PREDIKSI INTERAKSI ANTIBODI-ANTIGEN (VAKSIN) VIRUS H1N1 MELALUI METODE *MOLECULAR DOCKING* SECARA *IN SILICO*

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FAKULTAS MATEMATIKA DAN ILMU PENGETAHUAN ALAM
DEPARTEMEN KIMIA
DEPOK
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Tesis diajukan sebagai salah satu syarat untuk
Memperoleh gelar Master Sains

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ABSTRAK

PREDIKSI INTERAKSI ANTIBODI-ANTIGEN (VAKSIN) VIRUS H1N1 MELALUI METODE *MOLECULAR DOCKING* SECARA *IN SILICO*. Flu babi H1N1 merupakan salah satu penyakit menular akibat virus influenza tipe A yang telah menjadi pandemik dan mortalitasnya sangat tinggi pada manusia. Salah satu pencegahan penularan penyakit tersebut dengan cara vaksinasi. Mengetahui bagian antigenik (*epitope*) suatu virus merupakan hal penting untuk merancang suatu vaksin. Beberapa *epitope* telah diprediksi dari perwakilan protein *hemagglutinin* (HA)*, neuramidase* (NA)*,* dan *matrik* 2 (M2). Pendekatan *in silico* dilakukan melalui kombinasi prediksi pada tahap-tahap respon imun oleh adanya antigen yaitu; *proteasomal cleavage* (NetChop), *Transporter Antigen Processing* (TAP) *binding* (TAPPred), dan *Major Histocompatibility complex* (MHCPred). Upaya meningkatkan respon imun juga dilakukan dengan memprediksi e*pitope* sel B menggunakan *server* DiscoTope (*conformational epitope*) dan BepiPred (*sequential epitope*). Enam vaksin, yaitu NHM, MHN, HNM, MNH, HMN, dan NMH diperoleh dari 21 kombinasi terbaik *epitope* sel T dan sel B sebagai representasi variasi *allele Human Leukocyte Antigen* (HLA) dan protein virus sehingga diharapkan mampu memberikan respon imun. Struktur 3D vaksin diprediksi dan dimodeling menggunakan *server* CPHModels dan program *Swiss-Pdb Viewer* (*Deep View*). Hasil struktur 3D vaksin dievaluasi menggunakan Ramachandran Plot, BLASTp (*database* PDB virus), dan FeatureMap3D. Vaksin terdiri dari 258 asam amino dan memiliki kesamaan struktur 3D dengan protein dalam *database* lebih besar dari 50 %. Terakhir dilakukan *molecular docking* antara vaksin dengan antibodi dalam *database* diperoleh 14 *clustering* dengan waktu yang dibutuhkan sekitar 18 detik dan data energi minimum interaksi antibodi dengan vaksin NHM sebesar -13,6859 kkal/mol.

Kata Kunci: Antibodi, Antigen, Flu babi (H1N1), *In Silico, Molecular docking,* Vaksin.

ABSTRACT

IN SILICO PREDICTION OF ANTIBODY-ANTIGEN (VACCINE) INTERACTION OF H1N1 VIRUS USING MOLECULAR DOCKING METHOD. Swine flu H1N1 is one of the diseases due to influenza type A virus that has become pandemic and very high mortality to humans. One of the prevention of this disease with a vaccination. Knowing the antigenic (epitope) of a virus is important for designing a vaccine. Some have predicted epitope of representatives from protein hemagglutinin (HA), neuramidase (NA), and matrix 2 (M2). In silico approach was undertaken through a combination of input stages by immune response, namely antigen; proteasomal cleavage (NetChop), Transporter Antigen Processing (TAP) binding (TAPPred), and Major Histocompatibility Complex (MHCPred). An effort to improve the immune response is also conducted to predict the B-cell epitope using DiscoTope (conformational epitope) and BepiPred (sequential epitope) server. Six vaccines (vaccine NHM, MHN, HNM, MNH, HMN, and NMH) are the best combinations of 21 B-cell epitope and T-cell variations in allele representation as Human Leukocyte antigen (HLA) and protein the virus are expected to provide the immune response. The 3D structure and predicted vaccine was modeled by CPHModels program and the Swiss-PDB Viewer (Deep View). The results of 3D structure of vaccines evaluated using the Ramachandran Plot, BLASTp (protein database human - virus GDP), and FeatureMap3D. Vaccines consist of 258 amino acids have a similar 3D structure with protein in the database bigger than 50 %. The last performed molecular docking between vaccines and antibody was found in the database received 14 of clustering with the time needed about 18 seconds and the minimum energy of antibody interaction with NHM vaccine was -13,6859 kkal/mol.

Keywords: Antibody, Antigen, In Silico, Molecular Docking, Swine Influenza (H1N1), Vaccine.

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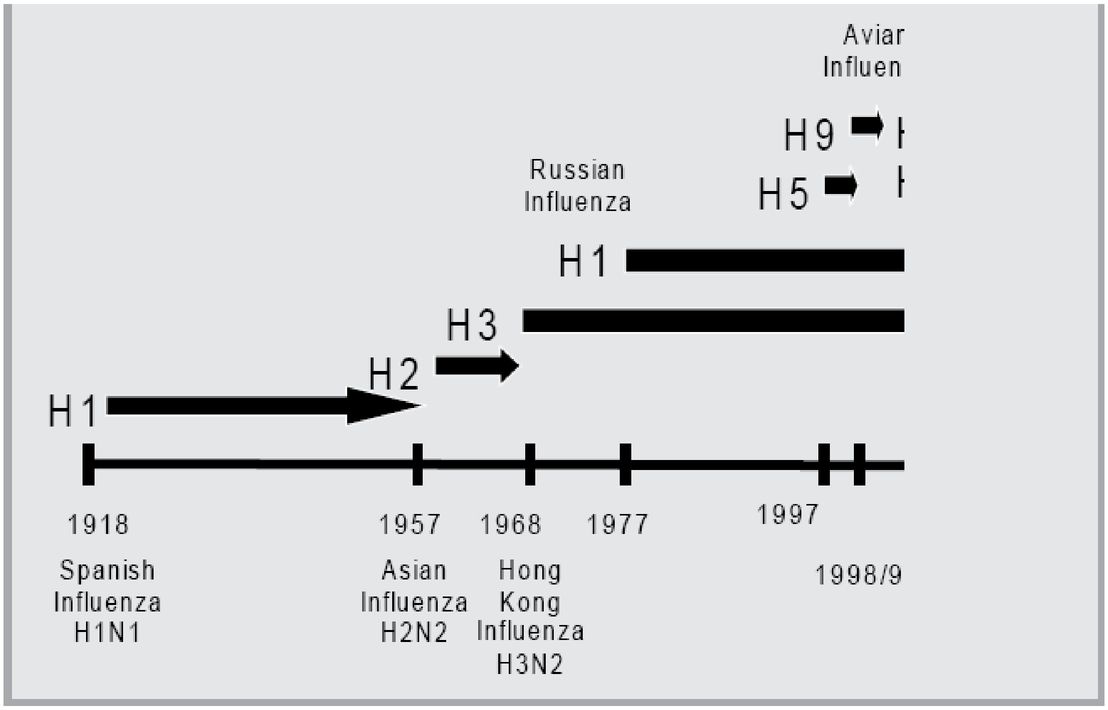
BAB I

PENDAHULUAN

Penyakit flu babi (*swine* influenza) adalah suatu penyakit menular disebabkan oleh virus influenza tipe A, khususnya subtipe H1N1. Flu babi menular dari babi ke babi, babi ke manusia, dan manusia ke manusia. Penularan virus tersebut dapat terjadi melalui kontak hidung antar babi atau melalui pengeringan mukus. Penularan melalui udara juga dapat terjadi ketika babi batuk atau bersin.

Virus Influenza tipe A umumnya tidak menyerang manusia, tapi terbukti virus tersebut dapat menyerang manusia. Gejala-gejala klinis yang ditemui seperti gejala flu umumnya, yaitu; demam, sakit tenggorokan, batuk, nyeri otot, sakit kepala, lemas, muntah-muntah, sulit bernafas, dan berakhir pada kematian.

Penyakit flu babi H1N1 pertama kali terjadi pada tahun 1918 dikenal sebagai “*Spanish Flu*“ menyebabkan kematian lebih dari 50 juta manusia di seluruh dunia dan dinyatakan sebagai wabah pandemik dalam kurun waktu satu tahun, yaitu tahun 1918-1919. Pandemik kedua terjadi pada tahun 1957 dikenali sebagai H2N2 menyerang kawasan asia atau “*Asian Flu*” menyebabkan kematian kurang lebih 1 juta manusia. Pandemik ketiga pada tahun 1968, “*Hongkong Flu*” disebabkan oleh virus influenza A H3N2 menewaskan 700.000 manusia (**Gambar 1**).



Gambar 1. Beberapa subtipe virus influenza A yang menjadi penyebab wabah pandemik (Radji, 2006)

Sebanyak 327 kasus infeksi *avian influenza* H5N1 di dunia dengan angka kematian rerata 60,96 % mayoritas terjadi di Indonesia, Vietnam, dan Thailand, serta Cina pada tahun 2003 (http://www.who.int.).

Kasus-kasus yang disebabkan oleh virus influenza A terus bermunculan. Data terakhir WHO sampai bulan Juni 2009, jumlah kasus influenza A H1N1 di seluruh dunia telah mencapai 59.814 kasus termasuk 263 menyebabkan kematian (http://www.who.int/csr/disease/swineflu/en/).

Usaha untuk menekan tingginya angka kematian yang disebabkan oleh virus H1N1 memerlukan suatu tindakan pencegahan dini melalui vaksinasi. Penelitian telah banyak dilakukan dalam rangka mendapatkan vaksin H1N1. Namun terapi lebih banyak digunakan berupa obat antivirus yang hanya berfungsi sebagai inhibitor dalam proses replikasi virus dalam sel inang. Vaksin H1N1 untuk manusia sangat sulit dihasilkan terkait virus H1N1 mudah bermutasi melalui *antigenic drift* dan *reassortment*.

Salah satu alternatif vaksin H1N1 untuk mencegah penyebaran virus adalah vaksin peptida. Vaksin peptida terdiri dari sekuen-sekuen peptida penyusun protein permukaan virus dan bersifat antigenik (dapat memicu timbulnya respon imunitas).

Tujuan penelitian adalah merancang vaksin H1N1 secara *in silico* dan memprediksi energi minimum interaksi antara vaksin sebagai antigen dengan antibodi manusia yang terdapat pada *database* melalui metode *molecular docking.*

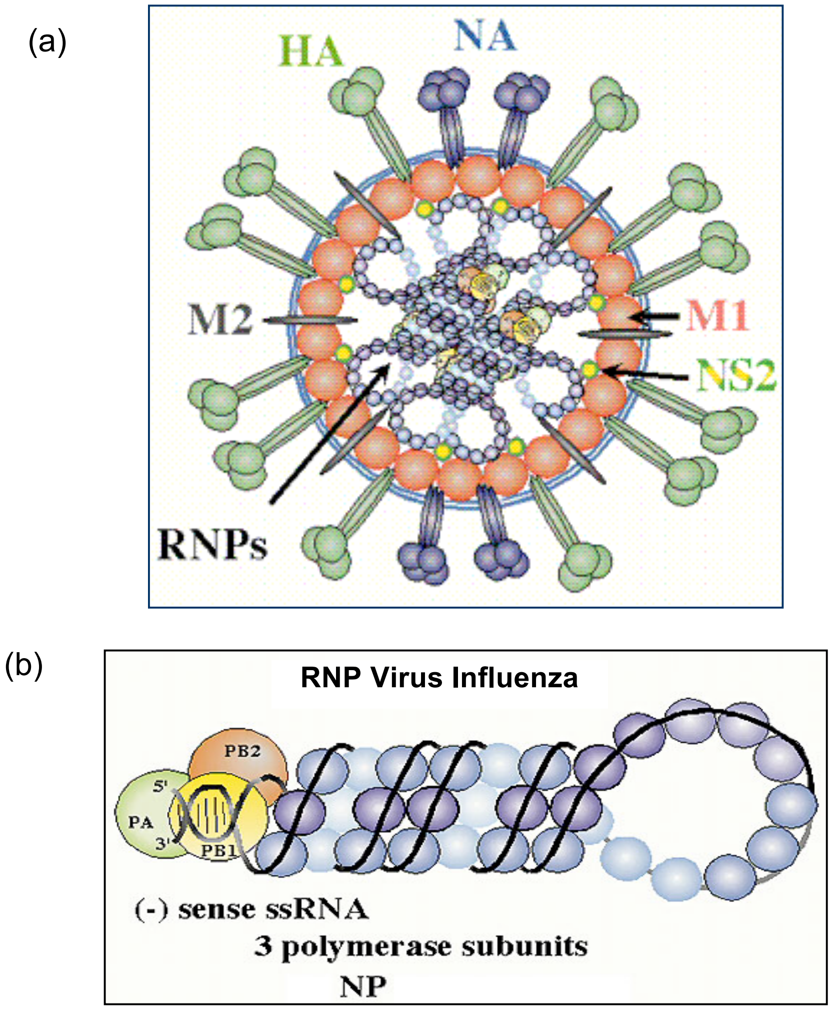
BAB II

TINJAUAN PUSTAKA

2.1 Virus Influenza

Virus influenza dikelompokkan ke dalam ordo *Mononegavirales*, famili *Orthomyxoviridae*. Berdasarkan *ribonucleoprotein* virus influenza dibagi ke dalam tiga tipe, yaitu tipe A, B, dan C. Influenza A bersifat endemik dan pandemik serta memerlukan inang, influenza B bersifat endemik dan tidak memerlukan inang, sedangkan influenza C merupakan penyakit flu biasa, tidak endemik maupun pandemik. Selain menginfeksi manusia, virus influenza tipe A dapat pula menginfeksi hewan seperti unggas dan mamalia, sedangkan virus tipe B dan C terutama menyerang pada manusia (Menno dan Hien, 2005).

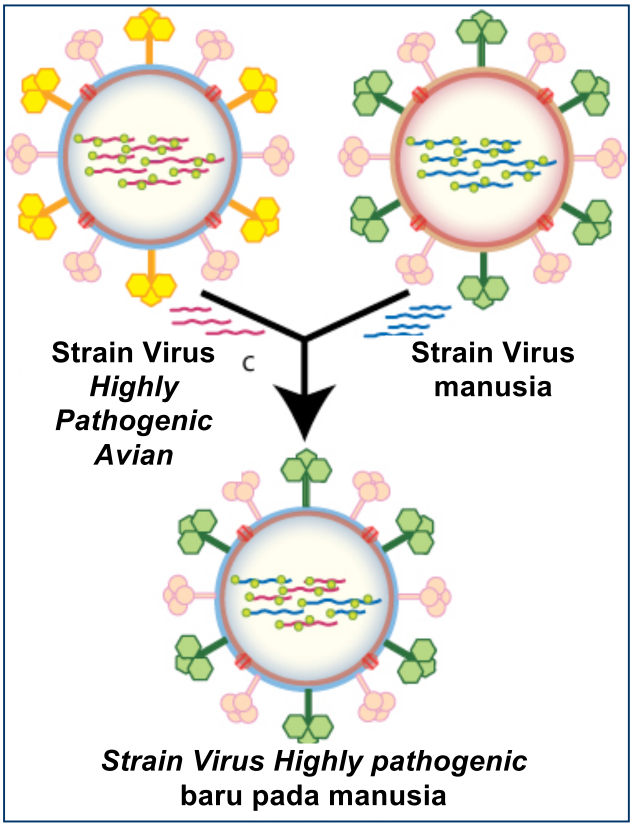
Virus influenza merupakan RNA virus, artinya RNA berfungsi sebagai pembawa informasi genetik. Genom virus adalah (-) ssRNA, memiliki 8 segmen, yaitu *Polymerase Basidic subunit 1* (PB1), *Polymerase Basidic subunit 2* (PB2), *Polymerase Acidic* (PA), *Nucleoprotein* (NP), *Neuraminidase* (NA), *Hemagglutinin* (HA), protein M*atrix subunit* 1 (M1), protein *Matrix subunit 2* (M2), protein *nonstructural subunit 1*(NS1), dan protein *nonstructural subunit* 2 (NS2). Antigen virus influenza terdiri dari beberapa komponen yaitu antigen internal, terdiri dari genom RNA dan protein M1; dan antigen eksternal terdapat pada permukaan virus, yaitu protein HA, NA, dan M2 . Antigen yang terdapat pada lapisan permukaan merupakan pembeda antar virus influenza. Virus influenza A memiliki 16 jenis HA dan 9 jenis NA (Maasab *et. al*.,1999). Protein HA dan NA digunakan sebagai identifikasi kode subtipe virus yang banyak jenisnya. Pada manusia terdapat subtipe H1N1, H2N2, H3N3, H5N1, H9N2, H1N2, H7N7, sedangkan pada babi terdapat subtipe H1N1, H1N2, H3N2, dan H2N3. Kelompok-kelompok tersebut ditetapkan setelah analisis filogenetik terhadap nukleotida dan penetapan sekuen gen-gen HA dan NA melalui cara deduksi asam amino (Fouchier, *et. al*., 2005). Struktur virus influenza ditunjukkan pada **Gambar 2**.



Gambar 2. (a) Struktur virus influenza; (b) Genom virus influenza (Digard, 2000)

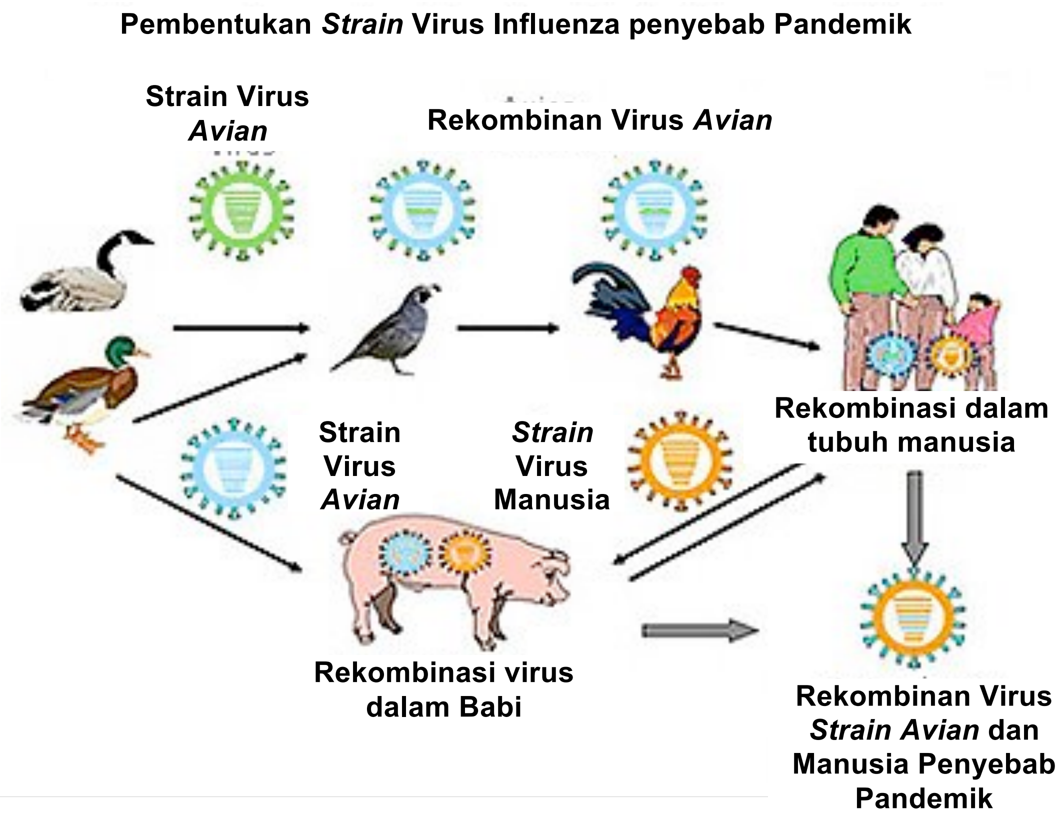
2.2 Virus H1N1 (Virus *Influenza* 1918*, "Spanish Flu")*

Perubahan *strain* virus seperti yang terjadi pada tahun 1957 dan 1968 dapat dimungkinkan terjadi ketika virus menginfeksi manusia kemudian menggunakan genom manusia untuk memproduksi virus-virus yang memiliki sifat patogenik baru seperti tampak pada **Gambar 3**.



Gambar 3. Pembentukan *strain* virus baru akibat rekombinasi genetik antara virus *strain avian* dan virus *strain* manusia (http://en.wikipedia.org/wiki/File:Influenza_geneticshift.jpg)

Berdasarkan analisis filogenetik, virus H1N1 1918 diperkirakan muncul dengan cara yang berbeda dengan virus pandemik tahun 1957 dan 1968, yaitu bukan dengan rekombinasi antara virus *strain avian* dengan virus *strain* manusia melainkan melalui transmisi langsung dari virus *strain avian* yang beradaptasi dalam tubuh manusia atau dengan perantara lain seperti babi (Reid, *et al.*, 2004) (**Gambar 4**).



Gambar 4. Pembentukan *strain* virus influenza A yang menyebabkan pandemik (http://www.cdc.gov/eid)

Analisis tersebut didukung dengan adanya observasi bahwa *strain* pandemik tahun 1918 mengandung residu asam amino pada posisi 226 dan 228 dari protein HA yang diperkirakan sebagai tempat pengikatan dengan *reseptor* dari *strain avian* (Taubenberger, *et al.*, 1997).

Protein HA virus yang menyebabkan pandemik pada tahun 1918 mempunyai perbedaan spesifisitas *reseptor* antar *strain*. Isolat A/South Carolina/1/1918 cenderung berikatan dengan *reseptor strain* manusia, sedangkan isolat A/New York/1/1918 dapat berikatan baik dengan *reseptor strain* manusia maupun *strain avian* (Srinivasan, *et. al.,* 2007).

Hasil studi kristalografi menjelaskan bahwa virus dapat menginfeksi dan menyebar antar manusia karena adanya perubahan struktur pada H1 dari protein HA membuat virus dapat mengenali reseptor manusia (Gamblin, *et.al*. 2004; Stevens, *et al.,* 2004).

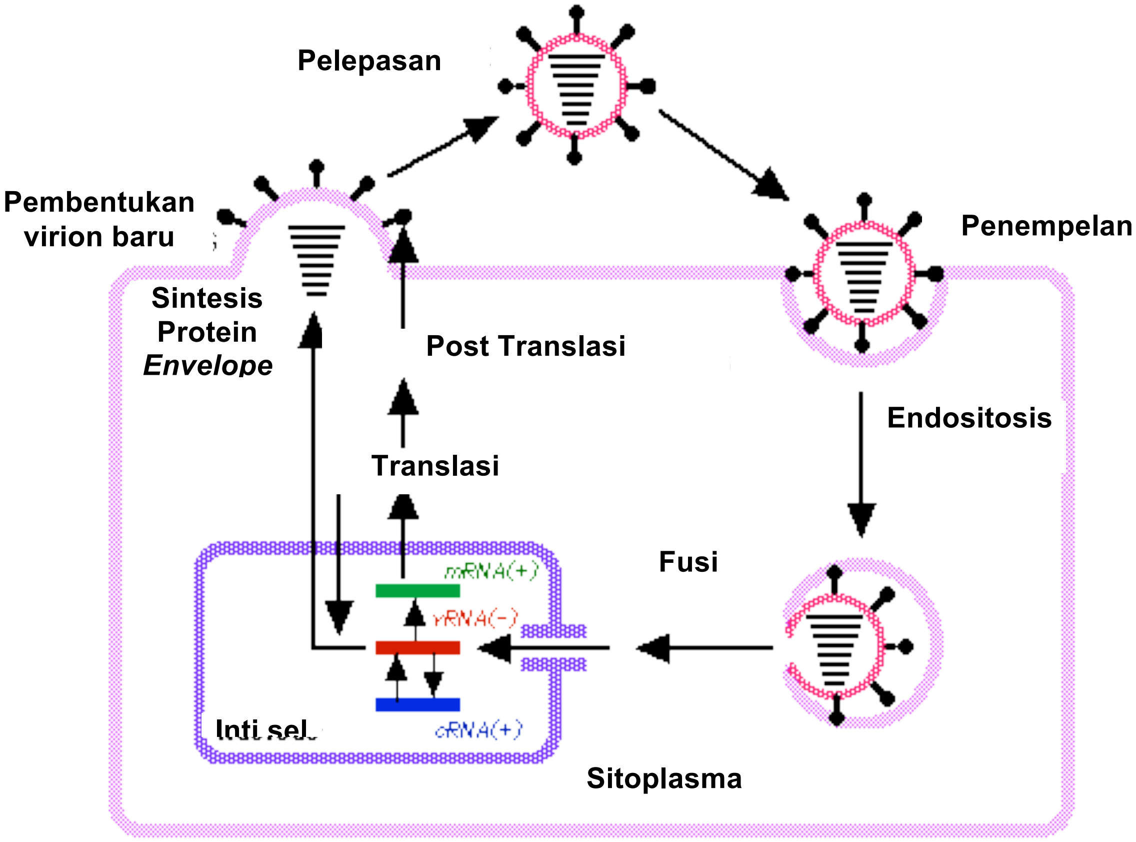
Virus H1N1 dapat bertahan hidup di air sampai 4 hari pada suhu 22°C dan lebih dari 30 hari pada 0°C. Virus akan mati pada pemanasan 60°C selama 30 menit atau 56°C selama 3 jam atau dengan detergen, desinfektan misalnya formalin, serta cairan yang mengandung *iodine*. Masa inkubasi virus influenza bervariasi antara 1 – 7 hari. (http://www.litbang.depkes.go.id/)

2.3. Infeksi virus H1N1 Pada Manusia

Salah satu faktor yang mempengaruhi tingkat patogen virus influenza adalah protein HA di permukaan virus atau *spike* (tonjolan) protein. Protein HA juga berperan pada proses infeksi virus ke dalam sel melalui interaksi dengan *reseptor* di permukaan sel inang. Mutasi pada protein HA dapat meningkatkan daya tular virus influenza.

Penginfeksian virus dimulai ketika virus memasuki sel inang setelah terjadi penempelan *spikes* virus dengan *reseptor* spesifik yang ada di permukaan sel inang. Virus akan menyusup ke sitoplasma sel inang dan mengintegrasikan materi genetiknya ke dalam inti sel. Virus menggunakan mesin genetik sel inang untuk bereplikasi membentuk virion-virion baru. Kemudian virion-virion baru dapat menginfeksi kembali sel-sel di sekitarnya (Menno dan Hien, 2005).

Fase penempelan (*attachment*) merupakan fase paling menentukan proses virus masuk ke dalam sel inang untuk melanjutkan replikasinya. Virus influenza A melalui *spikes* HA akan berikatan dengan reseptor yang mengandung asam sialat pada permukaan sel inang. Mekanisme virus masuk dan bereplikasi dalam sel inang ditunjukkan pada **Gambar 5**.



Gambar 5. Mekanisme virus masuk dan bereplikasi dalam sel inang. (Módena, *et. al*. 2006)

Gambar di atas menunjukkan proses virus masuk ke dalam sel inang melalui endositosis dan bereplikasi dengan mereproduksi materi genetik virus. Virus *influenza* termasuk kelas virus yang mengandung RNA sebagai materi genetiknya. Virus bereplikasi dengan memasuki sel inang dan menggunakan sel inang untuk memproduksi cetakan virus RNA.

Virus melekat pada bagian luar sel inang dan RNA virus masuk ke dalam inti sel. Gen virus mengalami *reverse* transkripsi kemudian ditranslasikan oleh enzim-enzim sel dan ribosom. Melalui proses tersebut, virus mengambil alih fungsi produktif sel.

Genom virus bereplikasi dalam inti sel inang. Virus RNA (vRNA) dikopi dari (-) *sense* menjadi (+) cRNA dan mRNA. cRNA tetap pada inti yang berfungsi sebagai *template* pada produksi (-) *sense* vRNA baru, sedangkan mRNA akan berpindah ke sitoplasma untuk memproduksi protein. *Nucleoprotein* (NP) kembali ke inti dan berasosiasi dengan vRNA membentuk *nucleocapsid.*

Salah satu faktor virus influenza dapat menginfeksi manusia disebabkan karena adanya kecocokan antara virus dengan *reseptor* pada permukaan sel inang. Virus influenza akan berikatan dengan glikoprotein atau glikolipid permukaan sel yang mengandung asam sialat.

2.3.1. Protein *Hemagglutinin* (HA)

Hemaglutinin (HA) adalah suatu protein yang mengalami glikosilasi dan asilasi (*glycosylated and acylated protein*) terdiri dari 562 – 566 asam amino terikat dalam sampul virus. Kepala membran distal protein HA berbentuk bulat, daerah permukaan berbentuk seperti tombol dan berkaitan dengan kemampuannya melekat pada reseptor sel, terdiri dari oligosakharida (Watowich, *et.al.*, 1994).

Protein HA berfungsi untuk mengikat dan menempel pada dinding sel inang, berbentuk paku–paku tajam saat menginfeksi sel sehingga dapat mengikat dan menempel erat pada dinding sel saat proses penginfeksian. Bagian protein HA yang berikatan dengan *reseptor* pada sel inang (*Receptor Binding Site)* mempunyai susunan asam amino khas. Setelah berikatan dengan reseptor sel inang, virus akan masuk melalui fusi *envelope* virus dengan membran endosomal sel inang. Proses tersebut memerlukan *protease* sel inang untuk mengaktivasi prekursor HAo menjadi fragmen1 (HA1) dan fragmen2 (HA2) digunakan virus melepaskan RNA kemudian bereplikasi di dalam sel inang. Aktivasi proteolitik protein HA merupakan faktor penting untuk infektivitas dan penyebaran virus ke seluruh tubuh.

2.3.2. Protein *Neuraminidase* (NA)

Protein *neuraminidase* (NA) berfungsi untuk melepaskan partikel virus setelah replikasi dalam sel dan mencegah virus menempel kembali pada reseptor sel inang melalui protein HA. Efisiensi replikasi virus sangat tergantung pada kerjasama protein HA dan NA virus (Nidom, 2005).

2.3.3. Protein Matrik 2

Protein M2 mempunyai peran dalam penyusunan virus. Bersama dengan protein HA dan NA, protein M2 menyusun struktur *envelope* virus. Protein M2 juga berperan pada awal infeksi dalam pemisahan protein M1 dari *Ribonucleoprotein* (RNP) masuk ke dalam sitoplasma sel inang.

