSASACHDGMGWLTI GI SGPNDGAVAVLK YNG
I I TGTI KSWKKQI LRTQSEECV CMNGSCFTI MTDGSPNKAASYKI FKI EKGKVT KSI ELNAPNFHYEECS
CYPDTGKVMCVC RDNNHGSNRPWVW SFDONLDYQI GYI CSGVFGDNPRPKDGK GSCGPVYVDGANGVKGF S
YRYGNGVWI GR TKSNSRRKGFEMI WDPNGWTE TDSNFFTKQDVAVT DWSGYSGSFVQHP ELTGLDCMRP
CFWVELI RGRPREKTTI WTS GSSI SFCGVNSDTVDWSPDGAELPFTI DK

>gi |189303424|gb|ACD85787.1| neurami ni dase [Influenza A virus (A/Mi ssi ssi ppi /06/2008(H1N1))]
MNPNQKI I TI GSI SI AI GI I SLMLQI GNI I SI WASHSI QTGSONNTGI CNQRI I TYENSTWVNHTYVNI N
NTNVVAGEDKTSVTLAGNSSLCSI SGWAI YTKDNGVRI GSKGDV FVI REPFI SCSHLECR TFFLTQ GALL
NDKHSNGTVKDRSPYRALM SCPLGEAPSPYNSK FESVAWSASACHDGMGWLTI GI SGPNDGAVAVLK YNG
I I TGTI KSWKKQI LRTQSEECV CMNGSCFTI MTDGSPNKAASYKI FKI EKGKVT KSI ELNAPNFHYEECS
CYPDTGKVMCVC RDNNHGSNRPWVW SFDONLDYQI GYI CSGVFGDNPRPKDGK GSCGPVYVDGANGVKGF S
YRYGNGVWI GR TKSNSRRKGFEMI WDPNGWTE TDSNFFTKQDVAVT DWSGYSGSFVQHP ELTGLDCMRP
CFWVELI RGRPREKTTI WTS GSSI SFCGVNSDTVDWSPDGAELPFTI DK

>gi |193084899|gb|ACF10339.1| neurami ni dase [Influenza A virus (A/Mi ssi ssi ppi /06/2008(H1N1))]
MNPNQKI I TI GSI SI AI GI I SLMLQI GNI I SI WASHSI QTGSONNTGI CNQRI I TYENSTWVNHTYVNI N
NTNVVAGEDKTSVTLAGNSSLCSI SGWAI YTKDNGVRI GSKGDV FVI REPFI SCSHLECR TFFLTQ GALL
NDKHSNGTVKDRSPYRALM SCPLGEAPSPYNSK FESVAWSASACHDGMGWLTI GI SGPNDGAVAVLK YNG
I I TGTI KSWKKQI LRTQSEECV CMNGSCFTI MTDGSPNKAASYKI FKI EKGKVT KSI ELNAPNFHYEECS
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 >gi |148276802|gb|ABQ53685.1| neurami ni dase [Influenza A virus
 (A/Nei menggu/63/1997(H1N1))]
 MNPNQKI I TI GSI CMAI GI I SLI LQI GNI VSI WI SHSI QTGSONYTG I CNQRI I TYENSTWVNQTYVNI N
 NTNVAAGDQTTVALAGNSSLCP I SGWAI YSKDNSI RI GSKGDV FVI RE PFI SC SHLE CRT FF LTO GALL
 NDKHSNGTVKDRSPYRALMSCPLGEAPSPYNSRFESVAWSASACHDGLGWLTI GI SGPDDGAVAVLK YNG
 I I TETI KSWRKRI LRTQESECVCVNGSCFTI MTDGPNNGPASYKI FKI EKGKTKSI ELDAPNSHYEECS
 CYPDAGTVMCVC RDNWHG SNRPWV SFNQNL DYQI GYI CSGVFGDNPRPKDGE GSCNPVTVDGADGVKGF S
 YRYGNGVWI GRTKSNRRRKFEMI WDPNGWTD TDSKFLVKQDVVAMTDWSGYSGSFVQHP ELTGLDCMRP
 CFWVELIRGRPRENTTI WTSGSSI SFCGVNGDTANWSWPDGSEL PFTI DK
 >gi |148276804|gb|ABQ53686.1| neurami ni dase [Influenza A virus
 (A/Tai wan/1348/1997(H1N1))]
 MNPNQKI I TI GSI SI AI GI I SLI LQI GNI I SI WASHSI QTGSONHTGI CNQRI I TYENSTWVNHTYVNI N
 NTNVAAGDKDTSVTLAGNSSLCSI SGWAI YTKDNSI RI GSKGDV FVI RE PFI SC SHME CRT FF LTO GALL
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 I I TETI KSWKKRI LRTQESECVCVNGSCFTI MTDGPSDGAASYKI FKI EKGKTKSI ELNAPNSHYEECS
 CYPDTGTVMCVC RDNWHG SNRPWV SFNQNL DYQI GYI CSGVFGDNPRPRDGE GSCNPVTVDGADGVKGF S
 YRYGNGVWI GRTKSNRLRKG FEMI WDPNGWTD TDSDFAVKQDVVAI TDWSGYSGSFVQHP ELTGLDCI RP
 CFWVELVRGLPRENTTI WTSGSSI SFCGVNSDTANWSWPDGAELPFTI DK
 >gi |148276806|gb|ABQ53687.1| neurami ni dase [Influenza A virus
 (A/Austri a/262/1997(H1N1))]
 MNPNQKI I TI GSI SVAI GI I SLI LQI GNI I SI WASHSI QTGSONYTG I CNQRI I TYENSTWVNQTYVNI N
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 I I TETI KSWKKRI LRTQESECVCVNGSCFTI MTDGPSDRAASYRI FKI DKGRVTKSI ELDAPNYHYEECS
 CYPDTGTVMCVC RDNWHG SNRPWV SFNQNL DYQI GYI CSGVFGDNPRPKDGE GSCNPVTVDGADGVKGF S
 YRYGNGVWI GRTKSNRLRKG FEMI WDPNGWTD TDSDFSMKQDVVAMTDWSGYSGSFVQHP ELTGLDCMRP
 CFWVELVRGLPRENTTI WTSGSSI SFCGVNSETANWSWPDGAELPFTI DK
 >gi |148276808|gb|ABQ53688.1| neurami ni dase [Influenza A virus
 (A/Durbi n/113/1997(H1N1))]
 MNPNQKI I TI GSI SVAI GI I SLI LQI GNI I SI WASHSI QTGSONYTG I CNQRI I TYENSTWVNQTYVNI N
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 YKYGNGVWI GRTKSNRLRKGFEI WDPNGWTTDSDSFVSKQDVVAI TDWGSYSGSFVQHPPELTGLDCI
 CFWVELVRGLPRENTTI WTSGSSI SFCGVNSDTANWSWPDGAELPFTI DK
 >gi |148276814|gb|ABQ53691.1| neurami ni dase [Influenza A virus (A/Hong
 Kong/364/1997(H1N1))]
 MNPNQI I TI GSI SI AI GI I SLMLOI GNI I SI WASHSI QTGSQNTGTI CNQRI I TYENSTWVNHTYVNI
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 CFWVELVRGLPRENTTI WTSGSSI SFCGVNSDTANWSWPDGAELPFTI DK
 >gi |148356750|dbj|BAF63047.1| neurami ni dase [Influenza A virus
 (A/Hanoi /1928/2002(H1N1))]
 MNPNQI I TI GSI SI AI GI I SLMLOI GNI I SI WASHSI QTGSQNTGTI CNQRI I TYENSTWVNHTYVNI
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 YKYGNGVWI GRTKSNRLRKGFEI WDPNGWTTDSDSFVSKQDVVAI TDWGSYSGSFVQHPPELTGLDCI
 CFWVELVRGLPRENTTI WTSGSSI SFCGVNSDTANWSWPDGAELPFTI DK
 >gi |148356757|dbj|BAF63051.1| neurami ni dase [Influenza A virus
 (A/Hanoi /2006/2002(H1N1))]
 MNPNQI I TI GSI SI AI GI I SLMLOI GXI I SI WASHSI QTGSQNTGTI CNQRI I TYENSTWVNHTYVNI
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 YKYGNGVWI GRTKSNRLRKGFEI WDPNGWTTDSDSFVSKQDVVAI TDWGSYSGSFVQHPPELTGLDCI
 CFWVELVRGLPRENTTI WTSGSSI SFCGVNSDTANWSWPDGAELPFTI DK
 >gi |183396529|dbj|BAG28189.1| neurami ni dase [Influenza A virus
 (A/Mori oka/27/2002(H1N1))]
 MNPNQI I TI GSI SI AI GI I SLMLOI GNI I SI WASHSI QTGSQNTGTI CNQRI I TYENSTWVNHTYVNI
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 I I TETI KSWKKQI LRTQSEECVNGSCFTI MTDGSPNGAASYKI FKI EKGVRTKSI ELNAPNSHYEES
 CYPDTGTVMCVCRDNDWHGNSRNPWVSFNQNLDYQI GYI CSGVFGDNPRPKDGECSNPVTVDGADGVKGF
 YKYGNGVWI GRTKSNRLRKGFEI WDPNGWTTDSDSFVSKQDVVAI TDWGSYSGSFVQHPPELTGLDCI
 CFWVELVRGLPRENTTI WTSGSSI SFCGVNSDTANWSWPDGAELPFTI DK
 >gi |170675942|dbj|BAG14285.1| neurami ni dase [Influenza A virus
 (A/Mori oka/17/2002(H1N1))]
 MNPNQI I TI GSI SI AI GI I SLMLOI GNI I SI WASHSI QTGSQNTGTI CNQRI I TYENSTWVNHTYVNI
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 I I TETI KSWKKQI LRTQSEECVNGSCFTI MTDGSPNGAASYKI FKI EKGVRTKSI ELNAPNSHYEES
 CYPDTGTVMCVCRDNDWHGNSRNPWVSFNQNLDYQI GYI CSGVFGDNPRPKDGECSNPVTVDGADGVKGF
 YKYGNGVWI GRTKSNRLRKGFEI WDPNGWTTDSDSFVSKQDVVAI TDWGSYSGSFVQHPPELTGLDCI
 CFWVELVRGLPRENTTI WTSGSSI SFCGVNSDTANWSWPDGAELPFTI DK
 >gi |148356769|dbj|BAF63058.1| neurami ni dase [Influenza A virus
 (A/Hanoi /191/2002(H1N1))]
 MNPNQI I TI GSI SI AI GI I SLMLOI GNI I SI WASHSI QTGSQNTGTI CNQRI I TYENSTWVNHTYVNI
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 I I TETI KSWKKRI LRTQSEECVNGSCFTI MTDGSPNEAASYKI FKI EKGVRTKSI ELNAPNSHYEES
 CYPDTGTVMCVCRDNDWHGNSRNPWVSFNQNLDYQI GYI CSGVFGDNPRPKDGECSNPVTVDGADGVKGF
 YKYGNGVWI GRTKSNRLRKGFEI WDPNGWTTDSDSFVSKQDVVAI TDWGSYSGSFVQHPPELTGLDCI
 CFWVELVRGLPRENTTI WTSGSSI SFCGVNSDTANWSWPDGAELPFTI DK
 >gi |82546780|gb|ABB82219.1| neurami ni dase [Influenza A virus (A/New
 York/494/2002(H1N1))]
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 CYPDTGTVMCVCRDNDWHGNSRNPWVSFNQNLDYQI GYI CSGVFGDNPRPKDGECSNPVTVDGADGVKGF
 YKYGNGVWI GRTKSNRLRKGFEI WDPNGWTTDSDSFVSKQDVVAI TDWGSYSGSFVQHPPELTGLDCI
 CFWVELVRGLPRENTTI WTSGSSI SFCGVNSDAADWSWPDGAELPFTI DK
 >gi |77543347|gb|ABA87083.1| neurami ni dase [Influenza A virus (A/New
 York/291/2002(H1N1))]
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 YKYGNGVWI GRTKSNRLRKGFEI WDPNGWTTDSDSFVSKQDVVAI TDWGSYSGSFVQHPPELTGLDCI
 CFWVELVRGLPRENTTI WTSGSSI SFCGVNSDTANWSWPDGAELPFTI DK

>gi |73761479|gb|AAZ83256.1| neurami ni dase [Influenza A virus (A/New York/220/2002(H1N1))]
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NTNVVAGDKDTSVTLAGNSSLCSI SGWAI YTKDNSI RI GSKGDV FVI REPFI SCSHLECRTEFFLTQGALL
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I I TETI KSWKKRI LRTQSEECVNGSCFTI MTDGPNNGAASYKI FKI EKGKVTKSI ELNAPNFHYEECS
CYPDTGTVMCVCRDNDWHGSRNPWVSFNQNLDYQI GYI CSGVFGDNP RPDKGKSGCNPVTVDGADGVKGF S
YKYGNGVWI GRTKSNRLRKG FEMI WDPNGWTD TDSDFSVKQDVVAI TDWSGYSGSFVQHP ELTGLDCI RP
CFWVELVRGLPRENTTI WTSGSSI SFCGVSDTANWSWPDGAELPFTI DK

>gi |125664181|gb|ABN51091.1| neurami ni dase [Influenza A virus
(A/Memphis/5/2003(H1N1))]
MNPNQKI I TI GSI SI AI GI I SLMLQI GNI I SI WASHSI QTGSQNHGTI CNQRI I TYENSTWVNHTYVNI N
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I I TETI KSWKKRI LRTQSEECVNGSCFTI MTDGPNNGAASYKI FKI EKGKVTKSI ELNAPNFHYEECS
CYPDTGTVMCVCRDNDWHGSRNPWVSFNQNLDYQI GYI CSGVFGDNP RPDKGKSGCNPVTVDGADGVKGF S
YKYGNGVWI GRTKSNRLRKG FEMI WDPNGWTD TDSDFSVKQDVVAI TDWSGYSGSFVQHP ELTGLDCI RP
CFWVELVRGLPRENTTI WTSGSSI SFCGVSDTANWSWPDGAELPFTI DK

>gi |122855951|gb|ABM67054.1| neurami ni dase [Influenza A virus
(A/Memphis/6/2003(H1N1))]
MNPNQKI I TI GSI SI AI GI I SLMLQI GNI I SI WASHSI QTGSQNHGTI CNQRI I TYENSTWVNHTYVNI N
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NDKHSNGTVKDRSPYRALMSPCLGEAPSPYNSKFESVAWSASACHDGMGWLTI GI SGPDNGAVAVLKYNG
I I TETI KSWKKRI LRTQSEECVNGSCFTI MTDGPNNGAASYKI FKI EKGKVTKSI ELNAPNFHYEECS
CYPDTGTVMCVCRDNDWHGSRNPWVSFNQNLDYQI GYI CSGVFGDNP RPDKGKSGCNPVTVDGADGVKGF S
YKYGNGVWI GRTKSNRLRKG FEMI WDPNGWTD TDSDFSVKQDVVAI TDWSGYSGSFVQHP ELTGLDCI RP
CFWVELVRGLPRENTTI WTSGSSI SFCGVSDTANWSWPDGAELPFTI DK

>gi |156123510|gb|ABU50639.1| neurami ni dase [Influenza A virus
(A/Oklahoma/3/2006(H1N1))]
MNPNQKI I TI GSI SI AI GI I SLMLQI GNI I SI WASHSI QTGSQNHGTI CNQRI I TYENSTWVNHTYVNI N
NTNVVAGDKDTSVTLAGNSSLCSI SGWAI YTKDNSI RI GSKGDV FVI REPFI SCSHLECRTEFFLTQGALL
NDKHSNGTVKDRSPYRALMSPCLGEAPSPYNSKFESVAWSASACHDGMGWLTI GI SGPDNGAVAVLKYNG
I I TETI KSWKKRI LRTQSEECVNGSCFTI MTDGPNNGAASYKI FKI EKGKVTKSI ELNAPNFHYEECS
CYPDTGTVMCVCRDNDWHGSRNPWVSFNQNLDYQI GYI CSGVFGDNP RPDKGKSGCNPVTVDGADGVKGF S
YKYGNGVWI GRTKSNRLRKG FEMI WDPNGWTD TDSDFSVKQDVVAI TDWSGYSGSFVQHP ELTGLDCI RP
CFWVELVRGLPRENTTI WTSGSSI SFCGVSDTANWSWPDGAELPFTI DK

>gi |168825256|gb|ACA33565.1| neurami ni dase [Influenza A virus
(A/California/09/2006(H1N1))]
MNPNQKI I TI GSI SI AI GI I SLMLQI GNI I SI WASHSI QTGSQNHGTI CNQRI I TYENSTWVNHTYVNI N
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NDKHSNGTVKDRSPYRALMSPCLGEAPSPYNSKFESVAWSASACHDGMGWLTI GI SGPDNGAVAVLKYNG
I I TETI KSWKKRI LRTQSEECVNGSCFTI MTDGPNNGAASYKI FKI EKGKVTKSI ELNAPNFHYEECS
CYPDTGTVMCVCRDNDWHGSRNPWVSFNQNLDYQI GYI CSGVFGDNP RPDKGKSGCNPVTVDGADGVKGF S
YKYGNGVWI GRTKSNRLRKG FEMI WDPNGWTD TDSDFSVKQDVVAI TDWSGYSGSFVQHP ELTGLDCI RP
CFWVELVRGLPRENTTI WTSGSSI SFCGVSDTANWSWPDGAELPFTI DK

>gi |158188202|gb|ABW23387.1| neurami ni dase [Influenza A virus
(A/Massachusetts/08/2006(H1N1))]
MNPNQKI I TI GSI SI AI GI I SLMLQI GNI I SI WASHSI QTGSQNHGTI CNQRI I TYENSTWVNHTYVNI N
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NDKHSNGTVKDRSPYRALMSPCLGEAPSPYNSKFESVAWSASACHDGMGWLTI GI SGPDNGAVAVLKYNG
I I TETI KSWKKRI LRTQSEECVNGSCFTI MTDGPNNGAASYKI FKI EKGKVTKSI ELNAPNFHYEECS
CYPDTGTVMCVCRDNDWHGSRNPWVSFNQNLDYQI GYI CSGVFGDNP RPDKGKSGCNPVTVDGADGVKGF S
YKYGNGVWI GRTKSNRLRKG FEMI WDPNGWTD TDSDFSVKQDVVAI TDWSGYSGSFVQHP ELTGLDCI RP
CFWVELVRGLPRENTTI WTSGSSI SFCGVSDTANWSWPDGAELPFTI DK

>gi |156123514|gb|ABU50641.1| neurami ni dase [Influenza A virus
(A/Missouri/11/2006(H1N1))]
MNPNQKI I TI GSI SI AI GI I SLMLQI GNI I SI WASHSI QTGSQNHGTI CNQRI I TYENSTWVNHTYVNI N
NTNVVAGDKDTSVTLAGNSSLCSI SGWAI YTKDNSI RI GSKGDV FVI REPFI SCSHLECRTEFFLTQGALL
NDKHSNGTVKDRSPYRALMSPCLGEAPSPYNSKFESVAWSASACHDGMGWLTI GI SGPDNGAVAVLKYNG
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CFWVELVRGLPRENTTI WTSGSSI SFCGVSDTANWSWPDGAELPFTI DK

>gi |158188218|gb|ABW23395.1| neurami ni dase [Influenza A virus
(A/Memphis/13/2006(H1N1))]
MNPNQKI I TI GSI SI AI GI I SLMLQI GNI I SI WASHSI QTGSQNHGTI CNQRI I TYENSTWVNHTYVNI N
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NDKHSNGTVKDRSPYRALMSPCLGEAPSPYNSKFESVAWSASACHDGMGWLTI GI SGPDNGAVAVLKYNG
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YKYGNGVWI GRTKSNRLRKG FEMI WDPNGWTD TDSDFSVKQDVVAI TDWSGYSGSFVQHP ELTGLDCI RP
CFWVELVRGLPRENTTI WTSGSSI SFCGVSDTANWSWPDGAELPFTI DK

>gi |168827347|gb|ACA33620.1| neurami ni dase [Influenza A virus
(A/Georgia/20/2006(H1N1))]
MNPNQKI I TI GSI SI AI GI I SLMLQI GNI I SI WASHSI QTGSQNHGTI CNQRI I TYENSTWVNHTYVNI N
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I I TETI KSWKKRI LRTQESECVCVNGSCFTI MTDGPSNGAASYKI FKI EKGKVTKSI ELNAPNFYEECS
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 >gi |168827351|gb|ACA33622.1| neurami ni dase [Influenza A virus
 (A/Georgi a/20/2006(H1N1))]
 MNPNQKI I TI GSI SI AI GI I SLMLQI GNI I SI WASHSI QTGSONHTGI CNQRI I TYENSTWVNHHTYVNI N
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 I I TETI KSWKKRI LRTQESECVCVNGSCFTI MTDGPSNGAASYKI FKI EKGKVTKSI ELNAPNFYEECS
 CYPDTGTVMCVCARDNWHGSRNPWVWVFNQNLDYQI GYI CSGVFGDNPRPKDGKGCSCNPVTVGDGADGVKGF
 YKYGNGVWI GRTKSNRLRKGFEI WDPNGWNTDSDFSVKQDVVAI TDWSGYSGSFVQHPGLTGLDCI RP
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 >gi |168827349|gb|ACA33621.1| neurami ni dase [Influenza A virus
 (A/Georgi a/20/2006(H1N1))]
 MNPNQKI I TI GSI SI AI GI I SLMLQI GNI I SI WASHSI QTGSONHTGI CNQRI I TYENSTWVNHHTYVNI N
 NTNVAAGKDKTSVTLAGNSSLCSI SGWAI YTKDNSI RI GSKGDVFI REFFI SCSHLECRFFLTQGALL
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 I I TETI KSWKKRI LRTQESECVCVNGSCFTI MTDGPSNGAASYKI FKI EKGKVTKSI ELNAPNFYEECS
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 >gi |158524906|gb|ABW71297.1| neurami ni dase [Influenza A virus (A/North Carolina/UR06-
 0011/2006(H1N1))]
 MNPNQKI I TI GSI SI AI GI I SLMLQI GNI I SI WASHSI QTGSONHTGI CNQRI I TYENSTWVNHHTYVNI N
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 NDKHNSGTVKDRSPYRALMSCPLGEAPSPYNSKFEVAVSASACHDGMGLTI GI SGPDNGAVAVLKYNIG
 I I TETI KSWKKRI LRTQESECVCVNGSCFTI MTDGPSNGAASYKI FKI EKGKVTKSI ELNAPNFYEECS
 CYPDTGTVMCVCARDNWHGSRNPWVWVFNQNLDYQI GYI CSGVFGDNPRPKDGKGCSCNPVTVGDGADGVKGF
 YKYGNGVWI GRTKSNRLRKGFEI WDPNGWNTDSDFSVKQDVVAI TDWSGYSGSFVQHPGLTGLDCI RP
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 0010/2006(H1N1))]
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 YKYGNGVWI GRTKSNRLRKGFEI WDPNGWNTDSDFSVKQDVVAI TDWSGYSGSFVQHPGLTGLDCI RP
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 (A/Singapore/1/1957(H2N2))]
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 LVDSI GSWSONI LRTQESECVCV NGTCTVVMTDGSASGRADTRI LFI KEGKI VHI SPLSGSAQHI EECSC
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 GWAFDNGDDVMMGRTI NKDSRSGYETFKVI GGWSTPNSKSQVNRQVI VDNNNWSGYSGI FSVEGKSCI NR
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 (A/Singapore/1/57(H2N2))]
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 (A/EI Salvador/2/57(H2N2))]
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LVDSI GSWSONI LRTQSEECVCI NGTCTVMTDGSASGRADTRI LFI KEGKI VHI SPLSGSAQHI EECSC
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CFYVELI RGRPQETRVVWTSNSI VVFCGTSYGTGSGWPDGANI NFMPPI
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(A/Adachi /2/1957(H2N2))]
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CFYVELI RGRPQETRVVWTSNSI VVFCGTSYGTGSGWPDGANI NFMPPI
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(A/Singapore/1/57(H2N2))]
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LVDSI GSWSONI LRTQSEECVCI NGTCTVMTDGSASGRADTRI LFI KEGKI VHI SPLSGSAQHI EECSC
YPRYPDVRCI CRDNWKGSNRPVI DI NMEDYSI DSSYVCSGLVGDTPRNDSSSNCRDPNNERGNPGVK
GWAFDNGDDVMMGRTI NKDSRSYG YETFKVI GGWSTPNSKSQVNRQVI VDNNNWSGYSGI FSVEGKSCI NR
CFYVELI RGRPQETRVVWTSNSI VVFCGTSYGTGSGWPDGANI NFMPPI
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I CPEVVEYRNWSKPOCOI TGFAPFSKDNSI RLSAGGDI WVTREPYVSCDPGKCYQFALGQGTTLDNKHSN
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VRCI CKDNWKGSNRPVI DI NMEDYSI DSSYVCSGLVGDTPRNDSSSNCRDPNNERGNPGVKWAFDN
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LVDSI GSWSONI LRTQSEECVCI NGTCTVMTDGSASGRADTRI LFI KEGKI VHI GPLSGSAQHI EECSC
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CFYVELI RGRPQETRVVWTSNSI VVFCGTSYGTGSGWPDGANI NFMPPI
>gi |145279043|gb |ABP49462.1| neurami ni dase [Influenza A vi rus
(A/AI bany/22/1957(H2N2))]
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LVDSI GSWSONI LRTQSEECVCI NGTCTVMTDGSASGRADTRI LFI KEGKI VHI SPLSGSAQHI EECSC
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>gi |146760071|gb |ABQ44463.1| neurami ni dase [Influenza A vi rus
(A/AI bany/20/1957(H2N2))]
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YPRYPDVRCI CRDNWKGSNRPVI DI NMEDYSI DSSYVCSGLVGDTPRNDSSSNCRDPNNERGNPGVK
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Arbor/23/1957(H2N2))]
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LVDSI GSWSONI LRTQSEECVCI NGTCTVMTDGSASGRADTRI LFI KEGKI VHI SPLSGSAQHI EECSC
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CFYVELI RGRPQETRVVWTSNSI VVFCGTSYGTGSGWPDGANI NFMPPI
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(A/Gui yang/1/1957(H2N2))]
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LVDSI GSWSONI LRTQSEECVCI NGTCTVMTDGSASGRADTRI LFI KEGKI VHI SPLSGSAQHI EECSC
YPRYPDVRCI CRDNWKGSNRPVI DI NMEDYSI DSSYVCSGLVGDTPRNDSSSNCRDPNNERGNPGVK
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>gi |194352167|gb|ACF54480.1| neurami ni dase [Infl uenza A vi rus (A/Si ngapore/1/1957(H2N2))]
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>gi |194352186|gb|ACF54491.1| neurami ni dase [Infl uenza A vi rus (A/Si ngapore/1-
MA12/1957(H2N2))]
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MA12B/1957(H2N2))]
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MA12D/1957(H2N2))]
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GWAFDNGDDVMMGR TI NKDSRSGYETFKVI GGWSTPNSKSQVNRQVI VDNNNWSGYSGI FSVEGKSCI NR
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>gi |324510|gb|AAA43413.1| neurami ni dase [Infl uenza A vi rus (A/RI/5-/1957(H2N2))]
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>gi |8250669|gb|AAA96709.2| neurami ni dase [Infl uenza A vi rus (A/Leni ngrad/134/57
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YPRYPDVRCI CRDNWKGSNRPVI DI NMEDYSI DSSYVCSGLVGDTPRNDSSSN SNCRDPNNERGNPGVK
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>gi |565252|gb|AAA96710.1| neurami ni dase [Infl uenza A vi rus
(A/Leni ngrad/134/17/1957(H2N2))]
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 (A/Leni ngrad/134/47/1957(H2N2))]
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 DNKHSNGTI HDRI PHRTLLMNLGVPFHLGTRQVCI AWSSSSCHDGKAWLHVCTGDDRNATASFI YDGR
 LVDSI GSWSONI LRTQSECEVCI NGCTVVMTDGSASGRADTRI LFI KEGKI VHI SPLSGSAQHI EECS
 YPRYPDVRCI CRDNWKGSNRPVI DI NMEDYSI DSSYVCSGLVGDTPRNDSSSNCRDPNNERGNPGVK
 GWAFDNGDDVMMGRTI SKDSRSGYETFVKVI GGWSTPNSKSQVNRQVI VDNNNWSGYSGI FSVEGKSCI NR
 CFYVELI RGRPQETRVWWTNSI VVFCGTSYGTGSGWPDGANI NFMP1
 >gi |106725724|gb|ABF82433.1| neurami ni dase [Influenza A virus (A/RI/5+/1957(H2N2))]
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 TTI EKEI CPKVVVEYRNWSKPQCCI TGFAPFSKDNSI RLSAGGDI WVTREPYVSCDPGKCYQFALGQGTTL
 DNKHSNDTVHRI PHRTLLMNLGVPFHLGTRQVCI AWSSSSCHDGKAWLHVCI TGDDKNATASFI YDGR
 LVDSI GSWSONI LRTQSECEVCI NGCTVVMTDGSASGRADTRI LFI EEGKI VHI SPLSGSAQHI EECS
 YPRYPGVRCI CRDNWKGSNRPVVDI NMEDYSI DSSYVCSGLVGDTPRNDSSSNCRDPNNERGTQGVK
 GWAFDNGDNLMMGRTI SKESRSGYETFVKVI GGWSTPNSKSQVNRQVI VDNNNWSGYSGI FSVEGKSCI NR
 CFYVELI RGRPQETRVWWTNSI VVFCGTSYGTGSGWPDGANI NFMP1
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 LVDSI GSWSONI LRTQSECEVCI NGCTVVMTDGSASGRADTRI LFI EEGKI VHI SPLSGSAQHI EECS
 YPRYPDVRCI CRDNWKGSNRPVVDI NMEDYSI DSSYVCSGLVGDTPRNDSSSNCRDPNNERGTQGVK
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 >gi |106725732|gb|ABF82435.1| neurami ni dase [Influenza A virus (A/RI/5+/1957(H2N2))]
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 TTI EKEI CPKVVVEYRNWSKPQCCI TGFAPFSKDNSI RLSAGGDI WVTREPYVSCDPGKCYQFALGQGTTL
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 LVDSI GSWSONI LRTQSECEVCI NGCTVVMTDGSASGRADTRI LFI KEGKI VHI SPLSGSAQHI EECS
 YPRYPDVRCI CRDNWKGSNRPVI DI NMEDYSI DSGYVCSGLVGDTPRNDSSSNCRDPNNERGNPGVK
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 >gi |115279067|gb|ABI 84962.1| neurami ni dase [Influenza A virus
 (A/Japan/305/1957(H2N2))]
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 LVDSI GSWSONI LRTQSECEVCI NGCTVVMTDGSASGRADTRI LFI KEGKI VHI SPLSGSAQHI EECS
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 CFYVELI RGRPQETRVWWTNSI VVFCGTSYGTGSGWPDGANI NFMP1
 >gi |133753662|gb|AB038310.1| neurami ni dase [Influenza A virus
 (A/AI bany/26/1957(H2N2))]
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 LVDSI GSWSONI LRTQSECEVCI NGCTVVMTDGSASGRADTRI LFI KEGKI VHI SPLSGSAQHI EECS
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 CFYVELI RGRPQETRVWWTNSI VVFCGTSYGTGSGWPDGANI NFMP1
 >gi |133752963|gb|AB038101.1| neurami ni dase [Influenza A virus
 (A/AI bany/2/1958(H2N2))]
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 LVDSI GSWSONI LRTQSECEVCI NGCTVVMTDGSASGRADTRI LFI KEGKI VHI SPLSGSAQHI EECS
 YPRYPDVRCI CRDNWKGSNRPVI DI NMEDYSI DSSYVCSGLVGDTPRNDSSSNCRDPNNERGNPGVK
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 CFYVELI RGRPQETRVWWTNSI VVFCGTSYGTGSGWPDGANI NFMP1
 >gi |133753643|gb|AB038299.1| neurami ni dase [Influenza A virus
 (A/AI bany/4/1958(H2N2))]
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 LVDSI GSWSONI LRTQSECEVCI NGCTVVMTDGSASGRADTRI LFI KEGKI VHI SPLSGSAQHI EECS
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 CFYVELI RGRPQETRVWWTNSI VVFCGTSYGTGSGWPDGANI NFMP1
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 (A/AI bany/1/1958(H2N2))]
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 LVDSI GSWSONI LRTQSECEVCI NGCTVVMTDGSASGRADTRI LFI KEGKI VHI SPLSGSAQHI EECS

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 CFYVELI RGRPQETRVWVWTSNSI VVFCGTSYGTGSGWPDGANI NFMPPI
 >gi |134047528|gb|AB052305.1| neurami ni dase [Influenza A vi rus
 (A/AI bany/3/1958(H2N2))]
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 TTI EKEI CPEVVEYRNWSKPQCOI TGFAPFSKDNSI RLSAGGDI WVTREPYVSCDPGKCYQFALGQGTTL
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 LVDSI GSWSONI LRTQESECVC I NGTCTVVMTDGSASGRADTRI LFI KEGKI VHI SPLSGSAQHI EECS
 YPRYPDVRCI CRDNWKGSRPVI DI NMEDYSI DSSYVCSGLVGDTPRNDSSSSNSNCRDPNNERGNPGVK
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 >gi |145279005|gb|ABP49440.1| neurami ni dase [Influenza A vi rus
 (A/AI bany/24/1958(H2N2))]
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 TTI EKEI CPEVVEYRNWSKPQCOI TGFAPFSKDNSI RLSAGGDI WVTREPYVSCDPGKCYQFALGQGTTL
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 LVDSI GSWSONI LRTQESECVC I NGTCTVVMTDGSASGRADTRI LFI KEGKI VHI SPLSGSAQHI EECS
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 GWAFDNGDDVMMGRTI SKDSRSGYETFKVI GGWSTPNSKSQANROVI VDKNNWSGYSI FSVEGKSCI NR
 CFYVELI RGRPQETRVWVWTSNSI VVFCGTSYGTGSGWPDGANI NFMPPI
 >gi |37784792|gb|AA046215.1| neurami ni dase [Influenza A vi rus (A/AI bany/6/58(H2N2))]
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 LVDSI GSWSONI LRTQESECVC I NGTCTVVMTDGSASGRADTRI LFI KEGKI VHI SPLSGSAQHI EECS
 YPRYPDVRCI CRDNWKGSRPVI DI NMEDYSI DSSYVCSGLVGDTPRNDSSSSNSNCRDPNNERGNPGVK
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 >gi |37784794|gb|AA046216.1| neurami ni dase [Influenza A vi rus (A/Malaya/16/58(H2N2))]
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 TTI EKEI CPEVVEYRNWSKPQCOI TGFAPFSKDNSI RLSAGGDI WVTREPYVSCDPGKCYQFALGQGTTL
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 LVDSI VSWSONI LRTQESECVC I NGTCTVVMTDGSASGRADTRI LFI KEGKI VHI SPLSGSAQHI EECS
 YPRYPDVRCI CRDNWKGSRPVI DI NMEDYSI DSSYVCSGLVGDTPRNDSSSSNSNCRDPNNERGNPGVK
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 (A/AI bany/5/1958(H2N2))]
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 DNKHSNGTI HDRI PHRTLLMNLGVPFHLGKQVCAWSSSSCHDGKAWLHVCVTGDDRNATASFI YDGR
 LVDSI GSWSONI LRTQESECVC I NGTCTVVMTDGSASGRADTRI LFI KEGKI VHI SPLSGSAQHI EECS
 YPRYPDVRCI CRDNWKGSRPVI DI NMEDYSI DSSYVCSGLVGDTPRNDSSSSNSNCRDPNNERGNPGVK
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 CFYVELI RGRPQETRVWVWTSNSI VVFCGTSYGTGSGWPDGANI NFMPPI
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 LEDSI GSWSONI LRTQESECVC I NGTCTVVMTDGSASGRADTRI LFI KEGKI VHI SPLSGSAQHI EECS
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 (A/Victoria/15681/59(H2N2))]
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 LEDSI GSWSONI LRTQESECVC I NGTCTVVMTDGSASGRADTRI LFI KEGKI VHI SPLSGSAQHI EECS
 YPRYPDVRCI CRDNWKGSRPVLDI SMEDYSI DSSYVCSGLVGDTPRNDSSSSNSNCRDPNNERGNPGVK
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 (A/Krasnodar/101/1959(H2N2))]
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 LVDSI GSWSONI LRTQESECVC I NGTCTVVMTDGSASGRADTRI LFI KEGKI VHI SPLSGSAQHI EECS
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 (A/AI bany/1/1959(H2N2))]
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 DNKHSNGTI HDRI PHRTLLMNLGVPFHLGKQVCAWSSSSCHDGKAWLHVCVTGDDRNATASFI YDGR

LVDSI GSWSONI LRTQSEECVCI NGTCTVVMTDGSASGRADTRI LFI KEGKI VHI SPLSGSAQHI EECSC
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 >gi |46401574|dbj |BAD16639.1| neurami ni dase [Influenza A virus (A/Ann
 Arbor/6/60(H2N2))]
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 LVDSI GSWSONI LRTQSEECVCI NGTCTVVMTDGSASGRADTRI LFI KEGKI VHI SPLSGSAQHI EECSC
 YPRYPDVRCI CRDNWKGNSRNPVI DI NMEDYSI DSSYVCSGLVGDTPRNDSSSNCRDPNNERGNPGVK
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 (A/AI bany/1/1960(H2N2))]
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 LEDSI GSWSONI LRTQSEECVCI NGTCTVVMTDGNASGRADTRI LFI KEGKI VHI SPLSGSAQHI EECSC
 YPRYPDVRCI CRDNWKGNSRNPVLDI SMEDYSI DSSYVCSGLVGDTPRNDSSSNCRDPNNERGNPGVK
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 Arbor/6/60(H2N2))]
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 LVDSI GSWSONI LRTQSEECVCI NGTCTVVMTDGSASGRADTRI LFI KEGKI VHI SPLSGSAQHI EECSC
 YPRYPDVRCI CRDNWKGNSRNPVI DI NMEDYSI DSSYVCSGLVGDTPRNDSSSNCRDPNNERGNPGVK
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 LVDSI GSWSONI LRTQSEECVCI NGI CTVMTDGSASGRADTRI LFI EEGKI VHI SPLSGSAQHVEECSC
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 DNKHSNDTI HDRI PHRTLLMNLGVPFHLGTRQVCVAWSSSSCHDGKAWLHVCTGDDRNATASFI YDGR
 LVDSI GSWSONI LRTQSEECVCI NGI CTVMTDGSASGRADTRI LFI EEGKI VHI SPLSGSAQHVEECSC
 YPRYPDVRCI CRDNWKGNSRNPVI DI NMEDYSI DSSYVCSGLVGDTPRNDSSSNCRDPNNERGNPGVK
 GWAFDNGDDVVMGRTI SKDLRSGYETFKVI GGWSTPNSKSQVNRQVI VDNNNWSGYSYGI FSVEGKSCI NR
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 >gi |37784806|gb |AA046222.1| neurami ni dase [Influenza A virus (A/Taiwan/1/62(H2N2))]
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 DNKHSNDTI HDRI PHRTLLMNLGVPFHLGTRQVCVAWSSSSCHDGKAWLHVCTGDDRNATASFI YDGR
 LVDSI GSWSONI LRTQSEECVCI NGTCTVVMTDGSASGRADTRI LFI EEGKI VHI SPLSGSAQHVEECSC
 YPRYPDVRCI CRDNWKGNSRNPVI DI NMEDYSI DSSYVCSGLVGDTPRNDSSSNCRDPNNERGNPGVK
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 CFYVELI RGRSQETRVWVWTSNSI VVFCGTSYGTGSGWPDGANI NFMP
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 LVDSI GSWSONI LRTQSEECVCI NGTCTVVMTDGSASGRADTRI LFI EEGKI VHI SPLSGSAQHVEECSC
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 (A/Netherlands/60/62(H2N2))]
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 (A/Netherl ands/65/63(H2N2))]
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 (A/Berl i n/3/1964(H2N2))]
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 LVDSI GSWSONI LRTQSECEVCI NGCTVVMTDGSASGRADTRI LFI EEGKI VHI SPLSGSAQHVEECSC
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 LMDSI GSWSONI LRTQSECEVCI NGCTVVMTDGSASGRADTRI LFI EEGKI VHI SPLSGSAQHVEECSC
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 (A/Cottbus/1/1964(H2N2))]
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 LMDSI GSWSONI LRTQSECEVCI NGCTVVMTDGSASGRADTRI LFI EEGKI VHI SPLSGSAQHVEECSC
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 (A/Potsdam/2/1965(H2N2))]
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 LVDSI GSWSONI LRTQSEECVCI NGTCTVVMTDGSASGRADTRI LFI EEGKI VHI SPLSGSAQHVEECS
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 (A/Moscow/1019/1965(H2N2))]
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 LVDSI GSWSONI LRTQSEECVCI NGTCTVVMTDGSASGRADTRI LFI EEGKI VHI SPLSGSAQHI EECSC
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 (A/NewJersey/3/65(H2N2))]
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 DNKHSNDTI HDRI PHRTLLMNELGVPFHLGTRQVCI AWSSSSCHDGKAWLHVCVTGDDKNATASFI YDGR
 LVDSI GSWSONI LRTQSEECVCI NGTCTVVMTDGSASGRADTRI LFI EEGKI VHI SPLSGSAQHVEECS
 YPRYPDVRCI CRDNWKGNSRPV DI NMEDYSI DSSYVCSGLVGDTPRNDRRSSNSNCRPNPNERGNPVGK
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 (A/Pittsburgh/2/65(H2N2))]
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 LVDSI GSWSONI LRTQSEECVCI NGTCTVVMTDGSASGRADTRI LFI EEGKI VHI SPLSGSAQHVEECS
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 (A/California/1/66(H2N2))]
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TTI EKEI CPKVVVEYRNWSKPOCQI TGFAPFSKDNSI RLSAGGDI WVTREPYVSCDPVKCYQFALGQGTTL
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LVDSI GSWSONI LRTQSEECVCI NGTCTVVMTDGSASGRADTRI LFI EEGKI VHI SPLSGSAQHVEECSC
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CFYVELI RGRKQETRVWVWTSNSI VVFCGTSGYGTGSWPDGANI NFMPPI
>gi |37784854|gb|AA046246.1| neurami ni dase [Influenza A virus
(A/Johannesburg/567/67(H2N2))]
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LVDSI GSWSONI LRTQSEECVCI NGTCTVVMTDGSASGRADTRI LFI EEGKI VHI SPLSGSAQHVEECSC
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GWAFDNGDDVWVMGRTI SKDLRSYG YETFKVI GGWSTPNSKSQI NROVI VSDNDRSGYSI FSVEGKSCI NR
CFYVELI RGRKQETRVWVWTSNSI VVFCGTSGYGTGSWPDGANI NFMPPI
>gi |37784856|gb|AA046247.1| neurami ni dase [Influenza A virus
(A/Cordoba/522/67(H2N2))]
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LVDSI GSWSONI LRTQSEECVCI NGTCTVVMTDGSASGRADTRI LFI EEGKI VHI SPLSGSAQHVEECSC
YPRYPGVRCI CRDNWKGSNRPVI DI NMEDYSI DSSYVCSGLVGDTPRNDRRSSNSNCRPNPNERGNQGVK
GWAFDNGDDVWVMGRTI SKDLRSYG YETFKVI GGWSTPNSKSQI NROVI VSDNDRSGYSI FSVEGKSCI NR
CFYVELI RGRKQETRVWVWTSNSI VVFCGTSGYGTGSWPDGANI NFMPPI
>gi |133981982|gb|AB044060.1| neurami ni dase [Influenza A virus
(A/AI bany/9/1967(H2N2))]
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LVDSI GSWSONI LRTQSEECVCI NGTCTVVMTDGSASGRADTRI LFI EEGKI VHI SPLSGSAQHVEECSC
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CFYVELI RGRKQETRVWVWTSNSI VVFCGTSGYGTGSWPDGANI NLMPPI
>gi |146760033|gb|AB044441.1| neurami ni dase [Influenza A virus
(A/AI bany/4/1967(H2N2))]
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LVDSI GSWSONI LRTQSEECVCI NGTCTVVMTDGSASGRADTRI LFI EEGKI VHI SPLSGSAQHVEECSC
YPRYPDVRCI CRDNWKGSNRPVI VDI NMEDYSI DSSYVCSGLVGDTPRNDRRSSNSNCRPNPNERGNQGVK
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CFYVELI RGRKQETRVWVWTSNSI VVFCGTSGYGTGSWPDGANI NFMPPI
>gi |133982576|gb|AB044104.1| neurami ni dase [Influenza A virus
(A/AI bany/8/1967(H2N2))]
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LVDSI GSWSONI LRTQSEECVCI NGTCTVVMTDGSASGRADTRI LFI EEGKI VHI SPLSGSAQHVEECSC
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CFYVELI RGRKQETRVWVWTSNSI VVFCGTSGYGTGSWPDGANI NLMPPI
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(A/AI bany/6/1967(H2N2))]
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LVDSI GSWSONI LRTQSEECVCI NGTCTVVMTDGSASGRADTRI LFI EEGKI VHI SPLSGSAQHVEECSC
YPRYPDVRCI CRDNWKGSNRPVI VDI NMEDYSI DSSYVCSGLVGDTPRNDRRSSNSNCRPNPNERGNQGVK
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CFYVELI RGRKQETRVWVWTSNSI VVFCGTSGYGTGSWPDGANI NFMPPI
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(A/AI bany/7/1967(H2N2))]
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LVDSI GSWSONI LRTQSEECVCI NGTCTVVMTDGSASGRADTRI LFI EEGKI VHI SPLSGSAQHVEECSC
YPRYPDVRCI CRDNWKGSNRPVI VDI NMEDYSI DSSYVCSGLVGDTPRNDRRSSNSNCRPNPNERGNQGVK
GWAFDNGDDVWVMGRTI SKDLRSYG YETFKVI GGWSTPNSKSQI NROVI VSDNDRSGYSI FSVEGKSCI NR
CFYVELI RGRKQETRVWVWTSNSI VVFCGTSGYGTGSWPDGANI NFMPPI
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(A/AI bany/3/1967(H2N2))]
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LVDSI GSWSONI LRTQSEECVCI NGTCTVVMTDGSASGRADTRI LFI EEGKI VHI SPLSGSAQHVEECSC
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 (A/Tashkent/1046/1967(H2N2))]
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 LVDSI GSWSONI LRTQSEECVCI NGCTVVMVDGSASGRADTRI LFI EEGKI VHI SPLSGSAQHVEECSC
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 (A/Johannesburg/617/1967(H2N2))]
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 LVDSI GSWSONI LRTQSEECVCI NGCTVVMVDGSASGRADTRI LFI EEGKI VHI SPLSGSAQHVEECSC
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 LVDSI GSWSONI LRTQSEECVCI NGCTVVMVDGSASGRADTRI LFI EEGKI VHI SPLSGSAQHVEECSC
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 >gi |194351984|gb|ACF54392.1| neurami ni dase [Influenza A virus
 (A/Georgi a/1/1967(H2N2))]
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 LVDSI GSWSONI LRTQSEECVCI NGCTVVMVDGSASGRADTRI LFI EEGKI VHI SPLSGSAQHVEECSC
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 (A/Berkeley/1/1968(H2N2))]
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 EKEI CPKVVVEYRNWSKPOCKI TGFAPFSKDNSI RLSAGGDI WVTREPVVSCDPGKCYQFALGQGTTL
 DNKHSNDTI HDRI PHRTLLMNLGVPFHLGTROVCI AWSSSSCHDGKAWLHVCI TGDDKNATASFI YDGR
 LVDSI GSWSONI LRTQSEECVCI NGCTVVMVDGSASGRADTRI LFI EEGKI VHI SPLSGSAQHVEECSC
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 (A/AI bany/2/1968(H2N2))]
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 LVDSI GSWSONI LRTQSEECVCI NGCTVVMVDGSASGRADTRI LFI EEGKI VHI SPLSGSAQHVEECSC
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 CFYVELI RGRKQETRVWVWTSNSI VVFCGTSYGTGSGWPDGANI NFMP
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 TTI EKEI CPKVVVEYRNWSKPOCKI TGFAPFSKDNSI RLSAGGDI WVTREPVVSCDPGKCYQFALGQGTTL
 DNKHSNDTI HDRI PHRTLLMNLGVPFHLGTROVCI AWSSSSCHDGKAWLHVCI TGDDKNATASFI YDGR
 LVDSI GSWSONI LRTQSEECVCI NGCTVVMVDGSASGRADTRI LFI EEGKI VHI SPLSGSAQHVEECSC
 YPRYPGVRCI CRDNWKGNSRNPVVDI NMEDYSI DSSYVCSGLVGDTPRNDRRSSNSNCRPNNEKGNQGVK
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 (A/Berkeley/1/1968(H2N2))]
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 DNKHSNDTI HDRI PHRTLLMNLGVPFHLGTROVCI AWSSSSCHDGKAWLHVCI TGDDKNATASFI YDGR
 LVDSI GSWSONI LRTQSEECVCI NGCTVVMVDGSASGRADTRI LFI EEGKI VHI SPLSGSAQHVEECSC
 YPRYPGVRCI CRDNWKGNSRNPVVDI NMEDYSI DSSYVCSGLVGDTPRNDRRSSNSNCRPNNEKGNQGVK
 GWAFDNGDDVVMGRTI SKDLRSGYETFKVI GGWSTPNSKSQI NROVI VSDNRSYGYSI FSVEGKSCI NR
 CFYVELI RGRKQETRVWVWTSNSI VVFCGTSYGTGSGWPDGANI NFMP
 >gi |134047432|gb|AB052250.1| neurami ni dase [Influenza A virus
 (A/AI bany/1/1968(H2N2))]
 MNPNQKI I TI GSASLI ATVCFLMQI AI LVTTVTLHFQHECDSPASNOVMPCEPI I I ERNI TEI VYLN
 TTI EKEI CPKVVVEYRNWSKPOCKI TGFAPFSKDNSI RLSAGGDI WVTREPVVSCDPGKCYQFALGQGTTL
 DNKHSNDTI HDRI PHRTLLMNLGVPFHLGTROVCI AWSSSSCHDGKAWLHVCI TGDDKNATASFI YDGR
 LVDSI GSWSONI LRTQSEECVCI NGCTVVMVDGSASGRADTRI LFI EEGKI VHI SPLSGSAQHVEECSC

YPRYPDVRCI CRDNWKGSNRPVVDI NMEDYSI DSSYVCSGLVGDTPRNDRRSSNSNCRPNPNEKGNQGVK
 GWAFDNGDDVMMGRTI SKDLRSYGETFKVI GGWSTPNSKSQI NROVI VSDNRSRGYSI FSVEGKSCI NR
 CFYVELI RGRKQETRVWWTNSI VVFCGTSGYGTGSWPDGANI NLMPI
 >gi |188504374|gb|ACD56305.1| neurami ni dase [Influenza A virus (A/North
 Carolina/1/1968(H2N2))]
 MNPNQKI I TI GSVSLTI ATVCFLMQI AI LVTTVTLHFQHECDSPASNQVMPCEPI I I ERNI TEI VYLNN
 TTI EKEI CPEVVEYRNWSKPQCQI TGFAPFSKDNSI RLSAGGDI WVTREPYVSCDPGKCYQFALGQGTTL
 DNKHSNDTI HDRI PHRTLLMNELGVPFHLGTROQVCVAWSSSSCHDGKAWLHVCVTGDDKNATASFI YDGR
 LVDSI GWSQNI LRTQSEECVCI NGTCTVVMTDGSASGRADTRI LFI EEGKI VHI SPLSGSAQHVEECSC
 YPRYPDVRCI CRDNWKGSNRPVI DI NMEDYSI DSSYVCSGLVGDTPRNDRRSSNSNCRPNPNERGNQGVK
 GWAFDNGDDVMMGRTI SKDLRSYGETFKVI GGWSTPNSKSQI NROVI VSDNRSRGYSI FSVEGKSCI NR
 CFYVELI RGRKQETRVWWTNSI VVFCGTSGYGTGSWPDGANI NLMPI
 >gi |188504393|gb|ACD56316.1| neurami ni dase [Influenza A virus
 (A/Korea/426/1968(H2N2))]
 MNPNQKI I TI GSVSLTI ATVCFLMQI AI LVTTVTLHFQHECDSPASNQVMPCEPI I I ERNI TEI VYLNN
 TTI EKEI CPEVVEYRNWSKPQCQI TGFAPFSKDNSI RLSAGGDI WVTREPYVSCDPGKCYQFALGQGTTL
 DNKHSNDTI HDRI PHRTLLMNELGVPFHLGTROQVCVAWSSSSCHDGKAWLHVCVTGDDKNATASFI YDGR
 LVDSI GWSQNI LRTQSEECVCI NGTCTVVMTDGSASGRADTRI LFI EEGKI VHI SPLSGSAQHVEECSC
 YPRYPDVRCI CRDNWKGSNRPVI DI NMEDYSI DSSYVCSGLVGDTPRNDRRSSNSNCRPNPNERGNQGVK
 GWAFDNGDDVMMGRTI SKDLRSYGETFKVI GGWSTPNSKSQI NROVI VSDNRSRGYSI FSVEGKSCI NR
 CFYVELI RGRKQETRVWWTNSI VVFCGTSGYGTGSWPDGANI NLMPI
 >gi |37784858|gb|AA046248.1| neurami ni dase [Influenza A virus (A/Korea/426/68(H2N2))]
 MNPNQKI I TI GSVSLTI ATVCFLMQI AI LVTTVTLHFQHECDSPASNQVMPCEPI I I ERNI TEI VYLNN
 TTI EKEI CPEVVEYRNWSKPQCQI TGFAPFSKDNSI RLSAGGDI WVTREPYVSCDPGKCYQFALGQGTTL
 DNKHSNDTI HDRI PHRTLLMNELGVPFHLGTROQVCVAWSSSSCHDGKAWLHVCVTGDDKNATASFI YDGR
 LVDSI GWSQNI LRTQSEECVCI NGTCTVVMTDGSASGRADTRI LFI EEGKI VHI SPLSGSAQHVEECSC
 YPRYPDVRCI CRDNWKGSNRPVI DI NMEDYSI DSSYVCSGLVGDTPRNDRRSSNSNCRPNPNERGNQGVK
 GWAFDNGDDVMMGRTI SKDLRSYGETFKVI GGWSTPNSKSQI NROVI VSDNRSRGYSI FSVEGKSCI NR
 CFYVELI RGRKQETRVWWTNSI VVFCGTSGYGTGSWPDGANI NLMPI
 >gi |37784860|gb|AA046249.1| neurami ni dase [Influenza A virus (A/Berkeley/1/68(H2N2))]
 MNPNQKI I TI GSVSLTI ATVCFLMQI AI LVTTVTLHFQHECDSPASNQVMPCEPI I I ERNTEI VYLNN
 TTI EKEI CPKVVVEYRNWSKPQCQI TGFAPFSKDNSI RLSAGGDI WVTREPYVSCDPGKCYQFALGQGTTL
 DNKHSNDTI HDRI PHRTLLMNELGVPFHLGTROQVCVAWSSSSCHDGKAWLHVCVTGDDKNATASFI YDGR
 LVDSI GWSQNI LRTQSEECVCI NGTCTVVMTDGSASGRADTRI LFI EEGKI VHI SPLSGSAQHVEECSC
 YPRYPDVRCI CRDNWKGSNRPVVDI NMEDYSI DSSYVCSGLVGDTPRNDRRSSNSNCRPNPNEKGNQGVK
 GWAFDNGDDVMMGRTI SKDLRSYGETFKVI GGWSTPNSKSQI NROVI VSDNRSRGYSI FSVEGKSCI NR
 CFYVELI RGRKQETRVWWTNSI VVFCGTSGYGTGSWPDGANI NLMPI
 >gi |63054904|gb|AAY28988.1| neurami ni dase [Influenza A virus (A/Canada/720/05(H2N2))]
 MNPNQKI I TI GSVSLTI ETVCFLMQI AI LATTVTLHFQHECDSPASNQVMPCEPI I I ERNI TEI VYLNN
 TTI EKEI CPEVVEYRNWSKPQCQI TGFAPFSKDNSI RLSAGGDI WVTREPYVSCDPGKCYQFALGQGTTL
 DNKHSNDTI HDRI PHRTLLMNELGVPFHLGTROQVCVAWSSSSCHDGKAWLHVCVTGDDKNATASFI YDGR
 LVDSI GWSQNI LRTQSEECVCI NGTCTVVMTDGSASGRADTRI LFI EEGKI VHI SPLSGSAQHVEECSC
 YPRYPDVRCI CRDNWKGSNRPVI DI NMEDYSI DSSYVCSGLVGDTPRNDRRSSNSNCRPNPNERGNQGVK
 GWAFDNGDDVMMGRTI GKDSRSYGETFKVI GGWSTPNSKSQVNRQVI VDNNRSRGYSI FSVEGKSCI NR
 CFYVELI RGRKQETRVWWTNSI VVFCGTSGYGTGSWPDGANI NLMPI
 >gi |106907951|gb|ABF83450.1| neurami ni dase [Influenza A virus (A/Northern
 Territory/60/1968(H3N2))]
 NPNQKI I TI GSVSLTI ATVCFLMQTAI LVTTVTLHFQKQYECDSASNQVMPCEPI I I ERNI TEI VYLNN
 TTI EKEI CPKVVVEYRNWSKPQCQI TGFAPFSKDNSI RLSAGGDI WVTREPYVSCDPGKCYQFALGQGTTL
 DNKHSNDTI HDRI PHRTLLMNELGVPFHLGTROQVCVAWSSSSCHDGKAWLHVCI TGDDKNATASFI YDGR
 LVDSI GWSQNI LRTQSEECVCI NGTCTVVMTDGSASGRADTRI LFI EEGKI VHI SPLSGSAQHVEECSC
 YPRYPDVRCI CRDNWKGSNRPVVDI NMEDYSI DSSYVCSGLVGDTPRNDRRSSNSNCRPNPNERGNQGVK
 WAFDNGDDVMMGRTI SKDLRSYGETFKVI GGWSTPNSKSQI NROVI VSDNRSRGYSI FSVEGKSCI NRC
 FYVELI RGRKQEARVWWTNSI VVFCGTSGYGTGSWPDGANI NLMPI
 >gi |37785264|gb|AA046470.1| neurami ni dase [Influenza A virus
 (A/Georgia/122/68(H3N2))]
 MNPNQKI I TI GSVSLTI ATVCFLMQI AI LVTTVTLHFQKQYECDSASNQVMPCEPI I I ERNI TEI VYLNN
 TTI EKEI CPKVVVEYRNWSKPQCQI TGFAPFSKDNSI RLSAGGDI WVTREPYVSCDPGKCYQFALGQGTTL
 DNKHSNDTI HDRI PHRTLLMNELGVPFHLGTROQVCVAWSSSSCHDGKAWLHVCI TGDDKNATASFI YDGR
 LVDSI GWSQNI LRTQSEECVCI NGTCTVVMTDGSASGRADTRI LFI EEGKI VHI SPLSGSAQHVEECSC
 YPRYPDVRCI CRDNWKGSNRPVVDI NMEDYSI DSSYVCSGLVGDTPRNDRRSSNSNCRPNPNERGNQGVK
 GWAFDNGDDVMMGRTI SKDLRSYGETFKVI GGWSTPNSKSQI NROVI VSDNRSRGYSI FSVEGKSCI NR
 CFYVELI RGRKQETRVWWTNSI VVFCGTSGYGTGSWPDGANI NLMPI
 >gi |37785268|gb|AA046472.1| neurami ni dase [Influenza A virus (A/Tehran/101/68(H3N2))]
 MNPNQKI I TI GSVSLTI ATVCFLMQI AI LVTTVTLHFQKQYECDSASNQVMPCEPI I I ERNI TEI VYLNN
 TTI EKEI CPKVVVEYRNWSKPQCQI TGFAPFSKDNSI RLSAGGDI WVTREPYVSCDPGKCYQFALGQGTTL
 DNKHSNDTI HDRI PHRTLLMNELGVPFHLGTROQVCVAWSSSSCHDGKAWLHVCI TGDDKNATASFI YDGR
 LVDSI GWSQNI LRTQSEECVCI NGTCTVVMTDGSASGRADTRI LFI EEGKI VHI SPLSGSAQHVEECSC
 YPRYPDVRCI CRDNWKGSNRPVVDI NMEDYSI DSSYVCSGLVGDTPRNDRRSSNSNCRPNPNERGNQGVK
 GWAFDNGDDVMMGRTI SKDLRSYGETFKVI GGWSTPNSKSQI NROVI VSDNRSRGYSI FSVEGKSCI NR
 CFYVELI RGRKQETRVWWTNSI VVFCGTSGYGTGSWPDGANI NLMPI
 >gi |85816057|gb|ABC84392.1| neurami ni dase [Influenza A virus (A/Beijing/1/68(H3N2))]
 MNPNQKI I TI GSVSLTI ATVCFLMQI AI LVTTVTLHFQKQYECDSASNQVMPCEPI I I ERNI TEI VYLNN
 TTI EKEI CPKVVVEYRNWSKPQCQI TGFAPFSKDNSI RLSAGGDI WVTREPYVSCDPGKCYQFALGQGTTL
 DNKHSNDTI HDRI PHRTLLMNELGVPFHLGTROQVCVAWSSSSCHDGKAWLHVCI TGDDKNATASFI YDGR
 LVDSI GWSQNI LRTQSEECVCI NGTCTVVMTDGSASGRADTRI LFI EEGKI VHI SPLSGSAQHVEECSC
 YPRYPDVRCI CRDNWKGSNRPVVDI NMEDYSI DSSYVCSGLVGDTPRNDRRSSNSNCRPNPNERGNQGVK

GWAFDNGDDVVMGRTI SKDLRSGYETFKVI GGWSTPNSKSOI NROVI VSDNRSYSGI FSVEGKSCI NR
 CFYVELI RGRKQETRVWWTNSI VVFCGTSYGTGSGWPDGANI NFMP
 >gi |46401580|dbj |BAD16642.1| neurami ni dase [Influenza A virus (A/Ai chi /2/1968(H3N2))]

MNPNQKI I TI GSVSLTI ATVCFLMQI AI LVTTVTLHFQYECDSASPANQVMPCEPI I I ERNI TEI VYLNN
 TTI EKEI CPKVVEYRNWSKPOCQI TGFAPFSKDNSI RLSAGGDI WVTREPVVSCDHGKCYQFALGQGTTL
 DNKHSNDTI HDRI PHRTLLMNLGVPFHLGTRQVCI AWSSSSCHDGKAWLHVCI TGDDKNATASFI YDGR
 LVDSI GSWSONI LRTQSEECVCI NGTCTVMTDGSASGRADTRI LFI EEGKI VHI SPLSGSAQHVEECSCY
 YPRYPGVRCI CRDNWKGSNRPVVDI NMEDYSI DSSYVCSGLVGDTPRNDRRSSNSNCRNPNNERGNQGVK
 GWAFDNGDDVVMGRTI SKDLRSGYETFKVI GGWSTPNSKSOI NROVI VSDNRSYSGI FSVEGKSCI NR
 CFYVELI RGRKQETRVWWTNSI VVFCGTSYGTGSGWPDGANI NFMP
 >gi |193805119|gb |ACF22213.1| neurami ni dase [Influenza A virus (A/Hong Kong/1-
 1/1968(H3N2))]

PNQKI I TI GSVSLTI ATVCFLMQI AI LVTTVTLHFQYECDSASPANQVMPCEPI I I ERNI TEI VYLNN
 TTI EKEI CPKVVEYRNWSKPOCQI TGFAPFSKDNSI RLSAGGDI WVTREPVVSCDHGKCYQFALGQGTTL
 DNKHSNDTI HDRI PHRTLLMNLGVPFHLGTRQVCI AWSSSSCHDGKAWLHVCI TGDDKNATASFI YDGR
 LVDSI GSWSONI LRTQSEECVCI NGTCTVMTDGSASGRADTRI LFI EEGKI VHI SPLSGSAQHVEECSCY
 YPRYPGVRCI CRDNWKGSNRPVVDI NMEDYSI DSSYVCSGLVGDTPRNDRRSSNSNCRNPNNERGNQGVK
 GWAFDNGDDVVMGRTI SKDLRSGYETFKVI GGWSTPNSKSOI NROVI VSDNRSYSGI FSVEGKSCI NR
 CFYVELI RGRKQETRVWWTNSI VVFCGTSYGTGSGWPDGANI NFMP
 >gi |193805157|gb |ACF22235.1| neurami ni dase [Influenza A virus (A/Hong Kong/1-
 4/1968(H3N2))]

PNQKI I TI GSVSLTI ATVCFLMQI AI LVTTVTLHFQYECDSASPANQVMPCEPI I I ERNI TEI VYLNN
 TTI EKEI CPKVVEYRNWSKPOCQI TGFAPFSKDNSI RLSAGGDI WVTREPVVSCDHGKCYQFALGQGTTL
 DNKHSNDTI HDRI PHRTLLMNLGVPFHLGTRQVCI AWSSSSCHDGKAWLHVCI TGDDKNATASFI YDGR
 LVDSI GSWSONI LRTQSEECVCI NGTCTVMTDGSASGRADTRI LFI EEGKI VHI SPLSGSAQHVEECSCY
 YPRYPGVRCI CRDNWKGSNRPVVDI NMEDYSI DSSYVCSGLVGDTPRNDRRSSNSNCRNPNNERGNQGVK
 GWAFDNGDDVVMGRTI SKDLRSGYETFKVI GGWSTPNSKSOI NROVI VSDNRSYSGI FSVEGKSCI NR
 CFYVELI RGRKQETRVWWTNSI VVFCGTSYGTGSGWPDGANI NFMP
 >gi |193805176|gb |ACF22246.1| neurami ni dase [Influenza A virus (A/Hong Kong/1-
 5/1968(H3N2))]

MNPNQKI I TI GSVSLTI ATVCFLMQI AI LVTTVTLHFQYECDSASPANQVMPCEPI I I ERNI TEI VYLNN
 TTI EKEI CPKVVEYRNWSKPOCQI TGFAPFSKDNSI RLSAGGDI WVTREPVVSCDHGKCYQFALGQGTTL
 DNKHSNDTI HDRI PHRTLLMNLGVPFHLGTRQVCI AWSSSSCHDGKAWLHVCI TGDDKNATASFI YDGR
 LVDSI GSWSONI LRTQSEECVCI NGTCTVMTDGSASGRADTRI LFI EEGKI VHI SPLSGSAQHVEECSCY
 YPRYPGVRCI CRDNWKGSNRPVVDI NMEDYSI DSSYVCSGLVGDTPRNDRRSSNSNCRNPNNERGNQGVK
 GWAFDNGDDVVMGRTI SKDLRSGYETFKVI GGWSTPNSKSOI NROVI VSDNRSYSGI FSVEGKSCI NR
 CFYVELI RGRKQETRVWWTNSI VVFCGTSYGTGSGWPDGANI NFMP
 >gi |193805214|gb |ACF22268.1| neurami ni dase [Influenza A virus (A/Hong Kong/1-
 7/1968(H3N2))]

PNQKI I TI GSVSLTI ATVCFLMQI AI LVTTVTLHFQYECDSASPANQVMPCEPI I I ERNI TEI VYLNN
 TTI EKEI CPKVVEYRNWSKPOCQI TGFAPFSKDNSI RLSAGGDI WVTREPVVSCDHGKCYQFALGQGTTL
 DNKHSNDTI HDRI PHRTLLMNLGVPFHLGTRQVCI AWSSSSCHDGKAWLHVCI TGDDKNATASFI YDGR
 LVDSI GSWSONI LRTQSEECVCI NGTCTVMTDGSASGRADTRI LFI EEGKI VHI SPLSGSAQHVEECSCY
 YPRYPGVRCI CRDNWKGSNRPVVDI NMEDYSI DSSYVCSGLVGDTPRNDRRSSNSNCRNPNNERGNQGVK
 GWAFDNGDDVVMGRTI SKDLRSGYETFKVI GGWSTPNSKSOI NROVI VSDNRSYSGI FSVEGKSCI NR
 CFYVELI RGRKQETRVWWTNSI VVFCGTSYGTGSGWPDGANI NFMP
 >gi |194304637|gb |ACF41738.1| neurami ni dase [Influenza A virus (A/Hong Kong/1-1-MA-
 12/1968(H3N2))]

MNPNQKI I TI GSVSLTI ATVCFLMQI AI LVTTVTLHFQYECDSASPANQVMPCEPI I I ERNI TEI VYLNN
 TTI EKEI CPKVVEYRNWSKPOCQI TGFAPFSKDNSI RLSAGGDI WVTREPVVSCDHGKCYQFALGQGTTL
 DNKHSNDTI HDRI PHRTLLMNLGVPFHLGTRQVCI AWSSSSCHDGKAWLHVCI TGDDKNATASFI YDGR
 LVDSI GSWSONI LRTQSEECVCI NGTCTVMTDGSASGRADTRI LFI EEGKI VHI SPLSGSAQHVEECSCY
 YPRYPGVRCI CRDNWKGSNRPVVDI NMEDYSI DSSYVCSGLVGDTPRNDRRSSNSNCRNPNNERGNQGVK
 GWAFDNGDDVVMGRTI SKDLRSGYETFKVI GGWSTPNSKSOI NROVI VSDNRSYSGI FSVEGKSCI NR
 CFYVELI RGRKQETRVWWTNSI VVFCGTSYGTGSGWPDGANI NFMP
 >gi |194304751|gb |ACF41804.1| neurami ni dase [Influenza A virus (A/Hong Kong/1-11-MA21-
 3/1968(H3N2))]

MNPNQKI I TI GSVSLTI ATVCFLMQI AI LVTTVTLHFQYECDSASPANQVMPCEPI I I ERNI TEI VYLNN
 TTI EKEI CPKVVEYRNWSKPOCQI TGFAPFSKDNSI RLSAGGDI WVTREPVVSCDHGKCYQFALGQGTTL
 DNKHSNDTI HDRI PHRTLLMNLGVPFHLGTRQVCI AWSSSSCHDGKAWLHVCI TGDDKNATASFI YDGR
 LVDSI GSWSONI LRTQSEECVCI NGTCTVMTDGSASGRADTRI LFI EEGKI VHI SPLSGSAQHVEECSCY
 YPRYPGVRCI CRDNWKGSNRPVVDI NMEDYSI DSSYVCSGLVGDTPRNDRRSSNSNCRNPNNERGNQGVK
 GWAFDNGDDVVMGRTI SKDLRSGYETFKVI GGWSTPNSKSOI NROVI VSDNRSYSGI FSVEGKSCI NR
 CFYVELI RGRKQETRVWWTNSI VVFCGTSYGTGSGWPDGANI NFMP
 >gi |194352003|gb |ACF54403.1| neurami ni dase [Influenza A virus (A/Hong Kong/1-1-MA-
 12D/1968(H3N2))]

MNPNQKI I TI GSVSLTI ATVCFLMQI AI LVTTVTLHFQYECDSASPANQVMPCEPI I I ERNI TEI VYLNN
 TTI EKEI CPKVVEYRNWSKPOCQI TGFAPFSKDNSI RLSAGGDI WVTREPVVSCDHGKCYQFALGQGTTL
 DNKHSNDTI HDRI PHRTLLMNLGVPFHLGTRQVCI AWSSSSCHDGKAWLHVCI TGDDKNATASFI YDGR
 LVDSI GSWSONI LRTQSEECVCI NGTCTVMTDGSASGRADTRI LFI EEGKI VHI SPLSGSAQHVEECSCY
 YPRYPGVRCI CRDNWKGSNRPVVDI NMEDYSI DSSYVCSGLVGDTPRNDRRSSNSNCRNPNNERGNQGVK
 GWAFDNGDDVVMGRTI SKDLRSGYETFKVI GGWSTPNSKSOI NROVI VSDNRSYSGI FSVEGKSCI NR
 CFYVELI RGRKQETRVWWTNSI VVFCGTSYGTGSGWPDGANI NFMP
 >gi |126567437|dbj |BAF48362.1| neurami ni dase [Influenza A virus
 (A/Ai chi /2/1968(H3N2))]

MNPNQKI I TI GSVSLTI ATVCFLMQI AI LVTTVTLHFQYECDSASPANQVMPCEPI I I ERNI TEI VYLNN
 TTI EKEI CPKVVEYRNWSKPOCQI TGFAPFSKDNSI RLSAGGDI WVTREPVVSCDHGKCYQFALGQGTTL

DNKHSNDTI HDRI PHRTLLMNELGVPFHLGTRQVCI AWSSSSCHDGGKAWLHVCI TGDDKNATASFI YDGR
 LVDSI GSWSONI LRTQSEECVCI NGCTVVMTDGSASGRADTRI LFI EEGKI VHI SPLSGSAQHVEECSC
 YPRYPGVRCI CRDNWKGNSRNPVVDI NMEDYSI DSSYVCSGLVGDTPRNDRRSSNSNCRPNPNERGNQGVK
 GWAFDNGDDVVMGRTI SKDLRSGYETFVKVI GGWSTPNKSKQI NRQVI VDSNDRSGYSI FSVEGKSCI NR
 CFYVELI RGRKQETRVWVWTSNSI VVFCGTSYGTGSGWPDGANI NFMP1
 >gi | 37785250 | gb | AA046463.1 | neurami ni dase [Influenza A virus (A/Canada/228/68(H3N2))] |
 MNPNQKI I TI GSVSLTI ATVCFLMCI AI LVTTVTLHFQYECDSPPASNOVMPCEPI I I ERNI TEI VYLN
 TTI EKEI CPKVVVEYRNWSKQDCI TGFAPFSKDNSI RLSAGGDI VWTREPVVSCDHGKCYQFALGQGTTL
 DNKHSNDTI HDRI PHRTLLMNELGVPFHLGTRQVCI AWSSSSCHDGGKAWLHVCI TGDDKNATASFI YDGR
 LVDSI GSWSONI LRTQSEECVCI NGCTVVMTDGSASGRADTRI LFI EEGKI VHI SPLSGSAQHVEECSC
 YPRYPGVRCI CRDNWKGNSRNPVVDI NMEDYSI DSSYVCSGLVGDTPRNDRRSSNSNCRPNPNERGNQGVK
 GWAFDNGDDVVMGRTI SKDLRSGYETFVKVI GGWSTPNKSKQI NRQVI VDSNDRSGYSI FSVEGKSCI NR
 CFYVELI RGRKQETRVWVWTSNSI VVFCGTSYGTGSGWPDGANI NFMP1
 >gi | 37785252 | gb | AA046464.1 | neurami ni dase [Influenza A virus
 (A/Singapore/1/68(H3N2))] |
 MNPNQKI I TI GSVSLTI ATVCFLMCI AI LVTTVTLHFQYECDSPPASNOVMPCEPI I I ERNI TEI VYLN
 TTI EKEI CPKVVVEYRNWSKQDCI TGFAPFSKDNSI RLSAGGDI VWTREPVVSCDHGKCYQFALGQGTTL
 DNKHSNDTI HDRI PHRTLLMNELGVPFHLGTRQVCI AWSSSSCHDGGKAWLHVCI TGDDKNATASFI YDGR
 LVDSI GSWSONI LRTQSEECVCI NGCTVVMTDGSASGRADTRI LFI EEGKI VHI SPLSGSAQHVEECSC
 YPRYPGVRCI CRDNWKGNSRNPVVDI NMEDYSI DSSYVCSGLVGDTPRNDRRSSNSNCRPNPNERGNQGVK
 GWAFDNGDDVVMGRTI SKDLRSGYETFVKVI GGWSTPNKSKQI NRQVI VDSNDRSGYSI FSVEGKSCI NR
 CFYVELI RGRKQETRVWVWTSNSI VVFCGTSYGTGSGWPDGANI NFMP1
 >gi | 194293977 | gb | ACF40083.1 | neurami ni dase [Influenza A virus
 (A/Washington/03/2008(H3N2))] |
 MNPNQKI I TI GSVSLTI STI CFFMQI AI LI TTVTLHFQYEFNSPPNNQVLMCEPTI I ERNI TEI VYLTN
 TTI EKEI CPKLAEYRNWSKQDCI TGFAPFSKDNSI RLSAGGDI VWTREPVVSCDPDKCYQFALGQGTTL
 NNWHSNNTVVRBTPYRTRLLMNELGVPFHLGTRQVCI AWSSSSCHDGGKAWLHVCI TGDDKNATASFI YNGR
 LVDSVVSWSKEI LRTQSEECVCI NGCTVVMTDGSASGKADTKI LFI EEGKI VHTSTLGSQAQHVVEECSC
 YPRYPGVRCVCRDNWKGNSRPI VDI NI KDHSI VSSYVCSGLVGDTPRKNDSSSSSSHCLDPNNEEGGHGVK
 GWAFDDGNDVVMGRTI SEKSRLYGYETFVKVI EGWSNPKSKLQI NRQVI VDRGNRSGYSI FSVEGKSCI NR
 CFYVELI RGRKEETEVWTSNSI VVFCGTSYGTGSGWPDGADI NLMP1
 >gi | 194294013 | gb | ACF40101.1 | neurami ni dase [Influenza A virus
 (A/Oregon/01/2008(H3N2))] |
 MNPNQKI I TI GSVSLTI STI CFFMQI AI LI TTVTLHFQYEFNSPPNNQVLMCEPTI I ERNI TEI VYLTN
 TTI EKEI CPKLAEYRNWSKQDCI TGFAPFSKDNSI RLSAGGDI VWTREPVVSCDPDKCYQFALGQGTTL
 NNWHSNNTVVRBTPYRTRLLMNELGVPFHLGTRQVCI AWSSSSCHDGGKAWLHVCI TGDDKNATASFI YNGR
 LVDSVVSWSKEI LRTQSEECVCI NGCTVVMTDGSASGKADTKI LFI EEGKI VHTSTLGSQAQHVVEECSC
 YPRYPGVRCVCRDNWKGNSRPI VDI NI KDHSI ASSYVCSGLVGDTPRKNDSSSSSSHCLDPNNEEGGHGVK
 GWAFDDGNDVVMGRTI SEKSRLYGYETFVKVI EGWSNPKSKLQI NRQVI VDRGNRSGYSI FSVEGKSCI NR
 CFYVELI RGRKEETEVWTSNSI VVFCGTSYGTGSGWPDGADI NLMP1
 >gi | 189303165 | gb | ACD85639.1 | neurami ni dase [Influenza A virus
 (A/Texas/05/2008(H3N2))] |
 NQKI I TI GSVSLTI STI CFFMQI AI LI TTVTLHFQYEFNSPPNNQVLMCEPTI I ERNI TEI VYLTNTTI
 EKEI CPKLAEYRNWSKQDCI TGFAPFSKDNSI RLSAGGDI VWTREPVVSCDPDKCYQFALGQGTTLN
 HSNNTVVRBTPYRTRLLMNELGVPFHLGTRQVCI AWSSSSCHDGGKAWLHVCI TGDDKNATASFI YNGRLVD
 SI VVSWSKEI LRTQSEECVCI NGCTVVMTDGSASGKADTKI LFI EEGKI VHTSTLGSQAQHVVEECSCYPR
 YPGVRCVCRDNWKGNSRPI VDI NI KDHSI VSSYVCSGLVGDTPRKNDSSSSSSHCLDPNNEEGGHGVK
 FDDGNDVVMGRTI SEKSRLYGYETFVKVI EGWSNPKSKLQI NRQVI VDRGNRSGYSI FSVEGKSCI NR
 CFYVELI RGRKEETEVWTSNSI VVFCGTSYGTGSGWPDGADI NLMP1
 >gi | 194294017 | gb | ACF40103.1 | neurami ni dase [Influenza A virus
 (A/Minnesota/06/2008(H3N2))] |
 MNPNQKI I TI GSVSLTI STI CFFMQI AI LI TTVTLHFQYEFNSPPNNQVLMCEPTI I ERNI TEI VYLTN
 TTI EKEI CPKLAEYRNWSKQDCI TGFAPFSKDNSI RLSAGGDI VWTREPVVSCDPDKCYQFALGQGTTL
 NNWHSNNTVVRBTPYRTRLLMNELGVPFHLGTRQVCI AWSSSSCHDGGKAWLHVCI TGDDKNATASFI YNGR
 LVDSVVSWSKEI LRTQSEECVCI NGCTVVMTDGSASGKADTKI LFI EEGKI VHTSTLGSQAQHVVEECSC
 YPRYPGVRCVCRDNWKGNSRPI VDI NI KDHSI VSSYVCSGLVGDTPRKNDSSSSSSHCLDPNNEEGGHGVK
 GWAFDDGNDVVMGRTI SEKSRLYGYETFVKVI EGWSNPKSKLQI NRQVI VDRGNRSGYSI FSVEGKSCI NR
 CFYVELI RGRKEETEVWTSNSI VVFCGTSYGTGSGWPDGADI NLMP1
 >gi | 194293993 | gb | ACF40091.1 | neurami ni dase [Influenza A virus
 (A/Washington/04/2008(H3N2))] |
 MNPNQKI I TI GSVSLTI STI CFFMQI AI LI TTVTLHFQYEFNSPPNNQVLMCEPTI I ERNI TEI VYLTN
 TTI EKEI CPKLAEYRNWSKQDCI TGFAPFSKDNSI RLSAGGDI VWTREPVVSCDPDKCYQFALGQGTTL
 NNWHSNNTVVRBTPYRTRLLMNELGVPFHLGTRQVCI AWSSSSCHDGGKAWLHVCI TGDDKNATASFI YNGR
 LVDSVVSWSKEI LRTQSEECVCI NGCTVVMTDGSASGKADTKI LFI EEGKI VHTSTLGSQAQHVVEECSC
 YPRYPGVRCVCRDNWKGNSRPI VDI NI KDHSI VSSYVCSGLVGDTPRKNDSSSSSSHCLDPNNEEGGHGVK
 GWAFDDGNDVVMGRTI SEKSRLYGYETFVKVI EGWSNPKSKLQI NRQVI VDRGNRSGYSI FSVEGKSCI NR
 CFYVELI RGRKEETEVWTSNSI VVFCGTSYGTGSGWPDGADI NLMP1
 >gi | 194293981 | gb | ACF40085.1 | neurami ni dase [Influenza A virus (A/New
 Jersey/15/2008(H3N2))] |
 MNPNQKI I TI GSVSLTI STI CFFMQI AI LI TTVTLHFQYEFNSPPNNQVLMCEPTI I ERNI TEI VYLTN
 TTI EKEI CPKLAEYRNWSKQDCI TGFAPFSKDNSI RLSAGGDI VWTREPVVSCDPDKCYQFALGQGTTL
 NNWHSNNTVVRBTPYRTRLLMNELGVPFHLGTRQVCI AWSSSSCHDGGKAWLHVCI TGDDKNATASFI YNGR
 LVDSVVSWSKEI LRTQSEECVCI NGCTVVMTDGSASGKADTKI LFI EEGKI VHTSTLGSQAQHVVEECSC
 YPRYPGVRCVCRDNWKGNSRPI VDI NI KDHSI VSSYVCSGLVGDTPRKNDSSSSSSHCLDPNNEEGGHGVK
 GWAFDDGNDVVMGRTI SEKSRLYGYETFVKVI EGWSNPKSKLQI NRQVI VDRGNRSGYSI FSVEGKSCI NR
 CFYVELI RGRKEETEVWTSNSI VVFCGTSYGTGSGWPDGADI NLMP1

>gi |194294021|gb|ACF40105.1| neurami ni dase [Influenza A virus (A/Mi nnesota/07/2008(H3N2))]
MNPNQI I TI GSVSLTI STI CFFMQI AI LI TTVTLHFQYEFNSPPNNQVLMCEPTI I ERNI TEI VYL TN
TTI EKEI CPKLA EYRNWSKPOCDI TGFAPFSKDNSI RLSAGGDI WVTREPYVSCDPDKCYQFALGQGTTL
NNVHNSNNTVRDRTPYRLLMNLGVPFHLGKQVCI AWSSSSCHDGKAWLHVCI TGDDKNATASFI YNGR
LVDSVVSWSKEI LRTQSEECVCI NGTCTVVM TDGSASGKADTKI LFI EEGKI VHTSTL SSGSAQHVEECSC
YPRYPGVRVCVRDNWKGSRPI VDI NI KDHSI VSSYVCSGLVGDTPRKN DSSSSSHCLDPNNEEGGHGVK
GWAFDDGNDVVMGRTI SEKSRLGYETFKVI EGWSNPKSKLQI NROVI VDRGNRSGYSGI FSVEGKSCI NR
CFYVELI RGRKEETEVLWTSNSI VVFCGTSGYGTGSWPDGADI NLMP I

>gi |193084877|gb|ACF10328.1| neurami ni dase [Influenza A virus (A/Texas/06/2008(H3N2))]
MNPNHKI I TI GSVSLTI STI CFFMQI AI LI TTVTLHFQYEFNSPPNNQVLMCEPTI I ERNI TEI VYL TN
TTI EKEI CPKLA EYRNWSKPOCDI TGFAPFSKDNSI RLSAGGDI WVTREPYVSCDPDKCYQFALGQGTTL
NNVHNSNNTVRXRTPYRLLMNLGVPFHLGKQVCI AWSSSSCHDGKAWLHVCI TGDDKNATASFI YNGR
LVDSVVSWSKEI LRTQSEECVCI NGTCTVVM TDGSASGKADTKI LFI EEGKI VHTSTL SSGSAQHVEECSC
YPRYPGVRVCVRDNWKGSRPI VDI NI KDHSI VSSYVCSGLVGDTPRKN DSSSSSHCLDPNNEEGGHGVK
GWAFDDGNDVVMGRTI SEKSRLGYETFKVI EGWSNPKSKLQI NROVI VDRGNRSGYSGI FSVEGKSCI NR
CFYVELI RGRKEETEVLWTSNSI VVFCGTSGYGTGSWPDGADI NLMP I

>gi |194294009|gb|ACF40099.1| neurami ni dase [Influenza A virus (A/South Carol i na/03/2008(H3N2))]
MNPNQI I TI GSVSLTI STI CFFMQI AI LI TTVTLHFQYEFNSPPNNQVLMCEPTI I ERNI TEI VYL TN
TTI EKEI CPKLA EYRNWSKPOCDI TGFAPFSKDNSI RLSAGGDI WVTREPYVSCDPDKCYQFALGQGTTL
NNVHNSNNTVRXRTPYRLLMNLGVPFHLGKQVCI AWSSSSCHDGKAWLHVCI TGDDKNATASFI YNGR
LVDSVVSWSKEI LRTQSEECVCI NGTCTVVM TDGSASGKADTKI LFI EEGKI VHTSTL SSGSAQHVEECSC
YPRYPGVRVCVRDNWKGSRPI VDI NI KDHSI VSSYVCSGLVGDTPRKN DSSSSSHCLDPNNEEGGHGVK
GWAFDDGNDVVMGRTI SEKSRLGYETFKVI EGWSNPKSKLQI NROVI VDRGNRSGYSGI FSVEGKSCI NR
CFYVELI RGRKEETEVLWTSNSI VVFCGTSGYGTGSWPDGADI NLMP I

>gi |193084881|gb|ACF10330.1| neurami ni dase [Influenza A virus (A/Iowa/01/2008(H3N2))]
MNPNQI I TI GSVSLTI STI CFFMQI AI LI TTVTLHFQYEFNSPPNNQVLMCEPTI I ERNI TEI VYL TN
TTI EKEI CPKLA EYRNWSKPOCDI TGFAPFSKDNSI RLSAGGDI WVTREPYVSCDPDKCYQFALGQGTTL
NNVHNSNNTVRXRTPYRLLMNLGVPFHLGKQVCI AWSSSSCHDGKAWLHVCI TGDDKNATASFI YNGR
LVDSVVSWSKEI LRTQSEECVCI NGTCTVVM TDGSASGKADTKI LFI EEGKI VHTSTL SSGSAQHVEECSC
YPRYPGVRVCVRDNWKGSRPI VDI NI KDHSI VSSYVCSGLVGDTPRKN DSSSSSHCLDPNNEEGGHGVK
GWAFDDGNDVVMGRTI SEKSRLGYETFKVI EGWSNPKSKLQI NROVI VDRGNRSGYSGI FSVEGKSCI NR
CFYVELI RGRKEETEVLWTSNSI VVFCGTSGYGTGSWPDGADI NLMP I

>gi |194293985|gb|ACF40087.1| neurami ni dase [Influenza A virus (A/Tennessee/04/2008(H3N2))]
MNPNQI I TI GSVSLTI STI CFFMQI AI LI TTVTLHFQYEFNSPPNNQVLMCEPTI I ERNI TEI VYL TN
TTI EKEI CPKLA EYRNWSKPOCDI TGFAPFSKDNSI RLSAGGDI WVTREPYVSCDPDKCYQFALGQGTTL
NNVHNSNNTVRDRTPYRLLMNLGVPFHLGKQVCI AWSSSSCHDGKAWLHVCI TGDDKNATASFI YNGR
LVDSI VWSKEI LRTQSEECVCI NGTCTVVM TDGSASGKADTKI LFI EEGKI VHTSTL SSGSAQHVEECSC
YPRYPGVRVCVRDNWKGSRPI VDI NI KDHSI VSSYVCSGLVGDTPRKN DSSSSSHCLDPNNEEGGHGVK
GWAFDDGNDVVMGRTI SEKSRLGYETFKVI EGWSNPKSKLQI NROVI VDRGNRSGYSGI FSVEGKSCI NR
CFYVELI RGRKEETEVLWTSNSI VVFCGTSGYGTGSWPDGADI NLMP I

>gi |194294005|gb|ACF40097.1| neurami ni dase [Influenza A virus (A/Ill i noi s/09/2008(H3N2))]
MNPNQI I TI GSVSLTI STI CFFMQI AI LI TTVTLHFQYEFNSPPNNQVLMCEPTI I ERNI TEI VYL TN
TTI EKEI CPKLA EYRNWSKPOCDI TGFAPFSKDNSI RLSAGGDI WVTREPYVSCDPDKCYQFALGQGTTL
NNVHNSNNTVRDRTPYRLLMNLGVPFHLGKQVCI AWSSSSCHDGKAWLHVCI TGDDKNATASFI YNGR
LVDSVVSWSKEI LRTQSEECVCI NGTCTVVM TDGSASGKADTKI LFI EEGKI VHTSTL SSGSAQHVEECSC
YPRYPGVRVCVRDNWKGSRPI VDI NI KDHSI VSSYVCSGLVGDTPRKN DSSSSSHCLDPNNEEGGHGVK
GWAFDDGNDVVMGRTI SEKSRLGYETFKVI EGWSNPKSKLQI NROVI VDRGNRSGYSGI FSVEGKSCI NR
CFYVELI RGRKEETEVLWTSNSI VVFCGTSGYGTGSWPDGADI NLMP I

>gi |193084885|gb|ACF10332.1| neurami ni dase [Influenza A virus (A/Iowa/02/2008(H3N2))]
MNPNQI I TI GSVSLTI STI CFFMQI AI LI TTVTLHFQYEFNSPPNNQVLMCEPTI I ERNI TEI VYL TN
TTI EKEI CPKLA EYRNWSKPOCDI TGFAPFSKDNSI RLSAGGDI WVTREPYVSCDPDKCYQFALGQGTTL
NNVHNSNNTVRDRTPYRLLMNLGVPFHLGKQVCI AWSSSSCHDGKAWLHVCI TGDDKNATASFI YNGR
LVDSI VWSKEI LRTQSEECVCI NGTCTVVM TDGSASGKADTKI LFI EEGKI VHTSTL SSGSAQHVEECSC
YPRYPGVRVCVRDNWKGSRPI VDI NI KDHSI VSSYVCSGLVGDTPRKN DSSSSSHCLDPNNEEGGHGVK
GWAFDDGNDVVMGRTI SEKSRLGYETFKVI EGWSNPKSKLQI NROVI VDRGNRSGYSGI FSVEGKSCI NR
CFYVELI RGRKEETEVLWTSNSI VVFCGTSGYGTGSWPDGADI NLMP I