2.4. Antigen

Antigen adalah zat yang mampu menginduksi suatu respon imunitas spesifik. Suatu molekul dapat dikatakan antigen apabila molekul tersebut mempunyai sifat *immunogenicity* dan *antigenicity*. *Immunogenicity* adalah kemampuan suatu molekul untuk menginduksi respon imunitas spesifik. Antigen yang mempunyai sifat *immunogenicity* disebut sebagai *immunogen*. Sedangkan *antigenicity* adalah kemampuan suatu molekul untuk bereaksi secara spesifik dengan produk-produk hasil respon imunitas yang diinduksinya (Kuby, 1992).

Bagian tertentu molekul antigen dapat menginduksi respon imunitas. Bagian antigen yang menginduksi respon imunitas dinamakan *antigenic determinat* (*epitope*) yang berikatan dengan *antigen-binding site* (situs pengikatan antigen) pada antibodi maupun reseptor limfosit. Semakin banyak *antigenic determinat* pada suatu antigen, maka respon imunitas akibat antigen tersebut akan semakin beragam (Abbas, *et al.*, 1994; Kuby, 1992)

2.5. Vaksin

Vaksin adalah bahan antigenik yang digunakan untuk menghasilkan kekebalan aktif terhadap suatu penyakit sehingga dapat mencegah atau mengurangi pengaruh infeksi oleh patogen. Vaksin dapat berupa galur virus atau bakteri yang telah dilemahkan sehingga tidak menimbulkan penyakit. Vaksin dapat juga berupa organisme mati atau hasil-hasil pemurniannya (protein/peptida/dsb.). Vaksin akan menginduksi sistem kekebalan tubuh untuk bertahan terhadap serangan patogen tertentu, terutama bakteri, virus, atau toksin.

2.6. Respon dan Sistem Imunitas

Respon imun adalah suatu aktivitas pertahanan terhadap zat asing yang masuk ke dalam tubuh. Semua mekanisme tubuh untuk mempertahankan keutuhannya, sebagai perlindungan terhadap bahaya karena zat asing masuk ke dalam tubuh disebut sistem imun. Ada dua macam sistem imun, yaitu sistem imun spesifik dan sistem imun non-spesifik.

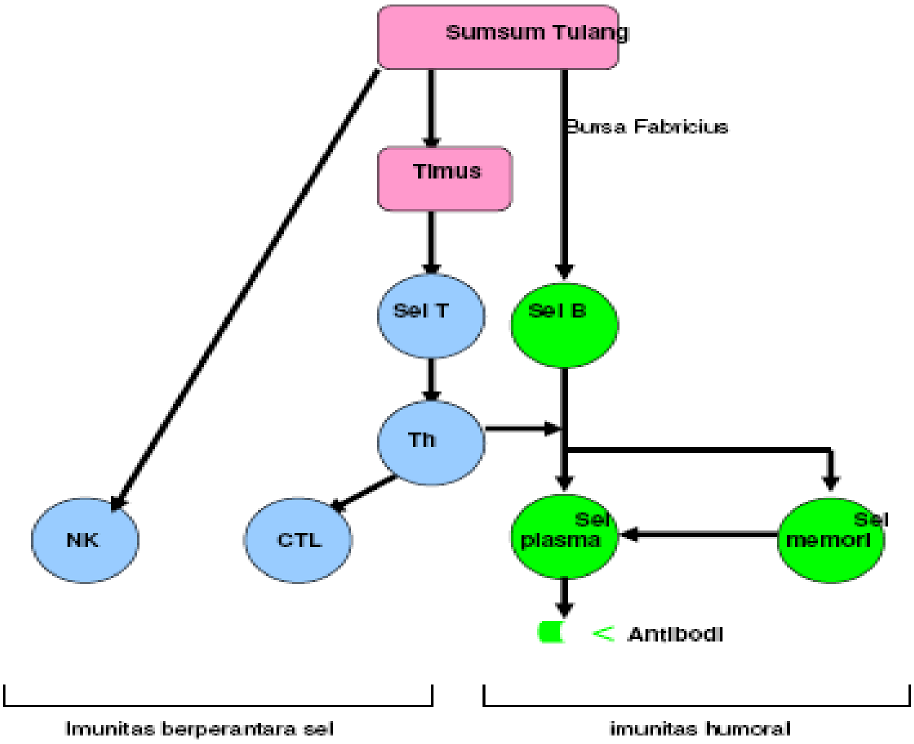
Sistem imun non-spesifik bersifat terstandarisasi untuk semua molekul asing yang memasuki tubuh, tanpa memori, dan tidak memiliki spesifisitas. Sedangkan sistem imun spesifik mengenali antigen dan memiliki memori, sehingga apabila antigen tersebut pernah menyerang tubuh sebelumnya, maka respon terhadapnya akan lebih cepat dan terarah. Sel B dan sel T berperan dalam sistem imun spesifik.

Resistensi dan pemulihan karena infeksi virus bergantung pada interaksi antara virus dan inangnya. Pertahanan inang bekerja langsung pada virus atau secara tidak langsung pada replikasi virus untuk merusak atau membunuh sel yang terinfeksi. Fungsi pertahanan non-spesifik inang pada awal infeksi untuk menghancurkan virus adalah mencegah atau mengendalikan infeksi, kemudian adanya fungsi pertahanan spesifik dari inang.

2.6.1. Komponen Sistem Imun Spesifik

Limfosit merupakan salah satu jenis sel darah putih selain fagosit yang dihasilkan di sumsum tulang belakang dan mempunyai peran penting dalam sistem imunitas. Sel B dan sel T merupakan tipe utama limfosit. Sel B terdapat pada darah perifer (10 – 20%), sumsum tulang, jaringan limfoid perifer, lien, dan tonsil, bertugas mensekresikan molekul antibodi ke seluruh cairan tubuh apabila terdapat antigen kemudian menangkapnya. Antigen yang mampu dijangkau oleh antibodi adalah antigen pada peredaran darah dan di luar sel, padahal beberapa bakteri patogen, parasit, dan virus perkembangan replikasinya berada di dalam sel sehingga tidak dapat dideteksi oleh antibodi sehingga tugas menyerang sel terinfeksi oleh virus dijalankan oleh sel T. Sel T terdapat pada darah perifer (60 – 70 %), parakortek kel limfa dan periarterioler lien.

Mekanisme kerja sistem imun ditunjukkan pada **Gambar 6.**



Gambar 6. Mekanisme secara umum sistem imun (http://www.damandiri.or.id/file/muhamadsamsiipbbab2.pdf)

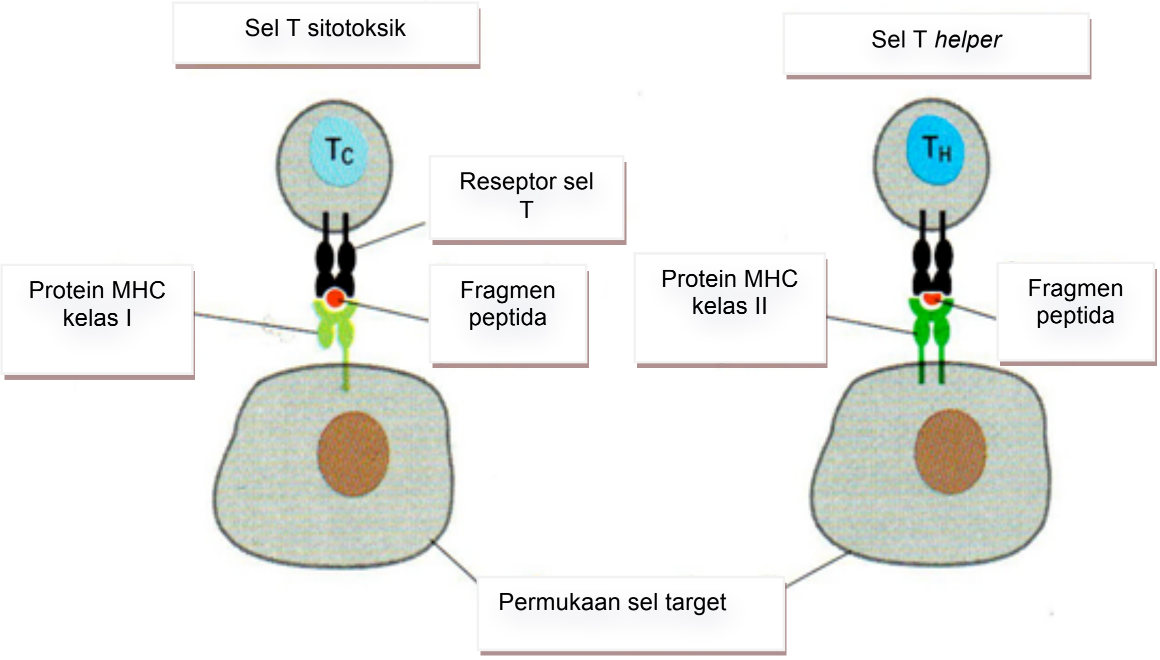
Ketika sel B menemukan antigen, maka perkembangan sel plasma akan diperbanyak. Masing-masing sel plasma akan memproduksi satu antibodi yang identik dan kemudian molekul-molekul antibodi akan menuju ke aliran darah. Suatu antigen akan berikatan dengan molekul antibodi seperti kunci dan gembok. Pada saat antigen dan antibodi saling berikatan, maka antigen tersebut telah ditandai oleh molekul antibodi untuk dilakukan perusakan.

Sel T berkontribusi dalam sistem imun dengan dua cara. Pertama, mengatur respon imun, dilakukan oleh sel T *Helper* (sel Th atau CD4) yang mengkoordinasikan respon imun dan berkomunikasi dengan sel-sel lain dengan cara melepaskan suatu sinyal yang disebut *cytokine*. Kedua, membunuh sel yang telah terinfeksi, dilakukan oleh sel *cytotoxic T lymphocyte* (CTLs) atau CD8. CTLs mampu mengenali fragmen kecil virus yang ada pada membran sel tempat virus bersembunyi, kemudian menyerang dan membunuh sel tersebut.

Sel T hanya mengenali antigen apabila antigen tersebut dibawa ke permukaan sel oleh molekul *major histocompatibility complex* (MHC) (**Gambar 7**). MHC dibagi atas dua kelas: protein MHC kelas I menampilkan fragmen antigen pada CTLs dan protein MHC kelas II menampilkan fragmen antigen pada *Th-cell*. Protein MHC kelas I berikatan dengan fragmen peptida antigen intraseluler setelah antigen diproses oleh *proteosome*, suatu kompleks protease sitoplasma, kemudian ditampilkan pada permukaan sel target atau A*ntigen Presenting Cell* (APC). Sedangkan protein MHC kelas II berikatan dengan fragmen peptida antigen ekstraseluler (Alberts, *et al.*, 2002; Tannock dan Hill, 1998).

Jajaran ketiga sel limfoid adalah *natural killer cells* (sel NK) yang tidak memiliki reseptor antigen spesifik. Sel NK merupakan bagian dari sistem imun nonspesifik. Beredar dalam darah sebagai limfosit yang memiliki kemampuan mengenal dan membunuh sel abnormal, seperti sel tumor dan sel yang terinfeksi oleh virus. Sel NK berperan penting dalam imunitas nonspesifik pada patogen intraseluler (Janeway, *et al.,* 2001).

Antigen eksogen masuk ke dalam tubuh melalui endosistosis atau fagositosis. Makrofag, sel denrit, dan sel B merombak antigen eksogen menjadi fragmen peptida melalui jalan endositosis. Sel T mengeluarkan subsetnya, yaitu CD4, untuk mengenal antigen bekerja sama dengan MHC kelas II. Antigen endogen dihasilkan oleh tubuh inang. Sebagai contoh adalah protein yang disintesis virus. Antigen endogen dirombak menjadi fraksi peptida yang selanjutnya berikatan dengan MHC kelas I pada retikulum endoplasma. Limfosit T mengeluarkan subsetnya, yaitu CD8, mengenali antigen endogen untuk berikatan dengan MHC kelas I (Tizard, *et. al.*, 2000).



Gambar 7. Pengenalan fragmen protein asing pada MHC oleh sel T (Alberts, *et al.*, 2002)

2.6.2. Antibodi

Antibodi merupakan makromolekul protein. Bertugas melawan sel-sel asing yang masuk ke tubuh manusia. Antibodi mempunyai dua fungsi, pertama untuk mengikatkan diri kepada sel-sel antigen. Fungsi kedua untuk melumpuhkan struktur biologi antigen lalu menghancurkannya. Antibodi berada dalam aliran darah dan cairan non selular.

2.7. Protein

Protein berasal dari kata *protos* dalam bahasa Yunani yang berarti “yang paling utama”. Merupakan senyawa organik kompleks berbobot molekul besar tersusun dari monomer-monomer asam amino yang dihubungkan satu sama lain dengan ikatan peptida. Molekul protein mengandung atom karbon, hidrogen, oksigen, nitrogen, terkadang mengandung sulfur dan fosfor. Protein berperan penting dalam struktur dan fungsi sel makhluk hidup.

Kebanyakan protein merupakan enzim atau subunit enzim. Protein terlibat dalam sistem kekebalan (imun) sebagai antibodi. Protein merupakan makromolekul selain polisakarida, lipida, dan polinukleotida penyusun utama makhluk hidup.

Protein tersusun oleh kombinasi asam amino melalui ikatan peptida membentuk struktur primer, sekunder, tersier, dan kuartener. Protein bisa merupakan satu rantai polipeptida maupun beberapa rantai polipeptida yang satu dengan lainnya membentuk ikatan atau interaksi tertentu. Perbedaan komposisi dan urutan asam amino penyusun mengakibatkan perbedaan sifat protein satu dengan lainnya.

Struktur primer protein merupakan polipeptida yang menunjukkan urutan asam amino penyusun serta ikatan disulfida (bila ada). Struktur sekunder menggambarkan struktur primer dan ikatan Hidrogen antar residu asam amino yang berdekatan membentuk struktur α-*heliks* dan β-*sheet* (Alberts, *et. al*., 2002). Struktur tersier protein adalah nama lain dari struktur tiga dimensi (3-D) suatu protein, terbentuk dari interaksi berbagai struktur sekunder yang berbeda dan membentuk *folding* dengan konformasi paling stabil (Baxevanis dan Ouellette, 2005).

2.8. Bioinformatika

Bioinformatika adalah aplikasi alat komputasi dan analisis untuk menginterpretasikan data-data biologi. Merupakan pengkombinasian berbagai disiplin ilmu termasuk ilmu komputer, matematika, fisika, biologi, dan ilmu kedokteran yang saling menunjang dan bermanfaat satu sama lain (Utama, 2003).

Bioinformatika berperan dalam identifikasi dan klasifikasi virus, dengan adanya *database* seperti GenBank yang didirikan oleh *National Center for Biotechnology Information* (NCBI) bersama dengan DNA *Data Bank of Japan* (DDBJ) dan *European Bioinformatics Institute* (EBI) (Baxevanis dan Oullette, 2005). *European Molecular Biology Laboratory* (EMBL) dan DDBJ berisikan data sekuen berbagai virus. *Software* untuk menganalisis kemiripan sekuen genom virus, seperti *Basic Local Alignment Search Tool* (BLAST) merupakan program penelusuran basis data sekuen untuk mencari sekuen asam nukleat maupun protein yang mirip dengan sekuen tertentu yang dimilikinya. Bioinformatika berfungsi untuk menganalisis posisi sejauh mana perbedaan suatu virus dengan virus lainnya menggunakan CLUSTALW.

Bioinformatika, khususnya pada bidang biologi molekuler, membuka sudut pandang baru dalam menyelesaikan persoalan biologi molekuler (Baxevanis dan Oullette, 2005).

2.8.1. Database

Database merupakan sekumpulan data sekuen DNA atau protein diperoleh melalui percobaan laboratorium yang disimpan dalam *file* komputer. Setiap *file* suatu sekuen berisi informasi mengenai asal organisme, nama sekuen, dan juga nomor akses yang digunakan untuk mengidentifikasi sekuen tersebut (Mount, 2004). *GenBank FlatFile Format* (GBFF) dan FASTA merupakan format umum digunakan dalam *database* bioinformatika. Tempat menyimpan serta mengelola *database* sekuen DNA suatu gen dan ekspresi asam aminonya disebut GenBank. Sekuen DNA dalam *database* diperoleh dari berbagai penelitian.

2.8.2. *Influenza Virus Resource* (IVR-NCBI)

Server Influenza Virus Resource (IVR) yang terintegrasi dalam NCBI menyimpan serta mendistribusikan data virus *influenza* dari *Influenza Genome Sequencing Project* dan *GenBank.*

NCBI didirikan oleh *U.S. National Library of Medicine* dan *National Institute of Health* sejak 1988. NCBI merupakan *database* informasi biologi molekuler khususnya terkait kesehatan manusia dan penyakit, selain analisis data *genome*, serta menyimpan dan mendistribusikan informasi biomedis.

2.8.3. Multiple Sequence Alignment

Multiple Sequence Alignment merupakan metode penjajaran lebih dari dua sekuens DNA atau asam amino menggunakan algoritma tertentu dengan bantuan komputer, sehingga didapatkan area yang memiliki urutan relatif identik satu sama lain. Metode *alignment* berfungsi mencari kemiripan, konservatifitas, dan homologi antar sekuens nukleotida atau protein didasarkan atas prinsip kesamaan struktural, fungsional, dan sekuen (Claverie dan Notredame, 2003).

2.8.4. Conserved Region

Conserved region menunjukkan sekuens yang tidak berubah selama proses evolusi, karena sekuens tersebut berperan penting dalam aktivitas biologis makhluk hidup. Walaupun demikian, tidak tertutup kemungkinan bahwa *conserved region* terbentuk dari sekuens nukleotida non-fungsional sehingga menyandikan sekuen tidak berfungsi penting pada protein (Baxevanis dan Oullette, 2005).

2.8.5. *Epitope Prediction Server*

Epitope prediction server merupakan *server* untuk memprediksi *epitope* yang terdapat pada suatu antigen dengan bantuan penggunaan metode algoritma.

Beberapa *server* untuk memprediksi epitope sel T antara lain NetChop memprediksi *proteasomal cleavage,* TAPPred memprediksi *Transporter Antigen Processing* (TAP) *binding*, dan SVMHC memprediksi *Major Histocompability Complex* (MHC) *binding*. Prediksi *epitope* sel B menggunakan *server* BepiPred menghasilkan *sequential epitope* dan Discotope menghasilkan *conformational epitope*.

2.8.6. *Protein Data Bank* (PDB)

Protein Data Bank (PDB) adalah sekumpulan file struktur makromolekul. Penentuan struktur molekul protein yang ada pada file PDB umumnya didapatkan dengan menggunakan data eksperimen kristalografi sinar-X atau spektroskopi *nuclear magnetic resonance* (NMR), kemudian dibantu dengan berbagai program komputer untuk membuat model molekul yang paling sesuai dengan data eksperimen (Baxevanis dan Ouellette, 2005; Schmidt, 2002).

2.8.7. Database Similarity Searching

Similarity searching digunakan untuk mencari kesamaan antara sekuen *unknown* dengan sekuens yang terdapat dalam *database.* Interpretasi hasil berupa suatu daftar (*hit list*) beserta berbagai nilai statistik (Baxevanis dan Oullette, 2005).

Program pertama kali yang dipakai secara luas dalam *database similarity searching* adalah FASTA. Program *Basic Local Alignment Search Tool* (BLAST) dikembangkan sesuai dengan tipe sekuen *query* dan *subject*, protein atau nukleotida. Jika tipe sekuens berbeda, sekuens 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 TBLASX dimana sekuen *query* dan *subject* merupakan nukleotida, tetapi keduanya ditranslasikan terlebih dahulu dan dibandingkan sebagai protein (Baxevanis dan Ouellette, 2005).

2.8.8. Homology Modeling

Homology modeling atau *comparative modeling* merupakan teknik untuk memprediksi struktur tiga dimensi protein berdasarkan sekuen asam aminonya. Prediksi struktur tiga dimensi suatu sekuen protein (disebut sebagai protein target) berdasarkan *alignment* terhadap satu atau lebih protein yang strukturnya telah diketahui secara eksperimen menggunakan kristalografi sinar-X dan spektroskopi *nuclear magnetic resonance* (NMR) (disebut sebagai protein *template*). Kualitas model tergantung dari tingkat kesamaan antara sekuen protein target dan sekuen protein *template*. gSemakin besar tingkat kesamaan antara sekuen protein target dan sekuen protein *template*, maka model yang dihasilkan akan semakin baik (Baxevanis dan Oullette, 2005).

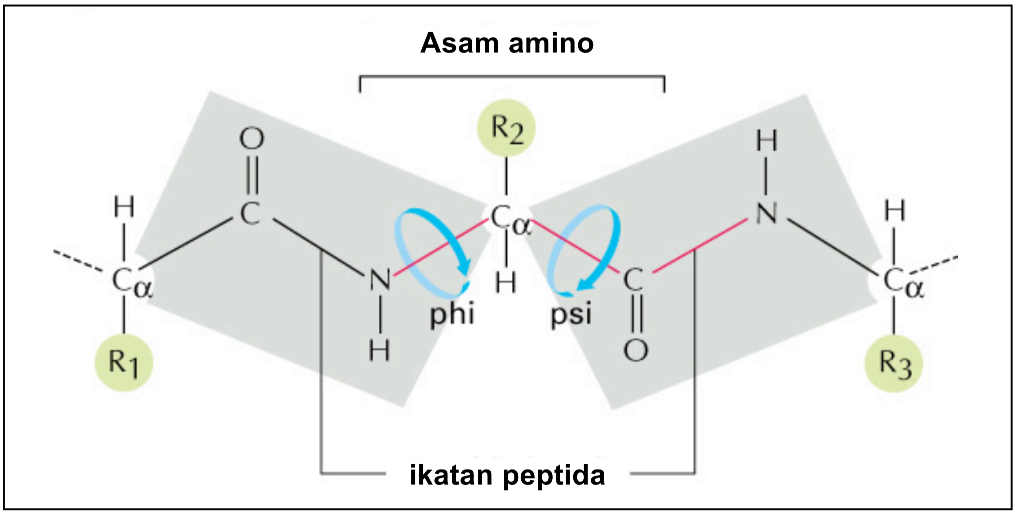
Salah satu *server* yang digunakan untuk *homology modeling* adalah SwissModel. Secara umum, pada *server* SwissModel terdapat dua metode untuk memprediksi struktur 3-D protein, yaitu *First Approach Mode* dan *Optimise Mode*.

Prediksi struktur tersier dengan *First Approach Mode* dilakukan dengan men-*submit* secara langsung sekuen protein yang akan dimodelkan (target) ke *server* SwissModel dalam format FASTA. *Homology modeling* dengan *First Approach mode* akan melakukan *alignment* otomatis terhadap sekuen *template* dan sekuen target.

Prediksi struktur tersier dengan *Optimise Mode* dilakukan dengan bantuan *software DeepView/Swiss-PdbViewer*. Struktur protein yang akan dimodel tidak dimasukkan melalui *web interface* namun dimasukkan sebagai *modeling-project* dari *software DeepView/SwissPdbViewer*. *Optimise mode* memberi kesempatan untuk memperbaiki *alignment* terlebih dahulu sebelum dimasukkan ke *server* SwissModel. Pengguna *server* dapat melakukan koreksi hasil pemodelan sekuen dari *software DeepView/Swiss-PdbViewer* untuk kemudian dioptimasi menggunakan *Optimise Mode*.

2.8.9. *Ramachandran Plot*

Ramachandran plot merupakan *plot* untuk memvisualisasikan koordinat tiga dimensi protein yang telah berhasil ditentukan secara eksperimen ke dalam koordinat internal. Koordinat internal terdiri dari sudut *Φ* (*phi*) sebagai sumbu x dan sudut *Ψ* (*psi*) sebagai sumbu y (Baxevanis dan Ouellette, 2005).



Gambar 8. Sudut ϕ (*phi*) dan sudut ψ (*psi*) pada dimensi dipeptida (Baxevanis dan Ouellette, 2005)

Sudut *Φ* merupakan sudut dihedral sepanjang ikatan N-C*α*, sedangkan sudut *Ψ* merupakan sudut dihedral sepanjang ikatan C*α*-C (**Gambar 8**). Setiap residu pada protein mempunyai satu sudut *Φ* dan sudut *Ψ*, sehingga setiap residu dapat digambarkan sebagai satu *plot. Plot-plot* yang menggambarkan residu pada suatu struktur protein disebut *Ramachandran plot* (Baxevanis dan Ouellette, 2005).

Cluster Ramachandran plot terbentuk dari beberapa residu menunjukkan bentuk struktur sekunder. Melalui *Ramachandran plot* dapat diketahui suatu struktur protein mempunyai kualitas baik atau tidak dengan cara melihat adanya plot residu non glisin yang terletak pada wilayah sudut dihedral terlarang (*disallowed region*). Struktur protein dengan plot residu non glisin pada *disallowed region* >15% memiliki kualitas yang buruk (Baxevanis dan Ouellette, 2005).

2.8.10. Molecular Docking

Molecular docking adalah metode yang didesain dan digunakan untuk memprediksi interaksi ikatan diantara keduanya selama pembentukan molekular kompleks protein secara tiga dimensi (3D). Kebanyakan algoritma *docking* menggunakan dua pendekatan. Pendekatan pertama adalah pencarian konformasi ruang antara ligan dan reseptor. Transformasi bentuk rigid ligan dan reseptor diperlihatkan pada saat simulasi *docking*. Pendekatan kedua adalah penghitungan nilai energi terendah ikatan yang terbentuk antara ligan dan reseptor. Penghitungan energi ini menggunakan beberapa kriteria termasuk geometri ruang dan pengukuran sifat fisiko kimia seperti ikatan hidrogen dan energi bebas. Penggunaan informasi biologi dan biokimia memegang peranan penting untuk menentukan model ikatan yang tepat terhadap protein target (Ting-Che Lu, 2005).

BAB III

METODOLOGI PENELITIAN

Penelitian dilakukan secara *in silico* selama satu tahun, sejak bulan Juni 2008 sampai bulan Juni 2009. *Database* merupakan sumber data penelitian. Alamat situs *database* diakses secara bebas menggunakan seperangkat komputer terhubung internet. Sistem operasi yang digunakan adalah *Microsoft Windows XP Professional* dengan *browser Mozilla FireFox* versi 3.1 beta 1. Bagan kerja ditunjukkan pada **Lampiran 1.**

3.1. Pencarian Sekuen Protein HA, NA, dan M2 Virus H1N1

Pencarian data sekuen protein *hemagglutinin* (HA), *neuraminidase* (NA), dan matrik 2 (M2) virus H1N1 pada inang manusia dan babi dilakukan melalui *server GenBank Influenza Virus Resource* (IVR-NCBI). *Homepage server* IVR-NCBI dapat diakses pada alamat situs: http://ncbi.nlm.nih.gov/genomes/FLU/Database.html. Format sekuen yang dipakai untuk menyimpan sekuen protein HA, NA, dan M2 adalah format FASTA karena format tersebut paling banyak digunakan untuk analisis pada *software-software* selanjutnya dibandingkan format GBFF. Sekuen protein terdiri dari urutan huruf-huruf, setiap huruf merupakan kode dari suatu asam amino (**Lampiran 2**).

3.2. *Multiple Sequence Alignments*

Sekuen protein HA, NA, dan M2 virus H1N1 inang manusia dan babi dalam format FASTA dimasukkan sebagai *input* ke dalam *server* ClustalW2 yang tampilan *homepage server* tersebut dapat diakses secara *on line* pada situs: http://www.ebi.ac.uk/Tools/clustalw2/. Melalui *server* tersebut dilakukan penyejajaran terhadap setiap protein HA, NA, dan M2 virus H1N1. Kemudian ditentukan perwakilan sekuen protein HA, NA, dan M2 berdasarkan skor tertinggi untuk digunakan sebagai input analisis selanjutnya.

3.3. Prediksi *Proteosomal Cleavage* Protein HA, NA, dan M2 Virus H1N1

Proteosomal cleavage diprediksi dengan menggunakan *server* NetChop yang dapat diakses bebas melalui internet dengan alamat situs *homepage* http://www.cbs.dtu.dk/services/NetChop/ . *Server* NetChop membutuhkan *input* data berupa sekuen protein untuk dapat memprediksi *proteosomal cleavage* protein HA, NA, dan M2 virus H1N1 inang manusia dan babi. Hasil prediksi *proteosomal cleavage* oleh NetChop adalah berupa sekuen peptida serta skor prediksi *cleavage* tiap sekuen peptida.

3.4. Prediksi TAP *Binding* Protein HA, NA dan M2 Virus H1N1

TAP *(Transporter Antigen Processing) binding* diprediksi dengan menggunakan *server* TAPPred yang dapat diakses bebas melalui internet dengan alamat situs *homepage* http://bioinformatics.coms.edu/mirror/tappred/. Hasil prediksi TAP *binding* oleh *server* TAPPred adalah berupa sekuen peptida beserta posisinya serta skor prediksi afinitas *binding* untuk tiap sekuen peptida.

3.5. Prediksi *Epitope* sel T Protein HA, NA, dan M2 Virus H1N1

Prediksi e*pitope* sel T protein HA, NA, dan M2 virus H1N1 inang manusia dan babi didasarkan atas skor *binding* terbesar. Hasil prediksi terdiri atas dua kelas MHC, yaitu MHC Kelas I dan MHC Kelas II. Seleksi kandidat peptida penyusun vaksin dilakukan dari hasil prediksi *epitope* sel T protein HA, NA, dan M2 virus H1N1. SVMHC memprediksi *epitope* sel T dengan data *input* sekuen asam amino protein HA, NA, dan M2 dalam format FASTA. *Epitope* MHC kelas I dan MHC kelas II diprediksi melalui *server* SVMHC dengan alamat situs *homepage* http://www-bs.informatik.uni-tuebingen.de/SVMHC/

3.6. Prediksi *Epitope* sel B Protein HA, NA, dan M2 Virus H1N1

Prediksi *epitope* sel B protein HA, NA, dan M2 virus H1N1 inang manusia dan babi dilakukan melalui *server* BepiPred melalui situs *homepage* http://tools.immuneepitope.org/tools/bcell/iedb input dan *server* DiscoTope melalui situs *homepage* http://tools.immuneepitope.org/stools/discotope/discotope.do

3.7. Penentuan Sekuen Vaksin

Penentuan sekuen vaksin hasil prediksi sel T didasarkan dari skor peptida-peptida hasil prediksi *server* SVMHC, NetChop, dan TAPPred. Sekuen vaksin yang dirancang berupa sekuen peptida dalam format FASTA.

Penentuan sekuen vaksin dilakukan melalui kombinasi peptida atas dasar hasil prediksi *epitope* sel B dan sel T. *Epitope* yang digunakan untuk kombinasi adalah *epitope* sel T (MHC-I dan MHC-II) dan *epitope* sel B adalah yang mempunyai skor *binding* paling tinggi (*high-binder*).

3.8. Homology Modeling

3.8.1. Pencarian *Template*

Pencarian *template* dilakukan melalui *server CPHModels* yang terkoneksi secara langsung dengan *database* PDB melalui koneksi internet. *Homepage server CPHModels* dapat diakses pada situs http://www.cbs.dtu.dk/services/CPHmodels/. Pencarian *template* dilakukan untuk protein HA, NA, dan M2 virus H1N1.

3.8.2. *Modeling* Struktur Tersier Vaksin

Modeling struktur tersier vaksin berdasarkan *template* dilakukan melalui program *Swiss-PdbViewer/DeepView.* Residu-residu penyusun struktur dapat dilihat melalui menu *Control Panel.* Pelekatan struktur vaksin pada *template* dilakukan melalui menu *Magic Fit*. Residu-residu yang melekat dapat dilihat melalui menu *alignment.*

Visualisasi struktur tersier vaksin hasil pelekatan dilakukan dengan memindahkan struktur tersier *template*, sehingga terlihat struktur tersier vaksin.

Perbaikan struktur tersier vaksin dilakukan dua tahap. Tahap pertama adalah perbaikan struktur vaksin pada *viewer DeepView* dengan memperbaiki residu-residu yang saling tumpang tindih. Sedangkan tahap kedua adalah melalui *server Swiss-Model* dengan cara mengirim struktur masing-masing vaksin yang telah diperbaki pada *DeepView* ke *server*

Swiss-Model dalam bentuk PDB untuk dilakukan pengoptimasian struktur, yaitu dengan cara memilih menu *Optimise Mode* pada *server Swiss-Model*.

3.8.3. Evaluasi Struktur Tersier Vaksin

Evaluasi struktur tersier vaksin dilakukan dengan melihat residu yang saling tumpang tindih dan menganalisis *Ramachandran Plot* struktur vaksin melalui menu *Ramachandran Plot* pada program*DeepView*.

3.8.4. Pembandingan Struktur Tersier Vaksin dengan *Database*

Pembandingan struktur tersier masing-masing vaksin dengan *database* protein dalam bentuk PDB dilakukan melalui *FeatureMap3*D pada situs *Center for Biological Sequence Analysis* (CBS). Alamat situs *homepage* dapat diakses di http://cbs.dtu.dk/services/FeatureMap3D.

3.8.5. Validasi Vaksin dengan *Database*

Validasi sekuen vaksin dengan *database* menggunakan BLASTp terhadap *database* protein *human* dan data PDB virus influenza A. Alamat situs homepage dapat diakses di

http://blast.ncbi.nlm.nih.gov/Blast.cgi.

3.9. *Molecular Docking*

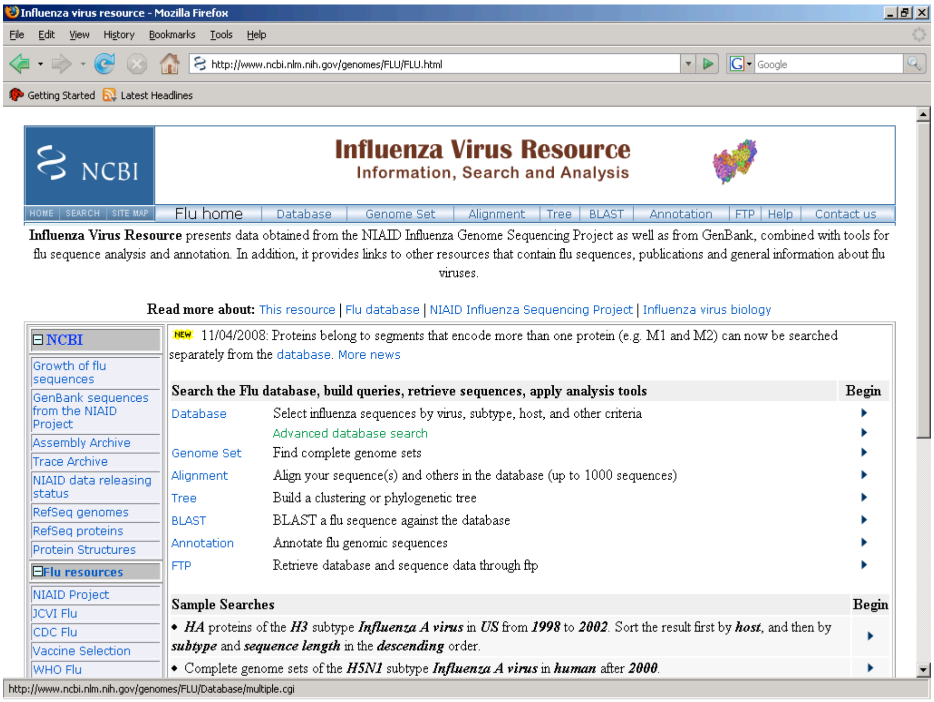
Prediksi molekular docking antara antigen (ligan) dengan antibodi pada manusia (reseptor) dilakukan menggunakan *software* Arguslab 4.0.1. Sebelum memulai docking, diunduh terlebih dahulu *file* PDB yang memiliki kesamaan dengan sekuen vaksin. diunduh juga *file* PDB yang berisikan *database* antibodi virus H1N1.

BAB IV

HASIL DAN PEMBAHASAN

4.1. Pencarian Sekuen Protein HA, NA, dan M2 Virus H1N1

Sekuen protein virus H1N1 yang dicari adalah sekuen protein *hemagglutinin* (HA), *neuraminidase* (NA), dan matrik 2 (M2). Protein HA dan NA merupakan komponen spesifik *antigenic* untuk menginduksi respon sistem imun terhadap subtipe H1N1, sedangkan protein M2 merupakan komponen *conserved antigenic* untuk menginduksi respon sistem imun terhadap *virus influenza* tipe A. Pencarian sekuen protein HA, NA, dan M2 dilakukan melalui *server GenBank Influenza Virus Resource* (IVR-NCBI) dengan alamat situs *homepage* http://ncbi.nlm.nih.gov/genomes/FLU/Database.html (**Gambar 8**) yang dapat diakses bebas melalui koneksi internet. *Database* dalam *GenBank* merupakan data yang lengkap karena tidak hanya memuat sekuen dan keterangan-keterangan mengenai protein, namun juga memuat sekuen *nucleotide* dari protein tersebut. Agar lebih memudahkan penggunaannya dalam *software* maupun *server* dalam penelitian, semua sekuen protein diubah ke dalam format FASTA (**Lampiran 3**).



Influenza Virus Resource presents data obtained from the NIAID Influenza Genome Sequencing Project as well as from GenBank, combined with tools for flu sequence analysis and annotation. In addition, it provides links to other resources that contain flu sequences, publications and general information about flu viruses.

Read more about: This resource | Flu database | NIAID Influenza Sequencing Project | Influenza virus biology

NEW 11/04/2008: Proteins belong to segments that encode more than one protein (e.g. M1 and M2) can now be searched separately from the database. More news

Search the Flu database, build queries, retrieve sequences, apply analysis tools		**Begin**
Database	Select influenza sequences by virus, subtype, host, and other criteria	▶
	Advanced database search	▶
Genome Set	Find complete genome sets	▶
Alignment	Align your sequence(s) and others in the database (up to 1000 sequences)	▶
Tree	Build a clustering or phylogenetic tree	▶
BLAST	BLAST a flu sequence against the database	▶
Annotation	Annotate flu genomic sequences	▶
FTP	Retrieve database and sequence data through ftp	▶

Sample Searches	**Begin**
• ***HA*** proteins of the ***H3*** subtype ***Influenza A virus*** in ***US*** from ***1998*** to ***2002***. Sort the result first by ***host***, and then by ***subtype*** and ***sequence length*** in the ***descending*** order.	▶
• Complete genome sets of the ***H5N1*** subtype ***Influenza A virus*** in ***human*** after ***2000***.	▶

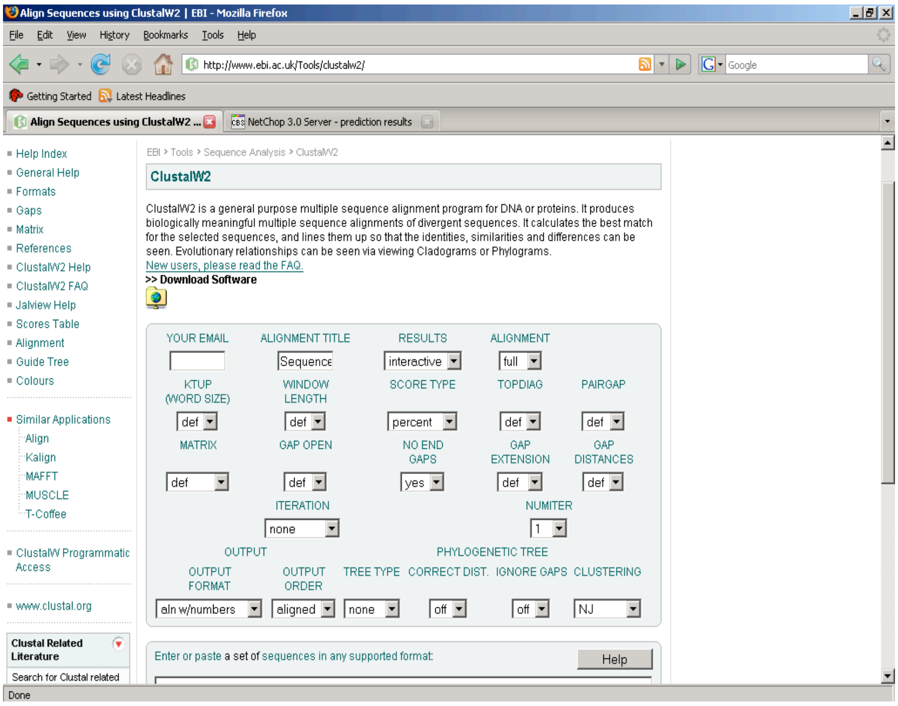
Gambar 8. Tampilan *Homepage* dari *Server GenBank Influenza Virus Resource* (IVR-NCBI) (http://ncbi.nlm.nih.gov/genomes/FLU/Database.html)

Sekuen protein yang diperoleh melalui *server GenBank Influenza Virus Resource* (IVR-NCBI) terlalu banyak, sehingga dilakukan seleksi dan pengelompokkan data. Seleksi dilakukan melalui pengurangan sekuens identik dan menggunakan sekuens *full-length*. Sedangkan pengelompokkan data dilakukan untuk memudahkan *multiple alignment*. Setelah dilakukan seleksi dan pengelompokkan data didapat hasil berikut:

- HA inang manusia : 36 sekuens (dari 753 sekuens)
- HA inang babi : 21sekuens (dari 170 sekuens)
- NA inang manusia : 30 sekuens (dari 713 sekuens)
- NA inang babi : 17 sekuens (dari 155 sekuens)
- M2 inang manusia : 20 sekuens (dari 182 sekuens)
- M2 inang babi : 11 sekuens (dari 87 sekuens)

4.2. *Multiple Sequence Alignments*

Data yang telah diseleksi dan dikelompokkan dimasukkan sebagai input *multiple alignment*. Tujuan *alignment* untuk melihat perbedaan sekuen protein dan untuk menentukan satu perwakilan protein HA, NA, dan M2 virus H1N1 pada inang manusia dan babi. *Server* yang digunakan untuk *multiple alignments* adalah ClustalW2. *Server* dapat diakses secara *on line* pada situs *homepage* http://wwwebi.ac.uk/Tools/clustalw2 (**Gambar 9**).



ClustalW2 is a general purpose multiple sequence alignment program for DNA or proteins. It produces biologically meaningful multiple sequence alignments of divergent sequences. It calculates the best match for the selected sequences, and lines them up so that the identities, similarities and differences can be seen. Evolutionary relationships can be seen via viewing Cladograms or Phylograms.

YOUR EMAIL:
ALIGNMENT TITLE: Sequence
RESULTS: interactive
ALIGNMENT: full
KTUP (WORD SIZE): def
WINDOW LENGTH: def
SCORE TYPE: percent
TOPDIAG: def
PAIRGAP: def
MATRIX: def
GAP OPEN: def
NO END GAPS: yes
GAP EXTENSION: def
GAP DISTANCES: def
ITERATION: none
NUMITER: 1
OUTPUT
OUTPUT FORMAT: aln w/numbers
OUTPUT ORDER: aligned
PHYLOGENETIC TREE
TREE TYPE: none
CORRECT DIST.: off
IGNORE GAPS: off
CLUSTERING: NJ

Enter or paste a set of sequences in any supported format:

Gambar 9. Tampilan *Homepage* dari *Server* Clustalw2 (http://wwwebi.ac.uk/Tools/clustalw2)

Data hasil analisis *multiple alignments* ditunjukkan dalam **Lampiran 4.** *Display* hasil *multiple alignments* pada ClustalW2 terdiri atas kode (*), (:), dan (.) (**Tabel 1**). Tanda (*) menandakan *conserve column* atau kesamaan asam amino pada satu kolom, tanda (:) menandakan bahwa ada kemiripan ukuran dan kesamaan kelarutan dalam air (hidrofilik atau hidrofobik) pada satu kolom, dan tanda (.) menandakan bahwa kemiripan ukuran sifat kelarutan dalam air telah dipertahankan dalam proses evolusi.

Tabel 1. Hasil perhitungan *conserve column* (*) pada hasil *multiple alignments*

Sekuen Protein	**Keterangan**
HA inang manusia	Rerata 391 (*) dalam 575aa: 34 (*) tiap 50aa
HA inang babi	Rerata 337 (*) dalam 579aa: 29 (*) tiap 50aa
NA inang manusia	Rerata 385 (*) dalam 470aa: 35 (*) tiap 50aa
NA inang babi	Rerata 302 (*) dalam 479aa: 32 (*) tiap 50aa
M2 inang manusia	Rerata 68 (*) dalam 98aa: 35 (*) tiap 50aa
M2 inang babi	Rerata 64 (*) dalam 97aa: 33 (*) tiap 50aa

Berdasarkan data di atas terlihat bahwa perbedaan antara sekuen protein virus H1N1 kurang signifikan karena didapat *conserve column* yang jumlahnya lebih besar dari 5 pada tiap 50 asam amino untuk semua protein (Baxevanis dan Oullette, 2001).

Berdasarkan hasil terdapat *range* skor yang cukup jauh, yaitu antara 78 sampai dengan 100. Data tersebut sangat dimungkinkan, sekuen dalam penelitian merupakan perwakilan tahun 1918 sampai dengan 2009 berasal dari lima benua di dunia, yaitu Afrika, Asia, Eropa, Australia, dan Amerika. Sekuen protein HA, NA, dan M2 Virus H1N1 inang manusia dan babi digunakan untuk prediksi *epitope* diperoleh berdasarkan skor tertinggi. *Header* Sekuen protein HA, NA, dan M2 dalam format FASTA digunakan sebagai input untuk prediksi *epitope* ditunjukkan pada **Tabel 2**.

Tabel 2. *Header* Sekuen Protein HA, NA, dan M2 virus H1N1

Protein	Header Sekuen (Format FASTA)
HA inang manusia	>gi|238695727|gb|ACR55004.1| hemagglutinin [Influenza A virus (A/Beijing/3/2009(H1N1))]
HA inang babi	>gi|4585155|gb|AAD25301.1|AF091306_1 hemagglutinin precursor [influenza A virus (A/swine/Hokkaido/2/81 (H1N1))]
NA inang manusia	>gi|237689850|gb|ACR15757.1| neuraminidase [Influenza A virus (A/Israel/644/2009(H1N1))]
NA inang babi	>gi|190403800|gb|ACE77987.1| neuraminidase [Influenza A virus (A/swine/Korea/CAN01/2004(H1N1))]
M2 inang manusia	>gi|229783371|gb|ACQ84453.1| matrix protein 2 [Influenza A virus (A/Korea/01/2009(H1N1))]
M2 inang babi	>gi|216409292|dbj|BAH02073.1| matrix protein 2 [Influenza A virus (A/swine/Chonburi/NIAH589/2005(H1N1))]

Sekuen protein dipilih dari skor ClustalW2 tertinggi dan memiliki *polybasic amino acid region,* yaitu mengandung 5 Arginin dan 2 Lisin (PQRERRRKKRGLF) sebagai indikator termasuk virus *highly pathogenic* (Nidom, 2005).

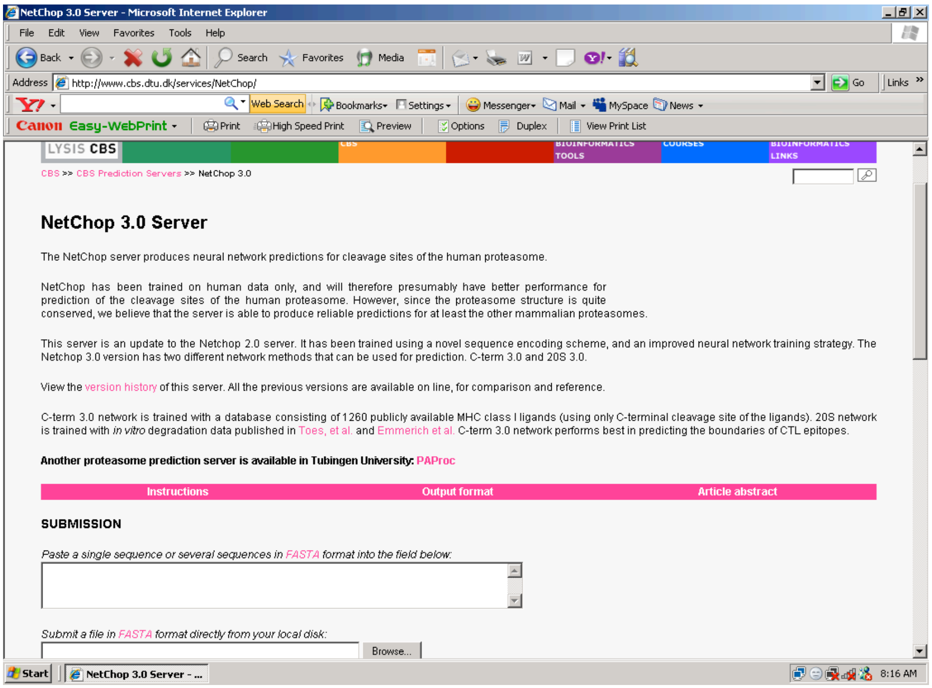
4.3. Prediksi *Epitope* sel T Protein HA, NA, dan M2 Virus H1N1

Beberapa *server* prediksi *epitope proteasomal cleavage* diantaranya PAProC, MAPPP, dan NetChop (Kesmir *et. al.,* 2002). *Server* NetChop merupakan metode *neural network-based* didasarkan pada ligan MHC kelas I dihasilkan oleh *proteosomal* manusia. Penggunaan *server proteasomal cleavage* mendekati proses *in vivo* direpresentasikan melalui *in silico*. Pemilihan *server* NetChop didasarkan pada prediksi *epitope* lebih akurat dan tampilan *output* data lebih informatif (Saxova, *et. al.,* 2003).

Data output *server* MAPPP berupa barisan-barisan peptida dengan panjang menyamping mengakibatkan pembacaan data kurang efisien. Sedangkan *server* PaProc menghasilkan data output berupa tabel yang berisikan peptida hasil pemotongan oleh server.

Prediksi *epitope proteasomal cleavage* juga dapat dilakukan menggunakan program *Bayesian Sequence Learning* merupakan teknik prediksi posisi pemotongan sekuen protein oleh *proteasomal* manusia (Mayo, 2006).

Prediksi *epitope* dalam penelitian dilakukan melalui *server* NetChop 3.0 (**Gambar 10**).



CBS >> CBS Prediction Servers >> NetChop 3.0

NetChop 3.0 Server

The NetChop server produces neural network predictions for cleavage sites of the human proteasome.

NetChop has been trained on human data only, and will therefore presumably have better performance for prediction of the cleavage sites of the human proteasome. However, since the proteasome structure is quite conserved, we believe that the server is able to produce reliable predictions for at least the other mammalian proteasomes.

This server is an update to the Netchop 2.0 server. It has been trained using a novel sequence encoding scheme, and an improved neural network training strategy. The Netchop 3.0 version has two different network methods that can be used for prediction. C-term 3.0 and 20S 3.0.

View the version history of this server. All the previous versions are available on line, for comparison and reference.

C-term 3.0 network is trained with a database consisting of 1260 publicly available MHC class I ligands (using only C-terminal cleavage site of the ligands). 20S network is trained with *in vitro* degradation data published in Toes, et al. and Emmerich et al. C-term 3.0 network performs best in predicting the boundaries of CTL epitopes.

Another proteasome prediction server is available in Tubingen University: PAProc

Instructions Output format Article abstract

SUBMISSION

Paste a single sequence or several sequences in FASTA format into the field below:

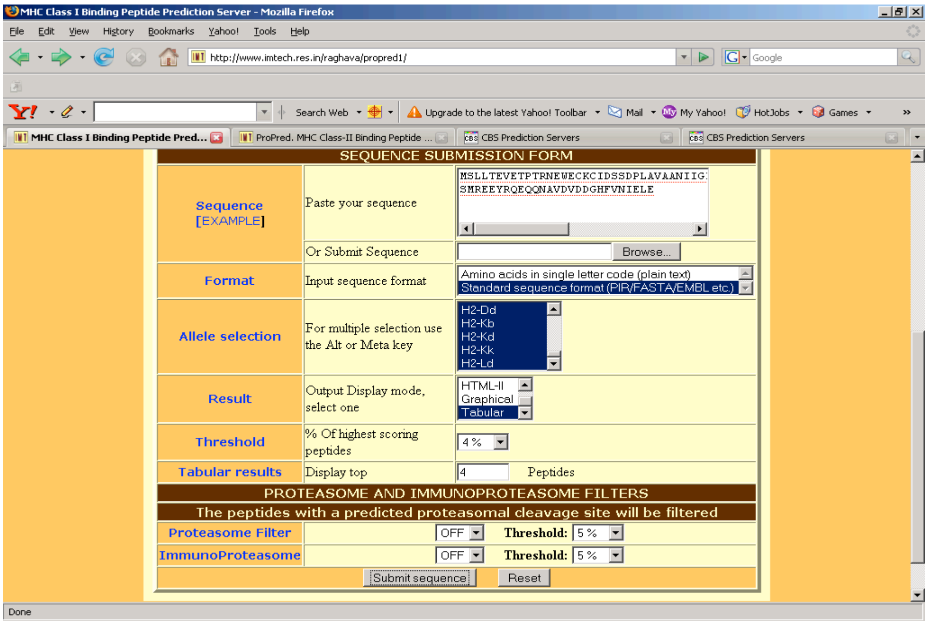
Submit a file in FASTA format directly from your local disk:

Browse...

Gambar 10. Tampilan *Homepage* dari *Server* NetChop 3.0 (http://www.cbs.dtu.dk/services/NetChop/)

Server NetChop memprediksi *epitope proteasomal cleavage* pada sel T dengan data *input* sekuen asam amino protein HA , NA, dan M2 virus H1N1 inang manusia dan babi dalam format FASTA. Data Output berupa sekuen protein yang ditandai sisi pemotongannya dengan huruf "S" (*cleavage site*). Hasil prediksi ditunjukkan dalam **Lampiran 5**.

Dilanjutkan dengan prediksi skor TAP (*Transporter Antigen Processing) binding* sekuen protein HA, NA, dan M2 dengan menggunakan *server* TapPred (**Gambar 11**). Data hasil prediksi ditunjukkan dalam **Lampiran 6**.



SEQUENCE SUBMISSION FORM

Sequence [EXAMPLE]	Paste your sequence	MSLLTEVETPTRNEWECKCIDSSDPLAVAANIIG: SMREEYRQEQQNAVDVDDGHFVNIELE
	Or Submit Sequence	
Format	Input sequence format	Amino acids in single letter code (plain text) Standard sequence format (PIR/FASTA/EMBL etc.)
Allele selection	For multiple selection use the Alt or Meta key	H2-Dd H2-Kb H2-Kd H2-Kk H2-Ld
Result	Output Display mode, select one	HTML-II Graphical Tabular
Threshold	% Of highest scoring peptides	4 %
Tabular results	Display top	4 Peptides

PROTEASOME AND IMMUNOPROTEASOME FILTERS

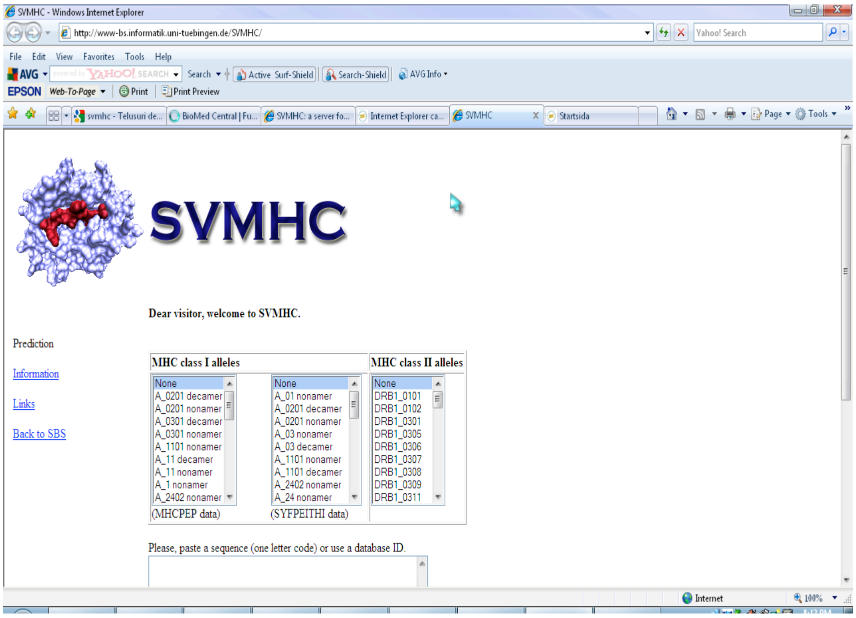
The peptides with a predicted proteasomal cleavage site will be filtered

Proteasome Filter	OFF	Threshold: 5 %
ImmunoProteasome	OFF	Threshold: 5 %

Gambar 11. Tampilan *Homepage* dari *Server* TapPred (http://bioinformatics.coms.edu/mirror/tappred/)

Analisis dan prediksi TAP binding peptida menggunakan metode *Support Vector Machine* (SVM) (Bhasin dan Raghava, 2003). SVM dikembangkan oleh Boser, *et. al* pertama kali dipresentasikan tahun 1992 dalam *Annual Workshop on Computational Learning Theory*, konsep dasar SVM merupakan kombinasi harmonis dari teori komputasi yang telah ada puluhan tahun sebelumnya (*dalam* Byun dan Lee, 2003). Berbagai metode dikenal sebelumnya seperti *linear discrimination analysis*, *hidden markov model* (HMM) hingga metode kecerdasan buatan seperti *artificial neural network* (ANN) (Lara, *et. al*., 2008) prediksi affinitas binding melalui TAP merupakan langkah yang efisien untuk memprediksi *epitope* suatu protein (Peters, *et al.,* 2003).

Epitope MHC kelas I dan II diprediksi melalui *server* SVMHC (**Gambar 12**). Data hasil prediksi ditunjukkan dalam **Lampiran 7**. Beberapa *server* prediksi *epitope* MHC antara lain MULTIPRED, HLAPred, ProPred I, dan ProPred II (Lin *et al.,* 2008). *Server* SVMHC digunakan berdasarkan metode SVM (Dönnes dan Elofsson, 2002). Server tersebut memprediksi *epitope* MHC kelas I dan kelas II dengan cepat dan memberikan tampilan output yang komprehensif (Dönnes dan Elofsson, 2006).



Dear visitor, welcome to SVMHC.

Please, paste a sequence (one letter code) or use a database ID.

Gambar 12. Tampilan *Homepage* dari *Server* SVMHC (http://www-bs.informatik.uni-tuebingen.de/SVMHC/)

Hasil prediksi e*pitope* sel T protein HA, NA, dan M2 virus H1N1 ditampilkan berupa sekuen peptida dengan skor *binding* yang berbeda-beda (**Lampiran 5-7**). Berdasarkan hasil prediksi, dipilih peptida-peptida yang akan digunakan sebagai kandidat *epitope* penyusun pada vaksin, yang didasarkan atas skor *binding* terbesar. Seleksi *epitope* diperoleh dari perbandingan prediksi *proteasomal cleavage*, *TAP binding,* dan MHC kelas I. Data tersebut ditunjukkan pada **Tabel 3 – 8**.

Tabel 3. *Epitope* sel T Protein HA inang manusia

NetChop	**TAPPred**	**SVMHC**
VHDCNTT	VHDCNTTCQ	VHDCNTTCQ
SIQSRGLFGAIAGF	SIQSRGLFG	SIQSRGLFG
KVDDGFLDI	KKVDDGFLD	KKVDDGFLD
LNREEIDGVKL	DGVKLESTR	IDGVKLEST
LQCRICI	GSLQCRICI	GSLQCRICI

Tabel 4. *Epitope* sel T Protein HA inang babi

NetChop	**TAPPred**	**SVMHC**
SDAPVHDCNTT	VHDCNTTCQ	VHDCNTTCQ
IQSRGLF	SIQSRGLFG	SIQSRGLFG
KVDDGFLDV	KKVDDGFLD	KKVDDGFLD
IDGVKLES	DGVKLESTR	IDGVKLEST
SLQCRICI	GSLQCRICI	GSLQCRICI

Tabel 5. *Epitope* sel T Protein NA inang manusia

NetChop	**TAPPred**	**SVMHC**
LTQGALL	LTQGALLND	FLTQGALLN
LNDKHSNGTV	ALLNDKHSN	ALLNDKHSN
LCPVSGWA	SLCPVSGWA	SLCPVSGWA
YNSRFESVA	SPYNSRFES	PYNSRFESV
ISGPDNGAVAV	GISGPDNGA	GISGPDNGA

Tabel 6. *Epitope* sel T Protein NA inang babi

NetChop	TAPPred	SVMHC
LTQGALL	LTQGALLND	FLTQGALLN
LNDKHSNGTV	ALLNDKHSN	ALLNDKHSN
LCPVSGWA	SLCPVSGWA	SLCPVSGWA
YNSRFESVA	SPYNSRFES	PYNSRFESV
ISGPDNGAVAV	GISGPDNGA	GISGPDNGA

Tabel 7. *Epitope* sel T Protein M2 inang manusia

NetChop	TAPPred	SVMHC
RRFKYGLK	RRFKYGLKR	YRRFKYGLK
RLFFKCIY	LFFKCIYRR	DRLFFKCIY

Tabel 8. *Epitope* sel T Protein M2 inang babi

NetChop	TAPPred	SVMHC
RRFKYGLK	RFKYGLKRG	FKYGLKRGP
RLFFKCIY	LDRLFFKCI	ILDRLFFKC

Ketika protein virus masuk ke dalam sel target, maka *epitope* pada protein tersebut akan dipecah menjadi fragmen peptida oleh protease, dan kemudian akan berikatan dengan MHCkelas II yang akan membawa *fragmen* peptida tersebut ke permukaan sel agar dapat dikenali oleh *reseptor* pada sel T yang kemudian akan mengaktifkan sistem imunitas sehingga akan menghasilkan respon imunitas. Usaha menghasilkan respon imunitas yang maksimal dengan memprediksi *epitope* MHC kelas II melalui *server* SVMHC (**Lampiran 7**). Data hasil seleksi prediksi *epitope* MHC kelas II ditunjukkan pada **Tabel 9 dan 10**.