>gi |194293997|gb|ACF40093.1| neurami ni dase [Influenza A virus (A/New Jersey/14/2008(H3N2))]
MNPNQI I TI GSVSLTI STI CFFMQI AI LI TTVTLHFQYEFNSPPNNQVLMCEPTI I ERNI TEI VYL TN
TTI EKEI CPKLA EYRNWSKPOCDI TGFAPFSKDNSI RLSAGGDI WVTREPYVSCDPDKCYQFALGQGTTL
NNVHNSNNTVRDRTPYRLLMNLGVPFHLGKQVCI AWSSSSCHDGKAWLHVCI TGDDKNATASFI YNGR
LVDSVVSWSKEI LRTQSEECVCI NGTCTVVM TDGSASGKADTKI LFI EEGKI VHTSTL SSGSAQHVEECSC
YPRYPGVRVCVRDNWKGSRPI VDI NI KDHSI VSSYVCSGLVGDTPRKN DSSSSSHCLDPNNEEGGHGVK
GWAFDDGNDVVMGRTI SEKSRLGYETFKVI EGWSNPKSKLQI NROVI VDRGNRSGYSGI FSVEGKSCI NR
CFYVELI RGRKEETEVLWTSNSI VVFCGTSGYGTGSWPDGADI NLMP I

>gi |194294025|gb|ACF40107.1| neurami ni dase [Influenza A virus (A/New York/09/2008(H3N2))]
MNPNQI I TI GSVSLTMSTI CFFMQI AI LI TTVTLHFQYEFNSPPNNQVLMCEPTI I ERNI TEI VYL TN
TTI EKEI CPKLA EYRNWSKPOCDI TGFAPFSKDNSI RLSAGGDI WVTREPYVSCDPDKCYQFALGQGTTL
NNVHNSNNTVRDRTPYRLLMNLGVPFHLGKQVCI AWSSSSCHDGKAWLHVCI TGDDKNATASFI YNGR
LVDSVVSWSKDI LRTQSEECVCI NGTCTVVM TDGSASGKADTKI LFI EEGKI VHTSTL SSGSAQHVEECSC
YPRYPGVRVCVRDNWKGSRPI VDI NI KDHSI VSSYVCSGLVGDTPRKN DSSSSSHCLDPNNEEGGHGVK

GWAFDDGNDVMMGRTI SEKSRLGYETFKVI EGWSNPKSKLQI NROVI VDRGNRSGYSGI FSVEGKSCI NR
 CFYVELI RGRKEETEVLWTSNSI VVFCGTSPTYGTGSPWPDGADI NLMP1
 >gi |37785256|gb|AA046466.1| neurami ni dase [Influenza A vi rus (A/Mal aysi a/1/68(H3N2))]

MNPNQKI I TI GSVSLTI ATVCFLMOI AI LVTTVTLHFQYECDSPASNQVMPCEPI I I ERNI TEI VYLNN
 TTI EKEI CPKVVVEYRNWSKQPCQI TGFAPFSKDNSI RLSAGGDI VWTREPYVSCDHGKCYQFALGQGTTL
 DNKHSNDTI HDRI PHRTLLMNLGVPFHLGTROVCI AWSSSSCHDGKAWLHVCI TGDDKNATASFI YDGR
 LVDSI GSWSONI LRTQSEECVCI NGTCTVVMTDGSASGRADTRI LFI EEGKI VHI SPLSGSAQHVEECSC
 YPRYPGVRCI CRDNWKGSNRPVVDI NMEDYSI DSSYVCSGLVGDTPRNDRRSSNSNCRPNPNERGNQGVK
 GWAFDNGDDVMMGRTI SKDLRSYETFKVI GGWSTPNSKSQI NROVI VSDNRSYSGI FSVEGKSCI NR
 CFYVELI RGRKQETRVWTSNSI VVFCGTSPTYGTGSPWPDGANI NFMP1

>gi |37785258|gb|AA046467.1| neurami ni dase [Influenza A vi rus (A/USSR/039/68(H3N2))]

MNPNQKI I TI GSVSLTI ATVCFLMOI AI LVTTVTLHFQYECDSPASNQVMPCEPI I I ERNI TEI VYLNN
 TTI EKEI CPKVVVEYRNWSKQPCQI TGFAPFSKDNSI RLSAGGDI VWTREPYVSCDHGKCYQFALGQGTTL
 DNKHSNDTI HDRI PHRTLLMNLGVPFHLGTROVCI AWSSSSCHDGKAWLHVCI TGDDKNATASFI YDGR
 LVDSI GSWSONI LRTQSEECVCI NGTCTVVMTDGSASGRADTRI LFI EEGKI VHI SPLSGSAQHVEECSC
 YPRYPGVRCI CRDNWKGSNRPVVDI NMEDYSI DSSYVCSGLVGDTPRNDRRSSNSNCRPNPNERGNQGVK
 GWAFDNGDDVMMGRTI SKDLRSYETFKVI GGWSTPNSKSQI NROVI VSDNRSYSGI FSVEGKSCI NR
 CFYVELI RGRKQETRVWTSNSI VVFCGTSPTYGTGSPWPDGANI NFMP1

>gi |37785260|gb|AA046468.1| neurami ni dase [Influenza A vi rus
 (A/Mal aysi a/221/68(H3N2))]

MNPNQKI I TI GSVSLTI ATVCFLMOI AI LVTTVTLHFQYECDFPASNQVMPCEPI I I ERNI TEI VYLNN
 TTI EKEI CPKVVVEYRNWSKQPCQI TGFAPFSKDNSI RLSAGGDI VWTREPYVSCDHGKCYQFALGQGTTL
 DNKHSNDTI HDRI PHRTLLMNLGVPFHLGTROVCI AWSSSSCHDGKAWLHVCI TGDDKNATASFI YDGR
 LVDSI GSWSONI LRTQSEECVCI NGTCTVVMTDGSASGRADTRI LFI EEGKI VHI SPLSGSAQHVEECSC
 YPRYPGVRCI CRDNWKGSNRPVVDI NMEDYSI DSSYVCSGLVGDTPRNDRRSSNSNCRPNPNERGNQGVK
 GWAFDNGDDVMMGRTI SKDLRSYETFKVI GGWSTPNSKSQI NROVI VSDNRSYSGI FSVEGKSCI NR
 CFYVELI RGRKQETRVWTSNSI VVFCGTSPTYGTGSPWPDGANI NFMP1

>gi |37785262|gb|AA046469.1| neurami ni dase [Influenza A vi rus
 (A/HongKong/16/68(H3N2))]

MNPNQKI I TI GSVSLTI ATVCFLMOI AI LVTTVTLHFQYECDSPASNQVMPCEPI I I ERNI TEI VYLNN
 TTI EKEI CPKVVVEYRNWSKQPCQI TGFAPFSKDNSI RLSAGGDI VWTREPYVSCDHGKCYQFALGQGTTL
 DNKHSNDTI HDRI PHRTLLMNLGVPFHLGTROVCI AWSSSSCHDGKAWLHVCI TGDDKNATASFI YDGR
 LVDSI GSWSONI LRTQSEECVCI NGTCTVVMTDGSASGRADTRI LFI EEGKI VHI SPLSGSAQHVEECSC
 YPRYPGVRCI CRDNWKGSNRPVVDI NMEDYSI DSSYVCSGLVGDTPRNDRRSSNSNCRPNPNERGNQGVK
 GWAFDNGDDVMMGRTI SKDLRSYETFKVI GGWSTPNSKSQI NROVI VSDNRSYSGI FSVEGKSCI NR
 CFYVELI RGRKQETRVWTSNSI VVFCGTSPTYGTGSPWPDGANI NFMP1

>gi |14009708|gb|AAK51726.1| neurami ni dase [Influenza A vi rus (A/Hong
 Kong/1/68(H3N2))]

MNPNQKI I TI GSVSLTI ATVCFLMOI AI LVTTVTLHFQYECDSPASNQVMPCEPI I I ERNI TEI VYLNN
 TTI EKEI CPKVVVEYRNWSKQPCQI TGFAPFSKDNSI RLSAGGDI VWTREPYVSCDHGKCYQFALGQGTTL
 DNKHSNDTI HDRI PHRTLLMNLGVPFHLGTROVCI AWSSSSCHDGKAWLHVCI TGDDKNATASFI YDGR
 LVDSI GSWSONI LRTQSEECVCI NGTCTVVMTDGSASGRADTRI LFI EEGKI VHI SPLSGSAQHVEECSC
 YPRYPGVRCI CRDNWKGSNRPVVDI NMEDYSI DSSYVCSGLVGDTPRNDRRSSNSNCRPNPNERGNQGVK
 GWAFDNGDDVMMGRTI SKDLRSYETFKVI GGWSTPNSKSQI NROVI VSDNRSYSGI FSVEGKSCI NR
 CFYVELI RGRKQETRVWTSNSI VVFCGTSPTYGTGSPWPDGANI NFMP1

>gi |193805271|gb|ACF22301.1| neurami ni dase [Influenza A vi rus (A/Hong Kong/1-
 12/1968(H3N2))]

MNPNQKI I TI GSVSLTI ATVCFLMOI AI LVTTVTLHFQYECDSPASNQVMPCEPI I I ERNI TEI VYLNN
 TTI EKEI CPKVVVEYRNWSKQPCQI TGFAPFSKDNSI RLSAGGDI VWTREPYVSCDHGKCYQFALGQGTTL
 DNKHSNDTI HDRI PHRTLLMNLGVPFHLGTROVCI AWSSSSCHDGKAWLHVCI TGDDKNATASFI YDGR
 LVDSI GSWSONI LRTQSEECVCI NGTCTVVMTDGSASGRADTRI LFI EEGKI VHI SPLSGSAQHVEECSC
 YPRYPGVRCI CRDNWKGSNRPVVDI NMEDYSI DSSYVCSGLVGDTPRNDRRSSNSNCRPNPNERGNQGVK
 GWAFDNGDDVMMGRTI SKDLRSYETFKVI GGWSTPNSKSQI NROVI VSDNRSYSGI FSVEGKSCI NR
 CFYVELI RGRKQETRVWTSNSI VVFCGTSPTYGTGSPWPDGANI NFMP1

>gi |133982222|gb|AB044071.1| neurami ni dase [Influenza A vi rus
 (A/AI bany/18/1968(H3N2))]

MNPNQKI I TI GFVFLTI ATVCFLMOI AI LVTTVTLHFQYECDSPASNQVMPCEPI I I ERNI TEI VYLNN
 TTI EKEI CPKVVVEYRNWSKQPCQI TGFAPFSKDNSI RLSAGGDI VWTREPYVSCDHGKCYQFALGQGTTL
 DNKHSNDTI HDRI PHRTLLMNLGVPFHLGTROVCI AWSSSSCHDGKAWLHVCI TGDDKNATASFI YDGR
 LVDSI GSWSONI LRTQSEECVCI NGTCTVVMTDGSASGRADTRI LFI EEGKI VHI SPLSGSAQHVEECSC
 YPRYPGVRCI CRDNWKGSNRPVVDI NMEDYSI DSSYVCSGLVGDTPRNDRRSSNSNCKPNPNERGNQGVK
 GWAFDNGDDVMMGRTI SKDLRSYETFKVI GGWSTPNSKSQI NROVI VSDNRSYSGI FSVEGKSCI NR
 CFYVELI RGRKQETRVWTSNSI VVFCGTSPTYGTGSPWPDGANI NFMP1

>gi |194304675|gb|ACF41760.1| neurami ni dase [Influenza A vi rus (A/Hong Kong/1-9-MA21-
 2/1968(H3N2))]

MNPNQKI I TI GSVSLTI ATVCFLMOI AI LVTTVTLHFQYECDSPASNQVMPCEPI I I ERNI TEI VYLNN
 TTI EKEI CPKVVVEYRNWSKQPCQI TGFAPFSKDNSI RLSAGGDI VWTREPYVSCDRGKCYQFALGQGTTL
 DNKHSNDTI HDRI PHRTLLMNLGVPFHLGTROVCI AWSSSSCHDGKAWLHVCI TGDDKNATASFI YDGR
 LVDSI GSWSONI LRTQSEECVCI NGTCTVVMTDGSASGRADTRI LFI EEGKI VHI SPLSGSAQHVEECSC
 YPRYPGVRCI CRDNWKGSNRPVVDI NMEDYSI DSSYVCSGLVGDTPRNDRRSSNSNCRPNPNERGNQGVK
 GWAFDNGDDVMMGRTI SKDLRSYETFKVI GGWSTPNSKSQI NROVI VSDNRSYSGI FSVEGKSCI NR
 CFYVELI RGRKQETRVWTSNSI VVFCGTSPTYGTGSPWPDGANI NFMP1

>gi |194304713|gb|ACF41782.1| neurami ni dase [Influenza A vi rus (A/Hong Kong/1-11-MA21-
 1/1968(H3N2))]

MNPNQKI I TI GSVSLTI ATVCFLMOI AI LVTTVTLHFQYECDSPASNQVMPCEPI I I ERNI TEI VYLNN
 TTI EKEI CPKVVVEYRNWSKQPCQI TGFAPFSKDNSI RLSAGGDI VWTREPYVSCDHGKCYQFALGQGTTL
 DNKHSNDTI HDRI PHRTLLMNLGVPFHLGTROVCI AWSSSSCHDGKAWLHVCI TGDDKNATASFI YDGR

LVDSI GSWSONI LRTQSEECVCI NGTCTVVMTDGSASGRADTRI LFI EEGKI VHI SPLSGSAQHVEECSC YPRYPGVRCI CRDNWKGNSRNPVVDI NMEDYSI DSSYVCSGLVGDTPRNDRRSSNSNCRPNPNERGNQGVK GWAFDNGDDVVMGRTI SKDLRSGYETFKVI GGWSTPNSKSI NROVI VSDNRSYGYSI FSVEGKSCI NR CFYVELI RGRKQETRVWVWTSNSI VVFCGTSYGTGSGWPDGANI NFMPPI

>gi |125664200|gb|ABN51102.1| neurami ni dase [Influenza A vi rus (A/AI bany/11/1968(H3N2))]

MNPNQKI I TI GSVSLTI ATVCFLMQI AI LVTTVTLHFQYECDSPASNQVMPCEPI I I ERNI TEI VYLLN TTI EKEI CPKVVEYRNWSKPOCOI TGFAPFSKDNSI RLSAGGDI WVTREPYVSCDHGKCYQFALGQGTLL DNKHSNDTI HDRI PHRTLLMNLGVPFHLGTROVCI AWSSSSCHDGKAWLHVCI TGDDKNATASFI YDGR LVDSI GSWSONI LRTQSEECVCI NGTCTVVMTDGSASGRADTRI LFI EEGKI VHI SPLSGSAQHVEECSC YPRYPGVRCI CRDNWKGNSRNPVVDI NMEDYSI DSSYVCSGLVGDTPRNDRRSSNSNCRPNPNERGNQGVK GWAFDNGDDVVMGRTI SKDLRSGYETFKVI GGWSTPNSKSI NROVI VSDNRSYGYSI FSVEGKSCI NR CFYVELI RGRKQETRVWVWTSNSI VVFCGTSYGTGSGWPDGANI NFMPPI

>gi |125664238|gb|ABN51124.1| neurami ni dase [Influenza A vi rus (A/AI bany/19/1968(H3N2))]

MNPNQKI I TI GSVSLTI ATVCFLMQI AI LVTTVTLHFQYECDSPASNQVMPCEPI I I ERNI TEI VYLLN TTI EKEI CPKVVEYRNWSKPOCOI TGFAPFSKDNSI RLSAGGDI WVTREPYVSCDPGKCYQFALGQGTLL DNKHSNDTI HDRI PHRTLLMNLGVPFHLGTROVCI AWSSSSCHDGKAWLHVCI TGDDKNATASFI YDGR LVDSI GSWSONI LRTQSEECVCI NGTCTVVMTDGSASGRADTRI LFI EEGKI VHI SPLSGSAQHVEECSC YPRYPGVRCI CRDNWKGNSRNPVVDI NMEDYSI DSSYVCSGLVGDTPRNDRRSSNSNCRPNPNERGNQGVK GWAFDNGDDVVMGRTI SKDLRSGYETFKVI GGWSTPNSKSI NROVI VSDNRSYGYSI FSVEGKSCI NR CFYVELI RGRKQETRVWVWTSNSI VVFCGTSYGTGSGWPDGANI NFMPPI

>gi |194352098|gb|ACF54458.1| neurami ni dase [Influenza A vi rus (A/Hong Kong/1-8-MA21-3/1968(H3N2))]

MNPNQKI I TI GSVSLTI ATVCFLMQI AI LVTTVTLHFQYECDSPASNQVMPCEPI I I ERNI TEI VYLLN TTI EKEI CPKVVEYRNWSKPOCOI TGFAPFSKDNSI RI SAGGDI WVTREPYVSCDHGKCYQFALGQGTLL DNKHSNDTI HDRI PHRTLLMNLGVPFHLGTROVCI AWSSSSCHDGKAWLHVCI TGDDKNATASFI YDGR LVDSI GSWSONI LRTQSEECVCI NGTCTVVMTDGSASGRADTRI LFI EEGKI VHI SPLSGSAQHVEECSC YPRYPGVRCI CRDNWKGNSRNPVVDI NMEDYSI DSSYVCSGLVGDTPRNDRRSSNSNCRPNPNERGNQGVK GWAFDNGDDVVMGRTI SKDLRSGYETFKVI GGWSTPNSKSI NROVI VSDNRSYGYSI FSVEGKSCI NR CFYVELI RGRKQETRVWVWTSNSI VVFCGTSYGTGSGWPDGANI NFMPPI

>gi |37785254|gb|AA046465.1| neurami ni dase [Influenza A vi rus (A/Phi I i ppi nes/3/68(H3N2))]

MNPNQKI I TI GSVSLTI ATVCFLMQI AI LVTTVTLHFQYECDSPASNQVMPCEPI I I ERNI TEI VYLLN TTI EKEI CPKVVEYRNWSKPOCOI TGFAPFSKDNSI RLSAGGDI WVTREPYVSCDHGKCYQFALGQGTLL DNKHSNDTI HDRI PHRTLLMNLGVPFHLGTROVCI AWSSSSCHDGKAWLHVCI TGDDKNATASFI YDGR LVDSI GSWSONI LRTQSEECVCI NGTCTVVMTDGSASGRADTRI LFI EEGKI VHI SPLSGSAQHVEECSC YPRYPGVRCI CRDNWKGNSRNPVVDI NMEDYSI DSSYVCSGLVGDTPRNDRRSSNSNCRPNPNERGNQGVK GWAFDNGDDVVMGRTI SKDLRSGYETFKVI GGWSTPNSKSI NROVI VSDNRSYGYSI FSVEGKSCI NR CFYVELI RGRKQETRVWVWTSNSI VVFCGTSYGTGSGWPDGANI NFMPPI

>gi |37785266|gb|AA046471.1| neurami ni dase [Influenza A vi rus (A/PuertoRi co/1/68(H3N2))]

MNPNQKI I TI GSVSLTI ATVCFLMQI AI LVTTVTLHFQYECDSPASNQVMPCEPI I I ERNI TEI VYLLN TTI EKEI CPKVVEYRNWSKPOCOI TGFAPFSKDNSI RLSAGGDI WVTREPYVSCDPGKCYQFALGQGTLL DNKHSNDTI HDRI PHRTLLMNLGVPFHLGTROVCI AWSSSSCHDGKAWLHVCI TGDDKNATASFI YDGR LVDSI GSWSONI LRTQSEECVCI NGTCTVVMTDGSASGRADTRI LFI EEGKI VHI SPLSGSAQHVEECSC YPRYPGVRCI CRDNWKGNSRNPVVDI NMEDYSI DSSYVCSGLVGDTPRNDRRSSNSNCRPNPNERGNQGVK GWAFDNGDDVVMGRTI SKDLRSGYETFKVI GGWSTPNSKSI NROVI VSDNRSYGYSI FSVEGKSCI NR CFYVELI RGRKQETRVWVWTSNSI VVFCGTSYGTGSGWPDGANI NFMPPI

>gi |37785270|gb|AA046473.1| neurami ni dase [Influenza A vi rus (A/Panama/1/68(H3N2))]

MNPNQKI I TI GSVSLTI ATVCFLMQI AI LVTTVTLHFQYECDSPASNQVMPCEPI I I ERNI TEI VYLLN TTI EKEI CPKVVEYRNWSKPOCOI TGFAPFSKDNSI RLSAGGDI WVTREPYVSCDHGKCYQFALGQGTLL DNKHSNDTI HDRI PHRTLLMNLGVPFHLGTROVCI AWSSSSCHDGKAWLHVCI TGDDKNATASFI YDGR LVDSI GSWSONI LRTQSEECVCI NGTCTVVMTDGSASGRADTRI LFI EEGKI VHI SPLSGSAQHVEECSC YPRYPGVRCI CRDNWKGNSRNPVVDI NMEDYSI DSSYVCSGLVGDTPRNDRRSSNSNCRPNPNERGNQGVK GWAFDNGDDVVMGRTI SKDLRSGYETFKVI GGWSTPNSKSI NROVI VSDNRSYGYSI FSVEGKSCI NR CFYVELI RGRKQETRVWVWTSNSI VVFCGTSYGTGSGWPDGANI NFMPPI

>gi |80977933|gb|ABB54517.1| neurami ni dase [Influenza A vi rus (A/Memphis/1/68(H3N2))]

MNPNQKI I TI GSVSLTI ATVCFLMQI AI LVTTVTLHFQYECDSPASNQVMPCEPI I I ERNI TEI VYLLN TTI EKEI CPKVVEYRNWSKPOCOI TGFAPFSKDNSI RLSAGGDI WVTREPYVSCDPGKCYQFALGQGTLL DNKHSNDTI HDRI PHRTLLMNLGVPFHLGTROVCI AWSSSSCHDGKAWLHVCI TGDDKNATASFI YDGR LVDSI GSWSONI LRTQSEECVCI NGTCTVVMTDGSASGRADTRI LFI EEGKI VHI SPLSGSAQHVEECSC YPRYPGVRCI CRDNWKGNSRNPVVDI NMEDYSI DSSYVCSGLVGDTPRNDRRSSNSNCRPNPNERGNQGVK GWAFDNGDDVVMGRTI SKDLRSGYETFKVI GGWSTPNSKSI NROVI VSDNRSYGYSI FSVEGKSCI NR CFYVELI RGRKQETRVWVWTSNSI VVFCGTSYGTGSGWPDGANI NFMPPI

>gi |1517824|gb|AAB06964.1| neurami ni dase

MNPNQKI I TI GSVSLTI ATVCFLMQI AI LVTTVTLHFQYECDSPASNQVMPCEPI I I ERNI TEI VYLLN TTI EKEI CPKLVVEYRNWSKPOCKI TGFAPFSKDNSI RLSAGGDI WVTREPYVSCDPGKCYQFALGQGTLL DNKHSNDTI HDRI PHRTLLMNLGVPFHLGTROVCI AWSSSSRHDGKAWLHVCI TGDDKNATASFI YDGR LVDSI GSWSONI LRTQSEECVCI NGTCTVVMTDGSASGRADTRI LFI EEGKI VHI SPLSGSAQHVEECSC YPRYPGVRCI CRDNWKGNSRNPVVDI NMEDYSI DSSYVCSGLVGDTPRNDRRSSNSNCRPNPNERGNQGVK GWAFDNGDDVVMGRTI SKDLRSGYETFKVI GGWSTPNSKSI NROVI VSDNRSYGYSI FSVEGKSCI NR CFYVELI RGRKQETRVWVWTSNSI VVFCGTSYGTGSGWPDGANI NFMPPI

>gi |134047623|gb|AB052360.1| neurami ni dase [Influenza A vi rus (A/AI bany/17/1968(H3N2))]

MNPNQKI I TI GSVSLTI ATVCFLMQI AI LVTTVTLHFQYECDSPASNQVMPCEPI I I ERNI TEI VYLLN TTI EKEI CPKVVEYRNWSKPOCOI TGFAPFSKDNSI RLSAGGDI WVTREPYVSCDHGKCYQFALGQGTLL

DNKHSNDTI HDRI PHRTLLMNLGVPFHLGTRQVCI AWSSSSCHDGGKAWLHVCI TGDDKNATASFI YDGR
 LVDSI GSWSONI LRTQSECEVCICI NGCTVVMVDGSASGRADTRI LFI EEGKI VHI SPLSGSAQHVEECSC
 YPRYPGVRCI CRDNWKGSNRPVVDI NMEDYSI DSSYVCSGLVGDTPRNDRRSSNSNCRPNPNERGNQGVK
 GWAFDNGNDVVMGRTI SKDLRSGYETFKVI GGWSTPNKSKQI NROVI VDSNDRSGYSGI FSVEGKSCI NR
 CFYVELI RGRKQETRVWWTNSI VVFCGTSYGTGSGWPDGANI NFMP1
 >gi |31790582|dbj |BAC77663.1| neurami ni dase [Influenza A vi rus (A/Hong
 Kong/1/68(H3N2))]
 MNPNQKI I TI GSVSLTI ATVCFLMQI AI LVTTVTLHFQYECDSASPANQVMPCEPI I I ERNI TEI VYLNN
 TTI EKEI CPKVVEYRNWSKPOCQI TGFAPFSKDNSI RLSAGGDI WVTREPYVSCDHGKCYQFALGQGTTL
 DNKHSNDTI HDRI PHRTLLMNLGVPFHLGTRQVCI AWSSSSCHDGGKAWLHVCI TGDDKNATASFI YDGR
 LVDSI GSWSONI LRTQSECEVCICI NGCTVVMVDGSASGRADTRI LFI EEGKI VHI SPLSGSAQHVEECSC
 YPRYPGVRCI CRDNWKGSNRPVVDI NMEDYSI DSSYVCSGLVGDTPRNDRRSSNSNCRPNPNERGNQGVK
 GWAFDNGDDVVMGRTI SKDLRSGYETFKVI GGWSTPNKSKQI NROVI VDSNDRSGYSGI FSVEGKSCI NR
 CFYVELI RGRKQETRVWWTNSI VVFCGTSYGTGSGWPDGANI NFMP1
 >gi |148628616|gb|ABQ97206.1| neurami ni dase [Influenza A vi rus (A/Hong Kong/68(H3N2))]
 MNPNQKI I TI GSVSLTI ATVCFLMQI AI LVTTVTLHFQYECDSASPANQVMPCEPI I I ERNI TEI VYLNN
 TTI EKEI CPKVVEYRNWSKPOCQI TGFAPFSKDNSI RLSAGGDI WVTREPYVSCDHGKCYQFALGQGTTL
 DNKHSNDTI HDRI PHRTLLMNLGVPFHLGTRQVCI AWSSSSCHDGGKAWLHVCI TGDDKNATASFI YDGR
 LVDSI GSWSONI LRTQSECEVCICI NGCTVVMVDGSASGRADTRI LFI EEGKI VHI SPLSGSAQHVEECSC
 YPRYPGVRCI CRDNWKGSNRPVVDI NMEDYSI DSSYVCSGLVGDTPRNDRRSSNSNCRPNPNERGNQGVK
 GWAFDDGNDVVMGRTI SEKSRLYGNETFKVI EGWSTPNKSKQI NROVI VDSNDRSGYSGI FSVEGKSCI NR
 CFYVELI RGRKQETRVWWTNSI VVFCGTSYGTGSGWPDGANI NFMP1
 >gi |188076309|gb|ACD47181.1| neurami ni dase [Influenza A vi rus
 (A/Wi sconsi n/06/2008(H3N2))]
 MNPNQKI I TI GSVSLTI STI CFFMQI AI LI TTVTLHFQYEFNSPPNNQVLMCEPTI I ERNI TEI VYLTN
 TTI EKEI CPKLAERYNWSKPOCDI TGFAPFSKDNSI RLSAGGDI WVTREPYVSCDPDKCYQFALGQGTTL
 NNVHSNDTVRBRTPYRTRLLMNLGVPFHLGTRQVCI AWSSSSCHDGGKAWLHVCI TGDDKNATASFI YNGR
 LI DSVVSWSKAI LRTQSECEVCICI NGCTVVMVDGSASGKADTKI LFI EEGKI VHTSTLSGSAQHVEECSC
 YPRYPGVRCVCRDNWKGSNRPDI VDI NI KDHSI VSSYVCSGLVGDTPRKNDSSSSSSHCLDPNNEEGGHGVK
 GWAFDDGNDVVMGRTI SEKSRLYGNETFKVI EGWSTPNKSKLQI NROVI VDRGNRSGYSGI FSVEGKSCI NR
 CFYVELI RGRKEETEVLWTSNSI VVFCGTSYGTGSGWPDGADI NLMP1
 >gi |189303145|gb|ACD85629.1| neurami ni dase [Influenza A vi rus
 (A/I daho/03/2008(H3N2))]
 MNPNQKI I TMGSVSLTI STI CFFMQI AI LI TTVTLHFQYEFNSPPNNQVLMCEPTI I ERNI TEI VYLTN
 TTI EKEI CPKLAERYNWSKPOCDI TGFAPFSKDNSI RLSAGGDI WVTREPYVSCDPDKCYQFALGQGTTL
 NNVHSNDTVRBRTPYRTRLLMNLGVPFHLGTRQVCI AWSSSSCHDGGKAWLHVCI TGDDKNATASFI YNGR
 LVDSI VSWSKAI LRTQSECEVCICI NGCTVVMVDGSASGKADTKI LFI EEGKI VHTSTLSGSAQHVEECSC
 YPRYPGVRCVCRDNWKGSNRPDI VDI NI KDHSI VSSYVCSGLVGDTPRKNDSSSSSGHCLDPNNEEGGHGVK
 GWAFDDGNDVVMGRTI SEKSRLYGNETFKVI EGWSTPNKSKLQI NROVI VDRGNRSGYSGI FSVEGKSCI NR
 CFYVELI RGRKEETEVLWTSNSI VVFCGTSYGTGSGWPDGADI NLMP1
 >gi |188076293|gb|ACD47173.1| neurami ni dase [Influenza A vi rus
 (A/Wi sconsi n/03/2008(H3N2))]
 MNPNQKI I TI GSVSLTI STI CFFMQI AI LI TTVTLHFQYEFNSPPNNQVLMCEPTI I ERNI TEI VYLTN
 TTI EKEI CPKLAERYNWSKPOCDI TGFAPFSKDNSI RLSAGGDI WVTREPYVSCDPDKCYQFALGQGTTL
 NNVHSNDTVRBRTPYRTRLLMNLGVPFHLGTRQVCI AWSSSSCHDGGKAWLHVCI TGDDKNATASFI YNGR
 LVDSI VSWSKAI LRTQSECEVCICI NGCTVVMVDGSASGKADTKI LFI EEGKI VHTSTLSGSAQHVEECSC
 YPRYPGVRCVCRDNWKGSNRPDI VDI NI KDHSI VSSYVCSGLVGDTPRKNDSSSSSSHCLDPNNEEGGHGVK
 GWAFDDGNDVVMGRTI SEKSRLYGNETFKVI EGWSTPNKSKLQI NROVI VDRGNRSGYSGI FSVEGKSCI NR
 CFYVELI RGRKEETEVLWTSNSI VVFCGTSYGTGSGWPDGADI NLMP1
 >gi |189303105|gb|ACD85609.1| neurami ni dase [Influenza A vi rus
 (A/Tennessee/02/2008(H3N2))]
 MNPNQKI I TI GSVSLTI STI CFFMQI AI LI TTVTLHFQYEFNSPPNNQVLMCEPTI I ERNI TEI VYLTN
 TTI EKEI CPKLAERYNWSKPOCDI TGFAPFSKDNSI RLSAGGDI WVTREPYVSCDPDKCYQFALGQGTTL
 NNVHSNDTVRBRTPYRTRLLMNLGVPFHLGTRQVCI AWSSSSCHDGGKAWLHVCI TGDDKNATASFI YNGR
 LVDSI VSWSKAI LRTQSECEVCICI NGCTVVMVDGSASGKADTKI LFI EEGKI VHTSTLSGSAQHVEECSC
 YPRYPGVRCVCRDNWKGSNRPDI VDI NI KDHSI VSSYVCSGLVGDTPRKNDSSSSSSHCLDPNNEEGGHGVK
 GWAFDDGNDVVMGRTI SEKSRLYGNETFKVI EGWSTPNKSKLQI NROVI VDRGNRSGYSGI FSVEGKSCI NR
 CFYVELI RGRKEETEVLWTSNSI VVFCGTSYGTGSGWPDGADI NLMP1
 >gi |188076307|gb|ACD47180.1| neurami ni dase [Influenza A vi rus
 (A/Wi sconsi n/07/2008(H3N2))]
 MNPNQKI I TI GSVSLTI STI CFFMQI AI LI TTVTLHFQYEFNSPPNNQVLMCEPTI I ERNI TEI VYLTN
 TTI EKEI CPKLAERYNWSKPOCDI TGFAPFSKDNSI RLSAGGDI WVTREPYVSCDPDKCYQFALGQGTTL
 NNVHSNDTVRBRTPYRTRLLMNLGVPFHLGTRQVCI AWSSSSCHDGGKAWLHVCI TGDDKNATASFI YNGR
 LVDSI VSWSKAI LRTQSECEVCICI NGCTVVMVDGSASGKADTKI LFI EEGKI VHTSTLSGSAQHVEECSC
 YPRYPGVRCVCRDNWKGSNRPDI VDI NI KDHSI VSSYVCSGLVGDTPRKNDSSSSSSHCLDPNNEEGGHGVK
 GWAFDDGNDVVMGRTI SEKSRLYGNETFKVI EGWSTPNKSKLQI NROVI VDRGNRSGYSGI FSVEGKSCI NR
 CFYVELI RGRKEETEVLWTSNSI VVFCGTSYGTGSGWPDGADI NLMP1
 >gi |194293955|gb|ACF40072.1| neurami ni dase [Influenza A vi rus
 (A/Memphi s/28/2008(H3N2))]
 MNPNQKI I TI GSVSLTI STI CFFMQI AI LI TTVTLHFQYEFNSPPNNQVLMCEPTI I ERNI TEI VYLTN
 TTI EKEI CPKLAERYNWSKPOCDI TGFAPFSKDNSI RLSAGGDI WVTREPYVSCDPDKCYQFALGQGTTL
 NNVHSNDTVRBRTPYRTRLLMNLGVPFHLGTRQVCI AWSSSSCHDGGKAWLHVCI TGDDKNATASFI YNGR
 LVDSI VSWSKAI LRTQSECEVCICI NGCTVVMVDGSASGKADTKI LFI EEGKI VHTSTLSGSAQHVEECSC
 YPRYPGVRCVCRDNWKGSNRPDI VDI NI KDHSI VSSYVCSGLVGDTPRKNDSSSSSSHCLDPNNEEGGHGVK
 GWAFDDGNDVVMGRTI SEKSRLYGNETFKVI EGWSTPNKSKLQI NROVI VDRGNRSGYSGI FSVEGKSCI NR
 CFYVELI RGRKEETEVLWTSNSI VVFCGTSYGTGSGWPDGADI NLMP1

>gi |189303153|gb|ACD85633.1| neurami ni dase [Influenza A virus (A/Wi sconsi n/10/2008(H3N2))]
MNPNOKI I TI GSVSLTI STI CFFMOI AI LI TTVTLHFQYEFNPPNNQVLMCEPTI I ERNI TEI VYLTN
TTI EKEI CPKLAERYNWSKPOCDI TGFAPFSKDNSI RLSAGGDI WVTREPYVSCDPDKCYQFALGQGTTL
NNVHNSNNTVXRTRPYRTLLMNLGVPFHLGKQVCI AWSSSSCHDGKAWLHVCI TGDDKNATASFI YNGR
LVDSVVSWSKEI LRTQESECVCICI NGTCTVMTDGSASGKADTKI LFI EEGKI VHTSTLGSQAQHVVEECSC
YPRYPGVRVCVRDNWKGSRNRPDI VDI NI KDHSI VSSYVCSGLVGDTPRKNDSSSSSHCLDPNNEEGGHGVK
GWAFDDGNDVVMGRTI SEKSRLGYETFKVI EGWSNPKSKLQI NROVI VDRGNRSGYSGI FSVEGKSCI NR
CFYVELI RGRKEETEVLWTSNSI VVFCGTSPTYGTGSWPDGADI NLMPDI

>gi |194293951|gb|ACF40070.1| neurami ni dase [Influenza A virus (A/FI ori da/10/2008(H3N2))]
MNPNOKI I TI GSVSLTI STI CFFMOI AI LI TTVTLHFQYEFNPPNNQVLMCEPTI I ERNI TEI VYLTN
TTI EKEI CPKLAERYNWSKPOCDI TGFAPFSKDNSI RLSAGGDI WVTREPYVSCDPDKCYQFALGQGTTL
NNVHNSNNTVXRTRPYRTLLMNLGVPFHLGKQVCI AWSSSSCHDGKAWLHVCI TGDDKNATASFI YNGR
LVDSI VVSWSKEI LRTQESECVCICI NGTCTVMTDGSASGKADTKI LFI EEGKI VHTSTLGSQAQHVVEECSC
YPRYPGVRVCVRDNWKGSRNRPDI VDI NI KDHSI VSSYVCSGLVGDTPRKNDSSSSSHCLDPNNEEGGHGVK
GWAFDDGNDVVMGRTI SEKSRLGYETFKVI EGWSNPKSKLQI NROVI VDRGNRSGYSGI FSVEGKSCI NR
CFYVELI RGRKEETEVLWTSNSI VVFCGTSPTYGTGSWPDGADI NLMPDI

>gi |188076301|gb|ACD47177.1| neurami ni dase [Influenza A virus (A/Vi rgi ni a/01/2008(H3N2))]
MNPNOKI I TI GSVSLTI STI CFFMOI AI LI TTVTLHFQYEFNPPNNQVLMCEPTI I ERNI TEI VYLTN
TTI EKEI CPKLAERYNWSKPOCDI TGFAPFSKDNSI RLSAGGDI WVTREPYVSCDPDKCYQFALGQGTTL
NNVHNSNNTVBRTRPYRTLLMNLGVPFHLGKQVCI AWSSSSCHDGKAWLHVCI TGDDNNATASFI YNGR
LVDSI VVSWSKEI LRTQESECVCICI NGTCTVMTDGSASGKADTKI LFI EEGKI VHTSTLGSQAQHVVEECSC
YPRYPGVRVCVRDNWKGSRNRPDI VDI NI KDHSI VSSYVCSGLVGDTPRKNDSSSSSHCLDPNNEEGGHGVK
GWAFDDGNDVVMGRTI SEKSRLGYETFKVI EGWSNPKSKLQI NROVI VDRGNRSGYSGI FSVEGKSCI NR
CFYVELI RGRKEETEVLWTSNSI VVFCGTSPTYGTGSWPDGADI NLMPDI

>gi |189303117|gb|ACD85615.1| neurami ni dase [Influenza A virus (A/FI ori da/07/2008(H3N2))]
MNPNOKI I TI GSVSLTI STI CFFMOI AI LI TTVTLHFQYEFNPPNNQVLMCEPTI I ERNI TEI VYLTN
TTI EKEI CPKLAERYNWSKPOCDI TGFAPFSKDNSI RLSAGGDI WVTREPYVSCDPDKCYQFALGQGTTL
NNVHNSNNTVBRTRPYRTLLMNLGVPFHLGKQVCI AWSSSSCHDGKAWLHVCI TGDDKNATASFI YNGK
LVDSI VVSWSKEI LRTQESECVCICI NGTCTVMTDGSASGKADTKI LFI EEGKI VHTSTLGSQAQHVVEECSC
YPRYPGVRVCVRDNWKGSRNRPDI VDI NI KDHSI VSSYVCSGLVGDTPRKNDSSSSSHCLDPNNEEGGHGVK
GWAFDDGNDVVMGRTI SEKSRLGYETFKVI EGWSNPKSKLQI NROVI VDRGNRSGYSGI FSVEGKSCI NR
CFYVELI RGRKEETEVLWTSNSI VVFCGTSPTYGTGSWPDGADI NLMPDI

>gi |194293959|gb|ACF40074.1| neurami ni dase [Influenza A virus (A/Georgi a/07/2008(H3N2))]
MNPNOKI I TI GSVSLTI STI CFFMOI AI LI TTVTLHFQYEFNPPNNQVLMCEPTI I ERNI TEI VYLTN
TTI EKEI CPKLAERYNWSKPOCDI TGFAPFSKDNSI RLSAGGDI WVTREPYVSCDPDKCYQFALGQGTTL
NNVHNSNNTVBRTRPYRTLLMNLGVPFHLGKQVCI AWSSSSCHDGKAWLHVCI TGDDKNATASFI YNGR
LVDSVVSWSKEI LRTQESECVCICI NGTCTVMTDGSASGKADTKI LFI EEGKI VHTSTLGSQAQHVVEECSC
YPRYPGVRVCVRDNWKGSRNRPDI VDI NI KDHSI VSSYVCSGLVGDTPRKNDSSSSSHCLDPNNEEGGHGVK
GWAFDDGNDVVMGRTI SEKSRLGYETFKVI EGWSNPKSKLQI NROVI VDRGNRSGYSGI FSVEGKSCI NR
CFYVELI RGRKEETEVLWTSNSI VVFCGTSPTYGTGSWPDGADI NLMPDI

>gi |188076299|gb|ACD47176.1| neurami ni dase [Influenza A virus (A/Wi sconsi n/08/2008(H3N2))]
MNPNOKI I TI GSVSLTI STI CFFMOI AI LI TTVTLHFQYEFNPPNNQVLMCEPTI I ERNI TEI VYLTN
TTI EKEI CPKLAERYNWSKPOCDI TGFAPFSKDNSI RLSAGGDI WVTREPYVSCDPDKCYQFALGQGTTL
NNVHNSNNTVBRTRPYRTLLMNLGVPFHLGKQVCI AWSSSSCHDGKAWLHVCI TGDDKNATASFI YNGR
LVDSVVSWSKEI LRTQESECVCICI NGTCTVMTDGSASGKADTKI LFI EEGKI VHTSTLGSQAQHVVEECSC
YPRYPGVRVCVRDNWKGSRNRPDI VDI NI KDHSI VSSYVCSGLVGDTPRKNDSSSSSHCLDPNNEEGGHGVK
GWAFDDGNDVVMGRTI SEKSRLGYETFKVI EGWSNPKSKLQI NROVI VDRGNRSGYSGI FSVEGKSCI NR
CFYVELI RGRKEETEVLWTSNSI VVFCGTSPTYGTGSWPDGADI NLMPDI

>gi |193084869|gb|ACF10324.1| neurami ni dase [Influenza A virus (A/North Carol i na/01/2008(H3N2))]
MNPNOKI I TI GSVSLTI STI CFFMOI AI LI TTVTLHFQYEFNPPNNQVLMCEPTI I ERNI TEI VYLTN
TTI EKEI CPKLAERYNWSKPOCDI TGFAPFSKDNSI RLSAGGDI WVTREPYVSCDPDKCYQFALGQGTTL
NNVHNSNNTVXRTRPYRTLLMNLGVPFHLGKQVCI AWSSSSCHDGKAWLHVCI TGDDKNATASFI YNGR
LVDSVVSWSKEI LRTQESECVCICI NGTCTVMTDGSASGKADTKI LFI EEGKI VHTSTLGSQAQHVVEECSC
YPRYPGVRVCVRDNWKGSRNRPDI VDI NI KDHSI VSSYVCSGLVGDTPRKNDSSSSSHCLDPNNEEGGHGVK
GWAFDDGNDVVMGRTI SEKSRLGYETFKVI EGWSNPKSKLQI NROVI VDRGNRSGYSGI FSVEGKSCI NR
CFYVELI RGRKEETEVLWTSNSI VVFCGTSPTYGTGSWPDGADI NLMPDI

>gi |193084865|gb|ACF10322.1| neurami ni dase [Influenza A virus (A/New York/06/2008(H3N2))]
MNPNOKI I TI GSVSLTI STI CFFLOI AI LI TTVTLHFQYEFNPPNNQVLMCEPTI I ERNI TEI VYLTN
TTI EKEI CPKLAERYNWSKPOCDI TGFAPFSKDNSI RLSAGGDI WVTREPYVSCDPDKCYQFALGQGTTL
NNVHNSNNTVBRTRPYRTLLMNLGVPFHLGKQVCI AWSSSSCHDGKAWLHVCI TGDDKNATASFI YNGR
LVDSI VVSWSKEI LRTQESECVCICI NGTCTVMTDGSASGKADTKI LFI EEGKI VHTSTLGSQAQHVVEECSC
YPRYPGVRVCVRDNWKGSRNRPDI VDI NI KDHSI VSSYVCSGLVGDTPRKNDSSSSSHCLDPNNEEGGHGVK
GWAFDDGNDVVMGRTI SEKSRLGYETFKVI EGWSNPKSKLQI NROVI VDRGNRSGYSGI FSVEGKSCI NR
CFYVELI RGRKEETEVLWTSNSI VVFCGTSPTYGTGSWPDGADI NLMPDI

>gi |194293969|gb|ACF40079.1| neurami ni dase [Influenza A virus (A/New York/08/2008(H3N2))]
MNPNOKI I TI GSVSLTI STI CFFLOI AI LI TTVTLHFQYEFNPPNNQVLMCEPTI I ERNI TEI VYLTN
TTI EKEI CPKLAERYNWSKPOCDI TGFAPFSKDNSI RLSAGGDI WVTREPYVSCDPDKCYQFALGQGTTL
NNVHNSNNTVBRTRPYRTLLMNLGVPFHLGKQVCI AWSSSSCHDGKAWLHVCI TGDDKNATASFI YNGR

LVDSI VSWSK EI LRTQSEECVCI NGTCTVVM TDGSASGKADTKI LFI EEGKI VHTSTL SGSAQHVEECSC
 YPRYPGVRVCVRDNWKGSRNPI VDI NI KDHSI VSSYVCSGLVGDTPRKN DSSSSSHCLDPNNEEGGHGVK
 GWAFDDGNDVVMGRTI SEKSR LGYETFVKVI EGWSNPKSKLQI NRQVI VDRGNRSGYSGI FSVEGKSCI NR
 CFYVELI RGRKEETEVLWTSNSI VVFCGTS GYGTGSGWPDGADI NLMPI
 >gi |189303149|gb|ACD85631.1| neurami ni dase [Influenza A vi rus
 (A/Okl ahoma/01/2008(H3N2))]
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 LVDSI VSWSK EI LRTQSEECVCI NGTCTVVM TDGSASGKADTKI LFI EEGKI VHTSTL SGSAQHVEECSC
 YPRYPGVRVCVRDNWKGSRNPI VDI NI KDHSI VSSYVCSGLVGDTPRKN DSSSSSHCLDPNNEEGGHGVK
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 CFYVELI RGRKEETEVLWTSNSI VVFCGTS GYGTGSGWPDGADI NLMPI
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 (A/Mi ssouri /01/2008(H3N2))]
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 >gi |194293963|gb|ACF40076.1| neurami ni dase [Influenza A vi rus
 (A/I ndi ana/05/2008(H3N2))]
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 YPRYPGVRVCVRDNWKGSRNPI VDI NI KDHSI VSSYVCSGLVGDTPRKN DSSSSSHCLDPNNEEGGHGVK
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 (A/Georgi a/04/2008(H3N2))]
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 (A/Arkansas/05/2008(H3N2))]
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 York/329/1999(H3N2))]
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 YPRYPGVRVCVRDNWKGSRNPI VDI NVKDYSI VSSYVCSGLVGDTPRKN DSSSSSHCLNPNNNEEGGHGVK
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YPRYPGVRVCVCRDNWKGSRPI VDI NVKDYSI VSSYVCSGLVGDTPRKNDSSSSSHCLNPNNEEGGHGK
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YPRYPGVRVCVCRDNWKGSRPI VDI NVKDYSI VSSYVCSGLVGDTPRKNDSSSSSHCLNPNNEEGGHGK
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CFYVELI RGRKQETEVWTSNSI VVFCGTSPTYGTGSWPDGADI NLMP
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LVDSI GSWSKKI LRTQSEECVCI NGTCTVMTDGSASGRADTKI LFI EEGKI I HI SQLSGSAQHVEECSC
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CFYVELI RGRKQETEVWTSNSI VVFCGTSPTYGTGSWPDGADI NLMP
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LVDSI GSWSKKI LRTQSEECVCI NGTCTVMTDGSASGRADTKI LFI EEGKI I HI SQLSGSAQHVEECSC
YPRYPGVRVCVCRDNWKGSRPI VDI NVKDYSI VSSYVCSGLVGDTPRKNDSSSSSHCLNPNNEEGGHGK
GWAFDDGNDVMMGRTI SEKFRSGYETFKVI EGWSKPNKLOI NROVI VDRDNRSYGSGI FSVEGKSCI NR
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YPRYPGVRVCVCRDNWKGSRPI VDI NVKDYSI VSSYVCSGLVGDTPRKNDSSSSSHCLDPNNEEGGHGK
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CFYVELI RGRKQETEVWTSNSI VVFCGTSPTYGTGSWPDGADI NLMP
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NNEHSNDTVHTRTPYRLLMNLGVPFHLGKQVCI AWSSSSCHDGKAWLHVCTGDENATASFI YNGR

LVDSI GSWSKKI LRTQSEECVCI NGTCTVVMTDGSASGRADTKI LFI EEGKI I HI SQLSGSAQHVEECSC
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 (A/human/Montreal/MTL500/00(H3N2))]
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 YPRYPGVRVCVRDNNWKGSRPI VDI NVKDYSI VSSYVCSGLVGDTPRKNDSSSSSSHCLDPNNEEGGHGVK
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 (A/human/Montreal/MTL169/00(H3N2))]
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 (A/human/Montreal/MTL63286/00(H3N2))]
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 (A/Perugia/7/2000(H3N2))]
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 (A/Denmark/41/2000(H3N2))]
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 YPRYPGVRVCVRDNNWKGSRPI VDI NI KDYSI VSSYVCSGLVGDTPRKNDSSSSSSHCLDPNNEEGGHGVK
 GWAFDDGNDVVMGRTI SEKLRSGYETFKVI EGWSKPNSKLOI NRQVI VDRGNRSGYSGI FSVEGKSCI NR
 CFYVELI RGRKQETEVWVWTSNSI VVFCGTSYGTGSGWPDGADI NLMP1
 >gi|149132956|gb|ABR20818.1|neuramindase [Influenza A virus
 (A/Niedersachsen/56/00(H3N2))]
 MNPNQKI I TI GSVSLTI ATI CFLMQI AI LVTTVTLHFQYECNSPPNNQVLMCEPTI I ERNI TEI VYLTN
 TTI EKEI CPKLAEYRNWSKPOCNI TGFAPFSKDNSI RLSAGGDI WVTREPVVSCDPDKCYQFALGQGTTL
 NNGHSNDTVHDRTPYRRTLLMNLGVPFHLGKQVCI AWSSSSCHDGKAWLHVCVTGDDENATASFI YNGR
 LVDSI GSWSKKI LRTQSEECVCI NGTCTVVMTDGSASGRADTKI LFI EEGKI VHTSTLSGSAQHVEECSC
 YPRYPGVRVCVRDNNWKGSRPI VDI NVKDYSI VSSYVCSGLVGDTPRKNDSSSSSSHCLDPNNEEGGHGVK
 GWAFDDGNDVVMGRTI SEKLRSGYETFKVI EGWSKPNSKLOI NRQVI VDRGNRSGYSGI FSVEGKSCI NR
 CFYVELI RGRKQETEVWVWTSNSI VVFCGTSYGTGSGWPDGADI NL
 >gi|115291184|gb|ABI93086.1|neuramindase [Influenza A virus (A/New South
 Wales/27/2000(H3N2))]
 MNPNQKI I TI GSVSLTI ATI CFLMQI AI LVTTVTLHFQYECNSPPNNQVLMCEPTI I ERNI TEI VYLTN
 TTI EKEI CPKLAEYRNWSKPOCNI TGFAPFSKDNSI RLSAGGDI WVTREPVVSCDPDKCYQFALGQGTTL
 NNGHSNDTVHDRTPYRRTLLMNLGVPFHLGKQVCI AWSSSSCHDGKAWLHVCVTGDDENATASFI YNGR
 LVDSI GSWSKKI LRTQSEECVCI NGTCTVVMTDGSASGRADTKI LFI EEGKI VHTSSLSGSAQHVEECSC
 YPRYPGVRVCVRDNNWKGSRPI VDI NVKDYSI VSSYVCSGLVGDTPRKNDSSSSSSHCLDPNNEEGGHGVK
 GWAFDDGNDVVMGRTI SEKLRSGYETFKVI EGWSKPNSKLOI NRQVI VDRGNRSGYSGI FSVEGKSCI NR
 CFYVELI RGRKQETEVWVWTSNSI VVFCGTSYGTGSGWPDGADI NLMP1

>gi |83752056|gb|ABC43053.1| neurami ni dase [Influenza A virus
(A/Canterbury/437/2003(H3N2))]
MNPNOKI I TI GSVSLTI ATI CFLMOI AI LVTTVTLHFQHECN SPPNNQVMLCEPTI I ERNI TEI VYLTN
TTI EKEI CPKLV EYRNWSKPOCNI TGFAF PFSKDNSI RLSAGGDI WVTREPYVSCDPDKCYQFALGQGTTL
NNGHSNDTVH DTRPYRTLLMNLGVPFHLGTROVCI AWSSSSCHDGKAWLHV CVTGDDKNATASFI YNGR
LVDSI GSWSKKI LRTQESECVC I NGTCTVVM TDGSASGKADTKI LFI EEGKI VHI STL S GSAQHVEECSC
YPRYPGVR CVC RDNNWKGSRNRI VDI NVKDYSI VSSYVCSGLVGDTPRKNDSFSSSHCLDPNNEEGGHGVK
GWAFDDGNDVVMGRTI SEKLRSGYETFVKI EGWSKPN SKLQI NROVI VERGNRSGYSGI FSVEGKSCI NR
CFYVELI RGRKEETE VVWTSNSI VVFCGTS GTYGTGSWPDGADI NLMP I

>gi |83752094|gb|ABC43075.1| neurami ni dase [Influenza A virus
(A/Canterbury/439/2003(H3N2))]
MNPNOKI I TI GSVSLTI ATI CFLMOI AI LVTTVTLHFQHECN SPPNNQVMLCEPTI I ERNI TEI VYLTN
TTI EKEI CPKLV EYRNWSKPOCNI TGFAF PFSKDNSI RLSAGGDI WVTREPYVSCDPDKCYQFALGQGTTL
NNGHSNDTVH DTRPYRTLLMNLGVPFHLGTROVCI AWSSSSCHDGKAWLHV CVTGDDKNATASFI YNGR
LVDSI GSWSKKI LRTQESECVC I NGTCTVVM TDGSASGKADTKI LFI EEGKI VHI STL S GSAQHVEECSC
YPRYPGVR CVC RDNNWKGSRNRI VDI NVKDYSI VSSYVCSGLVGDTPRKNDSFSSSHCLDPNNEEGGHGVK
GWAFDDGNDVVMGRTI SEKLRSGYETFVKI EGWSKPN SKLQI NROVI VERGNRSGYSGI FSVEGKSCI NR
CFYVELI RGRKEETE VVWTSNSI VVFCGTS GTYGTGSWPDGADI NLMP I

>gi |84873522|gb|ABC67820.1| neurami ni dase [Influenza A virus
(A/Canterbury/429/2003(H3N2))]
MNPNOKI I TI GSVSLTI ATI CFLMOI AI LVTTVTLHFQHECN SPPNNQVMLCEPTI I ERNI TEI VYLTN
TTI EKEI CPKLV EYRNWSKPOCNI TGFAF PFSKDNSI RLSAGGDI WVTREPYVSCDPDKCYQFALGQGTTL
NNGHSNDTVH DTRPYRTLLMNLGVPFHLGTROVCI AWSSSSCHDGKAWLHV CVTGDDKNATASFI YNGR
LVDSI GSWSKKI LRTQESECVC I NGTCTVVM TDGSASGKADTKI LFI EEGKI VHI STL S GSAQHVEECSC
YPRYPGVR CVC RDNNWKGSRNRI VDI NVKDYSI VSSYVCSGLVGDTPRKNDSFSSSHCLDPNNEEGGHGVK
GWAFDDGNDVVMGRTI SEKLRSGYETFVKI EGWSKPN SKLQI NROVI VERGNRSGYSGI FSVEGKSCI NR
CFYVELI RGRKEETE VVWTSNSI VVFCGTS GTYGTGSWPDGADI NLMP I

>gi |83751804|gb|ABC42914.1| neurami ni dase [Influenza A virus
(A/Canterbury/387/2003(H3N2))]
MNPNOKI I TI GSVSLTI ATI CFLMOI AI LVTTVTLHFQHECN SPPNNQVMLCEPTI I ERNI TEI VYLTN
TTI EKEI CPKLV EYRNWSKPOCNI TGFAF PFSKDNSI RLSAGGDI WVTREPYVSCDPDKCYQFALGQGTTL
NNGHSNDTVH DTRPYRTLLMNLGVPFHLGTROVCI AWSSSSCHDGKAWLHV CVTGDDKNATASFI YNGR
LVDSI GSWSKKI LRTQESECVC I NGTCTVVM TDGSASGKADTKI LFI EEGKI VHI STL S GSAQHVEECSC
YPRYPGVR CVC RDNNWKGSRNRI VDI NVKDYSI VSSYVCSGLVGDTPRKNDSFSSSHCLDPNNEEGGHGVK
GWAFDDGNDVVMGRTI SEKLRSGYETFVKI EGWSKPN SKLQI NROVI VERGNRSGYSGI FSVEGKSCI NR
CFYVELI RGRKEETE VVWTSNSI VVFCGTS GTYGTGSWPDGADI NLMP I

>gi |85838433|gb|ABC86127.1| neurami ni dase [Influenza A virus
(A/Canterbury/432/2003(H3N2))]
MNPNOKI I TI GSVSLTI ATI CFLMOI AI LVTTVTLHFQHECN SPPNNQVMLCEPTI I ERNI TEI VYLTN
TTI EKEI CPKLV EYRNWSKPOCNI TGFAF PFSKDNSI RLSAGGDI WVTREPYVSCDPDKCYQFALGQGTTL
NNGHSNDTVH DTRPYRTLLMNLGVPFHLGTROVCI AWSSSSCHDGKAWLHV CVTGDDKNATASFI YNGR
LVDSI GSWSKKI LRTQESECVC I NGTCTVVM TDGSASGKADTKI LFI EEGKI VHI STL S GSAQHVEECSC
YPRYPGVR CVC RDNNWKGSRNRI VDI NVKDYSI VSSYVCSGLVGDTPRKNDSFSSSHCLDPNNEEGGHGVK
GWAFDDGNDVVMGRTI SEKLRSGYETFVKI EGWSKPN SKLQI NROVI VERGNRSGYSGI FSVEGKSCI NR
CFYVELI RGRKEETE VVWTSNSI VVFCGTS GTYGTGSWPDGADI NLMP I

>gi |194269503|gb|ACF36675.1| neurami ni dase [Influenza A virus (A/Hong
Kong/CUHK51353/2003(H3N2))]
MNPNOKI I TI GSVSLTI STI CFFMOI AI LI TTVTLHFQYEFN SPPNNQVMLCEPTI I ERNI TEI VYLTN
TTI EKEI CPKLA EYRNWSKPOCNI TGFAF PFSKDNSI RLSAGGDI WVTREPYVSCDPDKCYQFALGQGTTL
NNVHSNDTVH DTRPYRTLLMNLGVPFHLGTROVCI AWSSSSCHDGKAWLHV CVTGDDENATASFI YNGR
LVDSI VSWSKKI LRTQESECVC I NGTCTVVM TDGSASGKADTKI LFI EEGKI VHI STL S GSAQHVEECSC
YPRYPGVR CVC RDNNWKGSRNRI VDI NI KDYSI VSSYVCSGLVGDTPRKNDS SSSSHCLDPNNEEGGHGVK
GWAFDDGNDVVMGRTI SEKLRSGYETFVKI EGWSNPN SKLQI NROVI VDRGNRSGYSGI FSVEGKSCI NR
CFYVELI RGRNQETE VLWTSNSI VVFCGTS GTYGTGSWPDGADI NLMP I

>gi |194269505|gb|ACF36676.1| neurami ni dase [Influenza A virus (A/Hong
Kong/CUHK51380/2003(H3N2))]
MNPNOKI I TI GSVSLTI STI CFFMOI AI LI TTVTLHFQYEFN SPPNNQVMLCEPTI I ERNI TEI VYLTN
TTI EKEI CPKLA EYRNWSKPOCNI TGFAF PFSKDNSI RLSAGGDI WVTREPYVSCDPDKCYQFALGQGTTL
NNVHSNDTVH DTRPYRTLLMNLGVPFHLGTROVCI AWSSSSCHDGKAWLHV CVTGDDKNATASFI YNGR
LVDSI VSWSKKI LRTQESECVC I NGTCTVVM TDGSASGKADTKI LFI EEGKI VHI STL S GSAQHVEECSC
YPRYPGVR CVC RDNNWKGSRNRI VDI NI KDYSI VSSYVCSGLVGDTPRKNDS SSSSHCLDPNNEEGGHGVK
GWAFDDGNDVVMGRTI SEKLRSGYETFVKI EGWSNPN SKLQI NROVI VDRGNRSGYSGI FSVEGKSCI NR
CFYVELI RGRNQETE VLWTSNSI VVFCGTS GTYGTGSWPDGADI NLMP I

>gi |110333367|gb|ABG67637.1| neurami ni dase [Influenza A virus
(A/Wai kato/139/2003(H3N2))]
MNPNOKI I TI GSVSLTI ATI CFLMOI AI LVTTVTLHFQHECN SPPNNQVMLCEPTI I ERNI TEI VYLTN
TTI EKEI CPKLV EYRNWSKPOCNI TGFAF PFSKDNSI RLSAGGDI WVTREPYVSCDPDKCYQFALGQGTTL
NNGHSNDTVH DTRPYRTLLMNLGVPFHLGTROVCI AWSSSSCHDGKAWLHV CVTGDDKNATASFI YNGR
LVDSI GSWSKKI LRTQESECVC I NGTCTVVM TDGSASGKADTKI LFI EEGKI VHI STL S GSAQHVEECSC
YPRYPGVR CVC RDNNWKGSRNRI VDI NVKDYSI VSSYVCSGLVGDTPRKNDSFSSSHCLDPNNEEGGHGVK
GWAFDDGNDVVMGRTI SEKLRSGYETFVKI EGWSKPN SKLQI NROVI VERGNRSGYSGI FSVEGKSCI NR
CFYVELI RGRKEETE VVWTSNSI VVFCGTS GTYGTGSWPDGADI NLMP I

>gi |110333405|gb|ABG67659.1| neurami ni dase [Influenza A virus
(A/Wai kato/148/2003(H3N2))]
MNPNOKI I TI GSVSLTI ATI CFLMOI AI LVTTVTLHFQHECN SPPNNQVMLCEPTI I ERNI TEI VYLTN
TTI EKEI CPKLV EYRNWSKPOCNI TGFAF PFSKDNSI RLSAGGDI WVTREPYVSCDPDKCYQFALGQGTTL
NNGHSNDTVH DTRPYRTLLMNLGVPFHLGTROVCI AWSSSSCHDGKAWLHV CVTGDDKNATASFI YNGR

LVDSI GSWSKKI LRTQSEECVCI NGTCTVVMTDGSASGKADTKI LFI EEGKI VHI STLSGSAQHVEECSC
YPRYPGVRVCVRDNWKGSRPI VDI NVKDYSI VSSYVCSGLVGDTPRKNDSSFSSHCCLDPNNEEGGHGVK
GWAFDDGNDVWWMGRTI SEKLRSGYETFKVI EGWSKPNSKLOI NRQVI VERGNRSGYSGI FSVEGKSCI NR
CFYVELI RGRKEETEVMWTSNSI VVFCGTSYGTGSGWPDGADI NLMP

>gi | 83730009 | gb | ABC42128.1 | neurami ni dase [Influenza A virus
(A/Canterbury/395/2003 (H3N2))]

MNPNQKI | TI GSLSLTI | ATIFLMI | ALVTTVTLHFQHECNSPPNNQVMLCEPTI | ERNI TEI VYLTN
TTI EKEI CPKLVYERNWSPQCNITGFAPFSKDNSI RLSAGGDI WVTREPVVSCDPDKCYQFALGQGTTL
NNGHSNDTVHTRTPYRTRLLMNLGVPFHLGTRQVCI AWSSSSCHDGKAWLHVCVTGDDKNATASFI YNGR
LVDSI GSWSKKI LRTQSEECVCI NGTCTVVMTDGSASGKADTKI LFI EEGKI VHI STLSGSAQHVEECSC
YPRYPGVRVCVRDNWKGSRPI VDI NVKDYSI VSSYVCSGLVGDTPRKNDSSFSSHCCLDPNNEEGGHGVK
GWAFDDGNDVWWMGRTI SEKLRSGYETFKVI EGWSKPNSKLOI NRQVI VERGNRSGYSGI FSVEGKSCI NR
CFYVELI RGRKEETEVMWTSNSI VVFCGTSYGTGSGWPDGADI NLMP

>gi | 2865378 | gb | AAC40507.1 | neurami ni dase [Influenza A virus (A/Hong
Kong/156/97 (H5N1))]

MNPNQKI | TI GSI CMVVG I | SLMLQI | GNI | SVWVSHI | QTWHPNQPEPCNQSI NFYTEQAAASVTLAGNS
SLCPI SGWAI YSKDNSI RI GSKGDVFI REPII SCSHLECRFTFFLTQGALLNDKHSNGTVKDRSPYRTLM
SCPVGEAPSPYNSRFESVAWSASACHDGI SWLTI GI SGPDNGAVAVLKYNGI | TDTI KSWRNNI LRTQES
ECACVNGSCFTVMTDGPNEQASYKI FKI EKGRVVKVELNAPNYHYEECSYPDAGEI TCVCARDNWHGS
NRPWVSFNONLEYQI GYI CSGVFGDSPRPNDGTGSCGPVSLNGAYGVKGFSEFKYNGVWVI GRTKSTSSRS
GFEMI WDPNGWTEETDSSFSLKQDI | AI TDWSGYSGSFI QHELTGLNMRPCFWVELI RGRPKKTI WTS
GSI SFCGVNSDVTGWSWPDGADLPFTI DK

>gi | 4324308 | gb | AAD16786.1 | neurami ni dase [Influenza A virus (A/Hong
Kong/482/97 (H5N1))]

MNPNQKI | TI GSI CMVVG I | SLMLQI | GNTI | SVWVSHI | KTWHPNQPEPCNQSI NFYTEQAAASVTLAGNS
SLCPI SGWAI YSKDNSI RI GSKGDVFI REPII SCSHLECRFTFFLTQGALLNDKHSNGTVKDRSPYRTLM
SCPVGEAPSPYNSRFESVAWSASACHDGI SWLTI GI SGPDNGAVAVLKYNGI | TDTI KSWRNNI LRTQES
ECACVNGSCFTVMTDGPNEQASYKI FKI EKGRVVKVELNAPNYHYEECSYPDAGEI TCVCARDNWHGS
NRPWVSFNONLEYQI GYI CSGVFGDSPRPNDGTGSCGPVSLNGAYGVKGFSEFKYNGVWVI GRTKSTSSRS
GFEMI WDPNGWTEETDSSFSLKQDI | AI TDWSGYSGSFI QHELTGLNMRPCFWVELI RGRPKKTI WTS
GSI SFCGVNSDVTGWSWPDGADLPFTI DK

>gi | 4324312 | gb | AAD16790.1 | neurami ni dase [Influenza A virus (A/Hong
Kong/516/97 (H5N1))]

MNPNQKI | TI GSI CMVVG I | SLMLQI | GNTI | SVWVSHI | KTWHPNQPEPCNQSI NFYTEQAAASVTLAGNS
SLCPI SGWAI YSKDNSI RI GSKGDVFI REPII SCSHLECRFTFFLTQGALLNDKHSNGTVKDRSPYRTLM
SCPVGEAPSPYNSRFESVAWSASACHDGI SWLTI GI SGPDNGAVAVLKYNGI | TDTI KSWRNNI LRTQES
ECACVNGSCFTVMTDGPNEQASYKI FKI EKGRVVKVELNAPNYHYEECSYPDAGEI TCVCARDNWHGS
NRPWVSFNONLEYQI GYI CSGVFGDSPRPNDGTGSCGPVSLNGAYGVKGFSEFKYNGVWVI GRTKSTSSRS
GFEMI WDPNGWTEETDSSFSLKQDI | AI TDWSGYSGSFI QHELTGLNMRPCFWVELI RGRPKKTI WTS
GSI SFCGVNSDVTGWSWPDGADLPFTI DK

>gi | 4324314 | gb | AAD16792.1 | neurami ni dase [Influenza A virus (A/Hong
Kong/538/97 (H5N1))]

MNPNQKI | TI GSI CMVVG I | SLMLQI | GNTI | SVWVSHI | KTWHPNQPEPCNQSI NFYTEQAAASVTLAGNS
SLCPI SGWAI YSKDNSI RI GSKGDVFI REPII SCSHLECRFTFFLTQGALLNDKHSNGTVKDRSPYRTLM
SCPVGEAPSPYNSRFESVAWSASACHDGI SWLTI GI SGPDNGAVAVLKYNGI | TDTI KSWRNNI LRTQES
ECACVNGSCFTVMTDGPNEQASYKI FKI EKGRVVKVELNAPNYHYEECSYPDAGEI TCVCARDNWHGS
NRPWVSFNONLEYQI GYI CSGVFGDSPRPNDGTGSCGPVSLNGAYGVKGFSEFKYNGVWVI GRTKSTSSRS
GFEMI WDPNGWTEETDSSFSLKQDI | AI TDWSGYSGSFI QHELTGLNMRPCFWVELI RGRPKKTI WTS
GSI SFCGVNSDVTGWSWPDGADLPFTI DK

>gi | 4324317 | gb | AAD16795.1 | neurami ni dase [Influenza A virus (A/Hong
Kong/491/97 (H5N1))]

MNPNQKI | TI GSI CMVVG I | SLMLQI | GNI | SVWVSP I | QAWHPNQPEPCNQSI NFYTEQAAASVTLAGNS
SLCPI SGWAI YSKDNSI RI GSKGDVFI REPII SCSHLECRFTFFLTQGALLNDKHSNGTVKDRSPYRTLM
SCPVGEAPSPYNSRFESVAWSASACHDGI SWLTI GI SGPDNGAVAVLKYNGI | TDTI KSWRNNI LRTQES
ECACVNGSCFTVMTDGPNEQASYKI FKI EKGRVVKVELNAPNYHYEECSYPDAGEI TCVCARDNWHGS
NRPWVSFNONLEYQI GYI CSGVFGDSPRPNDGTGSCGPVSLNGAYGVKGFSEFKYNGVWVI GRTKSTSSRS
GFEMI WDPNGWTEETDSSFSLKQDI | AI TDWSGYSGSFI QHELTGLNMRPCFWVELI RGRPKKTI WTS
GSI SFCGVNSDVTGWSWPDGADLPFTI DK

>gi | 4324319 | gb | AAD16797.1 | neurami ni dase [Influenza A virus (A/Hong
Kong/532/1997 (H5N1))]

MNPNQKI | TI GSI CMVVG I | SLMLQI | GNTI | SVWVSHI | QAWHPNQPEPCNQSI NFYTEQAAASVTLAGNS
SLCPI SGWAI YSKDNSI RI GSKGDVFI REPII SCSHLECRFTFFLTQGALLNDKHSNGTVKDRSPYRTLM
SCPVGEAPSPYNSRFESVAWSASACHDGI SWLTI GI SGPDNGAVAVLKYNGI | TDTI KSWRNNI LRTQES
ECACVNGSCFTVMTDGPNEQASYKI FKI EKGRVVKVELNAPNYHYEECSYPDAGEI TCVCARDNWHGS
NRPWVSFNONLEYQI GYI CSGVFGDSPRPNDGTGSCGPVSLNGAYGVKGFSEFKYNGVWVI GRTKSTSSRS
GFEMI WDPNGWTEETDSSFSLKQDI | AI TDWSGYSGSFI QHELTGLNMRPCFWVELI RGRPKKTI WTS
GSI SFCGVNSDVTGWSWPDGADLPFTI DK

>gi | 4324322 | gb | AAD16800.1 | neurami ni dase [Influenza A virus (A/Hong
Kong/542/97 (H5N1))]

MNPNQKI | TI GSI CMVVG I | SLMLQI | GNTI | SVWVSP I | QAWHPNQPEPCNQSI NFYTEQAAASVTLAGNS
SLCPI SGWAI YSKDNSI RI GSKGDVFI REPII SCSHLECRFTFFLTQGALLNDKHSNGTVKDRSPYRTLM
SCPVGEAPSPYNSRFESVAWSASACHDGI SWLTI GI SGPDNGAVAVLKYNGI | TDTI KSWRNNI LRTQES
ECACVNGSCFTVMTDGPNEQASYKI FKI EKGRVVKVELNAPNYHYEECSYPDAGEI TCVCARDNWHGS
NRPWVSFNONLEYQI GYI CSGVFGDSPRPNDGTGSCGPVSLNGAYGVKGFSEFKYNGVWVI GRTKSTSSRS
GFEMI WDPNGWTEETDSSFSLKQDI | AVTDWSGYSGSFI QHELTGLNMRPCFWVELI RGRPKKTI WTS
GSI SFCGVNSDVTGWSWPDGADLPFTI DK

>gi |8307791|gb|AAF74324.1|AF084274_1 neurami ni dase subtype 1 [Influenza A virus (A/Hong Kong/485/97(H5N1))]
MNPNQKI I TI GSI CMVVG I SLMLQI GNI I SVWVSHI I QTWHPNQPEPCNQSI NFYTEQAAAASVTLAGNS
SLCPI SGWAI YSKDNSI RI GSKGDVFI REPF I SCSHLECRTEFFLTQGALLNDKHSNGTVKDRSPYRTLM
SCPVGAEAPSPYNSRFESVAWSASACHDGI SWLTI GI SGPDPNGAVAVLKYNIGI I TDTI KSWRNNI LRTQES
ECACVNGSCFTVMTDGPSENEQASYKI FK I EKGRVVKVELNAPNYHYEECSYDPAGEI TCVCRDNWHGS
NRPWVSFNQNLLEYQI GYI CSGVFGDSPRPNDGTGSCGPVSLNGAYGVKGF SFKYNGVWI GRKTSTSSRS
GFEMI WDPNGWTE TDSFSLKQDI I AI TDWGSYSGSFI QHPELTGLNCRPCFWVELI RGRPKKEKI WTS
GSSV SFCGVNSDTVGSWPDGAELPFTI DK

>gi |8307787|gb|AAF74322.1|AF084272_1 neurami ni dase subtype 1 [Influenza A virus (A/Hong Kong/482/97(H5N1))]
MNPNQKI I TI GSI CMVVG I SLMLQI GNTI SVWVSHI I KTWHPNQPEPCNQSI NFYTEQAAAASVTLAGNS
SLCPI SGWAI YSKDNSI RI GSKGDVFI REPF I SCSHLECRTEFFLTQGALLNDKHSNGTVKDRSPYRTLM
SCPVGAEAPSPYNSRFESVAWSASACHDGI SWLTI GI SGPDPNGAVAVLKYNIGI I TDTI KSWRNNI LRTQES
ECACVNGSCFTVMTDGPSENEQASYKI FK I EKGRVVKVELNAPNYHYEECSYDPAGEI TCVCRDNWHGS
NRPWVSFNQNLLEYQI GYI CSGVFGDSPRPNDGTGSCGPVSLNGAYGVKGF SFKYNGVWI GRKTSTSSRS
GFEMI WDPNGWTE TDSFSLKQDI I AI TDWGSYSGSFI QHPELTGLNCRPCFWVELI RGRPKKEKI WTS
GSSI SFCGVNSDTVGSWPDGAELPFTI DK

>gi |8307793|gb|AAF74325.1|AF084275_1 neurami ni dase subtype 1 [Influenza A virus (A/Hong Kong/486/97(H5N1))]
MNPNQKI I TI GSI CMVVG I SLMLQI GNTI SVWVSHI I KTWHPNQPEPCNQSI NFYTEQAAAASVTLAGNS
SLCPI SGWAI YSKDNSI RI GSKGDVFI REPF I SCSHLECRTEFFLTQGALLNDKHSNGTVKDRSPYRTLM
SCPVGAEAPSPYNSRFESVAWSASACHDGI SWLTI GI SGPDPNGAVAVLKYNIGI I TDTI KSWRNNI LRTQES
ECACVNGSCFTVMTDGPSENEQASYKI FK I EKGRVVKVELNAPNYHYEECSYDPAGEI TCVCRDNWHGS
NRPWVSFNQNLLEYQI GYI CSGVFGDSPRPNDGTGSCGPVSLNGAYGVKGF SFKYNGVWI GRKTSTSSRS
GFEMI WDPNGWTE TDSFSLKQDI I AI TDWGSYSGSFI QHPELTGLNCRPCFWVELI RGRPKKEKI WTS
GSSI SFCGVNSDTVGSWPDGAELPFTI DK

>gi |3335423|gb|AAC32089.1| neurami ni dase subtype 1 [Influenza A virus (A/Hong Kong/156/97(H5N1))]
MNPNQKI I TI GSI CMVVG I SLMLQI GNI I SVWVSHI I QTWHPNQPEPCNQSI NFYTEQAAAASVTLAGNS
SLCPI SGWAI YSKDNSI RI GSKGDVFI REPF I SCSHLECRTEFFLTQGALLNDKHSNGTVKDRSPYRTLM
SCPVGAEAPSPYNSRFESVAWSASACHDGI SWLTI GI SGPDPNGAVAVLKYNIGI I TDTI KSWRNNI LRTQES
ECACVNGSCFTVMTDGPSENEQASYKI FK I EKGRVVKVELNAPNYHYEECSYDPAGEI TCVCRDNWHGS
NRPWVSFNQNLLEYQI GYI CSGVFGDSPRPNDGTGSCGPVSLNGAYGVKGF SFKYNGVWI GRKTSTSSRS
GFEMI WDPNGWTE TDSFSLKQDI I AI TDWGSYSGSFI QHPELTGLNCRPCFWVELI RGRPKKEKI WTS
GSSI SFCGVNSDTVGSWPDGAELPFTI DK

>gi |4324310|gb|AAD16788.1| neurami ni dase [Influenza A virus (A/Hong Kong/486/97(H5N1))]
MNPNQKI I TI GSI CMVVG I NLMLQI GNTI SVWVSHI I KTWHPNQPEPCNQSI NFYTEQAAAASVTLAGNS
SLCPI SGWAI YSKDNSI RI GSKGDVFI REPF I SCSHLECRTEFFLTQGALLNDKHSNGTVKDRSPYRTLM
SCPVGAEAPSPYNSRFESVAWSASACHDGI SWLTI GI SGPDPNGAVAVLKYNIGI I TDTI KSWRNNI LRTQES
ECACVNGSCFTVMTDGPSENEQASYKI FK I EKGRVVKVELNAPNYHYEECSYDPAGEI TCVCRDNWHGS
NRPWVSFNQNLLEYQI GYI CSGVFGDSPRPNDGTGSCGPVSLNGAYGVKGF SFKYNGVWI GRKTSTSSRS
GFEMI WDPNGWTE TDSFSLKQDI I AI TDWGSYSGSFI QHPELTGLNCRPCFWVELI RGRPKKEKI WTS
GSSI SFCGVNSDTVGSWPDGAELPFTI DK

>gi |4324321|gb|AAD16799.1| neurami ni dase [Influenza A virus (A/Hong Kong/514/97(H5N1))]
MNPNQKI I TI GSI CMVVG I SLMLQI GNI I SVWVSHI I QTWHPNQPEPCNQSI NFYTEQAAAASVTLAGNS
SLCPI SGWAI YSKDKSI RI GSKGDVFI REPF I SCSHLECRTEFFLTQGALLNDKHSNGTVKDRSPYGTLM
SCPVGETPSPYNSRFESVAWSASACHDSI SWLTI GI SGPDPNGAVAVLKYNIGI I TDTI KSWRNNI LRTQES
ECACVNGSCFTVMTDGPSENEQASYKI FK I EKGRVVKVELNAPNYHYEECSYDPAGEI TCVCRDNWHGS
NRPWVSFNQNLLEYQI GYI CSGVFGDSPRPNDGTGSCGPVSLNGAYGVKGF SFKYNGVWI GRKTSTSSRS
GFEMI WDPNGWTE TDSFSLKQDI I AI TDWGSYSGSFI QHPELTGLNCRPCFWVELI RGRPKKEKI WTS
GSSI SFCGVNSDTVGSWPDGAELPFTI DK

>gi |8307785|gb|AAF74321.1|AF084271_1 neurami ni dase subtype 1 [Influenza A virus (A/Hong Kong/481/97(H5N1))]
MNPNQKI I TI GSI CMVVG I SLMLQI GNI I SVWVSHI I QTWHPNQPEPCNQSI NFYTEQAAAASVTLAGNS
SLCPI SGWAI YSKDNSI RI GSKGDVFI REPF I SCSHLECRTEFFLTQGALLNDKHSNGTVKDRSPYRTLM
SCPVGAEAPSPYNSRFESVAWSASACHDGI SWLTI GI SGPDPNGAVAVLKYNIGI I TDTI KSWRNNI LRTQES
ECACVNGSCFTVMTDGPSENEQASYKI FK I EKGRVVKVELNAPNYHYEECSYDPAGEI TCVCRDNWHGS
NRPWVSFNQNLLEYQI GYI CSGVFGDSPRPNDGTGSCGPVSLNGAYGVKGF SFKYNGVWI GRKTSTSSRS
GFEMI WDPNGWTE TDSFSLKQDI I AI TDWGSYSGSFI QHPELTGLNCRPCFWVELI RGRPKKEKI WTS
GSSI SFCGVNSDTVGSWPDGAELPFTI DK

>gi |8307789|gb|AAF74323.1|AF084273_1 neurami ni dase subtype 1 [Influenza A Virus (A/Hong Kong/483/97(H5N1))]
MNPNQKI I TI GSI CMVVG I SLMLQI GNI I SVWI SHI I QTWHPNQPEPCNQSI NFYTEQAAAASVTLAGNS
SLCPI SGWAI YSKDNSI RI GSKGDVFI REPF I SCSHLECRTEFFLTQGALLNDKHSNGTVKDRSPYRTLM
SCPVGAEAPSPYNSRFESVAWSASACHDGI SWLTI GI SGPDPNEAVAVLKYNIGI I TDTI RSWRNNI LRTQES
ECACVNGSCFTVMTDGPSENEQASYKI FK I EKGRVVKVELNAPNYHYEECSYDPAGEI TCVCRDNWHGS
NRPWVSFNQNLLEYQI GYI CSGVFGDSPRPNDGTGSCGPVSLNGAYGVKGF SFKYNGVWI GRKTSTSSRS
GFEMI WDPNGWTE TDSFSLKQDI I AVTDWGSYSGSFI QHPELTGLNCRPCFWVELI RGRPKKEKI WTS
GSSI SFCGVNSDTVGSWPDGAELPFTI DK

>gi |182382583|gb|ACB87566.1| neurami ni dase [Influenza A virus (A/Ji angsu/2/2007(H5N1))]
MNPNQKI I TI GSI CMVI GI VSLMLQI GNI I SI VVSHI I OTGNQHQDEPI RANFLTENAVASVTLAGNSS
LCPVIRGVAVHSDNSI RI GSKGDVFI REPF I SCSHLECRTEFFLTQGALLNDKHSNGTVKDRSPHRTLMS
CPVGEAPSPYNSRFESVAWSASACHDGT SWLTI GI SGPDPNGAVAVLKYNIGI I TDTI KSWRNNI LRTQES

CACVNGSCFTVMTDGPNSGQASYKI FKMEKGGKVVKSVELNAPNYHYEECSCYPDAGEI TCVCRDNWHGNS
 RPWVSNQNLLEYQI GYI CSGVFGDNPRPNDGTGSCDPVSPNGAYGI KGFSSFKYNGVWI GRKSTNSRSR
 FEMI WDPNGWTEGDSSFSVKQDI VAI TDWSGYSGSFVQHPPELTGLDCI RPCFWVELI RGRPKESTI WTS
 SSI SFCGVNSDTSVSWSPDGAELPFTI DK

>gi |157103052|gb|ABV23935.1| neurami ni dase [Influenza A virus
 (A/Ni geri a/6e/07(H5N1))]
 MNPNQKI I TI GSI CMVI GI VSLMLQI GNMI SI WVSHSI QTGNQROAEPI SNTKFLTERAVASVTLAGNSS
 LCPI SGWAVYSKDNI RI GSRGDV FVI REPFI SCSHLECRTFFLTQGALLNDKHSNGTVKDRSPHRTLMS
 CPVGEAPSPYNSRFESVAWSASACHDGT SWLTI GI SGPDN GAVAVLK YNGI I TDTI KSWRNNI LRTQESE
 CACVNGSCFTVMTDGPNSGQASYKI FKMEKGGKVVKSVELDAPNYHYEECSCYPDAGEI TCVCRDNWHGNS
 RPWVSNQNLLEYQI GYI CSGVFGDNPRPNDGTGSCDPVSPNGAYGVKGFSSFKYNGVWI GRKSTNSRSR
 FEMI WDPNGWTEGDSSFSVKQDI VAI TDWSGYSGSFVQHPPELTGLDCI RPCFWVELI RGRPKESTI WTS
 SSI SFCGVNSDTSVSWSPDGAELPFTI DK

>gi |162569002|gb|ABY19420.1| neurami ni dase [Influenza A virus (A/Viet
 Nam/HN31242/2007(H5N1))]
 MNPNQKI I TI GSI CMVI GI VSLMLQI GNMI SI WVSHSI QTGNQNOVEPI I NTNFLTGKAVASI TLAGNSS
 LCPI RGWAI HSKDNI RI GSKGDV FVI REPFI SCSHLECRTFFLTQGALLNDKHSNGTVKDRSPHRTLMS
 CPVGEAPSPYNSRFESVAWSASACHDGT SWLTI GI SGPDN GAVAVLK YNGI I TDTI KSWRNNI LRTQESE
 CACVNGSCFTVMTDGPNSGQASYKI FKMEKGGKVI KSVELDAPNYHYEECSCYPDAGEI TCVCRDNWHGNS
 RPWVSNQNLLEYQI GYI CSGVFGDNPRPNDGTGSCDPVSHNGAYGVKGFSSFKYNGVWI GRKSTNSRSR
 FEMI WDPNGWTEGDSSFSVKQDI VAI TDWSGYSGSFVQHPPELTGLDCI RPCFWVELI RGRPKESTI WTS
 SSI SFCGVNSDTSVSWSPDGAELPFTI DK

>gi |124244208|gb|ABM92274.1| neurami ni dase [Influenza A virus (A/Egypt/0636-
 NAMRU3/2007(H5N1))]
 MNPNQKI I TI GSI CMVI GI VSLMLQI GNMI SI WVSHSI QTGNQCODEPI SNTKFLTEKAVASVTLAGNSS
 LCPI SGWAVYSKDNI RI GSRGDV FVI REPFI SCSHLECRTFFLTQGALLNDKHSNGTVKDRSPHRTLMS
 CPVGEAPSPYNSRFESVAWSASACHDGT SWLTI GI SGPDN GAVAVLK YNGI I TDTI KSWRNNI LRTQESE
 CACVNGSCFTVMTDGPSSGQASYKI FKMEKGGKVVKSVELDAPNYHYEECSCYPDAGEI TCVCRDNWHGNS
 RPWVSNQNLLEYQI GYI CSGVFGDNPRPNDGTGSCDPVFPNGAYGVKGFSSFKYNGVWI GRKSTNSRSR
 FEMI WDPNGWTEGDSSFSVKQDI VAI TDWSGYSGSFVQHPPELTGLDCI RPCFWVELI RGRPKESTI WTS
 SSI SFCGVNSDTSVSWSPDGAELPFTT DK

>gi |124098908|gb|ABM90469.1| neurami ni dase [Influenza A virus
 (A/Indonesia/1031RE2/2007(H5N1))]
 MNPNQKI I TI GSI CMVI GI VSLMLQI GNMI SI WVSHSI QKGNQHOAEI SNTNPLTEKAVASVTLAGNSS
 LCPI RGWAVHSDNNI RI GSKGDV FVI REPFI SCSHLECRTFFLTQGALLNDKHSNGTVKDRSPHRTLMS
 CPVGEAPSPYNSRFESVAWSASACHDGT SWLTI GI SGPDN EAVAVLK YNGI I TDTI KSWRNNI LRTQESE
 CACVNGSCFTVMTDGPNSGQASYKI FKMKKGGKVVKSVELDAPNYHYEECSCYPDAGEI TCVCRDNWHGNS
 RPWVSNQNLLEYQI GYI CSGVFGDNPRPNDGTGSCGPMSPNGAYGVKGFSSFKYNGVWI GRKSTNSRSR
 FEMI WDPNGWTEGDSSFSVKQDI VAI TDWSGYSGSFVQHPPELTGLDCI RPCFWVELI RGRPKESTI WTS
 SSI SFCGVNSDTSVSWSPDGAELPFTI DK

>gi |124098582|gb|ABM90436.1| neurami ni dase [Influenza A virus
 (A/Indonesia/1031/2007(H5N1))]
 MNPNQKI I TI GSI CMVI GI VSLMLQI GNMI SI WVSHSI QKGNQHOAEI SNTNPLTEKAVASVTLAGNSS
 LCPI RGWAVHSDNNI RI GSKGDV FVI REPFI SCSHLECRTFFLTQGALLNDKHSNGTVKDRSPHRTLMS
 CPVGEAPSPYNSRFESVAWSASACHDGT SWLTI GI SGPDN EAVAVLK YNGI I TDTI KSWRNNI LRTQESE
 CACVNGSCFTVMTDGPNSGQASYKI FKMKKGGKVVKSVELDAPNYHYEECSCYPDAGEI TCVCRDNWHGNS
 RPWVSNQNLLEYQI GYI CSGVFGDNPRPNDGTGSCGPMSPNGAYGVKGFSSFKYNGVWI GRKSTNSRSR
 FEMI WDPNGWTEGDSSFSVKQDI VAI TDWSGYSGSFVQHPPELTGLDCI RPCFWVELI RGRPKESTI WTS
 SSI SFCGVNSDTSVSWSPDGAELPFTI DK

>gi |124098853|gb|ABM90447.1| neurami ni dase [Influenza A virus
 (A/Indonesia/1031T/2007(H5N1))]
 MNPNQKI I TI GSI CMVI GI VSLMLQI GNMI SI WVSHSI QKGNQHOAEI SNTNPLTEKAVASVTLAGNSS
 LCPI RGWAVHSDNNI RI GSKGDV FVI REPFI SCSHLECRTFFLTQGALLNDKHSNGTVKDRSPHRTLMS
 CPVGEAPSPYNSRFESVAWSASACHDGT SWLTI GI SGPDN EAVAVLK YNGI I TDTI KSWRNNI LRTQESE
 CACVNGSCFTVMTDGPNSGQASYKI FKMKKGGKVVKSVELDAPNYHYEECSCYPDAGEI TCVCRDNWHGNS
 RPWVSNQNLLEYQI GYI CSGVFGDNPRPNDGTGSCGPMSPNGAYGVKGFSSFKYNGVWI GRKSTNSRSR
 FEMI WDPNGWTEGDSSFSVKQDI VAI TDWSGYSGSFVQHPPELTGLDCI RPCFWVELI RGRPKESTI WTS
 SSI SFCGVNSDTSVSWSPDGAELPFTI DK

>gi |124098932|gb|ABM90480.1| neurami ni dase [Influenza A virus
 (A/Indonesia/1032/2007(H5N1))]
 MNPNQKI I TI GSI CMVI GI VSLMLQI GNMI SI WVSHSI QKGNQHOAEI SNTNPLTEKAVASVTLAGNSS
 LCPI RGWAVHSDNNI RI GSKGDV FVI REPFI SCSHLECRTFFLTQGALLNDKHSNGTVKDRSPHRTLMS
 CPVGEAPSPYNSRFESVAWSASACHDGT SWLTI GI SGPDN EAVAVLK YNGI I TDTI KSWRNNI LRTQESE
 CACVNGSCFTVMTDGPNSGQASYKI FKMKKGGKVI KSVELDATNYHYEECSCYPDAGEI TCVCRDNWHGNS
 RPWVSNQNLLEYQI GYI CSGVFGDNPRPNDGTGSCGPMSPNGAYGVKGFSSFKYNGVWI GRKSTNSRSR
 FEMI WDPNGWTEGDSSFSVKQDI VAI TDWSGYSGSFVQHPPELTGLDCI RPCFWVELI RGRPKESTI WTS
 SSI SFCGVNSDTSVSWSPDGAELPFTI DK

>gi |124098881|gb|ABM90458.1| neurami ni dase [Influenza A virus
 (A/Indonesia/1031T2/2007(H5N1))]
 MNPNQKI I TI GSI CMVI GI VSLMLQI GNMI SI WVSHSI QKGNQHOAEI SNTNPLTEKAVASVTLAGNSS
 LCPI RGWAVHSDNNI RI GSKGDV FVI REPFI SCSHLECRTFFLTQGALLNDKHSNGTVKDRSPHRTLMS
 CPVGEAPSPYNSRFESVAWSASACHDGT SWLTI GI SGPDN EAVAVLK YNGI I TDTI KSWRNNI LRTQESE
 CACVNGSCFTVMTDGPNSGQASYKI FKMKKGGKVVKSVELDAPNYHYEECSCYPDAGEI TCVCRDNWHGNS
 RPWVSNQNLLEYQI GYI CSGVFGDNPRPNDGTGSCGPMSPNGAYGVKGFSSFKYNGVWI GRKSTNSRSR
 FEMI WDPNGWTEGDSSFSVKQDI VAI TDWSGYSGSFVQHPPELTGLDCI RPCFWVELI RGRPKESTI WTS
 SSI SFCGVNSDTSVSWSPDGAELPFTI DK

>gi |124098984|gb|ABM90502.1| neurami ni dase [Influenza A virus (A/Indonesia/CDC1032T/2007(H5N1))]
MNPQKI I TI GSI CMVI GI VSLMLQI GNMI SI WVSHSI QKGNQHOAESI SNTNPLTEKAVASVTLAGNSS
LCPI RGWAVHSKDNNI RI GSKGDV FVI REPFI SCSHLECRTEFFLTQGALLNDKHSNGTVKDRSPHRTLMS
CPVGEAPSPYNSRFESVAWSASACHDGT SWLTI GI SGPDNEAVAVLKYNGI I TDTI KSWRNNI LRTQESE
CACVNGSCFTVMTDGPNSNGQASYKI FKMKGKVI KSVELDATNYHYEECSYPDAGEI TCVCRDNWHGNS
RPWVFNQONLEYQI GYI CSGVFGDNPRPNDGTGSCGPMSPNGAYGVKGF SFKYNGVWI GRKSTNSRSG
FEMI WDPNGWTGTDSSFSVKQDI VAI TDWSGYSGSFVQHP ELTGLDCI RPCFWVELI RGRPKESTI WTS
SSI SFCGVNSDTVSWSPDGAELPFTI DK

>gi |124098957|gb|ABM90491.1| neurami ni dase [Influenza A virus (A/Indonesia/CDC1032N/2007(H5N1))]
MNPQKI I TI GSI CMVI GI VSLMLQI GNMI SI WVSHSI QKGNQHOAESI SNTNPLTEKAVASVTLAGNSS
LCPI RGWAVHSKDNNI RI GSKGDV FVI REPFI SCSHLECRTEFFLTQGALLNDKHSNGTVKDRSPHRTLMS
CPVGEAPSPYNSRFESVAWSASACHDGT SWLTI GI SGPDNEAVAVLKYNGI I TDTI KSWRNNI LRTQESE
CACVNGSCFTVMTDGPNSNGQASYKI FKMKGKVI KSVELDATNYHYEECSYPDAGEI TCVCRDNWHGNS
RPWVFNQONLEYQI GYI CSGVFGDNPRPNDGTGSCGPMSPNGAYGVKGF SFKYNGVWI GRKSTNSRSG
FEMI WDPNGWTGTDSSFSVKQDI VAI TDWSGYSGSFVQHP ELTGLDCI RPCFWVELI RGRPKESTI WTS
SSI SFCGVNSDTVSWSPDGAELPFTI DK

>gi |124099031|gb|ABM90524.1| neurami ni dase [Influenza A virus (A/Indonesia/CDC1046T/2007(H5N1))]
MNPQKI I TI GSI CMVI GI VSLMLQI GNMI SI WVSHSI QTGNQHOAESI SNTNPLTEKAVASVTLAGNSS
LCPI RGWAVHSKDNNI RI GSKGDV FVI REPFI SCSHLECRTEFFLTQGALLNDKHSNGTVKDRSPHRTLMS
CPVGEAPSPYNSRFESVAWSASACHDGT SWLTI GI SGPDNEAVAVLKYNGI I TDTI KSWRNNI LRTQESE
CACVNGSCFTVMTDGPNSNGQASYKI FKMKGKVI KSVELDATNYHYEECSYPDAGEI TCVCRDNWHGNS
RPWVFNQONLEYQI GYI CSGVFGDNPRPNDGTGSCGPMSPNGAYGVKGF SFKYNGVWI GRKSTNSRSG
FEMI WDPNGWTGTDSSFSVKQDI VAI TDWSGYSGSFVQHP ELTGLDCI RPCFWVELI RGRPKESTI WTS
SSI SFCGVNSDTVSWSPDGAELPFTI DK

>gi |124099009|gb|ABM90513.1| neurami ni dase [Influenza A virus (A/Indonesia/CDC1046/2007(H5N1))]
MNPQKI I TI GSI CMVI GI VSLMLQI GNMI SI WVSHSI QTGNQHOAESI SNTNPLTEKAVASVTLAGNSS
LCPI RGWAVHSKDNNI RI GSKGDV FVI REPFI SCSHLECRTEFFLTQGALLNDKHSNGTVKDRSPHRTLMS
CPVGEAPSPYNSRFESVAWSASACHDGT SWLTI GI SGPDNEAVAVLKYNGI I TDTI KSWRNNI LRTQESE
CACVNGSCFTVMTDGPNSNGQASYKI FKMKGKVI KSVELDATNYHYEECSYPDAGEI TCVCRDNWHGNS
RPWVFNQONLEYQI GYI CSGVFGDNPRPNDGTGSCGPMSPNGAYGVKGF SFKYNGVWI GRKSTNSRSG
FEMI WDPNGWTGTDSSFSVKQDI VAI TDWSGYSGSFVQHP ELTGLDCI RPCFWVELI RGRPKESTI WTS
SSI SFCGVNSDTVSWSPDGAELPFTI DK

>gi |124099058|gb|ABM90535.1| neurami ni dase [Influenza A virus (A/Indonesia/CDC1047/2007(H5N1))]
MNPQKI I TI GSI CMVI GI VSLMLQI GNMI SI WVSHSI QTGNQHOAESI SNTNPLTEKAVASVTLAGNSS
LCPI RGWAVHSKDNNI RI GSKGDV FVI REPFI SCSHLECRTEFFLTQGALLNDKHSNGTVKDRSPHRTLMS
CPVGEAPSPYNSRFESVAWSASACHDGT SWLTI GI SGPDNEAVAVLKYNGI I TDTI KSWRNNI LRTQESE
CACVNGSCFTVMTDGPNSNGQASYKI FKMKGKVI KSVELDATNYHYEECSYPDAGEI TCVCRDNWHGNS
RPWVFNQONLEYQI GYI CSGVFGDNPRPNDGTGSCGPMSPNGAYGVKGF SFKYNGVWI GRKSTNSRSG
FEMI WDPNGWTGTDSSFSVKQDI VAI TDWSGYSGSFVQHP ELTGLDCI RPCFWVELI RGRPKESTI WTS
SSI SFCGVNSDTVSWSPDGAELPFTI DK

>gi |124099084|gb|ABM90546.1| neurami ni dase [Influenza A virus (A/Indonesia/CDC1047S/2007(H5N1))]
MNPQKI I TI GSI CMVI GI VSLMLQI GNMI SI WVSHSI QTGNQHOAESI SNTNPLTEKAVASVTLAGNSS
LCPI RGWAVHSKDNNI RI GSKGDV FVI REPFI SCSHLECRTEFFLTQGALLNDKHSNGTVKDRSPHRTLMS
CPVGEAPSPYNSRFESVAWSASACHDGT SWLTI GI SGPDNEAVAVLKYNGI I TDTI KSWRNNI LRTQESE
CACVNGSCFTVMTDGPNSNGQASYKI FKMKGKVI KSVELDATNYHYEECSYPDAGEI TCVCRDNWHGNS
RPWVFNQONLEYQI GYI CSGVFGDNPRPNDGTGSCGPMSPNGAYGVKGF SFKYNGVWI GRKSTNSRSG
FEMI WDPNGWTGTDSSFSVKQDI VAI TDWSGYSGSFVQHP ELTGLDCI RPCFWVELI RGRPKESTI WTS
SSI SFCGVNSDTVSWSPDGAELPFTI DK

>gi |2833659|gb|AAC34264.1| neurami ni dase [Influenza A virus (A/Hong Kong/156/97(H5N1))]
QKQEI KMNPQKI I TI GSI CMVVI I SLMLQI GNI I SVVSHI I QTWHPNQPEPCNQSI N FYTEQAAAASV
TLAGNSSLCPI SGWAI YSKDNSI RI GSKGDV FVI REPFI SCSHLECRTEFFLTQGALLNDKHSNGTVKDRS
PYRTLMSCPVGEAPSPYNSRFESVAWSASACHDGI SWLTI GI SGPDNGAVAVLKYNGI I TDTI KSWRNNI
LRTQESECACVNGSCFTVMTDGPNSNGQASYKI FKI EKGRVVKSVELNAPNYHYEECSYPDAGEI TCVC
RDNWHGNSRPWVFNQONLEYQI GYI CSGVFGDSPRPNDGTGSCGVPVSLNGAYGVKGF SFKYNGVWI GRK
STSSRSGFEMI WDPNGWTETDSSFSVKQDI I AI TDWSGYSGSFI QHP ELTGLNMRPCFWVELI RGRPK
E KTI WTS GSSI SFCGVNSDTVGSWPDGAELPFTI DK

>gi |4324309|gb|AAD16787.1| neurami ni dase [Influenza A virus (A/Hong Kong/488/97(H5N1))]
MNPQKI I TI GSI CMVVI I SLMLQI GNTI SVVSHI I QTWHPNQPEPCNQSI N FYTEQAAAASVTLAGNS
SLCPI SGWAI YSKDNSI RI GSKGDV FVI REPFI SCSHLECRTEFFLTQGALLNDKHSNGTVKDRSPYRTLM
SCPVGEAPSPYNSRFESVAWSASACHDGI SWLTI GI SGPDNGAVAVLKYNGI I TDTI KSWRNNI LRTQES
EACVNGSCFTVMTDGPNSNGQASYKI FKI EKGRVVKSVELNAPNYHYEECSYPDAGEI TCVCRDNWHGNS
NRPWVFNQONLEYQI GYI CSGVFGDSPRPNDGTGSCGVPVSLNGAYGVKGF SFKYNGVWI GRKSTSSRS
GFEMI WDPNGWTETDSSFSVKQDI I AI TDWSGYSGSFI QHP ELTGLNMRPCFWVELI RGRPKETI WTS
GSSI SFCGVNSDTVGSWPDGAELPFTI DK

>gi |4324311|gb|AAD16789.1| neurami ni dase [Influenza A virus (A/Hong Kong/507/97(H5N1))]
MNPQKI I TI GSI CMVVI I SLMLQI GNTI SVVSHI I QTWHPNQPEPCNQSI N FYTEQAAAASVTLAGNS
SLCPI SGWAI YSKDNSI RI GSKGDV FVI REPFI SCSHLECRTEFFLTQGALLNDKHSNGTVKDRSPYRTLM
SCPVGEAPSPYNSRFESVAWSASACHDGI SWLTI GI SGPDNGAVAVLKYNGI I TDTI KSWRNNI LRTQES

ECACVNGSCFTVMTDGPSPNEQASYKI FKI EKGRVVKVELNAPNYHYEECSYDPAGEI TCVCRDNWHGS
 NRPWVSFNONLEYQI GYI CSGVFGDSPRPNDGTGCGPVSLNGAYGVKGFSEFKYGNVWI GRKSTSSRS
 GFEMI WDPNGWTE TDSSFSLKQDI I AI TDWSGYSGSFI QHELTGLNMRPCFWVELI RGRPKKEITI WTS
 GSSI SFCGVNSDVTGWSWPDDAELPFTI DK
 >gi |4324320|gb|AAD16798.1| neurami ni dase [Influenza A vi rus (A/Hong
 Kong/483/1997(H5N1))]
 MNPNQKI I TI GSI CMVVG I SLMLQI GNI I SVWI SHI I QTWHPNOPEPCNQSI NFYTEQAAASVTLAGNS
 SLCPI SGWAI YSKDNSI RI GSKGDVFI REFFI SCSHLECRFTFFLTQGALLNDKHSNGTVKDRSPYRTLM
 SCPVGEAPSPYNSRFESVAWSASACHDGI SWLTI GI SGPDNGAVAVLKYNIGI I TDTI KSWRNNI LRTQES
 ECACVNGSCFTVMTDGPSPNEQASYKI FKI EKGRVVKVELNAPNYHYEECSYDPAGEI TCVCRDNWHGS
 NRPWVSFNONLEYQI GYI CSGVFGDSPRPNDGTGCGPVSLNGAYGVKGFSEFKYGNVWI GRKSTSSRS
 GFEMI WDPNGWTE TDSSFSLKQDI I AI TDWSGYSGSFI QHELTGLNMRPCFWVELI RGRPKKEITI WTS
 GSSI SFCGVNSDVTGWSWPDDAELPFTI DK
 >gi |4324315|gb|AAD16793.1| neurami ni dase [Influenza A vi rus (A/Hong
 Kong/481/97(H5N1))]
 MNPNQKI I TI GSI CMVVG I SLMLQI GNI I SVWVSHI I QTWHPNOPEPCNQSI NFYTEQAAASVTLAGNS
 SLCPI SGWAI YSKDNSI RI GSKGDVFI REFFI SCSHLECRFTFFLTQGALLNDKHSNGTVKDRSPYRTLM
 SCPVGEAPSPYNSRFESVAWSASACHDGI SWLTI GI SGPDNGAVAVLKYNIGI I TDTI KSWRNNI LRTQES
 ECACVNGSCFTVMTDGPSPNEQASYKI FKI EKGRVVKVELNAPNYHYEECSYDPAGEI TCVCRDNWHGS
 NRPWVSFNONLEYQI GYI CSGVFGDSPRPNDGTGCGPVSLNGAYGVKGFSEFKYGNVWI GRKSTSSRS
 GFEMI WDPNGWTE TDSSFSLKQDI I AI TDWSGYSGSFI QHELTGLNMRPCFWVELI RGRPKKEITI WTS
 GSSI SFCGVNSDVTGWSWPDDAELPFTI DK
 >gi |4324316|gb|AAD16794.1| neurami ni dase [Influenza A vi rus (A/Hong
 Kong/485/97(H5N1))]
 MNPNQKI I TI GSI CMVVG I SLMLQI GNI I SVWVSHI I QTWHPNOPEPCNQSI NFYTEQAAASVTLAGNS
 SLCPI SGWAI YSKDNSI RI GSKGDVFI REFFI SCSHLECRFTFFLTQGALLNDKHSNGTVKDRSPYRTLM
 SCPVGEAPSPYNSRFESVAWSASACHDGI SWLTI GI SGPDNGAVAVLKYNIGI I TDTI KSWRNNI LRTQES
 ECACVNGSCFTVMTDGPSPNEQASYKI FKI EKGRVVKVELNAPNYHYEECSYDPAGEI TCVCRDNWHGS
 NRPWVSFNONLEYQI GYI CSGVFGDSPRPNDGTGCGPVSLNGAYGVKGFSEFKYGNVWI GRKSTSSRS
 GFEMI WDPNGWTE TDSSFSLKQDI I AI TDWSGYSGSFI QHELTGLNMRPCFWVELI RGRPKKEITI WTS
 GSSI SFCGVNSDVTGWSWPDDAELPFTI DK
 >gi |4324318|gb|AAD16796.1| neurami ni dase [Influenza A vi rus (A/Hong
 Kong/503/97(H5N1))]
 MNPNQKI I TI GSI CMVVG I SLMLQI GNI I SVWVSHI I QAWHSNOPEPCNQSI NFYTEQAAASVTLAGNS
 SLCPI SGWAI YSKDNSI RI GSKGDVFMREFFI SCSHLECRFTFFLTQGALLNNKHSNGTVKDRSPYRTLM
 SCPVGEAPSPYNSRFESVAWSASACHDGI SWLTI GI SGPDNGAVAVLKYNIGI I TDTI KSWRNNI LRTQES
 ECACVNGSCFTVMTDGPSPNEQASYKI FKI EKGRVVKVELNAPNYHYEECSYDPAGEI TCVCRDNWHGS
 NRPWVSFNONLEYQI GYI CSGVFGDSPRPNDGTGCGPVSLNGAYGVKGFSEFKYGNVWI GRKSTSSRS
 GFEMI WDPNGWTE TDSSFSLKQDI I AI TDWSGYSGSFI QHELTGLNMRPCFWVELI RGRPKKEITI WTS
 GSSI SFCGVNSDVTGWSWPDDAELPFTI DK
 >gi |4324313|gb|AAD16791.1| neurami ni dase [Influenza A vi rus (A/HongKong/97/98(H5N1))]
 MNPNQKI I TI GSI CMVVG I SLMLQI GNTI SVWVSHI I KTWHPNOPEPCNQSI NFYTEQAAASVTLAGNS
 SLCPI SGWAI YSKDNSI RI GSKGDVFI REFFI SCSHLECRFTFFLTQGALLNDKHSNGTVKDRSPYRTLM
 SCPVGEAPSPYNSRFESVAWSASACHDGI SWLTI GI SGPDNGAVAVLKYNIGI I TDTI KSWRNNI LRTQES
 ECACVNGSCFTVMTDGPSPNEQASYKI FKI EKGRVVKVELNAPNYHYEECSYDPAGEI TCVCRDNWHGS
 NRPWVSFNONLEYQI GYI CSGVFGDSPRPNDGTGCGPVSLNGAYGVKGFSEFKYGNVWI GRKSTSSRS
 GFEMI WDPNGWTE TDSSFSLKQDI I AI TDWSGYSGSFI QHELTGLNMRPCFWVELI RGRPKKEITI WTS
 GSSI SFCGVNSDVTGWSWPDDAELPFTI DK
 >gi |47834892|gb|AAT39081.1| neurami ni dase [Influenza A vi rus (A/HK/212/03 (H5N1))]
 MNPNQKI TTI GSI CMVI GI VSLMLQI GNI I SI VVSHSI OTGNQHOAEPNCQSI I TYENNTWVNTQYVNI S
 NTNFLTEKAVASVTLAGNSSLCPI SGWAVYSKDNGI RI GSKGDVFI REFFI SCSHLECRFTFFLTQGALL
 NDKHSNGTVKDRSPHRTLMSCPVGEAPSPYNSRFESVAWSASACHDGT SWLTI GI SGPDNGAVAVLKYNIGI
 I I TDTI KSWRNNI MRTQESEACVNGSCFTVMTDGPSPNEQASYKI FRI EKGKVVKSAELNAPNYHYEECS
 YDPAGEI TCVCRDNWHGSNRPWVSFNONLEYRI GYI CSGVFGDNPRNDGTGCGPVSPNGAYGVKGFSEFKYGNVWI
 GRKSTSSRS GFEMI WDPNGWTE TDSSFSLKQDI I AI TDWSGYSGSFI QHELTGLNMRPCFWVELI RGRPKKEITI WTS
 GSSI SFCGVNSDVTGWSWPDDAELPFTI DK
 >gi |148340810|gb|ABQ58981.1| neurami ni dase [Influenza A vi rus
 (A/Bei j i ng/01/2003(H5N1))]
 MNPNQKI I TI GSI CMVI GI VSLMLQI GNI I SI VVSHSI OTGNQHOAEPNI SNTKFLTEKAVASVTLAGNSS
 LCPI SGWAVHSDNSI RI GSKGDVFI REFFI SCSHLECRFTFFLTQGALLNDKHSNGTVKDRSPHRTLM
 CPVGEAPSPYNSRFESVAWSASACHDGT SWLTI GI SGPDNGAVAVLKYNIGI I TDTI KSWRNNI LRTQES
 CACI NGSCFTVMTDGPSPNEQASYKI FKMEKGVVKSVELDAPNYHYEECSYDPAGEI TCVCRDNWHGS
 NRPWVSFNONLEYQI GYI CSGVFGDNPRNDGTGCGPVSPNGAYGVKGFSEFKYGNVWI GRKSTSSRS
 GFEMI WDPNGWTE TDSSFSLKQDI I AI TDWSGYSGSFI QHELTGLNMRPCFWVELI RGRPKKEITI WTS
 GSSI SFCGVNSDVTGWSWPDDAELPFTI DK
 >gi |71013506|dbj|BAE07203.1| neurami ni dase [Influenza A vi rus (A/Hong
 Kong/213/03(H5N1))]
 MNPNQKI TTI GSI CMVI GI VSLMLQI GNI I SI VVSHSI OTGNQHOAEPNCQSI I TYENNTWVNTQYVNI S
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 NDKHSNGTVKDRSPHRTLMSCPVGEAPSPYNSRFESVAWSASACHDGT SWLTI GI SGPDNGAVAVLKYNIGI
 I I TDTI KSWRNNI MRTQESEACVNGSCFTVMTDGPSPNEQASYKI FRI EKGKVVKSAELNAPNYHYEECS
 YDPAGEI TCVCRDNWHGSNRPWVSFNONLEYRI GYI CSGVFGDNPRNDGTGCGPVSPNGAYGVKGFSEFKYGNVWI
 GRKSTSSRS GFEMI WDPNGWTE TDSSFSLKQDI I AI TDWSGYSGSFI QHELTGLNMRPCFWVELI RGRPKKEITI WTS
 GSSI SFCGVNSDVTGWSWPDDAELPFTI DK
 >gi |47834894|gb|AAT39082.1| neurami ni dase [Influenza A vi rus (A/HK/213/03 (H5N1))]
 PNOKI TTI GSI CMVI GI VSLMLQI GNI I SI VVSHSI OTGNQHOAEPNCQSI I TYENNTWVNTQYVNI SNT
 NFLTEKAVASVTLAGNSSLCPI SGWAVYSKDNGI RI GSKGDVFI REFFI SCSHLECRFTFFLTQGALLND

KHSNGTVKDRSPHRTLMSCPVGEAPSPYNSRFESVAWSASACHDGTSWLTI GI SGPDNGAVAVLKYNIGI I
 YDTI KSWRNNI MRTQESEACVNGSCFTVMTDGPNSGOASYKI FRI EKGKVVKSAELNAPNYHYEECSY
 PDAGEI TCVCRDNWHGNSRNPWFNFONLEYRI GYI CSGVFGDNPRPNDGTGSCGPVSPKAYGI KGFSEK
 YGNGVWI GRKSTNSRSRSGFEMI WDPNGWTGTDNSFVSKQDI VAI TDWSGYSGSFVQHPPELTGLDCI RPCF
 WVELI RGRPKESTI WTSGSSI SFC

>gi |145284413|gb|ABP52010.1| neurami ni dase [Influenza A virus (A/Hong
 Kong/213/2003(H5N1))]
 MNPNQKI I TI GSI CMVI GI VSLMLOI GNLI SI WWSHSI OTGNQHOAEPNOSI I TYENNTWVNOQTVYVNI S
 NTNFLTEKAVASVTLAGNSSLCP I SGWAVYKDNIGI RI GSKGDVFI REFFI SCSHLECRFTFFLTQGALL
 NDKHSNGTVKDRSPHRTLMSCPVGEAPSPYNSRFESVAWSASACHDGTSWLTI GI SGPDNGAVAVLKYNIGI
 I I TDTI KSWRNNI MRTQESEACVNGSCFTVMTDGPNSGOASYKI FRI EKGKVVKSAELNAPNYHYEECS
 CYPDAGEI TCVCRDNWHGNSRNPWFNFONLEYRI GYI CSGVFGDNPRPNDGTGSCGPVSPKAYGI KGFSEK
 FKYGNGVWI GRKSTNSRSRSGFEMI WDPNGWTGTDNSFVSKQDI VAI TDWSGYSGSFVQHPPELTGLDCI RP
 CFWVELI RGRPKESTI WTSGSSI SFCGVNSDTVGWSWPDGAELPLT

>gi |145284415|gb|ABP52011.1| neurami ni dase [Influenza A virus
 (A/Thai Land/16/2004(H5N1))]
 MNPNKKI I TI GSI CMVTGMVSLMLOI GNLI SI WWSHSI HTGNQHOAEPNI SNTNFLTEKAVASVKL
 AGNSS LCPI NGWAVYKDNIGI RI GSKGDVFI REFFI SCSHLECRFTFFLTQGALLNDKHSNGTVKDRSPHRTLMS
 CPVGEAPSPYNSRFESVAWSASACHDGTSWLTI GI SGPDNGAVAVLKYNIGI I TDTI KSWRNNI LRTQ
 ESE CACVNGSCFTVMTDGPNSGOASHKI FKMEKGVVKSVELDAPNYHYEECSYCPDAGEI TCVCRDNWHGNS
 RNPWFNFONLEYQI GYI CSGVFGDNPRPNDGTGSCGPVSSNGAYGVKGFSEKYGNGVWI GRKSTNSRSRSG
 FEMI WDPNGWTETDSSFSVKQDI VAI TDWSGYSGSFVQHPPELTGLDCI RPCFWVELI RGRPKESTI WASG
 SSI SFCGVNSDTVGWSWPDGAELPFTI DK

>gi |145284421|gb|ABP52014.1| neurami ni dase [Influenza A virus
 (A/Thai Land/Chai yaphum/622/2004(H5N1))]
 MNPNKKI I TI GSI CMVTGMVSLMLOI GNLI SI WWSHSI HTGNQHOAEPNI SNTNFLTEKAVASVKL
 AGNSS LCPI NGWAVYKDNIGI RI GSKGDVFI REFFI SCSHLECRFTFFLTQGALLNDKHSNGTVKDRSPHRTLMS
 CPVGEAPSPYNSRFESVAWSASACHDGTSWLTI GI SGPDNGAVAVLKYNIGI I TDTI KSWRNNI LRTQ
 ESE CACVNGSCFTVMTDGPNSGOASHKI FKMEKGVVKSVELDAPNYHYEECSYCPDAGEI TCVCRDNWHGNS
 RNPWFNFONLEYQI GYI CSGVFGDNPRPNDGTGSCGPVSSNGAYGVKGFSEKYGNGVWI GRKSTNSRSRSG
 FEMI WDPNGWTETDSSFSVKQDI VAI TDWSGYSGSFVQHPPELTGLDCI RPCFWVELI RGRPKESTI WTSG
 SSI SFCGVNSDTVGWSWPDGAELPFTI DK

>gi |72398597|gb|AAZ72716.1| neurami ndase [Influenza A virus (A/Viet Nam/HG-
 178/2004(H5N1))]
 MNPNQKI I TI GSI CMVTGI VSLMLOVGNMI SI WWSHSI HTGNQHOAEPNI SNTNFLTEKAVASVKL
 AGNSS LCPI NGWAVYKDNIGI RI GSKGDVFI REFFI SCSHLECRFTFFLTQGALLNDKHSNGTVKDRSPHRTLMS
 CPVGEAPSPYNSRFESVAWSASACHDGTSWLTI GI SGPDNGAVAVLKYNIGI I TDTI KSWRNNI LRTQ
 ESE CACVNGSCFTVMTDGPNSGOASHKI FKMEKGVVKSVELDAPNYHYEECSYCPDAGEI TCVCRDNWHGNS
 RNPWFNFONLEYQI GYI CSGVFGDNPRPNDGTGSCGPVSSNGAYGVKGFSEKYGNGVWI GRKSTNSRSRSG
 FEMI WDPNGWTETDSSFSVKQDI VAI TDWSGYSGSFVQHPPELTGLDCI RPCFWVELI RGRPKESTI WTSG
 SSI SFCGVNSDTVGWSWPDGAELPFTI DK

>gi |93008563|gb|ABE97712.1| neurami ni dase [Influenza A virus
 (A/Vietnam/CL01/2004(H5N1))]
 MNPNQKI I TI GSI CMVTGI VSLMLOVGNMI SI WWSHSI HTGNQHOAEPNI SNTNFLTEKAVASVKL
 AGNSS LCPI NGWAVYKDNIGI RI GSKGDVFI REFFI SCSHLECRFTFFLTQGALLNDKHSNGTVKDRSPHRTLMS
 CPVGEAPSPYNSRFESVAWSASACHDGTSWLTI GI SGPDNGAVAVLKYNIGI I TDTI KSWRNNI LRTQ
 ESE CACVNGSCFTVMTDGPNSGOASHKI FKMEKGVVKSVELDAPNYHYEECSYCPDAGEI TCVCRDNWHGNS
 RNPWFNFONLEYQI GYI CSGVFGDNPRPNDGTGSCGPVSSNGAYGVKGFSEKYGNGVWI GRKSTNSRSRSG
 FEMI WDPNGWTETDSSFSVKQDI VAI TDWSGYSGSFVQHPPELTGLDCI RPCFWVELI RGRPKESTI WTSG
 SSI SFCGVNSDTVGWSWPDGAELPFTI DK

>gi |93008571|gb|ABE97712.1| neurami ni dase [Influenza A virus
 (A/Vietnam/CL26/2004(H5N1))]
 MNPNQKI I TI GSI CMVTGI VSLMLOVGNMI SI WWSHSI HTGNQHOAEPNI SNTNFLTEKAVASVKL
 AGNSS LCPI NGWAVYKDNIGI RI GSKGDVFI REFFI SCSHLECRFTFFLTQGALLNDKHSNGTVKDRSPHRTLMS
 CPVGEAPSPYNSRFESVAWSASACHDGTSWLTI GI SGPDNGAVAVLKYNIGI I TDTI KSWRNNI LRTQ
 ESE CACVNGSCFTVMTDGPNSGOASHKI FKMEKGVVKSVELDAPNYHYEECSYCPDAGEI TCVCRDNWHGNS
 RNPWFNFONLEYQI GYI CSGVFGDNPRPNDGTGSCGPVSSNGAYGVKGFSEKYGNGVWI GRKSTNSRSRSG
 FEMI WDPNGWTETDSSFSVKQDI VAI TDWSGYSGSFVQHPPELTGLDCI RPCFWVELI RGRPKESTI WTSG
 SSI SFCGVNSDTVGWSWPDGAELPFTI DK

>gi |134306634|gb|AB072355.1| neurami ni dase [Influenza A virus
 (A/Prachinburi/6231/2004(H5N1))]
 MNPNKKI I TI GSI CMVTGMVSLMLOI GNLI SI WWSHSI HTENQHOAEPNI SNTNLLTEKAVASVKL
 AGNSS LCPI NGWAVYKDNIGI RI GSKGDVFI REFFI SCSHLECRFTFFLTQGALLNDKHSNGTVKDRSPHRTLMS
 CPVGEAPSPYNSRFESVAWSASACHDGTSWLTI GI SGPDNGAVAVLKYNIGI I TDTI KSWRNNI LRTQ
 ESE CACVNGSCFTVMTDGPNSGOASHKI FKMEKGVVKSVELDAPNYHYEECSYCPDAGEI TCVCRDNWHGNS
 RNPWFNFONLEYQI GYI CSGVFGDNPRPNDGTGSCGPVSSNGAYGVKGFSEKYGNGVWI GRKSTNSRSRSG
 FEMI WDPNGWTETDSSFSVKQDI VAI TDWSGYSGSFVQHPPELTGLDCI RPCFWVELI RGRPKESTI WTSG
 SSI SFCGVNSDTVGWSWPDGAELPFTI DK

>gi |46360357|gb|AAS89005.1| neurami ni dase [Influenza A virus (A/Thai Land/3(SP-
 83)/2004(H5N1))]
 MNPNKKI I TI GSI CMVTGMVSLMLOI GNLI SI WWSHSI HTGNQHOAEPNI SNTNFLTEKAVASVKL
 AGNSS LCPI NGWAVYKDNIGI RI GSKGDVFI REFFI SCSHLECRFTFFLTQGALLNDKHSNGTVKDRSPHRTLMS
 CPVGEAPSPYNSRFESVAWSASACHDGTSWLTI GI SGPDNGAVAVLKYNIGI I TDTI KSWRNNI LRTQ
 ESE CACVNGSCFTVMTDGPNSGOASHKI FKMEKGVVKSVELDAPNYHYEECSYCPDAGEI TCVCRDNWHGNS
 RNPWFNFONLEYQI GYI CSGVFGDNPRPNDGTGSCGPVSSNGAYGVKGFSEKYGNGVWI GRKSTNSRSRSG
 FEMI WDPNGWTETDSSFSVKQDI VAI TDWSGYSGSFVQHPPELTGLDCI RPCFWVELI RGRPKESTI WTSG
 SSI SFCGVNSDTVGWSWPDGAELPFTI DK

>gi |113497374|gb|ABI 36476.1| neurami ni dase [Influenza A vi rus
(A/Indonesia/2006(H5N1))]
MNPNQKI I TI GSI CMVI GI VSLMLQI GNMI SI WWSHSI QKGNQHOAESI SNTNPLTEKAVASVTLAGNSS
LCPI RGWAVHVKDNNI RI GSKGDFVFI REPFI SCSHLECRTEFFLTQGALLNDKHSNGTVKDRSPHRTLMS
CPVGEAPSPYNSRFESVAWSASACHDGTSWLTI GI SGPDNEAVAVLKYNGI I TDTI KSWRNNI LRTQESE
CACVNGSCFTVMTDGPNSNGQASYKI FKMEKGGKVVKSVELDAPNYHYEECSYDPAGEI TCVCRDNWHGNS
RPWVFNQONLEYQI GYI CSGVFGDNPRPNDGTGSCGPMSPNGAYGVKGF SFKYNGVWI GRTKSTNSRSG
FEMI WDPNGWTGTDSSFSVKQDI VAI TDWSGYSGSFVQHPTELGLDCI RPCFWVELI RGRPKESTI WTSG
SSI SFCGVNSDTVSWSPDGAELPFTI DK

>gi |113497245|gb|ABI 36446.1| neurami ni dase [Influenza A vi rus
(A/Indonesia/2006(H5N1))]
MNPNQKI I TI GSI CMVI GI VSLMLQI GNMI SI WWSHSI QKGNQHOAESI SNTNPLTEKAVASVTLAGNSS
LCPI RGWAVHVKDNNI RI GSKGDFVFI REPFI SCSHLECRTEFFLTQGALLNDKHSNGTVKDRSPHRTLMS
CPVGEAPSPYNSRFESVAWSASACHDGTSWLTI GI SGPDNEAVAVLKYNGI I TDTI KSWRNNI LRTQESE
CACVNGSCFTVMTDGPNSNGQASYKI FKMEKGGKVVKSVELDAPNYHYEECSYDPAGEI TCVCRDNWHGNS
RPWI SFNQNLEYQI GYI CSGVFGDNPRPNDGTGSCGPMSPNGAYGVKGF SFKYNGVWI GRTKSTNSRSG
FEMI WDPNGWTGTDSSFSVKQDI VAI TDWSGYSGSFVQHPTELGLDCI RPCFWVELI RGRPKESTI WTSG
SSI SFCGVNSDTVSWSPDGAELPFTI DK

>gi |157955437|gb|ABW06116.1| neurami ni dase [Influenza A vi rus
(A/Indonesia/583H/2006(H5N1))]
MNPNQKI I TI GSI CMVI GI VSLMLQI GNMI SI WWSHSI QKGNQHOAESI SNTNPLTEKAVASVTLAGNSS
LCPI RGWAVHVKDNNI RI GSKGDFVFI REPFI SCSHLECRTEFFLTQGALLNDKHSNGTVKDRSPHRTLMS
CPVGEAPSPYNSRFESVAWSASACHDGTSWLTI GI SGPDNEAVAVLKYNGI I TDTI KSWRNNI LRTQESE
CACVNGSCFTVMTDGPNSNGQASYKI FKMEKGGKVVKSVELDAPNYHYEECSYDPAGEI TCVCRDNWHGNS
RPWI SFNQNLEYQI GYI CSGVFGDNPRPNDGTGSCGPMSPNGAYGVKGF SFKYNGVWI GRTKSTNSRSG
FEMI WDPNGWTGTDSSFSVKQDI VAI TDWSGYSGSFVQHPTELGLDCI RPCFWVELI RGRPKESTI WTSG
SSI SFCGVNSDTVSWSPDGAELP

>gi |113497198|gb|ABI 36435.1| neurami ni dase [Influenza A vi rus
(A/Indonesia/2006(H5N1))]
MNPNQKI I TI GSI CMVI GI VSLMLQI GNMI SI WWSHSI QKGNQHOAESI SNTNPLTEKAVASVTLAGNSS
LCPI RGWAVHVKDNNI RI GSKGDFVFI REPFI SCSHLECRTEFFLTQGALLNDKHSNGTVKDRSPHRTLMS
CPVGEAPSPYNSRFESVAWSASACHDGTSWLTI GI SGPDNEAVAVLKYNGI I TDTI KSWRNNI LRTQESE
CACVNGSCFTVMTDGPNSNGQASYKI FKMEKGGKVVKSVELDAPNYHYEECSYDPAGEI TCVCRDNWHGNS
RPWI SFNQNLEYQI GYI CSGVFGDNPRPNDGTGSCGPMSPNGAYGVKGF SFKYNGVWI GRTKSTNSRSG
FEMI WDPNGWTGTDSSFSVKQDI VAI TDWSGYSGSFVQHPTELGLDCI RPCFWVELI RGRPKESTI WTSG
SSI SFCGVNSDTVSWSPDGAELPFTI DK

>gi |113497296|gb|ABI 36457.1| neurami ni dase [Influenza A vi rus
(A/Indonesia/2006(H5N1))]
MNPNQKI I TI GSI CMVI GI VSLMLQI GNMI SI WWSHSI QKGNQHOAESI SNTNPLTEKAVASVTLAGNSS
LCPI RGWAVHVKDNNI RI GSKGDFVFI REPFI SCSHLECRTEFFLTQGALLNDKHSNGTVKDRSPHRTLMS
CPVGEAPSPYNSRFESVAWSASACHDGTSWLTI GI SGPDNEAVAVLKYNGI I TDTI KSWRNNI LRTQESE
CACVNGSCFTVMTDGPNSNGQASYKI FKMEKGGKVVKSVELDAPNYHYEECSYDPAGEI TCVCRDNWHGNS
RPWVFNQONLEYQI GYI CSGVFGDNPRPNDGTGSCGPMSPNGAYGVKGF SFKYNGVWI GRTKSTNSRSG
FEMI WDPNGWTGTDSSFSVKQDI VAI TDWSGYSGSFVQHPTELGLDCI RPCFWVELI RGRPKESTI WTSG
SSI SFCGVNSDTVSWSPDGAELPFTI DK

>gi |157955475|gb|ABW06138.1| neurami ni dase [Influenza A vi rus
(A/Indonesia/604H/2006(H5N1))]
MNPNQKI I TI GSI CMVI GI VSLMLQI GNMI SI WWSHSI QKGNQHOAESI SNTNPLTEKAVASVTLAGNSS
LCPI RGWAVHVKDNNI RI GSKGDFVFI REPFI SCSHLECRTEFFLTQGALLNDKHSNGTVKDRSPHRTLMS
CPVGEAPSPYNSRFESVAWSASACHDGTSWLTI GI SGPDNEAVAVLKYNGI I TDTI KSWRNNI LRTQESE
CACVNGSCFTVMTDGPNSNGQASYKI FKMEKGGKVVKSVELDAPNYHYEECSYDPAGEI TCVCRDNWHGNS
RPWVFNQONLEYQI GYI CSGVFGDNPRPNDGTGSCGPMSPNGAYGVKGF SFKYNGVWI GRTKSTNSRSG
FEMI WDPNGWTGTDSSFSVKQDI VAI TDWSGYSGSFVQHPTELGLDCI RPCFWVELI RGRPKESTI WTSG
SSI SFCGVNSDTVSWSPDGAELPFTI DK

>gi |113972297|gb|ABI 49398.1| neurami ni dase [Influenza A vi rus
(A/Indonesia/2006(H5N1))]
MNPNQKI I TI GSI CMVI GI VSLMLQI GNMI SI WWSHSI QKGNQHOAESI SNTNPLTEKAVASVTLAGNSS
LCPI RGWAVHVKDNNI RI GSKGDFVFI REPFI SCSHLECRTEFFLTQGALLNDKHSNGTVKDRSPHRTLMS
CPVGEAPSPYNSRFESVAWSASACHDGTSWLTI GI SGPDNEAVAVLKYNGI I TDTI KSWRNNI LRTQESE
CACVNGSCFTVMTDGPNSNGQASYKI FKMEKGGKVVKSVELDAPNYHYEECSYDPAGEI TCVCRDNWHGNS
RPWVFNQONLEYQI GYI CSGVFGDNPRPNDGTGSCGPMSPNGAYGVKGF SFKYNGVWI GRTKSTNSRSG
FEMI WDPNGWTGTDSSFSVKQDI VAI TDWSGYSGSFVQHPTELGLDCI RPCFWVELI RGRPKESTI WTSG
SSI SFCGVNSDTVSWSPDGAELPFTI DK

>gi |113972316|gb|ABI 49409.1| neurami ni dase [Influenza A vi rus
(A/Indonesia/2006(H5N1))]
MNPNRKI I TI GSI CMVI GMVSLMLQI GNMI SI WWSHSI QKGNQHOAESI SNTNPLTEKAVASVTLAGNSS
LCPI RGWAVHVKDNNI RI GSKGDFVFI REPFI SCSHLECRTEFFLTQGALLNDKHSNGTVKDRSPHRTLMS
CPVGEAPSPYNSRFESVAWSASACHDGTSWLTI GI SGPDNEAVAVLKYNGI I TDTI KSWRNNI LRTQESE
CACVNGSCFTVMTDGPNSNGQASYKI FKMEKGGKVVKSVELDAPNYHYEECSYDPAGEI TCVCRDNWHGNS
RPWVFNQONLEYQI GYI CSGVFGDNPRPNDGTGSCGPMSPNGAYGVKGF SFKYNGVWI GRTKSTNSRSG
FEMI WDPNGWTGTDSSFSVKQDI VAI TDWSGYSGSFVQHPTELGLDCI RPCFWVELI RGRPKESTI WTSG
SSI SFCGVNSDTASWSPDGAELPFTI DK

>gi |118864141|gb|ABL31746.1| neurami ni dase [Influenza A vi rus
(A/Indonesia/2006(H5N1))]
MNPNQKI I TI GSI CMVI GI VSLMLQI GNMI SI WWSHSI QKGNQHOAESI SNTNPLTEKAVASVTLAGNSS
LCPI RGWAVHVKDNNI RI GSKGDFVFI REPFI SCSHLECRTEFFLTQGALLNDKHSNGTVKDRSPHRTLMS
CPVGEAPSPYNSRFESVAWSASACHDGTSWLTI GI SGPDNEAVAVLKYNGI I TDTI KSWRNNI LRTQESE

CACVNGSCFTVMTDGPNSGQASYKI FKMEKGGKVVKSVELDAPNYHYEECSCYPDAGEI TCVCRDNWHGNS
 RPWVSNQNLLEYQI GYI CSGVFGDNPRPNDGTGSCGPMSPNGAYGVKGFSSFKYNGVWI GRKSTNSRSR
 FEMI WDPNGWTGTDSSFSVKQDI VAI TDWSGYSGSFVQHPGLTGLDCI RPCFWVELI RGRPKESTI WTS
 SSI SFCGVNSDTSVSWSPDGAELPFTI DK
 >gi |118864192|gb|ABL31757.1| neurami ni dase [Influenza A vi rus
 (A/I ndonesi a/CDC836/2006(H5N1))]
 MNPNQKI I TI GSI CMVI GI VSLMLQI GNMI SI WVSHSI QTGNQHOAESI SNTNPLTEKAVASVTLAGNSS
 LCPI RGWAVHSDNNI RI GSKGDV FVI REPFI SCSHLECRTFFLTQGALLNDKHSNGTVKDRSPHRTLMS
 CPVGEAPSPYNSRFESVAWSASACHDGT SWLTI GI SGPDNEAVAVLK YNGI I TDTI KSWRNNI LRTQESE
 CACVNGSCFTVMTDGPNSGQASYKI FKMEKGGKVVKSVELDAPNYHYEECSCYPDAGEI TCVCRDNWHGNS
 RPWVSNQNLLEYQI GYI CSGVFGDNPRPNDGTGSCGPMSPNGAYGVKGFSSFKYNGVWI GRKSTNSRSR
 FEMI WDPNGWTGTDSSFSVKQDI VAI TDWSGYSGSFVQHPGLTGLDCI RPCFWVELI RGRPKESTI WTS
 SSI SFCGVNSDTSVSWSPDGAELPFTI DK
 >gi |118864235|gb|ABL31768.1| neurami ni dase [Influenza A vi rus
 (A/I ndonesi a/CDC836T/2006(H5N1))]
 MNPNQKI I TI GSI CMVI GI VSLMLQI GNMI SI WVSHSI QTGNQHOAESI SNTNPLTEKAVASVTLAGNSS
 LCPI RGWAVHSDNNI RI GSKGDV FVI REPFI SCSHLECRTFFLTQGALLNDKHSNGTVKDRSPHRTLMS
 CPVGEAPSPYNSRFESVAWSASACHDGT SWLTI GI SGPDNEAVAVLK YNGI I TDTI KSWRNNI LRTQESE
 CACVNGSCFTVMTDGPNSGQASYKI FKMEKGGKVVKSVELDAPNYHYEECSCYPDAGEI TCVCRDNWHGNS
 RPWVSNQNLLEYQI GYI CSGVFGDNPRPNDGTGSCGPMSPNGAYGVKGFSSFKYNGVWI GRKSTNSRSR
 FEMI WDPNGWTGTDSSFSVKQDI VAI TDWSGYSGSFVQHPGLTGLDCI RPCFWVELI RGRPKESTI WTS
 SSI SFCGVNSDTSVSWSPDGAELPFTI DK
 >gi |122913049|gb|ABM68050.1| neurami ni dase [Influenza A vi rus (A/Egypt/12374-
 NAMRU3/2006(H5N1))]
 MNPNQKI I TI GSI CMVI GI VSLMLQI GNMI SI WVSHSI QTGNQCOAEPI SNTKFLTEKAVASVTLAGNSS
 LCPI SGWAVYSKDNSI RI GSRGDV FVI REPFI SCSHLECRTFFLTQGALLNDKHSNGTVKDRSPHRTLMS
 CPVGEAPSPYNSRFESVAWSASACHDGT SWLTI GI SGPDNEAVAVLK YNGI I TDTI KSWRNNI LRTQESE
 CACVNGSCFTVMTDGPSSGQASYKI FKMEKGGKVVKSVELDAPNYHYEECSCYPDAGEI TCVCRDNWHGNS
 RPWVSNQNLLEYQI GYI CSGVFGDNPRPNDGTGSCGPMSPNGAYGVKGFSSFKYNGVWI GRKSTNSRSR
 FEMI WDPNGWTGTDSSFSVKQDI VAI TDWSGYSGSFVQHPGLTGLDCI RPCFWVELI RGRPKESTI WTS
 SSI SFCGVNSDTSVSWSPDGAELPFTI DK
 >gi |118864393|gb|ABL31782.1| neurami ni dase [Influenza A vi rus
 (A/I ndonesi a/CDC887/2006(H5N1))]
 MNPNQKI I TI GSI CMVI GI VSLMLQI GNMI SI WVSHSI QKGNQHOAESI SNTNPLTEKAVASVTLAGNSS
 LCPI RGWAVHSDNNI RI GSKGDV FVI REPFI SCSHLECRTFFLTQGALLNDKHSNGTVKDRSPHRTLMS
 CPVGEAPSPYNSRFESVAWSASACHDGT SWLTI GI SGPDNEAVAVLK YNGI I TDTI KSWRNNI LRTQESE
 CACVNGSCFTVMTDGPNSGQASYKI FKMKKGGKVVKSVELDAPNYHYEECSCYPDAGEI TCVCRDNWHGNS
 RPWVSNQNLLEYQI GYI CSGVFGDNPRPNDGTGSCGPMSPNGAYGVKGFSSFKYNGVWI GRKSTNSRSR
 FEMI WDPNGWTGTDSSFSVKQDI VAI TDWSGYSGSFVQHPGLTGLDCI RPCFWVELI RGRPKESTI WTS
 SSI SFCGVNSDTSVSWSPDGAELPFTI DK
 >gi |118574893|gb|ABL07021.1| neurami ni dase [Influenza A vi rus
 (A/I ndonesi a/CDC938E/2006(H5N1))]
 MNPNQKI I TI GSI CMVI GI VSLMLQI GNMI SI WVSHSI QKGNQHOAESI SNTNPLTEKAVASI TLAGNSS
 LCPI RGWAVHSDNNI RI GSKGDV FVI REPFI SCSHLECRTFFLTQGALLNDKHSNGTVKDRSPHRTLMS
 CPVGEAPSPYNSRFESVAWSASACHDGT SWLTI GI SGPDNEAVAVLK YNGI I TDTI KSWRNNI LRTQESE
 CACVNGSCFTVMTDGPNSGQASYKI FKMKKGGKVVKSVELDAPNYHYEECSCYPDAGEI TCVCRDNWHGNS
 RPWVSNQNLLEYQI GYI CSGVFGDNPRPNDGTGSCGPMSPNGAYGVKGFSSFKYNGVWI GRKSTNSRSR
 FEMI WDPNGWTGTDSSFSVKQDI VAI TDWSGYSGSFVQHPGLTGLDCI RPCFWVELI RGRPKESTI WTS
 SSI SFCGVNSDTSVSWSPDGAELPFTI DK
 >gi |118574874|gb|ABL07010.1| neurami ni dase [Influenza A vi rus
 (A/I ndonesi a/CDC938/2006(H5N1))]
 MNPNQKI I TI GSI CMVI GI VSLMLQI GNMI SI WVSHSI QKGNQHOAESI SNTNPLTEKAVASI TLAGNSS
 LCPI RGWAVHSDNNI RI GSKGDV FVI REPFI SCSHLECRTFFLTQGALLNDKHSNGTVKDRSPHRTLMS
 CPVGEAPSPYNSRFESVAWSASACHDGT SWLTI GI SGPDNEAVAVLK YNGI I TDTI KSWRNNI LRTQESE
 CACVNGSCFTVMTDGPNSGQASYKI FKMKKGGKVVKSVELDAPNYHYEECSCYPDAGEI TCVCRDNWHGNS
 RPWVSNQNLLEYQI GYI CSGVFGDNPRPNDGTGSCGPMSPNGAYGVKGFSSFKYNGVWI GRKSTNSRSR
 FEMI WDPNGWTGTDSSFSVKQDI VAI TDWSGYSGSFVQHPGLTGLDCI RPCFWVELI RGRPKESTI WTS
 SSI SFCGVNSDTSVSWSPDGAELPFTI DK
 >gi |118574912|gb|ABL07032.1| neurami ni dase [Influenza A vi rus
 (A/I ndonesi a/CDC940/2006(H5N1))]
 MNPNQKI I TI GSI CMVI GI VSLMLQI GNMI SI WVSHSI QTGNQYQAEPI SNTNPLTEKAVASVTLAGNSS
 LCPI RGWAVHSDNNI RI GSKGDV FVI REPFI SCSHLECRTFFLTQGALLNDKHSNGTVKDRSPHRTLMS
 CPVGEAPSPYNSRFESVAWSASACHDGT SWLTI GI SGPDNEAVAVLK YNGI I TDTI KSWRNNI LRTQESE
 CACVNGSCFTVMTDGPNSGQASYKI FKMEKGGKVVKSVELDAPNYHYEECSCYPDAGEI TCVCRDNWHGNS
 RPWVSNQNLLEYQI GYI CSGVFGDNPRPNDGTGSCGPMSPNGAYGVKGFSSFKYNGVWI GRKSTNSRSR
 FEMI WDPNGWTGTDSSFSVKQDI VAI TDWSGYSGSFVQHPGLTGLDCI RPCFWVELI RGRPKESTI WTS
 SSI SFCGVNSDTSVSWSPDGAELPFTI DK
 >gi |122913045|gb|ABM68048.1| neurami ni dase [Influenza A vi rus (A/Egypt/14725-
 NAMRU3/2006(H5N1))]
 MNPNQKI I TI GSI CMVI GI VSLMLQI GNI I SI WI SHSI QTGNQCOAGPI SNTKFLTEKAVASVTLAGNSS
 LCPI SGWAVYSKDNSI RI GSRGDV FVI RESFI SCSHLECRTFFLTQGALLNDKHSNGTVKDRSPHRTLMS
 CPVGEAPSPYNSRFESVAWSASACHDGT SWLTI GI SGPDNEAVAVLK YNGI I TDTI KSWRNNI LRTQESE
 CACVNGSCFTVMTDGPNSGQASYKI FKMEKGGKVVKSVELDAPNYHYEECSCYPDAGEI TCVCRDWHGNS
 RPWVSNQNLLEYQI GYI CSGVFGDNPRPNDGTGSCGPMSPNGAYGVKGFSSFKYNGVWI GRKSTNSRSR
 FEMI WDPNGWTGTDSSFSVKQDI VAI TDWSGYSGSFVQHPGLTGLDCI RPCFWVELI RGRPKESTI WTS
 SSI SFCGVNSDTSVSWSPDGAELPFTI DK

>gi |122913047|gb|ABM68049.1| neurami ni dase [Influenza A virus (A/Egypt/14724-NAMRU3/2006 (H5N1))]
MNPNQKI I TI GSI CMVI GI VSLMLQI GNI I SI WI SHSI QTGNQCOAEPI SNTKFLTEKAVASVTLAGNSS
LCPI SGWAVYSKDNSI RI GSRGDFVFI REPFI SCSHLECRTEFFLTQGALLNDKHSNGTVKDRSPHRTLMS
CPVGEAPSPYNSRFESVAWSASACHDGTSWLTI GI SGPDNGAVAVLKYNGI I TDTI KSWRNNI LRTQESE
CACVNGSCFTVMTDGPSSGQASYKI FKMEKGGVVKSVELDAPNYHYEECSYDPAGEI TCVCRDNWHGNS
RPWVFNQONLEYQI GYI CSGVFGDNPRPNDGTGSCGPVSPNGAYGVKGF SFKYNGVWI GRKSTNSRSG
FEMI WDPNGWTGTDSSFSVKQDI VAI TDWSGYSGSFVQHPTELGLDCI RPCFWVELI RGRPKESTI WTSG
SSI SFCGVNSDTVWSWPDGAELPFTI DK

>gi |162569004|gb|ABY19421.1| neurami ni dase [Influenza A virus (A/Viet Nam/HN31242/2007 (H5N1))]
MNPNQKI I TI GSI CMVI GI VSLMLQI GNI SI WWSHSI QTGNQOQVEPI I NTNFLT GKAVASI TLAGNSS
LCPI RGWAI HSKDNSI RI GSKGDFVFI REPFI SCSHLECRTEFFLTQGALLNDKHSNGTVKDRSPHRTLMS
CPVGEAPSPYNSRFESVAWSASACHDGTSWLTI GI SGPDNGAVAVLKYNGI I TDTI KSWRNNI LRTQESE
CACVNGSCFTVMTDGPSSGQASYKI FKMEKGGVVKSVELDAPNYHYEECSYDPAGEI TCVCRDNWHGNS
RPWVFNQONLEYQI GYI CSGVFGDNPRPNDGTGSCGPVSHNGAYGVKGF SFKYNGVWI GRKSTNSRSG
FEMI WDPNGWSETDSSFSVKQDI VAI TDWSGYSGSFVQHPTELGLDCI RPCFWVELI RGRPKESTVWTS
SSI SFCGVNSDTVWSWPDGAELPFTI DK

>gi |182382601|gb|ACB87576.1| neurami ni dase [Influenza A virus (A/Ji angsu/1/2007 (H5N1))]
MNPNQKI I TI GSI CMVI GI VSLMLQI GNI I SI WWSHSI QTGNQHQDEPI RNANFLTENAVASVTLAGNSS
LCPVIRGWAHVSKDNSI RI GSKGDFVFI REPFI SCSHLECRTEFFLTQGALLNDKHSNGTVKDRSPHRTLMS
CPVGEAPSPYNSRFESVAWSASACHDGTSWLTI GI SGPDNGAVAVLKYNGI I TDTI KSWRNNI LRTQESE
CACVNGSCFTVMTDGPSSGQASYKI FKMEKGGVVKSVELNAPNYHYEECSYDPAGEI TCVCRDNWHGNS
RPWVFNQONLEYQI GYI CSGVFGDNPRPNDGTGSCDPVSPNGAYGI KGF SFKYNGVWI GRKSTNSRSG
FEMI WDPNGWTE TDSSFSVKQDI VAI TDWSGYSGSFVQHPTELGLDCI RPCFWVELI RGRPKESTI WTS
SSI SFCGVNSDTVWSWPDGAELPFTI DK

>gi |85680902|gb|ABC72646.1| neurami ni dase [Influenza A virus (A/Thailand/676/2005 (H5N1))]
MNPNKKI I TI GSI CMVTGMVSLMLQI GNLI SI WWSHSI HTGNQOQAEPI SNTNFLT EKAVASV KLAGNSS
LCPI NGWAVYSKDNSI RI GSKGDFVFI REPFI SCSHLECRTEFFLTQGSLLNDKHSNGTVKDRSPHRTLMS
CPVGEAPSPYNSRFESVAWSASACHDGTSWLTI GI SGPDSGAVAVLKYNGI I TDTI KSWRNNI LRTQESE
CACVNGSCFTVMTDGPSSGQASHKI FKMEKGGVVKSVELNAPNYHYEECSYDPAGEI TCVCRDNWHGNS
RPWVFNQONLEYQI GYI CSGVFGDTPRPNDGTGSCGPVSSNGTYGVKGF SFKYNGVWI GRKSTNSRSG
FEMI WDPNGWTE TDSSFSVKQDI VAI TDWSGYSGSFVQHPTELGLDCI RPCFWVELI RGRPKESTI WTS
SSI SFCGVNSDTVWSWPDGAELPFTI DK

>gi |116295114|gb|ABJ98530.1| neurami ni dase [Influenza A virus (A/Thailand/RNP/2005 (H5N1))]
KQEFKMNPNKKI I TI GSI CMVTGMVSLMLQI GNLI SI WLSRSI HTGNQOQAEPI SNTNFLT EKAVASV KL
AGNSSLCPI NGWAVYSKDNSI RI GSKGDFVFI REPFI SCSHLECRTEFFLTQGSLLNDKHSNGTVKDRSPH
RTLMSCPVGEAPSPYNSRFESVAWSASACHDGTSWLTI GI SGPDSGAVAVLKYNGI I TDTI KSWRNNI LRTQESE
TOESEACVNGSCFTVMTDGPSSGQASHKI FKMEKGGVVKSVELNAPNYHYEECSYDPAGEI TCVCRDNWHGNS
WHGNSRNPWVFNQONLEYQI GYI CSGVFGDTPRPNDGTGSCGPVSSNGTYGVKGF SFKYNGVWI GRKST
NSRSGFEMI WDPNGWTE TDSSFSVKQDI VAI TDWSGYSGSFVQHPTELGLDCI RPCFWVELI RGRPKEST
I WTSGSSI SFCGVNSDTVGGSWP

>gi |126361912|gb|AB010178.1| neurami ni dase [Influenza A virus (A/Viet Nam/JP4207/2005 (H5N1))]
MNPNQKI I TI GSI CMVTGI VSLMLQVGNMI SI WWSHSI HTGNQHQAEPI SNTNFLT EKAVASV KLAGNSS
LCPI NGWAVYSKDNSI RI GSKGDFVFI REPFI SCSHLECRTEFFLTQGALLNDKHSNGTVKDRSPHRTLMS
CPVGEAPSPYNSRFESVAWSASACHDGTSWLTI GI SGPDNGAVAVLKYNGI I TDTI KSWRNNI LRTQESE
CACVNGSCFTVMTDGPSSGQASHKI FKMEKGGVVKSVELDAPNYHYEECSYDPAGEI TCVCRDNWHGNS
RPWVFNQONLEYQI GYI CSGVFGDNPRPNDGTGSCGPVSSNGAYGVKGF SFKYNGVWI GRKSTNSRSG
FEMI WDPNGWTE TDSSFSVKQDI VAI TDWSGYSGSFVQHPTELGLDCI RPCFWVELI RGRPKESTI WTS
SSI SFCGVNSDTVWSWPDGAELPFTI DK

>gi |78096578|dbj|BAE46950.1| neurami ni dase [Influenza A virus (A/Hanoi /30408/2005 (H5N1))]
MNPNQKI I TI GSI CMVTGI VSLMLQI GNI SI WWSHSI HTGNQHQSEPI SNTKFLTEKAVASV KLAGNSS
LCPI NGWAVYSKDNSI RI GSKGDFVFI REPFI SCSHLECRTEFFLTQGALLNDKHSNGTVKDRSPHRTLMS
CPVGEAPSPYNSRFESVAWSASACHDGTSWLTI GI SGPDNGAVAVV KYNGI I TDTI KSWRNNI LRTQESE
CACVNGSCFTVMTDGPSSGQASHKI FKMEKGGVVKSVELDAPNYHYEECSYDPAGEI TCVCRDNWHGNS
RPWVFNQONLEYQI GYI CSGVFGDNPRPNDGTGSCGPVSSNGAYGVKGF SFKYNGVWI GRKSTNSRSG
FEMI WDPNGWTE TDSSFSVKQDI VAI TDWSGYSGSFVQHPTELGLDCI RPCFWVELI RGRPKESTI WTS
SSI SFCGVNSDTVWSWPDGAELPFTI DK

>gi |95116895|gb|ABF56651.1| neurami ni dase [Influenza A virus (A/Vietnam/PEV16T/2005 (H5N1))]
MNPNQKI I TI GSI CMVTGI VSLMLQVGNMI SI WWSHSI HTGSQHQAEPI SNTNFLT EKAVASV KLAGNSS
LCPI NGWAVYSKDNSI RI GSKGDFVFI REPFI SCSHLECRTEFFLTQGALLNDKHSNGTVKDRSPHRTLMS
CPVGEAPSPYNSRFESVAWSASACHDGTSWLTI GI SGPDNGAVAVLKYNGI I TDTI KSWRNNI LRTQESE
CACVNGSCFTVMTDGPSSGQASHKI FKMEKGGVVKSVELDAPNYHYEECSYDPAGEI TCVCRDNWHGNS
RPWVFNQONLEYQI GYI CSGVFGDNPRPNDGTGSCGPVSSNGAYGVKGF SFKYNGVWI GRKSTNSRSG
FEMI WDPNGWTE TDSSFSVKQDI VAI TDWSGYSGSFVQHPTELGLDCI RPCFWVELI RGRPKESTI WTS
SSI SFCGVNSDTVWSWPDGAELPFTI DK

>gi |116295106|gb|ABJ98526.1| neurami ni dase [Influenza A virus (A/Thailand/NKNP/2005 (H5N1))]
KTI EI I TI GSI CMVTGMVSLMLQI GNLDLNMGPFPYSHRAQHKAEPI SNTNFLT EKAVASV KLAGNSSLC
PI NGWAVYSKDNSI RI GSKGDFVFI REPFI SCSHLQCRTEFFLTQGALLNDKHSNGTVKDRSPHRTLMSCP
VGEAPSPYNSRFESVAWSASACHDGTSWLTI GI SGPDNGAVAVLKYNGI I TDTI KSWRNNI LRTQESECA

CVNGSCFTVMTDGPNSGOASHKI FQNGKRGKVVKSQVLDAPHYHYEECSRYPDAREI TCVCRDNWHGNSR
 PWVSNQNLLEYQI GYI CSGVFGDNPRPNDGTGSCGVPSSNGAYGVKGFYKNGVWI GRTKSTNSRSRG
 EMI WDPNGWTE TDSSFSVKQDI VAI TDWSGYSGSFVQHPPELTGLDCI RPCFWVELI RGRPKESTI WTS
 SSI SFCGVNSDTPVGSWPDGAELPFT

>gi |116295110|gb|ABJ98528.1| neurami ni dase [Influenza A virus
 (A/Thai Land/RPFE/2005(H5N1))]

FSGSQKQEFKMNPNKKI I TI GSI CMVTGMVSLMLQI GNLI SI WVSHSI HTGNOHKAXPI SNTNFLT
 EKAVASVKLAGNSS LCPI NGWAVYSKDNSI RI GSKGDV FVI REPFI SCSHLECRTFFLTQGALLNDKHSNGT
 VKDRSPHRTLMSCPVGEAPSPYNSRFESVAWSASACHDGT SWLTI GI SGPONGAVAVLKYNIGI I TDTI
 KSWRNNI LRTQESE CACVNGSCFTVMTDGPNSGOASHKI FKMEKGGKLVLDAPNYHYEECS
 CYPDAGEI TCVCRDNWHGNSR PWVSNQNLLEYQI GYI CSGVFGDTPRPNDGTGSCGVPSSNGT
 YGVKGFYKNGVWI GRTKSTNSRSRG FEMI WDPNGWTE TDSSFSVKQDI VAI TDWSGYSGSFVQHP
 PELTGLNCI RPCFWVELI RGRPK ERAI WNSGNSI SFYGEKHTVGSWPDGAELPFT

>gi |116295120|gb|ABJ98533.1| neurami ni dase [Influenza A virus
 (A/Thai Land/NA60/2005(H5N1))]

MNPNKKI I TI GSI CMVTGMVSLMLQI GNLI SI WVSHSI HTGNOHKAPEI SNTNFLT
 EKAVASVKLAGNSS LCPI NGWAVYSKDNSI RI GSKGDV FVI REPFI SCSHLECRTFFLTQGALLNDKHSNGT
 VKDRSPHRTLMSCPVGEAPSPYNSRFESVAWSASACHDGT SWLTI GI SGPONGAVAVLKYNIGI I TDTI
 KSWRNNI LRTQESE CACVNGSCFTVMTDGPNSGOASHKI FKMEKGGKLVLDAPNYHYEECS
 CYPDAGEI TCVCRDNWHGNSR PWVSNQNLLEYQI GYI CSGVFGDTPRPNDGTGSCGVPSSNGAYGVKGF
 YKNGVWI GRTKSTNSRSRG FEMI WDPNGWTE TDSSFSVKQDI VAI TDWSGYSGSFVQHPPELTGLDCI
 RPCFWVELI RGRPKESTI WTS SSI SFCGVNSDTPVGSWPDGAELPFTI DKY

>gi |126361908|gb|AB010176.1| neurami ni dase [Influenza A virus
 (A/Cambodi a/JP52a/2005(H5N1))]

MNPNQKI I TI GSI CMVTGI ASLMLQI GNMI SI WVSHSI HTGNOHQAPEI SNTNFLT
 EKAVASVKLAGNSS LCPI NGWAVYSKDNSI RI GSKGDV FVI REPFI SCSHLECRTFFLTQGALLNDKHSNGT
 VKDRSPHRTLMSCPVGEAPSPYNSRFESVAWSASACHDGT SWLTI GI SGPONGAVAVLKYNIGI I TDTI
 KSWRNNI LRTQESE CACVNGSCFTVMTDGPNSGOASHKI FKMEKGGKLVLDAPNYHYEECS
 CYPDAGEI TCVCRDNWHGNSR PWVSNQNLLEYQI GYI CSGVFGDTPRPNDGTGSCGVPSSNGAYGVKGF
 YKNGVWI GRTKSTNSRSRG FEMI WDPNGWTE TDSSFSVKQDI VAI TDWSGYSGSFVQHPPELTGLDCI
 RPCFWVELI RGRPKESTI WTS SSI SFCGVNSDTPVGSWPDGAELPFTI DK

>gi |157955787|gb|ABW06314.1| neurami ni dase [Influenza A virus
 (A/Indonesi a/245H/2005(H5N1))]

MNPNQKI I TI GSI CMVI GI VSLMLQI GNMI SI WVSHSI OTGNOHQAPEI SNTNPLTEKAVASVTL
 LAGNSS LCPI RGWAVHSKDNSI RI GSKGDV FVI REPFI SCSHLECRTFFLTQGALLNDKHSNGT
 VKDRSPHRTLMSCPVGEAPSPYNSRFESVAWSASACHDGT SWLTI GI SGPONGAVAVLKYNIGI I TDTI
 KSWRNNI LRTQESE CACVNGSCFTVMTDGPNSGOASYKI FKMEKGGKLVLDAPNYHYEECS
 CYPDAGEI TCVCRDNWHGNSR PWVSNQNLLEYQI GYI CSGVFGDTPRPNDGTGSCGVPSSNGAYGVKGF
 YKNGVWI GRTKSTNSRSRG FEMI WDPNGWTE TDSSFSVKQDI VAI TDWSGYSGSFVQHPPELTGLDCI
 RPCFWVELI RGRPKESTI WTS SSI SFCGVNSDTPVGSWPDGAELPFTI DK

>gi |113707438|gb|ABI 16506.1| neurami ni dase [Influenza A virus
 (A/Chi na/GD01/2006(H5N1))]

MNPNQKI I TI GSI CMVI GI VSLMLQI GNMI SI WVSHSI OTGNOHQVEPI SNTNPLTEKAVASVTL
 LAGNSS LCPI RGWAVHSKDNSI RI GSKGDV FVI REPFI SCSHLECRTFFLTQGALLNDKHSNGT
 VKDRSPHRTLMSCPVGEAPSPYNSRFESVAWSASACHDGT SWLTI GI SGPONGAVAVLKYNIGI I TDTI
 KSWRNNI LRTQESE CACVNGSCFTVMTDGPNSGOASYKI FKMEKGGKLVLDAPNYHYEECS
 CYPDAGEI TCVCRDNWHGNSR PWVSNQNLLEYQI GYI CSGVFGDTPRPNDGTGSCGVPSSNGAYGVKGF
 YKNGVWI GRTKSPSSRSRG FEMI WDPNGWTE TDSSFSVKQDI VAI TDWSGYSGSFVQHPPELTGLDCI
 RPCFWVELI RGRPKESTI WTS SSI SFCGVNSDTPVGSWPDGAELPFTI DK

>gi |157103086|gb|ABV23953.1| neurami ni dase [Influenza A virus (A/Azerbaijan/001-
 161/2006(H5N1))]

MNPNQKI I TI GSI CMVI GI VSLMLQI GNMI SI WVSHSI OTGNORQAPEI SNTKFLTEKAVASVTL
 LAGNSS LCPI SGWAVYSKDNSI RI GSRGDV FVI REPFI SCSHLECRTFFLTQGALLNDKHSNGT
 VKDRSPHRTLMSCPVGEAPSPYNSRFESVAWSASACHDGT SWLTI GI SGPONGAVAVLKYNIGI I TDTI
 KSWRNNI LRTQESE CACVNGSCFTVMTDGPNSGOASYKI FKMEKGGKLVLDAPNYHYEECS
 CYPDAGEI TCVCRDNWHGNSR PWVSNQNLLEYQI GYI CSGVFGDTPRPNDGTGSCGVPSSNGAYGVKGF
 YKNGVWI GRTKSTNSRSRG FEMI WDPNGWTE TDSSFSVKQDI VAI TDWSGYSGSFVQHPPELTGLDCI
 RPCFWVELI RGRPKESTI WTS SSI SFCGVNSDTPVGSWPDGAELPFTI DK

>gi |157103100|gb|ABV23961.1| neurami ni dase [Influenza A virus (A/Azerbaijan/011-
 162/2006(H5N1))]

NPQKI I TI GSI CMVI GI VSLMLQI GNMI SI WVSHSI OTGNORQAPEI SNTKFLTEKAVASVTL
 LAGNSS LCPI SGWAVYSKDNSI RI GSRGDV FVI REPFI SCSHLECRTFFLTQGALLNDKHSNGT
 VKDRSPHRTLMSCPVGEAPSPYNSRFESVAWSASACHDGT SWLTI GI SGPONGAVAVLKYNIGI I TDTI
 KSWRNNI LRTQESE CACVNGSCFTVMTDGPNSGOASYKI FKMEKGGKLVLDAPNYHYEECS
 CYPDAGEI TCVCRDNWHGNSR PWVSNQNLLEYQI GYI CSGVFGDTPRPNDGTGSCGVPSSNGAYGVKGF
 YKNGVWI GRTKSTNSRSRG FEMI WDPNGWTE TDSSFSVKQDI VAI TDWSGYSGSFVQHPPELTGLDCI
 RPCFWVELI RGRPKESTI WTS SSI SFCGVNSDTPVGSWPDGAELPFTI DK

>gi |157103119|gb|ABV23972.1| neurami ni dase [Influenza A virus (A/Azerbaijan/008-
 208/2006(H5N1))]

MNPNQKI I TI GSI CMVI GI VSLMLQI GNMI SI WVSHSI OTGNORQAPEI SNTKFLTEKAVASVTL
 LAGNSS LCPI SGWAVYSKDNSI RI GSRGDV FVI REPFI SCSHLECRTFFLTQGALLNDKHSNGT
 VKDRSPHRTLMSCPVGEAPSPYNSRFESVAWSASACHDGT SWLTI GI SGPONGAVAVLKYNIGI I TDTI
 KSWRNNI LRTQESE CACVNGSCFTVMTDGPNSGOASYKI FKMEKGGKLVLDAPNYHYEECS
 CYPDAGEI TCVCRDNWHGNSR PWVSNQNLLEYQI GYI CSGVFGDTPRPNDGTGSCGVPSSNGAYGVKGF
 YKNGVWI GRTKSTNSRSRG FEMI WDPNGWTE TDSSFSVKQDI VAI TDWSGYSGSFVQHPPELTGLDCI
 RPCFWVELI RGRPKESTI WTS SSI SFCGVNSDTPVGSWPDGAELPFTI DK

>gi |157103135|gb|ABV23981.1| neurami ni dase [Influenza A virus (A/Azerbaijan/006-207/2006(H5N1))]
MNPNQKI I TI GSI CMVI GI VSLMLQI GNMI SI WWSHSI QTGNQROAEPI SNTKFLTEKAVASVTLAGNSS
LCPI SGWAVYSKDNSI RI GSRGDFVFI REPFI SCSHLECRTEFFLTQGALLNDKHSNGTVKDRSPHRTLMS
CPVGEAPSPYNSRFESVAWSASACHDGTSWLTI GI SGPDNGAVAVLKYNIGI I TDTI KSWRNNI LRTQESE
CACVNGSCFTVMTDGPSSNGQASYKI FKMEKGGKVVKSVELDAPNYHYEECSYCPDAGEI TCVCARDNWHGNS
RPWVFNQONLEYQI GYI CSGVFGDNPRPNDGTGSCGPVSPNGAYGVKGF SFKYNGVWI GRKSTNSRSG
FEMI WDPNGWTGTDSSFSVKQDI VAI TDWSGYSGSFVQHPTELTGLDCI RPCFWVELI RGRPKESTI WTS
SSI SFCGVNSDTVSWSPDGAELPFTI DK

>gi |148340545|gb|ABQ58918.1| neurami ni dase [Influenza A virus
(A/Turkey/651242/2006(H5N1))]
MNPNQKI I TI GSI CMVI GI VSLMLQI GNMI SI WWSHSI QTGNQROAEPI SNTKFLTEKAVASVTLAGNSS
LCPI SGWAVYSKDNSI RI GSRGDFVFI REPFI SCSHLECRTEFFLTQGALLNDKHSNGTVKDRSPHRTLMS
CPVGEAPSPYNSRFESVAWSASACHDGTSWLTI GI SGPDNGAVAVLKYNIGI I TDTI KSWRNNI LRTQESE
CACVNGSCFTVMTDGPSSNGQASYKI FKMEKGGKVVKSVELDAPNYHYEECSYCPDAGEI TCVCARDNWHGNS
RPWVFNQONLEYQI GYI CSGVFGDNPRPNDGTGSCGPVSPNGAYGVKGF SFKYNGVWI GRKSTNSRSG
FEMI WDPNGWTGTDSSFSVKQDI VAI TDWSGYSGSFVQHPTELTGLDCI RPCFWVELI RGRPKESTI WTS
SSI SFCGVNSDTVSWSPDGAELPFTI DK

>gi |157103072|gb|ABV23945.1| neurami ni dase [Influenza A virus (A/Azerbaijan/002-115/2006(H5N1))]
MNPNQKI I TI GSI CMVI GI VSLMLQI GNMI SI WWSHSI QTGNQROAEPI SNTKFLTEKAVASVTLAGNSS
LCPI SGWAVYSKDNSI RI GSRGDFVFI REPFI SCSHLECRTEFFLTQGALLNDKHSNGTVKDRSPHRTLMS
CPVGEAPSPYNSRFESVAWSASACHDGTSWLTI GI SGPDNGAVAVLKYNIGI I TDTI KSWRNNI LRTQESE
CACVNGSCFTVMTDGPSSNGQASYKI FKMEKGGKVVKSVELDAPNYHYEECSYCPDAGEI TCVCARDNWHGNS
RPWVFNQONLEYQI GYI CSGVFGDNPRPNDGTGSCGPVSPNGAYGVKGF SFKYNGVWI GRKSTNSRSG
FEMI WDPNGWTGTDSSFSVKQDI VAI TDWSGYSGSFVQHPTELTGLDCI RPCFWVELI RGRPKESTI WTS
SSI SFCGVNSDTVSWSPDGAELPFTI DK

>gi |157103596|gb|ABV24001.1| neurami ni dase [Influenza A virus
(A/Iraq/755/2006(H5N1))]
MNPNQKI I TI GSI CMVI GI VSLMLQI GNMI SI WWSHSI QTGNQROAEPI SNTKFLTEKAVASVTLAGNSS
LCPI SGWAVYSKDNSI RI GSRGDFVFI REPFI SCSHLECRTEFFLTQGALLNDKHSNGTVKDRSPHRTLMS
CPVGEAPSPYNSRFESVAWSASACHDGTSWLTI GI SGPDNGAVAVLKYNIGI I TDTI KSWRNNI LRTQESE
CACVNGSCFTVMTDGPSSNGQASYKI FKMEKGGKVVKSVELDAPNYHYEECSYCPDAGEI TCVCARDNWHGNS
RPWVFNQONLEYQI GYI CSGVFGDNPRPNDGTGSCGPVSPNGAYGVKGF SFKYNGVWI GRKSTNSRSG
FEMI WDPNGWTGTDSSFSVKQDI VAI TDWSGYSGSFVQHPTELTGLDCI RPCFWVELI RGRPKESTI WTS
SSI SFCGVNSDTVSWSPDGAELPFTI DK

>gi |157955698|gb|ABW06265.1| neurami ni dase [Influenza A virus
(A/Indonesia/292H/2006(H5N1))]
MNPNQKI I TI GSI CMVI GI VSLMLQI GNMI SI WWSHSI QTGNQROAEPI SNTNPLTEKAVASVTLAGNSS
LCPI RGWAVHVKDNNI RI GSKGDFVFI REPFI SCSHLECRTEFFLTQGALLNDKHSNGTVKDRSPHRTLMS
CPVGEAPSPYNSRFESVAWSASACHDGTSWLTI GI SGPDNEAVAVLKYNIGI I TDTI KSWRNNI LRTQESE
CACVNGSCFTVMTDGPSSNGQASYKI FKMEKGGKVVKSVELDAPNYHYEECSYCPDAGEI TCVCARDNWHGNS
RPWVFNQONLEYQI GYI CSGVFGDNPRPNDGTGSCGPVSPNGAYGVKGF SFKYNGVWI GRKSTNSRSG
FEMI WDPNGWTGTDSSFSVKQDI VAI TDWSGYSGSFVQHPTELTGLDCI RPCFWVELI RGRPKESTI WTS
SSI SFCGVNSDTVSWSPDGAELPFTI DK

>gi |148340541|gb|ABQ58916.1| neurami ni dase [Influenza A virus
(A/Turkey/12/2006(H5N1))]
MNPNQKI I TI GSI CMVI GI VSLMLQI GNMI SI WWSHSI QTGNQROAEPI SNTKFLTEKAVASVTLAGNSS
LCPI SGWAVYSKDNSI RI GSRGDFVFI REPFI SCSHLECRTEFFLTQGALLNDKHSNGTVKDRSPHRTLMS
CPVGEAPSPYNSRFESVAWSASACHDGTSWLTI GI SGPDNGAVAVLKYNIGI I TDTI KSWRNNI LRTQESE
CACVNGSCFTVMTDGPSSNGQASYKI FKMEKGGKVVKSVELDAPNYHYEECSYCPDAGEI TCVCARDNWHGNS
RPWVFNQONLEYQI GYI CSGVFGDNPRPNDGTGSCGPVSPNGAYGVKGF SFKYNGVWI GRKSTNSRSG
FEMI WDPNGWTGTDSSFSVKQDI VAI TDWSGYSGSFVQHPTELTGLDCI RPCFWVELI RGRPKESTI WTS
SSI SFCGVNSDTVSWSPDGAELPFTI DK

>gi |113496518|gb|ABI36298.1| neurami ni dase [Influenza A virus
(A/Indonesia/CDC582/2006(H5N1))]
MNPNQKI I TI GSI CMVI GI VSLMLQI GNMI SI WWSHSI QKGNQHOAEPI SNTNPLTEKAVASVTLAGNSS
LCPI RGWAVHVKDNNI RI GSKGDFVFI REPFI SCSHLECRTEFFLTQGALLNDKHSNGTVKDRSPHRTLMS
CPVGEAPSPYNSRFESVAWSASACHDGTSWLTI GI SGPDNEAVAVLKYNIGI I TDTI KSWRNNI LRTQESE
CACVNGSCFTVMTDGPSSNGQASYKI FKMEKGGKVVKSVELDAPNYHYEECSYCPDAGEI TCVCARDNWHGNS
RPWVFNQONLEYQI GYI CSGVFGDNPRPNDGTGSCGPVSPNGAYGVKGF SFKYNGVWI GRKSTNSRSG
FEMI WDPNGWTGTDSSFSVKQDI VAI TDWSGYSGSFVQHPTELTGLDCI RPCFWVELI RGRPKESTI WTS
SSI SFCGVNSDTVSWSPDGAELPFTI DK

>gi |157955603|gb|ABW06210.1| neurami ni dase [Influenza A virus
(A/Indonesia/538H/2006(H5N1))]
MNPNQKI I TI GSI CMVI GI VSLMLQI GNMI SI WWSHSI QTGNQHOAEPI SNTNPLTEKAVASVTLAGNSS
LCPI RGWAVHVKDNNI RI GSKGDFVFI REPFI SCSHSECRTEFFLTQGALLNDKHSNETVKDRSPHRTLMS
CPVGEAPSPYNSRFESVAWSASACHDGTSWLTI GI SGPDNGAVAVLKYNIGI I TDTI KSWRNNI LRTQESE
CACVNGSCFTVMTDGPSSNGQASYKI FKMEKGGKVVKSVELDAPNYHYEECSYCPDAGEI TCVCARDNWHGNS
RPWVFNQONLEYQI GYI CSGVFGDNPRPNDGTGSCGPVSPNGAYGVKGF SFKYNGVWI GRKSTNSRSG
FEMI WDPNGWTGTDSSFSVKQDI VAI TDWSGYSGSFVQHPTELTGLDCI RPCFWVELI RGRPKESTI WTS
SSI SFCGVNSDTVSWSPDGAELPFTI DK

>gi |157955565|gb|ABW06188.1| neurami ni dase [Influenza A virus
(A/Indonesia/536H/2006(H5N1))]
MNPNQKI I TI GSI CMVI GI VSLMLQI GNMI SI WWSHSI QTGNQHOAEPI SNTNPLTEKAVASVTLAGNSS
LCPI RGWAVHVKDNNI RI GSKGDFVFI REPFI SCSHSECRTEFFLTQGALLNDKHSNETVKDRSPHRTLMS
CPVGEAPSPYNSRFESVAWSASACHDGTSWLTI GI SGPDNGAVAVLKYNIGI I TDTI KSWRNNI LRTQESE

CACVNGSCFTVMTDGPNSGQASYKI FKMEKGGKVVKSVELDAPNYHYEEECSCYPDAGEI TCVCRDNWHGNS
 RPWVSFNQONLEYQI GYI CSGVFGDNPRPNDGTGSCGPMSSNGAYGVKGFSSFKYNGVWI GRKSTNSRSRSG
 FEMI WDPNGWTGTDSSFSVKQDI VAI TDWSGYSGSFVQHPPELTGLDCI RPCFWVELI RGRPKESTI WTS
 SSI SFCGVNSDTSVSWSPDGAELPFT

>gi |157955641|gb|ABW06232.1| neurami ni dase [Influenza A virus
 (A/Indonesia/534H/2006(H5N1))]

MNPNQKI I TI GSI CMAI GTVSLMLQI GNMI SI WVSHSI QTGNQHOAESI SNTNPLTEKAVASVTLAGNSS
 LCPI RGWAVHSDNSI RI GSKGDV FVI REPFI SCSSHSECRFFFLTQGALLNDKHSNETVKDRSPHRTLMS
 CPVGEAPSPYNSRFESVAWSASACHDGT SWLTI GI SGPDNGAVAVLK YNGI I TDTI KSWRNNI LRTQESE
 CACVNGSCFTVMTDGPNSGQASYKI FKMEKGGKVVKSVELDAPNYHYEEECSCYPDAGEI TCVCRDNWHGNS
 RPWVSFNQONLEYQI GYI CSGVFGDNPRPNDGTGSCGPMSSNGAYGVKGFSSFKYNGVWI GRKSTNSRSRSG
 FEMI WDPNGWTGTDSSFSVKQDI VAI TDWSGYSGSFVQHPPELTGLDCI RPCFWVELI RGRPKESTI WTS
 SSI SFCGVNSDTSVSWSPDGAELPFT

>gi |113495792|gb|ABI 36146.1| neurami ni dase [Influenza A virus
 (A/Indonesia/534H/2006(H5N1))]

MNPNQKI I TI GSI CMAI GTVSLMLQI GNMI SI WVSHSI QTGNQHOAESI SNTNPLTEKAVASVTLAGNSS
 LCPI RGWAVHSDNSI RI GSKGDV FVI REPFI SCSSHSECRFFFLTQGALLNDKHSNETVKDRSPHRTLMS
 CPVGEAPSPYNSRFESVAWSASACHDGT SWLTI GI SGPDNGAVAVLK YNGI I TDTI KSWRNNI LRTQESE
 CACVNGSCFTVMTDGPNSGQASYKI FKMEKGGKVVKSVELDAPNYHYEEECSCYPDAGEI TCVCRDNWHGNS
 RPWVSFNQONLEYQI GYI CSGVFGDNPRPNDGTGSCGPMSSNGAYGVKGFSSFKYNGVWI GRKSTNSRSRSG
 FEMI WDPNGWTGTDSSFSVKQDI VAI TDWSGYSGSFVQHPPELTGLDCI RPCFWVELI RGRPKESTI WTS
 SSI SFCGVNSDTSVSWSPDGAELPFT DK

>gi |113495851|gb|ABI 36157.1| neurami ni dase [Influenza A virus
 (A/Indonesia/535H/2006(H5N1))]

MNPNQKI I TI GSI CMAI GTVSLMLQI GNMI SI WVSHSI QTGNQHOAESI SNTNPLTEKAVASVTLAGNSS
 LCPI RGWAVHSDNSI RI GSKGDV FVI REPFI SCSSHSECRFFFLTQGALLNDKHSNETVKDRSPHRTLMS
 CPVGEAPSPYNSRFESVAWSASACHDGT SWLTI GI SGPDNGAVAVLK YNGI I TDTI KSWRNNI LRTQESE
 CACVNGSCFTVMTDGPNSGQASYKI FKMEKGGKVVKSVELDAPNYHYEEECSCYPDAGEI TCVCRDNWHGNS
 RPWVSFNQONLEYQI GYI CSGVFGDNPRPNDGTGSCGPMSSNGAYGVKGFSSFKYNGVWI GRKSTNSRSRSG
 FEMI WDPNGWTGTDSSFSVKQDI VAI TDWSGYSGSFVQHPPELTGLDCI RPCFWVELI RGRPKESTI WTS
 SSI SFCGVNSDTSVSWSPDGAELPFT DK

>gi |157955584|gb|ABW06199.1| neurami ni dase [Influenza A virus
 (A/Indonesia/535H/2006(H5N1))]

MNPNQKI I TI GSI CMAI GTVSLMLQI GNMI SI WVSHSI QTGNQHOAESI SNTNPLTEKAVASVTLAGNSS
 LCPI RGWAVHSDNSI RI GSKGDV FVI REPFI SCSSHSECRFFFLTQGALLNDKHSNETVKDRSPHRTLMS
 CPVGEAPSPYNSRFESVAWSASACHDGT SWLTI GI SGPDNGAVAVLK YNGI I TDTI KSWRNNI LRTQESE
 CACVNGSCFTVMTDGPNSGQASYKI FKMEKGGKVVKSVELDAPNYHYEEECSCYPDAGEI TCVCRDNWHGNS
 RPWVSFNQONLEYQI GYI CSGVFGDNPRPNDGTGSCGPMSSNGAYGVKGFSSFKYNGVWI GRKSTNSRSRSG
 FEMI WDPNGWTGTDSSFSVKQDI VAI TDWSGYSGSFVQHPPELTGLDCI RPCFWVELI RGRPKESTI WTS
 SSI SFCGVNSDTSVSWSPDGAELPFT DK

>gi |157955529|gb|ABW06168.1| neurami ni dase [Influenza A virus
 (A/Indonesia/542H/2006(H5N1))]