Tabel 9. *Epitope* MHC kelas II Protein virus H1N1 inang manusia

Protein HA	**Protein NA**	**Protein M2**
KNVTVTHSV	FFLTQGALL	IIGILHLIL
YYWTLVEPG	YICSGIFGD	ITDRLFFKC
ISDTPVHDC	FSFKYGNGV	DDGHFVNIE

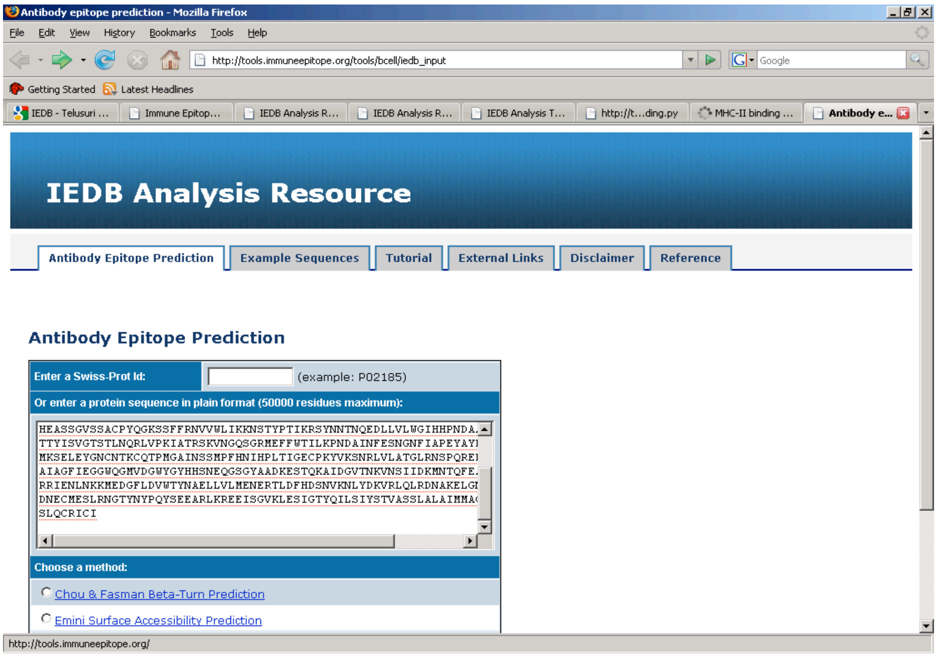
Tabel 10. *Epitope* MHC kelas II Protein virus H1N1 inang babi

Protein HA	**Protein NA**	**Protein M2**
YSDSSDPLV	FFLTQGALL	IIGILHLIL
SLLTEVETL	YICSGIFGD	ITDRLFFKC
GILHLILWI	FSFKYGNGV	DDGHFVNIE

Server SVMHC memprediksi *epitope* dengan panjang sembilan asam amino, analisisnya dilakukan setiap 30 asam amino protein HA, NA, dan M2 virus H1N1 inang manusia dan babi mulai dari asam amino posisi pertama hingga terakhir. Prediksi didasarkan atas kemampuan *epitope* untuk berikatan dengan tiap tipe molekul MHC, direpresentasikan dengan skor *binding* dengan kisaran nilai yang berbeda untuk masing-masing *allele*. Peptida dengan skor lebih besar dari *cut off (setting treshold)* digolongkan sebagai *binder* (*High binder, Moderate binder*, *Low binder*), sedangkan penelitian hanya memprediksi *High binder* peptida.

4.4. Prediksi *Epitope* Sel B Protein HA, NA, M2 Virus H1N1

Prediksi *epitope* sel B protein HA, NA, dan M2 virus H1N1 menggunakan *server* BepiPred terdapat dalam *homepage Immune Epitope Database Analysis Resource* (IEDB-AR) (**Gambar 13**).



Antibody Epitope Prediction

Enter a Swiss-Prot Id: (example: P02185)

Or enter a protein sequence in plain format (50000 residues maximum):

```
HEASSGVSSACPYQGKSSFFRNVVWLIKKNSTYPTIKRSYNNTNQEDLLVLWGIHHPNDA
TTYISVGTSTLNQRLVPKIATRSKVNGQSGRMEFFWTILKPNDAINFESNGNFIAPEYAY
MKSELEYGNCNTKCQTPMGAINSSMPFHNIHPLTIGECPKYVKSNRLVLATGLRNSPQRE
AIAGFIEGGWQGMVDGWYGYHHSNEQGSGYAADKESTQKAIDGVTNKVNSIIDKMNTQFE
RRIENLNKKMEDGFLDVWTYNAELLVLMENERTLDFHDSNVKNLYDKVRLQLRDNAKELG
DNECMESLRNGTYNYPQYSEEARLKREEISGVKLESIGTYQILSIYSTVASSLALAIMMA
SLQCRICI
```

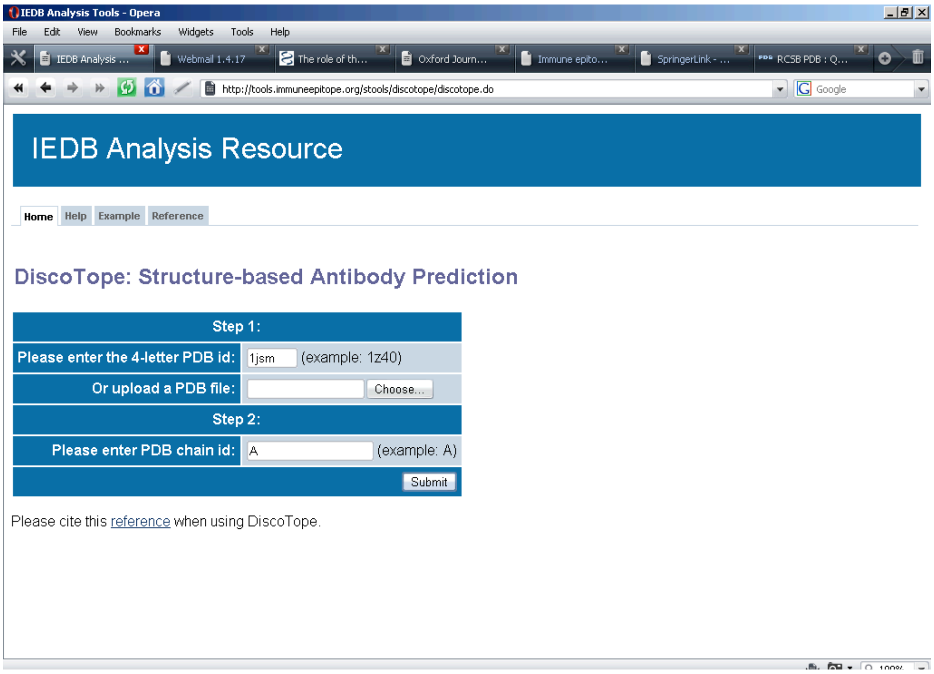
Choose a method:

○ Chou & Fasman Beta-Turn Prediction

○ Emini Surface Accessibility Prediction

Gambar 13. Tampilan *Homepage* dari *Server* BepiPred (http://tools.immuneepitope.org/tools/bcell/iedb input)

Kemudian prediksi *discontinous epitope* menggunakan *server* DiscoTope terdapat pula dalam *homepage* IEDB-AR (**Gambar 14**).



DiscoTope: Structure-based Antibody Prediction

Step 1:

Please enter the 4-letter PDB id: 1jsm (example: 1z40)

Or upload a PDB file:

Step 2:

Please enter PDB chain id: A (example: A)

Please cite this reference when using DiscoTope.

Gambar 14. Tampilan *Homepage* dari *Server* DiscoTope (http://tools.immuneepitope.org/stools/discotope/discotope.do)

Hasil prediksi *epitope* sel B protein HA menggunakan *server* BepiPred menghasilkan sekuen peptida dari beberapa *sequential epitope* dan *conformational epitope* dari *server* DiscoTope (**Lampiran 8**). Data hasil prediksi *epitope* sel B ditunjukkan pada **Tabel 11 – 16**.

Tabel 11. *Epitope* sel B Protein HA inang manusia

BepiPred	**DisCotope**
TSSWPNHDSNKGVTAACPHAGAKSF	TSSWPNH
YPKYSEEAKLNREEIDGVKL	KLNR

Tabel 12. *Epitope* sel B Protein HA inang babi

BepiPred	**DisCotope**
TSSWPDHETNRGVTAACPYAGANS	TSSYPDHETN

Tabel 13. *Epitope* sel B Protein NA inang manusia

BepiPred	**DisCotope**
TDGPSNGQA	GPSNGQ
FGDNPRPNDKTGSCGPVSSNGANGV	PNDG

Tabel 14. *Epitope* sel B Protein NA inang babi

BepiPred	**DisCotope**
FGDNPRSNDGKGNCGPVLSNGANGVK	GDNPRS

Tabel 15. *Epitope* sel B Protein M2 inang manusia

BepiPred	**DisCotope**
RCSDSSDP	DSSDP

Tabel 16. *Epitope* sel B Protein M2 inang babi

BepiPred	**DisCotope**
WECRYSDSSDP	CRYSDSS

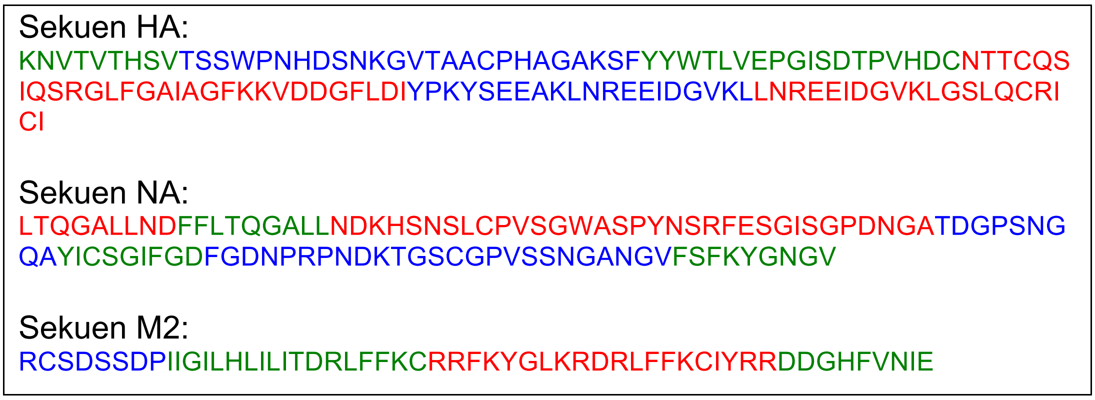
Pada hasil prediksi, ditampilkan posisi-posisi dari *epitope-epitope* tersebut namun prediksi ini tidak disertai dengan skor yang menggambarkan tingkat pengenalan *epitope* oleh sel B atau pengikatan dengan antibodi, sehingga untuk penentuan sekuen vaksin peptida nantinya, *epitope-epitop*e hasil prediksi ini diseleksi berdasarkan tingkat *accesible*. Semakin besar tingkat *accessibility*, maka semakin besar pula kemungkinan *epitope* tersebut untuk dapat dikenali oleh sel B atau berikatan dengan molekul antibodi.

4.5. Penentuan Sekuen Vaksin

Vaksin sebaiknya memiliki *epitope-epitope* binding dari subtipe H1N1 dan influenza tipe A tersebut. Penentuan sekuen vaksin peptida dilakukan melalui kombinasi peptida atas dasar hasil prediksi *epitope* sel B dan sel T. Berdasarkan hasil prediksi *epitope* yang telah dilakukan, terdapat banyak kesamaan antara protein HA inang manusia dengan inang babi begitu pula pada protein NA, dan M2. Sehingga protein yang dijadikan vaksin adalah protein HA, NA, dan M2 berasal dari inang manusia. Ada tiga *epitope* protein yang akan dikombinasi, yaitu *epitope* protein HA, NA, dan M2 dimana *epitope* untuk kombinasi adalah *epitope* sel T (MHC-I dan MHC-II) dan *epitope* sel B memiliki skor paling tinggi (*high-binder*).

Berdasarkan hasil diperoleh epitope-epitope protein HA, NA, dan M2 virus H1N1 ditunjukkan pada **Tabel 17**.

Tabel 17. *Epitope-epitope* protein HA, NA, dan M2 virus H1N1



Sekuen HA:
KNVTVTHSVTSSWPNHDSNKGVTAACPHAGAKSFYYWTLVEPGISDTPVHDCNTTCQS
IQSRGLFGAIAGFKKVDDGFLDIYPKYSEEAKLNREEIDGVKLLNREEIDGVKLGSLQCRI
CI

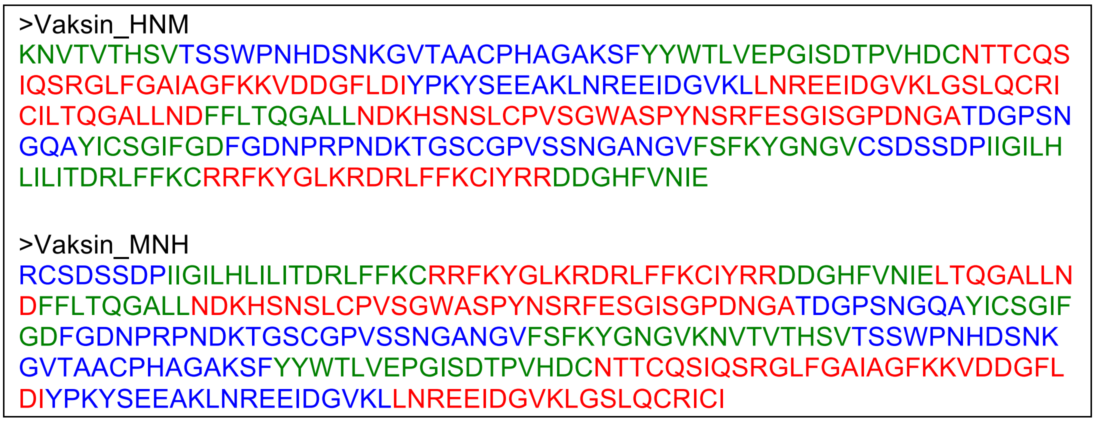
Sekuen NA:
LTQGALLNDFFLTQGALLNDKHSNSLCPVSGWASPYNSRFESGISGPDNGATDGPSNG
QAYICSGIFGDFGDNPRPNDKTGSCGPVSSNGANGVFSFKYGNGV

Sekuen M2:
RCSDSSDPIIGILHLILITDRLFFKCRRFKYGLKRDRLFFKCIYRRDDGHFVNIE

Bagian sekuen berwarna merah adalah *epitope* MHC-I, sedangkan hijau merupakan *epitope* MHC-II. Bagian sekuen berwarna biru adalah *epitope* sel B.

Berdasarkan hasil penentuan *epitope* tersebut, dibuat enam rancangan vaksin, dengan rincian dua vaksin berdasarkan pada *template* HA untuk vaksin MHN dan NHM; dua vaksin berdasarkan pada *template* NA untuk vaksin HNM dan MNH dan dua vaksin berdasarkan pada *template* M2 untuk vaksin HMN dan NMH. Sekuen vaksin ditunjukkan pada **Tabel 18**.

Tabel 18. Sekuen vaksin



>Vaksin_HNM
KNVTVTHSVTSSWPNHDSNKGVTAACPHAGAKSFYYWTLVEPGISDTPVHDCNTTCQS
IQSRGLFGAIAGFKKVDDGFLDIYPKYSEEAKLNREEIDGVKLLNREEIDGVKLGSLQCRI
CILTQGALLNDFFLTQGALLNDKHSNSLCPVSGWASPYNSRFESGISGPDNGATDGPSN
GQAYICSGIFGDFGDNPRPNDKTGSCGPVSSNGANGVFSFKYGNGVCSDSSDPIIGILH
LILITDRLFFKCRRFKYGLKRDRLFFKCIYRRDDGHFVNIE

>Vaksin_MNH
RCSDSSDPIIGILHLILITDRLFFKCRRFKYGLKRDRLFFKCIYRRDDGHFVNIELTQGALLN
DFFLTQGALLNDKHSNSLCPVSGWASPYNSRFESGISGPDNGATDGPSNGQAYICSGIF
GDFGDNPRPNDKTGSCGPVSSNGANGVFSFKYGNGVKNVTVTHSVTSSWPNHDSNK
GVTAACPHAGAKSFYYWTLVEPGISDTPVHDCNTTCQSIQSRGLFGAIAGFKKVDDGFL
DIYPKYSEEAKLNREEIDGVKLLNREEIDGVKLGSLQCRICI

```
>Vaksin_HMN
KNVTVTHSVTSSWPNHDSNKGVTAACPHAGAKSFYYWTLVEPGISDTPVHDCNTTCQS
IQSRGLFGAIAGFKKVDDGFLDIYPKYSEEAKLNREEIDGVKLLNREEIDGVKLGSLQCRI
CIRCSDSSDPIIGILHLILITDRLFFKCRRFKYGLKRDRLFFKCIYRRDDGHFVNIELTQGAL
LNDFFLTQGALLNDKHSNSLCPVSGWASPYNSRFESGISGPDNGATDGPSNGQAYICS
GIFGDFGDNPRPNDKTGSCGPVSSNGANGVFSFKYGNGV

>Vaksin_NMH
LTQGALLNDFFLTQGALLNDKHSNSLCPVSGWASPYNSRFESGISGPDNGATDGPSNG
QAYICSGIFGDFGDNPRPNDKTGSCGPVSSNGANGVFSFKYGNGVRCSDSSDPIIGILHL
ILITDRLFFKCRRFKYGLKRDRLFFKCIYRRDDGHFVNIEKNVTVTHSVTSSWPNHDSNK
GVTAACPHAGAKSFYYWTLVEPGISDTPVHDCNTTCQSIQSRGLFGAIAGFKKVDDGFL
DIYPKYSEEAKLNREEIDGVKLLNREEIDGVKLGSLQCRICI

>Vaksin_NHM
LTQGALLNDFFLTQGALLNDKHSNSLCPVSGWASPYNSRFESGISGPDNGATDGPSNG
QAYICSGIFGDFGDNPRPNDKTGSCGPVSSNGANGVFSFKYGNGVKNVTVTHSVTSSW
PNHDSNKGVTAACPHAGAKSFYYWTLVEPGISDTPVHDCNTTCQSIQSRGLFGAIAGFK
KVDDGFLDIYPKYSEEAKLNREEIDGVKLLNREEIDGVKLGSLQCRICIRCSDSSDPIIGIL
HLILITDRLFFKCRRFKYGLKRDRLFFKCIYRRDDGHFVNIE

>Vaksin_MHN
RCSDSSDPIIGILHLILITDRLFFKCRRFKYGLKRDRLFFKCIYRRDDGHFVNIEKNVTVTHS
VTSSWPNHDSNKGVTAACPHAGAKSFYYWTLVEPGISDTPVHDCNTTCQSIQSRGLFG
AIAGFKKVDDGFLDIYPKYSEEAKLNREEIDGVKLLNREEIDGVKLGSLQCRICILTQGALL
NDFFLTQGALLNDKHSNSLCPVSGWASPYNSRFESGISGPDNGATDGPSNGQAYICSGI
FGDFGDNPRPNDKTGSCGPVSSNGANGVFSFKYGNGV
```

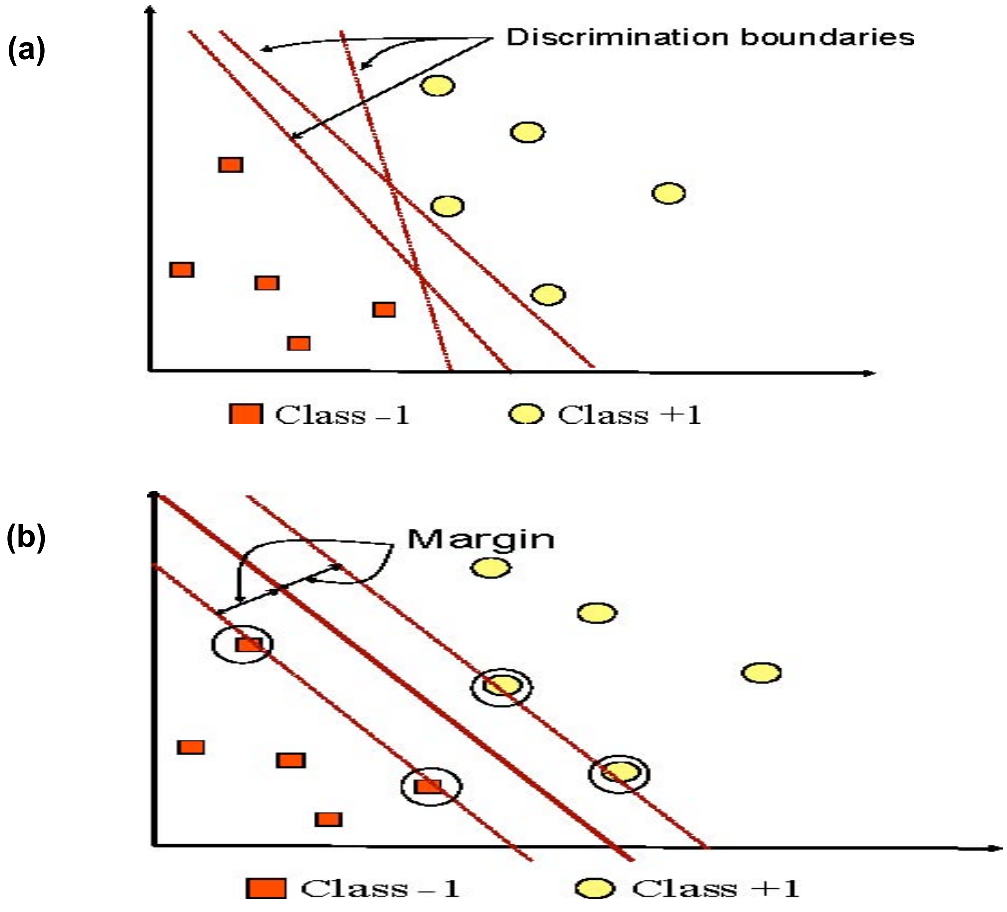
Vaksin MHN didapatkan melalui kombinasi urutan peptida *epitope* protein M2, HA, dan NA, sedangkan vaksin NHM merupakan kombinasi urutan peptida *epitope* protein NA, HA, dan M2. Vaksin HNM kombinasi urutan peptida *epitope* protein HA, NA, dan M2, sedangkan vaksin MNH kombinasi urutan peptida *epitope* protein M2, NA dan HA. Vaksin HMN kombinasi urutan peptida *epitope* protein HA, M2, dan NA, sedangkan vaksin NMH kombinasi urutan peptida *epitope* protein NA, M2, dan HA. Keenam sekuen vaksin peptida ditunjukkan dalam format FASTA.

Panjang sekuen vaksin H1N1 hasil penelitian sebanyak 258 asam amino hanya berbeda 2 asam amino dengan panjang sekuen vaksin

H5N1 hasil penelitian Rame (2007) sebanyak 260 asam amino dengan menggunakan metode yang sama.

Berbagai penelitian mengenai perancangan vaksin telah banyak dilakukan, penelitian Pradana (2006) metode HMM dan ANN, Syamsudin (2007) metode HMM, dan Suyono (2007) metode ANN. Berbeda dengan penelitian-penelitian sebelumnya, rancangan vaksin H1N1 menggunakan metode *Support Vector Machine* (SVM). Strategi SVM berbeda dengan HMM dan ANN yang mencari *hyperplane* pemisah antar *class*, SVM menemukan *hyperplane* terbaik pada *input space*. Konsep SVM dapat dijelaskan secara sederhana sebagai usaha mencari *hyperplane* terbaik berfungsi sebagai pemisah dua buah *class* pada *input space*.

Berbagai alternatif garis pemisah (*discrimination boundaries*) ditunjukkan pada **Gambar 15.** Beberapa *pattern* (disimbolkan kotak dan lingkaran) anggota terdiri dari dua buah *class*: +1 dan –1. *Pattern* pada *class* –1 disimbolkan dengan warna merah, sedangkan *pattern* pada *class* +1 warna kuning. Problem klasifikasi dapat diterjemahkan dengan usaha menemukan *hyperplane* (disimbolkan garis) yang memisahkan antara kedua kelompok tersebut (Byun dan Lee, 2003). **Gambar 15 (a)** menunjukkan garis pemisah yang tidak teratur.



Gambar 15 (a) dan (b). Alternatif garis pemisah (*discrimination boundaries*) (Byun dan Lee, 2003)

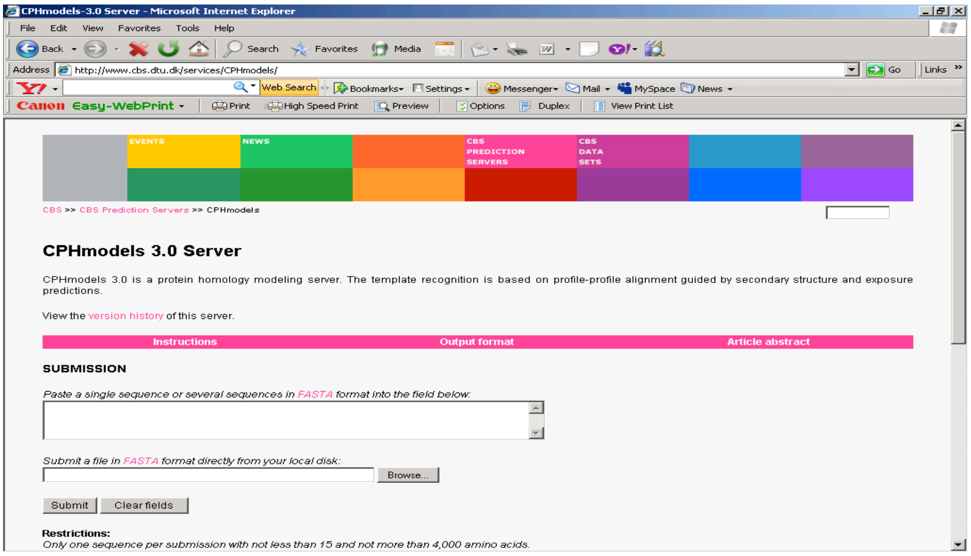
Hyperplane pemisah terbaik antara kedua class dapat ditemukan dengan mengukur *margin hyperplane* dan mencari titik maksimalnya. Margin adalah jarak antara *hyperplane* tersebut dengan *pattern* terdekat dari masing-masing *class*. *Pattern* yang paling dekat ini disebut sebagai *support vector*. Garis solid pada **Gambar 15 (b)** menunjukkan *hyperplane* yang terbaik, yaitu terletak tepat pada tengah-tengah kedua *class*, sedangkan titik merah dan kuning berada dalam lingkaran hitam adalah *support vector* (Byun dan Lee, 2003). Metode SVM merupakan metode yang tepat untuk merancang vaksin H1N1.

4.6. *Homology modeling*

Pendekatan *Homology modeling* dilakukan dalam penelitian untuk memprediksi struktur tersier dari vaksin. Prediksi struktur tersier suatu protein dengan *homology modelling* dapat dilakukan dengan syarat apabila kesamaan sekuen antara protein tersebut dengan protein database paling sedikit 20% (Bourne, 2003). Hasil sekuens *homology modelling* sekuen protein virus H1N1 dengan protein pada database menunjukkan lebih besar dari 50%*,* maka dapat dilakukan prediksi struktur vaksin dengan metode *homology modelling.*

4.6.1. Pencarian *Template*

Pencarian *template* dilakukan melalui *server* CPHModels terkoneksi dengan PDB *source* akses internet (**Gambar 16**). Pencarian *template* dilakukan apabila data PDB sekuen protein target tidak ada dalam *database*.



CPHmodels 3.0 Server

CPHmodels 3.0 is a protein homology modeling server. The template recognition is based on profile-profile alignment guided by secondary structure and exposure predictions.

View the version history of this server.

SUBMISSION

Paste a single sequence or several sequences in FASTA format into the field below:

Submit a file in FASTA format directly from your local disk:

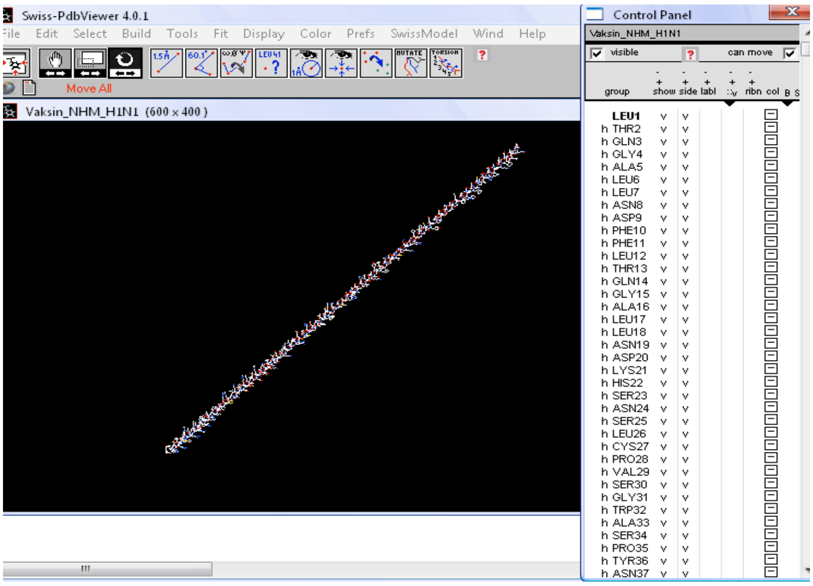
Restrictions:
Only one sequence per submission with not less than 15 and not more than 4,000 amino acids.