MNPNQKI I TI GSI CMVI GI VSLMLQI GNMI SI WVSHSI QTGNQHOAESI SNTNPLTEKAVASVTLAGNSS
 LCPI RGWAVHSDNSI RI GSKGDV FVI REPFI SCSHLECRFFFLTQGALLNDKHSNETVKDRSPHRTLMS
 CPVGEAPSPYNSRFESVAWSASACHDGT SWLTI GI SGPDNGAVAVLK YNGI I TDTI KSWRNNI LRTQESE
 CACVNGSCFTVMTDGPNSGQASYKI FKMEKGGKVVKSVELDAPNYHYEEECSCYPDAGEI TCVCRDNWHGNS
 RPWVSFNQONLEYQI GYI CSGVFGDNPRPNDGTGSCGPMSSNGAYGVKGFSSFKYNGVWI GRKSTNSRSRSG
 FEMI WDPNGWTGTDSSFSVKQDI VAI TDWSGYSGSFVQHPPELTGLDCI RPCFWVELI RGRPKESTI WTS
 SSI SFCGVNSDTSVSWSPDGAELPFT DK

>gi |113495963|gb|ABI 36179.1| neurami ni dase [Influenza A virus
 (A/Indonesia/597/2006(H5N1))]

MNPNQKI I TI GSI CMAI GTVSLMLQI GNMI SI WVSHSI QTGNQHOAESI SNTNPLTEKAVASVTLAGNSS
 LCPI RGWAVHSDNSI RI GSKGDV FVI REPFI SCSSHSECRFFFLTQGALLNDKHSNETVKDRSPHRTLMS
 CPVGEAPSPYNSRFESVAWSASACHDGT SWLTI GI SGPDNGAVAVLK YNGI I TDTI KSWRNNI LRTQESE
 CACVNGSCFTVMTDGPNSGQASYKI FKMEKGGKVVKSVELDAPNYHYEEECSCYPDAGEI TCVCRDNWHGNS
 RPWVSFNQONLEYQI GYI CSGVFGDNPRPNDGTGSCGPMSSNGAYGVKGFSSFKYNGVWI GRKSTNSRSRSG
 FEMI WDPNGWTGTDSSFSVKQDI VAI TDWSGYSGSFVQHPPELTGLDCI RPCFWVELI RGRPKESTI WTS
 SSI SFCGVNSDTSVSWSPDGAELPFT DK

>gi |113495914|gb|ABI 36168.1| neurami ni dase [Influenza A virus
 (A/Indonesia/596/2006(H5N1))]

MNPNQKI I TI GSI CMAI GTVSLMLQI GNMI SI WVSHSI QTGNQHOAESI SNTNPLTEKAVASVTLAGNSS
 LCPI RGWAVHSDNSI RI GSKGDV FVI REPFI SCSSHSECRFFFLTQGALLNDKHSNETVKDRSPHRTLMS
 CPVGEAPSPYNSRFESVAWSASACHDGT SWLTI GI SGPDNGAVAVLK YNGI I TDTI KSWRNNI LRTQESE
 CACVNGSCFTVMTDGPNSGQASYKI FKMEKGGKVVKSVELDAPNYHYEEECSCYPDAGEI TCVCRDNWHGNS
 RPWVSFNQONLEYQI GYI CSGVFGDNPRPNDGTGSCGPMSSNGAYGVKGFSSFKYNGVWI GRKSTNSRSRSG
 FEMI WDPNGWTGTDSSFSVKQDI VAI TDWSGYSGSFVQHPPELTGLDCI RPCFWVELI RGRPKESTI WTS
 SSI SFCGVNSDTSVSWSPDGAELPFT DK

Lampiran 4 : Hasil Alignment

Alignment: E:\1_Data Penelitian\9_Ridlo\Data\database\Ha\HA1\human\H1N1. aln

	10	20	30	40	50	60	
DTI CI GYHAN	N	S	T	D	T	V	56605625
DTI CI GYHAN	N	S	T	D	T	V	62291 emb
DTI CI GYHAN	N	S	T	D	T	V	89779321
DTI CI GYHAN	N	S	T	D	T	V	126599271
DTI CI GYHAN	N	S	T	D	T	V	125976181
DTI CI GYHAN	N	S	T	D	T	V	194304803
DTI CI GYHAN	N	S	T	D	T	V	133754132
DTI CI GYHAN	N	S	T	D	T	V	133754189
DTI CI GYHAN	N	S	T	D	T	V	89148077
DTI CI GYHAN	N	S	T	D	T	V	94960371
DTI CI GYHAN	N	S	T	D	T	V	324200 gb
DTI CI GYHAN	N	S	T	D	T	V	194352371
DTI CI GYHAN	N	S	T	D	T	V	94481538
DTI CI GYHAN	N	S	T	D	T	V	89782156
DTI CI GYHAN	N	S	T	D	T	V	133752882
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DTI CI GYHAN	N	S	T	D	T	V	145278810
DTI CI GYHAN	N	S	T	D	T	V	89152215
DTI CI GYHAN	N	S	T	D	T	V	89903056
DTI CI GYHAN	N	S	T	D	T	V	189303378
DTI CI GYHAN	N	S	T	D	T	V	188076435
DTI CI GYHAN	N	S	T	D	T	V	193084911
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DTI CI GYHAN	N	S	T	D	T	V	193084897
DTI CI GYHAN	N	S	T	D	T	V	189303368
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DTI CI GYHAN	N	S	T	D	T	V	194294061
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DTI CI GYHAN	N	S	T	D	T	V	194294063
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DTI CI GYHAN	N	S	T	D	T	V	189303388
DTI CI GYHAN	N	S	T	D	T	V	170181707
DTI CI GYHAN	N	S	T	D	T	V	193084905
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DTI CI GYHAN	N	S	T	D	T	V	158830221
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DTI CI GYHAN	N	S	T	D	T	V	158830223
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DTI CI GYHAN	N	S	T	D	T	V	158830231
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DTI CI GYHAN	N	S	T	D	T	V	145278924
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DTI CI GYHAN	N	S	T	D	T	V	115607765
DTI CI GYHAN	N	S	T	D	T	V	115607784
DTI CI GYHAN	N	S	T	D	T	V	117571148
DTI CI GYHAN	N	S	T	D	T	V	14587061
DTI CI GYHAN	N	S	T	D	T	V	14587059
DTI CI GYHAN	N	S	T	D	T	V	89033079

DTI	CI	GYHAN	NSTDTVDTVL	EKNVTVTHSV	NLLEDSSHNGK	LCLLKGI	APL	QLGNCSVAGW	gi	112789450				
DTI	CI	GYHAN	NSTDTVDTVL	EKNVTVTHSV	NLLEDSSHNGK	LCLLKGI	APL	QLGNCSVAGW	gi	112789469				
DTI	CI	GYHAN	NSTDTVDTVL	EKNVTVTHSV	NLLEDSSHNGK	LCLLKGI	APL	QLGNCSVAGW	gi	14587051				
DTI	CI	GYHAN	NSTDTVDTVL	EKNVTVTHSV	NLLEDSSHNGK	LCLLKGI	APL	QLGNCSVAGW	gi	14587053				
DTI	CI	GYHAN	NSTDTVDTVL	EKNVTVTHSV	NLLEDSSHNGK	LCLLKGI	APL	QLGNCSVAGW	gi	14587055				
DPI	CI	GYHAN	NSTDTVDTVL	EKNVTVTHSV	NLLEDSSHNGK	LCLLKGI	APL	QLGNCSVAGW	gi	14587049				
DTI	CI	GYHAN	NSTDTVDTVL	EKNVTVTHSV	NLLEDSSHNGK	LCRLKGTAPL	QLGNCSVAGW	gi	134047389					
DTI	CI	GYHAN	NSTDTVDTVL	EKNVTVTHSV	NLLEDSSHNGK	LCRLKGTAPL	QLGNCSVAGW	gi	112787584					
DTI	CI	GYHAN	NSTDTVDTVL	EKNVTVTHSV	NLLEDSSHNGK	LCRLKGTAPL	QLGNCSVAGW	gi	94959685					
DTI	CI	GYHAN	NSTDTVDTVL	EKNVTVTHSV	NLLEDSSHNGK	LCRLKGTAPL	QLGNCSVAGW	gi	109914458					
DTI	CI	GYHAN	NSTDTVDTVL	EKNVTVTHSV	NLLEDSSHNGK	LCRLKGTAPL	QLGNCSVAGW	gi	94959704					
DTI	CI	GYHAN	NSTDTVDTVL	EKNVTVTHSV	NLLEDSSHNGK	LCRLKGTAPL	QLGNCSVAGW	gi	120434212					
DTI	CI	GYHAN	NSTDTVDTVL	EKNVTVTHSV	NLLEDSSHNGK	LCRLKGTAPL	QLGNCSVAGW	gi	86788144					
DTI	CI	GYHAN	NSTDTVDTVL	EKNVTVTHSV	NLLEDSSHNGK	LCRLKGTAPL	QLGNCSVAGW	gi	89114296					
DTI	CI	GYHAN	NSTDTVDTVL	EKNVTVTHSV	NLLEDSSHNGK	LCRLKGTAPL	QLGNCSVAGW	gi	112787546					
DTI	CI	GYHAN	NSTDTVDTVL	EKNVTVTHSV	NLLEDSSHNGK	LCRLKGTAPL	QLGNCSVAGW	gi	89903075					
DTI	CI	GYHAN	NSTDTVDTVL	EKNVTVTHSV	NLLEDSSHNGK	LCRLKGTAPL	QLGNCSVAGW	gi	89782382					
DTI	CI	GYHAN	NSTDTVDTVL	EKNVTVTHSV	NLLEDSSHNGK	LCRLKGTAPL	QLGNCSVAGW	gi	406042					
DTI	CI	GYHAN	NSTDTVDTVL	EKNVTVTHSV	NLLEDSSHNGK	LCRLKGTAPL	QLGNCSVAGW	gi	145279077					
DTI	CI	GYHAN	NSTDTVDTVL	EKNVTVTHSV	NLLEDSSHNGK	LCRLKGTAPL	QLGNCSVAGW	gi	148897951					
DTI	CI	GYHAN	NSTDTVDTVL	EKNVTVTHSV	NLLEDSSHNGK	LCRLKGTAPL	QLGNCSVAGW	gi	146760085					
DTI	CI	GYHAN	NSTDTVDTVL	EKNVTVTHSV	NLLEDSSHNGK	LCRLKGTAPL	QLGNCSVAGW	gi	146133734					
DTI	CI	GYHAN	NSTDTVDTVL	EKNVTVTHSV	NLLEDSSHNGK	LCRLKGTAPL	QLGNCSVAGW	gi	134047484					
DTI	CI	GYHAN	NSTDTVDTVL	EKNVTVTHSV	NLLEDSSHNGK	LCRLKGTAPL	QLGNCSVAGW	gi	89112489					
DTI	CI	GYHAN	NSTDTVDTVL	EKNVTVTHSV	NLLEDSSHNGK	LCRLKGTAPL	QLGNCSVAGW	gi	125976162					
DTI	CI	GYHAN	NSTDTVDTVL	EKNVTVTHSV	NLLEDSSHNGK	LCRLKGTAPL	QLGNCSVAGW	gi	145278791					
DTI	CI	GYHAN	NSTDTVDTVL	EKNVTVTHSV	NLLEDSSHNGK	LCRLKGTAPL	QLGNCSVAGW	gi	125976219					
DTI	CI	GYHAN	NSTDTVDTVL	EKNVTVTHSV	NLLEDSSHNGK	LCRLKGTAPL	QLGNCSVAGW	gi	324122					
DTI	CI	GYHAN	NSTDTVDTVL	EKNVTVTHSV	NLLEDSSHNGK	LCRLKGTAPL	QLGNCSVAGW	gi	4325039					
DTLCI	GYHAN	NSTDTVDTVL	EKNVTVTHSV	NLLEDSSHNGK	LCRLKGTAPL	QLGNCSVAGW	gi	112456302						
*	.	**	****	*****	.*	****	*****	****	.*	**	.*	.*	**	Clustal Cons

LLGNPECDPL	LPVRSWSYI	V	ETPNSENGI	C	YPGDFI	DYEE	LREQLSSVSS	FERFEI	FPKE	gi	56605625
LLGNPECDPL	LPVRSWSYI	V	ETPNSENGI	C	YPGDFI	DYEE	LREQLSSVSS	FERFEI	FPKE	gi	62291
LLGNPECDPL	LPVRSWSYI	V	ETPNSENGI	C	YPGDFI	DYEE	LREQLSSVSS	FERFEI	FPKE	gi	89779321
LLGNPECDPL	LPVRSWSYI	V	ETPNSENGI	C	YPGDFI	DYEE	LREQLSSVSS	FERFEI	FPKE	gi	126599271
LLGNPECDPL	LPVRSWSYI	V	ETPNSENGI	C	YPGDFI	DYEE	LREQLSSVSS	FERFEI	FPKE	gi	125976181
LLGNPECDPL	LPVRSWSYI	V	ETPNSENGI	C	YPGDFI	DYEE	LREQLSSVSS	FERFEI	FPKE	gi	194304803
LLGNPECDPL	LPARWSYI	V	ETPNSENGI	C	YPGAFI	DYEE	LREQLSSVSS	FERFEI	FPKE	gi	133754132
LLGNPECDPL	LPARWSYI	V	ETPNSENGI	C	YPGDFI	DYEE	LREQLSSVSS	FERFEI	FPKE	gi	133754189
LLGNPECDPL	LPARWSYI	V	ETPNSENGI	C	YPGDFI	DYEE	LREQLSSVSS	FERFEI	FPKE	gi	89148077
LLGNPECDPL	LPARWSYI	V	ETPNSENGI	C	YPGDFI	DYEE	LREQLSSVSS	FERFEI	FPKE	gi	94960371
LLGNPECDPL	LPARWSYI	V	ETPNSENGI	C	YPGDFI	DYEE	LREQLSSVSS	FERFEI	FPKE	gi	324200
LLGNPECDPL	LPARWSYI	V	ETPNSENGI	C	YPGDFI	DYEE	LREQLSSVSS	FERFEI	FPKE	gi	194352371
LLGNPECDPL	LPARWSYI	V	ETPNSENGI	C	YPGDFI	DYEE	LREQLSSVSS	FERFEI	FPKE	gi	94481538
LLGNPECDPL	LPARWSYI	V	ETPNSENGI	C	YPGDFI	DYEE	LREQLSSVSS	FERFEI	FPKE	gi	89782156
LLGNPECDPL	LSERSWSYI	V	ETPNSENGI	C	YPGDFI	DYEE	LREQLSSVSS	FERFEI	FSKE	gi	133752882
LLGNPECDPL	LSERSWSYI	V	ETPNSENGI	C	YPGDFI	DYEE	LREQLSSVSS	FERFEI	FSKE	gi	133754170
LLGNPECDPL	LSERSWSYI	V	ETPNSENGI	C	YPGDFI	DYEE	LREQLSSVSS	FERFEI	FPKE	gi	145278810
LLGNPECDPL	LSERSWSYI	V	ETPNSENGI	C	YPGDFI	DYEE	LREQLSSVSS	FERFEI	FPKE	gi	89152215
LLGNPECDPL	LSERSWSYI	V	ETPNSENGI	C	YPGDFI	DYEE	LREQLSSVSS	FERFEI	FPKE	gi	89903056
LLGNPECDPL	SKESWSYI	V	EKPNPENGTC	YPGHFDYEE	LREQLSSVSS	FERFEI	FPKE	gi	189303378		
LLGNPECDPL	SKESWSYI	V	EKPNPENGTC	YPGHFDYEE	LREQLSSVSS	FERFEI	FPKE	gi	188076435		
LLGNPECDPL	SKESWSYI	V	EKPNPENGTC	YPGHFDYEE	LREQLSSVSS	FERFEI	FPKE	gi	193084911		
LLGNPECDPL	SKESWSYI	V	EKPNPENGTC	YPGHFDYEE	LREQLSSVSS	FERFEI	FPKE	gi	189303374		
LLGNPECDPL	SKESWSYI	V	EKPNPENGTC	YPGHFDYEE	LREQLSSVSS	FERFEI	FPKE	gi	189303360		
LLGNPECDPL	SKESWSYI	V	EKPNPENGTC	YPGHFDYEE	LREQLSSVSS	FERFEI	FPKE	gi	189303392		
LLGNPECDPL	SKESWSYI	V	EKPNPENGTC	YPGHFDYEE	LREQLSSVSS	FERFEI	FPKE	gi	189303362		
LLGNPECDPL	SKESWSYI	V	EKPNPENGTC	YPGHFDYEE	LREQLSSVSS	FERFEI	FPKE	gi	188076427		
LLGNPECDPL	SKESWSYI	V	EKPNPENGTC	YPGHFDYEE	LREQLSSVSS	FERFEI	FPKE	gi	189303372		
LLGNPECDPL	SKESWSYI	V	EKPNPENGTC	YPGHFDYEE	LREQLSSVSS	FERFEI	FPKE	gi	193084897		
LLGNPECDPL	SKESWSYI	V	EKPNPENGTC	YPGHFDYEE	LREQLSSVSS	FERFEI	FPKE	gi	189303368		
LLGNPECDPL	SKESWSYI	V	EKPNPENGTC	YPGHFDYEE	LREQLSSVSS	FERFEI	FPKE	gi	188076425		
LLGNPECDPL	SKESWSYI	V	EKPNPENGTC	YPGHFDYEE	LREQLSSVSS	FERFEI	FPKE	gi	194294061		
LLGNPECDPL	SKESWSYI	V	EKPNPENGTC	YPGHFDYEE	LREQLSSVSS	FERFEI	FPKE	gi	170181715		
LLGNPECDPL	SKESWSYI	V	EKPNPENGTC	YPGHFDYEE	LREQLSSVSS	FERFEI	FPKE	gi	194294063		
LLGNPECDPL	SKESWSYI	V	EKPNPENGTC	YPGHFDYEE	LREQLSSVSS	FERFEI	FPKE	gi	189303386		
LLGNPECDPL	SKESWSYI	V	EKPNPENGTC	YPGHFDYEE	LREQLSSVSS	FERFEI	FPKE	gi	189303388		
LLGNPECDPL	SKESWSYI	V	EKPNPENGTC	YPGHFDYEE	LREQLSSVSS	FERFEI	FPKE	gi	170181707		
LLGNPECDPL	SKESWSYI	V	EKPNPENGTC	YPGHFDYEE	LREQLSSVSS	FERFEI	FPKE	gi	193084905		
LLGNPECDPL	SKESWSYI	V	EKPNPENGTC	YPGHFDYEE	LREQLSSVSS	FERFEI	FPKE	gi	189303366		
LLGNPECDPL	SKESWSYI	V	EKPNPENGTC	YPGHFDYEE	LREQLSSVSS	FERFEI	FPKE	gi	170786954		
LLGNPECDPL	SKESWSYI	V	EKPNPENGTC	YPGHFDYEE	LREQLSSVSS	FERFEI	FPKE	gi	194294065		
LLGNPECDPL	SKESWSYI	V	EKPNPENGTC	YPGHFDYEE	LREQLSSVSS	FERFEI	FPKE	gi	194294069		
LLGNPECDPL	SKESWSYI	V	EKPNPENGTC	YPGHFDYEE	LREQLSSVSS	FERFEI	FPKE	gi	189303400		

I LGNPECELL	I SKESWSYI V	EKNPNENGTC	YPGHFADYEE	LREQLSSVSS	FERFEI FPKE	gi	188076441
I LGNPECELL	I SKESWSYI V	EKNPNENGTC	YPGHFADYEE	LREQLSSVSS	FERFEI FPKE	gi	170181783
I LGNPECELL	I SKESWSYI V	EKNPNENGTC	YPGHFADYEE	LREQLSSVSS	FERFEI FPKE	gi	189303384
I LGNPECELL	I SKESWSYI V	EKNPNENGTC	YPGHFADYEE	LREQLSSVSS	FERFEI FPKE	gi	189303390
I LGNPECELL	I SKESWSYI V	EKNPNENGTC	YPGHFADYEE	LREQLSSVSS	FERFEI FPKE	gi	189303376
I LGNPECELL	I SKESWSYI V	EKNPNENGTC	YPGHFADYEE	LREQLSSVSS	FERFEI FPKE	gi	188076459
I LGNPECELL	I SKESWSYI V	EKNPNENGTC	YPGHFADYEE	LREQLSSVSS	FERFEI FPKE	gi	189303398
I LGNPECELL	I SKESWSYI V	EKNPNENGTC	YPGHFADYEE	LREQLSSVSS	FERFEMFPKE	gi	189303382
I LGNPECELL	I SKESWSYI V	EKNPNENGTC	YPGHFADYEE	LREQLSSVSS	FERFEI FPKE	gi	189303380
VLGNPECELL	I SKESWSYI V	EKNPNENGTC	YPGHFADYEE	LREQLSSVSS	FERFEI FPKE	gi	189303370
I LGNPECELL	I SKESWSYI V	ETPNPENGTG	YPGYFADYEE	LREQLSSVSS	FERFEI FPKE	gi	158830221
I LGNPECELL	I SKESWSYI V	ETPNPENGTG	YPGYFADYEE	LREQLSSVSS	FERFEI FPKE	gi	158830241
I LGNPECELL	I SKESWSYI V	ETPNPENGTG	YPGYFADYEE	LREQLSSVSS	FERFEI FPKE	gi	158830237
I LGNPECELL	I SKESWSYI V	ETPNPENGTG	YPGYFADYEE	LREQLSSVSS	FERFEI FPKE	gi	158830223
I LGNPECELL	I SKESWSYI V	ETPNPENGTG	YPGYFADYEE	LREQLSSVSS	FERFEI FPKE	gi	115607822
I LGNPECELL	I SKESWSYI V	ETPNPENGTG	YPGYFADYEE	LREQLSSVSS	FERFEI FPKE	gi	158830225
I LGNPECELL	I SKESWSYI V	ETPNPENGTG	YPGYFADYEE	LREQLSSVSS	FERFEI FPKE	gi	158830231
I LGNPECELL	I SKESWSYI V	ETPNPENGTG	YPGYFADYEE	LREQLSSVSS	FERFEI FPKE	gi	158830233
I LGNPECELL	I SKESWSYI V	ETPNPENGTG	YPGYFADYEE	LREQLSSI SS	FERFEI FPKE	gi	158830227
I LGNPECELL	I SKESWSYI V	ETPNPENGTG	YPGYFADYEE	LREQLSSVSS	FERFEI FPKE	gi	158830235
I LGNPECELL	I SKESWSYI V	ETPNPENGTG	YPGYFADYEE	LREQLSSVSS	FERFEI FPKE	gi	145278924
I LGNPECELL	I SKESWSYI V	ETPNPENGTG	YPGYFADYEE	LREQLSSVSS	FERFEI FPKE	gi	115607803
I LGNPECELL	I SKESWSYI V	ETPNPENGTG	YPGYFADYEE	LREQLSSVSS	FERFEI FPKE	gi	115607765
I LGNPECELL	I SKESWSYI V	ETPNPENGTG	YPGHFADYEE	LREQLSSVSS	FERFEI FPKE	gi	115607784
I LGNPECELL	I SKESWSYI V	ETPNPENGTG	YPGYFADYEE	LREQLSSVSS	FERFEI FPKE	gi	117571148
I LGNPECELL	I PKESWSYI V	ETPNPENGTG	YPGYFADYEE	LREQLSSVSS	FERFEI FPKE	gi	14587061
I LGNPECELL	I PKESWSYI V	ETPNPENGTG	YPGYFADYEE	LREQLSSVSS	FERFEI FPKE	gi	14587059
I LGNPECELL	I SKESWSYI V	ETPNPENGTG	YPGHFADYEE	LREQLSSVSS	FERFEI FPKE	gi	89033079
I LGNPECESL	I SKESWSYI V	ETPNPENGTG	YPGYFADYEE	LREQLSSVSS	FERFEI FPKE	gi	112789450
I LGNPECESL	I SKESWSYI V	ETPNPENGTG	YPGYFADYEE	LREQLSSVSS	FERFEI FPKE	gi	112789469
I LGNPECELL	I SKESWSYI V	ETPNPENGTG	YPGYFADYEE	LREQLSSVSS	FERFEI FPKE	gi	14587051
I LGNPECELL	I SKESWSYI V	ETPNPENGTG	YPGYFADYEE	LREQLSSVSS	FERFEI FPKE	gi	14587053
I LGNPECELL	I SKESWSYI V	ETPNPENGTG	YPGYFADYEE	LREQLSSVSS	FERFEI FPKE	gi	14587055
I LGNPECELL	I SKESWSYI V	ETPNPENGTG	YPGYFADYEE	LREQLSSVSS	FERFEI FPKE	gi	14587049
I LGNPECESL	FSKESWSYI A	ETPNPENGTG	YPGYFADYEE	LKEQLSSVSS	FERFEI FPKE	gi	134047389
I LGNPECESL	FSKESWSYI A	ETPNPENGTG	YPGYFADYEE	LKEQLSSVSS	FERFEI FPKE	gi	112787584
I LGNPECESL	FSKESWSYI A	ETPNPENGTG	YPGYFADYEE	LREQLSSVSS	FERFEI FPKE	gi	94959685
I LGNPECESL	FSKESWSYI A	ETPNPENGTG	YPGYFADYEE	LREQLSSVSS	FERFEI FPKE	gi	109914458
I LGNPECESL	FSKESWSYI A	ETPNPENGTG	YPGYFADYEE	LREQLSSVSS	FERFEI FPKE	gi	94959704
I LGNPECESL	FSKESWSYI A	ETPNPENGTG	YPGYFADYEE	LREQLSSVSS	FERFEI FPKE	gi	120434212
VLGNPECESL	LSNRSWSYI A	ETPNSENGTC	YPGDFADYEE	LREQLSSVSS	FERFEI FPKE	gi	86788144
I LGNPECESL	LSNRSWSYI A	ETPNSENGI C	YPGDFADYEE	LREQLSSVSS	FERFEI FPKE	gi	89114296
I LGNPECESL	LSKRSWSYI A	ETPNSENGTC	YPGDFADYEE	LREQLSSVSS	FERFEI FPKE	gi	112787546
I LGNPECESL	LSKRSWSYI A	ETPNSENGAC	YPGDFADYEE	LREQLSSVSS	FERFEI FPKG	gi	89903075
I LGNPECESL	LSKRSWSYI A	ETPNSENGTC	YPGDFADYEE	LREQLSSVSS	FERFEI FPKE	gi	89782382
I LGNPECESL	LSKRSWSYI A	ETPNSENGAC	YPGDFADYEE	LREQLSSVSS	FERFEI FPKE	gi	406042 gb
I LGNPECESL	LSNRSWSYI A	ETPNSENGTC	YPGDFADYEE	LREQLSSVSS	FERFEI FPKE	gi	145279077
I LGNPECESL	LSNRSWSYI A	ETPNSENGTC	YPGDFADYEE	LREQLSSVSS	FERFEI FPKE	gi	148897951
I LGNPECESL	LSNRSWSYI A	ETPNSENGTC	YPGDFADYEE	LREQLSSVSS	FERFEI FPKE	gi	146760085
I LGNPECESL	LSNRSWSYI A	ETPNSENGTC	YPGDFADYEE	LREQLSSVSS	FERFEI FPKE	gi	146133734
I LGNPECESL	LSNRSWSYI A	ETPNSENGI C	YPGDFADYEE	LREQLSSVSS	FERFEI FPKE	gi	134047484
I LGNPECESL	LSNRSWSYI A	ETPNSENGI C	YPGDFADYEE	LREQLSSVSS	FERFEI FPKE	gi	89112489
I LGNPECESL	FSKKSWSYI A	ETPNSENGTC	YPGYFADYEE	LREQLSSVSS	FERFEI FPKE	gi	125976162
I LGNPECESL	FSKKSWSYI A	ETPNSENGTC	YPGYFADYEE	LREQLSSVSS	FERFEI FPKE	gi	145278791
I LGNPECESL	FSKKSWSYI A	ETPNSENGTC	YPGYFADYEE	LREQLSSVSS	FERFEI FPKE	gi	125976219
I LGNPECESL	VSKKSWSYI A	ETPNSENGTC	YPGYFADYEE	LREQLSSVSS	FERFEI FPKE	gi	324122 gb
LLGNPECDLL	LTASSWSYI V	ETSNSENGTC	YPGDFI DYEE	LREQLSSVSS	FEKFEI FPKT	gi	4325039 g
I LGNPECESL	FTTSSWSYI V	ETPNSDNGTC	YPGDFI NYEE	LREHLSSVSS	FERFEI FPKA	gi	112456302
. ***** . *	. ***** . *	. ***** . *	. ***** . *	. ***** . *	. ***** . *	. ***** . *	Cl ustal Cons

SSWPNHNTTK	GVTAACSHAG	KSSFYRNLLW	LTEKEGSYPK	LKNSYVNKKG	KEVLVLWGI H	gi	56605625
SSWPNHNTTK	GVTAACSHAG	KSSFYRNLLW	LTEKEGSYPK	LKNSYVNKKG	KEVLVLWGI H	gi	62291 emb
SSWPNHNTTK	GVTAACSHAG	KSSFYRNLLW	LTEKEGSYPK	LKNSYVNKKG	KEVLVLWGI H	gi	89779321
SSWPNHNTTK	GVTAACSHAG	KSSFYRNLLW	LTEKEGSYPK	LKNSYVNKKG	KEVLVLWGI H	gi	126599271
SSWPNHNTTK	GVTAACSHAG	KSSFYRNLLW	LTEKEGSYPK	LKNSYVNKKG	KEVLVLWGI H	gi	125976181
SSWPNHNTTK	GVTAACSHAG	KSSFYRNLLW	LTEKEGSYPN	LKNSYVNKKG	KEVLVLWGI H	gi	194304803
SSWPNHNTTK	GVTAACSHAG	KSSFYRNLLW	LTKKGSYPK	LKNSYVNKKG	KEVLVLWGI H	gi	133754132
SSWPKHNTTK	GVTAACSHAG	KSSFYRNLLW	LTKKEDSYPK	LKNSYVNKKG	KEVLVLWGVH	gi	133754189
SSWPKHNTTK	GVTAACSHAG	KSSFYRNLLW	LTKKEDSYPK	LSNSYVNKKG	KEVLVLWGVH	gi	89148077
SSWPNH-TFN	GVTVSCSHRG	KSSFYRNLLW	LTKKGSYPK	LTNSYVNKKG	KEVLVLWGVH	gi	94960371
SSWPNH-TFN	GVTVSCSHRG	KSSFYRNLLW	LTKKGSYPK	LTNSYVNKKG	KEVLVLWGVH	gi	324200 gb
SSWPNH-TFN	GVTASCSHRG	KSSFYRNLLW	LTKKGSYPK	LTNSYVNKKG	KEVLVLWGVH	gi	194352371
SSWPNH-TFN	GVTASCSHRG	KSSFYRNLLW	LTKKGSYPK	LTNSYVNKKG	KEVLVLWGVH	gi	94481538
SSWPNHNTLK	GVTASCSHGG	KSSFYRNLLW	LTKXGDSYPK	LNNSYVNKKG	KEVLVLWGVH	gi	89782156
SSWPKHNTTR	GVTAACSHAG	KSSFYRNLLW	LTEKDGSPN	LNNSYVNKKG	KEVLVLWGVH	gi	133752882

SSWPKH-TTG	GVTAACSHAG	KSSFYRLLW	LTEKDGSYPN	LNNSYVNNKG	KEVLVLWGVH	gi	133754170
SSWPKHNTTR	GVTAACSHAG	KSSFYRLLW	LTEKDGSYPN	LNNSYVNNKG	KEVLVLWGVH	gi	145278810
TSWPKHNTTK	GVTAACSHAG	KCSFYRLLW	LTEKDGSYPN	LNNSYVNNKG	KEVLVLWGVH	gi	89152215
SSWPKHNTAR	GVTAACSHAG	KSSFYRLLW	LTEKDGSYPN	LKNSYVNNKG	KEVLVLWGVH	gi	89903056
SSWPNHVT-	GVSASC SHNG	ESSFYRLLW	LTGKNGLYPN	LSKSYANNKE	KEVLVLWGVH	gi	189303378
SSWPNHVT-	GVSASC SHNG	ESSFYRLLW	LTGKNGLYPX	LSKSYANNKE	KEVLVLWGVH	gi	188076435
SSWPNHVT-	GVSASC SHNG	ESSFYRLLW	LTGKNGLYPN	LSKSYANNKE	KEVLVLWGVH	gi	193084911
SSWPNHVT-	GVSASC SHNG	ESSFYRLLW	LTGKNGLYPS	LSKSYANNKE	KEVLVLWGVH	gi	189303374
SSWPNHVT-	GVSASC SHNG	ESSFYRLLW	LTGKNGLYPN	LSKSYANNKE	KEVLVLWGVH	gi	189303360
SSWPNHVT-	GVSASC SHNG	ESSFYRLLW	LTGKNGLYPN	LSKSYANNKE	KEVLVLWGVH	gi	189303392
SSWPNHVT-	GVSASC SHNG	ESSFYRLLW	LTGKNGLYPN	LSKSYANNKE	KEVLVLWGVH	gi	189303362
SSWPNHVT-	GVSASC SHNG	ESSFYRLLW	LTGKNGLYPN	LSKSYANNKE	KEVLVLWGVH	gi	188076427
SSWPNHVT-	GVSASC SHNG	ESSFYRLLW	LTGKNGLYPN	LSKSYANNKE	KEVLVLWGVH	gi	189303372
SSWPNHVT-	GVSASC SHNG	ESSFYRLLW	LTGKNGLYPN	LSKSYANNKE	KEVLVLWGVH	gi	193084897
SSWPNHVT-	GVSASC SHNG	ESSFYRLLW	LTGKNGLYPN	LSKSYANNKE	KEVLVLWGVH	gi	189303368
SSWPNHVT-	GVSASC SHNG	ESSFYRLLW	LTGKNGLYPN	LSKSYANNKE	KEVLVLWGVH	gi	188076425
SSWPNHVT-	GVSASC SHNG	ESSFYRLLW	LTGKNGLYPN	LSKSYANNKE	KEVLVLWGVH	gi	194294061
SSWPNHVT-	GVSASC SHNG	ESSFYRLLW	LTGKNGLYPN	LSKSYANNKE	KEVLVLWGVH	gi	189303388
SSWPNHVT-	GVSASC SHNG	ESSFYRLLW	LTGKNGLYPN	LSKSYANNKE	KEVLVLWGVH	gi	194294063
SSWPNHVT-	GVSASC SHNG	ESSFYRLLW	LTGKNGLYPN	LI KSYANNKE	KEVLVLWGVH	gi	189303386
SSWPNHVT-	GVSASC SHNG	ESSFYRLLW	LTGKNGLYPN	LRKSYANNKE	KEVLVLWGVH	gi	189303388
SSWPNHVT-	GVSASC SHNG	ESSFYRLLW	LTGKNGLYPN	LSKSYANNKE	KEVLVLWGVH	gi	170181707
SSWPNHVT-	GVSASC SHNG	ESSFYRLLW	LTGKNGLYPN	LSKSYANNKE	KEVLVLWGVH	gi	193084905
SSWPXHVT-	GVSASC SHNG	ESSFYRLLW	LTGKNGLYPN	LSKSYANNKE	KEVLVLWGVH	gi	189303366
SSWPXHVT-	GVSASC SHNG	ESSFYRLLW	LTGKNGLYPN	LSKSYANNKE	KEVLVLWGVH	gi	170786954
SSWPXHVT-	GVSASC SHNG	ESSFYRLLW	LTGKNGLYPX	LSKSYANNKE	KEVLVLWGVH	gi	194294065
SSWPXHVT-	GVSASC SHNG	ESSFYRLLW	LTGKNGLYPN	LSKSYANNKE	KEVLVLWGVH	gi	194294069
SSWPSHTVT-	GVSASC SHNG	ESSFYRLLW	LTGKNGLYPN	LSKSYANNKE	KEVLVLWGVH	gi	189303400
SSWPKHTVT-	GVSASC SHNG	ESSFYRLLW	LTGKNGLYPN	LSKSYANNKE	KEVLVLWGVH	gi	188076441
SSWPNHVT-	GVSASC SHNG	ESSFYRLLW	LTGKNGLYPN	LSKSYANNKE	KEVLVLWGVH	gi	170181783
SSWPNHVT-	GVSASC SHNG	ESSFYRLLW	LTGKNGLYPN	LSKSYANNKE	KEVLVLWGVH	gi	189303384
SSWPNHVT-	GVSASC SHNG	ESSFYRLLW	LTGKNGLYPN	LSKSYANNKE	KEVLVLWGVH	gi	189303390
SSWPNHVT-	GVSASC SHNG	ESSFYRLLW	LTRKNGLYPN	LSKSYANNKE	KEVLVLWGVH	gi	189303376
SSWPNHVT-	GVSASC SHNG	ESSFYRLLW	LTRKNGLYPN	LSKSYANNKE	KEVLVLWGVH	gi	188076459
SSWPNHVT-	GVSASC SHNG	ESSFYRLLW	LTRKNGLYPN	LSKSYANNKE	KEVLVLWGVH	gi	189303398
SSWPNHVT-	GVSASC SHNG	ESSFYRLLW	LTGKNGLYPN	LKSYANNKE	KEVLVLWGVH	gi	189303382
SSWPNHVT-	GVSASC SHNG	ESSFYRLLW	LTRKNGLYPN	LSKSYANNKE	KEVLVLWGVH	gi	189303380
SSWPNHVT-	GVSASC SHNG	ESSFYKLLW	LTGKNGLYPN	LSKSYANNKK	KEVLVLWGVH	gi	189303370
SSWPNHVT-	GVSASC SHNG	KSSFYRLLW	LTGKNGLYPN	LSKSYANNKE	KEVLVLWGVH	gi	158830221
SSWPNHVT-	GVSASC SHNG	KSSFYRLLW	LTGKNGLYPN	LSKSYANNKE	KEVLVLWGVH	gi	158830241
SSWPNHVT-	GVSASC SHNG	KSSFYRLLW	LTGKNGLYPN	LSKSYANNKE	KEVLVLWGVH	gi	158830237
SSWPNHVT-	GVSASC SHNG	KSSFYRLLW	LTGKNGLYPN	LSKSYANNKE	KEVLVLWGVH	gi	158830223
SSWPNHVT-	GVSASC SHNG	KSSFYRLLW	LTGKNGLYPN	LSKSYANNKE	KEVLVLWGVH	gi	115607822
SSWPNHVT-	GVSASC SHNG	KSSFYRLLW	LTGKNGLYPN	LSKSYANNKE	KEVLVLWGVH	gi	158830225
SSWPNHVT-	GVSASC SHNG	KSSFYRLLW	LTGKNGLYPN	LSKSYANNKE	KEVLVLWGVH	gi	158830231
SSWPNHVT-	GVSASC SHNG	KSSFYRLLW	LTGKNGLYPN	LSKSYANNKE	KEVLVLWGVH	gi	158830233
SSWPNHVT-	GVSASC SHNG	KSSFYRLLW	LTGKNGLYPN	LSKSYANNKE	KEVLVLWGVH	gi	158830227
SSWPNHVT-	GVSASC SHNG	KSSFYRLLW	LTGKNGLYPN	LSKSYANNKE	KEVLVLWGVH	gi	158830235
SSWPNHVT-	GVSASC SHNG	KSSFYRLLW	LTGKNGLYPN	LSKSYANNKE	KEVLVLWGI H	gi	145278924
SSWPNHVT-	GVSASC SHNG	KSSFYRLLW	LTGKNGLYPN	LSKSYANNKE	KEVLVLWGVH	gi	115607803
SSWPNHVT-	GVSASC SHNG	KSSFYRLLW	LTGKNGLYPN	LSKSYANNKE	KEVLVLWGVH	gi	115607765
SSWPNHVT-	GVSASC SHNG	KSSFYRLLW	LTGKNGLYPN	LSKSYANNKE	KEVLVLWGVH	gi	115607784
SSWPNHVT-	GVSASC SHNG	KSSFYRLLW	LTGKNGLYPN	LSKSYVNNKE	KEVLVLWGVH	gi	117571148
SSWPNHVT-	GVSASC SHNG	KSSFYRLLW	LTGKNGLYPN	LSKSYVNNKE	KEVLVLWGVH	gi	14587061
SSWPNHVT-	GVSASC SHNG	KSSFYRLLW	LTGKNGLYPN	LSKSYVNNKE	KEVLVLWGVH	gi	14587059
SSWPNHVT-	GVSASC SHNG	KSSFYRLLW	LTKKNGLYPN	LSKSYVNNKE	KEVLVLWGVH	gi	89033079
SSWPNHVT-	GVSASC SHNG	KSSFYRLLW	LTGKNGLYPN	LSKSYVNNKE	KEVLVLWGVH	gi	112789450
SSWPNHVT-	GVSASC SHNG	KSSFYRLLW	LTEKNGLYPN	LSKSYVNNKE	KEVLVLWGVH	gi	112789469
SSWPNHVT-	GVSASC SHNG	KSSFYRLLW	LTEKNGLYPN	LSKSYVNNKE	KEVLVLWGVH	gi	14587051
SSWPNHVT-	GVSASC SHNG	KSSFYRLLW	LTEKNGLYPN	LSKSYVNNKE	KEVLVLWGVH	gi	14587053
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SSWPNHVT-	GVSASC SHNG	KSSFYRLLW	LTEKNGLYPN	LSKSYVNNKE	KEVLVI WGVH	gi	14587049
SSWPNHVTVK	GVTASC SHNG	KSSFYKLLW	LTEKNGLYPN	LSKSYVNNKE	KEVLVLWGVH	gi	134047389
SSWPNHVTVK	GVTASC SHNG	KSSFYKLLW	LTEKNGLYPN	LSKSYVNNKE	KEVLVLWGVH	gi	112787584
SSWPNHVTVK	GVTASC SHNG	KSSFYKLLW	LTEKNGLYPN	LSKSYVNNKE	KEVLVLWGVH	gi	94959685
SSWPNHVTVK	GVTASC SHNG	KSSFYKLLW	LTEKNGLYPN	LSKSYVNNKE	KEVLVLWGVH	gi	109914458
SSWPNHVTVK	GVTASC SHNG	KSSFYKLLW	LTEKNGLYPN	LSKSYVNNKE	KEVLVLWGI H	gi	94959704
SSWPNHVTVK	GVTASC SHNG	KSSFYKLLW	LTEKNGLYPN	LSKSYVNNKE	KEVLVLWGVH	gi	120434212
RSWPNH-TTR	GVTAACPHAR	KSSFYKNLWV	LTEANGSYPN	LSRSYVNNQE	KEVLVLWGVH	gi	86788144
RSWPKHNTI R	GVTAACSHAG	KSSFYKNLWV	LTEANGSYPN	LSTSYVNNQE	KEVLVLWGVH	gi	89114296
RSWPNHNI NI	GVTAACSHAG	KSSFYKLLW	LTEKDGSYPN	LNKSYVNNKE	KEVLVLWGVH	gi	112787546
RSWPEHNI DI	GVTAACSHAG	KSSFYKNLWV	LTEKDGSYPN	LNKSYVNNKE	KEVLI LWGVH	gi	89903075
RSWPKHNI TR	GVTAACSHAG	KSSFYKLLW	LTETNGSYPK	LSKSYVNNKE	KEVLVLWGVH	gi	89782382
RSWPKHNI TR	GVTAACSHAG	KSSFYKLLW	LTETDGSYPK	LSKSYVNNKE	KEVLVLWGVH	gi	406042 gb
RSWPKHNI TR	GVTAACSHAK	KSSFYKLLW	LTEANGSYPN	LSKSYVNNKE	KEVLVLWGVH	gi	145279077
RSWPKHNI TR	GVTAACSHAK	KSSFYKLLW	LTEANGSYPN	LSKSYVNNKE	KEVLVLWGVH	gi	148897951
RSWPKHNI TR	GVTAACSHAK	KSSFYKLLW	LTEANGSYPN	LSKSYVNNKE	KEVLVLWGVH	gi	146760085

HPPNI GDQRA	LYHTENAYVS	VVSSHYSRRF	TPEI AKRPKV	RDQEGRI NYY	WTLLPEPGDTI	gi	115607803
HPPNI GBQRA	LYHTENAYVS	VVSSHYSRRF	TPEI AKRPKV	RDQEGRI NYY	WTLLPEPGDTI	gi	115607765
HPPNI GDQRA	LYHTENAYVS	VVSSHYSRRF	TPEI AKRPKV	RDQEGRI NYY	WTLLPEPGDTI	gi	115607784
HPPNI GDQRA	LYHTENAYVS	VVSSHYSRRF	TPEI AKRPKV	RDQEGRI NYY	WTLLPEPGDTI	gi	117571148
HPPNI GDQRA	IYHTENAYVS	VVSSHYSRRF	TPEI VKRPKV	RDQEGRI NYY	WTLLPEPGDTI	gi	14587061
HPPNI GDQRA	IYHTENAYVS	VVSSHYSRRF	TPEI VKRPKV	RDQEGRI NYY	WTLLPEPGDTI	gi	14587059
HPSNI GDQRA	IYHTENAYVS	VVSSHYSRRF	TPEI VKRPKV	RDQEGRI NYY	WTLLPEPGDTI	gi	89033079
HPSNI GVQRA	IYHTENAYVS	VVSSHYSRRF	TPEI AKRPKV	RDQEGRI NYY	WTLLPEPGDTI	gi	112789450
HPSNI GVQRA	IYHTENAYVS	VVSSHYSRRF	TPEI AKRPKV	RDQEGRI NYY	WTLLPEPGDTI	gi	112789469
NPSNI GDQRA	IYHTENAYVS	VVSSHYSRRF	TPEI AKRPKV	RDQEGRI NYY	WTLLPEPGDTI	gi	14587051
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HPSNI GDQRA	IYHTENAYVS	VVSSHYSRRF	TPEI AKRPKV	RDQEGRI NYY	WTLLPEPGDTI	gi	134047389
HPSNI GDQRA	IYHTENAYVS	VVSSHYSRRF	TPEI AKRPKV	RDQEGRI NYY	WTLLPEPGDTI	gi	112787584
HPSNI GDQRA	IYHTENAYVS	VVSSHYSRRF	TPEI TKRPKV	RDQEGRI NYY	WTLLPEPGDTI	gi	94959685
HPSNI GDQRA	IYHTENAYVS	VVSSHYSRRF	TPEI TKRPKV	RNQEGRY NYY	WTLLPEPGDTI	gi	109914458
HPSNI GDQRA	IYHTENAYVS	VVSSHYSRRF	TPEI AKRPKV	RDQEGRI NYY	WTLLPEPGDTI	gi	94959704
HPSNI GDQRA	IYHTENAYVS	VVSSHYSRRF	TPEI AKRPKV	RDQEGRI NYY	WTLLPEPGDTI	gi	120434212
HPSNI EEQRA	LYRKDNAYVS	VVSSNYNRRF	TPEI AKRPKV	RDQSGRMNYY	WTLLPEPGDTI	gi	86788144
HPSNI EEQRT	LYRKDNAYVS	VVSSNYNRRF	TPEI AKRPKV	RDQPGRMNYY	WTLLPEPGDTI	gi	89114296
HPSNI ENQKT	LYRKENAYVS	VVSSNYNRRF	TPEI AERP KV	RGQAGRMNYY	WTLLPEPGDTI	gi	112787546
HPPNI ENQKT	LYRKENAYVS	VVSSNYNRRF	TPEI AERP KV	RGQAGRI NYY	WTLLPEPGDTI	gi	89903075
HPSNI EDQKT	LYRKENAYVS	VVSSNYNRRF	TPEI AERP KV	RGQAGRMNYY	WTLLPEPGDTI	gi	89782382
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HPSNI EDQRT	LYRKENAYVS	VVSSNYNRRF	TPEI AERP KV	RGQAGRMNYY	WTLLPEPGDKI	gi	145279077
HPSNI EDQRT	LYRKENAYVS	VVSSNYNRRF	TPEI AERP KV	RGQAGRMNYY	WTLLPEPGDKI	gi	148897951
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HPSKI EDQRT	LYRKENAYVS	VVSSNYNRRF	TPEI AERP KV	RGQAGRMNYY	WTLLPEPGDKI	gi	146133734
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HPPTGTDQOS	LYQNADAYVS	VGSSKYNRRF	TPEI AERP KV	RDQAGRMNYY	WTLLPEPGDTI	gi	4325039 g
HPPTSTDQQT	LYQNADAYVF	VGSSKYSKRF	KPEI AARP KV	RDQAGRMDDY	WTLLPEPGDTI	gi	112456302
.*	*	*.*	*.*	***	**.*	..*	***.*.*
Cl	ustal	Cons					

	250	260	270	280	290	300		
I FEANGNLI A	PRYAFALSRG	FGSGI I	TSNA	SMHECNTKCC	TPLGAI NSSL	PFQNI HPVTI	gi	56605625
I FEANGNLI A	PRYAFALSRG	FGSGI I	TSNA	SMHECNTKCC	TPLGAI NSSL	PFQNI HPVTI	gi	62291 emb
I FEANGNLI A	PMYAFALSRG	FGSGI I	TSNA	SMHECNTKCC	TPLGAI NSSL	PYQNI HPVTI	gi	89779321
I FEANGNLI A	PMYAFALSRG	FGSGI I	TSNA	SMHECNTKCC	TPLGAI NSSL	PYQNI HPVTI	gi	126599271
I FEANGNLI A	PMYAFALSRG	FGSGI I	TSNA	SMHECNTKCC	TPLGAI NSSL	PYQNI HPVTI	gi	125976181
I FEANGNLI A	PMYAFALSRG	FGSGI I	TSNA	SMHECNTKCC	TPLGAI NSSL	PYQNI HPVTI	gi	194304803
MFEANGNLVA	PWYAFALSRG	FGSGI I	TSNA	SMHECNTKCC	TPQGA I NSSL	PFQNI HPVTI	gi	133754132
I FEANGNLI A	PWYAFALSRG	FGSGI I	TSNA	SMHECNTKCC	TPQGA I NSSL	PFQNI HPVTI	gi	133754189
I FEANGNLI A	PWYAFALSRG	FGSGI I	TSNA	SMHECNTKCC	TPQGA I NSSL	PFQNI HPVTI	gi	89148077
I FEATGNLI A	PWYAFALSRG	FESGI I	TSNA	SMHECNTKCC	TPQGS I NSNL	PFQNI HPVTI	gi	94960371
I FEATGNLI A	PWYAFALSRG	FESGI I	TSNA	SMHECNTKCC	TPQGS I NSNL	PFQNI HPVTI	gi	324200 gb
I FEATGNLI A	PWYAFALSRG	FESGI I	TSNA	SMHECNTKCC	TPQGS I NSNL	PFQNI HPVTI	gi	194352371
I FEATGNLI A	PWYAFALSRG	FESGI I	TSNA	SMHECNTKCC	TPQGS I NSNL	PFQNI HPVTI	gi	94481538
I FEATGNLI A	PWYAFALSRG	FGSGI I	TSNA	SMHECNTKCC	TPQGA I NSSL	PFQNI HPVTI	gi	89782156
MFEANGNLI A	PWYAFALSRG	FGSGI I	TSNA	SMHECDTKCC	TPQGA I NSSL	PFQNI HPVTI	gi	133752882
MFEANGNLI A	PWYAFALSRG	FGSGI I	TSNA	SMHECDTKCC	TPQGA I NSSL	PFQNI HPVTI	gi	133754170
MFEANGNLI A	PWYAFALSRG	FGSGI I	TSNA	SMHECDTKCC	TPQGA I NSSL	PFQNI HPVTI	gi	145278810
I FEANGNLI A	PWYAFALSRG	FGSGI I	TSNA	SMHECNTKCC	TPQGA I NSSL	PFQNI HPVTI	gi	89152215
I FEANGNLI A	PWYAFALSRG	FGSGI I	TSNA	SMHECDTKCC	TPQGA I NSSL	PFQNI HPVTI	gi	89903056
I FEANGNLI A	PRYAFALSRG	FGSGI I	NSNA	PMDKCDAKCC	TPQGA I NSSL	PFQNVHPVTI	gi	189303378
I FEANGNLI A	PRYAFALSRG	FGSGI I	NSNA	PMDKCDAKCC	TPQGA I NSSL	PFQNVHPVTI	gi	188076435
I FEANGNLI A	PRYAFALSRG	FGSGI I	NSNA	PMDKCDAKCC	TPQGA I NSSL	PFQNVHPVTI	gi	193084911
I FEANGNLI A	PRYAFALSRG	FGSGI I	NSNA	PMDKCDAKCC	TPQGA I NSSL	PFQNVHPVTI	gi	189303374
I FEANGNLI A	PRYAFALSRG	FGSGI I	NSNA	PMDKCDAKCC	TPQGA I NSSL	PFQNVHPVTI	gi	189303360
I FEANGNLI A	PRYAFALSRG	FGSGI I	NSNA	PMDKCDAKCC	TPQGA I NSSL	PFQNVHPVTI	gi	189303392
I FEANGNLI A	PRYAFALSRG	FGSGI I	NSNA	PMDKCDAKCC	TPQGA I NSSL	PFQNVHPVTI	gi	189303362
I FEANGNLI A	PRYAFALSRG	FGSGI I	NSNA	PMDKCDAKCC	TPQGA I NSSL	PFQNVHPVTI	gi	188076427
I FEANGNLI A	PRYAFALSRG	FGSGI I	NSNA	PMDKCDAKCC	TPQGA I NSSL	PFQNVHPVTI	gi	189303372
I FEANGNLI A	PRXAFALSRG	FGSGI I	NSNA	PMDKCDAKCC	TPQGA I NSSL	PFQNVHPVTI	gi	193084897
I FEANGNLI A	PRYAFALSRG	FGSGI I	NSNA	PMDKCDAKCC	TPQGA I NSSL	PFQNVHPVTI	gi	189303368
I FEANGNLI A	PRYAFALSRG	FGSGI I	NSNA	PMDKCDAKCC	TPQGA I NSSL	PFQNVHPVTI	gi	188076425
I FEANGNLI A	PRYAFALSRG	FGSGI I	NSNA	PMDKCDAKCC	TPQGA I NSSL	PFQNVHPVTI	gi	194294061
I FEANGNLI A	PRYAFALSRG	FGSGI I	NSNA	PMDKCDAKCC	TPQGA I NSSL	PFQNVHPVTI	gi	170181715
I FEANGNLI A	PRYAFALSRG	FGSGI I	NSNA	PMDKCDAKCC	TPQGA I NSSL	PFQNVHPVTI	gi	194294063
I FEANGNLI A	PRYAFALSRG	FGSGI I	NSNA	PMDKCDAKCC	TPQGA I NSSL	PFQNVHPVTI	gi	189303386
I FEANGNLI A	PRYAFALSRG	FGSGI I	NSNA	PMDKCDAKCC	TPQGA I NSSL	PFQNVHPVTI	gi	189303388

I FEANGNLI A	PRYAFTLSRG	FGSGI I	NSNA	PMDKCDAKCQ	TPOGAI NSSL	PFQNVHPVTI	gi	170181707
I FEANGNLI A	PRYAFALSRG	FGSGI I	NSNA	PMDKCDAKCQ	TPOGAI NSSL	PFQNVHPVTI	gi	193084905
I FEANGNLI A	PRYAFALSRG	FGSGI I	NSNA	PMDKCDAKCQ	TPOGAI NSSL	PFQNVHPVTI	gi	189303366
I FEANGNLI A	PRYAFALSRG	FGSGI I	NSNA	PMDKCDAKCQ	TPOGAI NSSL	PFQNVHPVTI	gi	170786954
I FEANGNLI A	PRLAFALSRG	FGSGI I	NSNA	PMDKCDAKCQ	TPOGAI NSSL	PFQNVHPVTI	gi	194294065
I FEANGNLI A	PRYAFALSRG	FGSGI I	NSNA	PMDKCDAKCQ	TPOGAI NSSL	PFQNVHPVTI	gi	194294069
I FEANGNLI A	PRYAFALSRG	FGSGI I	NSNA	PMDKCDAKCQ	TPOGAI NSSL	PFQNVHPVTI	gi	189303400
I FEANGNLI A	PRYAFALSRG	FGSGI I	NSNA	PMDKCDAKCQ	TPOGAI NSSL	PFQNVHPVTI	gi	188076441
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I FEANGNLI A	PRYAFALSRG	FGSGI I	NSNA	PMDKCDAKCQ	TPOGAI NSSL	PFQNVHPVTI	gi	189303384
I FEANGNLI A	PRYAFALSRG	FGSGI I	NSNA	PMDKCDAKCQ	TPOGAI NSSL	PFQNVHPVTI	gi	189303390
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I FEANGNLI A	PRYAFALSRG	FGSGI I	NSNA	PMDKCDAKCQ	TPOGAI NSSL	PFQNVHPVTI	gi	189303382
I FEANGNLI A	PRYAFALSRG	FGSGI I	NSNA	PMDKCDAKCQ	TPOGAI NSSL	PFQNVHPVTI	gi	189303380
I FEANGNLI A	PRYAFALSRG	FGSGI I	NSNA	PMDECDAKCQ	TPOGAI NSSL	PFQNVHPVTI	gi	189303370
I FEANGNLI A	PRYAFALSRG	FGSGI I	NSNA	PMDECDAKCQ	TPOGAI NSSL	PFQNVHPVTI	gi	158830221
I FEANGNLI A	PRYAFALSRG	FGSGI I	NSNA	PMDECDAKCQ	TPOGAI NSSL	PFQNVHPVTI	gi	158830241
I FEANGNLI A	PRYAFALSRG	FGSGI I	NSNA	PMDECDAKCQ	TPOGAI NSSL	PFQNVHPVTI	gi	158830237
I FEANGNLI A	PRYAFALSRG	FGSGI I	NSNA	PMDECDAKCQ	TPOGAI NSSL	PFQNVHPVTI	gi	158830223
I FEANGNLI A	PRYAFALSRG	FGSGI I	NSNA	PMDECDAKCQ	TPOGAI NSSL	PFQNVHPVTI	gi	115607822
I FEANGNLI A	PRYAFALSRG	FGSGI I	NSNA	PMDECDAKCQ	TPOGAI NSSL	PFQNVHPVTI	gi	158830225
I FEANGNLI A	PRYAFALSRG	FGSGI I	NSNA	PMDECDAKCQ	TPOGAI NSSL	PFQNVHPVTI	gi	158830231
I FEANGNLI A	PRYAFALSRG	FGSGI I	NSNA	PMDECDAKCQ	TPOGAI NSSL	PFQNVHPVTI	gi	158830233
I FEANGNLI A	PRYAFALSRG	FGSGI I	NSNA	PMDECDAKCQ	TPOGAI NSSL	PFQNVHPVTI	gi	158830227
I FEANGNLI A	PRYAFALSRG	FGSGI I	NSNA	PMDECDAKCQ	TPOGAI NSSL	PFQNVHPVTI	gi	158830235
I FEANGNLI A	PRYAFALSRG	FGSGI I	NSNA	PMDECDAKCQ	TPOGAI NSSL	PFQNVHPVTI	gi	145278924
I FEANGNLI A	PRYAFALSRG	FGSGI I	NSNA	PMDECDAKCQ	TPOGAI NSSL	PFQNVHPVTI	gi	115607803
I FEANGNLI A	PRYAFALSRG	FGSGI I	NSNA	PMDECDAKCQ	TPOGAI NSSL	PFQNVHPVTI	gi	115607765
I FEANGNLI A	PRYAFALSRG	FGSGI I	NSNA	PMDECDAKCQ	TPOGAI NSSL	PFQNVHPVTI	gi	115607784
I FEANGNLI A	PWYAFALSRG	FGSGI I	NSNA	PMDECDAKCQ	TPOGAI NSSL	PFQNVHPVTI	gi	117571148
I FEANGNLI A	PWYAFALSRG	FGSGI I	NSNA	PMDECDAKCQ	TPOGAI NSSL	PFQNVHPVTI	gi	14587061
I FEANGNLI A	PWYAFALSRG	FGSGI I	NSNA	PMDECDAKCQ	TPOGAI NSSL	PFQNVHPVTI	gi	14587059
I FEANGNLI A	PWYAFALSRG	FGSGI I	NSNA	SMDECDAKCQ	TPOGAI NSSL	PFQNVHPVTI	gi	89033079
I FEANGNLI A	PWYAFALSRG	FESGI I	NSNA	PMDECDAKCQ	TPOGAI NSSL	PFQNVHPVTI	gi	112789450
I FEANGNLI A	PWYAFALSRG	FESGI I	NSNA	PMDECDAKCQ	TPOGAI NSSL	PFQNVHPVTI	gi	112789469
I FEANGNLI A	PWYAFALSRG	FGSGI I	NSNA	PMDECDAKCQ	TPOGAI NSSL	PFQNVHPVTI	gi	14587051
I FEANGNLI A	PWYAFALSRG	FGSGI I	NSNA	PMDECDAKCQ	TPOGAI NSSL	PFQNVHPVTI	gi	14587053
I FEANGNLI A	PWYAFALSRG	FGSGI I	NSNA	PMDECDAKCQ	TPOGAI NSSL	PFQNVHPVTI	gi	14587055
I FEANGNLI A	PWYAFALSRG	FGSGI I	NSNA	PMDECDTKCQ	TPOGAI NSSL	PFQNVHPVTI	gi	14587049
I FEANGNLI A	PWYAFALSRG	FGSGI I	NSNA	SMGECDAKCCQ	TPOGAI NSSL	PFQNVHPVTI	gi	134047389
I FEANGNLI A	PWYAFALSRG	FGSGI I	NSNA	SMGECDAKCCQ	TPOGAI NSSL	PFQNVHPVTI	gi	112787584
I FEANGNLI A	PWYAFALSRG	FGSGI I	NSNA	SMGECDAKCCQ	TPOGAI NSSL	PFQNVHPVTI	gi	94959685
I FEANGNLI A	PWYAFALSRG	FGSGI I	NSNA	SMGECDAKCCQ	TPOGAI NSSL	PFQNVHPVTI	gi	109914458
I FEANGNLI A	PWYAFALSRG	FGSGI I	NSNA	SMGDCDAKCCQ	TPOGAI NSSL	PFQNVHPVTI	gi	94959704
I FEANGNLI A	PWYAFALSRG	FGSGI I	NSNA	SMGECDAKCCQ	TPOGAI NSSL	PFQNVHPVTI	gi	120434212
I FEATGNLI A	PWYAFALSRG	PGSGI I	NSNA	PLDECDTKCCQ	TPOGAI NSSL	PFQNI HPVTI	gi	86788144
I FEATGNLI A	PWYAFALSRG	PGSGI I	NSNA	PMDECDTKCCQ	TPOGAI NSSL	PFQNI HPVTI	gi	89114296
I FEANGNLI A	PWYAFALSRG	LGSGI I	NSNA	SMDECDTKCCQ	TPOGAI NSSL	PFQNI HPFTI	gi	112787546
I FEANGNLI A	PWYAFALNNG	IGSGI I	NSNA	SMDECDTKCCQ	TPOGAI NSSL	PFQNI HPFTI	gi	89903075
I FEANGNLI A	PWYAFALSRG	FGSGI I	NSNA	SMDECDTKCCQ	TPOGAI NSSL	PFQNI HPVTI	gi	89782382
I FEANGNLI A	PWYAFALSRD	FGSGI I	NSNA	SMDECDTKCCQ	TPOGAI NSSL	PFQNI HPVTI	gi	406042
I FEANGNLI A	PWYAFALSRG	LGSGI I	NSNA	SMDECDTKCCQ	TPOGAI NSSL	PFQNI HPVTI	gi	145279077
I FEANGNLI A	PWYAFALSRG	LGSGI I	NSNA	SMDECDTKCCQ	TPOGAI NSSL	PFQNI HPVTI	gi	148897951
I FEANGNLI A	PWYAFALSRG	LGSGI I	NSNA	SMDECDTKCCQ	TPOGAI NSSL	PFQNI HPVTI	gi	146760085
I FEANGNLI A	PWYAFALSRG	LGSGI I	NSNA	SMDECDTKCCQ	TPOGAI NSSL	PFQNI HPVTI	gi	146133734
I FEANGNLI A	PWYAFALSRG	PGSGI I	NSNA	SMDECDTKCCQ	TPOGAI NSSL	PFQNI HPVTI	gi	134047484
I FEANGNLI A	PWYAFALSRG	PGSGI I	NSNA	SMDECDTKCCQ	TPOGAI NSSL	PFQNI HPVTI	gi	89112489
I FEANGNLI A	PWHAFALSRG	FGSGI I	NSNA	SMDECDTKCCQ	TPOGAI NSSL	PFQNI HPVTI	gi	125976162
I FEANGNLI A	PWHAFALSRG	FGSGI I	NSNA	SMDECDTKCCQ	TPOGAI NSSL	PFQNI HPVTI	gi	145278791
I FEANGNLI A	PWHAFALSRG	FGSGI I	NSNA	SMDECDTKCCQ	TPOGAI NSSL	PFQNI HPVTI	gi	125976219
I FEANGNLI A	PWHAFALNNG	FGSGI I	NSNA	SMDECDTKCCQ	TPOGAI NSSL	PFQNI HPVTI	gi	324122
T FEATGNLI A	PWYAFALNNG	SGSGI I	TSNA	PVHDCNTKCCQ	TPHGAI NSSL	PFQNI HPVTI	gi	4325039
T FEATGNLNV	PRYAFTMKRG	SGSGI I	VSDA	PVHDCNTTCCQ	TPKGAI NSSL	PFQNI HPVTI	gi	112456302
*** **	*	**	..**	**	..**	..**	..**	Clustal Cons

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310 320
GECPKYVRS A KLRMTGRLN I PSI QSR gi 56605625
GECPKYVRS A KLRMTGRLN I PSI QSR gi 62291 emb
GECPKYVRS A KLRMTGRLN I PSI QSR gi 89779321
GECPKYVRS A KLRMTGRLN N PSI QSR gi 126599271
GECPKYVRS A KLRMTGRLN I PSI QSR gi 125976181
GECPKYVRS A KLRMTGRLN I PSI QSR gi 194304803
GECPKYVRS A KLRMTGRLN I PSI QSR gi 133754132
GECPKYVRS A KLRMTGRLN I PSI QSR gi 133754189

GECPKYVKS	KLRMTGLRN	I PSI QSR	gi	89148077
GECPKYVRST	KLRMTGLRN	I PSI QYR	gi	94960371
GECPKYVRST	KLRMTGLRN	I PSI QYR	gi	324200 gb
GECPKYVRST	KLRMTGLRN	I PSI QYR	gi	194352371
GECPKYVRST	KLRMTGLRN	I PSI QYR	gi	94481538
GECPKYVRST	KLRMTGLRN	I PSI QSR	gi	89782156
GECPKYVRST	KLRMTGLRN	I PSI QSR	gi	133752882
GECPKYVRST	KLRMTGLRN	I PSI QSR	gi	133754170
GECPKYVRST	KLRMTGLRN	I PSI QSR	gi	145278810
GECPKYVRST	KLRMTGLRN	I PSI QSR	gi	89152215
GECPKYVRST	KLRMTGLRN	I PSI QSR	gi	89903056
GECPKYVRSA	KLRMTGLRN	I PSI QSR	gi	189303378
GECPKYVRSA	KLRMTGLRN	I PSI QSR	gi	188076435
GECPKYVRSA	KLRMTGLRN	I PSI QSR	gi	193084911
GECPKYVRSA	KLRMTGLRN	I PSI QSR	gi	189303374
GECPKYVRSA	KLRMTGLRN	I PSI QSR	gi	189303360
GECPKYVRSA	KLRMTGLRN	I PSI QSR	gi	189303392
GECPKYVRSA	KLRMTGLRN	I PSI QSR	gi	189303362
GECPKYVRSA	KLRMTGLRN	I PSI QSR	gi	188076427
GECPKYVRSA	KLRMTGLRN	I PSI QSR	gi	189303372
GECPKYVRSA	KLRMTGLRN	I PSI QSR	gi	193084897
GECPKYVRSA	KLRMTGLRN	I PSI QSR	gi	189303368
GECPKYVRSA	KLRMTGLRN	I PSI QSR	gi	188076425
GECPKYVRSA	KLRMTGLRN	I PSI QSR	gi	194294061
GECPKYVRSA	KLRMTGLRN	I PSI QSR	gi	170181715
GECPKYVRSA	KLRMTGLRN	I PSI QSR	gi	194294063
GECPKYVRSA	KLRMTGLRN	I PSI QSR	gi	189303386
GECPKYVRSA	KLRMTGLRN	I PSI QSR	gi	189303388
GECPKYVRSA	KLRMTGLRN	I PSI QSR	gi	170181707
GECPKYVRSA	KLRMTGLRN	I PSI QSR	gi	193084905
GECPKYVRSA	KLRMTGLRN	I PSI QSR	gi	189303366
GECPKYVRSA	KLRMTGLRN	I PSI QSR	gi	170786954
GECPKYVRSA	KLRMTGLRN	I PSI QSR	gi	194294065
GECPKYVRSA	KLRMTGLRN	I PSI QSR	gi	194294069
GECPKYVRSA	KLRMTGLRN	I PSI QSR	gi	189303400
GECPKYVRSA	KLRMTGLRN	I PSI QSR	gi	188076441
GECPKYVRSA	KLRMTGLRN	I PSI QSR	gi	170181783
GECPKYVRSA	KLRMTGLRN	I PSI QSR	gi	189303384
GECPKYVRST	KLRMTGLRN	I PSI QSR	gi	189303390
GECPKYVRSA	KLRMTGLRN	I PSI QSR	gi	189303376
GECPKYVRSA	KLRMTGLRN	I PSI QSR	gi	188076459
GECPKYVRSA	KLRMTGLRN	I PSI QSR	gi	189303398
GECPKYVRSA	KLRMTGLRN	I PSI QSR	gi	189303382
GECPKYVRSA	KLRMTGLRN	I PSI QSR	gi	189303380
GECPKYVRSA	KLRMTGLRN	I PSI QSR	gi	189303370
GECPKYVRSA	KLRMATGLRN	I PSI QSR	gi	158830221
GECPKYVRSA	KLRMATGLRN	I PSI QSR	gi	158830241
GECPKYVRSA	KLRMATGLRN	I PSI QSR	gi	158830237
GECPKYVRSA	KLRMATGLRN	I PSI QSR	gi	158830223
GECPKYVRSA	KLRMATGLRN	I PSI QSR	gi	115607822
GECPKYVRSA	KLRMATGLRN	I PSI QSR	gi	158830225
GECPKYVRSA	KLRMATGLRN	I PSI QSR	gi	158830231
GECPKYVRSA	KLRMATGLRN	I PSI QSR	gi	158830233
GECPKYVRSA	KLRMATGLRN	I PSI QSR	gi	158830227
GECPKYVRSA	KLRMATGLRN	I PSI QSR	gi	158830235
GECPKYVRSA	KLRMTGLRN	I PSI QSR	gi	145278924
GECPKYVRSA	KLRMTGLRN	I PSI QSR	gi	115607803
GECPKYVRSA	KLRMTGLRN	I PSI QSR	gi	115607765
GECPKYVRSA	KLRMTGLRN	I PSI QSR	gi	115607784
GECPKYVRSA	KLRMTGLRN	I PSI QSR	gi	117571148
GECPKYVRSA	KLRMTGLRN	I PSI QSR	gi	14587061
GECPKYVRSA	KLRMTGLRN	I PSI QSR	gi	14587059
GECPKYVRSA	KLRMTGLRN	I PSI QSR	gi	89033079
GECPKYVRSA	KLRMTGLRN	I PSI QSR	gi	112789450
GECPKYVRSA	KLRMTGLRN	I PSI QSR	gi	112789469
GECPKYVRSA	KLRMTGLRN	I PSI QSR	gi	14587051
GECPKYVRSA	KLRMTGLRN	I PSI QSR	gi	14587053
GECPKYVRSA	KLRMTGLRN	I PSI QSR	gi	14587055
GECPKYVRSA	KLRMTGLRN	I PSI QSR	gi	14587049
GECPKYVRST	KLRMTGLRN	I PSI QSR	gi	134047389
GECPKYVRST	KLRMTGLRN	I PSI QSR	gi	112787584
GECPKYVRST	KLRMTGLRN	I PSI QSR	gi	94959685
GECPKYVRST	KLRMTGLRN	I PSI QSR	gi	109914458
GECPKYVRST	KLRMTGLRN	I PSI QSR	gi	94959704
GECPKYVRST	KLRMTGLRN	I PSI QSR	gi	120434212
GECPKYVRST	KLRMTGLRN	I PSVQSR	gi	86788144
GECPKYVRST	KLRMTGLRN	I PSI QSR	gi	89114296

GECPKYVRST	KLRMVTGLRN	I PSI QSR	gi	112787546
GECPKYVRST	KLRMVTGLRN	I PSI QSR	gi	89903075
GECPKYVKST	KLRMVTGLRN	I PSI QSR	gi	89782382
GECPKYVKST	KLRMVTGLRN	I PSI QSR	gi	406042 gb
GECPKYVRST	KLRMVTGLRN	I PSI QSR	gi	145279077
GECPKYVRST	KLRMVTGLRN	I PSI QSR	gi	148897951
GECPKYVRST	KLRMVTGLRN	I PSI QSR	gi	146760085
GECPKYVRST	KLRMVTGLRN	I PSI QSR	gi	146133734
GECPKYVRST	KLRMVTGLRN	I PSI QSR	gi	134047484
GECPKYVRST	KLRMVTGLRN	I PSI QSR	gi	89112489
GECPKYVRST	KLRMVTGLRN	I PSI QSR	gi	125976162
GECPKYVRST	KLRMVTGLRN	I PSI QSR	gi	145278791
GECPKYVRST	KLRMVTGLRN	I PSI QSR	gi	125976219
GECPKYVRST	KLRMVTGLRN	I PSI QSR	gi	324122 gb
GECPKYVRST	KLRMATGLRN	I PSI QSR	gi	4325039 g
GECPKYVKST	KLRMATGLRN	I PSI QSR	gi	112456302
*****.*:	****.*****	**. * *	Cl	ustal Cons

Alignment: E:_1_Data Penelitan\9_Ridlo\Data\database\Ha\HA1\human\H2N2. al n

.....	10	20	30	40	50	60			
DQI	CI	GYHAN	NSTEKVDTI	L	ERNVTVTHAK	DI	LEKTHNGK	LCKLNGI PPL ELGDCSI AGW gi	73921184
DQI	CI	GYHAN	NSTEKVDTI	L	ERNVTVTHAK	DI	LEKTHNGK	LCKLNGI PPL ELGDCSI AGW gi	408523 gb
DQI	CI	GYHAN	NSTEKVDTI	L	ERNVTVTHAK	DI	LEKTHNGK	LCKLNGI PPL ELGDCSI AGW gi	133753638
DQI	CI	GYHAN	NSTEKVDTI	L	ERNVTVTHAK	DI	LEKTHNGK	LCKLNGI PPL ELGDCSI AGW gi	134047408
DQI	CI	GYHAN	NSTEKVDTI	L	ERNVTVTHAK	DI	LEKTHNGK	LCKLNGI PPL ELGDCSI AGW gi	133753657
DQI	CI	GYHAN	NSTEKVDTI	L	ERNVTVTHAK	DI	LEKTHNGK	LCKLNGI PPL ELGDCSI AGW gi	134047523
DQI	CI	GYHAN	NSTEKVDTI	L	ERNVTVTHAK	DI	LEKTHNGK	LCKLNGI PPL ELGDCSI AGW gi	145279057
DQI	CI	GYHAN	NSTEKVDTI	L	ERNVTVTHAK	DI	LEKTHNGK	LCKLNGI PPL ELGDCSI AGW gi	408525 gb
DQI	CI	GYHAN	NSTEKVDTI	L	ERNVTVTHAK	DI	LEKTHNGK	LCKLNGI PPL ELGDCSI AGW gi	189230461
DQI	CI	GYHAN	NSTEKVDTI	L	ERNVTVTHAK	DI	LEKTHNGK	LCKLNGI PPL ELGDCSI AGW gi	127057978
DQI	CI	GYHAN	NSTEKVDTNL	L	ERNVTVTHAK	DI	LEKTHNGK	LCKLNGI PPL ELGDCSI AGW gi	324146 gb
DQI	CI	GYHAN	NSTEKVDTI	L	ERNVTVTHAK	DI	LEKTHNGK	LCKLNGI PPL ELGDCSI AGW gi	305155 gb
DQI	CI	GYHAN	NSTEMVDTI	L	ERNVTVTHAK	DI	LEKTHNGK	LCKLNGI PPL ELGDCSI AGW gi	94481522
DQI	CI	GYHAN	NSTEKVDTI	L	ERNVTVTHAK	DI	LEKTHNGK	LCKLNGI PPL ELGDCSI AGW gi	63054902
DQI	CI	GYHAN	NSTEKVDTI	L	ERNVTVTHAK	DI	LEKTHNGK	LCKLNGI PPL ELGDCSI AGW gi	305117 gb
DQI	CI	GYHAN	NSTEKVDTI	L	ERNVTVTHAK	DI	LEKTHNGK	LCKLNGI PPL ELGDCSI AGW gi	133752958
DQI	CI	GYHAN	NSTEKVDTI	L	ERNVTVTHAK	DI	LEKTHNGK	LCKLNGI PPL ELGDCSI AGW gi	145279038
DQI	CI	GYHAN	NSTEKVDTI	L	ERNVTVTHAK	DI	LEKTHNGK	LCKLNGI PPL ELGDCSI AGW gi	146760066
DQI	CI	GYHAN	NSTEKVDTI	L	ERNVTVTHAK	DI	LEKTHNGK	LCKLNGI PPL ELGDCSI AGW gi	305163 gb
DQI	CI	GYHAN	NSTETVDTI	L	ERNVTVTHAK	DI	LEKTHNGK	LCKLNGI PPL ELGDCSI AGW gi	194352181
DQI	CI	GYHAN	NSTETVDTI	L	ERNVTVTHAK	DI	LEKTHNGK	LCKLNGI PPL ELGDCSI AGW gi	194352200
DQI	CI	GYHAN	NSTETVDTI	L	ERNVTVTHAK	DI	LEKTHNGK	LCKLNGI PPL ELGDCSI AGW gi	194352219
DQI	CI	GYHAN	NSTETVDTI	L	ERNVTVTHAK	DI	LEKTHNGK	LCKLNGI PPL ELGDCSI AGW gi	194352238
DQI	CI	GYHAN	NSTEKVDTI	L	ERNVTVTHAK	DI	LEKTHNGK	LCKLNGI PPL ELGDCSI AGW gi	194352162
DQI	CI	GYHAN	NSTEKVDTI	L	ERNVTVTHAK	DI	LEKTHNGK	LCKLNGI PPL ELGDCSI AGW gi	305171 gb
DQI	CI	GYHAN	NSTEKVDTI	L	ERNVTVTHAK	NI	LEKTHNGK	LCKLNGI PPL ELGDCSI AGW gi	26453383
DQI	CI	GYHAN	NSTEKVDTI	L	ERNVTVTHAK	NI	LEKTHNGR	LCKLNGI PPL ELGDCSI AGW gi	188504407
DQI	CI	GYHAN	NSTEKVDTI	L	ERNVTVTHAK	DI	LEKTHNGK	LCKLNGI PPL ELGDCSI AGW gi	133982551
DQI	CI	GYHAN	NSTEKVDTI	L	ERNVTVTHAK	DI	LEKTHNGK	LCKLNGI PPL ELGDCSI AGW gi	146133810
DQI	CI	GYHAN	NSTEKVDTI	L	ERNVTVTHAK	DI	LEKTHNGK	LCKLNGI PPL ELGDCSI AGW gi	115279062
DQI	CI	GYHAN	NSTEKVDTI	L	ERNVTVTHAK	DI	LEKTHNGK	LCKLNGI PPL ELGDCSI AGW gi	145279000
DQI	CI	GYHAN	NSTEKVDTI	L	ERNVTVTHAK	DI	LEKTHNGK	LCKLNGI PPL ELGDCSI AGW gi	189230499
DQI	CI	GYHAN	NSTEKVDTI	L	ERNVTVTHAK	DI	LEKTHNGK	LCKLNGI PPL ELGDCSI AGW gi	408677 gb
DQI	CI	GYHAN	NSTEKVDTI	L	ERNVTVTHAK	DI	LEKTHNGK	LCKLNGI PPL ELGDCSI AGW gi	305115 gb
DQI	CI	GYHAN	NSTEKVDTI	L	ERNVTVTHAK	DI	LEKTHNGK	LCKLNGI PPL ELGDCSI AGW gi	188504350
DQI	CI	GYHAN	NSTEKVDTI	L	ERNVTVTHAK	DI	LEKTHNGK	LCKLNGI PPL ELGDCSI AGW gi	189230518
DQI	CI	GYHAN	NSTEKVDTI	L	ERNVTVTHAK	DI	LEKTHNGK	LCKLNGI PPL ELGDCSI AGW gi	194351979
DQI	CI	GYHAN	NSTEKVDTI	L	ERNVTVTHAK	DI	LEKTHNGK	LCKLNGI PPL ELGDCSI AGW gi	189230423
DQI	CI	GYHAN	NSTEKVDTI	L	ERNVTVTHAK	DI	LEKTHNGK	LCKLNGI PPL ELGDCSI AGW gi	133755366
DQI	CI	GYHAN	NSTEKVDTI	L	ERNVTVTHAK	DI	LEKTHNGK	LCKLNGI PPL ELGDCSI AGW gi	133755385
DQI	CI	GYHAN	NSTEKVDTI	L	ERNVTVTHAK	DI	LEKTHNGK	LCKLNGI PPL ELGDCSI AGW gi	133755404
DQI	CI	GYHAN	NSTEKVDTI	L	ERNVTVTHAK	DI	LEKTHNGK	LCKLNGI PPL ELGDCSI TGW gi	146760028
DQI	CI	GYHAN	NSTEKVDTI	L	ERNVTVTHAK	DI	LEKTHNGK	LCKLNGI PPL ELGDCSI AGW gi	133981962
DQI	CI	GYHAN	NSTEKVDTI	L	ERNVTVTHAK	DI	LEKTHNGK	LCKLNGI PPL ELGDCSI AGW gi	133982571
DQI	CI	GYHAN	NSTEKVDTI	L	ERNVTVTHAK	DI	LEKTHNGK	LCKLNGI PPL ELGDCSI AGW gi	133755423
DQI	CI	GYHAN	NSTEKVDTI	L	ERNVTVTHAK	DI	LEKTHNGK	LCKLNGI PPL ELGDCSI AGW gi	134047427
DQI	CI	GYHAN	NSTEKVDTI	L	ERNVTVTHAK	DI	LEKTHNGK	LCKLNGI PPL ELGDCSI AGW gi	194304556
DQI	CI	GYHAN	NSTEKVDTI	L	ERNVTVTHAK	DI	LEKTHNGK	LCKLNGI PPL ELGDCSI AGW gi	189230442
DQI	CI	GYHAN	NSTEKVDTI	L	ERNVTVTHAK	DI	LEKTHNGK	LCKLNGI PPL ELGDCSI AGW gi	189230480
DQI	CI	GYHAN	NSTEKVDTI	L	ERNVTVTHAK	DI	LEKTHNGK	LCKLNGI PPL ELGDCSI AGW gi	221326 db
DQI	CI	GYHAN	NSTEKVDTI	L	ERNVTVTHAK	DI	LEKTHNGK	LCKLNGI PPL ELGDCSI AGW gi	221324 db
DQI	CI	GYHAN	NSTEKVDTI	L	ERNVTVTHAK	DI	LEKTHNGK	LCKLNGI PPL ELGDCSI AGW gi	189230537
DQI	CI	GYHAN	NSTEKVDTI	L	ERNVTVTHAK	DI	LEKTHNGK	LCKLNGI PPL ELGDCSI AGW gi	94481532
DQI	CI	GYHAN	NSTEKVDTI	L	ERNVTVTHAK	DI	LEKTHNGK	LCKLNGI PPL ELGDCSI AGW gi	188504388
DQI	CI	GYHAN	NSTEKVDTI	L	ERNVTVTHAK	DI	LEKTHNGK	LCKLNGI PPL ELGDCSI AGW gi	188504369
DQI	CI	GYHAN	NSTEKVDTI	L	ERNVTVTHAK	DI	LEKTHNGK	LCKLNGI PPL ELGDCSI AGW gi	408515 gb

DQI CI GYHAN NSTEKVDTI L ERNVTVTHAK DI LEKTHNGK LCKLNGI PPL ELGDCSI AGW gi |408513|gb
***** ** * * ***** .*****; ***** ** *.***:***.** Cl ustal Cons

. | | | | | | | | | | |
70 80 90 100 110 120
LLGNPECDRL LSVPEWSYI M EKENPRYSLC YPGSFNDYEE LKHLLSSVKH FEKVKI LPKD gi |73921184|
LLGNPECDRL LSVPEWSYI M EKENPRYSLC YPGSFNDYEE LKHLLSSVKH FEKVKI LPKD gi |408523|gb
LLGNPECDRL LSVPEWSYI M EKENPRDGLC YPGSFNDYEE LKHLLSSVKH FEKVKI LPKD gi |133753638|
LLGNPECDRL LSVPEWSYI M EKENPRDGLC YPGSFNDYEE LKHLLSSVKH FEKVKI LPKD gi |134047408|
LLGNPECDRL LSVPEWSYI M EKENPRDGLC YPGSFNDYEE LKHLLSSVKH FEKVKI LPKD gi |133753657|
LLGNPECDRL LSVPEWSYI M EKENPRDGLC YPGSFNDYEE LKHLLSSVKH FEKVKI LPKD gi |134047523|
LLGNPECDRL LSVPEWSYI M EKENPRDGLC YPGSFNDYEE LKHLLSSVKH FEKVKI LPKD gi |145279057|
LLGNPECDRL LSVPEWSYI M EKENPRDGLC YPGSFNDYEE LKHLLSSVKH FEKVKI LPKD gi |408525|gb
LLGNPECDRL LSVPEWSYI M EKENPRDGLC YPGSFNDYEE LKHLLSSVKH FEKVKI LPKD gi |189230461|
LLGNPECDRL LSVPEWSYI M EKENPRDGLC YPGSFNDYEE LKHLLSSVKH FEKVKI LPKD gi |127057978|
LLGNPECDRL LSVPEWSYI M EKENPRDGLC YPGSFNDYEE LKHLLSSVKH FEKVKI LPKD gi |324146|gb
LLGNPECDRL LSVPEWSYI M EKENPRDGLC YPGSFNDYEE LKHLLSSVKH FEKVKI LPKD gi |305155|gb
LLGNPECDRL LSVPEWSYI M EKENPRDGLC YPGSFNDYEE LKHLLSSVKH FEKVKI LPKD gi |94481522|
LLGNPECDRL LSVPEWSYI M EKENPRDGLC YPGSFNDYEE LKHLLSSVKH FEKVKI LPKD gi |63054902|
LLGNPECDRL LSVPEWSYI M EKENPRDGLC YPGSFNDYEE LKHLLSSVKH FEKVKI LPKD gi |305117|gb
LLGNPECDRL LSVPEWSYI M EKENPRDGLC YPGSFNDYEE LKHLLSSVKH FEKVKI LPKD gi |133752958|
LLGNPECDRL LSVPEWSYI M EKENPRDGLC YPGSFNDYEE LKHLLSSVKH FEKVKI LPKD gi |145279038|
LLGNPECDRL LSVPEWSYI M EKENPRDGLC YPGSFNDYEE LKHLLSSVKH FEKVKI LPKD gi |146760066|
LLGNPECDRL LSVPEWSYI M EKENPRDGLC YPGSFNDYEE LKHLLSSVKH FEKVKI LPKD gi |305163|gb
LLGNPECDRL LSVPEWSYI M EKENPRDGLC YPGSFNDYEE LKHLLSSVKH FEKVKI LPKD gi |194352181|
LLGNPECDRL LSVPEWSYI M EKENPRDGLC YPGSFNDYEE LKHLLSSVKH FEKVKI LPKD gi |194352200|
LLGNPECDRL LSVPEWSYI M EKENPRDGLC YPGSFNDYEE LKHLLSSVKH FEKVKI LPKD gi |194352238|
LLGNPECDRL LSVPEWSYI M EKENPRDGLC YPGSFNDYEE LKHLLSSVKH FEKVKI LPKD gi |194352162|
LLGNPECDRL LSVPEWSYI M EKENPRDGLC YPGSFNDYEE LKHLLSSVKH FEKVKI LPKD gi |305171|gb
LLGNPECDRL LSVPEWSYI M EKENPRDGLC YPGSFNDYEE LKHLLSSVKH FEKVKI LPKD gi |26453383|
LLGNPECDRL LRVPEWSYI M EKENPRDGLC YPGSFNDYEE LKHLLSSVKH FEKVKI LPKD gi |188504407|
LLGNPECDRL LRVPEWSYI M EKENPRDGLC YPGSFNDYEE LKHLLSSVKH FEKVKI LPKD gi |133982551|
LLGNPECDRL LRVPEWSYI M EKENPRDGLC YPGSFNDYEE LKHLLSSVKH FEKVKI LPKD gi |146133810|
LLGNPECDRL LSVPEWSYI M EKENPRDGLC YPGSFNDYEE LKHLLSSVKH FEKVKI LPKD gi |115279062|
LLGNPECDRL LSVPEWSYI M EKENPRDGLC YPGSFNDYEE LKHLLSSVKH FEKVKI LPKD gi |145279000|
LLGNPECDRL LSVPEWSYI M EKENPRDGLC YPGSFNDYEE LKHLLSSVTH FEKVKI LPRD gi |189230499|
LLGNPECDRL LSVPEWSYI M EKENPRDGLC YPGSFNDYEE LKHLLSSVKH FEKVKI LPKD gi |408677|gb
LLGNPECDRL LRVPEWSYI M EKENPRDGLC YPGSFNDYEE LKYLSSVKH FEKVKI LPKD gi |305115|gb
LLGNPECDRL LSVPEWSYI M EKENPRDGLC YPGSFNDYEE LKHLLSSVKH FEKVKI LPKD gi |188504350|
LLGNPECDRL LRVPEWSYI M EKENPRYSLC YPGSLNDYEE LKHLLSSVKH FEKVKI LPKD gi |189230518|
LLGNPECDRL LRVPEWSYI M EKENPRYSLC YPGSLNDYEE LKHLLSSVKH FEKVKI LPKD gi |194351979|
LLGNPECDRL LRVPEWSYI M EKENPRYSLC YPGSFNDYEE LKHLLSSVKH FEKVKI LPKD gi |189230423|
LLGNPECDRL LRVPEWSYI M EKENPRYSLC YPGSFNDYEE LKHLLSSVKH FEKVKI LPKD gi |133755366|
LLGNPECDRL LRVPEWSYI M EKENPRYSLC YPGSFNDYEE LKHLLSSVKH FEKVKI LPKD gi |133755385|
LLGNPECDRL LRVPEWSYI M EKENPRYSLC YPGSFNDYEE LKHLLSSVKH FEKVKI LPKD gi |133755404|
LLGNPECDRL LRVPEWSYI M EKENPRYSLC YPGSFNDYEE LKHLLSSVKH FEKVKI LPKD gi |146760028|
LLGNPECDRL LRVPEWSYI M EKENPRYSLC YPGSFNDYEE LKHLLSSVKH FEKVKI LPKD gi |133981962|
LLGNPECDRL LRVPEWSYI M EKENPRYSLC YPGSFNDYEE LKHLLSSVKH FEKVKI LPKD gi |133982571|
LLGNPECDRL LRVPEWSYI M EKENPRYSLC YPGSFNDYEE LKHLLSSVKH FEKVKI LPKD gi |133755423|
LLGNPECDRL LRVPEWSYI M EKENPRYSLC YPGSFNDYEE LKHLLSSVKH FEKVKI LPKD gi |134047427|
LLGNPECDRL LRVPEWSYI M EKENPRYSLC YPGSFNDYEE LKHLLSSVKH FEKVKI LPKD gi |194304556|
LLGNPECDRL LRVPEWSYI M EKENPRYSLC YPGSFNDYEE LKHLLSSVKH FEKVKI LPKD gi |189230442|
LLGNPECDRL LRVPEWSYI M EKENPRYSLC YPGSFNDYEE LKHLLSSVKH FEKVKI LPKD gi |189230480|
LLGNPECDRL LRVPEWSYI M EKENPRYSLC YPGSFNDYEE LKHLLSSVKH FEKVKI LPKD gi |221326|db
LLGNPECDRL LRVPEWSYI M EKENPRYSLC YPGSFNDYEE LKHLLSSVKH FEKVKI LPKD gi |221324|db
LLGNPECDRL LRVPEWSYI M EKENPRYNLC YPGSLNEYEE LKHLLSSVKH FEKVKI LPKD gi |189230537|
LLGNPECDRL LRVPEWSYI M EKENPRYSLC YPGSFNDYEE LKHLLSSVKH FEKVKI LPKD gi |94481532|
LLGNPECDRL LRVPEWSYI M EKENPRYSLC YPGSFNDYEE LKHLLSSVKH FEKVKI LPKD gi |188504388|
LLGNPECDRL LRVPEWSYI M EKENPRYSLC YPGSFNDYEE LKHLLSSVKH FEKVKI LPKD gi |188504369|
LLGNPECDRL LSVPEWSYI M EKENPRYSLC YPGSFNDYEE LKHLLSSVKH FEKVKI LPKD gi |408515|gb
LLGNPECDRL LSVPEWSYI M EKENPRYSLC YPGSFNDYEE LKHLLSSVKH FEKVKI LPKD gi |408513|gb
***** * ***** ** * * ***** .*****; ***** ** *.***:***.** Cl ustal Cons