Gambar 16. Tampilan *Homepage* dari *Server* CPHModels 3.0 (http://www.cbs.dtu.dk/services/CPHmodels/)

Data *template* hasil prediksi ditunjukkan dalam **Lampiran 9**. Pemilihan *template* untuk protein HA adalah kode PDB 1RUZ (*chain* H); protein NA adalah 2HTY (*chain* A); dan protein M2 adalah 2KIH (*chain* A). Kemudian masing-masing *template* diunduh dalam format PDB.

4.6.2. *Modeling* Struktur Tersier Vaksin

Struktur vaksin dalam DeepView dikonversi sebagai rantai lurus struktur primer (**Gambar 17**). Konversi ke bentuk rantai lurus memudahkan struktur vaksin mengikuti struktur *template*nya.



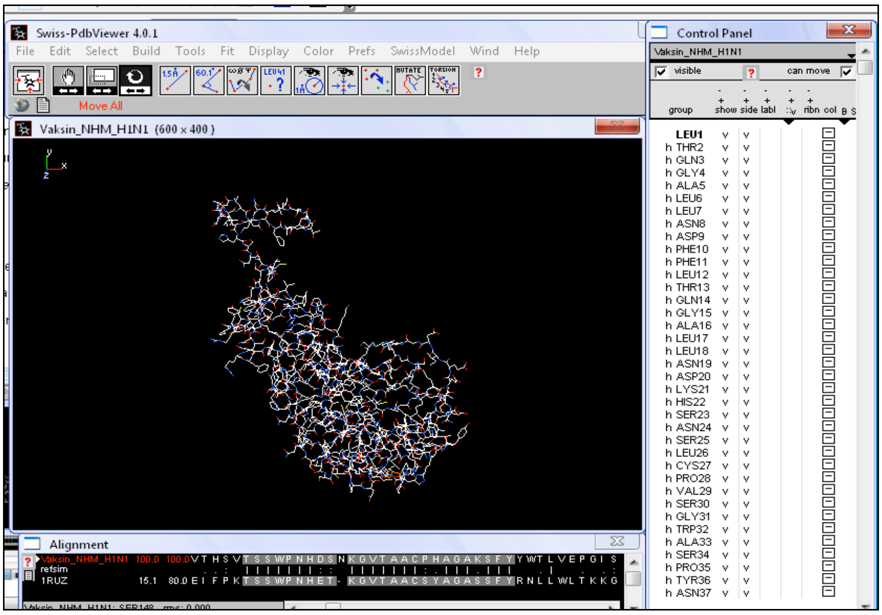
Gambar 17. Tampilan struktur vaksin NHM pada DeepView (Program *DeepView*)

Setelah *template* diunduh, struktur tersier *template* tersebut kemudian divisualisasikan menggunakan *DeepView* dengan cara membuka data PDB dari template. Hasil dari visualisasi didapatkan struktur tersier *template* dalam bentuk 3D dan dapat diputar sesuai sumbu putar. Residu-residu penyusun dapat dilihat melalui menu *Control Panel.*

Pelekatan struktur vaksin kepada *template* bertujuan agar struktur rantai lurus vaksin dapat berubah menjadi struktur tersier. Residu-residu yang sama akan saling melekat sehingga struktur vaksin akan ikut melipat (folding) mengikuti bentuk dari *template* dan akan merubah struktur rantai lurus menjadi struktur tersier. Melekatkan struktur vaksin pada *template* dapat dilakukan menggunakan program *DeepView* dengan memilih menu *Magic Fit* setelah membuka *file* PDB *template.*

4.6.3. Visualisasi Struktur Tersier Vaksin

Visualisasi struktur tersier vaksin hasil pelekatan dilakukan dengan memindahkan struktur tersier *template*, sehingga terlihat struktur tersier vaksin (**Gambar 18**). Enam struktur vaksin yang telah divisualisasikan ditunjukkan pada **Lampiran 10.**



```
Vaksin_NHM_H1N1  100.0  100.0 V T H S V T S S W P N H D S N K G V T A A C P H A G A K S F Y Y W T L V E P G I S
refsim                            . . :   | | | | | | | | : :   | | | | | | | | : . | | | . | | |       . |       .   . :
1RUZ              15.1   80.0 E I F P K T S S W P N H E T -   K G V T A A C S Y A G A S S F Y R N L L W L T K K G
```

Gambar 18. Tampilan struktur tersier vaksin NHM
(Program *DeepView*)

Tabel 19. Kesamaan Protein Vaksin dengan data PDB

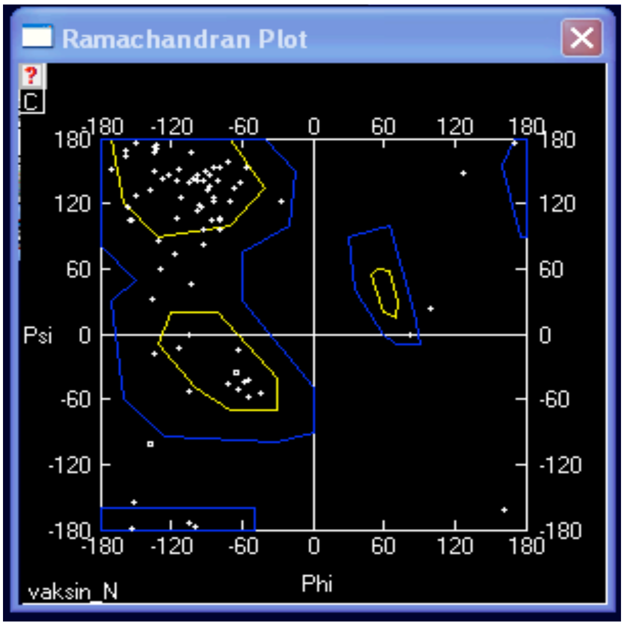
Vaksin	Data PDB	Sekuen *Homolog* (posisi)
NHM MHN	1RUZ (molecule: Hemagglutinin) (chain: H)	TSSWPNH (113-119) KGVTAACSYAGASSTY (123-138)
HNM MNH	2HTY (molecule: Neuramidase) (chain: A)	YICSGIFGD (181-189) NPRPNDKTGSCGPVSSNGANGV (198-219) FSFKYGNGV (216-224)
HMN NMH	2KIH (molecule: Matrik 2) (chain: A)	IIGILHL (130-136) ITDRLFFKC (139-147) RRFKYGLK (148-156)

Tabel 19 menunjukkan bahwa keenam rancangan vaksin memiliki kesamaan sekuen dengan protein virus influenza A H1N1, diharapkan memiliki fungsi yang sama dan memicu respon imunitas seperti pada protein virus.

Perbaikan struktur tersier vaksin perlu dilakukan untuk memperbaiki residu-residu yang saling tumpang tindih. Protein yang memiliki struktur asam amino sama dengan *template* belum tentu lipatan (*folding*) protein dalam bentuk tersiernya juga sama dikarenakan pengaruh interaksi antar asam amino dengan asam amino samping atau asam amino tetangga.

4.6.4. Evaluasi Struktur Tersier Vaksin

Evaluasi struktur tersier vaksin dilakukan dengan melihat residu yang saling tumpang tindih dan dengan cara menganalisis *Ramachandran Plot* dari struktur vaksin melalui menu *Ramachandran Plot* yang terintegrasi pada *DeepView* (**Gambar 19**).



Gambar 19. Ramachandran Plot dari struktur tersier vaksin NHM pada DeepView (Program *DeepView*)

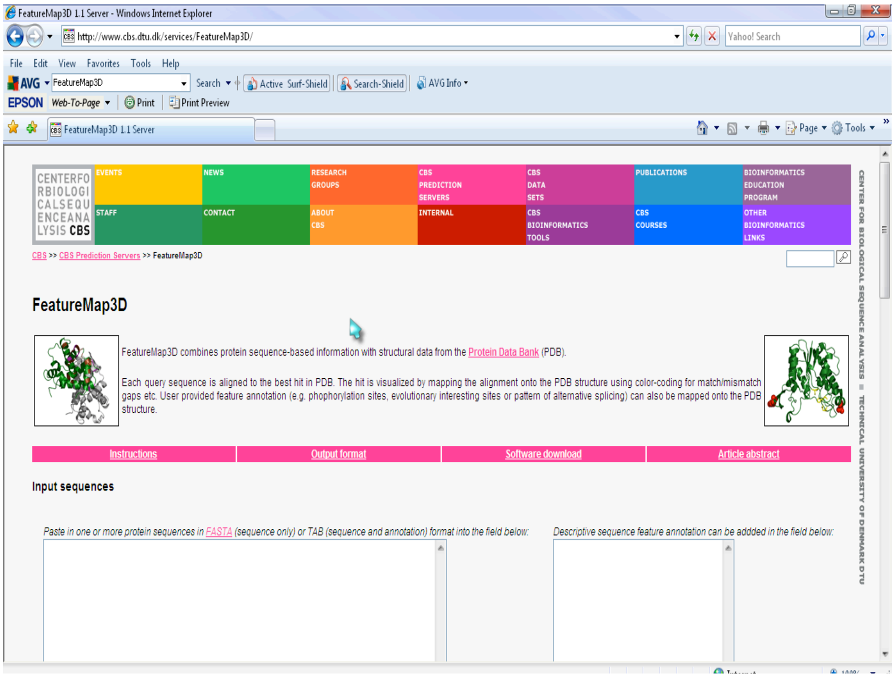
Ramachandran Plot keenam struktur vaksin divisualisasikan pada **Lampiran 11**. Kombinasi tertentu dari ϕ (*phi*) dan ψ (*psi*) tidak diperbolehkan karena akan menghasilkan *steric hindrance* atau tumpang tindih antara atom-atom dalam protein. *Ramachandran plot* digunakan untuk mengecek dan mengatur kembali konformasi idak realistik suatu model protein. *Ramachandran plot* memiliki suatu daerah ditandai oleh garis biru di sekelilingnya, merupakan daerah koordinat struktur sekunder protein. Daerah tersebut merupakan daerah diperbolehkan (*allowed region*), dimana sebagian besar asam amino di*plot*kan dalam dalam dua daerah yaitu daerah kuning, yaitu daerah secara sterik membolehkan nilai ϕ (*phi*) dan ψ (*psi*), dan daerah biru, yaitu daerah batasan toleransi maksimal *steric strain*. Sedangkan daerah tidak diperbolehkan (*disallowed region*), yaitu daerah di luar *allowed region*, dimana plot residu selain glisin tidak diperbolehkan ada di daerah tersebut.

Plot glisin dapat berada pada *disallowed region* karena glisin tidak mempunyai rantai samping, sehingga sudut ϕ (*phi*) dan sudut ψ (*psi*) yang dihasilkan pun tak terbatas. Jumlah plot residu selain glisin jika ada pada daerah terlarang menunjukkan kualitas struktur suatu protein. Apabila jumlahnya melebihi 15% dari seluruh jumlah residu protein tersebut, maka kualitas protein itu buruk (Baxevanis dan Ouellette, 2005).

Jumlah residu non glisin yang ada di *disallowed region* pada *Ramachandran Plot* untuk struktur vaksin hasil prediksi *First Approach Mode* maupun *Optimise Mode* jauh lebih kecil dari 15% jumlah keseluruhan residu (258 residu), yaitu berkisar 2 – 2,5%. Dengan demikian maka struktur keenam vaksin yang dihasilkan sudah baik kualitasnya.

4.6.5. Perbandingan Struktur Tersier Vaksin dengan *Database*

Pembandingan struktur tersier vaksin dengan data protein dalam bentuk PDB pada *database* dilakukan melalui *FeatureMap3*D pada situs *Center for Biological Sequence Analysis* (CBS) pada alamat situs http://cbs.dtu.dk/services/FeatureMap3D (**Gambar 20**). Data perbandingan vaksin hasil prediksi terhadap format PDB ditunjukkan pada **Lampiran 12**.



FeatureMap3D

FeatureMap3D combines protein sequence-based information with structural data from the Protein Data Bank (PDB).

Each query sequence is aligned to the best hit in PDB. The hit is visualized by mapping the alignment onto the PDB structure using color-coding for match/mismatch gaps etc. User provided feature annotation (e.g. phophorylation sites, evolutionary interesting sites or pattern of alternative splicing) can also be mapped onto the PDB structure.

Input sequences

Paste in one or more protein sequences in FASTA (sequence only) or TAB (sequence and annotation) format into the field below:

Descriptive sequence feature annotation can be addded in the field below:

Gambar 20. Tampilan *Homepage* dari *Server* FeatureMap3D (http://www.cbs.dtu.dk/services/FeatureMap3D/)

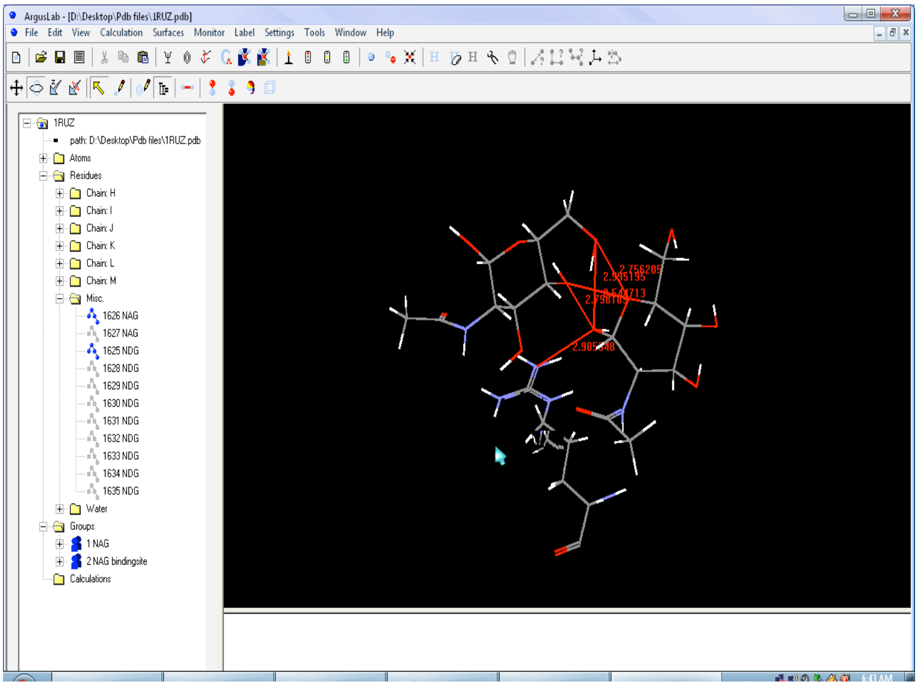
4.6.6. Validasi Vaksin dengan *Database*

Validasi sekuen vaksin dengan *database* menggunakan BLASTp terhadap *database* protein *human* dan data PDB virus influenza A. Analisis BLASTp terhadap protein *human* menunjukkan sekuen vaksin tidak ada yang sama dengan protein yang dihasilkan dalam tubuh manusia (**Lampiran 13**).

4.7. . Molecular Docking

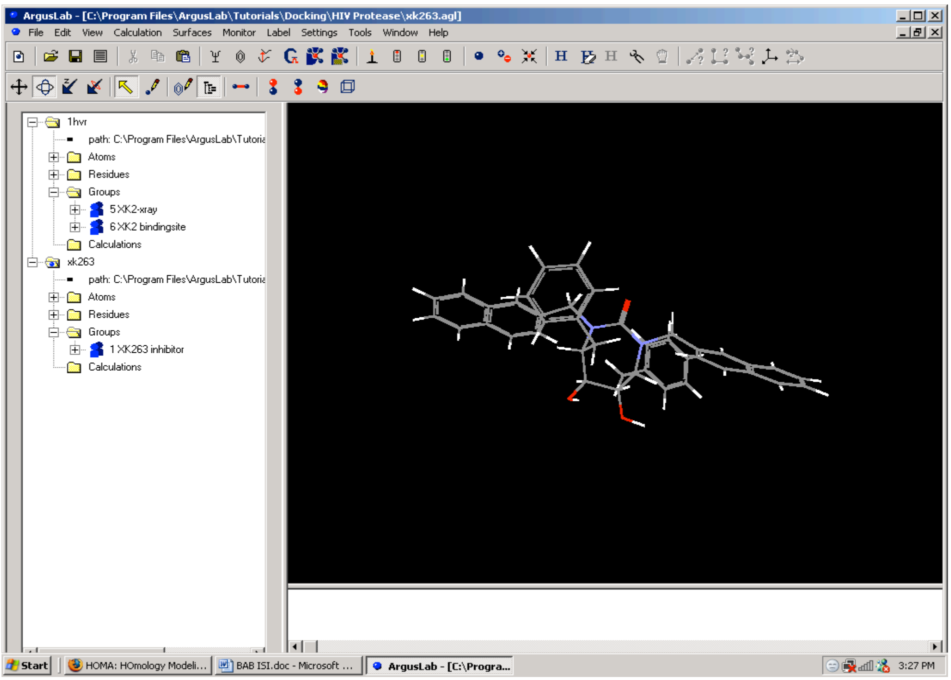
Enam vaksin dalam *file* PDB satu persatu dimasukkan ke dalam program Arguslab (**Gambar 21).** Analisis molecular docking ligan dan reseptor dalam program Arguslab hanya dapat dilakukan dalam format PDB. Kemudian binding site ligan ditentukan melalui koordinat *file* PDB.

Program Arguslab menganalisis docking dengan ketelitian tinggi dan fleksibilitas docking ligan (Chikhi dan Benseguenі, 2008).



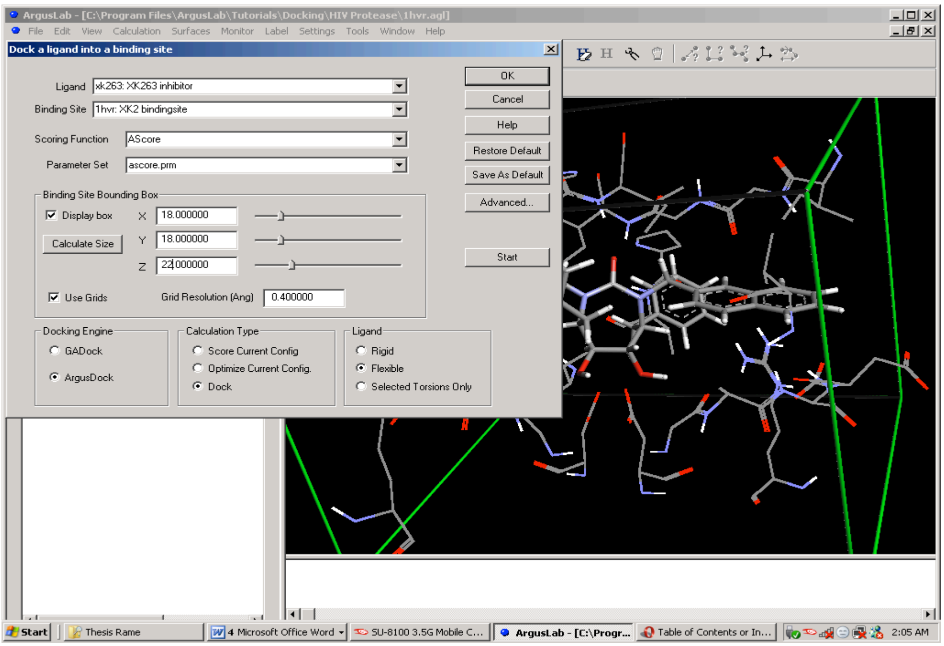
Gambar 21. Stuktur ligan dan binding site dari vaksin NHM (Program Arguslab)

Garis berwarna merah menunjukkan ikatan hidrogen antara ligan dengan *binding site* protein. Kemudian dimasukkan file PDB 3GBM yang telah diunduh sebelumnya (**Gambar 22**).



Gambar 22. Struktur antibodi reseptor (Program Arguslab)

Setelah itu dilakukan *calculation docking ligand* dengan mengatur *Binding Site Bounding Box* menjadi 18, 18, 22 Angstroms untuk x,y,z (**Gambar 23**).


ArgusLab - [C:\Program Files\ArgusLab\Tutorials\Docking\HIV Protease\1hvr.agl]

Dock a ligand into a binding site

Ligand: xk263: XK263 inhibitor

Binding Site: 1hvr: XK2 bindingsite

Scoring Function: AScore

Parameter Set: ascore.prm

Binding Site Bounding Box

☑ Display box

X: 18.000000

Y: 18.000000

Z: 22.000000

☑ Use Grids

Grid Resolution (Ang): 0.400000

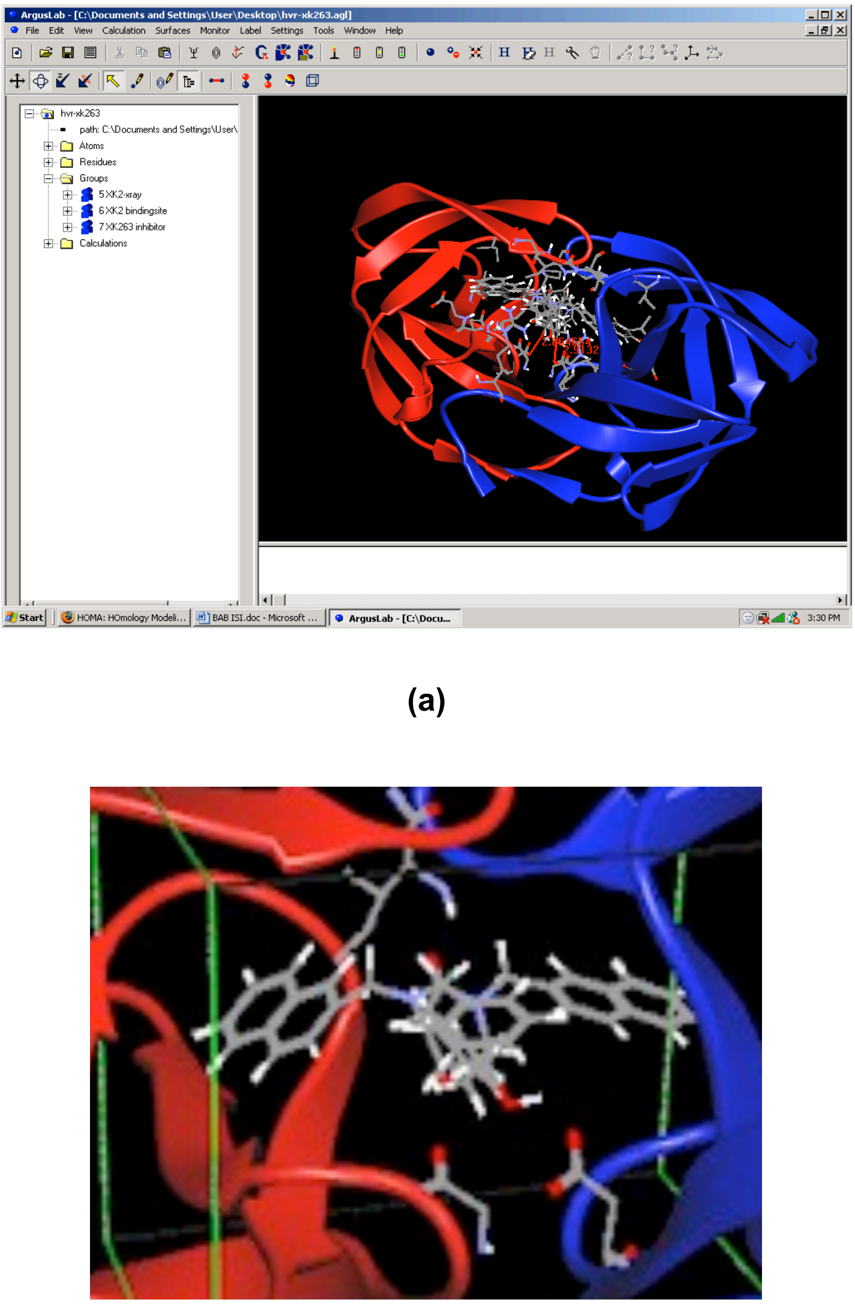
Docking Engine: ○ GADock ● ArgusDock

Calculation Type: ○ Score Current Config ○ Optimize Current Config. ● Dock

Ligand: ○ Rigid ● Flexible ○ Selected Torsions Only

Gambar 23. *Calculation docking ligand* (Program Arguslab)

Pengaturan *Binding Site Bounding Box* menjadi 18, 18, 22 Angstroms untuk x,y,z dilakukan agar visualisasi *docking* menjadi optimal. Hasil akhir visualisasi *docking* ditunjukkan pada **Gambar 24 (a)** dan **(b)**.



(a)

(b)

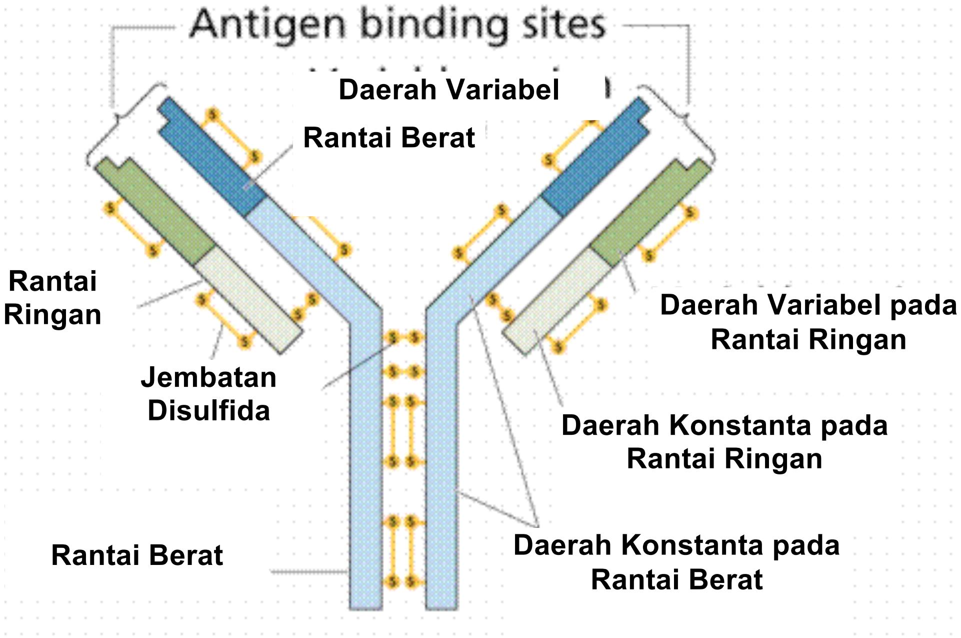
Gambar 24. **(a)** *Docking* antara ligan dengan *reseptor;* **(b)** Perbesaran gambar *Docking* antara ligan dengan *reseptor* (Program Arguslab)

Beberapa informasi yang diperoleh pada hasil akhir antara lain jarak ikatan atom C sebesar 1,9 Amstrong; N sebesar 1,8 Amstrong; O sebesar 1,7 Amstrong, dan S sebesar 2 Amstrong. *Grid docking* sebanyak 208 poin dari total *grid* sebesar 275684 poin. *Clustering* (pengelompokan) sebanyak 14 bentuk konformasi (**Tabel 20**), waktu yang dibutuhkan untuk optimasi *docking* selama 18 detik dan data energi minimum terbaik interaksi antibodi dengan vaksin sebesar -13,6859 kkal/mol.

Tabel 20. Energi minimum Interaksi 14 bentuk Konformasi hasil *clustering*

Pose	Energi minimum Interaksi (kkal/mol)
1	- 23,69
2	- 12,96
3	- 12,95
4	- 12,94
5	-12,53
6	- 11,49
7	- 11,40
8	- 11,27
9	- 11,18
10	- 11,04
11	- 10,98
12	- 10,75
13	-10,75
14	-10,67

Keberhasilan *docking* hanya ditunjukkan oleh vaksin NHM, sedangkan kelima vaksin lainnya tidak cocok dengan antibodi pada *database* yang bersifat spesifik terhadap antigen tertentu. Daerah pengikatan antibodi dengan antigen (*antigen binding site*) merupakan *variable region*, artinya daerah tersebut memiliki spesifitas yang berbeda untuk setiap molekul antibodi dan spesifik terhadap suatu antigen (**Gambar 25**).



Gambar 25. Struktur antibodi (http://www.emc.maricopa.edu/faculty/farabee/BIOBK/BioBookIMMUN)

BAB V

KESIMPULAN DAN SARAN

5.1 Kesimpulan

Berdasarkan hasil penelitian prediksi epitope dari *server* NetChop, TAPPred, dan MHCPred (MHC-I dan MHC-II) dan prediksi *epitope* sel B menggunakan *server* BepiPred dan Discotope diperoleh 21 *epitope*. 6 rancangan vaksin H1N1 diperoleh berdasarkan penyusunan *epitope* tersebut, yaitu vaksin HNM, MNH, HMN, NMH, NHM, dan MHN.

Struktur tersier vaksin dari hasil *homology modeling*, menunjukkan kemiripan struktur tersier lebih besar dari 50 % dengan data PDB database. Jumlah residu non glisin yang ada di *disallowed region* pada *Ramachandran Plot* untuk struktur vaksin hasil prediksi *First Approach Mode* maupun *Optimise Mode* kurang dari 15% jumlah keseluruhan residu (258 residu), yaitu berkisar 2 – 2,5%.

Prediksi *molecular docking* berhasil dilakukan pada vaksin NHM dengan jumlah *clustering* (pengelompokan) sebanyak 14 bentuk konformasi, waktu yang dibutuhkan untuk optimasi *docking* selama 18 detik dan data energi minimum terbaik interaksi antibodi dengan vaksin sebesar -13,6859 kkal/mol.

5.2 Saran

Analisis *molecular dynamics* struktur tersier hasil *modeling* dapat dilakukan untuk mengetahui stabilitas dan fleksibiltas rancangan vaksin.

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http://www.who.int 2008

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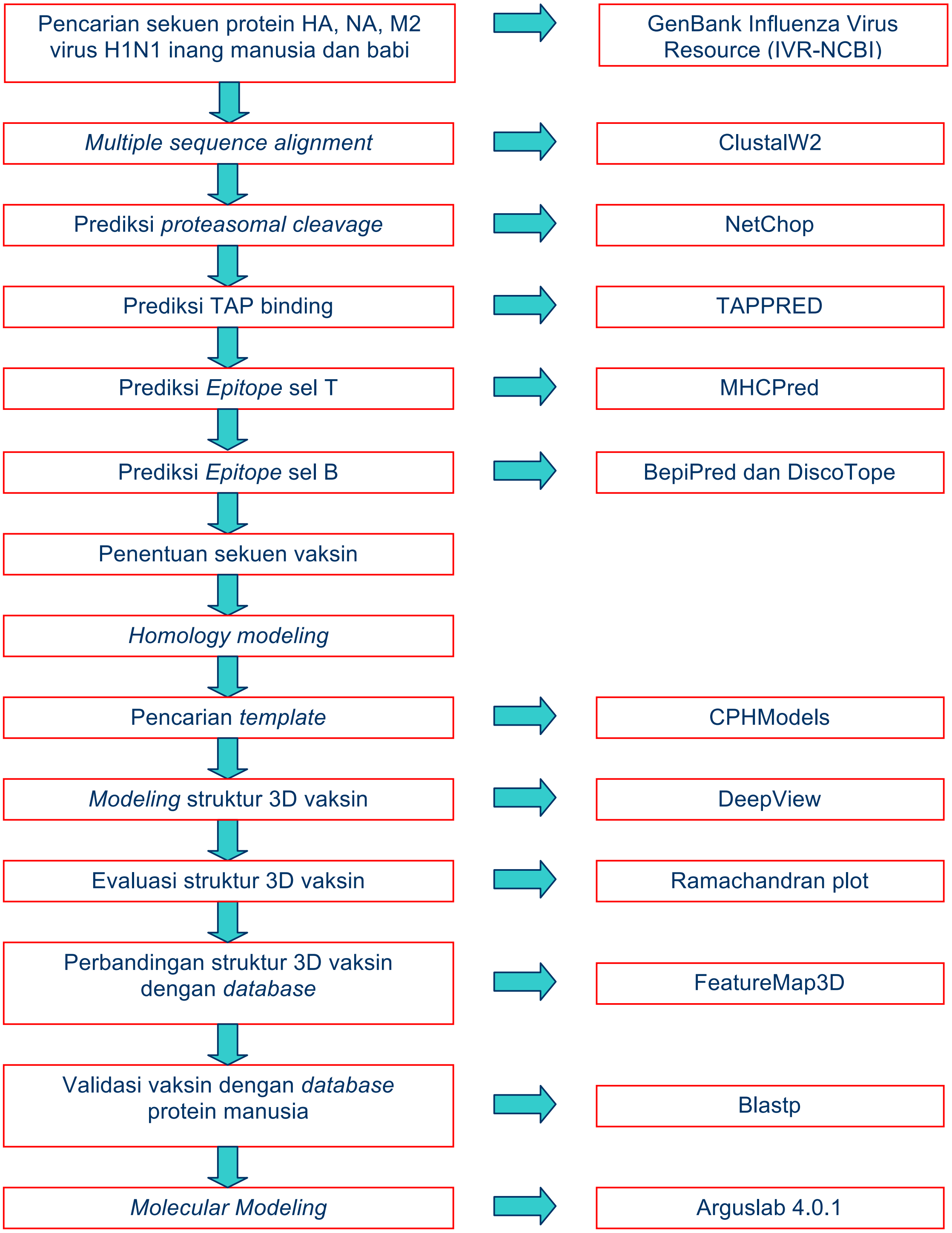
Lampiran 1. Bagan Kerja



Lampiran 2. Daftar *Official Codes* Dua Puluh Asam Amino

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

Lampiran 3. Sekuens Protein HA, NA, M2 Virus H1N1 dalam *Format* FASTA

3. 1. Sekuen Protein HA Inang Manusia

>gi|223551672|gb|ACM90863.1| hemagglutinin [Influenza A virus
(A/Johannesburg/28/2008(H1N1))]
MKVKLLVLLCTFTATYADTICIGYHANNSTDTVDTVLEKNVTVTHSVNLLENSHNGKLCLLKGIAPLQLG
NCSVAGWILGNPECELLISKESWSYIVEKPNPENGTCYPGHFADYEELREQLSSVSSFERFEIFPKESSW
PNHTVTGVSASCSHNGESSFYRNLLWLTGKNGLYPNLSKSYANNKEKEVLVLWGVHHPPNIGDQKALYHT
ENAYVSVVSSHYSRKFTPEIAKRPKVRDQEGRINYYWTLLEPGDTIIFEANGNLIAPRYAFALSRGFGSG
IINSNAPMDKCDAKCQTPQGAINSSLPFQNVHPVTIGECPKYVRSAKLRMVTGLRNIPSIQSRGLFGAIA
GFIEGGWTGMVDGWYGYHHQNEQGSGYAADQKSTQNAINGITNKVNSVIEKMNTQFTAVGKEFNKLERRM
ENLNKKVDDGFIDIWTYNAELLVLLENERTLDFHDSNVKNLYEKVKSQLKNNAKEIGNGCFEFYHKCNDE
CMESVKNGTYDYPKYSEESKLNREKIDGVKLESMGVYQILAIYSTVASSLVLLVSLGAISFWMCSNGSLQ
CRICI

**>gi|238618451|gb|ACR46992.1| hemagglutinin [Influenza A virus
(A/Osaka/2/2009(H1N1))]**
MKAILVVLLYTFATANADTLCIGYHANNSTDTVDTVLEKNVTVTHSVNLLEDKHNGKLCKLRGVAPLHLG
KCNIAGWILGNPECESLSTASSWSYIVETSSSDNGTCYPGDFIDYEELREQLSSVSSFERFEIFPKTSSW
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GIIISDTPVHDCNTTCQTPKGAINTSLPFQNIHPITIGKCPKYVKSTKLRLATGLRNVPSIQSRGLFGAI
AGFIEGGWTGMVDGWYGYHHQNEQGSGYAADLKSTQNAIDEITNKVNSVIEKMNTQFTAVGKEFNHLEKR
IENLNKKVDDGFLDIWTYNAELLVLLENERTLDYHDSNVKNLYEKVRSQLKNNAKEIGNGCFEFYHKCDN
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QCRICI

>gi|238695727|gb|ACR55004.1| hemagglutinin [Influenza A virus
(A/Beijing/3/2009(H1N1))]
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KCNIAGWILGNPECESLSTASSWSYIVETSSSDNGTCYPGDFIDYEELREQLSSVSSFERFEIFPKTSSW
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NADAYVFVGSSRYSKKFKPEIAIRPKVRDQEGRMNYYWTLVEPGDKITFEATGNLVVPRYAFAMERNAGS
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AGFIEGGWTGMVDGWYGYHHQNEQGSGYAADLKSTQNAIDEITNKVNSVIEKMNTQFTAVGKEFNHLEKR
IENLNKKVDDGFLDIWTYNAELLVLLENERTLDYHDSNVKNLYEKVRSQLKNNAKEIGNGCFEFYHKCDN
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QCRICI

>gi|238914630|gb|ACR78164.1| hemagglutinin [Influenza A virus
(A/Philippines/2003/2009(H1N1))]
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TCMESVKNGTYDYPKYSEEAKLNREEIDGVKLESTRIYQILAIYSTVASSLVLVVSLGAISFWMCSNGSL
QC

>gi|238695673|gb|ACR54974.1| hemagglutinin [Influenza A virus
(A/Shanghai/1/2009(H1N1))]

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QCRICI

>gi|238867295|gb|ACR67244.1| hemagglutinin [Influenza A virus
(A/Guangdong/02/2009(H1N1))]
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>gi|237688901|gb|ACR15238.1| hemagglutinin [Influenza A virus
(A/Taiwan/70013/2008(H1N1))]
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CRICI

>gi|229783367|gb|ACQ84451.1| hemagglutinin [Influenza A virus
(A/Korea/01/2009(H1N1))]
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QCRICI

>gi|237689852|gb|ACR15758.1| hemagglutinin [Influenza A virus
(A/Israel/644/2009(H1N1))]
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LGNPECESLSTASSWSYIVETSSSDNGTCYPGDFIDYEELREQLSSVSSFERFEIFPKTSSWPNHDSNKG
VTAACPHAGAKSFYKNLIWLVKKGNSYPKLSKSYINDKGKEVLVLWGIHHPSTSADQQSLYQNADAYVFV
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>gi|237847682|gb|ACR23302.1| hemagglutinin [Influenza A virus (A/Thailand/104/2009(H1N1))]
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MENLNKKVDDGFLDIWTYNAELLVLLENERTLDYHDSNVKNLYEKVRSQLKNNAKEIGNGCFEFYHKCDN
TCMESVKNGTYDYPKYSEEAKLNREEIDGVKLESTRIYQILAIYSTVASSLVLVVSLGAISFWMCSNGSL
QCRICI

>gi|228860929|gb|ACQ45338.1| hemagglutinin [Influenza A virus (A/Netherlands/602/2009(H1N1))]
MKAILVVLLYTFATANADTLCIGYHANNSTDTVDTVLEKNVTVTHSVNLLEDKHNGKLCKLRGVAPLHLG
KCNIAGWILGNPECESLSTASSWSYIVETSSSDNGTCYPGDFIDYEELREQLSSVSSFERFEIFPKTSSW
PNHDSNKGVTAACPHAGAKSFYKNLIWLVKKGNSYPKLSKSYINDKGKEVLVLWGIHHPSTSADQQSLYQ
NADAYVFVGSSRYSKKFKPEIAIRPKVRDQEGRMNYYWTLVEPGDKITFEATGNLVVPRYAFAMERNAGS
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QC

>gi|238914614|gb|ACR78156.1| hemagglutinin [Influenza A virus
(A/Victoria/2001/2009(H1N1))]
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KCNIAGWILGNPECESLSTASSWSYIVETSSSDNGTCYPGDFIDYEELREQLSSVSSFERFEIFPKTSSW
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GIIISDTPVHDCNTTCQTPKGAINTSLPFQNIHPITIGKCPKYVKSTKLRLATGLRNVPSIQSRGLFGAI
AGFIEGGWTGMVDGWYGYHHQNEQGSGYAADLKSTQNAIDEITNKVNSVIEKMNTQFTAVGKEFNHLEKR
IENLNKKIDDGFLDIWTYNAELLVLLENERTLDYHDSNVKNLYEKVRSQLKNNAKEIGNGCFEFYHKCDN
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QC

>gi|237604397|gb|ACR01019.1| hemagglutinin [Influenza A virus
(A/Christchurch/2/2009(H1N1))]
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NADAYVFVGSSRYSKKFKPEIAIRPKVRDQEGRMNYYWTLVEPGDKITFEATGNLVVPRYAFAMERNAGS
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IENLNKKVDDGFLDIWTYNAELLVLLENERTLDYHDSNVKNLYEKVRSQLKNNAKEIGNGCFEFYHKCDN
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QC

>gi|237651252|gb|ACR08500.1| hemagglutinin [Influenza A virus
(A/Auckland/1/2009(H1N1))]
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NADAYVFVGSSRYSKKFKPEIAIRPKVRDQEGRMNYYWTLVEPGDKITFEATGNLVVPRYAFAMERNAGS
GIIISDTPVHDCNTTCQTPKGAINTSLPFQNIHPITIGKCPKYVKSTKLRLATGLRNVPSIQSRGLFGAI
AGFIEGGWTGMVDGWYGYHHQNEQGSGYAADLKSTQNAIDEITNKVNSVIEKMNTQFTAVGKEFNHLEKR
IENLNKKVDDGFLDIWTYNAELLVLLENERTLDYHDSNVKNLYEKVRSQLKNNAKEIGNGCFEFYHKCDN
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QC

>gi|239504534|gb|ACR78585.1| hemagglutin [Influenza A virus (A/Sao
Paulo/1454/2009(H1N1))]
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NADAYVFVGSSRYSKKFKPEIAIRPKVRDQEGRMNYYWTLVEPGDKITFEATGNLVVPRYAFAMERNAGS
GIIISDTPVHDCNTTCQTPKGAINTSLPFQNIHPITIGKCPKYVKSTKLRLATGLRNVPSIQSRGLFGAI
AGFIEGGWTGMVDGWYGYHHQNEQGSGYAADLKSTQNAIDEITNKVNSVIEKMNTQFTAVGKEFNHLEKR
IENLNKKVDDGFLDIWTYNAELLVLLENERTLDYHDSNVKNLYEKVRSQLKNNAKEIGNGCFEFYHKCDN
TCMESVKNGTYDYPKYSEEAKLNREEIDGVKLESTRIYQILAIYSTVASSLVLVVSLGAISFWMCSNGSL
QCRICI

3.2. Sekuen Protein HA Inang Babi

**>gi|4585155|gb|AAD25301.1|AF091306_1 hemagglutinin precursor [influenza A virus
(A/swine/Hokkaido/2/81 (H1N1))]**
MKAILLVLLCTFAATNADTLCIGYHANNSTDTVDTILEKNVTVTHSVNLLEDKHNGKLCKLGGIAPLHLG
KCNIAGWLLGNPECELLFTVSSWSYIVETSNSDNGTCYPGDFINYEELREQLSSVSSFERFEIFPKTSSW
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QCRICI

>gi|163676476|gb|ABY40409.1| hemagglutinin [Influenza A virus
(A/swine/Chonburi/06CB2/2006(H1N1))]
MKAILLILLCTLAAANADTLCIGYHANNSTDTVDTVLEKNVTVTHSVNLLEDRHNGKLCNLRGKAPLHLG
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GIITSDAPVHDCNATCQTPKGAINTSLPFQNIHPITIGECPKYVKSTRLRMATGLRNIPSIQSRGLFGAI
AGFIEGGWTGMIDGWYGYHHQNGQGSGYAADQKSTQNAIDRITNKVNSVIEKMNIQFTAVGKEFNHLERR
IENLNKKVDDGFLDVWTYNAELLVLLENERTLDFHDSNVKTLYEKVKTQLRNNAKEIGNGCFEFYHKCDD
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QCRICI

>gi|210076637|gb|ACJ06667.1| hemagglutinin [Influenza A virus
(A/swine/Zhejiang/1/2007(H1N1))]
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NCNVAGWILGNPKCDLLLTANSWSYIIETSNSKNGACYPGEFADYEELKEQLSTVSSFERFEIFPKATSW
PNHDTTRGTTVACPHSGANSFYRNLLWIVKKGNSYPKLSKSYTNNKGKEVLVIWGVHHPPTDSDQQTLYQ
NNHTYVSVGSSKYYKRFTPEIVARPKVREQAGRMNYYWTLLDQGDTITFEATGNLIVPWHAFALKKGSNS
GIMMSDAQVHNCTTKCQTPHGALKSNLPFQNVHPVTIGECPKYVKSTQLRMATGLRNIPSIQSRGLFGAI
AGFIEGGWTGMIDGWYGYHHQNEQGSGYAADQKSTQIAIDGISNKVNSVIEKMNIQFTSMGKEFNNLEKR
MENLNKKVDDGFLDVWTYNAELLILLENERTLDFHDLNVKNLYEKVKSQLRNNAKEIGNGCFEFYHKCDN
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QCRVCI

>gi|190403701|gb|ACE77928.1| hemagglutinin [Influenza A virus
(A/swine/Korea/CAS08/2005(H1N1))]
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KCNIAGWLLGNPECESLFTASSWSYIVETPNSDNGTCYPGDFINYEELREHLSSVSSFERFEIFPKANSW
PNHDTDKGVTAACPYAGANSFYRNLIWLVKKGNSYPKLSKSYINNKKKEVLVIWGIHHPPTSTDQQTLYQ
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GIIVSDAPVHDCNTTCQTPKGAINTSLPFQNIHPVTIGECPKYVKSTKLRMATGLRNIPSIQSRGLFGAI
AGFIEGGWTGMIDGWYGYHHQNEQGSGYAADQKSTQNAIDGITNKVNSIIEKMNTQFTAVGKEFSQLEKR
IESLNNKVDDGFLDIWTYNAELLVLLENERTLDYHDSNVKNLYEKVRSQLKNNAKEIGNGCFEFYHKCDD
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QCRICI

>gi|151335575|gb|ABS00315.1| hemagglutinin [Influenza A virus
(A/swine/Henan/01/2006(H1N1))]
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NCSVAGWILGNPECESLFSKKSWSYIAETPNSENGTCYPGYFADYEELREQLSSVSSFERFEIFPKESSW
PNHTVTKGVSASCSHKGRSSFYRNLLWLTEKNGSYPNLSKSYVNNKEREVLVLWGVHHPSNIGEQRAIYH
TENAYVSVVSSHYNRRFTPEIAKRPKVRGQEGRINYYWTLLEPGDTIIFEANGNLIAPWYAFALSRGFGS
GIITSNASMDECDAKCQTPQGAINSSLPFQNVHPVTIGECPKYVRSTKLRMVTGLRNIPSIQSRGLFGAI
AGFIEGGWTGMIDGWYGYHHQNEQGSGYAADQKSTQNAINGITNKVNSVIEKMNTQFTAVGKEFNKLERR
MENLNKKVDDGFLDIWTYNAELLVLLENERTLDFHDSNVKNLYEKVKSQLKNNAKEIGNGCFEFYHKCNN
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QCRICI

>gi|238867285|gb|ACR67261.1| hemagglutinin [Influenza A virus
(A/swine/Parma/1997(H1N1))]
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GIITSDAPVHNCDTKCQTPHGALNSSLPFQNVHPITIGECPKYVKSTKLRMATGLRNVPSIQSRGLFGAI
AGFIEGGWTGMIDGWYGYHHQNEQGSGYAADQKSTQNAIDGISNKVNSVIEKMNTQFTAVGKEFNDLEKR
IENLNKKVDDGFLDVWTYNAELLVLLENERTLDFHDFNVRNLYEKVKSQLRNNAKEIGNGCFEFYHKCDD
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QCRICI

>gi|238057035|gb|ACR39188.1| hemagglutinin [Influenza A virus
(A/swine/Ennigerloh/IDT5803/2006(H1N1))]
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GIMMSDAHVHNCTTKCQTPHGALKSNLPFQNVHPITIGECPKYVKSTQLRMATGLRNIPSIPSRGLFGAI
AGFIEGGWTGMIDGWYGYHHQNEQGSGYAADQKSTQIAIDGISNKVNSVIEKMNIQFTSVGKEFNNLEKR
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QCRICI

>gi|224923729|gb|ACN67524.1| hemagglutinin [Influenza A virus
(A/swine/Belgium/1/1998(H1N1))]
MEAKLFVLFCVFNALKADTICVGYHANNSTDTVDTILEKNVTVTHSVNLLENSHNGKLCSLNGKAPLQLG
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IENLNKKVDDGFLDIWTYNAELLILLENERTLDFHDFNVKNLYEKVKSQLRNNAKEVGNGCFEFYHKCDN
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QCRICI

>gi|224979377|gb|ACN72617.1| hemagglutinin [Influenza A virus
(A/swine/Hungary/19774/2006(H1N1))]
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NCNVAGWILGNPECDLLLTANSWSYIIETSDSKNGACYPGEFADYEELREQLSTVSSFERFEIFPKATSW
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NKHTYVSVGSSKYYQRFTPEIVTRPKVREQAGRMNYYWTLLDQGDTITFEATGNLIAPWHAFALNKGSNS
GIMMSDAHVHNCTTKCQTPHGALKGNLPFQNVHPITIGECPKYVKSTQLRMATGLRNIPSIQSRGLFGAI
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QCRICI

>gi|20068267|emb|CAC86337.1| haemagglutinin [Influenza A virus (A/swine/Cotes
d'Armor/1488/99(H1N1))]
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HSGANSFYRNLLWIVKKGNSYPKLSKSYTNNKGKEVLVIWGVHHPPTDSDQQTLYQNNHTYVSVGSSKYY
QRFTPEIVARPKVRKQAGRINYYWTLLDQGDTITFEATGNLIAPWHAFALNKGSSSGIMMSDAHVHNCTT
KCQTPHGALKSNLPFQNVHPVTIGECPKYVKSTQLRMATGLRNIPSIQSRGLFGAIAGFIEGGWTGMIDG
WYGYHHQNEQGSGYAADQKSTQIAIDGISNKVNSVIEKMNIQFTSVGKEFNDLEKRIENLNKKVDDGFLD
VWTYNAELLILLENERTLDFHDFNVKNLYEKVKSQLRNNAKEIGNGCFEFYHKCDNECMESVKNGTYNYP
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(A/swine/Spain/53207/2004(H1N1))]
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IENLNKKVDDGFLDVWTYNAELLILLENERTLDFHDFNVKNLYEKVKSQLRNNAKEIGNGCFEFYHKCDN
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QCRICI

>gi|52078155|gb|AAU25851.1| hemagglutinin [Influenza A virus
(A/swine/Saskatchewan/18789/02(H1N1))]
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PNHETTKGVTAACSYSGASSFYRNLLWITKKGTSYPKLSKSYTNNKGKEVLVLWGVHHPPTTSDQQSIYQ
NTDAYVSVGSSKYNRRFTPEIAARPKVRGQAGRMNYYWTLLDQGDTITFEATGNLIAPWYAFALNKGSDS
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AGFIEGGWTGMIDGWYGYHHQNEQGSGYAADQKSTQNAIDGITNKVNSVIEKMNTQFTAVGKEFNNLERR
IENLNRKVDDGFLDVWTYNAELLVLLENERTLDFHDSNVRNLYEKVRSQLRNNAKELGNGCFEFYHKCDD
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QCRICI

>gi|157168452|gb|ABV25640.1| hemagglutinin [Influenza A virus (A/swine/North
Carolina/36883/2002(H1N1))]
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PNHDTDKGVTAACPYAGANSFYRNLIWLVKKGNSYPKLSKSYINNKKKEVLVIWGIHHPPTSTDQQTLYQ
NADAYVFVGSSKYSKEFKPEIAARPKVRDQAGRMNYYWTLIEPGDTITFEATGNLVVPRYAFAMKRGSGS
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>gi|157168458|gb|ABV25643.1| hemagglutinin [Influenza A virus
(A/swine/Iowa/00239/2004(H1N1))]
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QCRICI

>gi|237624328|gb|ACR01025.1| hemagglutinin [Influenza A virus
(A/swine/Alberta/OTH-33-8/2009(H1N1))]
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QCRICI

>gi|197344172|gb|ACH69547.1| hemagglutinin [Influenza A virus
(A/swine/OH/511445/2007(H1N1))]
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KCNIAGWLLGNPECESLSTASSWSYIVETSNSDNGTCYPGDFINYEELREQLSSVSSFERFEIFPKTSSW
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QCRICI

>gi|221327007|gb|ACM17276.1| hemagglutinin [Influenza A virus
(A/swine/IL/00685/2005(H1N1))]
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NCSVAGWILGNPECELLISKESWSYIVETPNPENGACYPGYFTDYEELREQLSSVSSFERFEIFPKESSW
PNHTVTGVSASCSHNGKSSFYRNLLWLTGKNGLYPNLSKSYTNNKEKEVLVLWGVHHPSNIGDQRALYHT
ENAYVSVVSSHCSRRFTPEIAKRPKVRDQEGRINYYWTLLEPGDTIIFEANGNLIAPRYAFALSRGFGSG
IITSNAPMDECNAKCQTPQGAINSSLPFQNVHPVTIGECPKYVRSAKLRMVTGLRNTPSIQSRGLFGAIA
GFIEGGWTGMVDGWYGYHHQNEQGSGYAADQKSTQNAINGITNKVNSVIEKMNTQFTAVGKEFNKLERRM
ENLNKKVDDGFLDIWTYNAELLVLLENERTLDFHDSNVKNLYEKVKSQLKNNAKEIGNGCFEFYHKCNDE
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CRICI

>gi|221326988|gb|ACM17265.1| hemagglutinin [Influenza A virus
(A/swine/NC/00573/2005(H1N1))]
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PNHTVTGVSASCSHNGKSSFYRNLLWLTGKNGLYPNLSKSYTNNKEKEVLVLWGVHHPPNIGNQRALYHT
ENAYVSVVSSHYSRRFTPEIAKRPKVRDQEGRINYYWTLLEPGDTIIFEANGNLIAPRYAFALSRGFGSG
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GFIEGGWTGMVDGWYGYHHQNEQGSGYAADQKSTQNAINGITNKVNSVIEKMNTQFTAVGKEFNKLERRM
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CRICI

>gi|82622903|gb|ABB86907.1| hemagglutinin [Influenza A virus
(A/swine/Ontario/53518/03(H1N1))]
MKAILLVLLYTFTSTNADTLCIGYHANNSTDTVDTVLEKNVTVTHSVNLLEDKHNGKLCRLGGIAPLHLG
KCNIAGWLLGNPECDLLLTVSSWSYIVETSNSYNGTCYPGDFTNYEELREQLSSVSSFERFEIFPKASSW
PNHETNRGVTAACPHAGTNSFYRNLIWLVKKGNTYPKLSKSYVNNKGKEVLVLWGIHHPSTSTDQQSLYQ
NADTYVFVGTSKYNKKFKPEIAVRPKVKDQAGRMNYYWTLVEPGDTITFEATGNLVVPRYAFAMNRGHGS
GIIISDTPVHDCNTTCQTPKGAINTSLPFQNVHPVTIGKCPKYVKSTRLRMATGLRNIPSIQSRGLFGAI
AGFIEGGWTGMIDGWYGYHHQNGQGSGYAADQKSTQNAIDGITNKVNSVIEKMNTQFTAVGKEFNHLEKR
IENLNKKVDDGFLDVWTYNAELLVLLENERTLDFHDSNVKNLYEKVRRQLKNNAKEIGNGCFEFYHNCDD
ACMESVKNGTYDYPKYSEESRLNREEINGIKLDSTRIYQILAIYSTVASSSVLLVSLGAISFWMCSNGSL
QCRICI

>gi|82622957|gb|ABB86937.1| hemagglutinin [Influenza A virus
(A/swine/Ontario/23866/04(H1N1))]
MKAILLVLLYTFTSTNADTLCIGYHANNSTDTVDTVLEKNVTVTHSVNLLEDKHNGRLCKLGGIAPLHLG
KCNIAGWLLGNPECELLFTVSSWSYIVETSNSYNGTCYPGDFINYEELREQLSSVSSFERFEIFPKASSW
PNHETNRGVTAACPHAGTNSFYRNLIWLVKKGNTYPKISKSYVNNKGKEVLVLWGIHHPSTSNDQQSLYQ
NADTYVFVGPSKYNKKFKPEIATRPKVRDQAGRMNYYWTLVEPGDTITFEATGNLVVPRYAFAMNRGSES

GIIISDTPVHDCNTTCQTPKGAINTSLPFQNVHPVTIGECPKYVKSTRLRMATGLRNIPSIQSRGLFGAI
AGFIEEGWTGMIDGWYGYHHQNGQGSGYAADQKSTQNAIDGITNKVNSVIEKMNTQFTAVGKEFNHLEKR
IENLNKKVDDGFLDVWTYNAELLVLLENERTLDFHDSNVKNLYEKVRRQLKNNAKEIGNGCFEFYHKCDD
ACMESVKNGTYDYPKYSEESRLNREEINGIKLDSTRIYQILAIYSTVASSSVLLVSLGAISFWMCSNGSL
QCRICI

>gi|237872683|gb|ACR26701.1| hemagglutinin [Influenza A virus (A/swine/North Carolina/7571/2003(H1N1))]
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KCNIAGWLLGNPECESLFTASSWSYIVETSNSDNGTCYPGDFINYEELREQLSSVSSFERFEIFPNASSW
PDHETNKGVTAACSHXGAKSFYRNLLWLVKRKNSYPKLSKSYINNKGKEVLVLWGIHHPSTNQDQETLYQ
NTDAYVFVGSSKYSKKFKPEIATRPKVRDQTGRMNYYWTLIEPGDTITFEATGNLVVPRYAFAMERGSGS
GIIISDATVHDCNATCQTPKGAINTSLPFQNIHPVTIGECPKYVKSTKLRMATGLRNVPSIQSRGLFGAI
AGFIEGGWTGMIDGWYGYHHQNEQGSGYAADRKSTQNAIDGITNKVNSVIEKMNTQFTAVGKEFNHLEKR
IENLNKKVDDGFLDVWTYNAELLVLLENERTLDYHDSNVKNLYEKVRSQLKNNAKEIGNGCFEFYHKCDD
TCMESVKNGTYDYPKYSEEAKLNREEIDGVKLESTRIYQILAIYSTVASSLVLVVSLGAISFWMCSNGSL
QCRICI

3.3. Sekuen Protein NA Inang Manusia

>gi|195661083|gb|ACG50708.1| neuraminidase [Influenza A virus (A/Johannesburg/12/2008(H1N1))]
QKIITIGSISIAIGIISLMLQIGNIISIWASHSIQTGSQNNTGICNQRIITYENSTWVNHTYVNINNTKV
VAGEDKTSVTLAGNSSLCSISGWAIYTKDNSIRIGSKGDVFVIREPFISCSHLECRTFFLTQGALLNDKH
SNGTVKDRSPYRALMSCPLGEAPSPYNSKFESVAWSASACHDGMGWLTIGISGPDNGAVAVLKYNGIITG
TIKSWKKQILRTQESECVCMNGSCFTIMTDGPSNKAASYKIFKIEKGKVTKSIELNAPNFYYEECSCYPD
TGIVMCVCRDNWHGSNRPWVSFNQNLDYQIGYICSGVFGDNPRPEDGEGSCNPVTVDGANGVKGFSYKYG
NGVWIGRTKSNRLRKGFEMIWDPNGWTNTDSDFSVKQDVVAITDWSGYSGSFVQHPELTGLDCIRPCFWV
ELVRGLPRENTTIWTSGSSISFCGVNSDTANWSWPDGAELPFTIDK

>gi|31096413|emb|CAD57261.1| neuraminidase [Influenza A virus (A/Hong Kong/437/2002(H1N1))]
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VAGKDKTSVTLAGNSSLCSISGWAIYTKDNSIRIGSKGDVFVIREPFISCSHLECRTFFLTQGALLNDKH
SNGTVKDRSPYRALMSCPLGEAPSPYNSKFESVAWSASACHDGMGWLTIGISGPDNGAVAVLKYNGIITE
TIKSWKKRILRTQESECVCVNGSCFTIMTDGPSNGAASYKIFKIEKGKVTKSVELNAPNFHYEECSCYPD
TGTVMCVCRDNWHGSNRPWVSFDQNLDYQIGYICSGVFGDNPRPKDGEGSCNPVTVDGADGVKGFSYKYG
NGVWIGRTKSNRLRKGFEMIWDPNGWTDTDSDFSVKQDVVAITDWSGYSGSFVQHPELTGLDCIRPCFWV
ELVRGLPRENTTIWTSGSSISFCGVNSATANWSWPDGAELPFTIDK