. | | | | | | | | | | |
130 140 150 160 170 180
RWTQHTTTGG SWACAVSGKP SFFRNMWLTL RKGSNYPVAK GSYNNTSSEQ MLI I WGVVHP gi |73921184|
RWTQHTTTGG SWACAVSGKP SFFRNMWLTL RKGSNYPVAK GSYNNTSSEQ MLI I WGVVHP gi |408523|gb
RWTQHTTTGG SRACAVSGNP SFFRNMWLTL KKGSNYPVAK GSYNNTSSEQ MLI I WGVVHP gi |133753638|
RWTQHTTTGG SRACAVSGNP SFFRNMWLTL KKGSNYPVAK GSYNNTSSEQ MLI I WGVVHP gi |134047408|
RWTQHTTTGG SRACAVSGNP SFFRNMWLTL KKGSNYPVAK GSYNNTSSEQ MLI I WGVVHP gi |133753657|
RWTQHTTTGG SRACAVSGNP SFFRNMWLTL KKGSNYPVAK GSYNNTSSEQ MLI I WGVVHP gi |134047523|
RWTQHTTTGG SRACAVSGNP SFFRNMWLTL KKGSNYPVAK GSYNNTSSEQ MLI I WGVVHP gi |145279057|
RWTQHTTTGG SRACAVSGNP SFFRNMWLTL KKGSNYPVAK GSYNNTSSEQ MLI I WGVVHP gi |408525|gb
RWTQHTTTGG SRACAVSGNP SFFRNMWLTL KKGSNYPVAK GSYNNTSSEQ MLI I WGVVHP gi |189230461|
RWTQHTTTGG SRACAVSGNP SFFRNMWLTL KKGSNYPVAK GSYNNTSSEQ MLI I WGVVHP gi |127057978|
RWTQHTTTGG SRACAVSGNP SFFRNMWLTL KEGSDYPVAK GSYNNTSSEQ MLI I WGVVHP gi |324146|gb

NDETEQRTLY	QNVGTYYSVV	TSTLNKRSTP	KI ATRPKVNG	LGGRMFSWT	LLDMWDTI	NF	gi	133982551
I DETEQRTLY	QNVETYYSVV	TSTLNKRSTP	KI ATRPKVNG	LGGRMFSWT	LLDMWDTI	NF	gi	146133810
NDETEQRTLY	QNVGTYYSVG	TSTLNKRSTP	EI ATRPKVNG	LGGRMFSWT	LLDMWDTI	NF	gi	115279062
NDETEQRTLY	QNVGTYYSVG	TSTLNKRSTP	EI ATRPKVNG	LGGRMFSWT	LLDMWDTI	NF	gi	145279000
NDETEQRTLY	QNVGTYYSVG	TSTLNKRSTP	EI ATRPKVNG	LGSRMFSWI	LLDMWDTI	NF	gi	189230499
NDETEQRTLY	QNVGTYYSVG	TSTLNKRSTP	DI ATRPKVNG	LGSRMFSWT	LLDMWDTI	NF	gi	408677 gb
NDETEQRTLY	QNVGTYYSVG	TSTLNKRSTP	EI ATRPKVNG	LGSRMFSWT	LLDMWDTI	NF	gi	305115 gb
NDETEQRTLY	QNVGTYYSVS	TSTLNKRSTP	EI ATRPKVNG	LGSRMFSWT	LLDMWDTI	NF	gi	188504350
KDEAEQRALY	QEVGTYYVSAS	TSTLNKRSTP	EI AARPEVNG	LGSRMFSWT	LLDVWDTI	NF	gi	189230518
I DEAEQRALY	QEVGTYYVSAS	TSTLNKRSTP	EI AARPEVNG	LGSRMFSWT	LLDVWDTI	NF	gi	194351979
KDEAEQRALY	QEVGTYYVSAS	TSTLNKRSTP	EI AARPEVNG	LGSRMFSWT	LLDVWDTI	NF	gi	189230423
KDEAEQRALY	QEVGTYYVSAS	TSTLNKRSTP	EI AARPEVNG	LGSRMFSWT	LLDVWDTI	NF	gi	133755366
KDEAEQRALY	QEVGTYYVSAS	TSTLNKRSTP	EI AARPEVNG	LGSRMFSWT	LLDVWDTI	NF	gi	133755385
NDEAEQRALY	QKVGTYVSAS	TSTLNKRSTP	EI AARPEVNG	LGSRMFSWT	LLDVWDTI	NF	gi	133755404
NDEAEQRALY	QKVGTYVSAS	TSTLNKRSTP	EI AARPEVNG	LGSRMFSWT	LLDVWDTI	NF	gi	146760028
KDEAEQRALY	QKVGTYVSAS	TSTLNKRSTP	EI AARPEVNG	LESRMFSWT	LLDVWDTI	NF	gi	133981962
NDEAEQRALY	QKVGTYVSAS	TSTLNKRSTP	EI AARPEVSG	LGSRMFSWT	LLDVWDTI	SF	gi	133982571
NDEAEQRALY	QKVGTYVSAS	TSTLNKRSTP	EI AARPEVSG	LGSRMFSWT	LLDVWDTI	SF	gi	133755423
NDEAEQRALY	QKVGTYVSAS	TSTLNKRSTP	EI AARPEVSG	LGSRMFSWT	LLDVWDTI	SF	gi	134047427
NDEAEQRALY	QEVGTYYVSAS	TSTLNKRSTP	EI AARPKVSG	LGSRMFSWT	LLDVWDTI	SF	gi	194304556
NDEAEQRALY	QKVGTYVSAS	TSTLNKRSTP	EI AARPEVNG	LRSRMFSWT	LLDVWDTI	NF	gi	189230442
KDEAEQRALY	QNVGTYYVSAS	TSTLNKRSTP	EI AARPEVNG	LGSRMFSWT	LLDVWDTI	NF	gi	189230480
NDEAEQRALY	QEVGTYYVSAS	TSTLNKRSTP	EI AARPKVNG	LGSRMFSWT	LLDVWDTI	NF	gi	221326 db
NDEAEQRALY	QEVGTYYVSAS	TSTLNKRSTP	EI AARPKVNG	LGSRMFSWT	LLDVWDTI	NF	gi	221324 db
NDEAEQRALY	QKVGTYVSAS	TSTLNKRSTP	EI AARPKVNG	LGSRMFSWT	LLDVWDTI	NF	gi	189230537
NDEAEQRALY	QKVGTYVSAS	TSTLNKRSTP	EI AARPKVNG	LGSRMFSWT	LLDMWDTI	NF	gi	94481532
NDEAEQRALY	QKVGTYVSAS	TSTLYKRSTP	EI AARPKVNG	LGSRMFSWT	LLDMWDTI	NF	gi	188504388
I DEAEQIALY	QKVGTYVSAS	TSTLNKRSTP	EI AARPEVNG	LGSRMFSWT	LLDMWDTI	NF	gi	188504369
NDEAEQRALY	QKVGTYVSEA	TSTLNKRSTP	EI AARPKVSG	LGSRMFSWT	LLDVWDTI	SF	gi	408515 gb
NDEAEQRALY	QEVGTYYVSEA	TSTLNKRSTP	EI AARPKVSG	LGSRMFSWT	LLDMWDTI	SF	gi	408513 gb
** ** *	*. * * * * *	* * * * * *	* * * * * *	* * * * *	* * * * * *	* * * * * *	Cl	ustal Cons

250	260	270	280	290	300			
ESTGNLVAPE	YGFKI SKRGS	SGI MKTEGTL	ENCETKQCTP	LGAI NTTLPF	HNHPLTI	GE	gi	73921184
ESTGNLVAPE	YGFKI SKRGS	SGI MKTEGTL	ENCETKQCTP	LGAI NTTLPF	HNHPLTI	GE	gi	408523 gb
ESTGNLI APE	YGFKI SKRGS	SGI MKTEGTL	GNCETKQCTP	LGAI NTTLPF	HNHPLTI	GE	gi	133753638
ESTGNLI APE	YGFKI SKRGS	SGI MKTEGTL	GNCETKQCTP	LGAI NTTLPF	HNHPLTI	GE	gi	134047408
ESTGNLI APE	YGFKI SKRGS	SGI MKTEGTL	GNCETKQCTP	LGAI NTTLPF	HNHPLTI	GE	gi	133753657
ESTGNLI APE	YGFKI SKRGS	SGI MKTEGTL	GNCETKQCTP	LGAI NTTLPF	HNHPLTI	GE	gi	134047523
ESTGNLI APE	YGFKI SKRGS	SGI MKTEGTL	GNCETKQCTP	LGAI NTTLPF	HNHPLTI	GE	gi	145279057
ESTGNLI APE	YGFKI SKRGS	SGI MKTEGTL	ENCETKQCTP	LGAI NTTLPF	HNHPLTI	GE	gi	408525 gb
ESTGNLI APE	YGFKI SKRGS	SGI MKTEGTL	ENCETKQCTP	LGAI NTTLPF	HNHPLTI	GE	gi	189230461
ESTGNLI APE	YGFKI SKRGS	SGI MKTEGTL	ENCETKQCTP	LGAI NTTLPF	HNHPLTI	GE	gi	127057978
ESTGNLI APE	YGFKI SKRGS	SGI MKTEGTL	ENCETKQCTP	LGAI NTTLPF	HNHPLTI	GE	gi	324146 gb
ESTGNLI APE	YGFKI SKRGS	SGI MKTEGTL	ENCETKQCTP	LGAI NTTLPF	HNHPLTI	GE	gi	305155 gb
ESTGNLI APE	YGFKI SKRGS	SGI MKTEGTL	ENCETKQCTP	LGAI NTTLPF	HNHPLTI	GE	gi	94481522
ESTGNLI APE	YGFKI SKRGS	SGI MKTEGTL	ENCETKQCTP	LGAI NTTLPF	HNHPLTI	GE	gi	63054902
ESTGNLI APE	YGFKI SKRGS	SGI MKTEGTL	GNCETKQCTP	LGAI NTTLPF	HNHPLTI	GE	gi	305117 gb
ESTGNLI APE	YGFKI SKRGS	SGI MKTEGTL	GNCETKQCTP	LGAI NTTLPF	HNHPLTI	GE	gi	133752958
ESTGNLI APE	YGFKI SKRGS	SGI MKTEGTL	GNCETKQCTP	LGAI NTTLPF	HNHPLTI	GE	gi	145279038
ESTGNLI APE	YGFKI SKRGS	SGI MKTEGTL	GNCETKQCTP	LGAI NTTLPF	HNHPLTI	GE	gi	146760066
ESTGNLI APE	YGFKI SKRGS	SGI MKTEGTL	GNCETKQCTP	LGAI NTTLPF	HNHPLTI	GE	gi	305163 gb
ESTGNLI APE	YGFKI SKRGS	SGI MKTEGTL	ENCETKQCTP	LGAI NTTLPF	HNHPLTI	GE	gi	194352181
ESTGNLI APE	YGFKI SKRGS	SGI MKTEGTL	ENCETKQCTP	LGAI NTTLPF	HNHPLTI	GE	gi	194352200
ESTGNLI APE	YGFKI SKRGS	SGI MKTEGTL	ENCETKQCTP	LGAI NTTLPF	HNHPLTI	GE	gi	194352219
ESTGNLI APE	YGFKI SKRGS	SGI MKTEGTL	ENCETKQCTP	LGAI NTTLPF	HNHPLTI	GE	gi	194352238
ESTGNLI APE	YGFKI SKRGS	SGI MKTEGTL	ENCETKQCTP	LGAI NTTLPF	HNHPLTI	GE	gi	194352162
ESTGNLI APE	YGFKI SKRGS	SGI MKTEGTL	ENCETKQCTP	LGAI NTTLPF	HNHPLTI	GE	gi	305171 gb
ESTGNLI APE	YGFKI SKRGS	SGI MKTEGTL	ENCETKQCTP	LGAI NTTLPF	HNHPLTI	GE	gi	26453383
ESTGNLI APE	YGFKI SKRGS	SGI MKTERTL	ENCETKQCTP	LGAI NTTLPF	HNHPLTI	GE	gi	188504407
ESTGNLI APE	YGFKI SKRGS	SGI MKTEGTL	ENCETKQCTP	LGAI NTTLPF	HNHPLTI	GE	gi	133982551
ESTGNLI APE	YGFKI SKRGS	SGI MKTEGTL	ENCETKQCTP	LGAI NTTLPF	HNHPLTI	GE	gi	146133810
ESTGNLI APE	YGFKI SKRGS	SGI MKTEGTL	ENCETKQCTP	LGAI NTTLPF	HNHPLTI	GE	gi	115279062
ESTGNLI APE	YGFKI SKRGS	SGI MKTEGTL	ENCETKQCTP	LGAI NTTLPF	HNHPLTI	GE	gi	145279000
ESTGNLI APE	YGFKI SKRGS	SGI MKTEGTL	ENCETKQCTP	LGAI NTTLPF	HNHPLTI	GE	gi	189230499
ESTGNLI APE	YGFKI SKRGS	SGI MKTEGTL	ENCETKQCTP	LGAI NTTLPF	HNHPLTI	GE	gi	408677 gb
ESTGNLI APE	YGFKI SKRGS	SGI MKTEGTL	ENCETKQCTP	LGAI NTTLPF	HNHPLTI	GE	gi	305115 gb
ESTGNLI APE	YGFKI SKRGS	SGI MKTEGTL	ENCETKQCTP	LGAI NTTLPF	HNHPLTI	GE	gi	188504350
ESTGNLVAPE	YGFKI SKRGS	SGI MKTEGTL	GNCETKQCTP	LGAI NTTLPF	HNHPLTI	GE	gi	189230518
ESTGNLVAPE	YGFKI SKRGS	SGI MKTEGTL	GNCETKQCTP	LGAI NTTLPF	HNHPLTI	GE	gi	194351979
ESTGNLVAPE	YGFKI SKRGS	SGI MKTEGTL	GNCETKQCTP	LGAI NTTLPF	HNHPLTI	GE	gi	189230423
ESTGNLVAPE	YGFKI SKRGS	SGI MKTEGTL	GNCETKQCTP	LGAI NTTLPF	HNHPLTI	GE	gi	133755366
ESTGNLVAPE	YGFKI SKRGS	SGI MKTEGTL	GNCETKQCTP	LGAI NTTLPF	HNHPLTI	GE	gi	133755385
ESTGNLVAPE	YGFKI SKRGS	SGI MKTEGTL	GNCETKQCTP	LGAI NTTLPF	HNHPLTI	GE	gi	133755404
ESTGNLVAPE	YGFKI SKRGS	SGI MKTEGTL	GNCETKQCTP	LGAI NTTLPF	HNHPLTI	GE	gi	146760028
ESTGNLVAPE	YGFKI SKRGS	SGI MKTEGTL	GNCETKQCTP	LGAI NTTLPF	HNHPLTI	GE	gi	133981962

ESTGNLVAPE	YGFKI SKRGS	SGI MKTEGTL	GNCETKCQTP	LGAI NNTLPPF	HNVHPLTI	GE	gi	133982571
ESTGNLVAPE	YGFKI SKRGS	SGI MKTEGTL	GNCETKCQTP	LGAI NNTLPPF	HNVHPLTI	GE	gi	133755423
ESTGNLVAPE	YGFKI SKRGS	SGI MKTEGTL	GNCETKCQTP	LGAI NNTLPPF	HNVHPLTI	GE	gi	134047427
ESTGNLVAPE	YGFKI SKRGS	SGI MKTEGTL	GNCETKCQTP	LGAI NNTLPPF	HNVHPLTI	GE	gi	194304556
ESTGNLVAPE	YGFKI SKRGS	SGI MKTEGTL	GNCETKCQTP	LGAI NNTLPPF	HNVHPLTI	GE	gi	189230442
ESTGNLVAPE	YGFKI SKRGS	SGI MKTEGTL	GNCETKCQTP	LGAI NNTLPPF	HNVHPLTI	GE	gi	189230480
ESTGNLVAPE	YGFKI SKRGS	SGI MKTEGTL	GNCETKCQTP	LGAI NNTLPPF	HNVHPLTI	GE	gi	221326 db
ESTGNLVAPE	YGFKI SKRGS	SGI MKTEGTL	GNCETKCQTP	LGAI NNTLPPF	HNVHPLTI	GE	gi	221324 db
ESTGNLVVPE	YGFKI SKRGS	SGI MKTEGTL	GNCETKCQTP	LGAI NNTLPPF	HNVHPLTI	GE	gi	189230537
ESTGNLVAPE	YGFKI SKRGS	SGI MKTEGTL	ENCETKCQTP	LGAI NNTLPPF	HNVHPLTI	GE	gi	94481532
ESTGNLVAPE	YGFKI SKRGS	SGI MKTEGTL	ENCETKCQTP	LGAI NNTLPPF	HNVHPLTI	GE	gi	188504388
ESTGNLVAPE	YGFKI SKRGS	SGI MKTEGTL	ENCETKCQTP	LGAI NNTLPPF	HNVHPLTI	GE	gi	188504369
ESTGNLVAPE	YGFKI SKRGS	SGI MKTEGTL	ENCETKCQTP	LGAI NNTLPPF	HNVHPLTI	GE	gi	408515 gb
ESTGNLVAPE	YGFKI SKRGS	SGI MKTEGTL	ENCETKCQTP	LGAI NNTLPPF	HNVHPLTI	GE	gi	408513 gb
*****	*****	*****	*****	*****	*****	*****	*****	Clustal Cons

.....								
	310		320					
CPKYVKSEKL	VLATGLRNVP	QI	ESR				gi	73921184
CPKYVKSEKL	VLATGLRNVP	QI	ESR				gi	408523 gb
CPKYVKSEKL	VLATGLRNVP	QI	ESR				gi	133753638
CPKYVKSEKL	VLATGLRNVP	QI	ESR				gi	134047408
CPKYVKSEKL	VLATGLRNVP	QI	ESR				gi	133753657
CPKYVKSEKL	VLATGLRNVP	QI	ESR				gi	134047523
CPKYVKSEKL	VLATGLRNVP	QI	ESR				gi	145279057
CPKYVKSEKL	VLATGLRNVP	QI	ESR				gi	408525 gb
CPKYVKSEKL	VLATGLRNVP	QI	ESR				gi	189230461
CPKYVKSEKL	VLATGLRNVP	QI	ESR				gi	127057978
CPKYVKSEKL	VLATGLRNVP	QI	ESR				gi	324146 gb
CPKYVKSEKL	VLATGLRNVP	QI	ESR				gi	305155 gb
CPKYVKSEKL	VLATGLRNVP	QI	ESR				gi	94481522
CPKYVKSEKL	VLATGLRNVP	QI	ESR				gi	63054902
CPKYVKSEKL	VLATGLRNVP	QI	ESR				gi	305117 gb
CPKYVKSEKL	VLATGLRNVP	QI	ESR				gi	133752958
CPKYVKSEKL	VLATGLRNVP	QI	ESR				gi	145279038
CPKYVKSEKL	VLATGLRNVP	QI	ESR				gi	146760066
CPKYVKSEKL	VLATGLRNVP	QI	ESR				gi	305163 gb
CPKYVKSEKL	VLATGLRNVP	QI	ESR				gi	194352181
CPKYVKSEKL	VLATGLRNVP	QI	ESR				gi	194352200
CPKYVKSEKL	VLATGLRNVP	QI	ESR				gi	194352219
CPKYVKSEKL	VLATGLRNVP	QI	ESR				gi	194352238
CPKYVKSEKL	VLATGLRNVP	QI	ESR				gi	194352162
CPKYVKSEKL	VLATGLRNVP	QI	ESR				gi	305171 gb
CPKYVKSEKL	VLATGLRNVP	QI	ESR				gi	26453383
CPKYVKSEKL	VLATGLRNVP	QI	EPR				gi	188504407
CPKYVKSEKL	VLATGLRNVP	QI	ESR				gi	133982551
CPKYVKSEKL	VLATGLRNVP	QI	ESR				gi	146133810
CPKYVKSEKL	VLATGLRNVP	QI	ESR				gi	115279062
CPKYVKSEKL	VLATGLRNVP	QI	ESR				gi	145279000
CPKYVKSEKL	VLATGLRNVP	QI	ESR				gi	189230499
CPKYVKSEKL	VLATGLRNVP	QI	ESR				gi	408677 gb
CPKYVKSEKL	VLATGLRNVP	QI	ESR				gi	305115 gb
CPKYVKSEKL	VLATGLRNVP	QI	ESR				gi	188504350
CPKYVKSEKL	VLATGLRNVP	QI	ESR				gi	189230518
CPKYVKSEKL	VLATGLRNVP	QI	ESR				gi	194351979
CPKYVKSEKL	VLATGLRNVP	QI	ESR				gi	189230423
CPKYVKSEKL	VLATGLRNVP	QI	ESR				gi	133755366
CPKYVKSEKL	VLATGLRNVP	QI	ESR				gi	133755385
CPKYVKSEKL	VLATGLRNVP	QI	ESR				gi	133755404
CPKYVKSEKL	VLATGLRNVP	QI	ESR				gi	146760028
CPKYVKSEKL	VLATGLRNVP	QI	ESR				gi	133981962
CPKYVKSEKL	VLATGLRNVP	QI	ESR				gi	133982571
CPKYVKSEKL	VLATGLRNVP	QI	ESR				gi	133755423
CPKYVKSEKL	VLATGLRNVP	QI	ESR				gi	134047427
CPKYVKSEKL	VLATGLRNVP	QI	ESR				gi	194304556
CPKYVKSEKL	VLATGLRNVP	QI	ESR				gi	189230442
CPKYVKSEKL	VLATGLRNVP	QI	ESR				gi	189230480
CPKYVKSEKL	VLATGLRNVP	QI	ESR				gi	221326 db
CPKYVKSEKL	VLATGLRNVP	QI	ESR				gi	221324 db
CPKYVKSEKL	VLATGLRNVP	QI	ESR				gi	189230537
CPKYVKSEKL	VLATGLRNVP	QI	ESR				gi	94481532
CPKYVKSEKL	VLATGLRNVP	QI	ESR				gi	188504388
CPKYVKSEKL	VLATGLRNVP	QI	ESR				gi	188504369
CPKYVKSEKL	VLATGLRNVP	QI	ESR				gi	408515 gb
CPKYVKSEKL	VLATGLRNVP	QI	ESR				gi	408513 gb
*****	*****	*****	*****	*****	*****	*****	*****	Clustal Cons

Alignment: E:\1_Data Penelitian\9_Ridlo\Data\database\Ha\HA1\human\H3N2. al n

Alignment table showing sequence coordinates (10-60) and corresponding amino acid residues (e.g., QKLPGNDNST, PNGTI VKTI T, NDQI EVT NAT, ELVQSSSTGE, ICDSPHQI LD gi) with accession numbers on the right (e.g., 193084867, 189303155, 188076387).

QDLPGNDNST	ATLCLGHHAV	PNGTLVKTI	DDQI EVTNAT	ELVQSSSTGK	I CNNPHRI	LD gi	194352074
QDLPGNDNST	ATLCLGHHAV	PNGTLVKTI	DDQI EVTNAT	ELVQSSSTGK	I CNNPHRI	LD gi	194304765
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QDLPGKGNNT	ATLCLGHHAV	PNGTLVKTI	DDQVEVTNAT	ELVQNLMSGK	I CSNPHRI	LD gi	14275704
..**.*	*****	***.*	..**.*	*****	****.*	**..**.*	Clustal Cons

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GENCTLI	DAL	LGDPQCDGFQ	NKKWDLFVER	SKAYSNCYPY	DVPDYASLRS	LVASSGTLEF	gi	189303155
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NNESFNWTGV	AQNGTSSACK	RRSI KSFSSR	LNWLHOLKYR	YPALNVTMPN	NDKFDKLYI	W gi	46981871
NNESFNWTGV	AQNGTSSACK	RRSI KSFSSR	LNWLHOLKYK	YPALNVTMPN	NEKFDKLYI	W gi	115607670
NNESFNWTGV	AQNGTSSACK	RRSI KSFSSR	LNWLHOLKYK	YPALNVTMPN	NEKFDKLYI	W gi	115521636
NNESFNWTGV	AQNGTSSACK	RRSNKSFFSR	LNWLHOLKYK	YPALNVTMPN	NEKFDKLYI	W gi	115521598
NNESFNWTGV	AQNGTSSACK	RRSNKSFFSR	LNWLHOLKYK	YPALNVTMPN	NEKFDKLYI	W gi	94481528
NNESFNWTGV	AQNGTSSACK	RRSNKSFFSR	LNWLHOLKYK	YPALNVTMPN	NEKFDKLYI	W gi	194352295
NNESFNWTGV	AQNGTSSACK	RRSNNSFFSR	LNWLHOLKYK	YPALNVTMPN	NEKFDKLYI	W gi	92090508
I TEGFTWTGV	TQNGGSNACK	RGPGSGFFSR	LNWLTSGST	YPVLNVTMPN	NDNFDKLYI	W gi	85816052
I TEGFTWTGV	TQNGGSNACK	RGPGSGFFSR	LNWLTSGST	YPVLNVTMPN	NDNFDKLYI	W gi	193805114
I TEGFTWTGV	TQNGGSNACK	RGPGSGFFSR	LNWLTSGST	YPVLNVTMPN	NDNFDKLYI	W gi	193805171
I TEGFTWTGV	TQNGGSNACK	RGPGSGFFSR	LNWLTSGST	YPVLNVTMPN	NDNFDKLYI	W gi	193805209
I TEGFTWTGV	TQNGGSNACK	RGPGSGFFSR	LNWLTSGST	YPVLNVTMPN	NDNFDKLYI	W gi	193805266
I TEGFTWTGV	TQNGGSNACK	RGPGSGFFSR	LNWLTSGST	YPVLNVTMPN	NDNFDKLYI	W gi	194352017
I TEGFTWTGV	TQNGGSNACK	RGPGSGFFSR	LNWLTSGST	YPVLNVTMPN	NDNFDKLYI	W gi	14009692
I TEGFTWTGV	TQNGGSNACK	RGPGSGFFSR	LNWLTSGST	YPVLNVTMPN	NDNFDKLYI	W gi	148910822
I TEGFTWTGV	TQNGGSNACK	RGPGSGFFSR	LNWLTSGST	YPVLNVTMPN	NDNFDKLYI	W gi	148910824
I TEGFTWTGV	TQNGGSNACK	RGPGSGFFSR	LNWLTSGST	YPVLNVTMPN	NDNFDKLYI	W gi	194352074
I TEGFTWTGV	TQNGGSNACK	RGPGSGFFSR	LNWLTSGST	YPVLNVTMPN	NDNFDKLYI	W gi	194304765
I TEGFTWTGV	TQNGGSNACK	RGPGSGFFSR	LNWLTSGST	YPVLNVTMPN	NDNFDKLYI	W gi	194352112
I TEGFTWTGV	TQNGGSNACK	RGPGSGFFSR	LNWLTSGST	YPVLNVTMPN	NDNFDKLYI	W gi	134047618
I TEGFTWTGV	TQNGGSNACK	RGPGSGFFSR	LNWLTSGST	YPVLNVTMPN	NDNFDKLYI	W gi	194352093
I TEGFTWTGV	TQNGGSNACK	RGPGSGFFSR	LNWLTSGST	YPVLNVTMPN	NDNFDKLYI	W gi	126567435
I TEGFTWTGV	TQNGGSNACK	RGPGSGFFSR	LNWLTSGST	YPVLNVTMPN	NDNFDKLYI	W gi	194304632
I TEGFTWTGV	TQNGGSNACK	RGPGSGFFSR	LNWLTSGST	YPVLNVTMPN	NDNFDKLYI	W gi	106907813
I TEGFTWTGV	TQNGGSNACK	RGPGSGFFSR	LNWLTSGST	YPVLNVTMPN	NDNFDKLYI	W gi	60753
I TEGFTWTGV	TQNGGSNACK	RGPGSGFFSR	LNWLTSGST	YPVLNVTMPN	NDNFDKLYI	W gi	194304670
I TEGFTWTGV	TQNGGSNACK	RGPGSGFFSR	LNWLTSGST	YPVLNVTMPN	NDNFDKLYI	W gi	194304651
I TEGFTWTGV	TQNGGSNACK	RGPGSGFFSR	LNWLTSGST	YPVLNVTMPN	NDNFDKLYI	W gi	194304746
I TEGFTWTGV	TQNGGSNACK	RGPSSGFFSR	LNWLTSGST	YPVLNVTMPN	NDNFDKLYI	W gi	118420992
I TEGFTWTGV	TQNGGSNACK	RGPSSGFFSR	LNWLTSGST	YPVLNVTMPN	NDNFDKLYI	W gi	145279136
I TEGFTWTGV	TQNGGSNACK	RGPGSGFFSR	LNWLTSGST	YPVLNVTMPN	NDNFDKLYI	W gi	125664195
I TEGFTWTGV	TQNGGSNACK	RGPGSGFFSR	LNWLTSGST	YPVLNVTMPN	NDNFDKLYI	W gi	80977928
I TEGFTWTGV	TQNGGSNACK	RGPGSGFFSR	LNWLTSGST	YPVLNVTMPN	NDNFDKLYI	W gi	125664233
I TEGFTWTGV	TQNGGSNACK	RGPNGGFFSR	LNWLTSGST	YPVLNVTMPN	NDNFDKLYI	W gi	148628604
VNESFNWTGV	TQNGGSNACK	RGPSSSFFSR	LNWLKSGNT	YPLMLNVTMPN	SDGFDKLYI	W gi	14275704
..*.*.*	*.*.*.*.*	*.*.*.*.*	*.*.*.*.*	*.*.*.*.*	*.*.*.*.*	Cl	ustal Cons

GVHHPGTDND	QI FLYAQASG	RI TVSTKRSQ	QTVI PNI GSR	PRVRNI PSRI	SI YWTI VKPG	gi	193084867
GVHHPGTDND	QI FLYAQASG	RI TVSTKRSQ	QTVI PNI GSR	PRVRNI PSRI	SI YWTI VKPG	gi	189303155
GVHHPGTDND	QI FLYAQASG	RI TVSTKRSQ	QTVI PNI GSR	PRVRNI PSRI	SI YWTI VKPG	gi	188076387
GVHHPGTDND	QI FLYAQASG	RI TVSTKRSQ	QTVI PNI GSR	PRVRNI PSRI	SI YWTI VKPG	gi	194293957
GVHHPGTDND	QI FLYAQASG	RI TVSTKRSQ	QTVI PNI GSR	PRVRNI PSRI	SI YWTI VKPG	gi	194293953
GVHHPGTDND	QI FLYAQASG	RI TVSTKRSQ	QTVI PNI GSR	PRVRNI PSRI	SI YWTI VKPG	gi	189303103
GVHHPGTDND	QI FLYAQASG	RI TVSTKRSQ	QTVI PNI GSR	PRVRNI PSRI	SI YWTI VKPG	gi	194294007
GVHHPGTDND	QI FLYAQASG	RI TVSTKRSQ	QTVI PNI GSR	PRVRNI PSRI	SI YWTI VKPG	gi	194294003
GVHHPGTDND	QI FLYAQASG	RI TVSTKRSQ	QTVI PNI GSR	PRVRNI PSRI	SI YWTI VKPG	gi	193084879
GVHHPGTDND	QI FLYAQASG	RI TVSTKRSQ	QTVI PNI GSR	PRVRNI PSRI	SI YWTI VKPG	gi	194294015
GVHHPGTDND	QI FLYAQASG	RI TVSTKRSQ	QTVI PNI GSR	PRVRNI PSRI	SI YWTI VKPG	gi	194580029
GVHHPGTDND	QI FLYAQASG	RI TVSTKRSQ	QTVI PNI GSR	PRVRNI PSRI	SI YWTI VKPG	gi	188076381
GVHHPGTDND	QI FLYAQASG	RI TVSTKRSQ	QTVI PNI GSR	PRVRNI PSRI	SI YWTI VKPG	gi	194293975
GVHHPGTDND	QI FLYAQASG	RI TVSTKRSQ	QTVI PNI XSR	PRVRNI PSRI	SI YWTI VKPG	gi	194294019

GVHHPGTDND	QI FLYAQASG	RI TVSTKRSQ	QTVI PNI GSR	XRXRNI PSRI	SI YWTI VKPG	gi	194293991
GVHHPGTDND	QI FLYAQASG	RI TVSTKRSQ	QTVI PNI GSR	XRVVNI PSRI	SI YWTI VKPG	gi	194294023
GVHHPGTDND	QI FLYAQASG	RI TVSTKRSQ	QTVI PNI GSR	PRVRNI PSRI	SI YWTI VKPG	gi	193084875
GVHHPGTDND	QI FLYAQASG	RI TVSTKRSQ	QTVI PNI GSR	PRVRDI PSRI	SI YWTI VKPG	gi	194293971
GVHHPGTDND	QI FLYAQASG	RI TVSTKRSQ	QTVI PNI GSR	PRVRNI PSRI	SI YWTI VKPG	gi	189303139
GVHHPGTDND	QI FLYAQASG	RI TVSTKRSQ	QTVI PNI GSR	PRVRDI PSRI	SI YWTI VKPG	gi	194293995
GVHHPGTDND	QI FLYAQASG	RI TVSTKRSQ	QTVI PNI GSR	PRVRBI PSRI	SI YWTI VKPG	gi	189303151
GVHHPGTDND	QI FLYAQASG	RI TVSTKRSQ	QTVI PNI GSR	PRVRNI PSRI	SI YWTI VKPG	gi	194294011
GVHHPGTDND	QI FLYAQASG	RI TVSTKRSQ	QTVI PNI GSR	PRVRNI PSRI	SI YWTI VKPG	gi	194293949
GVHHPGTDND	QI FLYAQASG	RI TVSTKRSQ	QTVI PNI GSR	PRVRNI PSRI	SI YWTI VKPG	gi	188076407
GVHHPGTDND	QI FLYAQASG	RI TVSTKRSQ	QTVI PNI GSR	PRVRNI PSRI	SI YWTI VKPG	gi	194293961
GI HHPGTDND	QI FLYAQASG	RI TVSTKRSQ	QTVI PNI GSR	PXVRNI PSRI	SI YWTI VKPG	gi	189303163
GI HHPGTDND	QI FLYAQASG	RI TVSTKRSQ	QTVI PNI GSR	PRVRNI PSRI	SI YWTI VKPG	gi	193084883
GVHHPGTDND	QI FLYAQASG	RI TVSTKRSQ	QTVI PNI RSR	PRVRNI PSRI	SI YWTI VKPG	gi	194293979
GVHHPGTDND	QI FLYAQASG	RI TVSTKRSQ	QTVI PNI GSR	PRVRNI PSRI	SI YWTI VKPG	gi	194293983
GVHHPGTDND	QI FLYAQASG	RI TVSTKRSQ	QTVI PNI GSR	PRVRDI PSRI	SI YWTI VKPG	gi	189303147
GVHHPGTDND	QI FLYAQASG	RI TVSTKRSQ	QTVI PNI GSR	PRVRNI PSRI	SI YWTI VKPG	gi	194293999
GVHHPGTDND	QI FLYAQASG	RI TVSTKRSQ	QTVI PNI GSR	PRVRNI PSRI	SI YWTI VKPG	gi	189303159
GVHHPGTDND	QI FLYAQASG	RI TVSTKRSQ	QTVI PNI GSR	PRVRNI PSRI	SI YWTI VKPG	gi	189303115
GVHHPGTDND	QI FLYAQASG	RI TVSTKRSQ	QTVI PNI GSR	PRVRDI PSRI	SI YWTI VKPG	gi	189303143
GVHHPGTDND	QI FLYAQASG	RI TVSTKRSQ	QTVI PNI GSR	LRVRDI PSRI	SI YWTI VKPG	gi	193084863
GVHHPGTDND	QI SLYAQASG	RI TVSTKRSQ	QTVI PSI GSR	PRI RDVPSRI	SI YWTI VKPG	gi	73921186
GVHHPSTDS	QTSLYVQASG	RVTVSTKRSQ	QTVI PNI GSR	PWVRGVSSRI	SI YWTI VKPG	gi	90571879
GVHHPSTDS	QTSLYVQASG	RVTVSTKRSQ	QTVI PNI GSR	PWVRGVSSRI	SI YWTI VKPG	gi	89923293
GVHHPSTDS	QTSLYVQASG	RVTVSTKRSQ	QTVI PNI GSR	PWVRGVSSRI	SI YWTI VKPG	gi	14030469
GVHHPSTDS	QTSLYVQASG	RVTVSTKRSQ	QTVI PNI GSR	PWVRGVSSRI	SI YWTI VKPG	gi	14030467
GVHHPSTDS	QTSLYVQASG	RVTVSTKRSQ	QTVI PNI GSR	PWVRGVSSRI	SI YWTI VKPG	gi	89938645
GVHHPSTDS	QTSLYVHASG	RVTVSTKRSQ	QTVI PNI GSR	PWVRGVSSRI	SI YWTI VKPG	gi	194268913
GVHHPSTDS	QTSLYVHASG	RVTVSTKRSQ	QTVI PNI GSR	PWVRGVSSRI	SI YWTI VKPG	gi	194268917
GVHHPSTDS	QTSLYVHASG	RVTVSTKRSQ	QTVI PNI GSR	PWVRGVSSRI	SI YWTI VKPG	gi	194268573
GVHHPSTDS	QTSLYVHASG	RVTVSTKRSQ	QTVI PNI GSR	PWVRGVSSRI	SI YWTI VKPG	gi	194268581
GVHHPSTDS	QTSLYVHASG	RVTVSTKRSQ	QTVI PNI GSR	PWVRGVSSRI	SI YWTI VKPG	gi	194268575
GVHHPSTDS	QTSLYVHASG	RVTVSTKRSQ	QTVI PNI GSR	PWVRGVSSRI	SI YWTI VKPG	gi	194268911
GVHHPSTDS	QTSLYVHASG	RVTVSTKRSQ	QTVI PNI GSR	PWVRGVSSRI	SI YWTI VKPG	gi	194268915
GI HHPSTDS	QTSLYVHASG	RVTVSTKRSQ	QTVI PNI GSR	PWVRGVSSRI	SI YWTI VKPG	gi	194268907
GVHHPSTDS	QTSLYVQASG	RVTVSTKRSQ	QTVI PNI GSR	PWVRGVSSRI	SI YWTI VKPG	gi	89789541
GVHHPSTDS	QTSLYVQASG	RVTVSTKRSQ	QTVI PNI GSR	PWVRGVSSRI	SI YWTI VKPG	gi	14030471
GVHHPSTDS	QTSLYVQASG	RVTVSTKRSQ	QTVI PNI GSR	PWVRGVSSRI	SI YWTI VKPG	gi	109675432
GVHHPSTDS	QTSLYVQASG	RVTVSTKRSQ	QTVI PNI GSR	PWVRGVSSRI	SI YWTI VKPG	gi	91126541
GVHHPSTDS	QTSLYVQASG	RVTVSTKRSQ	QTVI PNI GSR	PWVRGVSSRI	SI YWTI VKPG	gi	89784791
GVHHPSTDS	QTSLYVQASG	RVTVSTKRSQ	QTVI PNI GSR	PWVRGVSSRI	SI YWTI VKPG	gi	194268899
GVHHPSTDS	QTSLYVQASG	RVTVSTKRSQ	QTVI PNI GSR	PWVRGVSSRI	SI YWTI VKPG	gi	194268561
GVHHPSTDS	QTSLYVQASG	RVTVSTKRSQ	QTVI PNI GSR	PWVRGVSSRI	SI YWTI VKPG	gi	14486408
GVHHPSTDSV	QTSVYVQASG	RVTVSTKRSQ	QTVI PNI GSR	PWVRGVSSRI	SI YWTI VKPG	gi	92090510
GVHHPSTDS	QTSLYTOASG	RVTVSTKRSQ	QTVI PNI GSR	PWVRGI SSRI	SI YWTI VKPG	gi	46981871
GVHHPSTDS	QI SLYAQASG	RVTVSTKRSQ	QTVI PNI GSR	PWVRGVSSRI	SI YWTI VKPG	gi	115607670
GVHHPSTDS	QI SLYAQASG	RVTVSTKRSQ	QTVI PNI GSR	PWVRGVSSRI	SI YWTI VKPG	gi	115521636
GI HHPSTDS	QI SLYAQASG	RVTVSTKRSQ	QTVI PNI GSR	PWVRGVSSRI	SI YWTI VKPG	gi	115521598
GVHHPSTDS	QI SI YAQASG	RVTVSTKRSQ	QTVI PNI GSS	PWVRGVSSRI	SI YWTI VKPG	gi	94481528
GVHHPSTDS	QI SI YAQASG	RVTVSTKRSQ	QTVI PNI GSS	PWVRGVSSRI	SI YWTI VKPG	gi	194352295
GVHHPSTDS	QI SI YAQASG	RVTVSTKRSQ	QTVI PNI GSI	PWVRGVSSRI	SI YWTI VKPG	gi	92090508
GVHHPSTNOE	QTSLYVQASG	RVTVSTRRSQ	QTI I PNI GSR	PWVRGLSSRI	SI YWTI VKPG	gi	85816052
GVHHPSTNOE	QTSLYVQASG	RVTVSTRRSQ	QTI I PNI GSR	PWVRGLSSRI	SI YWTI VKPG	gi	193805114
GVHHPSTNOE	QTSLYVQASG	RVTVSTRRSQ	QTI I PNI GSR	PWVRGLSSRI	SI YWTI VKPG	gi	193805171
GVHHPSTNOE	QTSLYVQASG	RVTVSTRRSQ	QTI I PNI GSR	PWVRGLSSRI	SI YWTI VKPG	gi	193805209
GVHHPSTNOE	QTSLYVQASG	RVTVSTRRSQ	QTI I PNI GSR	PWVRGLSSRI	SI YWTI VKPG	gi	193805266
GVHHPSTNOE	QTSLYVQASG	RVTVSTRRSQ	QTI I PNI GSR	PWVRGLSSRI	SI YWTI VKPG	gi	194352017
GVHHPSTNOE	QTSLYVQASG	RVTVSTRRSQ	QTI I PNI GSR	PWVRGLSSRI	SI YWTI VKPG	gi	14009692
GVHHPSTNOE	QTSLYVQASG	RVTVSTRRSQ	QTI I PNI GSR	PWVRGLSSRI	SI YWTI VKPG	gi	148910822
GVHHPSTNOE	QTSLYVQASG	RVTVSTRRSQ	QTI I PNI GSR	PWVRGLSSRI	SI YWTI VKPG	gi	148910824
GVHHPSTNOE	QTSLYVQASG	RVTVSTRRSQ	QTI I PNI GSR	PWVRGLSSRI	SI YWTI VKPG	gi	194352074
GVHHPSTNOE	QTSLYVQASG	RVTVSTRRSQ	QTI I PNI GSR	PWVRGLSSRI	SI YWTI VKPG	gi	194304765
GVHHPSTNOE	QTSLYVQASG	RVTVSTRRSQ	QTI I PNI GSR	PWVRGLSSRI	SI YWTI VKPG	gi	194352112
GVHHPSTNOE	QTSLYVQASG	RVTVSTRRSQ	QTI I PNI GSR	PWVRGLSSRI	SI YWTI VKPG	gi	134047618
GVHHPSTNOE	QTSLYVQASG	RVTVSTRRSQ	QTI I PNI ESR	PWVRGLSSRI	SI YWTI VNP	gi	194352093
GVHHPSTNOE	QTSLYVQASG	RVTVSTRRSQ	QTI I PNI ESR	PWVRGLSSRI	SI YWTI VKPG	gi	126567435
GVHHPSTNOE	QTSLYVQASG	RVTVSTRRSQ	QTI I PNI WSR	PWVRGLSSRI	SI YWTI VKPG	gi	194304632
GVHHPSTNOE	QTSLYVQASG	RVTVSTRRSQ	QTI I PNI GSR	PWVRGLSSRI	SI YWTI VKPG	gi	106907813
GI HHPSTNOE	QTSLYVQASG	RVTVSTRRSQ	QTI I PNI GSR	PWVRGLSSRI	SI YWTI VKPG	gi	607531emb
GVHHPSTNOE	QTSLYVQASG	RVTVSTRRSQ	QTI I PNI GSR	PWVRGLSSRI	SI YWTI VKPG	gi	194304670
GVHHPSTNOE	QTSLYVQASG	RVTVSTRRSQ	QTI I PNI GSR	PWVRGLSSRI	SI YWTI VKPG	gi	194304651
GVHHPSTNOE	QTSLYVQASG	RVTVSTRRSQ	QTI I PNI GSR	PWVRGLSSRI	SI YWTI VKPG	gi	194304746
GVHHPSTNOE	QTSLYVQASG	RVTVSTRRSQ	QTI I PNI GSR	PWVRGLSSRI	SI YWTI VKPG	gi	118420992
GVHHPSTNOE	QTSLYVQASG	RVTVSTRRSQ	QTI I PNI GSR	PWVRGLSSRI	SI YWTI VKPG	gi	145279136
GVHHPSTNOE	QTSLYVQASG	RVTVSTRRSQ	QTI I PNI GSR	PWVRGLSSRI	SI YWTI VKPG	gi	125664195
GVHHPSTNOE	QTSLYVQASG	RVTVSTRRSQ	QTI I PNI GSR	PWVRGLSSRI	SI YWTI VKPG	gi	80977928
GVHHPSTNOE	QTSLYVQASG	RVTVSTRRSQ	QTI I PNI GSR	PWVRGLSSRI	SI YWTI VKPG	gi	125664233

GVHHPSTNQE QTSLYVQESG RVTVSTRRSQ OSI I PNI GSR PWVRGOSSRI SI YWTI VKPG gi 148628604
 GVHHPSTDRE QI NLYVQASG KI TVSTKRSQ QTI I PNVGSR PWVRGLSSRI SI YWTI VKPG gi 14275704 |
 *.***.*. * :.:. ** :****.*. :.:.**.* * :****.*.*** Clustal Cons

	250	260	270	280	290	300		
DI LLI NSTGN	LI APRGYFKI	RSGKSSI MRS	DAPI GKCENSE	CI TPNGSI PN	DKPFQNVNRI	gi	193084867	
DI LLI NSTGN	LI APRGYFKI	RSGKSSI MRS	DAPI GKCENSE	CI TPNGSI PN	DKPFQNVNRI	gi	189303155	
DI LLI NSTGN	LI APRGYFKI	RSGKSSI MRS	DAPI GKCENSE	CI TPNGSI PN	DKPFQNVNRI	gi	188076387	
DI LLI NSTGN	LI APRGYFKI	RSGKSSI MRS	DAPI GKCENSE	CI TPNGSI PN	DKPFQNVNRI	gi	194293957	
DI LLI NSTGN	LI APRGYFKI	RSGKSSI MRS	DAPI GKCENSE	CI TPNGSI PN	DKPFQNVNRI	gi	194293953	
DI LLI NSTGN	LI APRGYFKI	RSGKSSI MRS	DAPI GKCENSE	CI TPNGSI PN	DKPFQNVNRI	gi	189303103	
DI LLI NSTGN	LI APRGYFKI	RSGKSSI MRS	DAPI GKCENSE	CI TPNGSI PN	DKPFQNVNRI	gi	194294007	
DI LLI NSTGN	LI APRGYFKI	RSGKSSI MRS	DAPI GKCENSE	CI TPNGSI PN	DKPFQNVNRI	gi	194294003	
DI LLI NSTGN	LI APRGYFKI	RSGKSSI MRS	DAPI GKCENSE	CI TPNGSI PN	DKPFQNVNRI	gi	193084879	
DI LLI NSTGN	LI APRGYFKI	RSGKSSI MRS	DAPI GKCENSE	CI TPNGSI PN	DKPFQNVNRI	gi	194294015	
DI LLI NSTGN	LI APRGYFKI	RSGKSSI MRS	DAPI GKCENSE	CI TPNGSI PN	DKPFQNVNRI	gi	194580029	
DI LLI NSTGN	LI APRGYFKI	RSGKSSI MRS	DAPI GKCENSE	CI TPNGSI PN	DKPFQNI NRI	gi	188076381	
DI LLI NSTGN	LI APRGYFKI	RSGKSSI MRS	DAPI GKCENSE	CI TPNGSI PN	DKPFQNVNRI	gi	194293975	
DI LLI NSTGN	LI APRGYFKI	RSGKSSI MRS	DAPI GKCENSE	CI TPNGSI PN	DKPFQNVNRI	gi	194294019	
DI LLI NSTGN	LI APRGYFKI	RSGKSSI MRS	DAPI GKCENSE	CI TPNGSI PN	DKPFQNVNRI	gi	194293991	
DI LLI NSTGN	LI APRGYFKI	RSGKSSI MRS	DAPI GKCENSE	CI TPNGSI PN	DKPFQNVNRI	gi	194294023	
DI LLI NSTGN	LI APRGYFKI	RSGKSSI MRS	DAPI GKCENSE	CI TPNGSI PN	DKPFQNVNRI	gi	193084875	
DI LLI NSTGN	LI APRGYFKI	RSGKSSI MRS	DAPI GKCENSE	CI TPNGSI PN	DKPFQNVNRI	gi	194293971	
DI LLI NSTGN	LI APRGYFKI	RSGKSSI MRS	DAPI GKCENSE	CI TPNGSI PN	DKPFQNVNRI	gi	189303139	
DI LLI NSTGN	LI APRGYFKI	RSGKSSI MRS	DAPI GKCENSE	CI TPNGSI PN	DKPFQNVNRI	gi	194293995	
DI LLI NSTGN	LI APRGYFKI	RSGKSSI MRS	DAPI GKCENSE	CI TPNGSI PN	DKPFQNVNRI	gi	189303151	
DI LLI NSTGN	LI APRGYFKI	RSGKSSI MRS	DAPI GKCENSE	CI TPNGSI PN	DKPFQNVNRI	gi	194294011	
DI LLI NSTGN	LI APRGYFKI	RSGKSSI MRS	DAPI GKCENSE	CI TPNGSI PN	DKPFQNVNRI	gi	194293949	
DI LLI NSTGN	LI APRGYFKI	RSGKSSI MRS	DAPI GKCENSE	CI TPNGSI PN	DKPFQNVNRI	gi	188076407	
DI LLI NSTGN	LI APRGYFKI	RSGKSSI MRS	DAPI GKCENSE	CI TPNGSI PN	DKPFQNVNRI	gi	194293961	
DI LLI NSTGN	LI APRGYFKI	RSGKSSI MRS	DAPI GKCENSE	CI TPNGSI PN	DKPFQNVNRI	gi	189303163	
DI LLI NSTGN	LI APRGYFKI	RSGKSSI MRS	DAPI GKCENSE	CI TPNGSI PN	DKPFQNVNRI	gi	193084883	
DI LLI NSTGN	LI APRGYFKI	RSGKSSI MRS	DAPI GKCENSE	CI TPNGSI PN	DKPFQNVNRI	gi	194293979	
DI LLI NSTGN	LI APRGYFKI	RSGKSSI MRS	DAPI GKCENSE	CI TPNGSI PN	DKPFQNVNRI	gi	194293983	
DI LLI NSTGN	LI APRGYFKI	RSGKSSI MRS	DAPI GKCENSE	CI TPNGSI PN	DKPFQNVNRI	gi	194293983	
DI LLI NSTGN	LI APRGYFKI	RSGKSSI MRS	DAPI GKCENSE	CI TPNGSI PN	DKPFQNVNRI	gi	189303147	
DI LLI NSTGN	LI APRGYFKI	RSGKSSI MRS	DAPI GKCENSE	CI TPNGSI PN	DKPFQNVNRI	gi	194293999	
DI LLI NSTGN	LI APRGYFKI	RSGKSSI MRS	DAPI GKCENSE	CI TPNGSI PN	DKPFQNVNRI	gi	189303159	
DI LLI NSTGN	LI APRGYFKI	RSGKSSI MRS	DAPI GKCENSE	CI TPNGSI PN	DKPFQNVNRI	gi	189303115	
DI LLI NSTGN	LI APRGYFKI	RSGKSSI MRS	DAPI GKCENSE	CI TPNGSI PN	DKPFQNVNRI	gi	189303143	
DI LLI NSTGN	LI APRGYFKI	RSGKSSI MRS	DAPI GKCENSE	CI TPNGSI PN	DKPFQNVNRI	gi	193084863	
DI LLI NSTGN	LI APRGYFKI	RSGKSSI MRS	DAPI GKCENSE	CI TPNGSI PN	DKPFQNVNRI	gi	73921186	
DI LLI NSTGN	LI APRGYFKI	RSGKSSI MRS	DAPI DNCNSE	CI TPNGSI SN	DKPFQNVNRI	gi	90571879	
DI LLI NSTGN	LI APRGYFKI	RSGKSSI MRS	DAPI DNCNSE	CI TPNGSI SN	DKPFQNVNRI	gi	89923293	
DI LLI NSTGN	LI APRGYFKI	RSGKSSI MRS	DAPI DNCNSE	CI TPNGSI PN	DKPFQNVNRI	gi	14030469	
DI LLI NSTGN	LI APRGYFKI	RSGKSSI MRS	DAPI DNCNSE	CI TPNGSI PN	DKPFQNVNRI	gi	14030467	
DI LLI NSTGN	LI APRGYFKI	RSGKSSI MRS	DAPI DNCNSE	CI TPNGSI PN	DKPFQNVNRI	gi	89938645	
DI LLI NSTGN	LI APRGYFKI	RSGKSSI MRS	DAPI DNCNSE	CI TPNGSI PN	DKPFQNVNRI	gi	194268913	
DI LLI NSTGN	LI APRGYFKI	RSGKSSI MRS	DAPI DNCNSE	CI TPNGSI PN	DKPFQNVNRI	gi	194268917	
DI LLI NSTGN	LI APRGYFKI	RSGKSSI MRS	DAPI DNCNSE	CI TPNGSI PN	DKPFQNVNRI	gi	194268573	
DI LLI NSTGN	LI APRGYFKI	RSGKSSI MRS	DAPI DNCNSE	CI TPNGSI PN	DKPFQNVNRI	gi	194268581	
DI LLI NSTGN	LI APRGYFKI	RSGKSSI MRS	DAPI DNCNSE	CI TPNGSI PN	DKPFQNVNRI	gi	194268575	
DI LLI NSTGN	LI APRGYFKI	RSGKSSI MRS	DAPI DNCNSE	CI TPNGSI PN	DKPFQNVNRI	gi	194268911	
DI LLI NSTGN	LI APRGYFKI	RSGKSSI MRS	DAPI DNCNSE	CI TPNGSI PN	DKPFQNVNRI	gi	194268915	
DI LLI NSTGN	LI APRGYFKI	RSGKSSI MRS	DAPI DNCNSE	CI TPNGSI PN	DKPFQNVNRI	gi	194268907	
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DI LLI NSTGN	LI APRGYFKI	RSGKSSI MRS	DAPI GKCENSE	CI TPNGSI PN	DKPFQNVNRI	gi	194268899	
DI LLI NSTGN	LI APRGYFKI	RSGKSSI MRS	DAPI GKCENSE	CI TPNGSI PN	DKPFQNVNRI	gi	194268561	
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DVLVI NSNGN	LI APRGYFKM	RTGKSSI MRS	DAPI DTCI SE	CI TPNGSI PN	DKPFQNVNKI	gi	193805266	
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DVLVI NSNGN	LI APRGYFKM	RTGKSSI MRS	DAPI DTCI FE	CI TPNGSI PN	DKPFQNVNKI	gi	134047618
DVLVI NSNGN	LI APRGYFKM	RTGKSSI MRS	DAPI DTCI SE	CI TPNGSI PN	DKPFQNVNKI	gi	194352093
DVLVI NSNGN	LI APRGYFKM	RTGKSSI MRS	DAPI DTCI SE	CI TPNGSI PN	DKPFQNVNKI	gi	126567435
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DVLVI NSNGN	LI APRGYFKM	RTGKSSI MRS	DAPI DTCI SE	CI TPNGSI PN	DKPFQNVNKI	gi	60753 emb
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DVLVI NSNGN	LI APRGYFKM	RTGKSSI MRS	DAPI DTCI SE	CI TPNGSI PN	DKPFQNVNKI	gi	118420992
DVLVI NSNGN	LI APRGYFKM	RTGKSSI MRS	DAPI DTCI SE	CI TPNGSI PN	DKPFQNVNKI	gi	145279136
DVLVI NSNGN	LI APRGYFKM	RTGKSSI MRS	DAPI DTCI SE	CI TPNGSI PN	DKPFQNVNKI	gi	125664195
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DI LI I SNGN	LI APRGYFKV	HTGKSSI MRS	DAPI ETC SSE	CI TPNGSI PN	DKPFQNVNKI	gi	14275704
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TYGACPKYVK	QNTLKLATGM	RNVPEKQTR	gi	148628604
TYGACPKYVK	QNTLKLATGM	RNI PEKQTR	gi	14275704
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Alignment: D:\bwt skripsi\cari data\Data\database\Ha\HA1\human\H5N1_aln

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DQI	CI GYHAN	NSTEQVDTI	M	EKNVTVTHAQ	DI LEKTHNGK	LCDLDGVKPL	I LRDCSVAGW	gi 1134946
DQI	CI GYHAN	NSTEQVDTI	M	EKNVTVTHAQ	DI LEKTHNGK	LCDLDGVKPL	I LRDCSVAGW	gi 1579558
DQI	CI GYHAN	NSTEQVDTI	M	EKNVTVTHAQ	DI LEKTHNGK	LCDLDGVKPL	I LRDCSVAGW	gi 1579558
DQI	CI GYHAN	NSTEQVDTI	M	EKNVTVTHAQ	DI LEKTHNGK	LCDLDGVKPL	I LRDCSVAGW	gi 1185748
DQI	CI GYHAN	NSTEQVDTI	M	EKNVTVTHAQ	DI LEKTHNGK	LCDLDGVKPL	I LRDCSVAGW	gi 1185748
DQI	CI GYHAN	NSTEQVDTI	M	EKNVTVTHAQ	DI LEKTHNGK	LCDLDGVKPL	I LRDCSVAGW	gi 1240988
DQI	CI GYHAN	NSTEQVDTI	M	EKNVTVTHAQ	DI LEKTHNGK	LCDLDGVKPL	I LRDCSVAGW	gi 1188643
DQI	CI GYHAN	NSTEQVDTI	M	EKNVTVTHAQ	DI LEKTHNGK	LCDLDGVKPL	I LRDCSVAGW	gi 1134946
DQI	CI GYHAN	NSTEQVDTI	M	EKNVTVTHAQ	DI LEKTHNGK	LCDLDGVKPL	I LRDCSVAGW	gi 1134947
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DQI	CI GYHAN	NSTEQVDTI	M	EKNVTVTHAQ	DI LERTHNGK	LCDLNGVKPL	I LRDCSVAGW	gi 4457132

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FESNGNFI AP	EYAYKI VKKG	DSTI MKSELE	YGNCNTKCQT	PMGAI NSSMP	FHNI HPLTI G	gi	1162951
FESNGNFI AP	EYAYKI VKKG	DSAI MKSELE	YGNCNTKCQT	PMGAI NSSMP	FHNI HPLTI G	gi	7101349
FESNGNFI AP	EYAYKI VKKG	DSAI MKSELE	YGNCNTKCQT	PMGAI NSSMP	FHNI HPLTI G	gi	1452844
FESNGNFI AP	EYAYKI VKKG	DSAI LKSEVE	YGNCNTKCQT	PI GAI NSSMP	FHNI HPLTI G	gi	1487677
FESNGNFI AP	EYAYKI VKEG	DSAI MKSEVE	YGNCNTKCQT	PI GAI NSSMP	FHNI HPLTI G	gi	1823825
FESNGNFI AP	EYAYKI VKKG	DSAI MKSEVE	YGNCNTKCQT	PI GAI NSSMP	FHNI HPLTI G	gi	8713794
FESNGNFI AP	ENAYKI VKKG	DSTI MKSELE	YGNCNTKCQT	PI GAI NSSMP	FHNI HPLTI G	gi	1458436
FESNGNFI AP	ENAYKI VKKG	DSTI MKSELE	YGNCNTKCQT	PI GAI NSSMP	FHNI HPLTI G	gi	1458436
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FESNGNFI AP	ENAYKI VKKG	DSTI MKSELE	YGNCNTKCQT	PI GAI NSSMP	FHNI HPLTI G	gi	1458436
FESNGNFI AP	EYAYKI VKKG	DSTI MKSELE	YGNCNTKCQT	PI GAI NSSMP	FHNI HPLTI G	gi	1458436
FESNGNFI AP	EYAYKI VKKG	DSTI MKSELE	YGNCNTKCQT	PI GAI NSSMP	FHNI HPLTI G	gi	1458436
*****	* *****	** : * *****	* *****	* *****	*****	*****	Clustal Co

							310	320	330			
ECPKYVKSNR	LVLATGLRNS	PORESRRKKR	-	gi	1134946							
ECPKYVKSNR	LVLATGLRNS	PORESRRKKR	-	gi	1579558							
ECPKYVKSNR	LVLATGLRNS	PORESRRKKR	-	gi	1579558							
ECPKYVKSNR	LVLATGLRNS	PORESRRKKR	-	gi	1185748							
ECPKYVKSNR	LVLATGLRNS	PORESRRKKR	-	gi	1185748							
ECPKYVKSNR	LVLATGLRNS	PORESRRKKR	-	gi	1240988							
ECPKYVKSNR	LVLATGLRNS	PORESRRKKR	-	gi	1188643							
ECPKYVKSNR	LVLATGLRNS	PORESRRKKR	-	gi	1134946							
ECPKYVKSNR	LVLATGLRNS	PORESRRKKR	-	gi	1134947							
ECPKYVKSNR	LVLATGLRNS	PORESRRKKR	-	gi	1134947							
ECPKYVKSNR	LVLATGLRNS	PORESRRKKR	-	gi	1134947							
ECPKYVKSNR	LVLATGLRNS	PORESRRKKR	-	gi	1134947							
ECPKYVKSNR	LVLAKGLRNS	PORESRRKKR	-	gi	1134946							
ECPKYVKSNR	LVLATGLRNS	PORESRRKKR	-	gi	1579558							
ECPKYVKSNR	LVLATGLRNS	PORESRRKKR	-	gi	1134946							
ECPKYVKSNR	SVLATGLRNS	PORESRRKKR	-	gi	1586048							
ECPKYVKSNR	LVLATGLRNS	PORESRRKKR	-	gi	1188641							
ECPKYVKSNR	LVLATGLRNS	PORESRRKKR	-	gi	1134952							
ECPKYVKSNR	LVLATGLRNS	PORESRRKKR	-	gi	1134952							
ECPKYVKSNR	LVLATGLRNS	PORESRRKKR	-	gi	1188642							
ECPKYVKSNR	LVLATGLRNS	PORESRRKKR	-	gi	1188641							
ECPKYVKSNR	LVLATGLRNS	PORESRRKKR	-	gi	1185749							
ECPKYVKSNR	LVLATGLRNS	PORESRRKKR	-	gi	1188643							
ECPKYVKSNR	LVLATGLRNS	PORESRRKKR	-	gi	1579558							
ECPKYVKSNR	LVLATGLRNS	PORESRRKKR	-	gi	1134944							
ECPKYVKSNR	LVLATGLRNT	PORESRRKKR	-	gi	3421260							
ECPKYVKSNR	LVLATGLRNT	PORESRRKKR	-	gi	4457129							
ECPKYVKSNR	LVLATGLRNT	PORESRRKKR	-	gi	8307805							
ECPKYVKSNR	LVLATGLRNT	PHRESRRKKR	-	gi	4457132							
ECPKYVKSNR	LVLATGLRNT	PHRESRRKKR	-	gi	4457134							
ECPKYVKSNR	LVLATGLRNT	PHRESRRKKR	-	gi	4457138							
ECPKYVKSNR	LVLATGLRNT	PHRESRRKKR	-	gi	4457136							
ECPKYVKSNR	LVLATGLRNA	PORESRRKKR	-	gi	8307803							
ECPKYVKSNR	LVLATGLRNT	PORESRRKKR	-	gi	9009324							
ECPKYVKSNR	LVLATGLRNA	PORESRRKKR	-	gi	1483408							
ECPKYVKSNR	LVLATGLRNS	PORESRRKKR	-	gi	5029605							
ECPKYVKSNR	LVLATGLRNS	PORESRRKKR	-	gi	1187227							
ECPKYVKSNR	LVLATGLRNS	PORESRRKKR	-	gi	5440228							
ECPKYVKSNR	LVLATGLRNS	PORESRRKKR	-	gi	1452844							
ECPKYVKSNR	LVLATGLRNS	PORESRRKKR	-	gi	4657841							
ECPKYVKSNR	LVLATGLRNS	PORESRRKKR	-	gi	1452844							
ECPKYVKSNR	LVLATGLRNS	PORESRRKKR	-	gi	1569922							
ECPKYVKSNR	LVLATGLRNS	PORESRRKKR	-	gi	1452844							
ECPKYVKSNR	LVLATGLRNS	PORESRRKKR	-	gi	1598959							
ECPKYVKSNR	LVLATGLRNS	PORESRRKKR	-	gi	5861843							
ECPKYVKSNR	LVLATGLRNS	PORESRRKKR	-	gi	5029605							
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ECPKYVKSNR	LVLATGLRNS	PORESRRKKR	-	gi	1452844							
ECPKYVKSNR	LVLATGLRNS	PORETRAI AG	-	gi	1591449							
ECPKYVKSNR	LVLATGLRNS	PORETRAI AG	-	gi	1591449							
ECPKYVKSNR	LVLATGLRNS	PORETRAI AG	-	gi	1591449							
ECPKYVKSNR	LVLATGLRNS	PORETRAI AG	-	gi	1591449							
ECPKYVKSNR	LVLATGLRNS	PORETRAI AG	-	gi	1591449							
ECPKYVKSNR	LVLATGLRNS	PORETRAI AG	-	gi	1591449							
ECPKYVKSNR	LVLATGLRNS	PORETRAI AG	-	gi	1591449							
ECPKYVKSNR	LVLATGLRNS	PORETRAI AG	-	gi	1591449							
ECPKYVKSNR	LVLATGLRNS	PORETRAI AG	-	gi	1591449							

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ECPKYVKSNR LVLATGLRNS PORETRAI AG - gi | 1591449
ECPKYVKSNR LVLATGLRNS PORETRAI AG - gi | 1591449
ECPKYVKSNR LVLATGLRNS PORETRAI AG - gi | 1591449
ECPKYVKSNR LVLATGLRNS PORERRRKKR - gi | 7809657
ECPKYVKSNR LVLATGLRNS PORERRRKKR - gi | 9300839
ECPKYVKSNR LVLATGLRNS PORERRRKKR - gi | 1263619
ECPKYVKSNR LVLATGLRNS PORERRRKKR - gi | 1263619
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ECPKYVKSNR LVLATGLRNS PORERRRKKR - gi | 9300840
ECPKYVKSNR LVLATGLRNS POKERRRKKR - gi | 1162951
ECPKYVKSNR LVLATGLRNS POREKRRRKR - gi | 8568091
ECPKYVKSNR LVLATGLRNS POREXRRRKR - gi | 1162951
ECPKYVKSNR LVLATGLRNS PORERRRKKR - gi | 7101349
ECPKYVKSNR LVLATGLRNS PORERRRKKR - gi | 1452844
ECPKYVKSNR LVLATGLRNS PLRERRRKR - gi | 1487677
ECPKYVKSNR LVLATGLRNS PLRERRRKR - gi | 1823825
ECPKYVKSNR LVLATGLRNS PLRERRRKR - gi | 8713794
ECPKYVKSNR LVLATGLRNS POGERRRKKR A gi | 1458436
ECPKYVKSNR LVLATGLRNS POGERRRKKR A gi | 1458436
ECPKYVKSNR LVLATGLRNS POGERRRKKR - gi | 1458436
ECPKYVKSNR LVLATGLRNS POGERRRKKR - gi | 1458436
ECPKYVKSNR LVLATGLRNS POGERRRKKR - gi | 1458436
ECPKYVKSNR LVLATGLRNS POGERRRKKR - gi | 1571030
ECPKYVKSNR LVLATGLRNS POGERRRKKR - gi | 1458436
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ECPKYVKSNR LVLATGLRNS POGERRRKKR - gi | 1458436
ECPKYVKSNR LVLATGLRNS POGERRRKKR - gi | 1458436
*** ***. ***. * * *
Clustal Co

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Neurami ni dase

Alignment: G:\bwt skripsi\cari data\Data\database\Na\human\h1n1.aln

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.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....
      10          20          30          40          50          60
MNPNQKI | TI GSI SI AI GI | SLMLQI GNI | SI WASHSI QT GSNQNTGI CN QRI I TYENST gi | 189303446
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MNPNQKI | TI GSI SI AI GTI | SLMLQI GNMI | SI WASHSI QT GSNQHTGI CN QRI I TYENST gi | 122855951

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MNPNQKI	I	TI	GS	SI	AI	GI	SL	MLQI	GNI	I	SI	WASH	SI	QT	GSQNHT	GI	CN	QRI	I	TYEN	ST	gi	125664181	
MNPNQKI	I	TI	GS	SI	AI	GI	SL	MLQI	GNI	I	SI	WASH	SI	QT	GSQNHT	GI	CN	QRI	I	TYEN	ST	gi	158524906	
MNPNQKI	I	TI	GS	SI	AI	GI	SL	MLQI	GNI	I	SI	WASH	SI	QT	GSQNHT	GI	CN	QRI	I	TYEN	ST	gi	73761479	
MNPNQKI	I	TI	GS	SI	AI	GI	SL	MLQI	GNI	I	SI	WASH	SI	QT	GSQNHT	GI	CN	QRI	I	TYEN	ST	gi	156123510	
MNPNQKI	I	TI	GS	SI	AI	GI	SL	MLQI	GNI	I	SI	WASH	SI	QT	GSQNHT	GI	CN	QRI	I	TYEN	ST	gi	158188202	
MNPNQKI	I	TI	GS	SI	AI	GI	SL	MLQI	GNI	I	SI	WASH	SI	QT	GSQNHT	GI	CN	QRI	I	TYEN	ST	gi	168827347	
MNPNQKI	I	TI	GS	SI	AI	GI	SL	MLQI	GNI	I	SI	WASH	SI	QT	GSQNHT	GI	CN	QRI	I	TYEN	ST	gi	168827349	
MNPNQKI	I	TI	GS	SI	AI	GI	SL	MLQI	GNI	I	SI	WASH	SI	QT	GSQNHT	GI	CN	QRI	I	TYEN	ST	gi	168827351	
MNPNQKI	I	TI	GS	SI	AI	GI	SL	MLQI	GNI	I	SI	WASH	SI	QT	GSQNHT	GI	CN	QRI	I	TYEN	ST	gi	148276804	
MNPNQKI	I	TI	GS	SI	AI	GI	SL	MLQI	GNI	I	SI	WASH	SI	QT	GSQNHT	GI	CN	QRI	I	TYEN	ST	gi	148276814	
MNPNQKI	I	TI	GS	SI	AI	GI	SL	VLOI	GNI	I	SI	WASH	SI	QT	GSQNHT	GI	CN	QRI	I	TYEN	ST	gi	148356750	
MNPNQKI	I	TI	GS	SI	AI	GI	SL	MLQI	GNI	I	SI	WASH	SI	QT	GSQNHT	GI	CN	QRI	I	TYEN	ST	gi	82546780	
MNPNQKI	I	TI	GS	SI	AI	GI	SL	MLQI	GNI	I	SI	WASH	SI	QT	GSQNHT	GI	CN	QKI	I	TYK	ST	gi	77543347	
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MNPNQKI	I	TI	GS	SI	AI	GI	SL	LQV	GNI	I	SI	WASH	SI	QT	GSQNHT	GI	CN	QRI	I	TYEN	ST	gi	109914463	
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MNPNQKI	I	TI	GS	SI	AI	GI	SL	LQI	GNI	I	SI	WASH	SI	QT	GSQNHT	GI	CN	QRI	I	TYEN	ST	gi	134047394	
MNPNQKI	I	TI	GS	SI	VAI	GI	SL	LQI	GNI	I	SI	WASH	SI	QT	GSQNYT	GI	CN	QRI	I	TYEN	ST	gi	148276806	
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MNPNQKI	I	TI	GS	SI	CM	V	GI	SL	LQI	GNI	I	SI	W	SHS	QT	GNQ	-----	-----	HTG	gi				94960376
MNPNQKI	I	TI	GS	SI	CM	V	GI	SL	LQI	GNI	I	SI	W	SHS	QT	GNQ	-----	-----	HTG	gi				414313
MNPNQKI	I	TI	GS	SI	CM	V	GI	SL	LQI	GNI	I	SI	W	SHS	QT	GNQ	-----	-----	HTG	gi				324482
MNPNQKI	I	TI	GS	SI	CM	V	GI	SL	LQI	GNI	I	SI	W	SHS	QT	GNQ	-----	-----	HTG	gi				194352376
MNPNQKI	I	TI	GS	SI	CM	V	GI	SL	LQI	GNI	I	SI	W	SHS	QT	GNQ	-----	-----	HTG	gi				94481608
MNPNQKI	I	TI	GS	SI	CM	V	GI	SL	LQI	GNI	I	SI	W	SHS	QT	GNQ	-----	-----	HTG	gi				414309
MNPNQKI	I	TI	GS	SI	CM	V	GI	SL	LQI	GNI	I	SI	W	SHS	QT	GNQ	-----	-----	HTG	gi				414311
MNPNQKI	I	TI	GS	SI	CM	V	GI	SL	LQI	GNI	I	SI	W	SHS	QT	GNQ	-----	-----	HTG	gi				89782161
MNPNQKI	I	TI	GS	SI	CL	V	GI	SL	LQI	GNI	I	SI	W	SHS	QT	GSQ	-----	-----	HTG	gi				194304808
MNPNQKI	I	TI	GS	SI	CL	V	GI	SL	LQI	GNI	I	SI	W	SHS	QT	GSQ	-----	-----	HTG	gi				126599291
MNPNQKI	I	TI	GS	SI	CL	V	GI	SL	LQI	GNI	I	SI	W	SHS	QT	GSQ	-----	-----	HTG	gi				89779326
MNPNQKI	I	TI	GS	SI	CL	V	GI	SL	LQI	GNI	I	SI	W	SHS	QT	GSQ	-----	-----	HTG	gi				125976186
MNPNQKI	I	TI	GS	SI	CL	V	GI	SL	LQI	GNI	I	SI	W	SHS	QT	GSQ	-----	-----	HTG	gi				21693173
MNPNQKI	I	TI	GS	SI	CL	V	GI	SL	LQI	GNI	I	SI	W	SHS	QT	GSQ	-----	-----	HTG	gi				324508
MNPNQKI	I	TI	GS	SI	CM	V	GI	SL	LQI	GNI	I	SI	W	SHS	QT	GSQ	-----	-----	HTG	gi				133754137
MNPNQKI	I	TI	GS	SI	CM	V	GI	SL	LQI	GNI	I	SI	W	SHS	QA	GS	-----	-----	ST	gi				89148082
MNPNQKI	I	TI	GS	SI	CM	V	GI	SL	LQI	GNI	I	SI	W	SHS	QT	GSQNHT	GI	CN	QSI	I	TYK	ST	gi	133754194
MNPNQKI	I	TI	GS	SI	CM	V	GI	SL	LQI	GNI	I	SI	W	SHS	QT	GNQ	NHPET	CN	QSI	I	TYEN	ST	gi	8572169
MNPNQKI	I	TI	GS	SI	CM	V	GI	SL	LQI	GNI	V	SI	W	SHS	QT	GNQ	NHTGT	CN	QSI	I	TYK	ST	gi	89782392
MNPNQKI	I	TI	GS	SI	CM	V	GI	SL	LQI	GNI	V	SI	W	SHS	QT	GNQ	NHTGT	CN	QSI	I	TYK	ST	gi	21724204
MNPNQKI	I	TI	GS	SI	CM	V	GI	SL	LQI	GNI	V	SI	W	SHS	QT	GNQ	NHTGT	CN	QSI	I	TYK	ST	gi	112787551
MNPNQKI	I	TI	GS	SI	CM	V	GI	SL	LQI	GNI	V	SI	W	SHS	QT	GNQ	NHTGT	CD	QSI	I	TYK	ST	gi	4583795
MNPNQKI	I	TI	GS	SI	CM	V	GI	SL	LQI	GNI	V	SI	W	SHS	QT	GNQ	NHTGT	CD	QSI	I	TYK	ST	gi	8572171
MNPNQKI	I	TI	GS	SI	CM	V	GI	SL	FQI	GNI	V	SI	W	SHS	T	-----	-----	GTC	RSI	-----	-----	gi	89903080	
MNPNQKI	I	TI	GS	SI	CM	V	GI	SL	LQI	GNI	I	SI	W	SHS	QT	GSQNHT	GI	CN	QSI	I	TYK	ST	gi	133754175
MNPNQKI	I	TI	GS	SI	CM	V	GI	SL	LQI	GNI	I	SI	W	SHS	QT	GSQNHT	GI	CN	QSI	I	TYK	ST	gi	133752887
MNPNQKI	I	TI	GS	SI	CM	V	GI	SL	LQI	GNI	I	SI	W	SHS	QT	GSQNHT	GI	CN	QSI	I	TYK	ST	gi	21724202
MNPNQKI	I	TI	GS	SI	CM	V	GI	SL	LQI	GNI	V	SI	W	SHS	QT	GNQ	NHTGT	CD	QSI	I	TYK	ST	gi	21717612
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MNPNQKI	I	TI	GS	SI	CM	V	GI	SL	LQI	GNI	I	SI	W	SHS	QT	GSQNHT	GI	CN	QSI	I	TYK	ST	gi	145278815
MNPNQKI	I	TI	GS	SI	CM	V	GI	SL	LQI	GNI	I	SI	W	SHS	QT	GSQNHT	GI	CN	QSI	I	TYK	ST	gi	89152219
MNPNQKI	I	TI	GS	SI	CM	A	GI	SL	LQI	GNI	I	SI	W	SHS	QT	GSQNHT	GI	CN	QRI	I	TYEN	ST	gi	125976167
MNPNQKI	I	TI	GS	SI	CM	A	GI	SL	LQI	GNI	I	SI	W	SHS	QT	GSQNHT	GI	CN	QRI	I	TYEN	ST	gi	125976224
MNPNQKI	I	TI	GS	SI	CM	A	GI	SL	LQI	GNI	V	SI	W	SHS	QT	GSQNYT	GI	CN	QRI	I	TYEN	ST	gi	148276802
: ** **			*** : : *				** : * : *				** * **												Cl	ustal Cons

.....	70	80	90	100	110	120																								
WVNHTYVNI	N	NTN	V	V	A	---	-----	EDK	T	S	V	T	L	A	G	N	S	S	L	C	S	I	SGW	A	I	Y	T	K	D	N	S	I	R	gi	189303446
WVNHTYVNI	N	NTN	V	V	A	---	-----	EDK	T	S	V	T	L	A	G	N	S	S	L	C	S	I	SGW	A	A	Y	T	K	D	N	S	I	R	gi	189303436
WVNHTYVNI	N	NTN	V	V	A	---	-----	EDK	T	S	V	T	L	A	G	N	S	S	L	C	S	I	SGW	A	A	Y	T	K	D	N	S	I	R	gi	189303426
WVNHTYVNI	N	NTN	V	V	A	---	-----	EDK	T	S	V	T	L	A	G	N	S	S	L	C	S	I	SGW	A	A	Y	T	K	D	N	S	I	R	gi	194294067
WVNHTYVNI	N	NTN	V	V	A	---	-----	EDK	T	S	V	T	L	A	G	N	S	S	L	C	S	I	SGW	A	A	Y	T	K	D	N	S	I	R	gi	189303430
WVNHTYVNI	N	NTN	V	V	A	---	-----	EDK	T	S	V	T	L	A	G	N	S	S	L	C	S	I	SGW	A	A	Y	T	K	D	N	S	I	R	gi	189303428
WVNHTYVNI	N	NTN	V	V	A	---	-----	EDK	T	S	V	T	L	A	G	N	S	S	L	C	S	I	SGW	A	A	Y	T	K	D	N	S	I	R	gi	189303442
WVNHTYVNI	N	NTN	V	V	A	---	-----	EDK	T	S	V	T	L	A	G	N	S	S	L	C	S	I	SGW	A	A	Y	T	K	D	N	S	I	R	gi	193084915
WVNHTYVNI	N	NTN	V	V	A	---	-----	EDK	T	S	V	T	L	A	G	N	S	S	L	C	S	I	SGW	A	A	Y	T	K	D	N	S	I	R	gi	189303424
WVNHTYVNI	N	NTN	V	V	A	---	-----	EDK	T	S	V	T	L	A	G	N	S	S	L	C	S	I	SGW	A	A	Y	T	K	D	N	S	I	R	gi	193084899
WVNHTYVNI	N	NTN	V	V	A	---	-----	EDK	T	S	V	T	L	A	G	N	S	S	L	C	S	I	SGW	A	A	Y	T	K	D	N	S	I	R	gi	188076369
WVNHTYVNI	N	NTN	V	V	A	---	-----	EDK	T	S	V	T	L	A	G	N	S	S	L	C	S	I	SGW	A	A	Y	T	K	D	N	S	I	R	gi	189303410
WVNHTYVNI	N	NTN	V	V	A	---	-----	E	E	K	T	S	V	T	L	A	G	N	S	S	L	C	S	I	SGW	A	A	Y	T</						

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WVNHTYVNI N	NTNVVAG	----	EDKTSVTLAG	NSSLCSI	SGW	AI	YTKDNSI	R	gi	193084907
WVNHTYVNI N	NTNVVAG	----	EDKTSVTLAG	NSSLCSI	SGW	AI	YTKDNSI	R	gi	193084913
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WVNHTYVNI N	NTNVVAG	----	KDKTSVTLAG	NSSLCSI	SGW	AI	YTKDNSI	R	gi	125664181
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WVNHTYVNI N	NTNVVAG	----	KDKTSVTLAG	NSSLCSI	SGW	AI	YTKDNSI	R	gi	168827347
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WVNHTYVNI N	NTNVI AE	----	KDKTSVTLAG	NSSLCSI	SGW	AI	YTKDNSI	R	gi	82546780
WVNHTYVNI N	NTNVVAG	----	KDKTSVTLAG	NSSLCSI	SGW	AI	YTKDNSI	R	gi	77543347
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WVNQTYVNI N	NTNVVAG	----	KDKTSMTLAG	NSSLCPI	RGW	AI	YTKDNSI	R	gi	109914463
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I CNQGS I TYK	----VVAG	----	QDSTSVI LTG	NSSLCPI	RGW	AI	HSKDNGI	R	gi	94960376
I CNQGS I TYK	----VVAG	----	QDSTSVI LTG	NSSLCPI	RGW	AI	HSKDNGI	R	gi	414313 gb
I CNQGS I TYK	----VVAG	----	QDSTSVI LTG	NSSLCPI	RGW	AI	HSKDNGI	R	gi	324482 gb
I CNQGS I TYK	----VVAG	----	QDSTSVI LTG	NSSLCPI	RGW	AI	HSKDNGI	R	gi	194352376
I CNQGS I TYK	----VVAG	----	QDSTSVI LTG	NSSLCPI	RGW	AI	HSKDNGI	R	gi	94481608
I CNQGI I THK	----VVAG	----	QDSTSVI LTG	NSSLCPI	RGW	AI	HSKDNGI	R	gi	414309 gb
I CNQGI I TYN	----VVAG	----	QDSTSVI LTG	NSSLCPI	RGW	AI	HSKDNGI	R	gi	414311 gb
I CNQGI I TYN	----VVAG	----	QDSTSVI LTG	NSSLCPI	RGW	AI	HSKDNGI	R	gi	89782161 gb
I CNQNI I TYK	NSTWV	----	KDTTSVI LTG	NSSLCPI	RGW	AI	YSKDNSI	R	gi	194304808
I CNQNI I TYK	NSTWV	----	KDTTSVI LTG	NSSLCPI	RGW	AI	YSKDNSI	R	gi	126599291
I CNQNI I TYK	NSTWV	----	KDTTSVI LTG	NSSLCPI	RGW	AI	YSKDNSI	R	gi	89779326 gb
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I CNQNI I TYK	NSTWV	----	KDTTSVI LTG	NSSLCPI	RGW	AI	YSKDNSI	R	gi	21693173 gb
I CNQNI I TYK	NSTWV	----	KDTTSVI LTG	NSSLCPI	RGW	AI	YSKDNSI	R	gi	324508 gb
I CNQNI I TYK	NSTWVNTYV NI SNTNVVAG	----	QDSTSVI LTG	NSSLCPI	RGW	AI	YSKDNSI	R	gi	133754137
WVNQTYVNI S	NTNVVAG	----	PDATSVI LTG	NSSLCPI	RGW	AI	YSKDNGI	R	gi	89148082 gb
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WVNQTYV	----NVVAG	----	KDTTSVI LAG	NSSLCPI	RGW	AI	YSKDNGVR	R	gi	4583795 e
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----YVNI S	NTNVVAG	----	KDTTSVI LAG	NSSLCPI	RGW	AI	YSKDNGVR	R	gi	89903080 gb
WVNQTYVNI S	NTNVVAG	----	KDTTSVI LAG	NSSLCPI	RGW	AI	YSKDNGVR	R	gi	133754175 gb
WVNQTYVNI S	NTNVVAG	----	KDTTSVI LAG	NSSLCPI	RGW	AI	YSKDNGVR	R	gi	133752887 gb
WVNQTYVNI S	NTNVVAG	----	KDTTSVI LAG	NSSLCPI	RGW	AI	YSKDNGVR	R	gi	21724202 gb
WVNQTYVNI S	NTNVVAG	----	KDTTSVI LAG	NSSLCPI	RGW	AI	YSKDNGVR	R	gi	21717612 gb

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VVNQTYVNI S NTVVAG---- -KGTTSVI LAG NSSLCP I RGW AI YSKDNGI R gi 21717610|
VVNQTYVNI S NTVVAG---- -KGTTSVI LAG NSSLCP I RGW AI YSKDNGI R gi 89903061|
VVNQTYVNI S NTVVAG---- -KGTTSVI LAG NSSLCP I RGW AI YSKDNGI R gi 8572187|g
VVNQTYVNI S NTVVAG---- -KGTTPIV I LAG NSSLCP I RGW AI YSKDNGI R gi 145278815
VVNQTYVNI S NTVVAG---- -KDTTSMI LAG NSSLCP I RGW AI YSKDNGI R gi 89152219|
VVNQTYVNI S NTVVAG---- -KDTTSMI LAG NSSLCP I RGW AI YSKDNGI R gi 125976167
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VVNQTYVNI S NTVVAG---- -KDTTSMI LAG NSSLCP I RGW AI YSKDNGI R gi 148276802
VVNQTYVNI N NTVVAG---- -QDTTSVALAG NSSLCP I SGW AI YSKDNGI R gi 148276802
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IGSKGDVFI REPF I SCSHL ECRTFFLTQG ALLNDKHSNG TVKDRSPYRA LMSCPLGEAP gi 189303436
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*****.**** *****.***** **..**** ** **.. ***** Clustal Cons
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.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....
250   260   270   280   290   300
ESECVMNGS CFTI MTDGPS NKAASYKI FK I EKGKVTKSI ELNAPNFHYE ECSCYPDTGI gi 189303446
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ESECVCVNGS	CFTI	MTDGPS	DGPASYKI	FK	I	EKGKVTKSI	ELDAPNSHYE	ECSCYPDTGK	gi	89152219				
ESECVCVNGS	CFTI	MTDGPS	DGPASYRI	FK	I	EKGKI	TKSI	ELDAPNSHYE	ECSCYPDTGK	gi	125976167			
ESECVCVNGS	CFTI	MTDGPS	DGPASYRI	FK	I	EKGKI	TKSI	ELDAPNSHYE	ECSCYPDTGT	gi	125976224			
ESECVCVNGS	CFTI	MTDGNP	NGPASYKI	FK	I	EKGKI	TKSI	ELDAPNSHYE	ECSCYPDAGT	gi	148276802			
****	*	***	*****		.	***	*	*.*	***	****	***	*****	..	Clustal Cons

VMCVCRDNWH	GSNRPWVSFN	QNLDYQI	GYI	CSGVFGDNPR	PEDGEGSCNP	VTVDGANGVK	gi	189303446	
VMCVCRDNWH	GSNRPWVSFN	QNLDYQI	GYI	CSGVFGDNPR	PEDGEGSCNP	VTVDGANGVK	gi	189303436	
VMCVCRDNWH	GSNRPWVSFN	QNLDYQI	GYI	CSGVFGDNPR	PEDGEGSCNP	VTVDGANGVK	gi	189303426	
VMCVCRDNWH	GSNRPWVSFN	QNLDYQI	GYI	CSGVFGDNPR	PEDGEGSCNP	VTVDGANGVK	gi	194294067	
VMCVCRDNWH	GSNRPWVSFN	QNLDYQI	GYI	CSGVFGDNPR	PEDGEGSCNP	VTVDGANGVK	gi	189303430	
VMCVCRDNWH	GSNRPWVSFN	QNLDYQI	GYI	CSGVFGDNPR	PEDGEGSCNP	VTVDGANGVK	gi	189303428	
VMCVCRDNWH	GSNRPWVSFN	QNLDYQI	GYI	CSGVFGDNPR	PEDGEGSCNP	VTVDGANGVK	gi	189303442	
VMCVCRDNWH	GSNRPWVSFN	QNLDYQI	GYI	CSGVFGDNPR	PEDGEGSCNP	VTVDGANGVK	gi	193084915	
VMCVCRDNWH	GSNRPWVSFN	QNLDYQI	GYI	CSGVFGDNPR	PEDGEGSCNP	VTVDGANGVK	gi	189303424	
VMCVCRDNWH	GSNRPWVSFN	QNLDYQI	GYI	CSGVFGDNPR	PEDGEGSCNP	VTVDGANGVK	gi	193084899	
VMCVCRDNWH	GSNRPWVSFN	QNLDYQI	GYI	CSGVFGDNPR	PEDGEGSCNP	VTVDGANGVK	gi	188076369	
VMCVCRDNWH	GSNRPWVSFN	QNLDYQI	GYI	CSGVFGDNPR	PEDGEGSCNP	VTVDGANGVK	gi	189303410	
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VMCVCRDNWH	GSNRPWVSFN	QNLDYQI	GYI	CSGVFGDNPR	PEDGEGSCNP	VTVDGANGVK	gi	188076351	
VMCVCRDNWH	GSNRPWVSFN	QNLDYQI	GYI	CSGVFGDNPR	PEDGEGSCNP	VTVEGANGVK	gi	189303422	
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VMCVCRDNWH	GSNRPWVSFN	QNLDYQI	GYI	CSGVFGDNPR	PEDGEGSCNP	VTVDGANGVK	gi	193084913	
VMCVCRDNWH	GSNRPWVSFN	QNLDYQI	GYI	CSGVFGDNPR	PEDGEGSCNP	VTVDGANGVK	gi	189303412	
VMCVCRDNWH	GSNRPWVSFN	QNLDYQI	GYI	CSGVFGDNPR	PEDGEGSCNP	VTVDGANGVK	gi	195661085	
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VMCVCRDNWH	GSNRPWVSFN	QNLDYQI	GYI	CSGVFGDNPR	PEDGEGSCNP	VTVDGANGVK	gi	194294071	
VMCVCRDNWH	GSNRPWVSFN	QNLDYQI	GYI	CSGVFGDNPR	PEDGEGSCNP	VTVDGANGVK	gi	195661095	
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VI	CVCRDNWH	GSNRPWVSFN	QNLDYQI	GYI	CSGVFGDNPR	PEDGEGSCNP	VTVDGANGVK	gi	195661093
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VMCVCRDNWH	GSNRPWVSFN	QNLDYQI	GYI	CSGVFGDNPR	PEDGEGSCNP	VTVDGANGVK	gi	189303432	
VMCVCRDNWH	GSNRPWVSFN	QNLDYQI	GYI	CSGVFGDNPR	PEDGEGSCNP	VTVDGANGVK	gi	189303418	
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VMCVCRDNWH	GSNRPWVSFN	QNLDYQI	GYI	CSGVFGDNPR	PKDGECSNP	VTVDGADGVK	gi	189303420	
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VMCVCRDNWH	GSNRPWVSFN	QNLDYQI	GYI	CSGVFGDNPR	PKDKGSCNP	VTVDGADGVK	gi	156123510	
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VMCVCRDNWH	GSNRPWVSFN	QNLDYQI	GYI	CSGVFGDNPR	PKDKGSCNP	VTVDGADGVK	gi	168827347	
VMCVCRDNWH	GSNRPWVSFN	QNLDYQI	GYI	CSGVFGDNPR	PKDKGSCNP	VTVDGADGVK	gi	168827349	
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VMCVCRDNWH	GSNRPWVSFN	QNLDYQI	GYI	CSGVFGDNPR	PRDGECSNP	VTVDGADGVK	gi	148276804	
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VMCVCRDNWH	GSNRPWVSFN	QNLDYQI	GYI	CSGVFGDNPR	PKDGECSNP	VTVDGADGVK	gi	148356750	
VMCVCRDNWH	GSNRPWVSFN	QNLDYQI	GYI	CSGVFGDNPR	PKDGECSNP	VTVDGADGVK	gi	82546780	
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VMCVCRDNWH	GSNRPWVSFN	QNLDYQI	GYI	CSGVFGDNPR	PKDGECSNP	VTVDGADGVK	gi	134047394
VMCVCRDNWH	GSNRPWVSFN	QNLDYQI	GYI	CSGVFGDNPR	PKDGECSNP	VTVDGADGVK	gi	148276806
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VMCVCRDNWH	GSNRPWVSFD	QNLDYKI	GYI	CSGVFGDNPR	PKDGTGSCGP	VSADGANGVK	gi	324482 gb
VMCVCRDNWH	GSNRPWVSFD	QNLDYKI	GYI	CSGVFGDNPR	PKDGTGSCGP	VSADGANGVK	gi	194352376
VMCVCRDNWH	GSNRPWVSFD	QNLDYKI	GYI	CSGVFGDNPR	PKDGTGSCGP	VSADGANGVK	gi	94481608
VMCVCRDNWH	GSNRPWVSFD	QNLDYQI	GYI	CSGVFGDNPR	PKDGTGSCGP	VSADGANGVK	gi	414309 gb
VMCVCRDNWH	GSNRPWVSFD	QNLDYQI	GYI	CSGVFGDNPR	PKDGPSCGP	VSADGANGVK	gi	414311 gb
VMCVCRDNWH	GSNRPWVSFD	QNLDYQI	GYI	CSGVFGDNPR	PKDGTGSCGP	VSADGANGVK	gi	89782161
VMCVCRDNWH	GSNRPWVSFD	QNLDYQI	GYI	CSGVFGDNPR	PEDGTGSCGP	VYVDGANGVK	gi	194304808
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VMCVCRDNWH	GSNRPWVSFD	QNLDYQI	GYI	CSGVFGDNPR	PEDGTGSCGP	VYVDGANGVK	gi	89779326
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VMCVCRDNWH	GSNRPWVSFD	QNLDYQI	GYI	CSGVFGDNPR	PKDGTGSCGP	VYVDGANGVK	gi	133754194
VMCVCRDNWH	GSNRPWVSFD	QNLDYQI	GYI	CSGVFGDNPR	PNDGTGSCGP	VSSNGANGI	K	8572169 g
VMCVCRDNWH	GSNRPWVSFD	QNLDYQMGYI	CSGVFGDNPR	PKDGTGSCGP	VYVDGANGVK		gi	89782392
VMCVCRDNWH	GSNRPWVSFD	QNLDYQMGYI	CSGVFGDNPR	PKDGTGSCGP	VYVDGANGVK		gi	21724204
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VMCVCRDNWH	GSNRPWVSFD	QNLDYQMGYI	CSGVFGDNPR	PKDGTGSCGP	VYVDGANGVK		gi	4583795 e
VMCVCRDNWH	GSNRPWVSFD	QNLDYQMGYI	CSGVFGDNPR	PKDGTGSCGP	VYVDGANGVK		gi	8572171 g
VMCVCRDNWH	GSNRPWVSFD	QNLDYQMGYI	CSGVFGDNPR	PKDGTGSCGP	VYVDGANGVK		gi	89903080
VMCVCRDNWH	GSNRPWVSFD	QNLDYQMGYI	CSGVFGDNPR	PKDGTGSCGP	VYVDGANGVK		gi	133754175
VMCVCRDNWH	GSNRPWVSFD	QNLDYQMGYI	CSGVFGDNPR	PKDGTGSCGP	VYVDGANGVK		gi	133752887
VMCVCRDNWH	GSNRPWVSFD	QNLDYQMGYI	CSGVFGDNPR	PKDGTGSCGP	VYVDGANGVK		gi	21724202
VMCVCRDNWH	GSNRPWVSFD	QNLDYQMGYI	CSGVFGDNPR	PKDGTGSCGP	VYVDGANGVK		gi	21717612
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VMCVCRDNWH	GSNRPWVSFD	QNLDYQI	GYI	CSGVFGDNPR	PKDGTGSCGP	VYVDGANGVK	gi	89903061
VMCVCRDNWH	GSNRPWVSFD	QNLDYQI	GYI	CSGVFGDNPR	SKDGTGSCGP	VYVDGANGVK	gi	8572187 g
VMCVCRDNWH	GSNRPWVSFD	QNLDYQI	GYI	CSGVFGDNPR	PKDGTGSCGP	VYVDGANGVK	gi	145278815
VMCVCRDNWH	GSNRPWVSFD	QNLDYQI	GYI	CSGVFGDNPR	PKDGTGSCGP	VYVDGANGVK	gi	89152219
VMCVCRDNWH	GSNRPWVSFN	QNLDYQI	GYI	CSGVFGDNPR	PKDGTGSCDP	VYVDGANGVK	gi	125976167
VMCVCRDNWH	GSNRPWVSFN	QNLDYQI	GYI	CSGVFGDNPR	PKDGTGSCDP	VYVDGANGVK	gi	125976224
VMCVCRDNWH	GSNRPWVSFN	QNLDYQI	GYI	CSGVFGDNPR	PKDGTGSCDP	VYVDGANGVK	gi	148276802
*.*****	*****	****.	***	*****	**	..**.*.*	:	Clustal Cons

		370		380		390		400		410		420			
GFSYKYDNGV	WI	GRTKSNRL	RKGFEMI	WDP	NGWTNTDSD	SVKQDVVAI	T	DWSGYSGSFV	gi	189303446					
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GFSYKYGNV	WI	GRTKSNRL	RKGFEMI	WDP	NGWTNTDSD	SVKQDVVAI	T	DWSGYSGSFV	gi	125664181
GFSYKYGNV	WI	GRTKSNRL	RKGFEMI	WDP	NGWTNTDSD	SVKQDVVAI	T	DWSGYSGSFV	gi	168827351
GFSYKYGNV	WI	GRTKSNRL	RKGFEMI	WDP	NGWTDSD	AVKQDVVAI	T	DWSGYSGSFV	gi	148276804
GFSYKYGNV	WI	GRTKSNRL	RKGFEMI	WDP	NGWTDSD	SVKQDVVAI	T	DWSGYSGSFV	gi	148276814
GFSYKYGNV	WI	GRTKSNRL	RKGFEMI	WDP	NGWTDSD	SVKQDVVAI	T	DWSGYSGSFV	gi	148356750
GFSYKYGNV	WI	GRTKSNRL	RKGFEMI	WDP	NGWTDSD	SVKQDVVAI	T	DWSGYSGSFV	gi	82546780
GFSYKYGNV	WI	GRTKSNRL	RKGFEMI	WDP	NGWTDSD	SVKQDVVAI	T	DWSGYSGSFV	gi	77543347
GFSYKYGNV	WI	GRTKSNRL	RKGFEMI	WDP	NGWTDSD	SVKQDVVAI	T	DWSGYSGSFV	gi	148356757
GFSYKYGNV	WI	GRTKSNRL	RKGFEMI	WDP	NGWTDSD	SVKQDVVAI	T	DWSGYSGSFV	gi	148356769
GFSYRYGNV	WI	GRTKSNRL	RKGFEMI	WDP	NGWTDSD	SMKQDI VAMT		DWSGYSGSFV	gi	94959690
GFSYRYGNV	WI	GRTKSNRL	RKGFEMI	WDP	NGWTDSD	SMKQDI VAMT		DWSGYSGSFV	gi	109914463
GFSYRYGNV	WI	GRTKSNRL	RKGFEMI	WDP	NGWTDSD	SMKQDI VAMT		DWSGYSGSFV	gi	94959709
GFSYRYGNV	WI	GRTKSNRL	RKGFEMI	WDP	NGWTDSD	SMKQDI VAMT		DWSGYSGSFV	gi	112787589
GFSYRYGNV	WI	GRTKSNRL	RKGFEMI	WDP	NGWTDSD	SMKQDI VAMT		DWSGYSGSFV	gi	134047394
GFSYRYGNV	WI	GRTKSNRL	RKGFEMI	WDP	NGWTDSD	SMKQDVVAMT		DWSGYSGSFV	gi	148276806
GFSYKYGNV	WI	GRTKSNRL	RKGFEMI	WDP	NGWTDSD	SMKQDVVAMT		DWSGYSGSFV	gi	148276808
GFSYKYGNV	WI	GRTKSDSS	RHGFEMI	WDP	NGWTEDSRF	SMRQDVVAMT		DRSGYSGSFV	gi	94960376
GFSYKYGNV	WI	GRTKSDSS	RHGFEMI	WDP	NGWTEDSRF	SMRQDVVAMT		DRSGYSGSFV	gi	414313
GFSYKYGNV	WI	GRTKSDSS	RHGFEMI	WDP	NGWTEDSRF	SMRQDVVAI	T	NRSYSGSFV	gi	324482
GFSYKYGNV	WI	GRTKSDSS	RHGFEMI	WDP	NGWTEDSRF	SMRQDVVAMT		DRSGYSGSFV	gi	194352376
GFSYKYGNV	WI	GRTKSDSS	RHGFEMI	WDP	NGWTEDSRF	SMRQDVVAMT		DRSGYSGSFV	gi	94481608
GFSYRYGNV	WI	GRTKSDSS	RHGFEMI	WDP	NGWTEDSRF	SVRODVVAMT		DRSGYSGSFV	gi	414309
GFSYRYGNV	WI	GRTKSDSS	RHGFEMI	WDP	NGWTEDSRF	SVRODVVAMT		DRSGYSGSFV	gi	414311
GFSYRYGNV	WI	GRTKSDSS	RHGFEMI	WDP	NGWTEDSRF	SVRODVVAMT		DRSGYSGSFV	gi	89782161
GFSYRYGNV	WI	GRTKSHSS	RHGFEMI	WDP	NGWTEDSKF	SVRODVVAMT		DWSGYSGSFV	gi	194304808
GFSYRYGNV	WI	GRTKSHSS	RHGFEMI	WDP	NGWTEDSKF	SVRODVVAMT		DWSGYSGSFV	gi	126599291
GFSYRYGNV	WI	GRTKSHSS	RHGFEMI	WDP	NGWTEDSKF	SVRODVVAMT		DWSGYSGSFV	gi	89779326
GFSYRYGNV	WI	GRTKSHSS	RHGFEMI	WDP	NGWTEDSKF	SVRODVVAMT		DWSGYSGSFV	gi	125976186
GFSYRYGNV	WI	GRTKSHSS	RHGFEMI	WDP	NGWTEDSKF	SVRODVVAMT		DWSGYSGSFV	gi	21693173
GFSYRYGNV	WI	GRTKSHSS	RHGFEMI	WDP	NGWTEDSKF	SVRODVVAMT		DWSGYSGSFV	gi	324508
GFSYRYGNV	WI	GRTKSHSS	RHGFEMI	WDP	NGWTEDSKF	SVRODVVAMT		DWSGYSGSFV	gi	133754137
GFSYRYGNV	WI	GRTKSKSS	RHGFEMI	WDP	NGWTEDSRF	SVRODVVAMT		DWSGYSGSFV	gi	89148082
GFSYRYGNV	WI	GRTKSTSS	RHGFEMI	WDP	NGWTEDSKF	SVRODVVAMT		DWSGYSGSFV	gi	133754194
GFSYRYDNGV	WI	GRTKSTSS	RSGFEMI	WDP	NGWTEDSF	SVRODI VAI	T	DWSGYSGSFV	gi	8572169
GFSYRYGNV	WI	GRTKSNSS	ROGFEMI	WDP	NGWTEDSNF	FTKQDVAVT		DWSGYSGSFV	gi	89782392
GFSYRYGNV	WI	GRTKSNSS	ROGFEMI	WDP	NGWTEDSNF	FTKQDVAVT		DWSGYSGSFV	gi	21724204
GFSYRYGNV	WI	GRTKSNSS	ROGFEMI	WDP	NGWTEDSNF	FMKQDVAVT		DWSGYSGSFV	gi	112787551
GFSYKYGNV	WI	GRTKSNSS	ROGFEMI	WDP	NGWTEDSNF	FTKQDVAVT		DWSGYSGSFV	gi	4583795
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GFSYRYGNV	WI	GRTKSNSS	ROGFEMI	WDP	NGWTEDSNF	FMKQDVAVT		DWSGYSGSFV	gi	89903080
GFSYRYGNV	WI	GRTKSNSS	ROGFEMI	WDP	NGWTEDSNF	FVKQDVAVT		DWSGYSGSFV	gi	133754175
GFSYRYGNV	WI	GRTKSNSS	ROGFEMI	WDP	NGWTEDSNF	FVKQDVAVT		DWSGYSGSFV	gi	133752887
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GFSYRYDNGV	WI	GRTKSNSS	RKGFEMI	WDP	NGWTDPSNF	LVKQDI VAMT		DWSGYSGSFV	gi	21717612
GI SYRYGNV	WI	GRTKSDSS	ROGFEMI	WDP	NGWTEDSNF	FVKQDI VAMT		DWSGYSGSFV	gi	21717610
GFSYRYDNGV	WI	GRTKSDSS	ROGFEMI	WDP	NGWTEDSNF	FVKQDI VAMT		DWSGYSGSFV	gi	89903061
GFSYRYDNGV	WI	GRTKSDSS	ROGFEMI	WDP	NGWTEDSNF	FVKQDI VAMT		DWSGYSGSFV	gi	8572187
GFSYRYDNGV	WI	GRI KSNSS	ROGFEMI	WDP	NGWTEDSF	FVKQDVAVT		DWSGYSGSFV	gi	145278815
GFSYRYDNGV	WI	GRTKSNSS	ROGFEMI	WDP	NGWTEDSF	FVKQDVAVT		DWSGYSGSFV	gi	89152219
GFSYRYDNGV	WI	GRTKSNSS	RKGFEMI	WDP	NGWTDGDNF	LVKQDVAVT		DWSGYSGSFV	gi	125976167
GFSYRYDNGV	WI	GRTKSNSS	RKGFEMI	WDP	NGWTDGDNF	LVKQDVAVT		DWSGYSGSFV	gi	125976224
GFSYRYDNGV	WI	GRTKSNSS	RRGFEMI	WDP	NGWTDGSKF	LVKQDVAVT		DWSGYSGSFV	gi	148276802
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	430	440	450	460	470	480			
QHPELTGLDC	I	RPCFWVELV	RGLPRENTTI	WTSGSSI	SFC	GVNSDTANWS	WPDGAELPFT	gi	189303446
QHPELTGLDC	I	RPCFWVELV	RGLPRENTTI	WTSGSSI	SFC	GVNSDTANWS	WPDGAELPFT	gi	189303436
QHPELTGLDC	I	RPCFWVELV	RGLPRENTTI	WTSGSSI	SFC	GVNSDTANWS	WPDGAELPFT	gi	189303426
QHPELTGLDC	I	RPCFWVELV	RGLPRENTTI	WTSGSSI	SFC	GVNSDTANWS	WPDGAELPFT	gi	194294067
QHPELTGLDC	I	RPCFWVELV	RGLPRENTTI	WTSGSSI	SFC	GVNSDTANWS	WPDGAELPFT	gi	189303430
QHPELTGLDC	I	RPCFWVELV	RGLPRENTTI	WTSGSSI	SFC	GVNSDTANWS	WPDGAELPFT	gi	189303428
QHPELTGLDC	I	RPCFWVELV	RGLPRENTTI	WTSGSSI	SFC	GVNSDTANWS	WPDGAELPFT	gi	189303442

QHPELTGLDC	IRPCFWVELV	RGLPRENTTI	WTSGSSI	SFC	GVNSDTANWS	WPDGAELPFT	gi	193084915
QHPELTGLDC	IRPCFWVELV	RGLPRENTTI	WTSGSSI	SFC	GVNSDTANWS	WPDGAELPFT	gi	189303424
QHPELTGLDC	IRPCFWVELV	RGLPRENTTI	WTSGSSI	SFC	GVNSDTANWS	WPDGAELPFT	gi	193084899
QHPELTGLDC	IRPCFWVELV	RGLPRENTTI	WTSGSSI	SFC	GVNSDTANWS	WPDGAELPFT	gi	188076369
QHPELTGLDC	IRPCFWVELV	RGLPRENTTI	WTSGSSI	SFC	GVNSDTANWS	WPDGAELPFT	gi	189303410
QHPELTGLDC	IRPCFWVELV	RGLPRENTTI	WTSGSSI	SFC	GVNSDTANWS	WPDGAELPFT	gi	189303434
QHPELTGLDC	IRPCFWVELV	RGLPRENTTI	WTSGSSI	SFC	GVNSDTANWS	WPDGAELPFT	gi	193084909
QHPELTGLDC	IRPCFWVELV	RGLPRENTTI	WTSGSSI	SFC	GVNSDTANWS	WPDGAELPFT	gi	188076351
QHPELTGLDC	IRPCFWVELV	RGLPRENTTI	WTSGSSI	SFC	GVNSDTANWS	WPDGAELPFT	gi	189303422
QHPELTGLDC	IRPCFWVELV	RGLPRENTTI	WTSGSSI	SFC	GVNSDTANWS	WPDGAELPFT	gi	193084907
QHPELTGLDC	IRPCFWVELV	RGLPRENTTI	WTSGSSI	SFC	GVNSDTANWS	WPDGAELPFT	gi	193084913
QHPELTGLDC	IRPCFWVELV	RGLPRENTTI	WTSGSSI	SFC	GVNSDTANWS	WPDGAELPFT	gi	189303412
QHPELTGLDC	IRPCFWVELV	RGLPRENTTI	WTSGSSI	SFC	GVNSDTANWS	WPDGAELPFT	gi	195661085
QHPELTGLDC	IRPCFWVELV	RGLPRENTTI	WTSGSSI	SFC	GVNSDTANWS	WPDRAELPFT	gi	195661087
QHPELTGLDC	IRPCFWVELV	RGLPRENTTI	WTSGSSI	SFC	GVNSDTANWS	WPDGAELPFT	gi	194294071
QHPELTGLDC	IRPCFWVELV	RGLPRENTTI	WTSGSSI	SFC	GVNSDTANWS	WPDGAELPFT	gi	195661095
QHPELTGLDC	IRPCFWVELV	RGLPRENTTI	WTSGSSI	SFC	GVNSDTANWS	WPDGAELPFT	gi	195661089
QHPELTGLDC	IRPCFWVELV	RGLPRENTTI	WTSGSSI	SFC	GVNSDTANWS	WPDGAELPFT	gi	195661083
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QHPELTGLDC	IRPCFWVELV	RGLPRENTTI	WTSGSSI	SFC	GVNSDTANWS	WPDGAELPFT	gi	195661093
QHPELTGLDC	IRPCFWVELV	RGLPRENTTI	WTSGSSI	SFC	GVNSDTANWS	WPDGAELPFT	gi	170181723
QHPELTGLDC	IRPCFWVELV	RGLPRENTTI	WTSGSSI	SFC	GVNSDTANWS	WPDGAELPFT	gi	170181755
QHPELTGLDC	IRPCFWVELV	RGLPRENTTI	WTSGSSI	SFC	GVNSDTANWS	WPDGAELPFT	gi	189303432
QHPELTGLDC	IRPCFWVELV	RGLPRENTTI	WTSGSSI	SFC	GVNSDTANWS	WPDGAELPFT	gi	189303418
QHPELTGLDC	IRPCFWVELV	RGLPRENTTI	WTSGSSI	SFC	GVNSDTANWS	WPDGAELPFT	gi	195661097
QHPELTGLDC	IRPCFWVELV	RGLPRENTTI	WTSGSSI	SFC	GVNSDTANWS	WPDGAELPFT	gi	170181785
QHPELTGLDC	IRPCFWVELV	RGLPRENTTI	WTSGSSI	SFC	GVNSDTANWS	WPDGAELPFT	gi	170181779
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QHPELTGLDC	IRPCFWVELV	RGLPRENTTI	WTSGSSI	SFC	GVNGDI ANWS	WPDGAELPFT	gi	189303420
QHPELTGLDC	IRPCFWVELV	RGLPKENTTI	WTSGSSI	SFC	GVNSDTANWS	WPDGAELPFT	gi	183396529
QHPELTGLDC	IRPCFWVELV	RGLPKENTTI	WTSGSSI	SFC	GVNSDTANWS	WPDGAELPFT	gi	170675942
QHPELTGLDC	IRPCFWVELV	RGLPRENTTI	WTSGSSI	SFC	GVNSDTANWS	WPDGAELPFT	gi	156123514
QHPELTGLDC	IRPCFWVELV	RGLPRENTTI	WTSGSSI	SFC	GVNSDTANWS	WPDGAELPFT	gi	158188218
QHPELTGLDC	IRPCFWVELV	RGLPRENTTI	WTSGSSI	SFC	GVNSDTANWS	WPDGAELPFT	gi	157281301
QHPELTGLDC	IRPCFWVELV	RGLPRENTTI	WTSGSSI	SFC	GVNSDTANWS	WPDGAELPFT	gi	122855951
QHPELTGLDC	IRPCFWVELV	RGLPRENTTI	WTSGSSI	SFC	GVNSDTANWS	WPDGAELPFT	gi	125664181
QHPELTGLDC	IRPCFWVELV	RGLPRENTTI	WTSGSSI	SFC	GVNSDTANWS	WPDGAELPFT	gi	158524906
QHPELTGLDC	IRPCFWVELV	RGLPRENTTI	WTSGSSI	SFC	GVNSDTANWS	WPDGAELPFT	gi	73761479
QHPELTGLDC	IRPCFWVELV	RGLPRENTTI	WTSGSSI	SFC	GVNSDTANWS	WPDGAELPFT	gi	156123510
QHPELTGLDC	IRPCFWVELV	RGLPRENTTI	WTSGSSI	SFC	GVNSDTANWS	WPDGAELPFT	gi	158188202
QHPELTGLDC	IRPCFWVELV	RGLPRENTTI	WTSGSSI	SFC	GVNSDTANWS	WPDGAELPFT	gi	168827347
QHPELTGLDC	IRPCFWVELV	RGLPRENTTI	WTSGSSI	SFC	GVNSDTANWS	WPDGAELPFT	gi	168827349
QHPELTGLDC	IRPCFWVELV	RGLPRENTTI	WTSGSSI	SFC	GVNSDTANWS	WPDGAELPFT	gi	168827351
QHPELTGLDC	IRPCFWVELV	RGLPRENTTI	WTSGSSI	SFC	GVNSDTANWS	WPDGAELPFT	gi	148276804
QHPELTGLDC	IRPCFWVELV	RGLPRENTTI	WTSGSSI	SFC	GVNSDTANWS	WPDGAELPFT	gi	148276814
QHPELTGLDC	IRPCFWVELV	RGLPRENTTI	WTSGSSI	SFC	GVNSDTADWS	WPDGAELPFT	gi	148356750
QHPELTGLDC	IRPCFWVELV	RGLPRENTTI	WTSGSSI	SFC	GVNSDAADWS	WPDGAELPFT	gi	82546780
QHPELTGLDC	IRPCFWVELV	RGLPRENTTI	WTSGSSI	SFC	GVNSDTANWS	WPDGAELPFT	gi	77543347
QHPELTGLDC	IRPCFWVELV	RGLPRENTTI	WTSGSSI	SFC	GVNSDTANWS	WPDGAELPFT	gi	148356757
QHPELTGLDC	IRPCFWVELV	RGLPRENTTI	WTSGSSI	SFC	GVNSDTANWS	WPDGAELPFT	gi	148356769
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QHPELTGLDC	MRPCFWVELV	RGLPRENTTI	WTSGSSI	SFC	GVNSDTANWS	WPDGAELPFT	gi	94959709
QHPELTGLDC	MRPCFWVELV	RGLPRENTTI	WTSGSSI	SFC	GVNSDTANWS	WPDGAELPFT	gi	112787589
QHPELTGLDC	MRPCFWVELV	RGLPRENTTI	WTSGSSI	SFC	GVNSDTANWS	WPDGAELPFT	gi	134047394
QHPELTGLDC	MRPCFWVELV	RGLPRENTTI	WTSGSSI	SFC	GVNSDTANWS	WPDGAELPFT	gi	148276806
QHPELTGLDC	MRPCFWVELV	RGLPRENTTI	WTSGSSI	SFC	GVNSDTANWS	WPDGAELPFT	gi	148276808
QHPELTGLDC	MRPCFWVELV	RGLPEE -DAI	WTSGSI	I SFC	GVNSDTVDWS	WPDGAELPFT	gi	94960376
QHPELTGLDC	MRPCFWVELV	RGLPEE -DAI	WTSGSI	I SFC	GVNGDTVDWS	WPDGAELPFT	gi	414313
QHPELTGLDC	MRPCFWVELV	RGLPEE -DAI	WTSGSI	I SFC	GVNSDTVDWS	WPDGAELPFT	gi	324482
QHPELTGLDC	MRPCFWVELV	RGLPEE -NAI	WTSGSI	I SFC	GVNSDTVDWS	WPDGAELPFT	gi	194352376
QHPELTGLDC	MRPCFWVELV	RGLPEE -DAV	WTSGSI	I SFC	GVNSDTVDWS	WPDGAELPFT	gi	94481608
QHPELTGLDC	MRPCFWVELV	RGOPEE -ETI	WTSGSI	I SFC	GVNSDTVDWS	WPDGAELPFT	gi	414309
QHPELTGLDC	MRPCFWVELV	RGRPEE -ETI	WTSGSI	I SFC	GVNSDTVDWS	WPDGAELPFT	gi	414311
QHPELTGLDC	MRPCFWVELV	RGRPEE -ETI	WTSGSI	I SFC	GVNSDTVDWS	WPDGAELPFT	gi	89782161
QHPELTGLDC	MRPCFWVELV	RGRPKE -KTI	WTSASSI	SFC	GVNSDTVDWS	WPDGAELPFS	gi	194304808
QHPELTGLDC	MRPCFWVELV	RGRPKE -KTI	WTSASSI	SFC	GVNSDTVDWS	WPDGAELPFS	gi	126599291
QHPELTGLDC	MRPCFWVELV	RGRPKE -KTI	WTSASSI	SFC	GVNSDTVDWS	WPDGAELPFS	gi	89779326
QHPELTGLDC	MRPCFWVELV	RGRPKE -KTI	WTSASSI	SFC	GVNSDTVDWS	WPDGAELPFS	gi	125976186
QHPELTGLDC	MRPCFWVELV	RGRPKE -KTI	WTSASSI	SFC	GVNSDTVDWS	WPDGAELPFS	gi	21693173
QHPELTGLDC	IRPCFWVELV	RGRPKE -KTI	WTSASSI	SFC	GVNSDTVDWS	WPDGAELPFT	gi	324508
QHPELTGLDC	MRPCFWVELV	RGRPKE -NTI	WTSGSSI	SFC	GVNSDTVDWS	WPDGAELPFT	gi	133754137
QHPELTGLDC	MRPCFWVELV	RGOPKE -KTI	WTSGSSI	SFC	GVNSDTVDWS	WPDGAELPFT	gi	89148082
QHPELTGLDC	MRPCFWVELV	RGOPKE -KTI	WTSGSSI	SFC	GVNSDTVDWS	WPDGAELPFT	gi	133754194
QHPELTGLDC	MRPCFWVELV	RGOPKE -NTI	WTSGSSI	SFC	GVNSDTVDWS	WPDGAELPFS	gi	8572169
QHPELTGLDC	MRPCFWVELV	RGRPKE -NTI	WTSGSSI	SFC	GVNSDTVDWS	WPDGAELPFT	gi	89782392
QHPELTGLDC	MRPCFWVELV	RGRPKE -NTI	WTSGSSI	SFC	GVNSDTVDWS	WPDGAELPFT	gi	21724204

QHPELTGLDC	MRPCFWVELI	RGRPKE-NTI	WTSGSSI SFC	GVNSDTV DWS	WPDGAELPFT	gi	112787551
QHPELTGLDC	MRPCFWVELI	RGRPKE-NTI	WTSGSSI SFC	GVNSDTV DWS	WPDGAELPFT	gi	4583795 e
QHPELTGLDC	MRPCFWVELI	RGRPKE-NTI	WTSGSSI SFC	GVNSDTV DWS	WPDGAELPFT	gi	8572171 g
QHPELTGLDC	MRPCFWVELI	RGRPKE-NTI	WTSGSSI SFC	GVNSDTV DWS	WPDGAELPFT	gi	89903080
QHPELTGLDC	MRPCFWVELI	RGRPKEK-TI	WTSGSSI SFC	GVNSDTV DWS	WPDGAELPFT	gi	133754175
QHPELTGLDC	MRPCFWVELI	RGRPKEK-TI	WTSGSSI SFC	GVNSDTV DWS	WPDGAELPFT	gi	133752887
QHPELTGLDC	MRPCFWVELI	RGRPKEKTTI	WTSGSSI SFC	GVNSDTV DWS	WPDDAELPLT	gi	21724202
QHPELTGLDC	MRPCFWVELI	RGRPKE-NTI	WTSGSSI SFC	GVNSDTV DWS	WPDDAELPLN	gi	21717612
QHPELTGLDC	MRPCFWVELI	RGRPKE-KTI	WTSGSSI SFC	GVNSDTV DWS	WPDDAELPLT	gi	21717610
QHPELTGLDC	MRPCFWVELI	RGRPKE-KTI	WTSGSSI SFC	GVNSDTV DWS	WPDGAELPFT	gi	89903061
QHPELTGLDC	MRPCFWVELI	RGRPKE-KTI	WTSGSSI SFC	GVNSDTV DWS	WPDGAELPFT	gi	8572187 g
QHPELTGLDC	MRPCFWVELI	RGRPKE-KTI	WTSGSSI SFC	GVNSDTV DWS	WPDGAELPFT	gi	145278815
QHPELTGLNC	MRPCFWVELI	RGRPKE-KTI	WTSGSSI SFC	GVNSDTV DWS	WPDGAELPFT	gi	89152219
QHPELTGLDC	MRPCFWVELI	RGRPKEKTTI	WTSGSSI SFC	GVNSDTV NWS	WPDGAELPFT	gi	125976167
QHPELTGLDC	MRPCFWVELI	RGRPKEKTTI	WTSGSSI SFC	GVNSDTV NWS	WPDGAELPFT	gi	125976224
QHPELTGLDC	MRPCFWVELI	RGRPKEKTTI	WTSGSSI SFC	GVNGDTANWS	WPDGSELPFT	gi	148276802
*****:	*****:	** * * :	*** * : **	*::: . **	*** : **	Cl	ustal Cons

IDK	gi	189303446
IDK	gi	189303436
IDK	gi	189303426
IDK	gi	194294067
IDK	gi	189303430
IDK	gi	189303428
IDK	gi	189303442
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IDK	gi	193084907
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IDK	gi	189303412
IDK	gi	195661085
IDK	gi	195661087
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IDK	gi	195661095
IDK	gi	195661089
IDK	gi	195661083
IDK	gi	195661091
IDK	gi	195661093
IDK	gi	170181723
IDK	gi	170181755
IDK	gi	189303432
IDK	gi	189303418
IDK	gi	195661097
IDK	gi	170181785
IDK	gi	170181779
IDK	gi	168825256
IDK	gi	189303420
IDK	gi	183396529
IDK	gi	170675942
IDK	gi	156123514
IDK	gi	158188218
IDK	gi	157281301
IDK	gi	122855951
IDK	gi	125664181
IDK	gi	158524906
IDK	gi	73761479
IDK	gi	156123510
IDK	gi	158188202
IDK	gi	168827347
---	gi	168827349
IDK	gi	168827351
IDK	gi	148276804
IDK	gi	148276814
IDK	gi	148356750
IDK	gi	82546780
IDK	gi	77543347
IDK	gi	148356757
IDK	gi	148356769

IDK	gi	94959690
IDK	gi	109914463
IDK	gi	94959709
IDK	gi	112787589
IDK	gi	134047394
IDK	gi	148276806
VDK	gi	148276808
IDK	gi	94960376
IDK	gi	414313 gb
IDK	gi	324482 gb
IDK	gi	194352376
IDK	gi	94481608
IDK	gi	414309 gb
IDK	gi	414311 gb
IDK	gi	89782161
IDK	gi	194304808
IDK	gi	126599291
IDK	gi	89779326
IDK	gi	125976186
IDK	gi	21693173
IDK	gi	324508 gb
IDK	gi	133754137
IDK	gi	89148082
IDK	gi	133754194
IDK	gi	8572169 g
IDK	gi	89782392
IDK	gi	21724204
IDK	gi	112787551
IDK	gi	4583795 e
IDK	gi	8572171 g
IDK	gi	89903080
IDK	gi	133754175
IDK	gi	133752887
IDK	gi	21724202
IDK	gi	21717612
IDK	gi	21717610
IDK	gi	89903061
IDK	gi	8572187 g
IDK	gi	145278815
IDK	gi	89152219
IDK	gi	125976167
IDK	gi	125976224
IDK	gi	148276802
IDK	Cl	ustal Cons

Alignment: D:\bwt skripsi\cari data\Data\database\Na\human\h2n2. al n

.....	10	20	30	40	50	60																														
MNP	NQK	I	TI	GSV	SLT	ATV	CFL	MQ	AI	LA	TTV	TLH	FK	QH	EC	D	S	P	A	S	N	Q	V	M	P	C	E	P	I	I	E	R	gi	3778480		
MNP	NQK	I	TI	GSV	SLT	ATV	CFL	MQ	AI	LA	TTV	TLH	FK	QH	EC	D	S	P	A	S	N	Q	V	M	P	C	E	P	I	I	E	R	gi	3778480		
MNP	NQK	I	TI	GSV	SLT	ATV	CFL	MQ	AI	LA	TTV	TLH	FK	QH	EC	D	S	P	A	S	N	Q	V	M	P	C	E	P	I	I	E	R	gi	3778479		
MNP	NQK	I	TI	GSV	SLT	ETV	CFL	MQ	AI	LA	TTV	TLH	FK	QH	EC	D	S	P	A	S	N	Q	V	M	P	C	E	P	I	I	E	R	gi	3778478		
MNP	NQK	I	TI	DSV	SLT	ATV	CFL	MQ	AI	LA	TTV	TLH	FK	QH	EC	D	S	P	A	S	N	Q	V	M	P	C	E	P	I	I	E	R	gi	3778478		
-----	I	TI	GSV	SLT	ATV	CFL	MQ	AI	LA	TTV	TLH	FK	QH	KC	D	S	P	A	S	N	Q	V	M	P	C	E	P	I	I	E	R	gi	4947349			
MNP	NQK	I	TI	GSV	SLT	ATV	CFL	MQ	AI	LA	TTV	TLH	FK	QH	KC	D	S	P	A	S	N	Q	V	M	P	C	E	P	I	I	E	R	gi	9448159		
MNP	NQK	I	TI	GSV	SLT	ATV	CFL	MQ	AI	LA	TTV	TLH	FK	QH	EC	D	S	P	A	S	N	Q	V	M	P	C	E	P	I	I	E	R	gi	3179057		
MNP	NQK	I	TI	GSV	SLT	ATV	CFL	MQ	AI	LA	TTV	TLH	FK	QH	EC	D	S	P	A	S	N	Q	V	M	P	C	E	P	I	I	E	R	gi	4640157		
MNP	NQK	I	TI	GSV	SLT	ATV	CFL	MQ	AI	LA	TTV	TLH	FK	QH	EC	D	S	P	A	S	N	Q	V	M	P	C	E	P	I	I	E	R	gi	3778480		
MNP	NQK	I	TI	GSV	SLT	ATV	CFL	MQ	AI	LA	TTV	TLH	FK	QH	EC	D	S	P	A	S	N	Q	V	M	P	C	E	P	I	I	E	R	gi	3778479		
MNP	NQK	I	TI	GSV	SLT	ATV	CFL	MQ	AI	LA	TTV	TLH	FK	QH	EC	D	S	P	A	S	N	Q	V	M	P	C	E	P	I	I	E	R	gi	1461338		
MNP	NQK	I	TI	GSV	SLT	ATV	CFL	MQ	AI	LA	TTV	TLH	FK	QH	EC	D	S	P	A	S	N	Q	V	M	P	C	E	P	I	I	E	R	gi	3778479		
MNP	NQK	I	TI	GSV	SLT	ATV	CFL	MQ	AI	LA	TTV	TLH	FK	QH	EC	D	S	P	A	S	N	Q	V	M	P	C	E	P	I	I	E	R	gi	1339825		
MNP	NQK	I	TI	GSV	SLT	ATV	CFL	MQ	AI	LA	TTV	TLH	FK	QH	EC	D	S	P	A	S	N	Q	V	M	P	C	E	P	I	I	E	R	gi	1892305		
MNP	NQK	I	TI	GSV	SLT	ATV	CFL	M	H	I	AI	LA	TTV	TLH	FK	QH	EC	D	S	P	A	S	N	Q	A	M	P	C	E	P	I	I	E	R	gi	1885043
MNP	NQK	I	TI	GSV	SLT	ATV	CFL	MQ	AI	LA	TTV	TLH	FK	QH	EC	D	S	P	A	S	N	Q	V	M	P	C	E	P	I	I	E	R	gi	1270579		
MNP	NQK	I	TI	GSV	SLT	ATV	CFL	MQ	AI	LA	TTV	TLH	FK	QH	EC	D	S	P	A	S	N	Q	V	M	P	C	E	P	I	I	E	R	gi	1892304		
MNP	NQK	I	TI	GSV	SLT	ATV	CFL	MQ	AI	LA	TTV	TLH	FK	QH	EC	D	S	P	A	S	N	Q	V	M	P	C	E	P	I	I	E	R	gi	3778478		
MNP	NQK	I	TI	GSV	SLT	ATV	CFL	MQ	AI	LA	TTV	TLH	FK	QH	EC	D	S	P	A	S	N	Q	V	M	P	C	E	P	I	I	E	R	gi	1467600		
MNP	NQK	I	TI	GSV	SLT	ATV	CFL	MQ	AI	LA	TTV	TLH	FK	QH	EC	D	S	P	A	S	N	Q	V	M	P	C	E	P	I	I	E	R	gi	1943521		
MNP	NQK	I	TI	GSV	SLT	ATV	CFL	MQ	AI	LA	TTV	TLH	FK	QH	EC	D	S	P	A	S	N	Q	V	M	P	C	E	P	I	I	E	R	gi	1337529		
MNP	NQK	I	TI	GSV	SLT	ATV	CFL	MQ	AI	LA	TTV	TLH	FK	QH	EC	D	S	P	A	S	N	Q	V	M	P	C	E	P	I	I	E	R	gi	1452790		
MNP	NQK	I	TI	GSV	SLT	ATV	CFL	MQ	AI	LA	TTV	TLH	FK	QH	EC	D	S	P	A	S	N	Q	V	M	P	C	E	P	I	I	E	R	gi	4640157		
MNP	NQK	I	TI	GSV	SLT	ATV	CFL	MQ	AI	LA	TTV	TLH	FK	QH	EC	D	S	P	A	S	N	Q	V	M	P	C	E	P	I	I	E	R	gi	1337536		
MNP	NQK	I	TI	GSV	SLT	ATV	CFL	MQ	AI	LA	TTV	TLH	FK	QH	EC	D	S	P	A	S	N	Q	V	M	P	C	E	P	I	I	E	R	gi	1340474		
MNP	NQK	I	TI	GSV	SLT	ATV	CFL	MQ	AI	LA	TTV	TLH	FK	QH	EC	D	S	P	A	S	N	Q	V	M	P	C	E	P	I	I	E	R	gi	1452790		
MNP	NQK	I	TI	GSV	SLT	ATV	CFL	MQ	AI	LA	TTV	TLH	FK	QH	EC	D	S	P	A	S	N	Q	V	M	P	C	E	P	I	I	E	R	gi	1943521		
MNP	NQK	I	TI	GSV	SLT	ATV	CFL	MQ	AI	LA	TTV	TLH	FK	QH	EC	D	S	P	A	S	N	Q	V	M	P	C	E	P	I	I	E	R	gi	1943522		

NI TEI VYLNN	TI I EKEI XPK	VVEYRNWSKP	QCQI TGFAPF	SKDNSI RLSA	GGDI WVTREP	gi	1892305
NI TEI VYLNN	TTI EKEI CPK	VVEYRNWSKP	QCQI TGFAPF	SKDNSI RLSA	GGDI WVTREP	gi	3778484
NI TEI VYLNN	TTI EKEI CPK	VVEYRNWSKP	QCQI TGFAPF	SKDNSI RLSA	GGDI WVTREP	gi	3778485
NI TEI VYLNN	TTI EKEI CPK	VVEYRNWSKP	QCQI TGFAPF	SKDNSI RLSA	GGDI WVTREP	gi	3778484
NTTEI VYLNN	TTI EKEI CPK	VVEYRNWSKP	QCKI TGFAPF	SKDNSI RLSA	GGDI WVTREP	gi	1943045
NTTEI VYLNN	TTI EKEI CPK	VVEYRNWSKP	QCKI TGFAPF	SKDNSI RLSA	GGDI WVTREP	gi	4640157
NTTEI VYLNN	TTI EKEI CPK	VVEYRNWSKP	QCKI TGFAPF	SKDNSI RLSA	GGDI WVTREP	gi	3778486
NI TEI VYLNN	TTI EKEI CPK	VVEYRNWSKP	QCKI TGFAPF	SKDNSI RLSA	GGDI WVTREP	gi	1340474
NI TEI VYLNN	TTI EKEI CPK	VVEYRNWSKP	QCKI TGFAPF	SKDNSI RLSA	GGDI WVTREP	gi	3778483
NI TEI VYLNN	TTI EKEI CPK	VVEYRNWSKP	QCKI TGFAPF	SKDNSI RLSA	GGDI WVTREP	gi	1339825
NI TEI VYLNN	TTI EKEI CPK	VVEYRNWSKP	QCKI TGFAPF	SKDNSI RLSA	GGDI WVTREP	gi	1337554
NI TEI VYLNN	TTI EKEI CPK	VVEYRNWSKP	QCKI TGFAPF	SKDNSI RLSA	GGDI WVTREP	gi	3179058
NI TEI VYLNN	TTI EKEI CPK	VVEYRNWSKP	QCKI TGFAPF	SKDNSI RLSA	GGDI WVTREP	gi	3778484
NI TEI VYLNN	TTI EKEI CPK	VVEYRNWSKP	QCKI TGFAPF	SKDNSI RLSA	GGDI WVTREP	gi	1339819
NI TEI VYLNN	TTI EKETCPK	VVEYRSWSKP	QCKI TGFAPF	SKDNSI RLSA	GGDI WVTREP	gi	1467600
NI TEI VYLNN	TTI EKETCPK	VVEYRSWSKP	QCKI TGFAPF	SKDNSI RLSA	GGDI WVTREP	gi	1337553
NI TEI VYLNN	TTI EKETCPK	VVEYRSWSKP	QCKI TGFAPF	SKDNSI RLSA	GGDI WVTREP	gi	1337553
NI TEI VYLNN	TTI EKETCPK	VVEYRSWSKP	QCKI TGFAPF	SKDNSI RLSA	GGDI WVTREP	gi	1337554
NI TEI VYLNN	TTI EKEI CPE	VVEYRNWSKP	QCQI TGFAPF	SKDNSI RLSA	GGDI WVTREP	gi	3778481

Clustal Co

130	140	150	160	170	180		
YVSCDPGKCY	QFALGQGTTL	DNKHSNDTI H	DRI PHRTLLM	NELGVPFHHLG	TRQVCVAWSS	gi	3778480
YVSCDPGKCY	QFALGQGTTL	DNKHSNDTI H	DRI PHRTLLM	NELGVPFHHLG	TRQVCVAWSS	gi	3778480
YVSCDPGKCY	QFALGQGTTL	DNKHSNGTI H	DRI PHRTLLM	NELGVPFHHLG	TKQVCVAWSS	gi	3778479
YVSCDTGKCY	QFALGQGTTL	DNKHSNGTI H	DRI PHRTLLM	NELGVPFHHLG	TKQVCVAWSS	gi	3778478
YVSCDTGKCY	QFALGQGTTL	DNKHSNGTI H	DRI PHRTLLM	NELGVPFHHLG	TKQVCVAWSS	gi	3778478
YVSCDPGKCY	QFALGQGTTL	DNKHSNGTI H	DRI PHRTLLM	NELGVPFHHLG	TKQVCVAWSS	gi	4947349
YVSCDPGKCY	QFALGQGTTL	DNKHSNGTI H	DRI PHRTLLM	NELGVPFHHLG	TKQVCVAWSS	gi	9448159
YVSCDPGKCY	QFALGQGTTL	DNKHSNGTI H	DRI PHRTLLM	NELGVPFHHLG	TKQVCVAWSS	gi	3179057
YVSCDPGKCY	QFALGQGTTL	DNKHSNGTI H	DRSPHRTLLM	NELGVPFHHLG	TKQVCAAWSS	gi	4640157
YVSCDPGKCY	QFALGQGTTL	DNKHSNGTI H	DRSPHRTLLM	NELGVPFHHLG	TKQVCAAWSS	gi	3778480
YVSCDPGKCY	QFALGQGTTL	DNKHSNGTI H	DRI PHRTLLM	NELGVPFHHLG	TKQVCVAWSS	gi	3778479
YVSCDPGKCY	QFALGQGTTL	DNKHSNGTI H	DRI PHRTLLM	NELGVPFHHLG	TKQVCVAWSS	gi	1461338
YVSCDPGKCY	QFALGQGTTL	DNKHSNGTI H	DRI PHRTLLM	NELGVPFHHLG	TKQVCVAWSS	gi	3778479
YVSCDPGKCY	QFALGQGTTL	DNKHSNGTI H	DRI PHRTLLM	NELGVPFHHLG	TKQVCVAWSS	gi	1339825
YVSCDPGKCY	QFALGQGTTL	DNKHSNGTI H	DRI PHRTLLM	NELGVPFHHLG	TKQVCVAWSS	gi	1892305
YVSCDPGKCY	QFALGQGTTL	DNKHSNGTI H	DRI PHRTLLM	NELGVPFHHLG	TKQVCVAWSS	gi	1885043
YVSCDPGKCY	QFALGQGTTL	DNKHSNGTI H	DRI PHRTLLM	NELGVPFHHLG	TKQVCVAWSS	gi	1270579
YVSCDPGKCY	QFALGQGTTL	DNKHSNGTI H	DRI PHRTLLM	NELGVPFHHLG	TKQVCVAWSS	gi	1892304
YVSCDPGKCY	QFALGQGTTL	DNKHSNGTI H	DRI PHRTLLM	NELGVPFHHLG	TKQVCVAWSS	gi	3778478
YVSCDPGKCY	QFALGQGTTL	DNKHSNGTI H	DRI PHRTLLM	NELGVPFHHLG	TKQVCVAWSS	gi	1467600
YVSCDPGKCY	QFALGQGTTL	DNKHSNGTI H	DRI PHRTLLM	NELGVPFHHLG	TKQVCVAWSS	gi	1943521
YVSCDPGKCY	QFALGQGTTL	DNKHSNGTI H	DRI PHRTLLM	NELGVPFHHLG	TKQVCVAWSS	gi	1337529
YVSCDPGKCY	QFALGQGTTL	DNKHSNGTI H	DRI PHRTLLM	NELGVPFHHLG	TKQVCVAWSS	gi	1452790
YVSCDPGKCY	QFALGQGTTL	DNKHSNGTI H	DRI PHRTLLM	NELGVPFHHLG	TKQVCVAWSS	gi	4640157
YVSCDPGKCY	QFALGQGTTL	DNKHSNGTI H	DRI PHRTLLM	NELGVPFHHLG	TKQVCVAWSS	gi	1337536
YVSCDPGKCY	QFALGQGTTL	DNKHSNGTI H	DRI PHRTLLM	NELGVPFHHLG	TKQVCVAWSS	gi	1340474
YVSCDPGKCY	QFALGQGTTL	DNKHSNGTI H	DRI PHRTLLM	NELGVPFHHLG	TKQVCVAWSS	gi	1452790
YVSCDPGKCY	QFALGQGTTL	DNKHSNGTI H	DRI PHRTLLM	NELGVSFHLG	TKQVCVAWSS	gi	1943521
YVSCDPGKCY	QFALGQGTTL	DNKHSNGTI H	DRI PHRTLLM	NELGVSFHLG	TKQVCVAWSS	gi	1943522
YVSCDPGKCY	QFALGQGTTL	DNKHSNGTI H	DRI PHRTLLM	NELGVSFHLG	TKQVCVAWSS	gi	1943522
YVSCDPGKCY	QFALGQGTTL	DNKHSNGTI H	DRI PHRTLLM	NELGVSFHLG	TKQVCVAWSS	gi	1943522
YVSCDPGKCY	QFALGQGTTL	DNKHSNGTI H	DRI PHRTLLM	NELGVPFHHLG	TKQVCVAWSS	gi	324510
YVSCDPGKCY	QFALGQGTTL	DNKHSNGTI H	DRI PHRTLLM	NELGVPFHHLG	TKQVCVAWSS	gi	1340475
YVSCDPGKCY	QFALGQGTTL	DNKHSNGTI H	DRI PHRTLLM	NELGVPFHHLG	TKQVCVAWSS	gi	1337536
YVSCDPGKCY	QFALGQGTTL	DNKHSNGTI H	DRI PHRTLLM	NELGVPFHHLG	TKQVCVAWSS	gi	3778479
YVSCDPGKCY	QFALGQGTTL	DNKHSNGTI H	DRI PHRTLLM	NELGVPFHHLG	TKQVCVAWSS	gi	6305490
YVSCDPGKCY	QFALGQGTTL	DNKHSNGTI H	DRI PHRTLLM	NELGVPFHHLG	TKQVCVAWSS	gi	4640157
YVSCDPGKCY	QFALGQGTTL	DNKHSNGTI H	DRI PHRTLLM	NELGVPFHHLG	TKQVCVAWSS	gi	1152790
YVSCDPGKCY	QFALGQGTTL	DNKHSNGTI H	DRI PHRTLLM	NELGVPFHHLG	TKQVCVAWSS	gi	8250669
YVSCDPGKCY	QFALGQGTTL	DNKHSNGTI H	DRI PHRTLLM	NELGVPFHHLG	TKQVCVAWSS	gi	565252
YVSCDPGKCY	QFALGQGTTL	DNKHSNGTI H	DRI PHRTLLM	NELGVPFHHLG	TKQVCVAWSS	gi	565254
YVSCDPGKCY	QFALGQGTTL	DNKHSNGTI H	DRI PHRTLLM	NELGVPFHHLG	TKQVCVAWSS	gi	3778479
YVSCDPGKCY	QFALGQGTTL	DNKHSNGTI H	DRI PHRTLLM	NELGVPFHHLG	TKQVCVAWSS	gi	1885044
YVSCDPGKCY	QFALGQGTTL	DNKHSNGTI H	DRI PHRTLLM	NELGVPFHHLG	TKQVCVAWSS	gi	1452790
YVSCDPGKCY	QFALGQGTTL	DNKHSNDTVH	DRI PHRTLLM	NELGVPFHHLG	TRQVCI AWSS	gi	1067257
YVSCDPGKCY	QFALGQGTTL	DNKHSNGTVH	DRI PHRTLLM	NELGVPFHHLG	TRQVCI AWSS	gi	1067257
YVSCDPGKCY	QFALGQGTTL	DNKHSNDTVH	DRI PHRTLLM	NELGVPFHHLG	TRQVCI AWSS	gi	1067257
YVSCDPGKCY	QFALGQGTTL	DNKHSNDTI H	DRI PHRTLLM	NELGVPFHHLG	TRQVCVAWSS	gi	3778481
YVSCDPGKCY	QFALGQGTTL	DNKHSNDTI H	DRI PHRTLLM	NELGVPFHHLG	TRQVCVAWSS	gi	3778480
YVSCDPGKCY	QFALGQGTTL	DNKHSNDTI H	DRI PHRTLLM	NELGVPFHHLG	TRQVCVAWSS	gi	3778480
YVSCDPGKCY	QFALGQGTTL	DNKHSNDTI H	DRI PHRTLLM	NELGVPFHHLG	TRQVCVAWSS	gi	3778481
YVSCDPGKCY	QFALGQGTTL	DNKHSNDTI H	DRI PHRTLLM	NELGVPFHHLG	TRQVCVAWSS	gi	3778481
YVSCDPGKCY	QFALGQGTTL	DNKHSNDTI H	DRI PHRTLLM	NELGVPFHHLG	TRQVCVAWSS	gi	1885043
YVSCDPGKCY	QFALGQGTTL	DNKHSNDTI H	DRI PHRTLLM	NELGVPFHHLG	TRQVCVAWSS	gi	3778482

MTDGSASGRA	DTRI LFI EEG	KI VHI SPLAG	SAQHVEECSC	YPRYPGVRCI	CRDNWKGSNR	gi	3778485
MTDGSASGRA	DTRI LFI EEG	KI VHI SPLAG	SAQHVEECSC	YPRYPGVRCI	CRDNWKGSNR	gi	1480200
MTDGSASGRA	DTRI LFI EEG	KI VHI SPLSG	SAQHVEECSC	YPRYPGVRCI	CRDNWKGSNR	gi	1892305
MTDGSASGRA	DTRI LFI EEG	KI VHI SPLSG	SAQHVEECSC	YPRYPGVRCI	CRDNWKGSNR	gi	3778485
MTDGSASGRA	DTRI LFI EEG	KI VHI SPLSG	SAQHVEECSC	YPRYPGVRCI	CRDNWKGSNR	gi	1892305
MTDGSASGRA	DTRI LFI EEG	KI VHI SPLSG	SAQHVEECSC	YPRYPGVRCI	CRDNWKGSNR	gi	3778484
MTDGSASGRA	DTRI LFI EEG	KI VHI SPLSG	SAQHVEECSC	YPRYPGVRCI	CRDNWKGSNR	gi	3778485
MTDGSASGRA	DTRI LFI EEG	KI VHI SPLSG	SAQHVEECSC	YPRYPGVRCI	CRDNWKGSNR	gi	3778484
MTDGSASGRA	DTRI LFI EEG	KI VHI SPLSG	SAQHVEECSC	YPRYPDVRCI	CRDNWKGSNR	gi	1943045
MTDGSASGRA	DTRI LFI EEG	KI VHI SPLSG	SAQHVEECSC	YPRYPDVRCI	CRDNWKGSNR	gi	4640157
MTDGSASGRA	DTRI LFI EEG	KI VHI SPLSG	SAQHVEECSC	YPRYPDVRCI	CRDNWKGSNR	gi	3778486
-----	-----	-----	-----	-----	-----	gi	1340474
MTDGSASGRA	DTRI LFI EEG	KI VHI SPLSG	SAQHVEECSC	YPRYPDVRCI	CRDNWKGSNR	gi	3778483
MTDGSASGRA	DTRI LFI EEG	KI VHI SPLSG	SAQHVEECSC	YPRYPDVRCI	CRDNWKGSNR	gi	1339825
MTDGSASGRA	DTRI LFI EEG	KI VHI SPLSG	SAQHVEECSC	YPRYPDVRCI	CRDNWKGSNR	gi	1337554
MTDGSASGRA	DTRI LFI EEG	KI VHI SPLSG	SAQHVEECSC	YPRYPDVRCI	CRDNWKGSNR	gi	3179058
MTDGSASGRA	DTKI LFI EEG	KI VHI SPLSG	SAQHVEECSC	YPRYPDVRCI	CRDNWKGSNR	gi	3778484
MTDGSASGRA	DTRI LFI EEG	KI VHI SPLSG	SAQHVEECSC	YPRYPDVRCI	CRDNWKGSNR	gi	1943819
MTDGSASGRA	DTRI LFI EEG	KI VHI SPLSG	SAQHVEECSC	YPRYPDVRCI	CRDNWKGSNR	gi	1467600
MTDGSASGRA	DTRI LFI EEG	KI VHI SPLSG	SAQHVEECSC	YPRYPDVRCI	CRDNWKGSNR	gi	1337553
MTDGSASGRA	DTRI LFI EEG	KI VHI SPLSG	SAQHVEECSC	YPRYPDVRCI	CRDNWKGSNR	gi	1337553
MTDGSASGRA	DTRI LFI EEG	KI VHI SPLSG	SAQHVEECSC	YPRYPDVRCI	CRDNWKGSNR	gi	1337554
MTDGSASGRA	DTRI LFI EEG	KI VHI SPLSG	SAQHVEECSC	YPRYPDVRCI	CRDNWKGSNR	gi	3778481

Clustal Co

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	310	320	330	340	350	360	
PVI DI NMEDY	SI DSSYVCSG	LVGDTPRNDD	RSSNSNCRDP	NNERGNPGVK	GWAFDNGDDV	gi	3778480
PVI DI NMEDY	SI DSSYVCSG	LVGDTPRNDD	RSSNSNCRDP	NNERGNPGVK	GWAFDNGDDV	gi	3778480
PVI DI NMEDY	SI DSSYVCSG	LVGDTPRNDD	RSSNSNCRDP	NNERGNPGVK	GWAFDNGDDV	gi	3778479
PVI DI NMEDY	SI DSSYVCSG	LVGDTPRNDD	SSSNNSCRDP	NNERGNPGVK	GWAFDNGDDV	gi	3778478
PVI DI NMEDY	SI DSSYVCSG	LVGDTPRNDD	SSSNNSCRDP	NNERGNPGVK	GWAFDNGDDV	gi	3778478
PVI DI NMEDY	SI DSSYVCSG	LVGDTPRNDD	SSSNNSCRDP	NNERGNPGVK	GWAFDNGDDV	gi	4947349
PVI DI NMEDY	SI DSSYVCSG	LVGDTPRNDD	SSSNNSCRDP	NNERGNPGVK	GWAFDNGDDV	gi	9448159
PVI DI NMEDY	SI DSSYVCSG	LVGDTPRNDD	SSSNNSCRDP	NNERGNPGVK	GWAFDNGDDV	gi	3179057
PVI DI NMEDY	SI DSSYVCSG	LVGDTPRNDD	SSSNNSCRDP	NNERGNPGVK	GWAFDNGDDV	gi	4640157
PVI DI NMEDY	SI DSSYVCSG	LVGDTPRNDD	SSSNNSCRDP	NNERGNPGVK	GWAFDNGDDV	gi	3778480
PVLDI SMEDY	SI GSSYVCSG	LVGDTPRNDD	SSSNNSCRDP	NNERGNPGVK	GWAFDNGDDV	gi	3778478
PVLDI SMEDY	SI DSSYVCSG	LVGDTPRNDD	SSSNNSCRDP	NNERGNPGVK	GWAFDNGDDV	gi	1461339
PVLDI SMEDY	SI DSSYVCSG	LVGDTPRNDD	SSSNNSCRDP	NNERGNPGVK	GWAFDNGDDV	gi	3778479
PVLDI SMEDY	SI DSSYVCSG	LVGDTPRNDD	SSSNNSCRDP	NNERGNPGVK	GWAFDNGDDV	gi	1339825
PVI DI NMEDY	SI DSSYVCSG	LVGDTPRNDD	SSSNNSCRDP	NNERGNPGVK	GWAFDNGDDV	gi	1892305
PVI DI NMEDY	SI DSSYVCSG	LVGDTPRNDD	SSSNNSCRDP	NNERGNPGVK	GWAFDNGDDV	gi	1885043
PVI DI NMEDY	SI DSSYVCSG	LVGDTPRNDD	SSSNNSCRDP	NNERGNPGVK	GWAFDNGDDV	gi	1270579
PVI DI NMEDY	SI DSSYVCSG	LVGDTPRNDD	SSSNNSCRDP	NNERGNPGVK	GWAFDNGDDV	gi	1892304
PVI DI NMEDY	SI DSSYVCSG	LVGDTPRNDD	SSSNNSCRDP	NNERGNPGVK	GWAFDNGDDV	gi	3778478
PVI DI NMEDY	SI DSSYVCSG	LVGDTPRNDD	SSSNNSCRDP	NNERGNPGVK	GWAFDNGDDV	gi	1467600
PVI DI NMEDY	SI DSSYVCSG	LVGDTPRNDD	SSSNNSCRDP	NNERGNPGVK	GWAFDNGDDV	gi	1943521
PVI DI NMEDY	SI DSSYVCSG	LVGDTPRNDD	SSSNNSCRDP	NNERGNPGVK	GWAFDNGDDV	gi	1337529
PVI DI NMEDY	SI DSSYVCSG	LVGDTPRNDD	SSSNNSCRDP	NNERGNPGVK	GWAFDNGDDV	gi	1452790
PVI DI NMEDY	SI DSSYVCSG	LVGDTPRNDD	SSSNNSCRDP	NNERGNPGVK	GWAFDNGDDV	gi	4640157
PVI DI NMEDY	SI DSSYVCSG	LVGDTPRNDD	SSSNNSCRDP	NNERGNPGVK	GWAFDNGDDV	gi	1337536
PVI DI NMEDY	SI DSSYVCSG	LVGDTPRNDD	SSSNNSCRDP	NNERGNPGVK	GWAFDNGDDV	gi	1340474
PVI DI NMEDY	SI DSSYVCSG	LVGDTPRNDD	SSSNNSCRDP	NNERGNPGVK	GWAFDNGDDV	gi	1452790
PVI DI NMEDY	SI DSSYVCSG	LVGDTPRNDD	SSSNNSCRDP	NNERGNPGVK	GWAFDNGDDV	gi	1943521
PVI DI NMEDY	SI DSSYVCSG	LVGDTPRNDD	SSSNNSCRDP	NNERGNPGVK	GWAFDNGDDV	gi	1943522
PVI DI NMEDY	SI DSSYVCSG	LVGDTPRNDD	SSSNNSCRDP	NNERGNPGVK	GWAFDNGDDV	gi	1943522
PVI DI NMEDY	SI DSSYVCSG	LVGDTPRNDD	SSSNNSCRDP	NNERGNPGVK	GWAFDNGDDV	gi	1943522
PVI DI NMEDY	SI DSSYVCSG	LVGDTPRNDD	SSSNNSCRDP	NNERGNPGVK	GWAFDNGDDV	gi	324510
PVI DI NMEDY	SI DSSYVCSG	LVGDTPRNDD	SSSNNSCRDP	NNERGNPGVK	GWAFDNGDDV	gi	1340475
PVI DI NMEDY	SI DSSYVCSG	LVGDTPRNGD	SSSNNSCRDP	NNERGNPGVK	GWAFDNGDDV	gi	1337536
PVI DI NMEDY	SI DSSYVCSG	LVGDTPRNGD	SSSNNSCRDP	NNERGNPGVK	GWAFDNGDDV	gi	3778479
PVI DI NMEDY	SI DSSYVCSG	LVGDTPRNDD	SSSNNSCRDP	NNERGNPGVK	GWAFDNGDDV	gi	6305490
PVI DI NMEDY	SI DSSYVCSG	LVGDTPRNDD	SSSNNSCRDP	NNERGNPGVK	GWAFDNGDDV	gi	4640157
PVI DI NMEDY	SI DSSYVCSG	LVGDTPRNDD	SSSNNSCRDP	NNERGNPGVK	GWAFDNGDDV	gi	1152790
PVI DI NMEDY	SI DSSYVCSG	LVGDTPRNDD	SSSNNSCRDP	NNERGNPGVK	GWAFDNGDDV	gi	8250669
PVI DI NMEDY	SI DSSYVCSG	LVGDTPRNDD	SSSNNSCRDP	NNERGNPGVK	GWAFDNGDDV	gi	565252
PVI DI NMEDY	SI DSSYVCSG	LVGDTPRNDD	SSSNNSCRDP	NNERGNPGVK	GWAFDNGDDV	gi	565254
-----	-----	-----	-----	-----	-----	gi	3778479
PVI DI NMEDY	SI DSSYVCSG	LVGDTPRNDD	SSSNNSCRDP	NNERGNPGVK	GWAFDNGDDV	gi	1885044
PVI DI NMEDY	SI DSSYVCSG	LVGDTPRNDD	SSSNNSCRDP	NNERGNPGVK	GWAFDNGDDV	gi	1452790
PVVDI NMEDY	SI DSSYVCSG	LVGDTPRNDD	SSSNNSCRNP	NNERGTQGVK	GWAFDNGNDL	gi	1067257
PVVDI NMEDY	SI DSSYVCSG	LVGDTPRNDD	SSSNNSCRDP	NNERGTQGVK	GWAFDNGNDL	gi	1067257
PVI DI NMEDY	SI DSSYVCSG	LVGDTPRNDD	SSSNNSCRDP	NNERGNPGVK	GWAFDNGDDV	gi	1067257
PVI DI NMEDY	SI DSSYVCSG	LVGDTPRNDD	SSSNNSCRDP	NNERGNPGVK	GWAFDNGDDV	gi	3778481
PVI DI NMEDY	SI DSSYVCSG	LVGDTPRNDD	RSSNSNCRDP	NNERGNPGVK	GWAFDNGDDV	gi	3778480
PVI DI NMEDY	SI DSSYVCSG	LVGDTPRNDD	RSSNSNCRDP	NNERGNPGVK	GWAFDNGDDV	gi	3778480

CFYVELI RGR	KQETRVWVTS	NSI VVFCGTS	GTYGTGSWPD	GANI NFMPI	gi	3778483
CFYVELI RGR	KQETRVWVTS	NSI VVFCGTS	GTYGTGSWPD	GANI NFMPI	gi	3778485
CFYVELI RGR	KQETRVWVTS	NSI VVFCGTS	GTYGTGSWPD	GANI NFMPI	gi	1943519
CFYVELI RGR	KQETRVWVTS	NSI VVFCGTS	GTYGTGSWPD	GANI NFMPI	gi	3778485
CFYVELI RGR	KQETRVWVTS	NSI VVFCGTS	GTYGTGSWPD	GANI NFMPI	gi	1480200
CFYVELI RGR	KQETRVWVTS	NSI VVFCGTS	GTYGTGSWPD	GANI NFMPI	gi	1892305
CFYVELI RGR	KQETRVWVTS	NSI AVFCGTS	GTYGTGSWPD	GANI NFMPI	gi	3778485
CFYVELI RGR	KQETRVWVTS	NSI AVFCGTS	GTYGTGSWPD	GANI NFMPI	gi	1892305
CFYVELI RGR	KQETRVWVTS	NSI VVFCGTS	GTYGTGSWPD	GANI NFMPI	gi	3778484
CFYVELI RGR	KQETRVWVTS	NSI VVFCGTS	GTYGTGSWPD	GANI NFMPI	gi	3778485
CFYVELI RGR	KQETRVWVTS	NSI VVFCGTS	GTYGTGSWPD	GANI NFMPI	gi	3778484
CFYVELI RGR	KQETRVWVTS	NSI VVFCGTS	GTYGTGSWPD	GANI NFMPI	gi	1943045
CFYVELI RGR	KQETRVWVTS	NSI VVFCGTS	GTYGTGSWPD	GANI NLMPI	gi	4640157
CFYVELI RGR	KQETRVWVTS	NSI VVFCGTS	GTYGTGSWPD	GANI NLMPI	gi	3778486
CFYVELI RGR	KQETRVWVTS	NSI VVFCGTS	GTYGTGSWPD	GANI NLMPI	gi	1340474
CFYVELI RGR	KQETRVWVTS	NSI VVFCGTS	GTYGTGSWPD	GANI NLMPI	gi	3778483
CFYVELI RGR	KQETRVWVTS	NSI VVFCGTS	GTYGTGSWPD	GANI NLMPI	gi	1339825
CFYVELI RGR	KQETRVWVTS	NSI VVFCGTS	GTYGTGSWPD	GANI NLMPI	gi	1337554
CFYVELI RGR	KQETRVWVTS	NSI VVFCGTS	GTYGTGSWPD	GANI NLMPI	gi	3179058
CFYVELI RGR	KQETRVWVTS	NSI VVFCGTS	GTYGTGSWPD	GANI NLMPI	gi	3778484
CFYVELI RGR	KQETRVWVTS	NSI VVFCGTS	GTYGTGSWPD	GANI NLMPI	gi	1339819
CFYVELI RGR	KQETRVWVTS	NSI VVFCGTS	GTYGTGSWPD	GANI NFMPI	gi	1467600
CFYVELI RGR	KQETRVWVTS	NSI VVFCGTS	GTYGTGSWPD	GANI NFMPI	gi	1337553
CFYVELI RGR	KQETRVWVTS	NSI VVFCGTS	GTYGTGSWPD	GANI NFMPI	gi	1337553
CFYVELI RGR	KQETRVWVTS	NSI VVFCGTS	GTYGTGSWPD	GANI NFMPI	gi	1337554
CFYVELI RGR	KQETRVWVTS	NSI VVFCGTS	GTYGTGSWPD	GANI NFMPI	gi	3778481
*****	*****	*****	*****	*****	Clustal Co	

Alignment: G:\bwt skripsi\cari data\Data\database\Na\human\h3n2. al n

	10	20	30	40	50	60									
MNPNQKI	I	TI	GSVSLTI	STI	CFFMQI	AI	LI	TTVTLHFKQY	EFNSPPNNQV	MLCEPTI	I	ER	gi	188076309	
MNPNQKI	I	TI	GSVSLTI	STI	CFFMQI	AI	LI	TTVTLHFKQY	EFNSPPNNQV	MLCEPTI	I	ER	gi	188076307	
MNPNQKI	I	TI	GSVSLTI	STI	CFFMQI	AI	LI	TTVTLHFKQY	EFNSPPNNQV	MLCEPTI	I	ER	gi	194293955	
MNPNQKI	I	TI	GSVSLTI	STI	CFFMQI	AI	LI	TTVTLHFKQY	EFNSPPNNQV	MLCEPTI	I	ER	gi	194293993	
MNPNHKI	I	TI	GSVSLTI	STI	CFFMQI	AI	LI	TTVTLHFKQY	EFNSPPNNQV	MLCEPTI	I	ER	gi	193084877	
MNPNQKI	I	TI	GSVSLTI	STI	CFFMQI	AI	LI	TTVTLHFKQY	EFNSPPNNQV	MLCEPTI	I	ER	gi	189303105	
MNPNQKI	I	TI	GSVSLTI	STI	CFFMQI	AI	LI	TTVTLHFKQY	EFNSPPNNQV	MLCEPTI	I	ER	gi	193084869	
MNPNQKI	I	TI	GSVSLTI	STI	CFFMQI	AI	LI	TTVTLHFKQY	EFNSPPNNQV	MLCEPTI	I	ER	gi	194294017	
MNPNQKI	I	TI	GSVSLTI	STI	CFFMQI	AI	LI	TTVTLHFKQY	EFNSPPNNQV	MLCEPTI	I	ER	gi	189303153	
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MNPNQKI	I	TI	GSVSLTI	STI	CFFMQI	AI	LI	TTVTLHFKQY	EFNSPPNNQV	MLCEPTI	I	ER	gi	194294021	
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MNPNQKI	I	TI	GSVSLTI	STI	CFFMQI	AI	LI	TTVTLHFKQY	EFNSPPNNQV	MLCEPTI	I	ER	gi	194293977	
MNPNQKI	I	TI	GSVSLTI	STI	CFFMQI	AI	LI	TTVTLHFKQY	EFNSPPNNQV	MLCEPTI	I	ER	gi	194294013	
MNPNQKI	I	TI	GSVSLTI	STI	CFFMQI	AI	LI	TTVTLHFKQY	EFNSPPNNQV	MLCEPTI	I	ER	gi	193084885	
MNPNQKI	I	TI	GSVSLTI	STI	CFFMQI	AI	LI	TTVTLHFKQY	EFNSPPNNQV	MLCEPTI	I	ER	gi	194293951	
---	NQKI	I	TI	GSVSLTI	STI	CFFMQI	AI	LI	TTVTLHFKQY	EFNSPPNNQV	MLCEPTI	I	ER	gi	189303165
MNPNQKI	I	TI	GSVSLTI	STI	CFFMQI	AI	LI	TTVTLHFKQY	EFNSPPNNQV	MLCEPTI	I	ER	gi	189303149	
MNPNQKI	I	TI	GSVSLTI	STI	CFFMQI	AI	LI	TTVTLHFKQY	EFNSPPNNQV	MLCEPTI	I	ER	gi	188076301	
MNPNQKI	I	TI	GSVSLTI	STI	CFFMQI	AI	LI	TTVTLHFKQY	EFNSPPNNQV	MLCEPTI	I	ER	gi	194293985	
MNPNQKI	I	TI	GSVSLTI	STI	CFFMQI	AI	LI	TTVTLHFKQY	EFNSPPNNQV	MLCEPTI	I	ER	gi	194293963	
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MNPNQKI	I	TI	GSVSLTI	STI	CFFMQI	AI	LI	TTVTLHFKQY	EFNSPPNNQV	MLCEPTI	I	ER	gi	193084865	
MNPNQKI	I	TI	GSVSLTI	STI	CFFMQI	AI	LI	TTVTLHFKQY	EFNSPPNNQV	MLCEPTI	I	ER	gi	194293969	
MNPNQKI	I	TI	GSVSLTI	STI	CFFMQI	AI	LI	TTVTLHFKQY	EFNSPPNNQV	MLCEPTI	I	ER	gi	189303117	
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MNPNQKI	I	TI	GSVSLTI	STI	CFFMQI	AI	LI	TTVTLHFKQY	EFNSPPNNQV	MLCEPTI	I	ER	gi	194294009	
MNPNQKI	I	TI	GSVSLTM	STI	CFFMQI	AI	LI	TTVTLHFKQY	EFNSPPNNQV	MLCEPTI	I	ER	gi	194294025	
MNPNQKI	I	TI	GSVSLTI	STI	CFFMQI	AI	LI	TTVTLHFKQY	EFNSPPNNQV	MLCEPTI	I	TER	gi	193084881	
MNPNQKI	I	TI	GSVSLTI	STI	CFFMQI	AI	LI	TTVTLHFKQY	EFNSPPNNQV	MLCEPTI	I	ER	gi	194293959	
MNPNQKI	I	TI	GSVSLTI	STI	CFFMQI	AI	LI	TTVTLHFKQY	EFNSPPNNQV	MLCEPTI	I	ER	gi	188076299	
MNPNQKI	I	TI	GSVSLTI	STI	CFFMQI	AI	LI	TTVTLHFKQY	EFNSPPNNQV	MLCEPTI	I	ER	gi	194294005	
MNPNQKI	I	TI	GSVSLTI	STI	CFFMQI	AI	LI	TTVTLHFKQY	EFNSPPNNQV	MLCEPTI	I	ER	gi	188076293	
MNPNQKI	I	TI	GSVSLTI	STI	CFFMQI	AI	LI	TTVTLHFKQY	EFNSPPNNQV	MLCEPTI	I	ER	gi	194293973	
MNPNQKI	I	TI	GSVSLTI	STI	CFFMQI	AI	LI	TTVTLHFKQY	EFNSPPNNQV	MLCEPTI	I	ER	gi	189303145	
MNPNQKI	I	TI	GSVSLTI	STI	CFFMQI	AI	LI	TTVTLHFKQY	EFNSPPNNQV	MLCEPTI	I	ER	gi	194269505	
MNPNQKI	I	TI	GSVSLTI	STI	CFFMQI	AI	LI	TTVTLHFKQY	EFNSPPNNQV	MLCEPTI	I	ER	gi	194269503	
MNPNQKI	I	TI	GSVSLTI	STI	CFFMQI	AI	LV	TTVTLHFKQY	ECNSPPNNQV	MLCEPTI	I	ER	gi	22859349	
MNPNQKI	I	TI	GSVSLTI	ATI	CFLMQI	AI	LV	TTVTLHFKQY	ECNSPPNNQV	MLCEPTI	I	ER	gi	13548555	
MNPNQKI	I	TI	GSVSLTI	ATI	CFLMQI	AI	LV	TTVTLHFKQY	ECNSPPNNQV	MLCEPTI	I	ER	gi	149132956	
MNPNQKI	I	TI	GSVSLTI	ATI	CFLMQI	AI	LV	TTVTLHFKQY	ECNSPPNNQV	MLCEPTI	I	ER	gi	22859405	
MNPNQKI	I	TI	GSVSLTI	ATI	CFLMQI	AI	LV	TTVTLHFKQY	ECNSPPNNQV	MLCEPTI	I	ER	gi	13548549	
MNPNQKI	I	TI	GSVSLTI	ATI	CFLMQI	AI	LV	TTVTLHFKQY	ECNSPPNNQV	MLCEPTI	I	ER	gi	115291184	
MNPNQKI	I	TI	GSVSLTI	ATI	CFLMQI	AI	LV	TTVTLHFKQH	ECNSPPNNQV	MLCEPTI	I	ER	gi	83752056	
MNPNQKI	I	TI	GSVSLTI	ATI	CFLMQI	AI	LV	TTVTLHFKQH	ECNSPPNNQV	MLCEPTI	I	ER	gi	110333405	
MNPNQKI	I	TI	GSVSLTI	ATI	CFLMQI	AI	LV	TTVTLHFKQH	ECNSPPNNQV	MLCEPTI	I	ER	gi	83752094	


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NI TEI VYLN  TTI EKEI CPK VVEYRNWSKP QCQI TGFAPF SKDNSI RLSA  GDI WVTREP gi 37785268|
NI TEI VYLN  TTI EKEI CPK VVEYRNWSKP QCQI TGFAPF SKDNSI RLSA  GDI WVTREP gi 125664238
NI TEI VYLN  TTI EKEI CPK VVEYRNWSKP QCQI TGFAPF SKDNSI RLSA  GDI WVTREP gi 134047623
NI TEI VYLTN TTI EKEI CPK LVEYRNWSKP CCKI TGFAPF SKDNSI RLSA  GDI WVTREP gi 1517824|g
***** *  ***.* ** ** .***** ** *.******.* ** *.****** ** ***** Cl ustal Cons

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130	140	150	160	170	180		
YVSCDPDKCY	QFALGQGTTL	NNVHSNDTVR	BRTPYRRTLLM	NELGVPFHHLG	TKQVCI AWSS	gi	188076309
YVSCDPDKCY	QFALGQGTTL	NNVHSNDTVR	BRTPYRRTLLM	NELGVPFHHLG	TKQVCI AWSS	gi	188076307
YVSCDPDKCY	QFALGQGTTL	NNVHSNDTVR	BRTPYRRTLLM	NELGVPFHHLG	TKQVCI AWSS	gi	194293955
YVSCDPDKCY	QFALGQGTTL	NNVHSNDTVR	BRTPYRRTLLM	NELGVPFHHLG	TKQVCI AWSS	gi	194293993
YVSCDPDKCY	QFALGQGTTL	NNVHSNDTVR	XRTPYRRTLLM	NELGVPFHHLG	TKQVCI AWSS	gi	193084877
YVSCDPDKCY	QFALGQGTTL	NNVHSNDTVR	XRTPYRRTLLM	NELGVPFHHLG	TKQVCI AWSS	gi	189303105
YVSCDPDKCY	QFALGQGTTL	NNVHSNDTVR	XRTPYRRTLLM	NELGVPFHHLG	TKQVCI AWSS	gi	193084869
YVSCDPDKCY	QFALGQGTTL	NNVHSNDTVR	XRTPYRRTLLM	NELGVPFHHLG	TKQVCI AWSS	gi	194294017
YVSCDPDKCY	QFALGQGTTL	NNVHSNDTVR	XRTPYRRTLLM	NELGVPFHHLG	TKQVCI AWSS	gi	189303153
YVSCDPDKCY	QFALGQGTTL	NNVHSNDTVR	XRTPYRRTLLM	NELGVPFHHLG	TKQVCI AWSS	gi	189303157
YVSCDPDKCY	QFALGQGTTL	NNVHSNDTVR	DRTPYRRTLLM	NELGVPFHHLG	TKQVCI AWSS	gi	194294021
YVSCDPDKCY	QFALGQGTTL	NNVHSNDTVR	DRTPYRRTLLM	NELGVPFHHLG	TKQVCI AWSS	gi	194293997
YVSCDPDKCY	QFALGQGTTL	NNVHSNDTVR	BRTPYRRTLLM	NELGVPFHHLG	TKQVCI AWSS	gi	194293977
YVSCDPDKCY	QFALGQGTTL	NNVHSNDTVR	XRTPYRRTLLM	NELGVPFHHLG	TKQVCI AWSS	gi	194294013
YVSCDPDKCY	QFALGQGTTL	NNVHSNDTVR	XRTPYRRTLLM	NELGVPFHHLG	TKQVCI AWSS	gi	193084885
YVSCDPDKCY	QFALGQGTTL	NNVHSNDTVR	XRTPYRRTLLM	NELGVPFHHLG	TKQVCI AWSS	gi	194293951
YVSCDPDKCY	QFALGQGTTL	NNVHSNDTVR	BRTPYRRTLLM	NELGVPFHHLG	TKQVCI AWSS	gi	189303165
YVSCDPDKCY	QFALGQGTTL	NNVHSNDTVR	BRTPYRRTLLM	NELGVPFHHLG	TKQVCI AWSS	gi	189303149
YVSCDPDKCY	QFALGQGTTL	NNVHSNDTVR	XRTPYRRTLLM	NELGVPFHHLG	TKQVCI AWSS	gi	188076301
YVSCDPDKCY	QFALGQGTTL	NNVHSNDTVR	DRTPYRRTLLM	NELGVPFHHLG	TKQVCI AWSS	gi	194293985
YVSCDPDKCY	QFALGQGTTL	NNVHSNDTVR	DRTPYRRTLLM	NELGVPFHHLG	TKQVCI AWSS	gi	194293963
YVSCDPDKCY	QFALGQGTTL	NNVHSNDTVR	DRTPYRRTLLM	NELGVPFHHLG	TKQVCI AWSS	gi	194293981
YVSCDPDKCY	QFALGQGTTL	NNVHSNDTVR	DRTPYRRTLLM	NELGVPFHHLG	TKQVCI AWSS	gi	193084865
YVSCDPDKCY	QFALGQGTTL	NNVHSNDTVR	BRTPYRRTLLM	NELGVPFHHLG	TKQVCI AWSS	gi	194293969
YVSCDPDKCY	QFALGQGTTL	NNVHSNDTVR	BRTPYRRTLLM	NELGVPFHHLG	TKQVCI AWSS	gi	189303117
YVSCDPDKCY	QFALGQGTTL	NNVHSNDTVR	XRTPYRRTLLM	NELGVPFHHLG	TKQVCI AWSS	gi	189303161
YVSCDPDKCY	QFALGQGTTL	NNVHSNDTVR	XRTPYRRTLLM	NELGVPFHHLG	TKQVCI AWSS	gi	194294009
YVSCDPDKCY	QFALGQGTTL	NNVHSNDTVR	BRTPYRRTLLM	NELGVPFHHLG	TKQVCI AWSS	gi	194294025
YVSCDPDKCY	QFALGQGTTL	NNVHSNDTVR	XRTPYRRTLLM	NELGVPFHHLG	TKQVCI AWSS	gi	193084881
YVSCDPDKCY	QFALGQGTTL	NNVHSNDTVR	DRTPYRRTLLM	NELGVPFHHLG	TKQVCI AWSS	gi	194293959
YVSCDPDKCY	QFALGQGTTL	NNVHSNDTVR	DRTPYRRTLLM	NELGVPFHHLG	TKQVCI AWSS	gi	188076299
YVSCDPDKCY	QFALGQGTTL	NNVHSNDTVR	DRTPYRRTLLM	NELGVPFHHLG	TKQVCI AWSS	gi	194294005
YVSCDPDKCY	QFALGQGTTL	NNVHSNDTVR	DRTPYRRTLLM	NELGVPFHHLG	TKQVCI AWSS	gi	188076293
YVSCDPDKCY	QFALGQGTTL	NNVHSNDTVR	DRTPYRRTLLM	NELGVPFHHLG	TKQVCI AWSS	gi	194293973
YVSCDPDKCY	QFALGQGTTL	NNVHSNDTVR	DRTPYRRTLLM	NELGVPFHHLG	TKQVCI AWSS	gi	189303145
YVSCDPDKCY	QFALGQGTTL	NNVHSNDTVH	DRTPYRRTLLM	NELGVPFHHLG	TKQVCI AWSS	gi	194269505
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YVSCDPDKCY	QFALGQGTTL	NNVHSNDTVH	DRTPYRRTLLM	NELGVPFHHLG	TKQVCI AWSS	gi	13548555
YVSCDPDKCY	QFALGQGTTL	NNVHSNDTVH	DRTPYRRTLLM	NELGVPFHHLG	TKQVCI AWSS	gi	149132956
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YVSCDPDKCY	QFALGQGTTL	NNVHSNDTVH	DRTPYRRTLLM	NELGVPFHHLG	TKQVCI AWSS	gi	71564600
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YVSCDPDKCY	QFALGQGTTL	NNVHSNDTVH	DRTPYRRTLLM	NELGVPFHHLG	TKQVCI AWSS	gi	13548569
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YVSCDHGKCY	QFALGQGTTL	DNKHSNDTI H	DRI PHRTLLM	NELGVPFHHLG	TKQVCI AWSS	gi	193805119
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YVSCDHGKCY	QFALGQGTTL	DNKHSNDTI	H	DRI PHRTLLM	NELGVPFHGL	TRQVCI AWSS	gi	126567437	
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YVSCDPGKCY	QFALGQGTTL	DNKHSNDTI	H	DRI PHRTLLM	NELGVPFHGL	TRQVCI AWSS	gi	1517824	g
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190	200	210	220	230	240			
SSCHDGKAWL	HVCI TGDDKN	ATASFI YNGR	LI DSVVSWSK	EI LRTOESEC	VCI NGTCTVV	gi	188076309	
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SSCHDGKAWL	HVCI	TGDDKN	ATASFI	YDGR	LVDSI	GSWSQ	NI	LRTQSEEC	VCI	NGTCTVV	gi	37785270
SSCHDGKAWL	HVCI	TGDDKN	ATASFI	YDGR	LVDSI	GSWSQ	NI	LRTQSEEC	VCI	NGTCTVV	gi	31790582
SSCHDGKAWL	HVCI	TGDDKN	ATASFI	YDGR	LVDSI	GSWSQ	NI	LRTQSEEC	VCI	NGTCTVV	gi	46401580
SSCHDGKAWL	HVCI	TGDDKN	ATASFI	YDGR	LVDSI	GSWSQ	NI	LRTQSEEC	VCI	NGTCTVV	gi	194304713
SSCHDGKAWL	HVCI	TGDDKN	ATASFI	YDGR	LVDSI	GSWSQ	NI	LRTQSEEC	VCI	NGTCTVV	gi	194304637
SSCHDGKAWL	HVCI	TGDDKN	ATASFI	YDGR	LVDSI	GSWSQ	NI	LRTQSEEC	VCI	NGTCTVV	gi	133982222
SSCHDGKAWL	HVCI	TGDDKN	ATASFI	YDGR	LVDSI	GSWSQ	NI	LRTQSEEC	VCI	NGTCTVV	gi	148628616
SSCHDGKAWL	HVCI	TGDDKN	ATASFI	YDGR	LVDSI	GSWSQ	NI	LRTQSEEC	VCI	NGTCTVV	gi	194304675
SSCHDGKAWL	HVCI	TGDDKN	ATASFI	YDGR	LVDSI	GSWSQ	NI	LRTQSEEC	VCI	NGTCTVV	gi	37785264
SSCHDGKAWL	HVCI	TGDDKN	ATASFI	YDGR	LVDSI	GSWSQ	NI	LRTQSEEC	VCI	NGTCTVV	gi	37785266
SSCHDGKAWL	HVCI	TGDDKN	ATASFI	YDGR	LVDSI	GSWSQ	NI	LRTQSEEC	VCI	NGTCTVV	gi	80977933
SSCHDGKAWL	HVCI	TGDDKN	ATASFI	YDGR	LVDSI	GSWSQ	NI	LRTQSEEC	VCI	NGTCTVV	gi	37785268
SSCHDGKAWL	HVCI	TGDDKN	ATASFI	YDGR	LVDSI	GSWSQ	NI	LRTQSEEC	VCI	NGTCTVV	gi	125664238
SSCHDGKAWL	HVCI	TGDDKN	ATASFI	YDGR	LVDSI	GSWSQ	NI	LRTQSEEC	VCI	NGTCTVV	gi	134047623
SSRHGKAWL	HVCVTGDDKN	ATASFI	YDGR	LVDSI	GSWSQ	NI	LRTQSEEC	VCI	NGTCTVV	gi	1517824	
**	*****	***	** *	*****	*	* **	***	*****	*****	Cl	ustal Cons	