>gi|237681744|gb|ACR10236.1| neuraminidase [Influenza A virus (A/Narita/1/2009(H1N1))]
MNPNQKIITIGSVCMTIGMANLILQIGNIISIWISHSIQLGNQNQIETCNQSVITYENNTWVNQTYVNIS
NTNFAAGQSVVSVKLAGNSSLCPVSGWAIYSKDNSVRIGSKGDVFVIREPFISCSPLECRTFFLTQGALL
NDKHSNGTIKDRSPYRTLMSCPIGEVPSPYNSRFESVAWSASACHDGINWLTIGISGPDNGAVAVLKYNG
IITDTIKSWRNNILRTQESECACVNGSCFTVMTDGPSNGQASYKIFRIEKGKIVKSVEMNAPNYHYEECS
CYPDSSEITCVCRDNWHGSNRPWVSFNQNLEYQIGYICSGIFGDNPRPNDKTGSCGPVSSNGANGVKGFS
FKYGNGVWIGRTKSISSRNGFEMIWDPNGWTGTDNNFSIKQDIVGINEWSGYSGSFVQHPELTGLDCIRP
CFWVELIRGRPKENTIWTSGSSISFCGVNSDTVGWSWPDGAELPFTIDK

>gi|237689850|gb|ACR15757.1| neuraminidase [Influenza A virus (A/Israel/644/2009(H1N1))]
MNPNQKIITIGSVCMTIGMANLILQIGNIISIWISHSIQLGNQNQIETCNQSVITYENNTWVNQTYVNIS
NTNFAAGQSVVSVKLAGNSSLCPVSGWAIYSKDNSVRIGSKGDVFVIREPFISCSPLECRTFFLTQGALL
NDKHSNGTIKDRSPYRTLMSCPIGEVPSPYNSRFESVAWSASACHDGINWLTIGISGPDNGAVAVLKYNG
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CYPDSSEITCVCRDNWHGSNRPWVSFNQNLEYQIGYICSGIFGDNPRPNDKTGSCGPVSSNGANGVKGFS
FKYGNGVWIGRTKSISSRNGFEMIWDPNGWTGTDNNFSIKQDIVGINEWSGYSGSFVQHPELTGLDCIRP
CFWVELIRGRPKENTIWTSGSSISFCGVNSDTVGWSW

>gi|238914612|gb|ACR78155.1| neuraminidase [Influenza A virus
(A/Philippines/2009/2009(H1N1))]
MNPNQKIITIGSVCMTIGMANLILQIGNIISIWISHSIQLGNQNQIETCNQSVITYENNTWVNQTYVNIS
NTNFAAGQSVVSVKLAGNSSLCPVSGWAIYSKDNSIRIGSKGDVFVIREPFISCSPLECRTFFLTQGALL
NDKHSNGTIKDRSPYRTLMSCPIGEVPSPYNSRFESVAWSASACHDGINWLTIGISGPDNGAVAVLKYNG
IITDTIKSWRNNILRTQESECACVNGSCFTVMTDGPSDGQASYKIFRIEKGKIVKSVEMNAPNYHYEECS
CYPDSSEITCVCRDNWHGSNRPWVSFNQNLEYQIGYICSGIFGDNPRPNDKTGSCGPVSSNGANGVKGFS
FKYGNGVWIGRTKSISSRNGFEMIWDPNGWTGTDNNFSIKQDIVGINEWSGYSGSFVQHPELTGLDCIRP
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>gi|239812998|gb|ACS27784.1| neuraminidase [Influenza A virus
(A/Shanghai/37T/2009(H1N1))]
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NTNFAAGQSVVSVKLAGNSSLCPVSGWAIYSKDNSIRIGSKGDVFVIREPFISCSPLECRTFFLTQGALL
NDKHSNGTIKDRSPYRTLMSCPIGEVPSPYNSRFESVAWSASACHDGINWLTIGISGPDNGAVAVLKYNG
IITDTIKSWRNNILRTQESECAVVNGSCFTVMTDGPSDGQASNKIFRIEKGKIVKSVEMNAPNYHYEECS
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FKYGNGVWIGRTKSISSRNGFEMIWDPNGWTGTDNNFSIKQDIVGINEWSGYSGSFVQHPELTGLDCIRP
CFWVELIRGRPKENTIWTSGSSISFCGVNSDTVGWSWPDGAELPFTIDK

>gi|237604390|gb|ACR01015.1| neuraminidase [Influenza A virus
(A/Nonthaburi/102/2009(H1N1))]
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NDKHSNGTIKDRSPYRTLMSCPIGEVPSPYNSRFESVAWSASACHDGINWLTIGISGPDNGAVAVLKYNG
IITDTIKSWRNNILRTQESECACVNGSCFTVMTDGPSDGQASYKIFRIEKGKIVKSVEMNAPNYHYEECS
CYPDSSEITCVCRDNWHGSNRPWVSFNQNLEYQIGYICSGIFGDNPRPNDKTGSCGPVSSNGANGVKGFS
FKYGNGVWIGRTKSISSRNGFEMIWDPNGWTGTDNNFSIKQDIVGINEWSGYSGSFVQHPELTGLDCIRP
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>gi|229892682|gb|ACQ89891.1| neuraminidase [Influenza A virus
(A/Korea/01/2009(H1N1))]
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NDKHSNGTIKDRSPYRTLMSCPIGEVPSPYNSRFESVAWSASACHDGINWLTIGISGPDNGAVAVLKYNG
IITDTIKSWRNNILRTQESECACVNGSCFTVMTDGPSNGQASYKIFRIEKGKIVKSVEMNAPNYHYEECS
CYPDSSEITCVCRDNWHGSNRPWVSFNQNLEYQIGYICRGIFGDNPRPNDKTGSCGPVSSNGANGVKGFS
FKYGNGVWIGRTKSISSRNGFEMIWDPNGWTGTDNNFSIKQDIVGINEWSGYSGSFVQHPELTGLDCIRP
CFWVELIRGRPKENTIWTSGSSISFCGVNSDTVGWSWPDGAELPFTIDK

>gi|228860931|gb|ACQ45339.1| neuraminidase [Influenza A virus
(A/Netherlands/602/2009(H1N1))]
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NDKHSNGTIKDRSPYRTLMSCPIGEVPSPYNSRFESVAWSASACHDGINWLTIGISGPDNGAVAVLKYNG
IITDTIKSWRNNILRTQESECACVNGSCFTVMTDGPSNGQASYKIFRIEKGKIVKSVEMNAPNYHYEECS
CYPDSSEITCVCRDNWHGSNRPWVSFNQNLEYQIGYICSGIFGDNPRPNDKTGSCGPVSSNGANGVKGFS
FKYGNGVWIGRTKSISSRNGFEMIWDPNGWTGTDNNFSIKQDIVGINEWSGYSGSFXQHPELTGLDCIRP
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>gi|229609553|gb|ACQ83396.1| neuraminidase [Influenza A virus
(A/Stockholm/28/2009(H1N1))]
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VSVKLAGNSSLCPVSGWAIYSKDNSVRIGSKGDVFVIREPFISCSPLECRTFFLTQGALLNDKHSNGTIK
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NNILRTQESECACVNGSCFTVMTDGPSNGQASYKIFRIEKGKIVKSVEMNAPNYHYEECSCYPDSSEITC
VCRDNWHGSNRPWVSFNQNLEYQIGYICSGIFGDNPRPNDKTGSCGPVSSNGANGVKGFSFKYGNGVWIG
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PKENTIWTSGSSISFCGVNSDTVGWSWPDGAE

>gi|238618427|gb|ACR46980.1| neuraminidase [Influenza A virus
(A/Moscow/01/2009(H1N1))]
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NTNFAAGQSVVSVKLAGNSSLCPVSGWAIYSKDNSIRIGSKGDVFVIREPFISCSPLECRTFFLTQGALL
NDKHSNGTIKDRSPYRTLMSCPIGEVPSPYNSRFESVAWSASACHDGINWLTIGISGPDNGAVAVLKYNG
IITDTIKSWRNNILRTQESECACVNGSCFTVMTDGPSDGQASYKIFRIEKGKIVKSVEMNAPNYHYEECS
CYPDSSEITCVCRDNWHGSNRPWVSFNQNLEYQIGYICSGIFGDNPRPNDKTGSCGPVSSNGANGVKGFS
FKYGNGVWIGRTKSISSRNGFEMIWDPNGWTGTDNNFSIKQDIVGINEWSGYSGSFVQHPELTGLDCIRP
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>gi|238627784|gb|ACR49231.1| neuraminidase [Influenza A virus
(A/Poland/37/2009(H1N1))]
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IITDTIKSWRNNILRTQESECACVNGSCFTVMTDGPSDGQASYKIFRIEKGKIVKSVEMNAPNYHYEECS
CYPDSSEITCVCRDNWHGSNRPWVSFNQNLEYQIGYICSGIFGDNPRPNDKTGSXGPVSSNGANGVKGFS
FKYGNGVWIGRTKSISSRNGFEMIWDPNGWTGTDNNFSIKQDIVGINEWSGYSGSFVQHPELTGLDCIRP
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>gi|237689829|gb|ACR15745.1| neuraminidase [Influenza A virus
(A/Lisboa/26/2009(H1N1))]
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YPDSSEITCVCRDNWHGSNRPWVSFNQNLEYQIGYICSGIFGDNPRPNDKTGSCGPVSSNGANGVKGFSF
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>gi|237681728|gb|ACR10226.1| neuraminidase [Influenza A virus
(A/Bayern/63/2009(H1N1))]
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NDKHSNGTIKDRSPYRTLMSCPIGEVPSPYNSRFESVAWSASACHDGINWLTIGISGPDNGAVAVLKYNG
IITDTIKSWRNNILRTQESECACVNGSCFTVMTDGPSDGQASYKIFRIEKGKIVKSVEMNAPNYHYEECS
CYPDSSEITCVCRDNWHGSNRPWVSFNQNLEYQIGYICSGIFGDNPRPNDKTGSCGPVSSNGANGVKGFS
FKYGNGVWIGRTKSISSRNGFEMIWDPNGWTGTDNNFSIKQDIVGINEWSGYSGSFVQHPELTGLDCIRP
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>gi|229368679|gb|ACQ59196.1| neuraminidase [Influenza A virus
(A/Denmark/513/2009(H1N1))]
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IITDTIKSWRNNILRTQESECACVNGSCFTVMTDGPSNGQASYKIFRIEKGKIVKSVEMNAPNYHYEECS
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FKYGNGVWIGRTKSISSRNGFEMIWDPNGWTGTDNNFSIKQDIVGINEWSGYSGSFVQHPELTGLDCIRP
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>gi|229892732|gb|ACQ89919.1| neuraminidase [Influenza A virus
(A/Mexico/InDRE4114/2009(H1N1))]
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FKYGNGVWIGRTKSISSRNGFEMIWDPNGWTGTDNNFSIKQDIVGINEWSGYSGSFVQHPELTGLDCIRP
CFWVELIRGRPKENTIWTSGSSISFCGVNSDTVGWSWPDGAELPFTIDK

>gi|229396353|gb|ACQ63207.1| neuraminidase [Influenza A virus (A/New
York/12/2009(H1N1))]
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IITDTIKSWRNNILRTQESECACVNGSCFTVMTDGPSDGQASYKIFRIEKGKIVKSVEMNAPNYHYEECS
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FKYGNGVWIGRTKSISSRNGFEMIWDPNGWTGTDNNFSIKQDIVGINEWSGYSGSFVQHPELTGLDCIRP
CFWVELIRGRPKENTIWTSGSSISFCGVNSDTVGWSWPDGAELPFTIDK

>gi|227831797|gb|ACP41947.1| neuraminidase [Influenza A virus
(A/Texas/05/2009(H1N1))]
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NDKHSNGTIKDRSPYRTLMSCPIGEVPSPYNSRFESVAWSASACHDGINWLTIGISGPDNGAVAVLKYNG
IITDTIKSWRNNILRTQESECACVNGSCFTVMTDGPSNGQASYKIFRIEKGKIVKSVEMNAPNYHYEECS
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FKYGNGVWIGRTKSISSRNGFEMIWDPNGWTGTDNNFSIKQDIVGINEWSGYSGSFVQHPELTGLDCIRP
CFWVELIRGRPKENTIWTSGSSISFCGVNSDTVGWSWPDGAELPFTI

>gi|238623294|gb|ACR47008.1| neuraminidase [Influenza A virus
(A/Mexico/47N/2009(H1N1))]
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NDKHSNGTIKDRSPYRTLMSCPIGEVPSPYNSRFESVAWSASACHDGINWLTIGISGPDNGAVAVLKYNG
IITDTIKSWRNNILRTQESECACVNGSCFTVMTDGPSNGQASYKIFRIEKGKIVKSVEMNAPNYHYEECS
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FKYGNGVWIGRTKSISSRNGFEMIWDPNGWTGTDNNFSIKQDIVGINEWSGYSGSFVQHPELTGLDCIRP
CFWVELIRGRPKENTIWTSGSSISFCGVNSDTVGWSWPDGAELPFTIDK

>gi|227977158|gb|ACP44181.1| neuraminidase [Influenza A virus
(A/Ohio/07/2009(H1N1))]
MNPNQKIITIGSVCMTIGMANLILQIGNIISIWISHSIQLGNQNQIETCNQSVITYENNTWVNQTYVNIS
NTNFAAGQSVVSVKLAGNSSLCPVSGWAIYSKDNSIRIGSKGDVFVIREPFISCSPLECRTFFLTQGALL
NDKHSNGTIKDRSPYRTLMSCPIGEVPSPYNSRFESVAWSASACHDGINWLTIGISGPDNGAVAVLKYNG
IITDTIKSWRNNILRTQESECACVNGSCFTVMTDGPSDGQASYKIFRIEKGKIVKSVEMNAPNYHYEECS
CYPDSSEITCVCRDNWHGSNRPWVSFNQNLEYQIGYICSGIFGDNPRPNDKTGSCGPVSSNGANGVKGFS
FKYGNGVWIGRTKSISSRNGFEMIWDPNGWTGTDNNFSIKQDIVGINEWSGYSGSFVQHPELTGLDCIRP
CFWVELIRGRPKENTIWTSGSSISFCGVNSDTVGWSWPDGAELPFTIDK

>gi|238635095|gb|ACR40321.2| neuraminidase [Influenza A virus (A/New
York/3252/2009(H1N1))]
MNPNQKIITIGSVCMTIGMANLILQIGNIISIWISHSIQLGNQNQIETCNQSVITYENNTWVNQTYVNIS
NTNFAAGQSVVSVKLAGNSSLCPVSGWAIYSKDNSIRIGSKGDVFVIREPFISCSPLECRTFFLTQGALL
NDKHSNGTIKDRSPYRTLMSCPIGEVPSPYNSRFESVAWSASACHDGINWLTIGISGPDNGAVAVLKYNG
IITDTIKSWRNNILRTQESECACVNGSCFTVMTDGPSDGQASYKIFRIEKGKIVKSVEMNAPNYHYEECS
CYPDSSEITCVCRDNWHGSNRPWVSFNQNLEYQIGYICSGIFGDNPRPNDKTGSCGPVSSNGANGVKGFS
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FKYGNGVWIGRTKSISSRNGFEMIWDPNGWNGTDNNFSIKQDIVGINEWSGYSGSFVQHPELTGLDCIRP
CFWVELIRGRPKENTIWTSGSSISFCGVNSDTVGWSWPDGAELPFTIDK

>gi|238231184|gb|ACR40331.1| neuraminidase [Influenza A virus (A/New
York/3253/2009(H1N1))]
MNPNQKIITIGSVCMSIGMANLILQIGNIISIWISHSIQLGNQNQIETCNQSVITYENNTWVNQTYVNIS
NTNFAAGQSVVSVKLAGNSSLCPVSGWAIYSKDNSIRIGSKGDVFVIREPFISCSPLECRTFFLTQGALL
NDKHSNGTIKDRSPYRTLMSCPIGEVPSPYNSRFESVAWSASACHDGINWLTIGISGPDNGAVAVLKYNG
IITDTIKSWRNNILRTQESECACVNGSCFTVMTDGPSDGQASYKIFRIEKGKIVKSVEMNAPNYHYEECS
CYPDSSEITCVCRDNWHGSNRPWVSFNQNLEYQIGYICSGIFGDNPRPNDKTGSCGPVSSNGANGVKGFS
FKYGNGVWIGRTKSISSRNGFEMIWDPNGWTGTDNNFSIKQDIVGINEWSGYSGSFVQHPELTGLDCIRP
CFWVELIRGRPKENTIWTSGSSISFCGVNSDTVGWSWPDGAELPFTIDK

>gi|237689231|gb|ACR15428.1| neuraminidase [Influenza A virus
(A/Managua/2055.01/2008(H1N1))]
MNPNQKIITIGSISIAIGIISLMLQIGNIISIWASHSIQTGSQNNTGICNQRIITYENSTWVNHTYVNIN
NTNVVAGEDKTSVTLAGNSSLCSVSGWAIYTKDNSIRIGSKGDVFVIREPFISCSHLECRTFFLTKGALL
NDKHSNGTVKDRSPYRALMSCPLGEAPSPYNSKFESVAWSASACHDGMGWLTIGISGPDNGAVAVLKYNG
IITGTIKSWKKQILRTQESECVCMNGSCFTIMTDGPSNKAASYKIFKIEKGKVTKSIELNAPNFHYEECS
CYPDTGIVMCVCRDNWHGSNRPWVSFNQNLDYQIGYICSGVFGDNPRPEDGEGSCNPVTVDGANGVKGFS
YKYDNGVWIGRTKSNRLRKGFEMIWDPNGWTNTDSDFSVKQDVVAITDWSGYSGSFVQHPELTGLDCIRP
CFWVELVRGLPRENTTIWTSGSSISFCGVNSDTANWSWPDGAELPFTIDK

>gi|237511840|gb|ACQ99631.1| neuraminidase [Influenza A virus
(A/Mexico/4108/2009(H1N1))]
GSVCMTIGMANLILQIGNIISIWISHSIQLGNQNQIETCNQSVITYENNTWVNQTYVNISNTNFAAGQSV
VSVKLAGNSSLCPVSGWAIYSKDNSVRIGSKGDVFVIREPFISCSPLECRTFFLTQGALLNDKHSNGTIK
DRSPYRTLMSCPIGEVPSPYNSRFESVAWSASACHDGINWLTIGISGPDNGAVAVLKYNGIITDTIKSWR
NNILRTQESECACVNGSCFTVMTDGPSNGQASYKIFRIEKGKIVKSVEMNAPNYHYEECSCYPDSSEITC
VCRDNWHGSNRPWVSFNQNLEYQIGYICSGIFGDNPRPNDKTGSCGPVSSNGANGVKGFSFKYGNGVWIG
RTKSISSRNGFEMIWDPNGWTGTDNNFSIKQDIVGINEWSGYSGSFVQHPELTGLDCIRPCFWVELIRGR
PKENTIWTSGSSISFCGVNSDTVGWSWPDGAELPFTIDK

>gi|229598898|gb|ACQ83302.1| neuraminidase [Influenza A virus
(A/Christchurch/2/2009(H1N1))]
TIGSVCMTIGMANLILQIGNIISIWISHSIQLGNQNQIETCNQSVITYENNTWVNQTYVNISNTNFAAGQ
SVVSVKLAGNSSLCPVSGWAIYSKDNSVRIGSKGDVFVIREPFISCSPLECRTFFLTQGALLNDKHSNGT
IKDRSPYRTLMSCPIGEVPSPYNSRFESVAWSASACHDGINWLTIGISGPDNGAVAVLKYNGIITDTIKS
WRNNILRTQESECACVNGSCFTVMTDGPSNGQASYKIFRIEKGKIVKSVEMNAPNYHYEECSCYPDSSEI
TCVCRDNWHGSNRPWVSFNQNLEYQIGYICSGIFGDNPRPNDKTGSCGPVSSNGANGVKGFSFKYGNGVW
IGRTKSISSRNGFEMIWDPNGWTGTDNNFSIKQDIVGINEWSGYSGSFVQHPELTGLDCIRPCFWVELIR
GRPKENTIWTSGSSISFCGVNSDTVGWSWPDGAELP

>gi|237651246|gb|ACR08497.1| neuraminidase [Influenza A virus
(A/Brisbane/17/2009(H1N1))]
MNPNQKIITIGSVCMTIGMANLILQIGNIISIWISHSIQLGNQNQIETCNQSVITYENNTWVNQTYVNIS
NTNFAAGQSVVSVKLAGNSSLCPVSGWAIYSKDNSIRIGSKGDVFVIREPFISCSPLECRTFFLTQGALL
NDKHSNGTIKDRSPYRTLMSCPIGEVPSPYNSRFESVAWSASACHDGINWLTIGISGPDNGAVAVLKYNG
IITDTIKSWRNNILRTQESECACVNGSCFTVMTDGPSDGQASYKIFRIEKGKIVKSVEMNAPNYHYEECS
CYPDSSEITCVCRDNWHGSNRPWVSFNQNLEYQIGYICSGIFGDNPRPNDKTGSCGPVSSNGANGVKGFS
FKYGNGVWIGRTKSISSRNGFEMIWDPNGWTGTDNNFSIKQDIVGINEWSGYSGSFVQHPELTGLDCIRP
CFWVELIRGRPKENTIWTSGSSISFCGVNSDTVGWSWPDGAELPF

>gi|238914624|gb|ACR78161.1| neuraminidase [Influenza A virus
(A/Perth/29/2009(H1N1))]
MNPNQKIITIGSVCMTIGMANLILQIGNIISIWISHSIQLGNQNQIETCNQSVITYENNTWVNQTYVNIS
NTNFAAGQSVVSVKLAGNSSLCPVSGWAIYSKDNSVRIGSKGDVFVIREPFISCSPLECRTFFLTQGALL
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NDKHSNGTIKDRSPYRTLMSCPIGEVPSPYNSRFESVAWSASACHDGINWLTIGISGPDNGAVAVLKYNG
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CYPDSSEITCVCRDNWHGSNRPWVSFNQNLEYQIGYICSGIFGDNPRPNDKTGSCGPVSSNGANGVKGFS
FRYGNGVWIGRTKSISSRNGFEMIWDPNGWTGTDNNFSIKQDIVGINEWSGYSGSFVQHPELTGLDCIRP
CFWVELIRGRPKENTIWTSGSSISFCGVNSDTVGWSWPDGAELPF
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>gi|237604392|gb|ACR01016.1| neuraminidase [Influenza A virus
(A/Christchurch/2/2009(H1N1))]

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MNPNQKIITIGSVCMTIGMANLILQIGNIISIWISHSIQLGNQNQIETCNQSVITYENNTWVNQTYVNIS
NTNFAAGQSVVSVKLAGNSSLCPVSGWAIYSKDNSVRIGSKGDVFVIREPFISCSPLECRTFFLTQGALL
NDKHSNGTIKDRSPYRTLMSCPIGEVPSPYNSRFESVAWSASACHDGINWLTIGISGPDNGAVAVLKYNG
IITDTIKSWRNNILRTQESECACVNGSCFTVMTDGPSNGQASYKIFRIEKGKIVKSVEMNAPNYHYEECS
CYPDSSEITCVCRDNWHGSNRPWVSFNQNLEYQIGYICSGIFGDNPRPNDKTGSCGPVSSNGANGVKGFS
FKYGNGVWIGRTKSISSRNGFEMIWDPNGWTGTDNNFSIKQDIVGINEWSGYSGSFVQHPELTGLDCIRP
CFWVELIRGRPKENTIWTSGSSISFCGVNSDTVGWSWPDGAELPF
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>gi|60811|emb|CAA33354.1| neuraminidase [Influenza A virus
(A/Chile/1/1983(H1N1))]

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MNPNQKIITIGSICMTIGIISLILQIGNIISIWVSHSIQTGSQNHTGICNQRIITYENSTWVNQTYVNIN
NTNVVAGKDTTSVTLAGNSSLCPIRGWAIYSKDNSIRIGSKGDVFVIREPFISCSHLECRTFFLTQGALL
NDKHSNGTVKDRSPYRALMSCPIGEAPSPYNSRFESVAWSASACHDGMGWLTIGISGPDDGAVAVLKYNG
IITETIKSWRKRILRTQESECVCVNGSCFTIMTDGPSNGPASYRIFKIEKGKITKSIELDAPNSHYEECS
CYPDTGTVMCVCRDNWHGSNRPWVSFNQNLDYQIGYICSGVFGDNPRPKDGKGSCDPVTVDGADGVKGFS
YRYGNGVWIGRTKSNSSRKGFEMIWDPNGWTDTDSNFLVKQDVVAMTDWSGYSGSFVQHPELTGLDCMRP
CFWVELIRGRPREKTTIWTSGSSISFCGVNSDTANWSWPDGAELPFTIDK
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>gi|148276812|gb|ABQ53690.1| neuraminidase [Influenza A virus
(A/Brazil/199/1997(H1N1))]

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MNPNQKIITIGSISVAIGMISLILQIGNIISIWASHSIQTGSQNYTGICNQRIITYENSTWVNQTYVNIN
NTNVVAGKDKTSMTLAGNSSLCPIRGWAIYTKDNSIRIGSKGDVFVIREPFISCSHLECRTFFLTQGALL
NDKHSNGTVKDRSPYRALMSCPLGEAPSPYNSRFESVAWSASACHDGLGWLTIGISGPDNGAVAVLKYNG
IITETIKSWKKQILRTQESECVCVNGSCFTIMTDGPSDRAASYRIFKIEKGRVTKSIELDAPNYHYEECS
CYPDTGTVMCVCRDNWHGSNRPWVSFNQNLDYQIGYICSGVFGDNPRPKDGEGSCNPVTVDGADGVKGFS
YRYGNGVWIGRTKSNRLRKGFEMIWDPNGWTDTDSDFSMKQDVVAMTDWSGYSGSFVQHPELTGLDCMRP
CFWVELVRGLPRENTTIWTSGSSISFCGVNSETADWSWPDGAELPFTIDK
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3.4. Sekuen Protein NA Inang Babi

>gi|1212736|dbj|BAA06717.1| neuraminidase [Influenza A virus
(A/sw/Obihiro/5/1992(H1N1))]

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MNPNQKIITIGSISMAIGIISLILQIGNIISIWASHSIQTGSQNHTGICNQRMITYENSTWVNQTYVNIS
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NDKHSNGTVKDRSPYRALMSCPLGEAPSPYNSRFESVAWSASACHDGMGWLTIGISGPDDGAVAVLKYNG
IITETIKSWRKQILRTQESECVCVNGSCFTIMTDGPSDGPASYRIFKIEKGKVTKSIELDAPNYHYEECS
CYPDTGTVMCVCRDNWHGSNRPWVSFNQNLDYQIGYICSGVFGDNPRPKDGEGSCNPVTVDGADGVKGFS
YRYGNGVWIGRTKSNRLRKGFEMIWDPNGWTDTDSDFSVKQDVVAMTDWSGYSGSFVQHPELTGLDCMRP
CFWVELIRGRPREKTTIWTSGSSISFCGVNSDTANWSWPDGAELPFTIDK
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**>gi|190403800|gb|ACE77987.1| neuraminidase [Influenza A virus
(A/swine/Korea/CAN01/2004(H1N1))]**

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MNTNQRIITIGTVCLIVGIISLLLQIGNIVSLWISHSIQTGGKNHTEMCNQNVITYVNNTWVNRTYVNIS
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NDKHSNGTVKDRSPYRTLMSCPIGEAPSPYNSRFESVAWSASACHDGMGWLTIGISGPDNGAVAVLKYNG
IITDTIKSWRNKILRTQESECVCMNGSCFTVLTDGPSNGQASYKIFKVEKGKIIKSIELDAPNYHYEECS
CYPDTGKVMCVCRDNWHASNRPWVSFDQNLDYQMGYICSGVFGDNPRSNDGKGNCGPVLSNGANGVKGFS
YRYGNGVWIGRTKSIDSRSGFEMIWDPNGWTETDSSFSMKQDIIALTDWSGYSGSFVQHPELTGMNCIRP
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CFWVELIRGQPKESTIWASGSSISFCGVNSETASWSWPDGADLPFTIDK

>gi|190403802|gb|ACE77988.1| neuraminidase [Influenza A virus
(A/swine/Korea/CAS08/2005(H1N1))]
MNTNQRIITIGTVCLIVGIISLLLQIGNIVSLWISHSIQTGGKNHTEMCNQNVITYVNNTWVNRTYVNIS
NTNIAAVQDVTSVILAGNSSLCPVSGWAIYSKDNSIRIGSKGDIFVIREPFISCSQLECRTFFLTQGALL
NDKHSNGTVKDRSPYRTLMSCPIGEAPSPYNSRFESVAWSASACHDGMGWLTIGISGPDNGAVAVLKYNG
IITDTIKSWRNKILRTQESECVCMNGSCFTVLTDGPSNGQASYKIFKVEKGKIIKSIELDAPNYHYEECS
CYPDTGKVMCVCRDNWHASNRPWVSFDQNLDYQMGYICSGVFGDNPRSNDGKGNCGPVLSNGANGVKGFS
YRYGNGVWIGRTKSTDSRSGFEMIWDPNGWTETDSSFSMKQDIIALTDWSGYSGSFVQHPELTGMNCIRP
CFWVELIRGQPKESTIWASGSSISFCGVNSETASWSWPDGADLPFTIDK

>gi|163676450|gb|ABY40396.1| neuraminidase [Influenza A virus
(A/swine/Chonburi/05CB1/2005(H1N1))]
MNPNQKIITIGSVCVTIGIASLILQIGNIISIWISHSIQIGNQNQPETCNRSVITYENNTWVNQTFVNIN
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NDKHSNGTIKDRSPYRTLMSCLVGEVPSPYNSRFESVAWSASACHDGISWLTIGISGPDNEAVAVLKYNG
IITDTIKSWRKNILRTQESECACVNGSCFTVMTDGPSNGQASYKIFKIEKGKVVKSVELNAPNYHYEECS
CYPESGKITCVCRDNWHGSNRPWVSFNQNLEYQIGYICSGIFGDNPRPNDRTGSCGPVSSNGANGVKGFS
FKYGNGVWIGRTKSTSLRSGFEMIWDPNGWTGTDNNFSAKQDIIGINDWSGYSGSFVQHPELTGLDCMRP
CFWVELIRGRPKENTIWTSGSSISFCGVNSDTVGWSWPDGAELPFNYDK

>gi|163676452|gb|ABY40397.1| neuraminidase [Influenza A virus
(A/swine/Chonburi/06CB2/2006(H1N1))]
MNPNQKIITIGSVCVTIGIASLILQIGNIISIWISHSIQTGNQNQPETCNQSVITYENNTWVNQTFVNIN
NTNFVAEQAIVSVKLAGNSSLCPVSGWAIYSKDNSVRIGSKGDVFVIREPFISCSHLECRTFFLTQGALL
NDKHSNGTIKDRSPYRTLMSCLVGEVPSPYNSRFESVAWSASACHDGISWLTIGISGPDNEAVAVLKYNG
IITDTIKSWRKNILRTQESECACVNGSCFTVMTDGPSNGQASYKIFKIEKGKVVKSVELNAPNYHYEECS
CYPESGKITCVCRDNWHGSNRPWVSFNQNLEYQIGYICSGIFGDNPRPNDRTGSCGPVSSYGANGVKGFS
FKYGNGVWIGRTKSTSLRSGFEMIWDPNGWTGTDNNFSAKQDIIGINDWSGYSGSFVQHPELTGLDCMRP
CFWVELIRGRPKENTIWTSGSSISFCGVNSDTVGWSWPDGAELPFTIDK