MTDGSASGKA	DTKI	LFI	EEG	KI	VHTSTLSG	SAQHVEECSC	YPRYPGVRCV	CRDNWKGSNR	gi	188076309
MTDGSASGKA	DTKI	LFI	EEG	KI	VHTSTLSG	SAQHVEECSC	YPRYPGVRCV	CRDNWKGSNR	gi	188076307
MTDGSASGKA	DTKI	LFI	EEG	KI	VHTSTLSG	SAQHVEECSC	YPRYPGVRCV	CRDNWKGSNR	gi	194293955
MTDGSASGKA	DTKI	LFI	EEG	KI	VHTSTLSG	SAQHVEECSC	YPRYPGVRCV	CRDNWKGSNR	gi	194293993
MTDGSASGKA	DTKI	LFI	EEG	KI	VHTSTLSG	SAQHVEECSC	YPRYPGVRCV	CRDNWKGSNR	gi	193084877
MTDGSASGKA	DTKI	LFI	EEG	KI	VHTSTLSG	SAQHVEECSC	YPRYPGVRCV	CRDNWKGSNR	gi	189303105
MTDGSASGKA	DTKI	LFI	EEG	KI	VHTSTLSG	SAQHVEECSC	YPRYPGVRCV	CRDNWKGSNR	gi	193084869
MTDGSASGKA	DTKI	LFI	EEG	KI	VHTSTLSG	SAQHVEECSC	YPRYPGVRCV	CRDNWKGSNR	gi	194294017
MTDGSASGKA	DTKI	LFI	EEG	KI	VHTSTLSG	SAQHVEECSC	YPRYPGVRCV	CRDNWKGSNR	gi	189303153
MTDGSASGKA	DTKI	LFI	EEG	KI	VHTSTLSG	SAQHVEECSC	YPRYPGVRCV	CRDNWKGSNR	gi	189303157
MTDGSASGKA	DTKI	LFI	EEG	KI	VHTSTLSG	SAQHVEECSC	YPRYPGVRCV	CRDNWKGSNR	gi	194294021
MTDGSASGKA	DTKI	LFI	EEG	KI	VHTSTLSG	SAQHVEECSC	YPRYPGVRCV	CRDNWKGSNR	gi	194293997
MTDGSASGKA	DTKI	LFI	EEG	KI	VHTSTLSG	SAQHVEECSC	YPRYPGVRCV	CRDNWKGSNR	gi	194293977
MTDGSASGKA	DTKI	LFI	EEG	KI	VHTSTLSG	SAQHVEECSC	YPRYPGVRCV	CRDNWKGSNR	gi	194294013
MTDGSASGKA	DTKI	LFI	EEG	KI	VHTSTLSG	SAQHVEECSC	YPRYPGVRCV	CRDNWKGSNR	gi	193084885

MTDGSASGRA	DTRI LFI EEG	KI VHI SPLSG	SAQHVEECSC	YPRYPGVRCI	CRDNWKGSNR	gi	194304675
MTDGSASGRA	DTRI LFI EEG	KI VHI SPLSG	SAQHVEECSC	YPRYPGVRCI	CRDNWKGSNR	gi	37785264
MTDGSASGRA	DTRI LFI EEG	KI VHI SPLSG	SAQHVEECSC	YPRYPGVRCI	CRDNWKGSNR	gi	37785266
MTDGSASGRA	DTRI LFI EEG	KI VHI SPLSG	SAQHVEECSC	YPRYPGVRCI	CRDNWKGSNR	gi	80977933
MTDGSASGRA	DTRI LFI EEG	KI VHI SPLSG	SAQHVEECSC	YPRYPGVRCI	CRDNWKGSNR	gi	37785268
MTDGSASGRA	DTRI LFI EEG	KI VHI SPLSG	SAQHVEECSC	YPRYPGVRCI	CRDNWKGSNR	gi	125664238
MTDGSASGRA	DTRI LFI EEG	KI VHI SPLSG	SAQHVEECSC	YPRYPGVRCI	CRDNWKGSNR	gi	134047623
MTDGSASGRA	DTRI LFI EEG	KI VHI SPLSG	SAQHVEECSC	YPRYPGVRCV	CRDNWKGSNR	gi	1517824
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		310	320	330	340	350	360	
PI VDI NI KDH	SI VSSYVCSG	LVGDTPRKN	SSSSSHCLDP	NNEEGHGK	GWAFDDGNDV	gi	188076309	
PI VDI NI KDH	SI VSSYVCSG	LVGDTPRKN	SSSSSHCLDP	NNEEGHGK	GWAFDDGNDV	gi	188076307	
PI VDI NI KDH	SI VSSYVCSG	LVGDTPRKN	SSSSSHCLDP	NNEEGHGK	GWAFDDGNDV	gi	194293955	
PI VDI NI KDH	SI VSSYVCSG	LVGDTPRKN	SSSSSHCLDP	NNEEGHGK	GWAFDDGNDV	gi	194293993	
PI VDI NI KDH	SI VSSYVCSG	LVGDTPRKN	SSSSSHCLDP	NNEEGHGK	GWAFDDGNDV	gi	193084877	
PI VDI NI KDH	SI VSSYVCSG	LVGDTPRKN	SSSSSHCLDP	NNEEGHGK	GWAFDDGNDV	gi	189303105	
PI VDI NI KDH	SI VSSYVCSG	LVGDTPRKN	SSSSSHCLDP	NNEEGHGK	GWAFDDGNDV	gi	193084869	
PI VDI NI KDH	SI VSSYVCSG	LVGDTPRKN	SSSSSHCLDP	NNEEGHGK	GWAFDDGNDV	gi	194294017	
PI VDI NI KDH	SI VSSYVCSG	LVGDTPRKN	SSSSSHCLDP	NNEEGHGK	GWAFDDGNDV	gi	189303153	
PI VDI NI KDH	SI VSSYVCSG	LVGDTPRKN	SSSSSHCLDP	NNEEGHGK	GWAFDDGNDV	gi	189303157	
PI VDI NI KDH	SI VSSYVCSG	LVGDTPRKN	SSSSSHCLDP	NNEEGHGK	GWAFDDGNDV	gi	194294021	
PI VDI NI KDH	SI VSSYVCSG	LVGDTPRKN	SSSSSHCLDP	NNEEGHGK	GWAFDDGNDV	gi	194293997	
PI VDI NI KDH	SI VSSYVCSG	LVGDTPRKN	SSSSSHCLDP	NNEEGHGK	GWAFDDGNDV	gi	194293977	
PI VDI NI KDH	SI ASSYVCSG	LVGDTPRKN	SSSSSHCLDP	NNEEGHGK	GWAFDDGNDV	gi	194294013	
PI VDI NI KDH	SI VSSYVCSG	LVGDTPRKN	SSSSSHCLDP	NNEEGHGK	GWAFDDGNDV	gi	193084885	
PI VDI NI KDH	SI VSSYVCSG	LVGDTPRKN	SSSSSHCLDP	NNEEGHGK	GWAFDDGNDV	gi	194293951	
PI VDI NI KDH	SI VSSYVCSG	LVGDTPRKN	SSSSSHCLDP	NNEEGHGK	GWAFDDGNDV	gi	189303165	
PI VDI NI KDH	SI VSSYVCSG	LVGDTPRKN	SSSSSHCLDP	NNEEGHGK	GWAFDDGNDV	gi	189303149	
PI VDI NI KDH	SI VSSYVCSG	LVGDTPRKN	SSSSSHCLDP	NNEEGHGK	GWAFDDGNDV	gi	188076301	
PI VDI NI KDH	SI VSSYVCSG	LVGDTPRKN	SSSSSHCLDP	NNEEGHGK	GWAFDDGNDV	gi	194293985	
PI VDI NI KDH	SI VSSYVCSG	LVGDTPRKN	SSSSSHCLDP	NNEEGHGK	GWAFDDGNDV	gi	194293963	
PI VDI NI KDH	SI VSSYVCSG	LVGDTPRKN	SSSSSHCLDP	NNEEGHGK	GWAFDDGNDV	gi	194293981	
PI VDI NI KDH	SI VSSYVCSG	LVGDTPRKN	SSSSSHCLDP	NNEEGHGK	GWAFDDGNDV	gi	193084865	
PI VDI NI KDH	SI VSSYVCSG	LVGDTPRKN	SSSSSHCLDP	NNEEGHGK	GWAFDDGNDV	gi	194293969	
PI VDI NI KDH	SI VSSYVCSG	LVGDTPRKN	SSSSSHCLDP	NNEEGHGK	GWAFDDGNDV	gi	189303117	
PI VDI NI KDH	SI VSSYVCSG	LVGDTPRKN	SSSSSHCLDP	NNEEGHGK	GWAFDDGNDV	gi	189303161	
PI VDI NI KDH	SI VSSYVCSG	LVGDTPRKN	SSSSSHCLDP	NNEEGHGK	GWAFDDGNDV	gi	194294009	
PI VDI NI KDH	SI VSSYVCSG	LVGDTPRKN	SSSSSHCLDP	NNEEGHGK	GWAFDDGNDV	gi	194294025	
PI VDI NI KDH	SI VSSYVCSG	LVGDTPRKN	SSSSSHCLDP	NNEEGHGK	GWAFDDGNDV	gi	193084881	
PI VDI NI KDH	SI VSSYVCSG	LVGDTPRKN	SSSSSHCLDP	NNEEGHGK	GWAFDDGNDV	gi	194293959	
PI VDI NI KDH	SI VSSYVCSG	LVGDTPRKN	SSSSSHCLDP	NNEEGHGK	GWAFDDGNDV	gi	188076299	
PI VDI NI KDH	SI VSSYVCSG	LVGDTPRKN	SSSSSHCLDP	NNEEGHGK	GWAFDDGNDV	gi	194294005	
PI VDI NI KDH	SI VSSYVCSG	LVGDTPRKN	SSSSSHCLDP	NNEEGHGK	GWAFDDGNDV	gi	188076293	
PI VDI NI KDH	SI VSSYVCSG	LVGDTPRKN	SSSSSHCLDP	NNEEGHGK	GWAFDDGNDV	gi	194293973	
PI VDI NI KDH	SI VSSYVCSG	LVGDTPRKN	SSSSSHCLDP	NNEEGHGK	GWAFDDGNDV	gi	189303145	
PI VDI NI KDH	SI VSSYVCSG	LVGDTPRKN	SSSSSHCLDP	NNEEGHGK	GWAFDDGNDV	gi	194269505	
PI VDI NI KDH	SI VSSYVCSG	LVGDTPRKN	SSSSSHCLDP	NNEEGHGK	GWAFDDGNDV	gi	194269503	
PI VDI NI KDH	SI VSSYVCSG	LVGDTPRKN	SSSSSHCLDP	NNEEGHGK	GWAFDDGNDV	gi	22859349	
PI VDI NVKDY	SI VSSYVCSG	LVGDTPRKN	SSSSSHCLDP	NNEEGHGK	GWAFDDGNDV	gi	13548555	
PI VDI NVKDY	SI VSSYVCSG	LVGDTPRKN	SSSSSHCLDP	NNEEGHGK	GWAFDDGNDV	gi	149132956	
PI VDI NVKDY	SI VSSYVCSG	LVGDTPRKN	SSSSSHCLDP	NNEEGHGK	GWAFDDGNDV	gi	22859405	
PI VDI NVKDY	SI VSSYVCSG	LVGDTPRKN	SSSSSHCLDP	NNEEGHGK	GWAFDDGNDV	gi	13548549	
PI VDI NVKDY	SI VSSYVCSG	LVGDTPRKN	SSSSSHCLDP	NNEEGHGK	GWAFDDGNDV	gi	115291184	
PI VDI NVKDY	SI VSSYVCSG	LVGDTPRKN	SFSSSHCLDP	NNEEGHGK	GWAFDDGNDV	gi	83752056	
PI VDI NVKDY	SI VSSYVCSG	LVGDTPRKN	SFSSSHCLDP	NNEEGHGK	GWAFDDGNDV	gi	110333405	
PI VDI NVKDY	SI VSSYVCSG	LVGDTPRKN	SFSSSHCLDP	NNEEGHGK	GWAFDDGNDV	gi	83752094	
PI VDI NVKDY	SI VSSYVCSG	LVGDTPRKN	SFSSSHCLDP	NNEEGHGK	GWAFDDGNDV	gi	84873522	
PI VDI NVKDY	SI VSSYVCSG	LVGDTPRKN	SFSSSHCLDP	NNEEGHGK	GWAFDDGNDV	gi	83751804	
PI VDI NVKDY	SI VSSYVCSG	LVGDTPRKN	SFSSSHCLDP	NNEEGHGK	GWAFDDGNDV	gi	85838433	
PI VDI NVKDY	SI VSSYVCSG	LVGDTPRKN	SFSSSHCLDP	NNEEGHGK	GWAFDDGNDV	gi	110333367	
PI VDI NVKDY	SI VSSYVCSG	LVGDTPRKN	SFSSSHCLDP	NNEEGHGK	GWAFDDGNDV	gi	83730009	
PI VDI NVKDY	SI VSSYVCSG	LVGDTPRKN	SFSSSHCLDP	NNEEGHGK	GWAFDDGNDV	gi	22859395	
PI VDI NVKDY	SI VSSYVCSG	LVGDTPRKN	SSSSSHCLDP	NNEEGHGK	GWAFDDGNDV	gi	71564600	
PI VDI NVKDY	SI VSSYVCSG	LVGDTPRKN	SSSSSHCLNP	NNEEGHGK	GWAFDDGNDV	gi	68509317	
PI VDI NVKDY	SI VSSYVCSG	LVGDTPRKN	SSSSSHCLNP	NNEEGHGK	GWAFDDGNDV	gi	80974029	
PI VDI NVKDY	SI VSSYVCSG	LVGDTPRKN	SSSSSHCLNP	NNEEGHGK	GWAFDDGNDV	gi	68509898	
PI VDI NVKDY	SI VSSYVCSG	LVGDTPRKN	SSSSSHCLNP	NNEEGHGK	GWAFDDGNDV	gi	67057708	
PI VDI NVKDY	SI VSSYVCSG	LVGDTPRKN	SSSSSHCLNP	NNEEGHGK	GWAFDDGNDV	gi	68525445	
PI VDI NVKDY	SI VSSYVCSG	LVGDTPRKN	SSSSSHCLNP	NNEEGHGK	GWAFDDGNDV	gi	68508605	
PI VDI NVKDY	SI VSSYVCSG	LVGDTPRKN	SSSSSHCLNP	NNEEGHGK	GWAFDDGNDV	gi	68509231	
PI VDI NVKDY	SI VSSYVCSG	LVGDTPRKN	SSSSSHCLNP	NNEEGHGK	GWAFDDGNDV	gi	68510063	
PI VDI NVKDY	SI VSSYVCSG	LVGDTPRKN	SSSSSHCLNP	NNEEGHGK	GWAFDDGNDV	gi	13548565	
PI VDI NVKDY	SI VSSYVCSG	LVGDTPRKN	SSSSSHCLNP	NNEEGHGK	GWAFDDGNDV	gi	73761601	
PI VDI NVKDY	SI VSSYVCSG	LVGDTPRKN	SSSSSHCLNP	NNEEGHGK	GWAFDDGNDV	gi	13548569	
PI VDI NVKDY	SI VSSYVCSG	LVGDTPRKN	SSSSSHCLNP	NNEEGHGK	GWAFDDGNDV	gi	13548551	

PVVDI NMEDY	SI DSSYVCSG	LVGDTPRNDD	RSSNSNCRNP	NNERGNQGVK	GWAFDNGDDV	gi	193805119
PVVDI NMEDY	SI DSSYVCSG	LVGDTPRNDD	RSSNSNCRNP	NNERGNQGVK	GWAFDNGDDV	gi	193805157
PVVDI NMEDY	SI DSSYVCSG	LVGDTPRNDD	RSSNSNCRNP	NNERGNQGVK	GWAFDNGDDV	gi	193805214
PVVDI NMEDY	SI DSSYVCSG	LVGDTPRNDD	RSSNSNCRNP	NNERGNQGVK	GWAFDNGDDV	gi	106907951
PVVDI NMEDY	SI DSSYVCSG	LVGDTPRNDD	RSSNSNCRNP	NNERGNQGVK	GWAFDNGDDV	gi	85816057
PVVDI NMEDY	SI DSSYVCSG	LVGDTPRNDD	RSSNSNCRNP	NNERGNQGVK	GWAFDNGDDV	gi	193805176
PVVDI NMEDY	SI DSSYVCSG	LVGDTPRNDD	RSSNSNCRNP	NNERGNQGVK	GWAFDNGDDV	gi	194304751
PVVDI NMEDY	SI DSSYVCSG	LVGDTPRNDD	RSSNSNCRNP	NNERGNQGVK	GWAFDNGDDV	gi	194352003
PVVDI NMEDY	SI DSSYVCSG	LVGDTPRNDD	RSSNSNCRNP	NNERGNQGVK	GWAFDNGDDV	gi	37785258
PVVDI NMEDY	SI DSSYVCSG	LVGDTPRNDD	RSSNSNCRNP	NNERGNQGVK	GWAFDNGDDV	gi	37785260
PVVDI NMEDY	SI DSSYVCSG	LVGDTPRNDD	RSSNSNCRNP	NNERGNQGVK	GWAFDNGDDV	gi	194352098
PVVDI NMEDY	SI DSSYVCSG	LVGDTPRNDD	RSSNSNCRNP	NNERGNQGVK	GWAFDNGDDV	gi	126567437
PVVDI NMEDY	SI DSSYVCSG	LVGDTPRNDD	RSSNSNCRNP	NNERGNQGVK	GWAFDNGDDV	gi	37785250
PVVDI NMEDY	SI DSSYVCSG	LVGDTPRNDD	RSSNSNCRNP	NNERGNQGVK	GWAFDNGDDV	gi	37785252
PVVDI NMEDY	SI DSSYVCSG	LVGDTPRNDD	RSSNSNCRNP	NNERGNQGVK	GWAFDNGDDV	gi	37785256
PVVDI NMEDY	SI DSSYVCSG	LVGDTPRNDD	RSSNSNCRNP	NNERGNQGVK	GWAFDNGDDV	gi	37785262
PVVDI NMEDY	SI DSSYVCSG	LVGDTPRNDD	RSSNSNCRNP	NNERGNQGVK	GWAFDNGDDV	gi	14009708
PVVDI NMEDY	SI DSSYVCSG	LVGDTPRNDD	RSSNSNCRNP	NNERGNQGVK	GWAFDNGDDV	gi	193805271
PVVDI NMEDY	SI DSSYVCSG	LVGDTPRNDD	RSSNSNCRNP	NNERGNQGVK	GWAFDNGDDV	gi	125664200
PVVDI NMEDY	SI DSSYVCSG	LVGDTPRNDD	RSSNSNCRNP	NNERGNQGVK	GWAFDNGDDV	gi	37785254
PVVDI NMEDY	SI DSSYVCSG	LVGDTPRNDD	RSSNSNCRNP	NNERGNQGVK	GWAFDNGDDV	gi	37785270
PVVDI NMEDY	SI DSSYVCSG	LVGDTPRNDD	RSSNSNCRNP	NNERGNQGVK	GWAFDNGDDV	gi	31790582
PVVDI NMEDY	SI DSSYVCSG	LVGDTPRNDD	RSSNSNCRNP	NNERGNQGVK	GWAFDNGDDV	gi	46401580
PVVDI NMEDY	SI DSSYVCSG	LVGDTPRNDD	RSSNSNCRNP	NNERGNQGVK	GWAFDNGDDV	gi	194304713
PVVDI NMEDY	SI DSSYVCSG	LVGDTPRNDD	RSSNSNCRNP	NNERGNQGVK	GWAFDNGDDV	gi	194304637
PVVDI NMEDY	SI DSSYVCSG	LVGDTPRNDD	RSSNSNCRNP	NNERGNQGVK	GWAFDNGDDV	gi	133982222
PVVDI NMEDY	SI DSSYVCSG	LVGDTPRNDD	RSSNSNCRNP	NNERGNQGVK	GWAFDNGDDV	gi	148628616
PVVDI NMEDY	SI DSSYVCSG	LVGDTPRNDD	RSSNSNCRNP	NNERGNQGVK	GWAFDNGDDV	gi	194304675
PVVDI NMEDY	SI DSSYVCSG	LVGDTPRNDD	RSSNSNCRNP	NNERGNQGVK	GWAFDNGDDV	gi	37785264
PVVDI NMEDY	SI DSSYVCSG	LVGDTPRNDD	RSSNSNCRNP	NNERGNQGVK	GWAFDNGDDV	gi	37785266
PVVDI NMEDY	SI DSSYVCSG	LVGDTPRNDD	RSSNSNCRNP	NNERGNQGVK	GWAFDNGDDV	gi	80977933
PVVDI NMEDY	SI DSSYVCSG	LVGDTPRNDD	RSSNSNCRNP	NNERGNQGVK	GWAFDNGDDV	gi	37785268
PVVDI NMEDY	SI DSSYVCSG	LVGDTPRNDD	RSSNSNCRNP	NNERGNQGVK	GWAFDNGDDV	gi	125664238
PVVDI NMEDY	SI DSSYVCSG	LVGDTPRNDD	RSSNSNCRNP	NNERGNQGVK	GWAFDNGDDV	gi	134047623
PVADI NMEDY	SI DSSYVCSG	LVGDTPRNDD	RSSNSNCRNP	NNERGNQGVK	GWAFDNGDDV	gi	1517824
..***.*	*******	*****	*.*.*	***.*	*****	Clustal Cons	

WMGRTI SEKS	RLGYETFKVI	EGWSNPCKSL	QI NRQVI VDR	GNRSGYSGI F	SVEGKSCI NR	gi	188076309
WMGRTI SEKS	RLGYETFKVI	EGWSNPCKSL	QI NRQVI VDR	GNRSGYSGI F	SVEGKSCI NR	gi	188076307
WMGRTI SEKS	RLGYETFKVI	EGWSNPCKSL	QI NRQVI VDR	GNRSGYSGI F	SVEGKSCI NR	gi	194293955
WMGRTI SEKS	RLGYETFKVI	EGWSNPCKSL	QI NRQVI VDR	GNRSGYSGI F	SVEGKSCI NR	gi	194293993
WMGRTI SEKS	RLGYETFKVI	EGWSNPCKSL	QI NRQVI VDR	GNRSGYSGI F	SVEGKSCI NR	gi	193084877
WMGRTI SEKS	RLGYETFKVI	EGWSNPCKSL	QI NRQVI VDR	GNRSGYSGI F	SVEGKSCI NR	gi	189303105
WMGRTI SEKS	RLGYETFKVI	EGWSNPCKSL	QI NRQVI VDR	GNRSGYSGI F	SVEGKSCI NR	gi	193084869
WMGRTI SEKS	RLGYETFKVI	EGWSNPCKSL	QI NRQVI VDR	GNRSGYSGI F	SVEGKSCI NR	gi	194294017
WMGRTI SEKS	RLGYETFKVI	EGWSNPCKSL	QI NRQVI VDR	GNRSGYSGI F	SVEGKSCI NR	gi	189303153
WMGRTI SEKS	RLGYETFKVI	EGWSNPCKSL	QI NRQVI VDR	GNRSGYSGI F	SVEGKSCI NR	gi	189303157
WMGRTI SEKS	RLGYETFKVI	EGWSNPCKSL	QI NRQVI VDR	GNRSGYSGI F	SVEGKSCI NR	gi	194294021
WMGRTI SEKS	RLGYETFKVI	EGWSNPCKSL	QI NRQVI VDR	GNRSGYSGI F	SVEGKSCI NR	gi	194293997
WMGRTI SEKS	RLGYETFKVI	EGWSNPCKSL	QI NRQVI VDR	GNRSGYSGI F	SVEGKSCI NR	gi	194293977
WMGRTI SEKS	RLGYETFKVI	EGWSNPCKSL	QI NRQVI VDR	GNRSGYSGI F	SVEGKSCI NR	gi	194294013
WMGRTI SEKS	RLGYETFKVI	EGWSNPCKSL	QI NRQVI VDR	GNRSGYSGI F	SVEGKSCI NR	gi	193084885
WMGRTI SEKS	RLGYETFKVI	EGWSNPCKSL	QI NRQVI VDR	GNRSGYSGI F	SVEGKSCI NR	gi	194293951
WMGRTI SEKS	RLGYETFKVI	EGWSNPCKSL	QI NRQVI VDR	GNRSGYSGI F	SVEGKSCI NR	gi	189303165
WMGRTI SEKS	RLGYETFKVI	EGWSNPCKSL	QI NRQVI VDR	GNRSGYSGI F	SVEGKSCI NR	gi	189303149
WMGRTI SEKS	RLGYETFKVI	EGWSNPCKSL	QI NRQVI VDR	GNRSGYSGI F	SVEGKSCI NR	gi	188076301
WMGRTI SEKS	RLGYETFKVI	EGWSNPCKSL	QI NRQVI VDR	GNRSGYSGI F	SVEGKSCI NR	gi	194293985
WMGRTI SEKS	RLGYETFKVI	EGWSNPCKSL	QI NRQVI VDR	GNRSGYSGI F	SVEGKSCI NR	gi	194293963
WMGRTI SEKS	RLGYETFKVI	EGWSNPCKSL	QI NRQVI VDR	GNRSGYSGI F	SVEGKSCI NR	gi	194293981
WMGRTI SEKS	RLGYETFKVI	EGWSNPCKSL	QI NRQVI VDR	GNRSGYSGI F	SVEGKSCI NR	gi	193084865
WMGRTI SEKS	RLGYETFKVI	EGWSNPCKSL	QI NRQVI VDR	GNRSGYSGI F	SVEGKSCI NR	gi	194293969
WMGRTI SEKS	RLGYETFKVI	EGWSNPCKSL	QI NRQVI VDR	GNRSGYSGI F	SVEGKSCI NR	gi	189303117
WMGRTI SEKS	RLGYETFKVI	EGWSNPCKSL	QI NRQVI VDR	GDRSGYSGI F	SVEGKSCI NR	gi	189303161
WMGRTI SEKS	RLGYETFKVI	EGWSNPCKSL	QI NRQVI VDR	GNRSGYSGI F	SVEGKSCI NR	gi	194294009
WMGRTI SEKS	RLGYETFKVI	EGWSNPCKSL	QI NRQVI VDR	GNRSGYSGI F	SVEGKSCI NR	gi	194294025
WMGRTI SEKS	RLGYETFKVI	EGWSNPCKSL	QI NRQVI VDR	GNRSGYSGI F	SVEGKSCI NR	gi	193084881
WMGRTI SEKS	RLGYETFKVI	EGWSNPCKSL	QI NRQVI VDR	GNRSGYSGI F	SVEGKSCI NR	gi	194293959
WMGRTI SEKS	RLGYETFKVI	EGWSNPCKSL	QI NRQVI VDR	GNRSGYSGI F	SVEGKSCI NR	gi	188076299
WMGRTI SEKS	RLGYETFKVI	EGWSNPCKSL	QI NRQVI VDR	GNRSGYSGI F	SVEGKSCI NR	gi	194294005
WMGRTI SEKS	RLGYETFKVI	EGWSNPCKSL	QI NRQVI VDR	GNRSGYSGI F	SVEGKSCI NR	gi	188076293
WMGRTI SEKS	RLGYETFKVI	EGWSNPCKSL	QI NRQVI VDR	GNRSGYSGI F	SVEGKSCI NR	gi	194293973
WMGRTI SEKS	RLGYETFKVI	EGWSNPCKSL	QI NRQVI VDR	GNRSGYSGI F	SVEGKSCI NR	gi	189303145
WMGRTI SEKL	RSYETFKVI	EGWSNPCKSL	QI NRQVI VDR	GNRSGYSGI F	SVEGKSCI NR	gi	194269505
WMGRTI SEKL	RSYETFKVI	EGWSNPCKSL	QI NRQVI VDR	DNRSGYSGI F	SVEGKSCI NR	gi	194269503
WMGRTI SEKL	RSYETFKVI	EGWSNPCKSL	QI NRQVI VDR	GNRSGYSGI F	SVEGKSCI NR	gi	22859349

WMGRTI SEKL	RSGYETFKVI	EGWSKPNSKL	QI NRQVI VDR	GNRSGYSGI F	SVEGKSCI NR	gi	13548555
WMGRTI SEKL	RSGYETFKVI	EGWSKPNSKL	QI NRQVI VDR	GNRSGYSGI F	SVEGKSCI NR	gi	149132956
WMGRTI SEKL	RSGYETFKVI	EGWSKPNSKL	QI NRQVI VDR	GNRSGYSGI F	SVEGKSCI NR	gi	22859405
WMGRTI SEKL	RTGYETFKVI	EGWSKPNSKL	QI NRQVI VDR	GNRSGYSGI F	SVEGKSCI NR	gi	13548549
WMGRTI SEKL	RSGYETFKVI	EGWSKPNSKL	QI NRQVI VDR	GNRSGYSGI F	SVEGKSCI NR	gi	115291184
WMGRTI SEKL	RSGYETFKVI	EGWSKPNSKL	QI NRQVI VER	GNRSGYSGI F	SVEGKSCI NR	gi	83752056
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WMGRTI SEKL	RSGYETFKVI	EGWSKPNSKL	QI NRQVI VER	GNRSGYSGI F	SVEGKSCI NR	gi	83752094
WMGRTI SEKL	RSGYETFKVI	EGWSKPNSKL	QI NRQVI VER	GNRSGYSGI F	SVEGKSCI NR	gi	84873522
WMGRTI SEKL	RSGYETFKVI	EGWSKPNSKL	QI NRQVI VER	GNRSGYSGI F	SVEGKSCI NR	gi	83751804
WMGRTI SEKL	RSGYETFKVI	EGWSKPNSKL	QI NRQVI VER	GNRSGYSGI F	SVEGKSCI NR	gi	85838433
WMGRTI SEKL	RSGYETFKVI	EGWSKPNSKL	QI NRQVI VER	GNRSGYSGI F	SVEGKSCI NR	gi	110333367
WMGRTI SEKL	RSGYETFKVI	EGWSKPNSKL	QI NRQVI VER	GNRSGYSGI F	SVEGKSCI NR	gi	83730009
WMGRTI SEKL	RSGYETFKVI	EGWSKPNSKL	QI NRQVI VER	GNRSGYSGI F	SVEGKSCI NR	gi	22859395
WMGRTI SEKS	RSGYETFKVI	EGWSKPNSKL	QI NRQVI VER	GNRSGYSGI F	SVEGKSCI NR	gi	71564600
WMGRTI SEKF	RSGYETFKVI	EGWSKPNSKL	QI NRQVI VDR	DNRSGYSGI F	SVEGKSCI NR	gi	68509317
WMGRTI SEKF	RSGYETFKVI	EGWSKPNSKL	QI NRQVI VDR	DNRSGYSGI F	SVEGKSCI NR	gi	80974029
WMGRTI SEKF	RSGYETFKVI	EGWSKPNSKL	QI NRQVI VDR	DNRSGYSGI F	SVEGKSCI NR	gi	68509898
WMGRTI SEKF	RSGYETFKVI	EGWSKPNSKL	QI NRQVI VDR	DNRSGYSGI F	SVEGKSCI NR	gi	67057708
WMGRTI SEKF	RSGYETFKVI	EGWSKPNSKL	QI NRQVI VDR	DNRSGYSGI F	SVEGKSCI NR	gi	68525445
WMGRTI SEKF	RSGYETFKVI	EGWSKPNSKL	QI NRQVI VDR	DNRSGYSGI F	SVEGKSCI NR	gi	68508605
WMGRTI SEKF	RSGYETFKVI	EGWSKPNSKL	QI NRQVI VDR	DNRSGYSGI F	SVEGKSCI NR	gi	68509231
WMGRTI SEKF	RSGYETFKVI	EGWSKPNSKL	QI NRQVI VDR	DNRSGYSGI F	SVEGKSCI NR	gi	68510063
WMGRTI SEKF	RSGYETFKVI	EGWSKPNSKL	QI NRQVI VDR	DNRSGYSGI F	SVEGKSCI NR	gi	13548565
WMGRTI SEKF	RSGYETFKVI	EGWSKPNSKL	QI NRQVI VDR	DNRSGYSGI F	SVEGKSCI NR	gi	73761601
WMGRTI SEKF	RSGYETFKVI	EGWSKPNSKL	QI NRQVI VDR	GNRSGYSGI F	SVEGKSCI NR	gi	13548569
WMGRTI SEKF	RSGYETFKVI	EGWSKPNSKL	QI NRQVI VDR	DNRSGYSGI F	SVEGKSCI NR	gi	13548551
WMGRTI SKDL	RSGYETFKVI	GGWSTPNSKS	QI NRQVI VDS	DNRSGYSGI F	SVEGKSCI NR	gi	193805119
WMGRTI SKDL	RSGYETFKVI	GGWSTPNSKS	QI NRQVI VDS	DNRSGYSGI F	SVEGKSCI NR	gi	193805157
WMGRTI SKDL	RSGYETFKVI	GGWSTPNSKS	QI NRQVI VDS	DNRSGYSGI F	SVEGKSCI NR	gi	193805214
WMGRTI SKDL	RSGYETFKVI	GGWSTPNSKS	QI NRQVI VDS	DNRSGYSGI F	SVEGKSCI NR	gi	106907951
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WMGRTI SKDL	RSGYETFKVI	GGWSTPNSKS	QI NRQVI VDS	DNRSGYSGI F	SVEGKSCI NR	gi	193805176
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WMGRTI SKDL	RSGYETFKVI	GGWSTPNSKS	QI NRQVI VDS	DNRSGYSGI F	SVEGKSCI NR	gi	194352003
WMGRTI SKDL	RSGYETFKVI	GGWSTPNSKS	QI NRQVI VDS	DNRSGYSGI F	SVEGKSCI NR	gi	37785258
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WMGRTI SKDL	RSGYETFKVI	GGWSTPNSKS	QI NRQVI VDS	DNRSGYSGI F	SVEGKSCI NR	gi	194352098
WMGRTI SKDL	RSGYETFKVI	GGWSTPNSKS	QI NRQVI VDS	DNRSGYSGI F	SVEGKSCI NR	gi	126567437
WMGRTI SKDL	RSGYETFKVI	GGWSTPNSKS	QI NRQVI VDS	DNRSGYSGI F	SVEGKSCI NR	gi	37785250
WMGRTI SKDL	RSGYETFKVI	GGWSTPNSKS	QI NRQVI VDS	DNRSGYSGI F	SVEGKSCI NR	gi	37785252
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WMGRTI SKDL	RSGYETFKVI	GGWSTPNSKS	QI NRQVI VDS	DNRSGYSGI F	SVEGKSCI NR	gi	37785262
WMGRTI SKDL	RSGYETFKVI	GGWSTPNSKS	QI NRQVI VDS	DNRSGYSGI F	SVEGKSCI NR	gi	14009708
WMGRTI SKDL	RSGYETFKVI	GGWSTPNSKS	QI NRQVI VDS	DNRSGYSGI F	SVEGKSCI NR	gi	193805271
WMGRTI SKDL	RSGYETFKVI	GGWSTPNSKS	QI NRQVI VDS	DNRSGYSGI F	SVEGKSCI NR	gi	125664200
WMGRTI SKDL	RSGYETFKVI	GGWSTPNSKS	QI NRQVI VDS	DNRSGYSGI F	SVEGKSCI NR	gi	37785254
WMGRTI SKDL	RSGYETFKVI	GGWSTPNSKS	QI NRQVI VDS	DNRSGYSGI F	SVEGKSCI NR	gi	37785270
WMGRTI SKDL	RSGYETFKVI	GGWSTPNSKS	QI NRQVI VDS	DNRSGYSGI F	SVEGKSCI NR	gi	31790582
WMGRTI SKDL	RSGYETFKVI	GGWSTPNSKS	QI NRQVI VDS	DNRSGYSGI F	SVEGKSCI NR	gi	46401580
WMGRTI SKDL	RSGYETFKVI	GGWSTPNSKS	QI NRQVI VDS	DNRSGYSGI F	SVEGKSCI NR	gi	194304713
WMGRTI SKDL	RSGYETFKVI	GGWSTPNSKS	QI NRQVI VDS	DNRSGYSGI F	SVEGKSCI NR	gi	194304637
WMGRTI SKDL	RSGYETFKVI	GGWSTPNSKS	QI NRQVI VDS	DNRSGYSGI F	SVEGKSCI NR	gi	133982222
WMGRTI SKDL	RSGYETFKVI	GGWSTPNSKS	QI NRQVI VDS	DNRSGYSGI F	SVEGKSCI NR	gi	148628616
WMGRTI SKDL	RSGYETFKVI	GGWSTPNSKS	QI NRQVI VDS	DNRSGYSGI F	SVEGKSCI NR	gi	194304675
WMGRTI SKDL	RSGYETFKVI	GGWSTPNSKS	QI NRQVI VDS	DNRSGYSGI F	SVEGKSCI NR	gi	37785264
WMGRTI SKDL	RSGYETFKVI	GGWSTPNSKS	QI NRQVI VDS	DNRSGYSGI F	SVEGKSCI NR	gi	37785266
WMGRTI SKDL	RSGYETFKVI	GGWSTPNSKS	QI NRQVI VDS	DNRSGYSGI F	SVEGKSCI NR	gi	80977933
WMGRTI SKDL	RSGYETFKVI	GGWSTPNSKS	QI NRQVI VDS	DNRSGYSGI F	SVEGKSCI NR	gi	37785268
WMGRTI SKDL	RSGYETFKVI	GGWSTPNSKS	QI NRQVI VDS	DNRSGYSGI F	SVEGKSCI NR	gi	125664238
WMGRTI SKDL	RSGYETFKVI	GGWSTPNSKS	QI NRQVI VDS	DNRSGYSGI F	SVEGKSCI NR	gi	134047623
WMGRTI SKDL	RSGYETFKVI	GGWSTPNSKS	QI NRQVI VDS	DNRSGYSGI F	SVEGKSCI NR	gi	1517824
*****	* *****	*** . * . **	*****	.. *****	*** . *****	Clustal Cons	

CFYVELI RGR	KEETEVLTWS	NSI VVFCGTS	GTYGTGSWPD	GADI NLMPI	gi	188076309
CFYVELI RGR	KEETEVLTWS	NSI VVFCGTS	GTYGTGSWPD	GADI NLMPI	gi	188076307
CFYVELI RGR	KEETEVLTWS	NSI VVFCGTS	GTYGTGSWPD	GADI NLMPI	gi	194293955
CFYVELI RGR	KEETEVLTWS	NSI VVFCGTS	GTYGTGSWPD	GADI NLMPI	gi	194293993
CFYVELI RGR	KEETEVLTWS	NSI VVFCGTS	GTYGTGSWPD	GADLNLMPI	gi	193084877
CFYVELI RGR	KEETEVLTWS	NSI VVFCGTS	GTYGTGSWPD	GADI NLMPI	gi	189303105
CFYVELI RGR	KEETEVLTWS	NSI VVFCGTS	GTYGTGSWPD	GADI NLMPI	gi	193084869
CFYVELI RGR	KEETEVLTWS	NSI VVFCGTS	GTYGTGSWPD	GADI NLMPI	gi	194294017
CFYVELI RGR	KEETEVLTWS	NSI VVFCGTS	GTYGTGSWPD	GADI NLMPI	gi	189303153
CFYVELI RGR	KEETEVLTWS	NSI VVFCGTS	GTYGTGSWPD	GADI NLMPI	gi	189303157
CFYVELI RGR	KEETEVLTWS	NSI VVFCGTS	GTYGTGSWPD	GADI NLMPI	gi	194294021

CFYVELI RGR	KEKTEVLWTS	NSI VVFCGTS	GTYGTGSWPD	GADI NLMPI	gi	194293997
CFYVELI RGR	KEETEVLWTS	NSI VVFCGTS	GTYGTGSWPD	GADI NLMPI	gi	194293977
CFYVELI RGR	KEXTEVLWTS	NSI VVFCGTS	GTYGTGSWPD	GADI NLMPI	gi	194294013
CFYVELI RGR	KEXTEVLWTS	NSI VVFCGTS	GTYGTGSWPD	GADI NLMPI	gi	193084885
CFYVELI RGR	KEETEVLWTS	NSI VVFCGTS	GTYGTGSWPD	GADI NLMPI	gi	194293951
CFYVELI RGR	KEETEVLWTS	NSI VVFCGTS	GTYGTGSWPD	GADI NLMPI	gi	189303165
CFYVELI RGR	KEETEVLWTS	NSI VVFCGTS	GTYGTGSWPD	GADI NLMPI	gi	189303149
CFYVELI RGR	KEETEVLWTS	NSI VVFCGTS	GTYGTGSWPD	GADI NLMPI	gi	188076301
CFYVELI RGR	KEETEVLWTS	NSI VVFCGTS	GTYGTGSWPD	GADI NLMPI	gi	194293985
CFYVELI RGR	KEETEVLWTS	NSI VVFCGTS	GTYGTGSWPD	GADI NLMPI	gi	194293963
CFYVELI RGR	KEETEVLWTS	NSI VVFCGTS	GTYGTGSWPD	GADI NLMPI	gi	194293981
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CFYVELI RGR	KEETEVLWTS	NSI VVFCGTS	GTYGTGSWPD	GADI NLMPI	gi	194293969
CFYVELI RGR	KEETEVLWTS	NSI VVFCGTS	GTYGTGSWPD	GADI NLMPI	gi	189303117
CFYVELI RGR	KEETEVLWTS	NSI VVFCGTS	GTYGTGSWPD	GADI NLMPI	gi	189303161
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CFYVELI RGR	KEETEVLWTS	NSI VVFCGTS	GTYGTGSWPD	GADI NLMPI	gi	194294025
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CFYVELI RGR	KEETEVLWTS	NSI VVFCGTS	GTYGTGSWPD	GADI NLMPI	gi	194293959
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CFYVELI RGR	KEETEVLWTS	NSI VVFCGTS	GTYGTGSWPD	GADI NLMPI	gi	194294005
CFYVELI RGR	KEETEVLWTS	NSI VVFCGTS	GTYGTGSWPD	GADI NLMPI	gi	188076293
CFYVELI RGR	KEETEVLWTS	NSI VVFCGTS	GTYGTGSWPD	GADI NLMPI	gi	194293973
CFYVELI RGR	KEETEVLWTS	NSI VVFCGTS	GTYGTGSWPD	GADI NLMPI	gi	189303145
CFYVELI RGR	NOETEVLWTS	NSI VVFCGTS	GTYGTGSWPD	GADI NLMPI	gi	194269505
CFYVELI RGR	NOETEVLWTS	NSI VVFCGTS	GTYGTGSWPD	GADI NLMPI	gi	194269503
CFYVELI RGR	KOETEVLWTS	NSI VVFCGTS	GTYGTGSWPD	GADI NLMPI	gi	22859349
CFYVELI RGR	KOETEVLWTS	NSI VVFCGTS	GTYGTGSWPD	GADI NLMPI	gi	13548555
CFYVELI RGR	KOETEVLWTS	NSI VVFCGTS	GTYGTGSWPD	GADI NL---	gi	149132956
CFYVELI RGR	KOETEVLWTS	NSI VVFCGTS	GTYGTGSWPD	GADI NLMPI	gi	22859405
CFYVELI RGR	KOETEVLWTS	NSI VVFCGTS	GTYGTGSWPD	GADI NLMPI	gi	13548549
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CFYVELI RGR	KEETEVLWTS	NSI VVFCGTS	GTYGTGSWPD	GADI NLMPI	gi	83752094
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CFYVELI RGR	KEETEVLWTS	NSI VVFCGTS	GTYGTGSWPD	GADI NLMPI	gi	83751804
CFYVELI RGR	KEETEVLWTS	NSI VVFCGTS	GTYGTGSWPD	GADI NLMPI	gi	85838433
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CFYVELI RGR	KOETEVLWTS	NSI VVFCGTS	GTYGTGSWPD	GADI NLM--	gi	68509317
CFYVELI RGR	KOETEVLWTS	NSI VVFCGTS	GTYGTGSWPD	GADI NLM--	gi	80974029
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CFYVELI RGR	KOETEVLWTS	NSI VVFCGTS	GTYGTGSWPD	GADI NLMPI	gi	68525445
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CFYVELI RGR	KOETEVLWTS	NSI VVFCGTS	GTYGTGSWPD	GADI NLMPI	gi	68509231
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CFYVELI RGR	KOETEVLWTS	NSI VVFCGTS	GTYGTGSWPD	GADI NLMPI	gi	13548569
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CFYVELI RGR	KOETRVWTS	NSI VVFCGTS	GTYGTGSWPD	GANI NFMP	gi	193805119
CFYVELI RGR	KOETRVWTS	NSI VVFCGTS	GTYGTGSWPD	GANI NFMP	gi	193805157
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CFYVELI RGR	KOETRVWTS	NSI VVFCGTS	GTYGTGSWPD	GANI NFMP	gi	85816057
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CFYVELI RGR	KOETRVWTS	NSI VVFCGTS	GTYGTGSWPD	GANI NFMP	gi	194304751
CFYVELI RGR	KOETRVWTS	NSI VVFCGTS	GTYGTGSWPD	GANI NFMP	gi	194352003
CFYVELI RGR	KOETRVWTS	NSI VVFCGTS	GTYGTGSWPD	GANI NFMP	gi	37785258
CFYVELI RGR	KOETRVWTS	NSI VVFCGTS	GTYGTGSWPD	GANI NFMP	gi	37785260
CFYVELI RGR	KOETRVWTS	NSI VVFCGTS	GTYGTGSWPD	GANI NFMP	gi	194352098
CFYVELI RGR	KOETRVWTS	NSI VVFCGTS	GTYGTGSWPD	GANI NFMP	gi	126567437
CFYVELI RGR	KOETRVWTS	NSI VVFCGTS	GTYGTGSWPD	GANI NFMP	gi	37785250
CFYVELI RGR	KOETRVWTS	NSI VVFCGTS	GTYGTGSWPD	GANI NFMP	gi	37785252
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CFYVELI RGR	KOETRVWTS	NSI VVFCGTS	GTYGTGSWPD	GANI NFMP	gi	37785262
CFYVELI RGR	KOETRVWTS	NSI VVFCGTS	GTYGTGSWPD	GANI NFMP	gi	14009708
CFYVELI RGR	KOETRVWTS	NSI VVFCGTS	GTYGTGSWPD	GANI NFMP	gi	193805271
CFYVELI RGR	KOETRVWTS	NSI VVFCGTS	GTYGTGSWPD	GANI NFMP	gi	125664200
CFYVELI RGR	KOETRVWTS	NSI VVFCGTS	GTYGTGSWPD	GANI NFMP	gi	37785254
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CFYVELI RGR	KOETRVWTS	NSI VVFCGTS	GTYGTGSWPD	GANI NFMP	gi	31790582
CFYVELI RGR	KOETRVWTS	NSI VVFCGTS	GTYGTGSWPD	GANI NFMP	gi	46401580

CFYVELI RGR	KQETRVVWTS	NSI VVFCGTS	GTYGTGSPWD	GANI NFMPI	gi	194304713
CFYVELI RGR	KQETRVVWTS	NSI VVFCGTS	GTYGTGSPWD	GANI NFMHI	gi	194304637
CFYVELI RGR	KQETRVVWTS	NSI VVFCGTS	GTYGTGSPWD	GANI NFMPI	gi	133982222
CFYVELI RGR	KQETRVVWTS	NSI VVFCGTS	GTYGTGSPWD	GANI NFMPI	gi	148628616
CFYVELI RGR	KQETRVVWTS	NSI VVFCGTS	GTYGTGSPWD	GANI NFMPI	gi	194304675
CFYVELI RGR	KQETRVVWTS	NSI VVFCGTS	GTYGTGSPWD	GANI NFMPI	gi	37785264
CFYVELI RGR	KQETRVVWTS	NSI VVFCGTS	GTYGTGSPWD	GANI NFMPI	gi	37785266
CFYVELI RGR	KQETRVVWTS	NSI VVFCGTS	GTYGTGSPWD	GANI NFMPI	gi	80977933
CFYVELI RGR	KQETRVVWTS	NSI VVFCGTS	GTYGTGSPWD	GANI NFMPI	gi	37785268
CFYVELI RGR	KQETRVVWTS	NSI VVFCGTS	GTYGTGSPWD	GANI NFMPI	gi	125664238
CFYVELI RGR	KQETRVVWTS	NSI VVFCGTS	GTYGTGSPWD	GANI NFMPI	gi	134047623
CFYVELI RGR	KQETRVVWTS	NSI VVFCGTS	GTYGTGSPWD	GADI NFMPI	gi	1517824
*****	::: * **	*****	*****	***: *	Cl	ustal Cons

Alignment: G:\bwt skripsi\cari data\Data\database\Na\human\h5n1. al n

	10	20	30	40	50	60				
-----	MNPNQKI	IT	GSI CMVI GI V	SLMLQI GNMI	SI WVSHSI QT	GNQHQAES	--	gi	124099031	
-----	MNPNQKI	IT	GSI CMVI GI V	SLMLQI GNMI	SI WVSHSI QT	GNQHQAES	--	gi	124099009	
-----	MNPNQKI	IT	GSI CMVI GI V	SLMLQI GNMI	SI WVSHSI QT	GNQHQAES	--	gi	124099058	
-----	MNPNQKI	IT	GSI CMVI GI V	SLMLQI GNMI	SI WVSHSI QT	GNQHQAES	--	gi	124099084	
-----	MNPNQKI	IT	GSI CMVI GI V	SLMLQI GNMI	SI WVSHSI QT	GNQHQAES	--	gi	157955787	
-----	MNPNQKI	IT	GSI CMVI GI V	SLMLQI GNMI	SI WVSHSI QT	GNQHQAES	--	gi	113497245	
-----	MNPNQKI	IT	GSI CMVI GI V	SLMLQI GNMI	SI WVSHSI QT	GNQHQAES	--	gi	157955437	
-----	MNPNQKI	IT	GSI CMVI GI V	SLMLQI GNMI	SI WVSHSI QT	GNQHQAES	--	gi	113497198	
-----	MNPNQKI	IT	GSI CMVI GI V	SLMLQI GNMI	SI WVSHSI QT	GNQHQAES	--	gi	113972297	
-----	MNPNQKI	IT	GSI CMVI GI V	SLMLQI GNMI	SI WVSHSI QT	GNQHQAES	--	gi	118864192	
-----	MNPNQKI	IT	GSI CMVI GI V	SLMLQI GNMI	SI WVSHSI QT	GNQHQAES	--	gi	118864235	
-----	MNPNQKI	IT	GSI CMVI GI V	SLMLQI GNMI	SI WVSHSI QT	GNQHQAES	--	gi	157955698	
-----	MNPNQKI	IT	GSI CMVI GI V	SLMLQI GNMI	SI WVSHSI QT	GNQHQAES	--	gi	157955529	
-----	MNPNQKI	IT	GSI CMVI GI V	SLMLQI GNMI	SI WVSHSI QT	GNQHQAES	--	gi	118864141	
-----	MNPNQKI	IT	GSI CMVI GI V	SLMLQI GNMI	SI WVSHSI QK	GNQHQAES	--	gi	124098908	
-----	MNPNQKI	IT	GSI CMVI GI V	SLMLQI GNMI	SI WVSHSI QK	GNQHQAES	--	gi	124098582	
-----	MNPNQKI	IT	GSI CMVI GI V	SLMLQI GNMI	SI WVSHSI QK	GNQHQAES	--	gi	124098853	
-----	MNPNQKI	IT	GSI CMVI GI V	SLMLQI GNMI	SI WVSHSI QK	GNQHQAES	--	gi	124098881	
-----	MNPNQKI	IT	GSI CMVI GI V	SLMLQI GNMI	SI WVSHSI QK	GNQHQAES	--	gi	118864393	
-----	MNPNQKI	IT	GSI CMVI GI V	SLMLQI GNMI	SI WVSHSI QK	GNQHQAES	--	gi	124098932	
-----	MNPNQKI	IT	GSI CMVI GI V	SLMLQI GNMI	SI WVSHSI QK	GNQHQAES	--	gi	124098984	
-----	MNPNQKI	IT	GSI CMVI GI V	SLMLQI GNMI	SI WVSHSI QK	GNQHQAES	--	gi	124098957	
-----	MNPNQKI	IT	GSI CMVI GI V	SLMLQI GNMI	SI WVSHSI QK	GNQHQAES	--	gi	118574893	
-----	MNPNQKI	IT	GSI CMVI GI V	SLMLQI GNMI	SI WVSHSI QK	GNQHQAES	--	gi	118574874	
-----	MNPNQKI	IT	GSI CMVI GI V	SLMLQI GNMI	SI WVSHSI QK	GNQHQAES	--	gi	113497296	
-----	MNPNQKI	IT	GSI CMVI GI V	SLMLQI GNMI	SI WVSHSI QK	GNQHQAES	--	gi	157955475	
-----	MNPNQKI	IT	GSI CMVI GI V	SLMLQI GNMI	SI WVSHSI QK	GNQHQAES	--	gi	113496518	
-----	MNPNQKI	IT	GSI CMVI GI V	SLMLQI GNMI	SI WVSHSTQK	GNQHQAES	--	gi	113497374	
-----	MNPNRKI	IT	GSI CMVI GMV	SLMLQI GNMI	SI WVSHSI QT	GNQHQAES	--	gi	113972316	
-----	MNPNQKI	IT	GSI CMVI GI V	SLMLQI GNMV	STWVSHSI QT	GNQYQAES	--	gi	118574912	
-----	MNPNQKI	IT	GSI CMAI GTV	SLMLQI GNMI	SI WVSHSI QT	GNQHQAES	--	gi	157955603	
-----	MNPNQKI	IT	GSI CMAI GTV	SLMLQI GNMI	SI WVSHSI QT	GNQHQAES	--	gi	157955565	
-----	MNPNQKI	IT	GSI CMAI GTV	SLMLQI GNMI	SI WVSHSI QT	GNQHQAES	--	gi	157955641	
-----	MNPNQKI	IT	GSI CMAI GTV	SLMLQI GNMI	SI WVSHSI QT	GNQHQAES	--	gi	157955584	
-----	MNPNQKI	IT	GSI CMAI GTV	SLMLQI GNMI	SI WVSHSI QT	GNQHQAES	--	gi	113495792	
-----	MNPNQKI	IT	GSI CMAI GTV	SLMLQI GNMI	SI WVSHSI QT	GNQHQAES	--	gi	113495851	
-----	MNPNQKI	IT	GSI CMAI GTV	SLMLQI GNMI	SI WVSHSI QT	GNQHQAES	--	gi	113495963	
-----	MNPNQKI	IT	GSI CMAI GTV	SLMLQI GNMI	SI WVSHSI QT	GNQHQAES	--	gi	113495914	
-----	MNPNQKVI	IT	GSI CMVI GI V	SLMLQI GNMI	SI WVSHSI QT	GNQNVQEP	--	gi	162569002	
-----	MNPNQKI	IT	GSI CMVI GI V	SLMLQI GNMI	SI WVSHSI QT	GNQNVQEP	--	gi	162569004	
-----	MNPNQKI	IT	GSI CMVI GI V	SLMLQI GNMV	SLWVSHSI QT	GNQHVEP	--	gi	113707438	
-----	MNPNQKI	IT	GSI CMVI GI V	SLMLQI GNMI	SI WVSHSI QT	GNQQAEP	--	gi	157103086	
-----	-NP	NQKI	IT	GSI CMVI GI V	SLMLQI GNMI	SI WVSHSI QT	GNQQAEP	--	gi	157103100
-----	MNPNQKI	IT	GSI CMVI GI V	SLMLQI GNMI	SI WVSHSI QT	GNQQAEP	--	gi	157103119	
-----	MNPNQKI	IT	GSI CMVI GI V	SLMLQI GNMI	SI WVSHSI QT	GNQQAEP	--	gi	157103135	
-----	MNPNQKI	IT	GSI CMVI GI V	SLMLQI GNMI	SI WVSHSI QT	GNQQAEP	--	gi	157103072	
-----	MNPNQKI	IT	GSI CMVI GI V	SLMLQI GNMI	SI WVSHSI QT	GNQQAEP	--	gi	157103052	
-----	MNPNQKI	IT	GSI CMVI GI V	SLMLQI GNMI	SI WVSHSI QT	GNQQAEP	--	gi	124244208	
-----	MNPNQKI	IT	GSI CMVI GI V	SLMLQI GNMI	SI WVSHSI QT	GNQQAEP	--	gi	122913049	
-----	MNPNQKI	IT	GSI CMVI GI V	SLMLQI GNMI	SI WVSHSI QT	GNQQAEP	--	gi	148340545	
-----	-NP	NQKI	IT	GSI CMVI GI V	SLMLQI GNMI	SI WVSHSI QT	GNQQAEP	--	gi	148340541
-----	MNPNQKI	IT	GSI CMVI GI V	SLMLQI GNMI	SI WVSHSI QT	GNQQAEP	--	gi	157103596	
-----	MNPNQKI	IT	GSI CMVI GI V	SLMLQI GNI I	SI WI SHSI QT	GNQQAEP	--	gi	122913045	
-----	MNPNQKI	IT	GSI CMVI GI V	SLMLQI GNI I	SI WI SHSI QT	GNQQAEP	--	gi	122913047	
-----	MNPNQKI	IT	GSI CMVI GI V	SLMLQI GNMI	SI WVSHSI QT	GNQQAEP	--	gi	148340810	
-----	MNPNKKI	IT	GSI CMV TGMV	SLMLQI GNLI	SI WVSHSI HT	GNQKAEP	--	gi	145284421	
-----	MNPNKKI	IT	GSI CMV TGMV	SLMLQI GNLI	SI WVSHSI HT	GNQKAEP	--	gi	116295120	
-----	-KQEFK	MNPNKKI	IT	GSI CMV TGMV	SLMLQI GNLI	SI WLSRSI HT	GNQQAEP	--	gi	116295114
-----	FSGSQKQEFK	MNPNKKI	IT	GSI CMV TGMV	SLMLQI GNLI	SI WVSHSI HT	GNQKAXP	--	gi	116295110

-----	MNPNNKI	I	TI	GS	CMVTGMV	SLMLQI	GNLI	SI	WVSHSI	HT	GNQQAEP	--	gi	85680902				
-----	MNPNNKI	I	TI	GS	CMVTGMV	SLMLQI	GNLI	SI	WVSHSI	HT	GNQQAEP	--	gi	46360357				
-----	MNPNNKI	I	TI	GS	CMVTGMV	SLMLQI	GNLI	SI	WVSHSI	HT	ENOHKAEP	--	gi	134306634				
-----	--	KT	EI	I	TI	GS	CMVTGMV	SLMLQI	GNLD	LNMGP	FYSH	RAQHKAEP	--	gi	116295106			
-----	MNPNNKI	I	TI	GS	CMVTGMV	SLMLQI	GNLI	SI	WVSHSI	HT	GNQKAEP	--	gi	145284415				
-----	MNPNNKI	I	TI	GS	CMVTGI	V	SLMLQVGNMI	SI	WVSHSI	HT	GNQQAEP	--	gi	93008563				
-----	MNPNNKI	I	TI	GS	CMVTGI	V	SLMLQVGNMI	SI	WVSHSI	HT	GNQQAEP	--	gi	93008571				
-----	MNPNNKI	I	TI	GS	CMVTGI	V	SLMLQVGNMI	SI	WVSHSI	HT	GNQQAEP	--	gi	126361912				
-----	MNPNNKI	I	TI	GS	CMVTGI	V	SLMLQVGNMI	SI	WVSHSI	HT	GSQHQAEP	--	gi	95116895				
-----	MNPNNKI	I	TI	GS	CMVTGI	V	SLMLQVGNMI	SI	WVSHSI	HT	GNQQAEP	--	gi	72398597				
-----	MNPNNKI	I	TI	GS	CMVTGI	A	SLMLQI	GNMI	SI	WVSHSI	HT	GNQQAEP	--	gi	126361908			
-----	MNPNNKI	I	TI	GS	CMVTGI	V	SLMLQI	GNMI	SI	WVSHSI	HT	GNQHSEP	--	gi	78096578			
-----	MNPNNKI	I	TI	GS	CMVI	GI	V	SLMLQI	GNI	I	SI	WVSHSI	QT	GNQHQDEP	--	gi	182382583	
-----	MNPNNKI	I	TI	GS	CMVI	GI	V	SLMLQI	GNI	I	SI	WVSHSI	QT	GNQHQDEP	--	gi	182382601	
-----	--	PN	KI	TT	GS	CMVI	GI	V	SLMLQI	GNI	I	SI	WVSHSI	QT	GNQQAEP	PCN	gi	47834894
-----	MNPNNKI	TT	GS	CMVI	GI	V	SLMLQI	GNI	I	SI	WVSHSI	QT	GNQQAEP	PCN	gi	145284413		
-----	MNPNNKI	TT	GS	CMVI	GI	V	SLMLQI	GNI	I	SI	WVSHSI	QT	GNQQAEP	PCN	gi	47834892		
-----	MNPNNKI	TT	GS	CMVI	GI	V	SLMLQI	GNI	I	SI	WVSHSI	QT	GNQQAEP	PCN	gi	71013506		
-----	MNPNNKI	I	TI	GS	CMVVGI	I	NLMLQI	GNTI	SVVWSHI	I	KT	WHPNOPEP	--	gi	4324310			
-----	MNPNNKI	I	TI	GS	CMVVGI	I	SLMLQI	GNTI	SVVWSHI	I	KT	WHPNOPEP	--	gi	4324311			
-----	MNPNNKI	I	TI	GS	CMVVGI	I	SLMLQI	GNTI	SVVWSHI	I	KT	WHPNOPEP	--	gi	4324313			
-----	MNPNNKI	I	TI	GS	CMVVGI	I	SLMLQI	GNTI	SVVWSHI	I	KT	WHPNOPEP	--	gi	4324308			
-----	MNPNNKI	I	TI	GS	CMVVGI	I	SLMLQI	GNTI	SVVWSHI	I	KT	WHPNOPEP	--	gi	4324312			
-----	MNPNNKI	I	TI	GS	CMVVGI	I	SLMLQI	GNTI	SVVWSHI	I	KT	WHPNOPEP	--	gi	4324314			
-----	MNPNNKI	I	TI	GS	CMVVGI	I	SLMLQI	GNTI	SVVWSHI	I	KT	WHPNOPEP	--	gi	8307787			
-----	MNPNNKI	I	TI	GS	CMVVGI	I	SLMLQI	GNTI	SVVWSHI	I	KT	WHPNOPEP	--	gi	8307793			
-----	MNPNNKI	I	TI	GS	CMVVGI	I	SLMLQI	GNTI	SVVWSHI	I	QT	WHPNOPEP	--	gi	4324309			
-----	MNPNNKI	I	TI	GS	CMVVGI	I	SLMLQI	GNI	I	SVVWSPI	I	QA	WHPNOPEP	--	gi	4324317		
-----	MNPNNKI	I	TI	GS	CMVVGI	I	SLMLQI	GNTI	SVVWSPI	I	QD	WHPNOPEP	--	gi	4324322			
-----	MNPNNKI	I	TI	GS	CMVVGI	I	SLMLQI	GNTI	SVVWSPI	I	QA	WHPNOPEP	--	gi	4324319			
-----	MNPNNKI	I	TI	GS	CMVVGI	I	SLMLQI	GNI	I	SVVWSHI	I	QA	WHSNPEP	--	gi	4324318		
-----	MNPNNKI	I	TI	GS	CMVVGI	I	SLMLQI	GNI	I	SVVWSHI	I	QT	WHPNOPEP	--	gi	8307791		
-----	MNPNNKI	I	TI	GS	CMVVGI	I	SLMLQI	GNI	I	SVVWSHI	I	QT	WHPNOPEP	--	gi	4324316		
-----	MNPNNKI	I	TI	GS	CMVVGI	I	SLMLQI	GNI	I	SVVWSHI	I	QT	WHPNOPEP	--	gi	4324321		
-----	OKQEI	K	MNPNNKI	I	TI	GS	CMVVGI	I	SLMLQI	GNI	I	SVVWSHI	I	QT	WHPNOPEP	--	gi	2833659
-----	MNPNNKI	I	TI	GS	CMVVGI	I	SLMLQI	GNI	I	SVVWSHI	I	QT	WHPNOPEP	--	gi	4324315		
-----	MNPNNKI	I	TI	GS	CMVVGI	I	SLMLQI	GNI	I	SVVWSHI	I	QT	WHPNOPEP	--	gi	4324315		
-----	MNPNNKI	I	TI	GS	CMVVGI	I	SLMLQI	GNI	I	SVVWSHI	I	QT	WHPNOPEP	--	gi	8307789		
-----	MNPNNKI	I	TI	GS	CMVVGI	I	SLMLQI	GNI	I	SVVWSHI	I	QT	WHPNOPEP	--	gi	4324320		
-----	MNPNNKI	I	TI	GS	CMVVGI	I	SLMLQI	GNI	I	SVVWSHI	I	QT	WHPNOPEP	--	gi	3335423		
-----	MNPNNKI	I	TI	GS	CMVVGI	I	SLMLQI	GNI	I	SVVWSHI	I	QT	WHPNOPEP	--	gi	8307785		
-----	MNPNNKI	I	TI	GS	CMVVGI	I	SLMLQI	GNI	I	SVVWSHI	I	QT	WHPNOPEP	--	gi	2865378		
-----	..	**	*****	*		****	**											Clustal Cons

.....	70	80	90	100	110	120	-----	S	NTNPLTEKAV	VSVTL	LAGNSS	LCPI	RGWAVH	SKDNNI	RI	GS	gi	124099031
-----							-----	S	NTNPLTEKAV	VSVTL	LAGNSS	LCPI	RGWAVH	SKDNNI	RI	GS	gi	124099009
-----							-----	S	NTNPLTEKAV	VSVTL	LAGNSS	LCPI	RGWAVH	SKDNNI	RI	GS	gi	124099058
-----							-----	S	NTNPLTEKAV	VSVTL	LAGNSS	LCPI	RGWAVH	SKDNNI	RI	GS	gi	124099084
-----							-----	S	NTNPLTEKAV	ASVT	LAGNSS	LCPI	RGWAVH	SKDNNI	RI	GS	gi	157955787
-----							-----	S	NTNPLTEKAV	ASVT	LAGNSS	LCPI	RGWAVH	SKDNNI	RI	GS	gi	113497245
-----							-----	S	NTNPLTEKAV	ASVT	LAGNSS	LCPI	RGWAVH	SKDNNI	RI	GS	gi	157955437
-----							-----	S	NTNPLTEKAV	ASVT	LAGNSS	LCPI	RGWAVH	SKDNNI	RI	GS	gi	113497198
-----							-----	S	NTNPLTEKAV	ASVT	LAGNSS	LCPI	RGWAVH	SKDNNI	RI	GS	gi	113972297
-----							-----	S	NTNPLTEKAV	ASVT	LAGNSS	LCPI	RGWAVH	SKDNNI	RI	GS	gi	118864192
-----							-----	S	NTNPLTEKAV	ASVT	LAGNSS	LCPI	RGWAVH	SKDNNI	RI	GS	gi	118864235
-----							-----	S	NTNPLTEKAV	ASVT	LAGNSS	LCPI	RGWAVH	SKDNNI	RI	GS	gi	157955698
-----							-----	S	NTNPLTEKAV	ASVT	LAGNSS	LCPI	RGWAVH	SKDNNI	RI	GS	gi	157955529
-----							-----	S	NTNPLTEKAV	ASVT	LAGNSS	LCPI	RGWAVH	SKDNNI	RI	GS	gi	118864141
-----							-----	S	NTNPLTEKAV	ASVT	LAGNSS	LCPI	RGWAVH	SKDNNI	RI	GS	gi	124098908
-----							-----	S	NTNPLTEKAV	ASVT	LAGNSS	LCPI	RGWAVH	SKDNNI	RI	GS	gi	124098582
-----							-----	S	NTNPLTEKAV	ASVT	LAGNSS	LCPI	RGWAVH	SKDNNI	RI	GS	gi	124098853
-----							-----	S	NTNPLTEKAV	ASVT	LAGNSS	LCPI	RGWAVH	SKDNNI	RI	GS	gi	124098881
-----							-----	S	NTNPLTEKAV	ASVT	LAGNSS	LCPI	RGWAVH	SKDNNI	RI	GS	gi	118864393
-----							-----	S	NTNPLTEKAV	ASVT	LAGNSS	LCPI	RGWAVH	SKDNNI	RI	GS	gi	124098932
-----							-----	S	NTNPLTEKAV	ASVT	LAGNSS	LCPI	RGWAVH	SKDNNI	RI	GS	gi	124098984
-----							-----	S	NTNPLTEKAV	ASVT	LAGNSS	LCPI	RGWAVH	SKDNNI	RI	GS	gi	124098957
-----							-----	S	NTNPLTEKAV	ASI	TLAGNSS	LCPI	RGWAVH	SKDNNI	RI	GS	gi	118574893
-----							-----	S	NTNPLTEKAV	ASI	TLAGNSS	LCPI	RGWAVH	SKDNNI	RI	GS	gi	118574874
-----							-----	S	NTNPLTEKAV	ASVT	LAGNSS	LCPI	RGWAVH	SKDNNI	RI	GS	gi	113497296
-----							-----	S	NTNPLTEKAV	ASVT	LAGNSS	LCPI	RGWAVH	SKDNNI	RI	GS	gi	157955475
-----							-----	S	NTNPLTEKAV	ASVT	LAGNSS	LCPI	RGWAVH	SKDNNI	RI	GS	gi	113496518
-----							-----	S	NTNPLTEKAV	ASVT	LAGNSS	LCPI	RGWAVH	SKDNNI	RI	GS	gi	113497374
-----							-----	S	NTNPLTEKAV	ASVT	LAGNSS	LCPI	RGWAVH	SKDNNI	RI	GS	gi	113972316
-----							-----	S	NTNPLTEKAV	ASVT	LAGNSS	LCPI	RGWAVH	SKDNNI	RI	GS	gi	118574912
-----							-----	S	NTNPLTEKAV	ASVT	LAGNSS	LCPI	RGWAVH	SKDNNI	RI	GS	gi	157955603
-----							-----	S	NTNPLTEKAV	ASVT	LAGNSS	LCPI	RGWAVH	SKDNNI	RI	GS	gi	157955565

KGDVFI REP	FI SCSHLECR	TFFLTQGALL	NDKHSNGTVK	DRSPYRTLMS	CPVGEAPSPY	gi	4324314	g
KGDVFI REP	FI SCSHLECR	TFFLTQGALL	NDKHSNGTVK	DRSPYRTLMS	CPVGEAPSPY	gi	8307787	g
KGDVFI REP	FI SCSHLECR	TFFLTQGALL	NDKHSNGTVK	DRSPYRTLMS	CPVGEAPSPY	gi	8307793	g
KGDVFI REP	FI SCSHLECR	TFFLTQGALL	NDKHSNGTVK	DRSPYRTLMS	CPVGEAPSPY	gi	4324309	g
KGDVFI REP	FI SCSHLECR	TFFLTQGALL	NDKHSNGTVK	DRSPYRTLMS	CPVGEAPSPY	gi	4324317	g
KGDVFI REP	FI SCSHLECR	TFFLTQGALL	NDKHSNGTVK	DRSPYRTLMS	CPVGEAPSPY	gi	4324322	g
KGDVFI REP	FI SCSHLECR	TFFLTQGALL	NDKHSNGTVK	DRSPYRTLMS	CPVGEAPSPY	gi	4324319	g
KGDVFMREP	FI SCSHLECR	TFFLTQGALL	NNKHSNGTVK	DRSPYRTLMS	CPVGEAPSPY	gi	4324318	g
KGDVFI REP	FI SCSHLECR	TFFLTQGALL	NDKHSNGTVK	DRSPYRTLMS	CPVGEAPSPY	gi	8307791	g
KGDVFI REP	FI SCSHLECR	TFFLTQGALL	NDKHSNGTVK	DRSPYRTLMS	CPVGEAPSPY	gi	4324316	g
KGDVFI REP	FI SCSHLECR	TFFLTQGALL	NDKHSNGTVK	DRSPYRTLMS	CPVGEAPSPY	gi	4324321	g
KGDVFI REP	FI SCSHLECR	TFFLTQGALL	NDKHSNGTVK	DRSPYRTLMS	CPVGEAPSPY	gi	2833659	g
KGDVFI REP	FI SCSHLECR	TFFLTQGALL	NDKHSNGTVK	DRSPYRTLMS	CPVGEAPSPY	gi	4324315	g
KGDVFI REP	FI SCSHLECR	TFFLTQGALL	NDKHSNGTVK	DRSPYRTLMS	CPVGEAPSPY	gi	8307789	g
KGDVFI REP	FI SCSHLECR	TFFLTQGALL	NDKHSNGTVK	DRSPYRTLMS	CPVGEAPSPY	gi	4324320	g
KGDVFI REP	FI SCSHLECR	TFFLTQGALL	NDKHSNGTVK	DRSPYRTLMS	CPVGEAPSPY	gi	3335423	g
KGDVFI REP	FI SCSHLECR	TFFLTQGALL	NDKHSNGTVK	DRSPYRTLMS	CPVGEAPSPY	gi	8307785	g
KGDVFI REP	FI SCSHLECR	TFFLTQGALL	NDKHSNGTVK	DRSPYRTLMS	CPVGEAPSPY	gi	2865378	g
.*****. .*	***** .**	*****.*	*.*****.*	****.***	*****.***	Cl	ustal	Cons

		190	200		210		220		230		240		
NSRFESVAWS	ASACHDGTSW	LTI	GI	SGPDN	EAVAVLKYNG	II	TDTI	KSWR	NNI	LRTQESE	gi	124099031	
NSRFESVAWS	ASACHDGTSW	LTI	GI	SGPDN	EAVAVLKYNG	II	TDTI	KSWR	NNI	LRTQESE	gi	124099009	
NSRFESVAWS	ASACHDGTSW	LTI	GI	SGPDN	EAVAVLKYNG	II	TDTI	KSWR	NNI	LRTQESE	gi	124099058	
NSRFESVAWS	ASACHDGTSW	LTI	GI	SGPDN	EAVAVLKYNG	II	TDTI	KSWR	NNI	LRTQESE	gi	124099084	
NSRFESVAWS	ASACHDGTSW	LTI	GI	SGPDN	EAVAVLKYNG	II	TDTI	KSWR	NNI	LRTQESE	gi	157955787	
NSRFESVAWS	ASACHDGTSW	LTI	GI	SGPDN	EAVAVLKYNG	II	TDTI	KSWR	NNI	LRTQESE	gi	113497245	
NSRFESVAWS	ASACHDGTSW	LTI	GI	SGPDN	EAVAVLKYNG	II	TDTI	KSWR	NNI	LRTQESE	gi	157955437	
NSRFESVAWS	ASACHDGTSW	LTI	GI	SGPDN	EAVAVLKYNG	II	TDTI	KSWR	NNI	LRTQESE	gi	113497198	
NSRFESVAWS	ASACHDGTSW	LTI	GI	SGPDN	EAVAVLKYNG	II	TDTI	KSWR	NNI	LRTQESE	gi	113972297	
NSRFESVAWS	ASACHDGTSW	LTI	GI	SGPDN	EAVAVLKYNG	II	TDTI	KSWR	NNI	LRTQESE	gi	118864192	
NSRFESVAWS	ASACHDGTSW	LTI	GI	SGPDN	EAVAVLKYNG	II	TDTI	KSWR	NNI	LRTQESE	gi	118864235	
NSRFESVAWS	ASACHDGTSW	LTI	GI	SGPDN	EAVAVLKYNG	II	TDTI	KSWR	NNI	LRTQESE	gi	157955698	
NSRFESVAWS	ASACHDGTSW	LTI	GI	SGPDN	EAVAVLKYNG	II	TDTI	KSWR	NNI	LRTQESE	gi	157955529	
NSRFESVAWS	ASACHDGTNSW	LTI	GI	SGPDN	EAVAVLKYNG	II	TDTI	KSWR	KNI	LRTQESE	gi	118864141	
NSRFESVAWS	ASACHDGTSW	LTI	GI	SGPDN	EAVAVLKYNG	II	TDTI	KSWR	NNI	LRTQESE	gi	124098908	
NSRFESVAWS	ASACHDGTSW	LTI	GI	SGPDN	EAVAVLKYNG	II	TDTI	KSWR	NNI	LRTQESE	gi	124098582	
NSRFESVAWS	ASACHDGTSW	LTI	GI	SGPDN	EAVAVLKYNG	II	TDTI	KSWR	NNI	LRTQESE	gi	124098853	
NSRFESVAWS	ASACHDGTSW	LTI	GI	SGPDN	EAVAVLKYNG	II	TDTI	KSWR	NNI	LRTQESE	gi	124098881	
NSRFESVAWS	ASACHDGTSW	LTI	GI	SGPDN	EAVAVLKYNG	II	TDTI	KSWR	NNI	LRTQESE	gi	118864393	
NSRFESVAWS	ASACHDGTSW	LTI	GI	SGPDN	EAVAVLKYNG	II	TDTI	KSWR	NNI	LRTQESE	gi	124098932	
NSRFESVAWS	ASACHDGTSW	LTI	GI	SGPDN	EAVAVLKYNG	II	TDTI	KSWR	NNI	LRTQESE	gi	124098984	
NSRFESVAWS	ASACHDGTSW	LTI	GI	SGPDN	EAVAVLKYNG	II	TDTI	KSWR	NNI	LRTQESE	gi	124098957	
NSRFESVAWS	ASACHDGTSW	LTI	GI	SGPDN	EAVAVLKYNG	II	TDTI	KSWR	NNI	LRTQESE	gi	118574893	
NSRFESVAWS	ASACHDGTSW	LTI	GI	SGPDN	EAVAVLKYNG	II	TDTI	KSWR	NNI	LRTQESE	gi	118574874	
NSRFESVAWS	ASACHDGTSW	LTI	GI	SGPDN	EAVAVLKYNG	II	TDTI	KSWR	NNI	LRTQESE	gi	113497296	
NSRFESVAWS	ASACHDGTSW	LTI	GI	SGPDN	EAVAVLKYNG	II	TDTI	KSWR	NNI	LRTQESE	gi	157955475	
NSRFESVAWS	ASACHDGTSW	LTI	GI	SGPDN	EAVAVLKYNG	II	TDTI	KSWR	NNI	LRTQESE	gi	113496518	
NSRFESVAWS	ASACHDGTSW	LTI	GI	SGPDN	EAVAVLKYNG	II	TDTI	KSWR	NNI	LRTQESE	gi	113497374	
NSRFESVAWS	ASACHDGTSW	LTI	GI	SGPDN	EAVAVLKYNG	II	TDTI	KSWR	NNI	LRTQESE	gi	113972316	
NSRFESVAWS	ASACHDGTSW	LTI	GI	SGPDN	EAVAVLKYNG	II	TDTI	KSWR	NNI	LRTQESE	gi	118574912	
NSRFESVAWS	ASACHDGTSW	LTI	GI	SGPDN	GAVAVLKYNG	II	TDTI	KSWR	NNI	LRTQESE	gi	157955603	
NSRFESVAWS	ASACHDGTSW	LTI	GI	SGPDN	GAVAVLKYNG	II	TDTI	KSWR	NNI	LRTQESE	gi	157955565	
NSRFESVAWS	ASACHDGTSW	LTI	GI	SGPDN	GAVAVLKYNG	II	TDTI	KSWR	NNI	LRTQESE	gi	157955641	
NSRFESVAWS	ASACHDGTSW	LTI	GI	SGPDN	GAVAVLKYNG	II	TDTI	KSWR	NNI	LRTQESE	gi	157955584	
NSRFESVAWS	ASACHDGTSW	LTI	GI	SGPDN	GAVAVLKYNG	II	TDTI	KSWR	NNI	LRTQESE	gi	113495792	
NSRFESVAWS	ASACHDGTSW	LTI	GI	SGPDN	GAVAVLKYNG	II	TDTI	KSWR	NNI	LRTQESE	gi	113495851	
NSRFESVAWS	ASACHDGTSW	LTI	GI	SGPDN	GAVAVLKYNG	II	TDTI	KSWR	NNI	LRTQESE	gi	113495963	
NSRFESVAWS	ASACHDGTSW	LTI	GI	SGPDN	GAVAVLKYNG	II	TDTI	KSWR	NNI	LRTQESE	gi	113495914	
NSRFESVAWS	ASACHDGTSW	LTI	GI	SGPDN	GAVAVLKYNG	II	TDTI	KSWR	NNI	LRTQESE	gi	162569002	
NSRFESVAWS	ASACHDGTSW	LTI	GI	SGPDN	GAVAVLKYNG	II	TDTI	KSWR	NNI	LRTQESE	gi	162569004	
NSRFESVAWS	ASACHDGTSW	LTI	GI	SGPDN	GAVAVLKYNG	MI	TDTI	KSWR	NNI	LRTQESE	gi	113707438	
NSRFESVAWS	ASACHDGTSW	LTI	GI	SGPDN	GAVAVLKYNG	II	TDTI	KSWR	NNI	LRTQESE	gi	157103086	
NSRFESVAWS	ASACHDGTSW	LTI	GI	SGPDN	GAVAVLKYNG	II	TDTI	KSWR	NNI	LRTQESE	gi	157103100	
NSRFESVAWS	ASACHDGTSW	LTI	GI	SGPDN	GAVAVLKYNG	II	TDTI	KSWR	NNI	LRTQESE	gi	157103119	
NSRFESVAWS	ASACHDGTSW	LTI	GI	SGPDN	GAVAVLKYNG	II	TDTI	KSWR	NNI	LRTQESE	gi	157103135	
NSRFESVAWS	ASACHDGTSW	LTI	GI	SGPDN	GAVAVLKYNG	II	TDTI	KSWR	NNI	LRTQESE	gi	157103072	
NSRFESVAWS	ASACHDGASW	LTI	GI	SGPDN	GAVAVLKYNG	II	TDTI	KSWR	NNI	LRTQESE	gi	157103052	
NSRFESVAWS	ASACHDGTSW	LTI	GI	SGPDN	GAVAVLKYNG	II	TDTI	KSWR	NNI	LRTQESE	gi	124244208	
NSRFESVAWS	ASACHDGTSW	LTI	GI	SGPDN	GAVAVLKYNG	II	TDTI	KSWR	NNI	LRTQESE	gi	122913049	
NSRFESVAWS	ASACHDGTSW	LTI	GI	SGPDN	GAVAVLKYNG	II	TDTI	KSWR	NNI	LRTQESE	gi	148340545	
NSRFESVAWS	ASACHDGTSW	LTI	GI	SGPDN	GAVAVLKYNG	II	TDTI	KSWR	NNI	LRTQESE	gi	148340541	
NSRFESVAWS	ASACHDGTSW	LTI	GI	SGPDN	GAVAVLKYNG	II	TDTI	KSWR	NNI	LRTQESE	gi	157103596	
NSRFESVAWS	ASACHDGTSW	LTI	GI	SGPDN	GAVAVLKYNG	II	TDTI	KSWR	NNI	LRTQESE	gi	122913045	
NSRFESVAWS	ASACHDGTSW	LTI	GI	SGPDN	GAVAVLKYNG	II	TDTI	KSWR	NNI	LRTQESE	gi	122913047	
NSRFESVAWS	ASACHDGTSW	LTI	GI	SGPDN	GAVAVLKYNG	II	TDTI	KSWR	NNI	LRTQESE	gi	148340810	

NSRFESVAWS	ASACHDGTSW	LTI GI	SGPDN	GAVAVLKYN	II	TDTI	KSWR	NNI	LRTQESE	gi	145284421
NSRFESVAWS	ASACHDGTSW	LTI GI	SGPDN	GAVAVLKYN	II	TDTI	KSWR	NNI	LRTQESE	gi	116295120
NSRFESVAWS	ASACHDGTSW	LTI GI	SGPDS	GAVAVLKYN	II	TDTI	KSWR	NNI	LRTQESE	gi	116295114
NSRFESVAWS	ASACHDGTSW	LTI GI	SGPDN	GAVAVLKYN	II	TDTI	KSWR	NNI	LRTQESE	gi	116295110
NSRFESVAWS	ASACHDGTSW	LTI GI	SGPDS	GAVAVLKYN	II	TDTI	KSWR	NNI	LRTQESE	gi	85680902
NSRFESVAWS	ASACHDGTSW	LTI GI	SGPDS	GAVAVLKYN	II	TDTI	KSWR	NNI	LRTQESE	gi	46360357
NSRFESVAWS	ASACHDGTSW	LTI GI	SGPDN	GAVAVLKYN	II	TDTI	KSWR	NNI	LRTQESE	gi	134306634
NSRFESVAWS	ASACHDGTSW	LTI GI	SGPDN	GAVAVLKYN	II	TDTI	KSWR	NNI	LRTQESE	gi	116295106
NSRFESVAWS	ASACHDGTSW	LTI GI	SGPDN	GAVAVLKYN	II	TDTI	KSWR	NNI	LRTQESE	gi	145284415
NSRFESVAWS	ASACHDGTSW	LTI GI	SGPDN	GAVAVLKYN	II	TDTI	KSWR	NNI	LRTQESE	gi	93008563
NSRFESVAWS	ASACHDGTSW	LTI GI	SGPDN	GAVAVLKYN	II	TDTI	KSWR	NNI	LRTQESE	gi	93008571
NSRFESVAWS	ASACHDGTSW	LTI GI	SGPDN	GAVAVLKYN	II	TDTI	KSWR	NNI	LRTQESE	gi	126361912
NSRFESVAWS	ASACHDGTSW	LTI GI	SGPDN	GAVAVLKYN	II	TDTI	KSWR	NNI	LRTQESE	gi	95116895
NSRFESVAWS	ASACHDGTSW	LTI GI	SGPDN	GAVAVLKYN	II	TDTI	KSWR	NNI	LRTQESE	gi	72398597
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NSRFESVAWS	ASACHDGTSW	LTI GI	SGPDN	GAVAVLKYN	II	TDTI	KSWR	NNI	LRTQESE	gi	78096578
NSRFESVAWS	ASACHDGTSW	LTI GI	SGPDN	GAVAVLKYN	II	TDTI	KSWR	NNI	LRTQESE	gi	182382583
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NSRFESVAWS	ASACHDGTSW	LTI GI	SGPDN	GAVAVLKYN	II	TDTI	KSWR	NNI	LRTQESE	gi	47834894
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NSRFESVAWS	ASACHDGI SW	LTI GI	SGPDN	GAVAVLKYN	II	TDTI	KSWR	NNI	LRTQESE	gi	4324310
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NSRFESVAWS	ASACHDGI SW	LTI GI	SGPDN	GAVAVLKYN	II	TDTI	KSWR	NNI	LRTQESE	gi	4324308
NSRFESVAWS	ASACHDGI SW	LTI GI	SGPDN	GAVAVLKYN	II	TDTI	KSWR	NNI	LRTQESE	gi	4324312
NSRFESVAWS	ASACHDGI SW	LTI GI	SGPDN	GAVAVLKYN	II	TDTI	KSWR	NNI	LRTQESE	gi	4324314
NSRFESVAWS	ASACHDGI SW	LTI GI	SGPDN	GAVAVLKYN	II	TDTI	KSWR	NNI	LRTQESE	gi	8307787
NSRFESVAWS	ASACHDGI SW	LTI GI	SGPDN	GAVAVLKYN	II	TDTI	KSWR	NNI	LRTQESE	gi	8307793
NSRFESVAWS	ASACHDGI SW	LTI GI	SGPDN	GAVAVLKYN	II	TDTI	KSWR	NNI	LRTQESE	gi	4324309
NSRFESVAWS	ASACHDGI SW	LTI GI	SGPDN	GAVAVLKYN	II	TDTI	KSWR	NNI	LRTQESE	gi	4324317
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NSRFESVAWS	ASACHDGI SW	LTI GI	SGPDN	GAVAVLKYN	II	TDTI	KSWR	NNI	LRTQESE	gi	4324319
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NSRFESVAWS	ASACHDGI SW	LTI GI	SGPDN	GAVAVLKYN	II	TDTI	KSWR	NNI	LRTQESE	gi	8307791
NSRFESVAWS	ASACHDGI SW	LTI GI	SGPDN	GAVAVLKYN	II	TDTI	KSWR	NNI	LRTQESE	gi	4324316
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NSRFESVAWS	ASACHDGI SW	LTI GI	SGPDN	GAVAVLKYN	II	TDTI	KSWR	NNI	LRTQESE	gi	2833659
NSRFESVAWS	ASACHDGI SW	LTI GI	SGPDN	GAVAVLKYN	II	TDTI	KSWR	NNI	LRTQESE	gi	4324315
NSRFESVAWS	ASACHDGI SW	LTI GI	SGPDN	EAVAVLKYN	II	TDTI	RSWR	NNI	LRTQESE	gi	8307789
NSRFESVAWS	ASACHDGI SW	LTI GI	SGPDN	EAVAVLKYN	II	TDTI	RSWR	NNI	LRTQESE	gi	4324320
NSRFESVAWS	ASACHDGI SW	LTI GI	SGPDN	GAVAVLKYN	II	TDTI	KSWR	NNI	LRTQESE	gi	3335423
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NSRFESVAWS	ASACHDGI SW	LTI GI	SGPDN	GAVAVLKYN	II	TDTI	KSWR	NNI	LRTQESE	gi	2865378
*****	*****	**	*****	****	****	*****	***	*	..	**	Clustal Cons

	250	260	270	280	290	300	
CACVNGSCFT	VMTDGPNSGQ	ASYKI	FKMEK	-GKVVKSVEL	DAPNYHYEEC	SCYPDAGEI	T gi 124099031
CACVNGSCFT	VMTDGPNSGQ	ASYKI	FKMEK	-GKVVKSVEL	DAPNYHYEEC	SCYPDAGEI	T gi 124099009
CACVNGSCFT	VMTDGPNSGQ	ASYKI	FKMEK	-GKVVKSVEL	DAPNYHYEEC	SCYPDAGEI	T gi 124099058
CACVNGSCFT	VMTDGPNSGQ	ASYKI	FKMEK	-GKVVKSVEL	DAPNYHYEEC	SCYPDAGEI	T gi 124099084
CACVNGSCFT	VMTDGPNSGQ	ASYKI	FKMEK	-GKVVKSVEL	DAPNYHYEEC	SCYPDAGEI	T gi 157955787
CACVNGSCFT	VMTDGPNSGQ	ASYKI	FKMEK	-GKVVKSVEL	DAPNYHYEEC	SCYPDAGEI	T gi 113497245
CACVNGSCFT	VMTDGPNSGQ	ASYKI	FKMEK	-GKVVKSVEL	DAPNYHYEEC	SCYPDAGEI	T gi 157955437
CACVNGSCFT	VMTDGPNSGQ	ASYKI	FKMEK	-GKVVKSVEL	DAPNYHYEEC	SCYPDAGEI	T gi 113497198
CACVNGSCFT	VMTDGPNSGQ	ASYKI	FKMEK	-GKVVKSVEL	DAPNYHYEEC	SCYPDAGEI	T gi 113972297
CACVNGSCFT	VMTDGPNSGQ	ASYKI	FKMEK	-GKVVKSVEL	DAPNYHYEEC	SCYPDAGEI	T gi 118864192
CACVNGSCFT	VMTDGPNSGQ	ASYKI	FKMEK	-GKVVKSVEL	DAPNYHYEEC	SCYPDAGEI	T gi 118864235
CACVNGSCFT	VMTDGPNSGQ	ASYKI	FKMEK	-GKVVKSVEL	DAPNYHYEEC	SCYPDAGEI	T gi 157955698
CACVNGSCFT	VMTDGPNSGQ	ASYKI	FKMEK	-GKVVKSVEL	DAPNYHYEEC	SCYPDAGEI	T gi 157955529
CACVNGSCFT	VMTDGPNSGQ	ASYKI	FKMEK	-GKVVKSVEL	DAPNYHYEEC	SCYPDAGEI	T gi 118864141
CACVNGSCFT	VMTDGPNSGQ	ASYKI	FKMCK	-GKVVKSVEL	DAPNYHYEEC	SCYPDAGEI	T gi 124098908
CACVNGSCFT	VMTDGPNSGQ	ASYKI	FKMCK	-GKVVKSVEL	DAPNYHYEEC	SCYPDAGEI	T gi 124098582
CACVNGSCFT	VMTDGPNSGQ	ASYKI	FKMCK	-GKVVKSVEL	DAPNYHYEEC	SCYPDAGEI	T gi 124098853
CACVNGSCFT	VMTDGPNSGQ	ASYKI	FKMCK	-GKVVKSVEL	DAPNYHYEEC	SCYPDAGEI	T gi 124098881
CACVNGSCFT	VMTDGPNSGQ	ASYKI	FKMCK	-GKVVKSVEL	DAPNYHYEEC	SCYPDAGEI	T gi 118864393
CACVNGSCFT	VMTDGPNSGQ	ASYKI	FKMCK	-GKVI KVEL	DATNYHYEEC	SCYPDAGEI	T gi 124098932
CACVNGSCFT	VMTDGPNSGQ	ASYKI	FKMCK	-GKVI KVEL	DATNYHYEEC	SCYPDAGEI	T gi 124098984
CACVNGSCFT	VMTDGPNSGQ	ASYKI	FKMCK	-GKVI KVEL	DATNYHYEEC	SCYPDAGEI	T gi 124098957
CACVNGSCFT	VMTDGPNSGQ	ASYKI	FKMCK	-GKVVKSVEL	DAPNYHYEEC	SCYPDAGEI	T gi 118574893
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CACVNGSCFT	VMTDGPNSGQ	ASYKI	FKMEK	-GKVVKSVEL	DAPNYHYEEC	SCYPDAGEI	T gi 113497296
CACVNGSCFT	VMTDGPNSGQ	ASYKI	FKMEK	-GKVVKSVEL	DAPNYHYEEC	SCYPDAGEI	T gi 157955475
CACVNGSCFT	VMTDGPNSGQ	ASYKI	FKMEK	-GKVVKSVEL	DAPNYHYEEC	SCYPDAGEI	T gi 113496518
CACVNGSCFT	VMTDGPNSGQ	ASYKI	FKMEK	-GKVVKSVEL	DAPNYHYEEC	SCYPDAGEI	T gi 113497374

CACVNGSCFT VMTDGPSNGQ ASYKI FKMEK -GKVVKSVEL VAPNYHYEEC SCYPDAGEI T gi 113972316
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CACVNGSCFT VMTDGPSNGQ ASYKI FKMEK -GKVVKSVEL NAPNYHYEEC SCYPDAGEI T gi 182382601
CACVNGSCFT VMTDGPSNGQ ASYKI FRI EK -GKVVKSVEL NAPNYHYEEC SCYPDAGEI T gi 47834894
CACVNGSCFT VMTDGPSNGQ ASYKI FRI EK -GKVVKSVEL NAPNYHYEEC SCYPDAGEI T gi 145284413
CACVNGSCFT VMTDGPSNGQ ASYKI FRI EK -GKVVKSVEL NAPNYHYEEC SCYPDAGEI T gi 47834892
CACVNGSCFT VMTDGPSNGQ ASYKI FRI EK -GKVVKSVEL NAPNYHYEEC SCYPDAGEI T gi 71013506
CACVNGSCFT VMTDGPSSGQ ASYKI FKI EK -GRVKSVEL NAPNYHYEEC SCYPDAGEI T gi 4324310
CACVNGSCFT VMTDGPSSGQ ASYKI FKI EK -GRVKSVEL NAPNYHYEEC SCYPDAGEI T gi 4324311
CACVNGSCFT VMTDGPSSGQ ASYKI FKI EK -GRVKSVEL NAPNYHYEEC SCYPDAGEI T gi 4324313
CACVNGSCFT VMTDGPSSGQ ASYKI FKI EK -GRVKSVEL NAPNYHYEEC SCYPDAGEI T gi 4324308
CACVNGSCFT VMTDGPSSGQ ASYKI FKI EK -GRVKSVEL NAPNYHYEEC SCYPDAGEI T gi 4324312
CACVNGSCFT VMTDGPSSGQ ASYKI FKI EK -GRVKSVEL NAPNYHYEEC SCYPDAGEI T gi 4324314
CACVNGSCFT VMTDGPSSGQ ASYKI FKI EK -GRVKSVEL NAPNYHYEEC SCYPDAGEI T gi 8307787
CACVNGSCFT VMTDGPSSGQ ASYKI FKI EK -GRVKSVEL NAPNYHYEEC SCYPDAGEI T gi 8307793
CACVNGSCFT VMTDGPSSGQ ASYKI FKI EK -GRVKSVEL NAPNYHYEEC SCYPDAGEI T gi 4324309
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CACVNGSCFT VMTDGPSSGQ ASYKI FKI EK -GRVKSVEL NAPNYHYEEC SCYPDAGEI T gi 8307791
CACVNGSCFT VMTDGPSSGQ ASYKI FKI EK -GRVKSVEL NAPNYHYEEC SCYPDAGEI T gi 4324316
CACVNGSCFT VMTDGPSSGQ ASYKI FKI EK -GRVKSVEL NAPNYHYEEC SCYPDAGEI T gi 4324321
CACVNGSCFT VMTDGPSSGQ ASYKI FKI EK -GRVKSVEL NAPNYHYEEC SCYPDAGEI T gi 4324315
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CACVNGSCFT VMTDGPSSGQ ASYKI FKI EK -GRVKSVEL NAPNYHYEEC SCYPDAGEI T gi 8307785
CACVNGSCFT VMTDGPSSGQ ASYKI FKI EK -GRVKSVEL NAPNYHYEEC SCYPDAGEI T gi 2865378
*. *. *. *. *. * * * *. * * * *. * * * *. * * * *. * * * *. * * * *. * Clustal Cons

.....|.....||.....||.....||.....||.....||.....|

310	320	330	340	350	360				
CVCRDNWHGS	NRPWVSFNQN	LEYQI	GYI	CS	GVFGDNPRPN	DGTGSCGPMS	PNGAYGVKGF	gi	124099031
CVCRDNWHGS	NRPWVSFNQN	LEYQI	GYI	CS	GVFGDNPRPN	DGTGSCGPMS	PNGAYGVKGF	gi	124099009
CVCRDNWHGS	NRPWVSFNQN	LEYQI	GYI	CS	GVFGDNPRPN	DGTGSCGPMS	PNGAYGVKGF	gi	124099058
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CVCRDNWHGS	NRPWVSFNQN	LEYQI	GYI	CS	GVFGDNPRPN	DGTGSCGPMS	PNGAYGVKGF	gi	157955787
CVCRDNWHGS	NRPWI SFNQN	LEYQI	GYI	CS	GVFGDNPRPN	DGTGSCGPMS	PNGAYGVKGF	gi	113497245
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CVCRDNWHGS	NRPWI SFNQN	LEYQI	GYI	CS	GVFGDNPRPN	DGTGSCGPMS	PNGAYGVKGF	gi	113497198
CVCRDNWHGS	NRPWVSFNQN	LEYQI	GYI	CS	GVFGDNPRPN	DGTGSCGPMS	PNGAYGVKGF	gi	113972297
CVCRDNWHGS	NRPWVSFNQN	LEYQI	GYI	CS	GVFGDNPRPN	DGTGSCGPMS	PNGAYGVKGF	gi	118864192
CVCRDNWHGS	NRPWVSFNQN	LEYQI	GYI	CS	GVFGDNPRPN	DGTGSCGPMS	PNGAYGVKGF	gi	118864235
CVCRDNWHGS	NRPWVSFNQN	LEYQI	GYI	CS	GVFGDNPRPN	DGTGSCGPMS	PNGAYGVKGF	gi	157955698
CVCRDNWHGS	NRPWVSFNQN	LEYQI	GYI	CS	GVFGDNPRPN	DGTGSCGPMS	PNGAYGVKGF	gi	157955529
CVCRDNWHGS	NRPWVSFNQN	LEYQI	GYI	CS	GVFGDNPRPN	DGTGSCGPMS	PNGAYGVKGF	gi	118864141
CVCRDNWHGS	NRPWVSFNQN	LEYQI	GYI	CS	GVFGDNPRPN	DGTGSCGPMS	PNGAYGVKGF	gi	124098908
CVCRDNWHGS	NRPWVSFNQN	LEYQI	GYI	CS	GVFGDNPRPN	DGTGSCGPMS	PNGAYGVKGF	gi	124098582
CVCRDNWHGS	NRPWVSFNQN	LEYQI	GYI	CS	GVFGDNPRPN	DGTGSCGPMS	PNGAYGVKGF	gi	124098853
CVCRDNWHGS	NRPWVSFNQN	LEYQI	GYI	CS	GVFGDNPRPN	DGTGSCGPMS	PNGAYGVKGF	gi	124098881
CVCRDNWHGS	NRPWVSFNQN	LEYQI	GYI	CS	GVFGDNPRPN	DGTGSCGPMS	PNGAYGVKGF	gi	118864393
CVCRDNWHGS	NRPWVSFNQN	LEYQI	GYI	CS	GVFGDNPRPN	DGTGSCGPMS	PNGAYGVKGF	gi	124098932
CVCRDNWHGS	NRPWVSFNQN	LEYQI	GYI	CS	GVFGDNPRPN	DGTGSCGPMS	PNGAYGVKGF	gi	124098984
CVCRDNWHGS	NRPWVSFNQN	LEYQI	GYI	CS	GVFGDNPRPN	DGTGSCGPMS	PNGAYGVKGF	gi	124098957
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CVCRDNWHGS	NRPWVSFNQN	LEYQI	GYI	CS	GVFGDNPRPN	DGTGSCGPMS	SNGAYGVKGF	gi	157955603
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CVCRDNWHGS	NRPWVSFNQN	LEYQI	GYI	CS	GVFGDNPRPN	DGTGSCGPMS	SNGAYGVKGF	gi	157955641
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CVCRDNWHGS	NRPWVSFNQN	LEYQI	GYI	CS	GVFGDNPRPN	DGTGSCGPMS	SNGAYGVKGF	gi	113495792
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CVCRDNWHGS	NRPWVSFNQN	LEYQI	GYI	CS	GVFGDNPRPN	DGTGSCGPMS	HNGAYGVKGF	gi	162569004
CVCRDNWHGS	NRPWVSFNQN	LEYQI	GYI	CS	GVFGDNPRPN	DGTGSCGPMS	PNGAYGVKGF	gi	113707438
CVCRDNWHGS	NRPWVSFNQN	LEYQI	GYI	CS	GVFGDNPRPN	DGTGSCGPMS	PNGAYGVKGF	gi	157103086
CVCRDNWHGS	NRPWVSFNQN	LEYQI	GYI	CS	GVFGDNPRPN	DGTGSCGPMS	PNGAYGVKGF	gi	157103100
CVCRDNWHGS	NRPWVSFNQN	LEYQI	GYI	CS	GVFGDNPRPN	DGTGSCGPMS	PNGAYGVKGF	gi	157103119
CVCRDNWHGS	NRPWVSFNQN	LEYQI	GYI	CS	GVFGDNPRPN	DGTGSCGPMS	PNGAYGVKGF	gi	157103135
CVCRDNWHGS	NRPWVSFNQN	LEYQI	GYI	CS	GVFGDNPRPN	DGTGSCGPMS	PNGAYGVKGF	gi	157103072
CVCRDNWHGS	NRPWVSFNQN	LEYQI	GYI	CS	GVFGDNPRPN	DGTGSCGPMS	PNGAYGVKGF	gi	157103052
CVCRDNWHGS	NRPWVSFNQN	LEYQI	GYI	CS	GVFGDNPRPN	DGTGSCGPMS	PNGAYGVKGF	gi	124244208
CVCRDNWHGS	NRPWVSFNQN	LEYQI	GYI	CS	GVFGDNPRPN	DGTGSCGPMS	PNGAYGVKGF	gi	122913049
CVCRDNWHGS	NRPWVSFNQN	LEYQI	GYI	CS	GVFGDNPRPN	DGTGSCGPMS	PNGAYGVKGF	gi	148340545
CVCRDNWHGS	NRPWVSFNQN	LEYQI	GYI	CS	GVFGDNPRPN	DGTGSCGPMS	PNGAYGVKGF	gi	148340541
CVCRDNWHGS	NRPWVSFNQN	LEYQI	GYI	CS	GVFGDNPRPN	DGTGSCGPMS	PNGAYGVKGF	gi	157103596
CVCRDSWHGS	NRPWVSFNQN	LEYQI	GYI	CS	GVFGDNPRPN	DGTGSCGPMS	PNGAYGVKGF	gi	122913045
CVCRDSWHGS	NRPWVSFNQN	LEYQI	GYI	CS	GVFGDNPRPN	DGTGSCGPMS	PNGAYGVKGF	gi	122913047
CVCRDNWHGS	NRPWVSFNQN	LEYQI	GYI	CS	GVFGDNPRPN	DGTGSCGPMS	PNGAYGVKGF	gi	148340810
CVCRDNWHGS	NRPWVSFNQN	LEYQI	GYI	CS	GVFGDNPRPN	DGTGSCGPMS	SNGAYGVKGF	gi	145284421
CVCRDNWHGS	NRPWVSFNQN	LEYQI	GYI	CS	GVFGDNPRPN	DGTGSCGPMS	SNGAYGVKGF	gi	116295120
CVCRDNWHGS	NRPWVSFNQN	LEYQI	GYI	CS	GVFGDTPRPN	DGTGSCGPMS	SNGTYGVKGF	gi	116295114
CVCRDNWHGS	NRPWVSFNQN	LEYQI	GYI	CS	GVFGDTPRPN	DGTGSCGPMS	SNGTYGVKGF	gi	116295110
CVCRDNWHGS	NRPWVSFNQN	LEYQI	GYI	CS	GVFGDTPRPN	DGTGSCGPMS	SNGTYGVKGF	gi	85680902
CVCRDNWHGS	NRPWVSFNQN	LEYQI	GYI	CS	GVFGDNPRPN	DGTGSCGPMS	SNGAYGVKGF	gi	46360357
CVCRDNWHGS	NRPWVSFNQN	LEYQI	GYI	CS	GVFGDNPRPN	DGTGSCGPMS	SNGAYGVKGF	gi	134306634
CVCRDNWHGS	NRPWVSFNQN	LEYQI	GYI	CS	GVFGDNPRPN	DGTGSCGPMS	SNGAYGVKGF	gi	116295106
CVCRDNWHGS	NRPWVSFNQN	LEYQI	GYI	CS	GVFGDNPRPN	DGTGSCGPMS	SNGAYGVKGF	gi	145284415
CVCRDNWHGS	NRPWVSFNQN	LEYQI	GYI	CS	GVFGDNPRPN	DGTGSCGPMS	SNGAYGVKGF	gi	93008563
CVCRDNWHGS	NRPWVSFNQN	LEYQI	GYI	CS	GVFGDNPRPN	DGTGSCGPMS	SNGAYGVKGF	gi	93008571
CVCRDNWHGS	NRPWVSFNQN	LEYQI	GYI	CS	GVFGDNPRPN	DGTGSCGPMS	SNGAYGVKGF	gi	126361912
CVCRDNWHGS	NRPWVSFNQN	LEYQI	GYI	CS	GVFGDNPRPN	DGTGSCGPMS	SNGAYGVKGF	gi	95116895
CVCRDNWHGS	NRPWVSFNQN	LEYQI	GYI	CS	GVFGDNPRPN	DGTGSCGPMS	SNGAYGVKGF	gi	72398597
CVCRDNWHGS	NRPWVSFNQN	LEYQI	GYI	CS	GVFGDNPRPN	DGTGSCGPMS	SNGAHGVKGF	gi	126361908
CVCRDNWHGS	NRPWVSFNQN	LEYQI	GYI	CS	GVFGDNPRPN	DGTGSCGPMS	SNGAYGVKGF	gi	78096578
CVCRDNWHGS	NRPWVSFNQN	LEYQI	GYI	CS	GVFGDNPRPN	DGTGSCDPMS	PNGAYGI KGF	gi	182382583
CVCRDNWHGS	NRPWVSFNQN	LEYQI	GYI	CS	GVFGDNPRPN	DGTGSCDPMS	PNGAYGI KGF	gi	182382601
CVCRDNWHGS	NRPWVSFNQN	LEYRI	GYI	CS	GVFGDNPRPN	DGTGSCGPMS	PKGAYGI KGF	gi	47834894
CVCRDNWHGS	NRPWVSFNQN	LEYRI	GYI	CS	GVFGDNPRPN	DGTGSCGPMS	PKGAYGI KGF	gi	145284413
CVCRDNWHGS	NRPWVSFNQN	LEYRI	GYI	CS	GVFGDNPRPN	DGTGSCGPMS	PKGAYGI KGF	gi	47834892

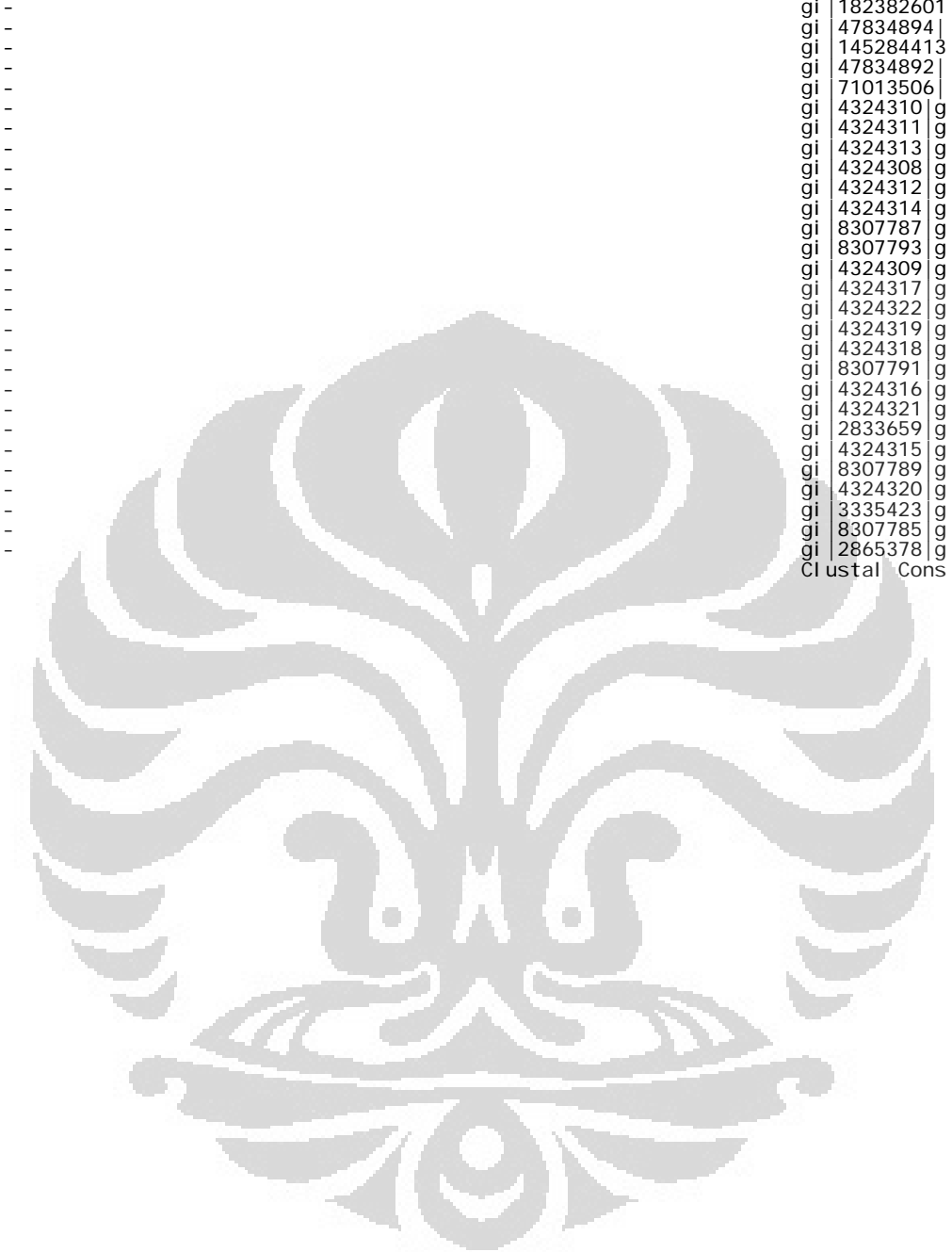
CVCARDNWHGS	NRPWVSFNQN	LEYRI GYI CS	GVFGDNPRPN	DGTGSCGPVS	PKGAYGI KGF	gi	71013506
CVCARDNWHGS	NRPWVSFNQN	LEYQI GYI CS	GVFGDSPRPN	DGTGSCGPVS	LNGAYGVKGF	gi	4324310
CVCARDNWHGS	NRPWVSFNQN	LEYQI GYI CS	GVFGDSPRPN	DGTGTCGPVS	LNGAYGVKGF	g	4324311
CVCARDNWHGS	NRPWVSFNQN	LEYQI GYI CS	GVFGDSPRPN	DGTGSCGPVS	LNGAYGVKGF	gi	4324313
CVCARDNWHGS	NRPWVSFNQN	LEYQI GYI CS	GVFGDSPRPN	DGTGSCGPVS	LNGAYGVKGF	gi	4324308
CVCARDNWHGS	NRPWVSFNQN	LEYQI GYI CS	GVFGDSPRPN	DGTGSCGPVS	LNGAYGVKGF	gi	4324312
CVCARDNWHGS	NRPWVSFNQN	LEYQI GYI CS	GVFGDSPRPN	DGTGSCGPVS	LNGAYGVKGF	gi	4324314
CVCARDNWHGS	NRPWVSFNQN	LEYQI GYI CS	GVFGDSPRPN	DGTGSCGPVS	LNGAYGVKGF	gi	8307787
CVCARDNWHGS	NRPWVSFNQN	LEYQI GYI CS	GVFGDSPRPN	DGTGSCGPVS	LNGAYGVKGF	gi	8307793
CVCARDNWHGS	NRPWVSFNQN	LEYQI GYI CS	GVFGDSPRPN	DGTGSCGPVS	LNGAYGVKGF	gi	4324309
CVCARDNWHGS	NRPWVSFNQN	LEYQI GYI CS	GVFGDSPRPN	DGTGSCGPVS	LNGAYGVKGF	gi	4324317
CVCARDNWHGS	NRPWVSFNQN	LEYQI GYI CS	GVFGDSPRPN	DGTGSCGPVS	LNGAYGVKGF	gi	4324322
CVCARDNWHGS	NRPWVSFNQN	LEYQI GYI CS	GVFGDSPRPN	DGTGSCGPVS	LNGAYGVKGF	gi	4324319
CVCARDNWHGS	NRPWVSFNQN	LEYQI GYI CS	GVFGDSPRPN	DGTGSCGPVS	LNGAYGVKGF	gi	4324318
CVCARDNWHGS	NRPWVSFNQN	LEYQI GYI CS	GVFGDSPRPN	DGTGSCGPVS	LNGAYGVKGF	gi	8307791
CVCARDNWHGS	NRPWVSFNQN	LEYQI GYI CS	GVFGDSPRPN	DGTGSCGPVS	LNGAYGVKGF	gi	4324316
CVCARDNWHGS	NRPWVSFNQN	LEYQI GYI CS	GVFGDSPRPN	DGTGSCGPVS	LNGAYGVKGF	gi	4324321
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CVCARDNWHGS	NRPWVSFNQN	LEYQI GYI CS	GVFGDSPRPN	DGTGSCGPVS	LNGAYGVKGF	gi	4324315
CVCARDNWHGS	NRPWVSFNQN	LEYQI GYI CS	GVFGDSPRPN	DGTGSCGPVS	LNGAYGVKGF	gi	8307789
CVCARDNWHGS	NRPWVSFNQN	LEYQI GYI CS	GVFGDSPRPN	DGTGSCGPVS	LNGAYGVKGF	gi	4324320
CVCARDNWHGS	NRPWVSFNQN	LEYQI GYI CS	GVFGDSPRPN	DGTGSCGPVS	LNGAYGVKGF	gi	3335423
CVCARDNWHGS	NRPWVSFNQN	LEYQI GYI CS	GVFGDSPRPN	DGTGSCGPVS	LNGAYGVKGF	gi	8307785
CVCARDNWHGS	NRPWVSFNQN	LEYQI GYI CS	GVFGDSPRPN	DGTGSCGPVS	LNGAYGVKGF	gi	2865378
*****	*****	* * * * *	*****	*****	* * * * *	Clustal Cons	

370	380	390	400	410	420		
SFKYGNVWI	GRTKSTNSRS	GFEMI WDPNG	WTGTDSSFSV	KQDI VAI TDW	SGYSGSFVQH	gi	124099031
SFKYGNVWI	GRTKSTNSRS	GFEMI WDPNG	WTGTDSSFSV	KQDI VAI TDW	SGYSGSFVQH	gi	124099009
SFKYGNVWI	GRTKSTNSRS	GFEMI WDPNG	WTGTDSSFSV	KQDI VAI TDW	SGYSGSFVQH	gi	124099058
SFKYGNVWI	GRTKSTNSRS	GFEMI WDPNG	WTGTDSSFSV	KQDI VAI TDW	SGYSGSFVQH	gi	124099084
SFKYGNVWI	GRTKSTNSRS	GFEMI WDPNG	WTGTDSSFSV	KQDI VAI TNW	SGYSGSFVQH	gi	157955787
SFKYGNVWI	GRTKSTNSRS	GFEMI WDPNG	WTGTDSSFSV	KQDI VAI TDW	SGYSGSFVQH	gi	113497245
SFKYGNVWI	GRTKSTNSRS	GFEMI WDPNG	WTGTDSSFSV	KQDI VAI TDW	SGYSGSFVQH	gi	157955437
SFKYGNVWI	GRTKSTNSRS	GFEMI WDPNG	WTGTDSSFSV	KQDI VAI TDW	SGYSGSFVQH	gi	113497198
SFKYGNVWI	GRTKSTNSRS	GFEMI WDPNG	WTGTDSSFSV	KQDI VAI TDW	SGYSGSFVQH	gi	113972297
SFKYGNVWI	GRTKSTNSRS	GFEMI WDPNG	WTGTDSSFSV	KQDI VAI TDW	SGYSGSFVQH	gi	118864192
SFKYGNVWI	GRTKSTNSRS	GFEMI WDPNG	WTGTDSSFSV	KQDI VAI TDW	SGYSGSFVQH	gi	118864235
SFKYGNVWI	GRTKSTNSRS	GFEMI WDPNG	WTGTDSSFSV	KQDI VAI TDW	SGYSGSFVQH	gi	157955698
SFKYGNVWI	GRTKSTNSRS	GFEMI WDPNG	WTGTDSSFSV	KQDI VAI TDW	SGYSGSFVQH	gi	157955529
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SFKYGNVWI	GRTKSTNSRS	GFEMI WDPNG	WTGTDSSFSV	KQDI VAI TDW	SGYSGSFVQH	gi	124098908
SFKYGNVWI	GRTKSTNSRS	GFEMI WDPNG	WTGTDSSFSV	KQDI VAI TDW	SGYSGSFVQH	gi	124098582
SFKYGNVWI	GRTKSTNSRS	GFEMI WDPNG	WTGTDSSFSV	KQDI VAI TDW	SGYSGSFVQH	gi	124098853
SFKYGNVWI	GRTKSTNSRS	GFEMI WDPNG	WTGTDSSFSV	KQDI VAI TDW	SGYSGSFVQH	gi	124098881
SFKYGNVWI	GRTKSTNSRS	GFEMI WDPNG	WTGTDSSFSV	KQDI VAI TDW	SGYSGSFVQH	gi	118864393
SFKYGNVWI	GRTKSTNSRS	GFEMI WDPNG	WTGTDSSFSV	KQDI VAI TDW	SGYSGSFVQH	gi	124098932
SFKYGNVWI	GRTKSTNSRS	GFEMI WDPNG	WTGTDSSFSV	KQDI VAI TDW	SGYSGSFVQH	gi	124098984
SFKYGNVWI	GRTKSTNSRS	GFEMI WDPNG	WTGTDSSFSV	KQDI VAI TDW	SGYSGSFVQH	gi	124098957
SFKYGNVWI	GRTKSTNSRS	GFEMI WDPNG	WTGTDSSFSV	KQDI VAI TDW	SGYSGSFVQH	gi	118574893
SFKYGNVWI	GRTKSTNSRS	GFEMI WDPNG	WTGTDSSFSV	KQDI VAI TDW	SGYSGSFVQH	gi	118574874
SFKYGNVWI	GRTKSTNSRS	GFEMI WDPNG	WTGTDSSFSV	KQDI VAI TDW	SGYSGSFVQH	gi	113497296
SFKYGNVWI	GRTKSTNSRS	GFEMI WDPNG	WTGTDSSFSV	KQDI VAI TDW	SGYSGSFVQH	gi	157955475
SFKYGNVWI	GRTKSTNSRS	GFEMI WDPNG	WTGTDSSFSV	KQDI VAI TDW	SGYSGSFVQH	gi	113496518
SFKYGNVWI	GRTKSTNSRS	GFEMI WDPNG	WTGTDSSFSV	KQDI VAI TDW	SGYSGSFVQH	gi	113497374
SFKYGNVWI	GRTKSTNSRS	GFEMI WDPNG	WTGTDSSFSV	KQDI VAI TDW	SGYSGSFVQH	gi	113972316
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SFKYGNVWI	GRTKSTNSRS	GFEMI WDPNG	WTGTDSSFSV	KQDI VAI TDW	SGYSGSFVQH	gi	157955584
SFKYGNVWI	GRTKSTNSRS	GFEMI WDPNG	WTGTDSSFSV	KQDI VAI TDW	SGYSGSFVQH	gi	113495792
SFKYGNVWI	GRTKSTNSRS	GFEMI WDPNG	WTGTDSSFSV	KQDI VAI TDW	SGYSGSFVQH	gi	113495851
SFKYGNVWI	GRTKSTNSRS	GFEMI WDPNG	WTGTDSSFSV	KQDI VAI TDW	SGYSGSFVQH	gi	113495963
SFKYGNVWI	GRTKSTNSRS	GFEMI WDPNG	WTGTDSSFSV	KQDI VAI TDW	SGYSGSFVQH	gi	113495914
SFKYGNVWI	GRTKSPNSRS	GFEMI WDPNG	WSETDSSFSV	KQDI VAI TDW	SGYSGSFVQH	gi	162569002
SFKYGNVWI	GRTKSPNSRS	GFEMI WDPNG	WSETDSSFSV	KQDI VAI TDW	SGYSGSFVQH	gi	162569004
SFKYGNVWI	GRTKSPNSRS	GFEMI WDPNG	WSETDSSFSV	KQDI VAI TDW	SGYSGSFVQH	gi	113707438
SFKYGNVWI	GRTKSTNSRS	GFEMI WDPNG	WTGTDSSFSV	KQDI VAI TDW	SGYSGSFVQH	gi	157103086
SFKYGNVWI	GRTKSTNSRS	GFEMI WDPNG	WTGTDSSFSV	KQDI VAI TDW	SGYSGSFVQH	gi	157103100
SFKYGNVWI	GRTKSTNSRS	GFEMI WDPNG	WTGTDSSFSV	KQDI VAI TDW	SGYSGSFVQH	gi	157103119
SFKYGNVWI	GRTKSTNSRS	GFEMI WDPNG	WTGTDSSFSV	KQDI VAI TDW	SGYSGSFVQH	gi	157103135
SFKYGNVWI	GRTKSTNSRS	GFEMI WDPNG	WTGTDSSFSV	KQDI VAI TDW	SGYSGSFVQH	gi	157103072
SFKYGNVWI	GRTKSTNSRS	GFEMI WDPNG	WTGTDSSFSV	KQDI VAI TDW	SGYSGSFVQH	gi	157103052
SFKYGNVWI	GRTKSTNSRS	GFEMI WDPNG	WTGTDSSFSV	KQDI VAI TDW	SGYSGSFVQH	gi	124244208
SFKYGNVWI	GRTKSTNSRS	GFEMI WDPNG	WTGTDSSFSV	KQDI VAI TDW	SGYSGSFVQH	gi	122913049

SFKYNGVWI	GRTKSTNSRS	GFEMI WDPNG	WTGTDSSFSV	KQDI VAI TDW	SGYSGSFVQH	gi	148340545
SFKYNGVWI	GRTKSTNSRS	GFEMI WDPNG	WTGTDSSFSV	KQDI VAI TDW	SGYSGSFVQH	gi	148340541
SFKYNGVWI	GRTKSTNSRS	GFEMI WDPNG	WTGTDSSFSV	KQDI VAI TDW	SGYSGSFVQH	gi	157103596
SFKYNGVWI	GRTKSTNSRS	GFEMI WDPNG	WTGTDSSFSV	KQDI VAI TDW	SGYSGSFVQH	gi	122913045
SFKYNGVWI	GRTKSTNSRS	GFEMI WDPNG	WTGTDSSFSV	KQDI VAI TDW	SGYSGSFVQH	gi	122913047
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SFKYNGVWI	GRTKSTNSRS	GFEMI WDPNG	WTETDSSFSV	KQDI VAI TDW	SGYSGSFVQH	gi	116295106
SFKYNGVWI	GRTKSTNSRS	GFEMI WDPNG	WTETDSSFSV	KQDI VAI TDW	SGYSGSFVQH	gi	145284415
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SFKYNGVWI	GRTKSTSSRS	GFEMI WDPNG	WTETDSSFSL	KQDI I AI TDW	SGYSGSFI QH	gi	4324315
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SFKYNGVWI	GRTKSTSSRS	GFEMI WDPNG	WTETDSSFSL	KQDI I AVTDW	SGYSGSFI QH	gi	4324320
SFKYNGVWI	GRTKSTSSRS	GFEMI WDPNG	WTETDSSFSL	KQDI I AI TDW	SGYSGSFI QH	gi	3335423
SFKYNGVWI	GRTKSTSSRS	GFEMI WDPNG	WTETDSSFSL	KQDI I AI TDW	SGYSGSFI QH	gi	8307785
SFKYNGVWI	GRTKSTSSRS	GFEMI WDPNG	WTETDSSFSX	KQDI I AI TDW	SGYSGSFI QH	gi	2865378
*****	*****	***	*****	*** **	****. *. *. *	*****. **	Clustal Cons

		430		440		450		460		470		480			
PELTGLDCI	R	PCFWVELI	RG	RPKESTI	WTS	GSSI	SFCGVN	SDTVSWSPD	GAELPFTI	DK	gi	124099031			
PELTGLDCI	R	PCFWVELI	RG	RPKESTI	WTS	GSSI	SFCGVN	SDTVSWSPD	GAELPFTI	DK	gi	124099009			
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PELTGLDCI	R	PCFWVELI	RG	RPKESTI	WTS	GSSI	SFCGVN	SDTVSWSPD	GAELPFTI	DK	gi	157955787			
PELTGLDCI	R	PCFWVELI	RG	RPKESTI	WTS	GSSI	SFCGVN	SDTVSWSPD	GAELPFTI	DK	gi	113497245			
PELTGLDCI	R	PCFWVELI	RG	RPKESTI	WTS	GSSI	SFCGVN	SDTVSWSPD	GAELP----	gi		157955437			
PELTGLDCI	R	PCFWVELI	RG	RPKESTI	WTS	GSSI	SFCGVN	SDTVSWSPD	GAELPFTI	DK	gi	113497198			
PELTGLDCI	R	PCFWVELI	RG	RPKESTI	WTS	GSSI	SFCGVN	SDTVSWSPD	GAELPFTI	DK	gi	113972297			
PELTGLDCI	R	PCFWVELI	RG	RPKESTI	WTS	GSSI	SFCGVN	SDTVSWSPD	GAELPFTI	DK	gi	118864192			
PELTGLDCI	R	PCFWVELI	RG	RPKESTI	WTS	GSSI	SFCGVN	SDTVSWSPD	GAELPFTI	DK	gi	118864235			
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PELTGLDCI	R	PCFWVELI	RG	RPKESTI	WTS	GSSI	SFCGVN	SDTVSWSPD	GAELPFTI	DK	gi	157955529			
PELTGLDCI	R	PCFWVELI	RG	RPKESTI	WTS	GSSI	SFCGVN	SDTVSWSPD	GAELPFTI	DK	gi	118864141			
PELTGLDCI	R	PCFWVELI	RG	RPKESTI	WTS	GSSI	SFCGVN	SDTVSWSPD	GAELPFTI	DK	gi	124098908			
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PELTGLDCI	R	PCFWVELI	RG	RPKESTI	WTS	GSSI	SFCGVN	SDTVSWSPD	GAELPFTI	DK	gi	124098853			
PELTGLDCI	R	PCFWVELI	RG	RPKESTI	WTS	GSSI	SFCGVN	SDTVSWSPD	GAELPFTI	DK	gi	124098881			
PELTGLDCI	R	PCFWVELI	RG	RPKESTI	WTS	GSSI	SFCGVN	SDTVSWSPD	GAELPFTI	DK	gi	118864393			
PELTGLDCI	R	PCFWVELI	RG	RPKESTI	WTS	GSSI	SFCGVN	SDTVSWSPD	GAELPFTI	DK	gi	124098932			
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PELTGLDCI	R	PCFWVELI	RG	RPKESTI	WTS	GSSI	SFCGVN	SDTVSWSPD	GAELPFTI	DK	gi	124098957			

PELTGLDCI R	PCFWVELI RG	RPKESTI WTS	GSSI SFCGVN	SDTVSWSWPD	GAELPFTI DK	gi	118574893
PELTGLDCI R	PCFWVELI RG	RPKESTI WTS	GSSI SFCGVN	SDTVSWSWPD	GAELPFTI DK	gi	118574874
PELTGLDCI R	PCFWVELI RG	RPKESTI WTS	GSSI SFCGVN	SDTVSWSWPD	GAELPFTI DK	gi	113497296
PELTGLDCI R	PCFWVELI RG	RPKESTI WTS	GSSI SFCGVN	SDTVSWSWPD	G-----	gi	157955475
PELTGLDCI R	PCFWVELI RG	RPKESTI WTS	GSSI SFCGVN	SDTVSWSWPD	GAELPFTI DK	gi	113496518
PELTGLDCI R	PCFWVELI RG	RPKESTI WTS	GSSI SFCGVN	SDTVSWSWPD	GAELPFTI DK	gi	113497374
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PELTGLDCI R	PCFWVELI RG	RPKESTI WTS	GSSI SFCGVN	SDTVSWSWPD	GAELPFT---	gi	157955641
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PELTGLDCI R	PCFWVELI RG	RPKESTI WTS	GSSI SFCGVN	SDTVSWSWPD	GAELPFTI DK	gi	113495792
PELTGLDCI R	PCFWVELI RG	RPKESTI WTS	GSSI SFCGVN	SDTVSWSWPD	GAELPFTI DK	gi	113495851
PELTGLDCI R	PCFWVELI RG	RPKESTI WTS	GSSI SFCGVN	SDTVSWSWPD	GAELPFTI DK	gi	113495963
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PELTGLDCI R	PCFWVELI RG	RPKESTVWTS	GSSI SFCGVN	SDTVSWSWPD	GAELPFSI DK	gi	162569002
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PELTGLDCI R	PCFWVELI RG	RPKESTI WTS	GSSI SFCGVN	SDTVSWSWPD	GAELPFTI DK	gi	157103086
PELTGLDCI R	PCFWVELI RG	RPKESTI WTS	GSSI SFCGVN	SDTVSWSWPD	GAELPFTI DK	gi	157103100
PELTGLDCI R	PCFWVELI RG	RPKESTI WTS	GSSI SFCGVN	SDTVSWSWPD	GAE-----	gi	157103119
PELTGLDCI R	PCFWVELI RG	RPKESTI WTS	GSSI SFCGVN	SDTVSWSWPD	GAELPFTI --	gi	157103135
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PELTGLDCI R	PCFWVELI RG	RPKESTI WTS	GSSI SFCGVN	SDTVSWSWPD	GAELPFTTDK	gi	124244208
PELTGLDCI R	PCFWVELI RG	RPKESTI WTS	GSSI SFCGVN	SDTVSWSWPD	GAELPFTI DK	gi	122913049
PELTGLDCI R	PCFWVELI RG	RPKESTI WTS	GSSI SFCGVN	SDTVSWSWPD	GAELPFTI DK	gi	148340545
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PELTGLDCI R	PCFWVELI RG	RPKESTI WTS	GSSI SFCGVN	SDTVSWSWPD	GAELPFTI DK	gi	122913045
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PELTGLDCI R	PCFWVELV RG	RPKESTI WTS	GSSI SFCGVN	SDTVGWSWPD	GAELPFTI DK	gi	148340810
PELTGLDCI R	PCFWVELI RG	RPKESTI WTS	GSSI SFCGVN	SDTVGWSWPD	GAELPFTI DK	gi	145284421
PELTGLDCI R	PCFWVELI RG	RPKESTI WTS	GSSI SFCGVN	SDTVGWSWPD	GAELPFTI DK	gi	116295120
PELTGLDCI R	PCFWVELI RG	RPKESTI WTS	GSSI SFCGVN	SDTVGWSWPD	-----	gi	116295114
PELTGLDCI R	PCFWVELI RG	RPKERAI WNS	GNSI SFYGEE	KHTVGWSWP-	-----	gi	116295110
PELTGLDCI R	PCFWVELI RG	RPKESTI WTS	GSSI SFCGVN	SDTVGWSWPD	GAELPFTI DK	gi	85680902
PELTGLDCI R	PCFWVELI RG	RPKESTI WTS	GSSI SFCGVN	SDTVGWSWPD	GAELPFTI DK	gi	46360357
PELTGLDCI R	PCFWVELI RG	RPKESTI WTS	GSSI SFCGVN	SGTVGWSWPD	GAELPFTI DK	gi	134306634
PELTGLDCI R	PCFWVELI RG	RPKESTI WTS	GSSI SFCGVN	SEAVGWSWPD	GAELPFT---	gi	116295106
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PELTGLDCI R	PCFWVELI RG	RPKESTI WTS	GSSI SFCGVN	SDTVGWSWPD	GAE-----	gi	93008571
PELTGLDCI R	PCFWVELI RG	RPKESTI WTS	GSSI SFCGVN	SDTVGWSWPD	GAELPFTI DK	gi	126361912
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PELTGLDCI R	PCFWVELI RG	RPKESTI WTS	GSSI SFCGVN	SDTVGWSWPD	GAELPFTI DK	gi	72398597
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PELTGLDCI R	PCFWVELI RG	RPKESTI WTS	GSSI SFCGVN	SDTVSWSWPD	GAELPFTI DK	gi	182382583
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PELTGLDCI R	PCFWVELI RG	RPKESTI WTS	GSSI SFC---	-----	-----	gi	47834894
PELTGLDCI R	PCFWVELI RG	RPKESTI WTS	GSSI SFCGVN	SDTVGWSWPD	DAELPLT---	gi	145284413
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PELTGLNDCMR	PCFWVELI RG	RPKEKTI WTS	GSSI SFCGVN	SDTVGWSWPD	DAELPFTI DK	g	4324308
PELTGLNDCMR	PCFWVELI RG	SPKEKTI WTS	GSSI SFCGVN	SDTVGWSWPD	GAELPFTI DK	g	4324312
PELTGLNDCMR	PCFWVELI RG	RPKEKTI WTS	GSSI SFCGVN	SDTVGWSWPD	DAELPFTI DK	g	4324314
PELTGLNDCMR	PCFWVELI RG	RPKEKTI WTS	GSSI SFCGVN	SDTVGWSWPD	GAELPFTI DK	g	8307787
PELTGLNDCMR	PCFWVELI RG	RPKEKTI WTS	GSSI SFCGVN	SDTVGWSWPD	GAELPYTI DK	g	8307793
PELTGLNDCMR	PCFWVELI RG	RPKEKTI WTS	GSSI SFCGVN	SDTVGWSWPD	DAELPFTI DK	g	4324309
PELTGLNDCMR	PCFWVELI RG	RPKEKTI WTS	GSSI SFCGVN	SDTVGWSWPD	DAELPFTI DK	g	4324317
PELTGLNDCMR	PCFWVELI RG	RPKEKTI WTS	GSSI SFCGVN	SDTVGWSWPD	DAELPLTI DK	g	4324322
PELTGLNDCMR	PCFWVELI RG	RPKEKTI WTS	GSSI SFCGVN	SDTVGWSWPD	DAELPFTI DK	g	4324319
PELTGLNDCMR	PCFWVELI RG	RPKEKTI WTS	GSSI SFCGVN	SDTVGWSWPD	DAELPFTI DK	g	4324318
PELTGLNDCMR	PCFWVELI RG	RPKEKTI WTS	GSSVSFCGVN	SDTMGWSWPD	GAELPFTI DK	g	8307791
PELTGLNDCMR	PCFWVELI RG	RPKEKTI WTS	GSSVSFCGVN	SDTMGWSWPD	DAELPFTI DK	g	4324316
PELTGLNDCMR	PCFWVELI RG	RPKEKTI WTS	GSSI SFCGVN	SDTVGWSWPD	DAELPFTI DK	g	4324321
PELTGLNDCMR	PCFWVELI RG	RPKEKTI WTS	GSSI SFCGVN	SDTVGWSWPD	DAELPFTI DK	g	2833659
PELTGLNDCMR	PCFWVELI RG	RPKEKTI WTS	GSSI SFCGVN	SDTVGWSWPD	DAELPFTI DK	g	4324315
PELTGLNDCMR	PCFWVELI RG	RPKEKTI WTS	GSSI SFCGVN	SDTVGWSWPD	GAELPFTI DK	g	8307789
PELTGLNDCMR	PCFWVELI RG	RPKEKTI WTS	GSSI SFCGVN	SDTVGWSWPD	DAELPFTI DK	g	4324320
PELTGLNDCMR	PCFWVELI RG	RPKEKTI WTS	GSSI SFCGVN	SDTVGWSWPD	GAELPFTI DK	g	3335423
PELTGLNDCMR	PCFWVELI RG	RPKEKTI WTS	GSSI SFCGVN	SDTVGWSWPD	GAELPFTI DK	g	8307785



Lampiran 5 :**Conserve Region**

BioEdit version 7.0.8.0 (6/17/07)
 Conserved region search
 Alignment file: G:\bwt skripsi\cari
 data\Data\database\Ha\HA1\human\H1N1.aln
 10/30/2008 1:33:27 PM

Minimum segment length (actual for each
 sequence): 10
 Maximum average entropy: 0.2
 Maximum entropy per position: 0.2
 Gaps limited to 2 per segment
 Contiguous gaps limited to 1 in any segment

3 conserved regions found

Region 1: Position 7 to 18
 Consensus:
 7 YHANNSTDTVDT 18

Segment Length: 12
 Average entropy (Hx): 0.0597
 Position 7 : 0.0551
 Position 8 : 0.0551
 Position 9 : 0.0551
 Position 10 : 0.0551
 Position 11 : 0.0551
 Position 12 : 0.0551
 Position 13 : 0.0551
 Position 14 : 0.0551
 Position 15 : 0.0551
 Position 16 : 0.1101
 Position 17 : 0.0551
 Position 18 : 0.0551

Region 2: Position 97 to 110
 Consensus:
 97 DYEELREQLSSVSS 110

Segment Length: 14
 Average entropy (Hx): 0.0934
 Position 97 : 0.1875
 Position 98 : 0.0551
 Position 99 : 0.0551
 Position 100 : 0.0551
 Position 101 : 0.0551
 Position 102 : 0.1875
 Position 103 : 0.1101
 Position 104 : 0.1197
 Position 105 : 0.0551
 Position 106 : 0.0551
 Position 107 : 0.0551
 Position 108 : 0.1514
 Position 109 : 0.1101
 Position 110 : 0.0551

Region 3: Position 316 to 327
 Consensus:

316 TGLRNIPSIQSR 327

Segment Length: 12
 Average entropy (Hx): 0.0705
 Position 316 : 0.0551
 Position 317 : 0.0551
 Position 318 : 0.0551
 Position 319 : 0.0551
 Position 320 : 0.0551
 Position 321 : 0.0648
 Position 322 : 0.0551
 Position 323 : 0.0551
 Position 324 : 0.1101
 Position 325 : 0.0551
 Position 326 : 0.1748
 Position 327 : 0.0551

BioEdit version 7.0.8.0 (6/17/07)
 Conserved region search
 Alignment file: G:\bwt skripsi\cari
 data\Data\database\Ha\HA1\human\H2N2.aln
 10/30/2008 1:37:07 PM

Minimum segment length (actual for each
 sequence): 10
 Maximum average entropy: 0.2
 Maximum entropy per position: 0.2
 Gaps limited to 2 per segment
 Contiguous gaps limited to 1 in any segment

8 conserved regions found

Region 1: Position 1 to 14
 Consensus:
 1 DQICIGYHANNSTE 14

Segment Length: 14
 Average entropy (Hx): 0.0871
 Position 1 : 0.0871
 Position 2 : 0.0871
 Position 3 : 0.0871
 Position 4 : 0.0871
 Position 5 : 0.0871
 Position 6 : 0.0871
 Position 7 : 0.0871
 Position 8 : 0.0871
 Position 9 : 0.0871
 Position 10 : 0.0871
 Position 11 : 0.0871
 Position 12 : 0.0871
 Position 13 : 0.0871
 Position 14 : 0.0871

Region 2: Position 16 to 30
 Consensus:
 16 VDTILERNVTVTHAK 30

Segment Length: 15
 Average entropy (Hx): 0.0882
 Position 16 : 0.0871
 Position 17 : 0.0871
 Position 18 : 0.0871
 Position 19 : 0.1039

Position 20 : 0.0871
 Position 21 : 0.0871
 Position 22 : 0.0871
 Position 23 : 0.0871
 Position 24 : 0.0871
 Position 25 : 0.0871
 Position 26 : 0.0871
 Position 27 : 0.0871
 Position 28 : 0.0871
 Position 29 : 0.0871
 Position 30 : 0.0871

Region 3: Position 32 to 71

Consensus:

32
 ILEKTHNGKLCCKLNGIPPLELGDCSIAGWLLG
 NPECDRL 71

Segment Length: 40
 Average entropy (Hx): 0.0936

Position 32 : 0.0871
 Position 33 : 0.0871
 Position 34 : 0.0871
 Position 35 : 0.0871
 Position 36 : 0.0871
 Position 37 : 0.0871
 Position 38 : 0.0871
 Position 39 : 0.0871
 Position 40 : 0.1739
 Position 41 : 0.0871
 Position 42 : 0.0871
 Position 43 : 0.0871
 Position 44 : 0.0871
 Position 45 : 0.0871
 Position 46 : 0.0871
 Position 47 : 0.0871
 Position 48 : 0.0871
 Position 49 : 0.0871
 Position 50 : 0.0871
 Position 51 : 0.0871
 Position 52 : 0.0871
 Position 53 : 0.0871
 Position 54 : 0.1739
 Position 55 : 0.0871
 Position 56 : 0.0871
 Position 57 : 0.0871
 Position 58 : 0.1739
 Position 59 : 0.0871
 Position 60 : 0.0871
 Position 61 : 0.0871
 Position 62 : 0.0871
 Position 63 : 0.0871
 Position 64 : 0.0871
 Position 65 : 0.0871
 Position 66 : 0.0871
 Position 67 : 0.0871
 Position 68 : 0.0871
 Position 69 : 0.0871
 Position 70 : 0.0871
 Position 71 : 0.0871

Region 4: Position 73 to 85

Consensus:

73 VPEWSYIMEKENP 85

Segment Length: 13
 Average entropy (Hx): 0.0871
 Position 73 : 0.0871
 Position 74 : 0.0871
 Position 75 : 0.0871
 Position 76 : 0.0871
 Position 77 : 0.0871
 Position 78 : 0.0871
 Position 79 : 0.0871
 Position 80 : 0.0871
 Position 81 : 0.0871
 Position 82 : 0.0871
 Position 83 : 0.0871
 Position 84 : 0.0871
 Position 85 : 0.0871

Region 5: Position 162 to 180

Consensus:

162 SYNNTSGEQMLIIVGVVHP 180

Segment Length: 19
 Average entropy (Hx): 0.0871

Position 162 : 0.0871
 Position 163 : 0.0871
 Position 164 : 0.0871
 Position 165 : 0.0871
 Position 166 : 0.0871
 Position 167 : 0.0871
 Position 168 : 0.0871
 Position 169 : 0.0871
 Position 170 : 0.0871
 Position 171 : 0.0871
 Position 172 : 0.0871
 Position 173 : 0.0871
 Position 174 : 0.0871
 Position 175 : 0.0871
 Position 176 : 0.0871
 Position 177 : 0.0871
 Position 178 : 0.0871
 Position 179 : 0.0871
 Position 180 : 0.0871

Region 6: Position 224 to 233

Consensus:

224 RMEFSWTL 233

Segment Length: 10
 Average entropy (Hx): 0.0905

Position 224 : 0.0871
 Position 225 : 0.0871
 Position 226 : 0.0871
 Position 227 : 0.0871
 Position 228 : 0.1039
 Position 229 : 0.0871
 Position 230 : 0.1039
 Position 231 : 0.0871
 Position 232 : 0.0871
 Position 233 : 0.0871

Region 7: Position 249 to 270

Consensus:

249 PEYGFKISKRGSSGIMKTEGTL 270

Segment Length: 22

Average entropy (Hx): 0.0879

Position 249 : 0.0871
 Position 250 : 0.0871
 Position 251 : 0.0871
 Position 252 : 0.0871
 Position 253 : 0.0871
 Position 254 : 0.0871
 Position 255 : 0.0871
 Position 256 : 0.0871
 Position 257 : 0.0871
 Position 258 : 0.0871
 Position 259 : 0.0871
 Position 260 : 0.0871
 Position 261 : 0.0871
 Position 262 : 0.0871
 Position 263 : 0.0871
 Position 264 : 0.0871
 Position 265 : 0.0871
 Position 266 : 0.0871
 Position 267 : 0.0871
 Position 268 : 0.1039
 Position 269 : 0.0871
 Position 270 : 0.0871

Region 8: Position 272 to 323

Consensus:
 272
 NCETKQCOTPLGAINITLPHFHNHPLTIGCEPK
 YVKSEKLVLATGLRNVQPQE 323

Segment Length: 52

Average entropy (Hx): 0.0891

Position 272 : 0.0871
 Position 273 : 0.0871
 Position 274 : 0.0871
 Position 275 : 0.0871
 Position 276 : 0.0871
 Position 277 : 0.0871
 Position 278 : 0.0871
 Position 279 : 0.0871
 Position 280 : 0.0871
 Position 281 : 0.0871
 Position 282 : 0.0871
 Position 283 : 0.0871
 Position 284 : 0.0871
 Position 285 : 0.0871
 Position 286 : 0.0871
 Position 287 : 0.0871
 Position 288 : 0.0871
 Position 289 : 0.0871
 Position 290 : 0.0871
 Position 291 : 0.0871
 Position 292 : 0.0871
 Position 293 : 0.0871
 Position 294 : 0.0871
 Position 295 : 0.0871
 Position 296 : 0.0871
 Position 297 : 0.0871
 Position 298 : 0.0871
 Position 299 : 0.0871
 Position 300 : 0.0871
 Position 301 : 0.0871
 Position 302 : 0.0871
 Position 303 : 0.1739
 Position 304 : 0.0871
 Position 305 : 0.0871

Position 306 : 0.0871
 Position 307 : 0.0871
 Position 308 : 0.0871
 Position 309 : 0.0871
 Position 310 : 0.0871
 Position 311 : 0.0871
 Position 312 : 0.0871
 Position 313 : 0.0871
 Position 314 : 0.0871
 Position 315 : 0.0871
 Position 316 : 0.1039
 Position 317 : 0.0871
 Position 318 : 0.0871
 Position 319 : 0.0871
 Position 320 : 0.0871
 Position 321 : 0.0871
 Position 322 : 0.0871
 Position 323 : 0.0871

BioEdit version 7.0.8.0 (6/17/07)

Conserved region search

Alignment file: G:\bwt skripsi\cari
 data\Data\database\Ha\HA1\human\H3N2.aln
 10/30/2008 1:36:49 PM

Minimum segment length (actual for each
 sequence): 10
 Maximum average entropy: 0.2
 Maximum entropy per position: 0.2
 Gaps limited to 2 per segment
 Contiguous gaps limited to 1 in any segment

8 conserved regions found

Region 1: Position 10 to 20

Consensus:
 10 TATLCLGHHAV 20

Segment Length: 11

Average entropy (Hx): 0.0599

Position 10 : 0.0694
 Position 11 : 0.0589
 Position 12 : 0.0589
 Position 13 : 0.0589
 Position 14 : 0.0589
 Position 15 : 0.0589
 Position 16 : 0.0589
 Position 17 : 0.0589
 Position 18 : 0.0589
 Position 19 : 0.0589
 Position 20 : 0.0589

Region 2: Position 32 to 44

Consensus:
 32 DQIEVTNATELVQ 44

Segment Length: 13

Average entropy (Hx): 0.0634

Position 32 : 0.0589
 Position 33 : 0.0589
 Position 34 : 0.1177
 Position 35 : 0.0589
 Position 36 : 0.0589
 Position 37 : 0.0589
 Position 38 : 0.0589
 Position 39 : 0.0589

Position 40 : 0.0589
 Position 41 : 0.0589
 Position 42 : 0.0589
 Position 43 : 0.0589
 Position 44 : 0.0589

Region 3: Position 64 to 74
 Consensus:
 64 CTLIDALLGDP 74

Segment Length: 11
 Average entropy (Hx): 0.0589
 Position 64 : 0.0589
 Position 65 : 0.0589
 Position 66 : 0.0589
 Position 67 : 0.0589
 Position 68 : 0.0589
 Position 69 : 0.0589
 Position 70 : 0.0589
 Position 71 : 0.0589
 Position 72 : 0.0589
 Position 73 : 0.0589
 Position 74 : 0.0589

Region 4: Position 107 to 120
 Consensus:
 107 SLRSLVASSGTLEF 120

Segment Length: 14
 Average entropy (Hx): 0.0631
 Position 107 : 0.0589
 Position 108 : 0.0589
 Position 109 : 0.0589
 Position 110 : 0.0589
 Position 111 : 0.0589
 Position 112 : 0.1177
 Position 113 : 0.0589
 Position 114 : 0.0589
 Position 115 : 0.0589
 Position 116 : 0.0589
 Position 117 : 0.0589
 Position 118 : 0.0589
 Position 119 : 0.0589
 Position 120 : 0.0589

Region 5: Position 232 to 241
 Consensus:
 232 IYWTIVKPGD 241

Segment Length: 10
 Average entropy (Hx): 0.0648
 Position 232 : 0.0589
 Position 233 : 0.0589
 Position 234 : 0.0589
 Position 235 : 0.0589
 Position 236 : 0.0589
 Position 237 : 0.0589
 Position 238 : 0.1177
 Position 239 : 0.0589
 Position 240 : 0.0589
 Position 241 : 0.0589

Region 6: Position 249 to 259

Consensus:
 249 GNLIAPRGYFK 259

Segment Length: 11
 Average entropy (Hx): 0.0589
 Position 249 : 0.0589
 Position 250 : 0.0589
 Position 251 : 0.0589
 Position 252 : 0.0589
 Position 253 : 0.0589
 Position 254 : 0.0589
 Position 255 : 0.0589
 Position 256 : 0.0589
 Position 257 : 0.0589
 Position 258 : 0.0589
 Position 259 : 0.0589

Region 7: Position 263 to 274
 Consensus:
 263 GKSSIMRSDAPI 274

Segment Length: 12
 Average entropy (Hx): 0.0598
 Position 263 : 0.0589
 Position 264 : 0.0589
 Position 265 : 0.0589
 Position 266 : 0.0589
 Position 267 : 0.0589
 Position 268 : 0.0589
 Position 269 : 0.0694
 Position 270 : 0.0589
 Position 271 : 0.0589
 Position 272 : 0.0589
 Position 273 : 0.0589
 Position 274 : 0.0589

Region 8: Position 308 to 329
 Consensus:
 308 YVKQNTLKLATGMRNVPEKQTR 329

Segment Length: 22
 Average entropy (Hx): 0.0616
 Position 308 : 0.0589
 Position 309 : 0.0589
 Position 310 : 0.0589
 Position 311 : 0.0589
 Position 312 : 0.0589
 Position 313 : 0.0589
 Position 314 : 0.0589
 Position 315 : 0.0589
 Position 316 : 0.0589
 Position 317 : 0.0589
 Position 318 : 0.0589
 Position 319 : 0.0589
 Position 320 : 0.0589
 Position 321 : 0.0589
 Position 322 : 0.0589
 Position 323 : 0.1177
 Position 324 : 0.0589
 Position 325 : 0.0589
 Position 326 : 0.0589
 Position 327 : 0.0589
 Position 328 : 0.0589
 Position 329 : 0.0589

BioEdit version 7.0.8.0 (6/17/07)
 Conserved region search
 Alignment file: G:\bwt skripsi\cari
 data\Data\database\Ha\HA1\human\H5N1.aln
 10/30/2008 1:36:06 PM

Minimum segment length (actual for each
 sequence): 10
 Maximum average entropy: 0.2
 Maximum entropy per position: 0.2
 Gaps limited to 2 per segment
 Contiguous gaps limited to 1 in any segment

10 conserved regions found

Region 1: Position 1 to 34

Consensus:

1
 DQICIGYHANNSTEQVDTIMEKNVTVTHAQDI
 LE 34

Segment Length: 34

Average entropy (Hx): 0.0675

Position 1 : 0.0646
 Position 2 : 0.0646
 Position 3 : 0.0646
 Position 4 : 0.0646
 Position 5 : 0.0646
 Position 6 : 0.0646
 Position 7 : 0.0763
 Position 8 : 0.0646
 Position 9 : 0.0646
 Position 10 : 0.0646
 Position 11 : 0.0763
 Position 12 : 0.0646
 Position 13 : 0.0646
 Position 14 : 0.0646
 Position 15 : 0.1290
 Position 16 : 0.0646
 Position 17 : 0.0646
 Position 18 : 0.0646
 Position 19 : 0.0646
 Position 20 : 0.0763
 Position 21 : 0.0646
 Position 22 : 0.0646
 Position 23 : 0.0646
 Position 24 : 0.0646
 Position 25 : 0.0646
 Position 26 : 0.0646
 Position 27 : 0.0646
 Position 28 : 0.0646
 Position 29 : 0.0646
 Position 30 : 0.0646
 Position 31 : 0.0646
 Position 32 : 0.0646
 Position 33 : 0.0646
 Position 34 : 0.0646

Region 2: Position 54 to 70

Consensus:

54 DCSVAGWLLGNPMCDEF 70

Segment Length: 17

Average entropy (Hx): 0.0646

Position 54 : 0.0646
 Position 55 : 0.0646

Position 56 : 0.0646
 Position 57 : 0.0646
 Position 58 : 0.0646
 Position 59 : 0.0646
 Position 60 : 0.0646
 Position 61 : 0.0646
 Position 62 : 0.0646
 Position 63 : 0.0646
 Position 64 : 0.0646
 Position 65 : 0.0646
 Position 66 : 0.0646
 Position 67 : 0.0646
 Position 68 : 0.0646
 Position 69 : 0.0646
 Position 70 : 0.0646

Region 3: Position 72 to 82

Consensus:

72 NVPEWSYIVEK 82

Segment Length: 11

Average entropy (Hx): 0.0646

Position 72 : 0.0646
 Position 73 : 0.0646
 Position 74 : 0.0646
 Position 75 : 0.0646
 Position 76 : 0.0646
 Position 77 : 0.0646
 Position 78 : 0.0646
 Position 79 : 0.0646
 Position 80 : 0.0646
 Position 81 : 0.0646
 Position 82 : 0.0646

Region 4: Position 95 to 119

Consensus:

95 FNDYEELKHLLSRINHFEEKIQIIPK 119

Segment Length: 25

Average entropy (Hx): 0.0728

Position 95 : 0.0646
 Position 96 : 0.1290
 Position 97 : 0.1290
 Position 98 : 0.0646
 Position 99 : 0.0646
 Position 100 : 0.0646
 Position 101 : 0.0646
 Position 102 : 0.0646
 Position 103 : 0.0646
 Position 104 : 0.0646
 Position 105 : 0.0646
 Position 106 : 0.0646
 Position 107 : 0.0646
 Position 108 : 0.0763
 Position 109 : 0.0646
 Position 110 : 0.0646
 Position 111 : 0.0646
 Position 112 : 0.0646
 Position 113 : 0.0646
 Position 114 : 0.0646
 Position 115 : 0.0646
 Position 116 : 0.1290
 Position 117 : 0.0646
 Position 118 : 0.0646
 Position 119 : 0.0646

Region 5: Position 163 to 173
 Consensus:
 163 SYNNTNQEDLL 173

Segment Length: 11
 Average entropy (Hx): 0.0704
 Position 163 : 0.0646
 Position 164 : 0.0646
 Position 165 : 0.0646
 Position 166 : 0.0646
 Position 167 : 0.0646
 Position 168 : 0.0646
 Position 169 : 0.0646
 Position 170 : 0.0646
 Position 171 : 0.1290
 Position 172 : 0.0646
 Position 173 : 0.0646

Region 6: Position 190 to 199
 Consensus:
 190 LYQNPTYIS 199

Segment Length: 10
 Average entropy (Hx): 0.0775
 Position 190 : 0.0646
 Position 191 : 0.0646
 Position 192 : 0.1290
 Position 193 : 0.0646
 Position 194 : 0.0646
 Position 195 : 0.1290
 Position 196 : 0.0646
 Position 197 : 0.0646
 Position 198 : 0.0646
 Position 199 : 0.0646

Region 7: Position 201 to 211
 Consensus:
 201 GTSTLNQRLVP 211

Segment Length: 11
 Average entropy (Hx): 0.0646
 Position 201 : 0.0646
 Position 202 : 0.0646
 Position 203 : 0.0646
 Position 204 : 0.0646
 Position 205 : 0.0646
 Position 206 : 0.0646
 Position 207 : 0.0646
 Position 208 : 0.0646
 Position 209 : 0.0646
 Position 210 : 0.0646
 Position 211 : 0.0646

Region 8: Position 236 to 251
 Consensus:
 236 NDAINFESNGNFIAP 251

Segment Length: 16
 Average entropy (Hx): 0.0686
 Position 236 : 0.0646
 Position 237 : 0.0646
 Position 238 : 0.0646

Position 239 : 0.0646
 Position 240 : 0.0646
 Position 241 : 0.0646
 Position 242 : 0.0646
 Position 243 : 0.0646
 Position 244 : 0.0646
 Position 245 : 0.0646
 Position 246 : 0.0646
 Position 247 : 0.0646
 Position 248 : 0.1290
 Position 249 : 0.0646
 Position 250 : 0.0646
 Position 251 : 0.0646

Region 9: Position 253 to 262
 Consensus:
 253 AYKIVKKGDS 262

Segment Length: 10
 Average entropy (Hx): 0.0710
 Position 253 : 0.0646
 Position 254 : 0.0646
 Position 255 : 0.0646
 Position 256 : 0.0646
 Position 257 : 0.0646
 Position 258 : 0.0646
 Position 259 : 0.1290
 Position 260 : 0.0646
 Position 261 : 0.0646
 Position 262 : 0.0646

Region 10: Position 283 to 303
 Consensus:
 283 GAINSSMPFHNIHPLTIG 303

Segment Length: 21
 Average entropy (Hx): 0.0676
 Position 283 : 0.0646
 Position 284 : 0.0646
 Position 285 : 0.0646
 Position 286 : 0.0646
 Position 287 : 0.0646
 Position 288 : 0.0646
 Position 289 : 0.0646
 Position 290 : 0.0646
 Position 291 : 0.1290
 Position 292 : 0.0646
 Position 293 : 0.0646
 Position 294 : 0.0646
 Position 295 : 0.0646
 Position 296 : 0.0646
 Position 297 : 0.0646
 Position 298 : 0.0646
 Position 299 : 0.0646
 Position 300 : 0.0646
 Position 301 : 0.0646
 Position 302 : 0.0646
 Position 303 : 0.0646

BioEdit version 7.0.8.0 (6/17/07)
 Conserved region search
 Alignment file: I:\cari
 data\database\Na\human\h1n1.aln
 1/11/2002 12:57:19 PM

Minimum segment length (actual for each sequence): 15
 Maximum average entropy: 0.2
 Maximum entropy per position: 0.2
 Gaps limited to 2 per segment
 Contiguous gaps limited to 1 in any segment

3 conserved regions found

Region 1: Position 120 to 158

Consensus:

120

RIGSKGDVVFVIREPFISCSHLECRFFLTQGAL

LNDKHS 158

Segment Length: 39

Average entropy (Hx): 0.0676

Position 120 : 0.0555

Position 121 : 0.0555

Position 122 : 0.0555

Position 123 : 0.0555

Position 124 : 0.0555

Position 125 : 0.0555

Position 126 : 0.0555

Position 127 : 0.1110

Position 128 : 0.0555

Position 129 : 0.0555

Position 130 : 0.0555

Position 131 : 0.0555

Position 132 : 0.0555

Position 133 : 0.0555

Position 134 : 0.0555

Position 135 : 0.0555

Position 136 : 0.0555

Position 137 : 0.0555

Position 138 : 0.0555

Position 139 : 0.1110

Position 140 : 0.1110

Position 141 : 0.0555

Position 142 : 0.0555

Position 143 : 0.1526

Position 144 : 0.1110

Position 145 : 0.0555

Position 146 : 0.0555

Position 147 : 0.0555

Position 148 : 0.0555

Position 149 : 0.1110

Position 150 : 0.0555

Position 151 : 0.0555

Position 152 : 0.0555

Position 153 : 0.0555

Position 154 : 0.0555

Position 155 : 0.0555

Position 156 : 0.1526

Position 157 : 0.0555

Position 158 : 0.0555

Region 2: Position 301 to 319

Consensus:

301 VMCVCRDNWHSNRPVVSF 319

Segment Length: 19

Average entropy (Hx): 0.0585

Position 301 : 0.0555

Position 302 : 0.1110

Position 303 : 0.0555

Position 304 : 0.0555

Position 305 : 0.0555

Position 306 : 0.0555

Position 307 : 0.0555

Position 308 : 0.0555

Position 309 : 0.0555

Position 310 : 0.0555

Position 311 : 0.0555

Position 312 : 0.0555

Position 313 : 0.0555

Position 314 : 0.0555

Position 315 : 0.0555

Position 316 : 0.0555

Position 317 : 0.0555

Position 318 : 0.0555

Position 319 : 0.0555

Region 3: Position 413 to 430

Consensus:

413 SGYSGSFVQHPGLTGLDC 430

Segment Length: 18

Average entropy (Hx): 0.0586

Position 413 : 0.0555

Position 414 : 0.0555

Position 415 : 0.0555

Position 416 : 0.0555

Position 417 : 0.0555

Position 418 : 0.0555

Position 419 : 0.0555

Position 420 : 0.0555

Position 421 : 0.0555

Position 422 : 0.0555

Position 423 : 0.0555

Position 424 : 0.0555

Position 425 : 0.0555

Position 426 : 0.0555

Position 427 : 0.0555

Position 428 : 0.0555

Position 429 : 0.1110

Position 430 : 0.0555

BioEdit version 7.0.8.0 (6/17/07)

Conserved region search

Alignment file: F:\cari

data\database\Na\human\h2n2.aln

1/11/2002 1:00:48 PM

Minimum segment length (actual for each sequence): 10

Maximum average entropy: 0.2

Maximum entropy per position: 0.2

Gaps limited to 2 per segment

Contiguous gaps limited to 1 in any segment

2 conserved regions found

Region 1: Position 432 to 443

Consensus:

432 QETRVWWTNSNI 443

Segment Length: 12

Average entropy (Hx): 0.0560

Position 432 : 0.0560

Position 433 : 0.0560

Position 434 : 0.0560

Position 435 : 0.0560
 Position 436 : 0.0560
 Position 437 : 0.0560
 Position 438 : 0.0560
 Position 439 : 0.0560
 Position 440 : 0.0560
 Position 441 : 0.0560
 Position 442 : 0.0560
 Position 443 : 0.0560

Region 2: Position 456 to 465
 Consensus:
 456 GSWPDGANIN 465

Segment Length: 10
 Average entropy (Hx): 0.0570
 Position 456 : 0.0560
 Position 457 : 0.0560
 Position 458 : 0.0560
 Position 459 : 0.0560
 Position 460 : 0.0560
 Position 461 : 0.0560
 Position 462 : 0.0560
 Position 463 : 0.0560
 Position 464 : 0.0659
 Position 465 : 0.0560

BioEdit version 7.0.8.0 (6/17/07)
 Conserved region search
 Alignment file: I:\cari
 data\database\Na\human\h3n2.aln
 1/11/2002 12:58:14 PM

Minimum segment length (actual for each
 sequence): 15
 Maximum average entropy: 0.2
 Maximum entropy per position: 0.2
 Gaps limited to 2 per segment
 Contiguous gaps limited to 1 in any segment

7 conserved regions found

Region 1: Position 94 to 125
 Consensus:
 94
 ITGFAPFSKDNSIRLSAGGDIWVTREPYVSCD
 125

Segment Length: 32
 Average entropy (Hx): 0.0590
 Position 94 : 0.0555
 Position 95 : 0.0555
 Position 96 : 0.0555
 Position 97 : 0.0555
 Position 98 : 0.0555
 Position 99 : 0.0555
 Position 100 : 0.0555
 Position 101 : 0.0555
 Position 102 : 0.1110
 Position 103 : 0.0555
 Position 104 : 0.0555
 Position 105 : 0.0555
 Position 106 : 0.0555
 Position 107 : 0.0555
 Position 108 : 0.1110
 Position 109 : 0.0555

Position 110 : 0.0555
 Position 111 : 0.0555
 Position 112 : 0.0555
 Position 113 : 0.0555
 Position 114 : 0.0555
 Position 115 : 0.0555
 Position 116 : 0.0555
 Position 117 : 0.0555
 Position 118 : 0.0555
 Position 119 : 0.0555
 Position 120 : 0.0555
 Position 121 : 0.0555
 Position 122 : 0.0555
 Position 123 : 0.0555
 Position 124 : 0.0555
 Position 125 : 0.0555

Region 2: Position 156 to 171
 Consensus:
 156 RTLLMNELGVPFHLGT 171

Segment Length: 16
 Average entropy (Hx): 0.0555
 Position 156 : 0.0555
 Position 157 : 0.0555
 Position 158 : 0.0555
 Position 159 : 0.0555
 Position 160 : 0.0555
 Position 161 : 0.0555
 Position 162 : 0.0555
 Position 163 : 0.0555
 Position 164 : 0.0555
 Position 165 : 0.0555
 Position 166 : 0.0555
 Position 167 : 0.0555
 Position 168 : 0.0555
 Position 169 : 0.0555
 Position 170 : 0.0555
 Position 171 : 0.0555

Region 3: Position 173 to 193
 Consensus:
 173 QVCIAWSSSSCHDGKAWLHVC 193

Segment Length: 21
 Average entropy (Hx): 0.0560
 Position 173 : 0.0555
 Position 174 : 0.0555
 Position 175 : 0.0555
 Position 176 : 0.0555
 Position 177 : 0.0555
 Position 178 : 0.0555
 Position 179 : 0.0555
 Position 180 : 0.0555
 Position 181 : 0.0555
 Position 182 : 0.0555
 Position 183 : 0.0653
 Position 184 : 0.0555
 Position 185 : 0.0555
 Position 186 : 0.0555
 Position 187 : 0.0555
 Position 188 : 0.0555
 Position 189 : 0.0555
 Position 190 : 0.0555
 Position 191 : 0.0555

Position 192 : 0.0555
Position 193 : 0.0555

Consensus:
415 KSCINRCFYVELIRGRK 431

Region 4: Position 222 to 248
Consensus:
222 ILRTQESECVCINGTCTVVMTDGSASG
248

Segment Length: 27
Average entropy (Hx): 0.0576
Position 222 : 0.0555
Position 223 : 0.0555
Position 224 : 0.0555
Position 225 : 0.0555
Position 226 : 0.0555
Position 227 : 0.0555
Position 228 : 0.0555
Position 229 : 0.0555
Position 230 : 0.0555
Position 231 : 0.0555
Position 232 : 0.0555
Position 233 : 0.0555
Position 234 : 0.0555
Position 235 : 0.0555
Position 236 : 0.0555
Position 237 : 0.0555
Position 238 : 0.0555
Position 239 : 0.0555
Position 240 : 0.0555
Position 241 : 0.1110
Position 242 : 0.0555
Position 243 : 0.0555
Position 244 : 0.0555
Position 245 : 0.0555
Position 246 : 0.0555
Position 247 : 0.0555
Position 248 : 0.0555

Region 5: Position 268 to 285
Consensus:
268 LSGSAQHVEECSCYPRYP 285

Segment Length: 18
Average entropy (Hx): 0.0592
Position 268 : 0.0555
Position 269 : 0.1110
Position 270 : 0.0555
Position 271 : 0.0555
Position 272 : 0.0555
Position 273 : 0.0555
Position 274 : 0.0555
Position 275 : 0.0653
Position 276 : 0.0555
Position 277 : 0.0555
Position 278 : 0.0555
Position 279 : 0.0555
Position 280 : 0.0555
Position 281 : 0.0555
Position 282 : 0.0555
Position 283 : 0.0555
Position 284 : 0.0555
Position 285 : 0.0555

Region 6: Position 415 to 431

Segment Length: 17
Average entropy (Hx): 0.0613
Position 415 : 0.0555
Position 416 : 0.0555
Position 417 : 0.0555
Position 418 : 0.0555
Position 419 : 0.0555
Position 420 : 0.0555
Position 421 : 0.0555
Position 422 : 0.0555
Position 423 : 0.0555
Position 424 : 0.0555
Position 425 : 0.0555
Position 426 : 0.0555
Position 427 : 0.0555
Position 428 : 0.0555
Position 429 : 0.0555
Position 430 : 0.0555
Position 431 : 0.1526

Region 7: Position 438 to 462
Consensus:
438 WTSNSIVFCGTSPTYGTGSWPDGA 462

Segment Length: 25
Average entropy (Hx): 0.0559
Position 438 : 0.0555
Position 439 : 0.0555
Position 440 : 0.0555
Position 441 : 0.0555
Position 442 : 0.0555
Position 443 : 0.0555
Position 444 : 0.0555
Position 445 : 0.0555
Position 446 : 0.0555
Position 447 : 0.0555
Position 448 : 0.0555
Position 449 : 0.0555
Position 450 : 0.0555
Position 451 : 0.0653
Position 452 : 0.0555
Position 453 : 0.0555
Position 454 : 0.0555
Position 455 : 0.0555
Position 456 : 0.0555
Position 457 : 0.0555
Position 458 : 0.0555
Position 459 : 0.0555
Position 460 : 0.0555
Position 461 : 0.0555
Position 462 : 0.0555

BioEdit version 7.0.8.0 (6/17/07)
Conserved region search
Alignment file: I:\cari
data\database\Na\human\h5n1.aln
1/11/2002 12:58:39 PM

Minimum segment length (actual for each
sequence): 15
Maximum average entropy: 0.2
Maximum entropy per position: 0.2
Gaps limited to 2 per segment

Contiguous gaps limited to 1 in any segment

5 conserved regions found

Region 1: Position 138 to 156

Consensus:

138 ECRTFFLTQGALLNDKHSN 156

Segment Length: 19

Average entropy (Hx): 0.0665

Position 138 : 0.1110

Position 139 : 0.0555

Position 140 : 0.0555

Position 141 : 0.0555

Position 142 : 0.0555

Position 143 : 0.0555

Position 144 : 0.0555

Position 145 : 0.0555

Position 146 : 0.0555

Position 147 : 0.0555

Position 148 : 0.1526

Position 149 : 0.0555

Position 150 : 0.0555

Position 151 : 0.0555

Position 152 : 0.1110

Position 153 : 0.0555

Position 154 : 0.0555

Position 155 : 0.0555

Position 156 : 0.0555

Region 2: Position 166 to 196

Consensus:

166

RTLMSCPVGEAPSPYNSRFESVAWSASACHD

196

Segment Length: 31

Average entropy (Hx): 0.0576

Position 166 : 0.0653

Position 167 : 0.0555

Position 168 : 0.0555

Position 169 : 0.0555

Position 170 : 0.0555

Position 171 : 0.0555

Position 172 : 0.0555

Position 173 : 0.0555

Position 174 : 0.0555

Position 175 : 0.0555

Position 176 : 0.1110

Position 177 : 0.0555

Position 178 : 0.0555

Position 179 : 0.0555

Position 180 : 0.0555

Position 181 : 0.0555

Position 182 : 0.0555

Position 183 : 0.0555

Position 184 : 0.0555

Position 185 : 0.0555

Position 186 : 0.0555

Position 187 : 0.0555

Position 188 : 0.0555

Position 189 : 0.0555

Position 190 : 0.0555

Position 191 : 0.0555

Position 192 : 0.0555

Position 193 : 0.0555

Position 194 : 0.0555

Position 195 : 0.0555

Position 196 : 0.0555

Region 3: Position 307 to 323

Consensus:

307 WHGSNRPWVSFNQNLEY 323

Segment Length: 17

Average entropy (Hx): 0.0640

Position 307 : 0.0555

Position 308 : 0.0555

Position 309 : 0.0555

Position 310 : 0.0555

Position 311 : 0.0555

Position 312 : 0.0555

Position 313 : 0.0555

Position 314 : 0.0555

Position 315 : 0.1890

Position 316 : 0.0555

Position 317 : 0.0555

Position 318 : 0.0555

Position 319 : 0.0555

Position 320 : 0.0555

Position 321 : 0.0555

Position 322 : 0.0653

Position 323 : 0.0555

Region 4: Position 358 to 375

Consensus:

358 KGFSEFKYGNVWIGRTKS 375

Segment Length: 18

Average entropy (Hx): 0.0555

Position 358 : 0.0555

Position 359 : 0.0555

Position 360 : 0.0555

Position 361 : 0.0555

Position 362 : 0.0555

Position 363 : 0.0555

Position 364 : 0.0555

Position 365 : 0.0555

Position 366 : 0.0555

Position 367 : 0.0555

Position 368 : 0.0555

Position 369 : 0.0555

Position 370 : 0.0555

Position 371 : 0.0555

Position 372 : 0.0555

Position 373 : 0.0555

Position 374 : 0.0555

Position 375 : 0.0555

Region 5: Position 430 to 444

Consensus:

430 RPCFWVELIRGRPKE 444

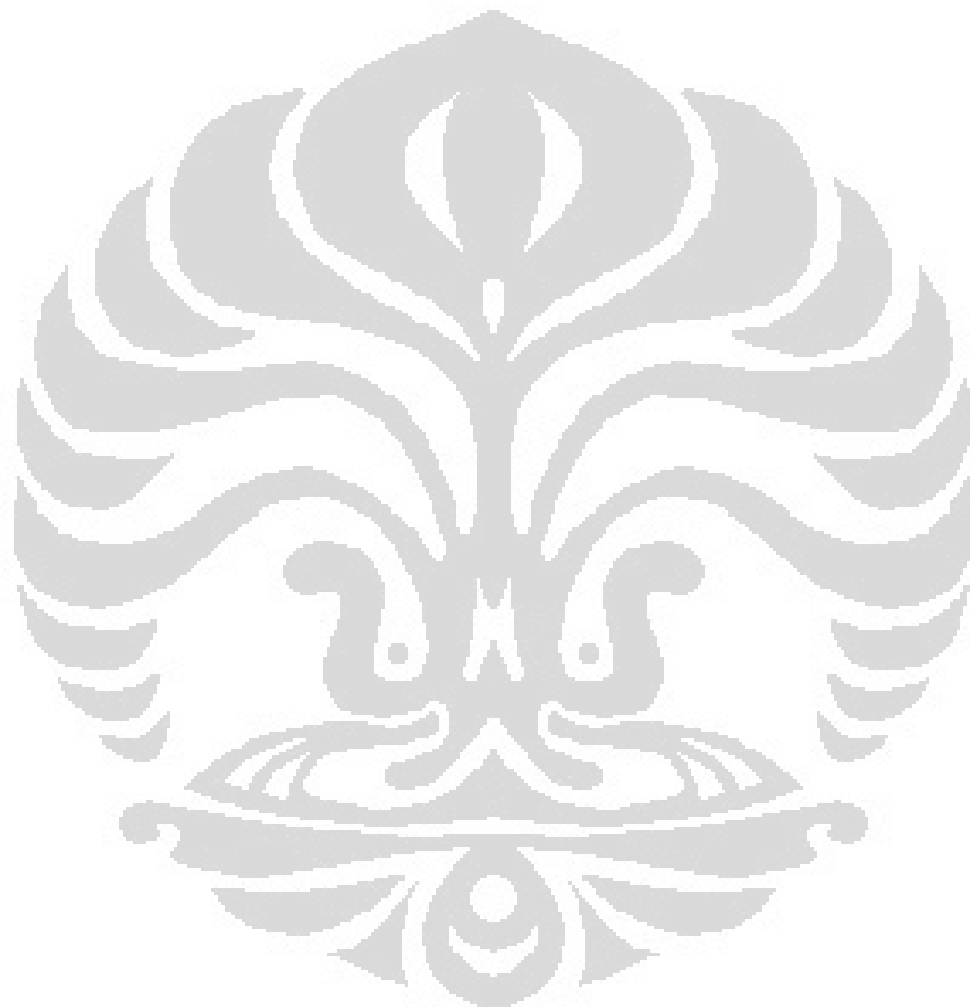
Segment Length: 15

Average entropy (Hx): 0.0599

Position 430 : 0.0555

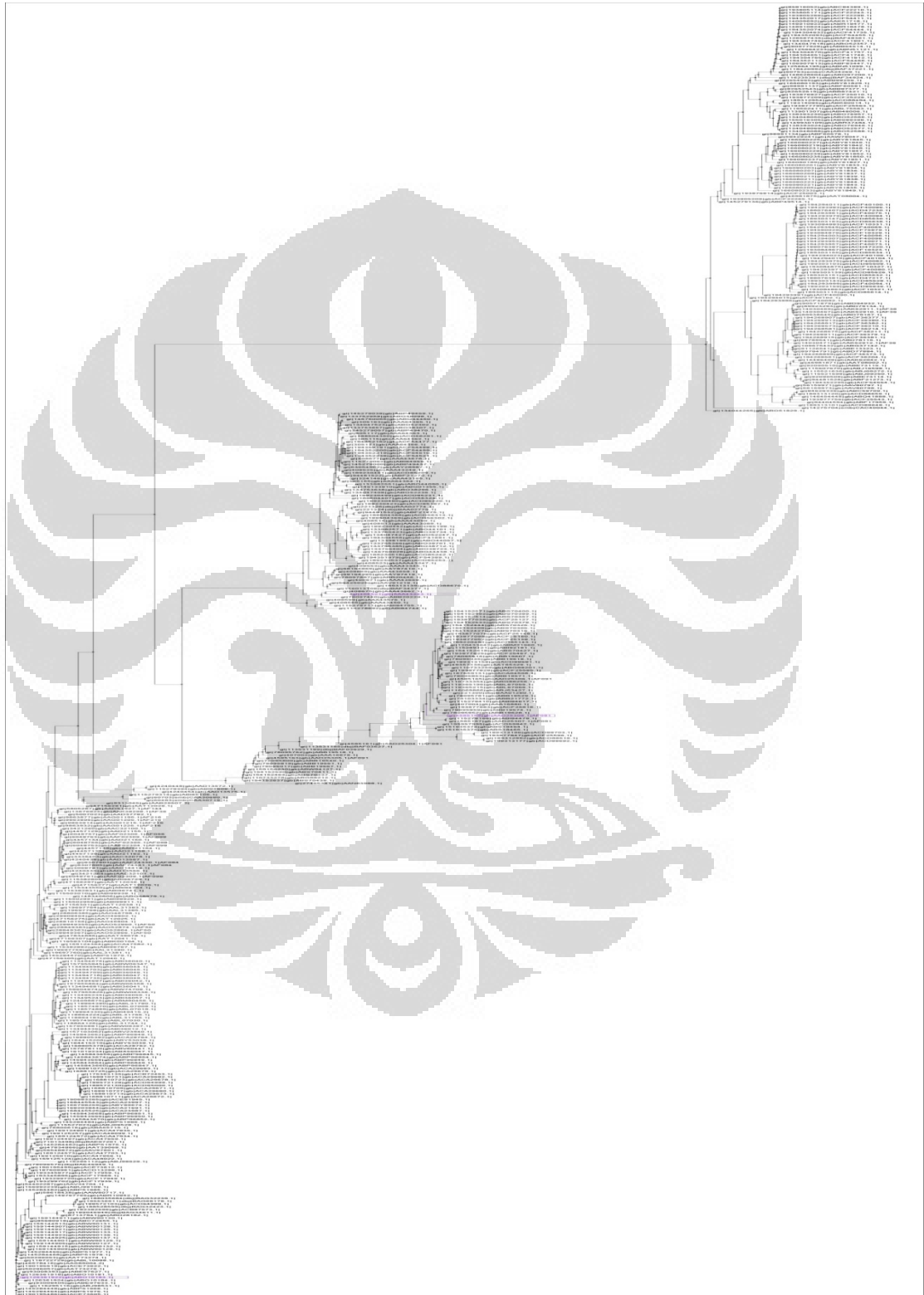
Position 431 : 0.0555

Position 432 : 0.0555
Position 433 : 0.0555
Position 434 : 0.0555
Position 435 : 0.0555
Position 436 : 0.0555
Position 437 : 0.0555
Position 438 : 0.1110
Position 439 : 0.0555
Position 440 : 0.0555
Position 441 : 0.0653
Position 442 : 0.0555
Position 443 : 0.0555
Position 444 : 0.0555



Lampiran 6 : Pohon filogenetik

Haemagglutinin



Neuraminidase