>gi|168487842|gb|ACA25342.1| neuraminidase [Influenza A virus
(A/swine/Shanghai/1/2005(H1N1))]
MNTNQRIITIGTACLIIGIVSLLLQIGNIVSLWISHSIQTGEKNHSETCNRNTITYENSTWVNQTYVNIS
NINIAGGQGVASIILAGNSSLCPVNGWAIYSKDNSIRIGSKGDIFVIREPFISCSHLECRTFFLTQGALL
NDRHSNGTVKDRSPYRTLMSCPIGEAPSPYNSKFESVAWSASACHDGMGWLTIGISGPDNGAVAVLKYNG
IITDTIKSWRNRILRTQESECVCINGSCFTIMTDGPSNGQASYKIFKMERGKIIKSVELDAPNYHYEECS
CYPDTGKVVCVCRDNWHASNRPWVSFDQNLDYQIGYICSGVFGDNPRSNDGKGNCGPVLSNGANGVKGFS
FRYGNGVWIGRTKSTNSRSGFEMIWDPNGWTETDSNFSMKQDIIALTDWSGYSGSFVQHPELTGMNCIRP
CFWVELIRGQPKESTIWTSGSSISFCGVDSETASWSWPDGADLPFTIDK

>gi|210076639|gb|ACJ06668.1| neuraminidase [Influenza A virus
(A/swine/Zhejiang/1/2007(H1N1))]
MNPNQKIITIGSICMTIGIASLILQIGNIISIWISHSIQTGNQNKPEICNQNVITYENNTWVNQTYVNIS
NTNFVAEQAVASVKLAGNSSLCPVSGWAIYSKDNSVRIGSKGDVFVIREPFISCSHLECRTFFLTQGALL
NDKHSNGTIKDRSPYRTLMSCPIGEVPSPYNSRFESVAWSASACHDGTSWLTIGISGPDNGAVAVLKYNG
IITDTIKSWRKNILRTQESECACVNGSCFTVMTDGPSNGQASYKVFKIERGKVVKSVELNAPNYHYEECS
CYPESGEITCVCRDNWHGSNRPWVSFNQNLEYQMGYICSGIFGDNPRPNDKTGSCGPVFSNGANGVKGFS
FKYGNGVWIGRTKSTSSRRGFEMIWDPDGWTRTDDKFSVKQDIIGITDWSGYSGSFVQHPELTGLDCMRP
CFWVELIRGRPKENTIWTSGSSISFCGVNSDTVGWSWPDGAELPFTIDK

>gi|224979384|gb|ACN72621.1| neuraminidase [Influenza A virus
(A/swine/Hungary/19774/2006(H1N1))]
MNPNQKIIIISSICMTNGIASLILQIGNIISIWISHSIQTGNQNQTETCNQSVIIYENNTWVNQTYVNIS
NNNFVAEQTVVPVKLVGSSPLCPVSGWAIYSKDNSVRIGSKGDVFVIREPFISCSHLECRTFFLTQGALL
NDKHSNGTVKDRSPYRTLMSCPIGEVPSPYNSRFESVAWSASACHDGSSWLTIGISGPDNGAVAVLKYND
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IITDTIKSWKNNILRTQESECACLNGSCFTVMTDGPSNGQASYKIFKIEKGKVVKSVELNAPNYHYEECS
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FKYGDGIWIGRTKSTSSRSGFEMIWDPNGWTGTDNNFSVKQDIVGITDWTGYSGSFVQHPELTGLDCIRP
CFWVELIRGRPKENTIWTSGSSISFCGVNSDTVGWSWPDGAELPFTIDK

>gi|89789284|gb|ABD78107.1| neuraminidase [Influenza A virus
(A/Swine/Spain/50047/2003(H1N1))]
MNPNQKIITIGSICMTTGIVSLILQIGNLISIWASHSIQIGNQNQPEICNQSVITYENNTWVNQTYVNIN
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NDKHSNGTIKDRSPYRTLMSCPIGEVPSPYNSRFESVAWSASACHDGTSWLTIGISGPDNGAVAVLKYNG
IITDTIKSWRNNILRTQESECACVNGSCFTVMTDGPSNGQASYKIFKIEKGKVVKSVELNAPNYHYEECS
CYPESGEITCVCRDNWHGSNRPWVSFNQNLEYQIGYICSGIFGDNPRPNDRTGSCGPVFSNGANGVKGFS
FKYGNGVWIGRTKSTSSRSGFEMIWDPNGWTRTDDNFSVKQDIIGMTDWSGYSGSFVQHPELTGLDCMRP
CFWVELIRGRPKENTIWTSGSSISFCGVNSDTVSWSWPDGAELPFTIDK

>gi|91177893|gb|ABE27156.1| neuraminidase [Influenza A virus
(A/swine/Spain/53207/2004(H1N1))]
MNPNQKIIIISSICMTNGIASLILQIGNIISIWISHSIQIGNQNQTETCNQSVIIYENNTWVNQTYVNIS
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NDKHSNGTVKDRSPYRTLMSCPIGEVPSPYNSRFESVAWSASACHDGTSWLTIGISGPDNGAVAVLKYND
IITDTIKSWKNNILRTQESECACLNGSCFTVMTDGPSNGQASYKIFKIEKGKVVKSVELNAPNYHYEECS
CYPDSGEIICVCRDNWHGSNRPWVTFNQNLEYQIGYICSGVLGDNPRPNDRTGSCGPVSSHGANGVKGFS
FKYGNGIWIGRTKSTSSRSGFEMIWDPNGWTGTDNNFSVKQDIVGITDWSGYSGSFVQHPELTGLDCIRP
CFWVELIRGRPKENTIWTSGSSISFCGVNSDTVGWSWPDGAELPFTIDK

>gi|238057618|gb|ACR39305.1| neuraminidase [Influenza A virus
(A/swine/Ennigerloh/IDT5803/2006(H1N1))]
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NDKHSNGTIKDRSPYRTLMSCPIGEVPSPYNSRFESVAWSASACHDGTSWLTIGISGPDNGAVAVLKYND
IITDTIKSWRNNILRTQESECACMNGSCFTVMTDGPSNGQASYKIFKIEKGKVVKSVELNAPNYHYEECS
CYPDSGEIICVCRDNWHGSNRPWVSFNQNLEYQIGYICSGVLGDNPRPNDRTGSCGPVSSNGANGVKGFS
FKYGNGVWIGRTKSTSSRSGFEMIWDPNGWTGTDNNFSVKQDIVGITDWSGYSGSFVQHPELTGLSCMRP
CFWVELIRGRPKENTIWTSGSSISFCGVNSDTVGWSWPDGAELPFTIDK

>gi|195933633|gb|ABS50330.2| neuraminidase [Influenza A virus
(A/swine/Italy/247578/2004(H1N1))]
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NNNFVAEQTVISVKLAGSSSLCPVSGWAIYSKDNSVRIGSKGDVFVIREPFISCSHLECRTFFLTQGALL
NDKHSNGTVKDRSPYRTLMSCPIGEVPSPYNSRFESVAWSASACHDGTSWLTIGISGPDNGAVAVLKYNG
IITDTIKSWKNNILRTQESECACLNGSCFTVMTDGPSNGQASYKIFKIEKGKVVKSVELNAPNYHYEECS
CYPDSGEIICVCRDNWHGSNRPWVSFNQNLEYQIGYICSGVLGDNPRPNDRTGSCGPVSSHGANGVKGFS
FKYGNGIWIGRTKSTSTRSGFEMIWDPNGWTGTDNKFSVKQDIVGITDWSGYSGSFVQHPELTGLDCIRP
CFWVELIRGRPKENTIWTSGSSISFCGVNSDTVDW

>gi|237872673|gb|ACR26696.1| neuraminidase [Influenza A virus (A/swine/North
Carolina/41265/2005(H1N1))]
NTNQRIIXIGTVCLIVGIVSLLLQIGNIVSLWISHSIQTGERNHPETCSQNVITYENNTWVNQTYVNISN
TNIADGQGVTSIILAGNSSLCPISGWAIYSKDNSIRIGSKGDIFVIREPFISCSQVECRTFFLTQGALLN
DRHSNGTVKDRSPYRTLMSCPIGEAPSPYNSRFESVAWSASACHDGMGWLTIGISGPDNGAVAVLKYNGI
ITDTIKSWRNKILRTQESECVCINGSCFTIMTDGPSNGQASYKIFKMEKGKIIKSVELDAPNYHYEECSC
YPDTGKVVCVCRDNWHASNRPWVSFDQNXNYQIGYICSGVFGDNPRSNDGKGNCGPVLSNGANGVKGFSF
RYGNGVWIGRTKSISSRSGFEMIWDPNGWTETDSSFXTKQDIIALTDWSGYSGSFVQHPELTGMNCIKPC
FWVELIRGQPKESTIWTSGSSISFCGVDSETASWSWPDGADLPFT
SWPDGAELPFTIDK
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>gi|237872673|gb|ACR26696.1| neuraminidase [Influenza A virus (A/swine/North
Carolina/41265/2005(H1N1))]
NTNQRIIXIGTVCLIVGIVSLLLQIGNIVSLWISHSIQTGERNHPETCSQNVITYENNTWVNQTYVNISN
TNIADGQGVTSIILAGNSSLCPISGWAIYSKDNSIRIGSKGDIFVIREPFISCSQVECRTFFLTQGALLN
DRHSNGTVKDRSPYRTLMSCPIGEAPSPYNSRFESVAWSASACHDGMGWLTIGISGPDNGAVAVLKYNGI
ITDTIKSWRNKILRTQESECVCINGSCFTIMTDGPSNGQASYKIFKMEKGKIIKSVELDAPNYHYEECSC
YPDTGKVVCVCRDNWHASNRPWVSFDQNXNYQIGYICSGVFGDNPRSNDGKGNCGPVLSNGANGVKGFSF
RYGNGVWIGRTKSISSRSGFEMIWDPNGWTETDSSFXTKQDIIALTDWSGYSGSFVQHPELTGMNCIKPC
FWVELIRGQPKESTIWTSGSSISFCGVDSETASWSWPDGADLPFT
```

```
>gi|52078153|gb|AAU25850.1| neuraminidase [Influenza A virus
(A/swine/Saskatchewan/18789/02(H1N1))]
MNPNQKIITIGSICMAIGVISLVLQIGNIISIWVNHSIQTGSQNHPETCNQSVITYENNTWVNQTYINIS
NTNLIAEQAVAPVTLAGNSSLCPISGWAIYSKDNGIRIGSKGDVFVIREPFISCSHLECRAFFLTQGALL
NDKHSNGTVKDRSPYRTLMSCPVGEAPSPYNSRFESVAWSASACHDGISWLTIGISGPDNGAVAVLKYNG
IITDTVKSWRNNILRTQESECACINGSCFTIMTDGPSNGQASYKIFKIEKGKVVKSVELNAPNYHYEECS
CYPDASEVMCVCRDNWHGSNRPWVSFNQNLEYQIGYICSGVFGDNPRPNDGTGSCGPVSSNGAYGVKGFS
FKYGNGVWIGRTKSTSSRSGFEMIWDPNGWTETDNSFSVKQDIVAITDWSGYSGSFVQHPELTGLDCMRP
CFWVELIRGRPKENTIWTSGSSISFCGVNSDTVGWSWPDGAELPFTIDK
```

```
>gi|237624332|gb|ACR01027.1| neuraminidase [Influenza A virus
(A/swine/Alberta/OTH-33-8/2009(H1N1))]
MNPNQKIITIGSVCMTIGMANLILQIGNIISIWISHSIQLGNQNQIETCNQSVITYENNTWVNQTYVNIS
NTNFAAGQSVVSVKLAGNSSLCPVGEWAIHSKDNSVRIGSKGDVFVIREPFILCSPLECRTFFLTQGALL
NDKHSNGTIKDRSPYRTLMSCPIGEVPSPYNSRFESVAWSASACHDGINWLTIGISGPDNGAVAVLKYNG
IITDTIKSWRNNILRTQESECACVNGSCFTVMTDGPSNGQASYKIFRIEKGKIVKSVEMNAPNYHYEECS
CYPDSSEITCVCRDNWHGSNRPWVSFNQNLEYQIGYICSGIFGDNPRPNDKTGCCGPVSSNGANGVKGFS
FKYGNGVWIGRTKSISSRNGFEMIWDPNGWTGTDNNFSIKQDIVGINEWSGYSGSFVQHPELTGLDCIRP
CFWVELIRGRPKENTIWTSGSSISFCGVNSDTVGWSWPDGAELPFTIDK
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```
>gi|188572592|gb|ACD65204.1| neuraminidase [Influenza A virus
(A/swine/Ohio/24366/07(H1N1))]
MNTNQRIITIGTVCLIVGIVSLLLQIGNIVSLWINHSIQTGEKNHPETCSQNVITYENNTWVNQTYVNIS
NTNIVDGQGVTSIILAGNSSLCPISGWAIYSKDNSIRIGSKGDIFVIREPFISCSHLECRTFFLTQGALL
NDRHSNGTVKDRSPYRTLMSCPIGEAPSPYNSRFESVAWSASACHDGMGWLTIGISGPDNGAVAVLKYNG
IITDTIKSWRNKILRTQESECVCINGSCFTIMTDGPSNGQASYKIFKMEKGKIIKSVELDAPNYHYEECS
CYPDTGKVVCVCRDNWHASNRPWVTFDQNLNYQIGYICSGVFGDNPRSNDGKGNCGPVPSNGANGVKGFS
FRYGNGVWIGRTKSISSRSGFEMIWDPNGWTETDSSFSIKQDIIALTDWSGYSGSFVQHPELTGMNCIKP
CFWVELIRGQPKESTIWTSGSSISFCGVDSETVSWSWPDGADLPFTIDK
```

```
>gi|197344174|gb|ACH69548.1| neuraminidase [Influenza A virus
(A/swine/OH/511445/2007(H1N1))]
MNTNQRIITIGTVCLIVGIVSLLLQIGNIVSLWINHSIQTGKRNHPETCSQNVITYENNTWVNQTYVNIS
NTNIVDGQGVTSIILAGNSSLCPISGWAIYSKDNSIRIGSKGDIFVIREPFISCSHLECRTFFLTQGALL
NDRHSNGTVKDRSPYRTLMSCPIGEAPSPYNSRFESVAWSASACHDGMGWLTIGISGPDNGAVAVLKYNG
IITDTIKSWRNKILRTQESECVCINGSCFTIMTDGPSNGQASYKIFKMEKGKIIKSVELDAPNYHYEECS
CYPDTGKVVCVCRDNWHASNRPWVTFDQNLNYQIGYICSGVFGDNPRSNDGKGNCGPVPSNGANGVKGFS
FRYGNGVWIGRTKSISSRSGFEMIWDPNGWTETDSSFSIKQDIIALTDWSGYSGSFVQHPELTGMNCIKP
CFWVELIRGQPKESTIWTSGSSISFCGVDSETVSWSWPDGADLPFTIDK
```

3.5. Sekuen Protein M2 Inang Manusia

>gi|229783371|gb|ACQ84453.1| matrix protein 2 [Influenza A virus (A/Korea/01/2009(H1N1))]

```
MSLLTEVETPTRSEWECRCSDSSDPLVIAANIIGILHLILWITDRLFFKCIYRRFKYGLKRGPSTEGVPE
SMREEYQQEQQSAVDVDDGHFVNIELE
```

```
>gi|224021238|gb|ACN32514.1| matrix protein 2 [Influenza A virus
(A/Japan/AF07/2008(H1N1))]
MSLLTEVETPIRNEWGCRCNDSSDPLVVAASIIGIVHLILWIIDRLFSKSIYRIFKHGLKRGPSTEGVPE
SMREEYREEQQNAVDADDDHFVSIELE

>gi|148356909|dbj|BAF63137.1| matrix protein 2 [Influenza A virus
(A/Hanoi/TX09/2006(H1N1))]
MSLLTEVETPIRNEWGCRCNDSSDPLVVAANIIGIVHLILWIIDRLFSKSIYRIFKHGLKRGPSTEGVPE
SMREEYREEQQNAVDADDGHFVSIELE

>gi|187935874|gb|ACD37435.1| matrix protein 2 [Influenza A virus
(A/Philippines/673/2006(H1N1))]
MSLLTEVETPIRNEWGCRCNDSSDPLVVAASIIGIVHLILWIIDRLFSKSIYRIFKHGLKGGPSTEGVPE
SMREEYREEQQNAVDADDGHFVSIEQ

>gi|133754211|gb|ABO38397.1| matrix protein 2 [Influenza A virus
(A/Singapore/6/1986(H1N1))]
MSLLTEVETPIRNEWGCRCNDSSDPLVVAASIIGILHLILWILDRLFFKCIYRLLKRGLKRGPSTEGVPE
SMREEYREEQQNAVDADDGHFVSIEL

>gi|239812968|gb|ACS27773.1| matrix protein 2 [Influenza A virus
(A/Kaluga/01/2009(H1N1))]
MSLLTEVETHTRSEWECRCSDSSDPLVIAANIIGILHLILWITDRLFFKCIYRRFKYGLKRGPSTEGVPE
SMREEYQQEQQSAVDVDDGHFVNIELE

>gi|237681732|gb|ACR10228.1| matrix protein 2 [Influenza A virus
(A/Bayern/63/2009(H1N1))]
MSLLTEVETPTRSEWECRCSDSSDPLVIAANIIGILHLILWITDRLFFKCIYRRFKYGLKRGPSTEGVPE
SMREEYQQEQQSAVDVDDGHFVNIDLE

>gi|229462687|gb|ACQ66059.1| matrix protein 2 [Influenza A virus (A/Castilla-La
Mancha/GP13/2009(H1N1))]
MSLLTEVETPTRSEWECRCSDSSDPLVIAANIIGILHLILWITDRLFFKCIYRRFKYGLKRGPSTEGVPE
SMREEYQQEQQSAVDVDDGHFVNIELE

>gi|238867514|gb|ACR67216.1| matrix protein 2 [Influenza A virus (A/New
York/33/2009(H1N1))]
MSLLTEVETPTRSEWECRCSDSSDPLVIAANIIGILHLILWITDRLFFKCIYRRFKYGLKRGPSTEGVPE
SMREEYQQEQQSAVDVDDGHFVNRELE

>gi|238058512|gb|ACR39405.1| matrix protein 2 [Influenza A virus (A/New
York/3221/2009(H1N1))]
MSLLTEVETPTRSEWECRCSDSSDPLVIAANIIGILHLILWITDRLFFKCIYRRFKYGLKRGPSTEGVPE
SMREEYQQEQQSAVDVDDGHFVNIEL

>gi|229536073|gb|ACQ76375.1| matrix protein 2 [Influenza A virus
(A/Texas/07/2009(H1N1))]
MSLLTEVETPTRSEWECRCSDSSDPLVIAANIIGILHLILWITDRLFFKCIYRRFKYGLKRGPSMEGVPE
SMREEYQQEQQSAVDVDDGHFVNIELE

>gi|237769932|gb|ACR18961.1| matrix protein 2 [Influenza A virus (A/New
York/13/2009(H1N1))]
MSLLTEVETPTRSEWECRCSDSSDPLVIAANIIGILHLILWITDRLFFKCIYRRFKYGLKRGPSTEGVPE
SLREEYQQEQQSAVDVDDGHFVNIELE
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>gi|237659610|gb|ACR09359.1| matrix protein 2 [Influenza A virus (A/Mexico/4486/2009(H1N1))]
MSLLTEVETPTRSEWECRCSDSSDPLVIAANIIGILHLILWITDRLFFKCIYRRFKYGLKRGPFTEGVPE
SMREEYQQEQQSAVDVDDGHFVNIELE

>gi|237769935|gb|ACR18963.1| matrix protein 2 [Influenza A virus (A/Oregon/05/2009(H1N1))]
MSLLTEVETPTXSEWECRCSDSSDPLVIAANIIGILHLILWITDRLFFKCIYRRFKYGLKRGPSTEGVPE
SMREEYQQEQQSAVDVDDGHFVNIELE

>gi|228481037|gb|ACQ42237.1| matrix protein 2 [Influenza A virus (A/Auckland/3/2009(H1N1))]
MSLLTEVETPTRSEWECRCSDSSDPLVIAANIIGILHLILWITDRLFFKCIYRRFKYGLKRGPSTEGVPE
SMREEYQQEQQSAVDVDDGHFVNIELE

>gi|187936002|gb|ACD37512.1| matrix protein 2 [Influenza A virus (A/Auckland/8/2007(H1N1))]
MSLLTEVETPIKNEWGCRCNDSSDPLVVAANIIGIVHLILWIIDRLFSKSIYRIFKHGLKRGPSTEGVPE
SMREEYREEQQNAVDADDGHFVSIELE

>gi|187935899|gb|ACD37450.1| matrix protein 2 [Influenza A virus (A/Victoria/501/2007(H1N1))]
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SMREEYREEQQNAVDADDGHFVSIELE

>gi|187935967|gb|ACD37491.1| matrix protein 2 [Influenza A virus (A/Brisbane/59/2007(H1N1))]
MSLLTEVETPIRNEWGCRCNDSSDPLVVAASIIGIVHLILWIIDRLFSKSIYRIFKHGLKRGPSTEGVPE
SMREEYREEQQNAVDADDDHFVSIELEG

>gi|187935959|gb|ACD37486.1| matrix protein 2 [Influenza A virus (A/South Australia/423//2007(H1N1))]
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SMREEYREEQQNAVDADDDHFVSIELE

>gi|239586243|gb|ACR83533.1| matrix protein 2 [Influenza A virus (A/Sao Paulo/1454/2009(H1N1))]
MSLLTEVETPTRSEWECRCSDSSDPLVIAANIIGILHLILWITDRLFFKCIYRRFKYGLKRGPSTEGVPE
SMREEYQQEQQSAVDVDDGHFVNIELE

3.6. Sekuen Protein M2 Host Swine

>gi|216409292|dbj|BAH02073.1| matrix protein 2 [Influenza A virus (A/swine/Chonburi/NIAH589/2005(H1N1))]
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SMREEYQQEQQSAVDVDDGHFVNIELE

>gi|224021238|gb|ACN32514.1| matrix protein 2 [Influenza A virus (A/Japan/AF07/2008(H1N1))]
MSLLTEVETPIRNEWGCRCNDSSDPLVVAASIIGIVHLILWIIDRLFSKSIYRIFKHGLKRGPSTEGVPE
SMREEYREEQQNAVDADDDHFVSIELE

>gi|148356909|dbj|BAF63137.1| matrix protein 2 [Influenza A virus (A/Hanoi/TX09/2006(H1N1))]
MSLLTEVETPIRNEWGCRCNDSSDPLVVAANIIGIVHLILWIIDRLFSKSIYRIFKHGLKRGPSTEGVPE
SMREEYREEQQNAVDADDGHFVSIELE

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>gi|187935874|gb|ACD37435.1| matrix protein 2 [Influenza A virus
(A/Philippines/673/2006(H1N1))]
MSLLTEVETPIRNEWGCRCNDSSDPLVVAASIIGIVHLILWIIDRLFSKSIYRIFKHGLKGGPSTEGVPE
SMREEYREEQQNAVDADDGHFVSIEQ

>gi|133754211|gb|ABO38397.1| matrix protein 2 [Influenza A virus
(A/Singapore/6/1986(H1N1))]
MSLLTEVETPIRNEWGCRCNDSSDPLVVAASIIGILHLILWILDRLFFKCIYRLLKRGLKRGPSTEGVPE
SMREEYREEQQNAVDADDGHFVSIEL

>gi|239812968|gb|ACS27773.1| matrix protein 2 [Influenza A virus
(A/Kaluga/01/2009(H1N1))]
MSLLTEVETHTRSEWECRCSDSSDPLVIAANIIGILHLILWITDRLFFKCIYRRFKYGLKRGPSTEGVPE
SMREEYQQEQQSAVDVDDGHFVNIELE

>gi|237681732|gb|ACR10228.1| matrix protein 2 [Influenza A virus
(A/Bayern/63/2009(H1N1))]
MSLLTEVETPTRSEWECRCSDSSDPLVIAANIIGILHLILWITDRLFFKCIYRRFKYGLKRGPSTEGVPE
SMREEYQQEQQSAVDVDDGHFVNIDLE

>gi|229462687|gb|ACQ66059.1| matrix protein 2 [Influenza A virus (A/Castilla-La
Mancha/GP13/2009(H1N1))]
MSLLTEVETPTRSEWECRCSDSSDPLVIAANIIGILHLILWITDRLFFKCIYRRFKYGLKRGPSTEGVPE
SMREEYQQEQQSAVDVDDGHFVNIELE

>gi|238867514|gb|ACR67216.1| matrix protein 2 [Influenza A virus (A/New
York/33/2009(H1N1))]
MSLLTEVETPTRSEWECRCSDSSDPLVIAANIIGILHLILWITDRLFFKCIYRRFKYGLKRGPSTEGVPE
SMREEYQQEQQSAVDVDDGHFVNRELE

>gi|238058512|gb|ACR39405.1| matrix protein 2 [Influenza A virus (A/New
York/3221/2009(H1N1))]
MSLLTEVETPTRSEWECRCSDSSDPLVIAANIIGILHLILWITDRLFFKCIYRRFKYGLKRGPSTEGVPE
SMREEYQQEQQSAVDVDDGHFVNIEL

>gi|229536073|gb|ACQ76375.1| matrix protein 2 [Influenza A virus
(A/Texas/07/2009(H1N1))]
MSLLTEVETPTRSEWECRCSDSSDPLVIAANIIGILHLILWITDRLFFKCIYRRFKYGLKRGPSMEGVPE
SMREEYQQEQQSAVDVDDGHFVNIELE

>gi|237769932|gb|ACR18961.1| matrix protein 2 [Influenza A virus (A/New
York/13/2009(H1N1))]
MSLLTEVETPTRSEWECRCSDSSDPLVIAANIIGILHLILWITDRLFFKCIYRRFKYGLKRGPSTEGVPE
SLREEYQQEQQSAVDVDDGHFVNIELE

>gi|237659610|gb|ACR09359.1| matrix protein 2 [Influenza A virus
(A/Mexico/4486/2009(H1N1))]
MSLLTEVETPTRSEWECRCSDSSDPLVIAANIIGILHLILWITDRLFFKCIYRRFKYGLKRGPFTEGVPE
SMREEYQQEQQSAVDVDDGHFVNIELE

>gi|237769935|gb|ACR18963.1| matrix protein 2 [Influenza A virus
(A/Oregon/05/2009(H1N1))]
MSLLTEVETPTXSEWECRCSDSSDPLVIAANIIGILHLILWITDRLFFKCIYRRFKYGLKRGPSTEGVPE
SMREEYQQEQQSAVDVDDGHFVNIELE
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```
>gi|228481037|gb|ACQ42237.1| matrix protein 2 [Influenza A virus
(A/Auckland/3/2009(H1N1))]
MSLLTEVETPTRSEWECRCSDSSDPLVIAANIIGILHLILWITDRLFFKCIYRRFKYGLKRGPSTEGVPE
SMREEYQQEQQSAVDVDDGHFVNIELE

>gi|187936002|gb|ACD37512.1| matrix protein 2 [Influenza A virus
(A/Auckland/8/2007(H1N1))]
MSLLTEVETPIKNEWGCRCNDSSDPLVVAANIIGIVHLILWIIDRLFSKSIYRIFKHGLKRGPSTEGVPE
SMREEYREEQQNAVDADDGHFVSIELE

>gi|187935899|gb|ACD37450.1| matrix protein 2 [Influenza A virus
(A/Victoria/501/2007(H1N1))]
MSLLTEVETPIRNEWGCRCNDSSDPLVVAANIIGIVHLILWIIDRLFSKSIYRIFKHGLKRGPSTEGVPE
SMREEYREEQQNAVDADDGHFVSIELE

>gi|187935967|gb|ACD37491.1| matrix protein 2 [Influenza A virus
(A/Brisbane/59/2007(H1N1))]
MSLLTEVETPIRNEWGCRCNDSSDPLVVAASIIGIVHLILWIIDRLFSKSIYRIFKHGLKRGPSTEGVPE
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>gi|187935959|gb|ACD37486.1| matrix protein 2 [Influenza A virus (A/South
Australia/423//2007(H1N1))]
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SMREEYREEQQNAVDADDDHFVSIELE

>gi|239586243|gb|ACR83533.1| matrix protein 2 [Influenza A virus (A/Sao
Paulo/1454/2009(H1N1))]
MSLLTEVETPTRSEWECRCSDSSDPLVIAANIIGILHLILWITDRLFFKCIYRRFKYGLKRGPSTEGVPE
SMREEYQQEQQSAVDVDDGHFVNIELE
```

Lampiran 4. Hasil *Multiple Alignment Protein* HA, NA, dan M2 Menggunakan *Server* ClustalW2

4. 1. Protein HA Inang Manusia

```
CLUSTAL 2.0.10 multiple sequence alignment


gi|237604397|gb|ACR01019.1|      ----------MKAILVVLLYTFATANADTLCIGYHANNSTDTVDTVLEKN 40
gi|237651252|gb|ACR08500.1|      ----------MKAILVVLLYTFATANADTLCIGYHANNSTDTVDTVLEKN 40
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gi|239504534|gb|ACR78585.1|      ----------MKAILVVLLYTFATANADTLCIGYHANNSTDTVDTVLEKN 40
gi|228860929|gb|ACQ45338.1|      ----------MKAILVVLLYTFATANADTLCIGYHANNSTDTVDTVLEKN 40
gi|229783367|gb|ACQ84451.1|      ----------MKAILVVLLYTFATANADTLCIGYHANNSTDTVDTVLEKN 40
gi|238695727|gb|ACR55004.1|      ----------MKAILVVLLYTFATANADTLCIGYHANNSTDTVDTVLEKN 40
gi|229536049|gb|ACQ76362.1|      ----------MKAILVVLLYTFATANADTLCIGYHANNSTDTVDTVLEKN 40
gi|237769990|gb|ACR18991.1|      ----------MKAILVVLLYTFATANADTLCIGYHANNSTDTVDTVLEKN 40
gi|238505424|gb|ACR43939.1|      ----------MKAILVVLLYTFATANADTLCIGYHANNSTDTVDTVLEKN 40
gi|237769863|gb|ACR18920.1|      ----------MKAILVVLLYTFATANADTLCIGYHANNSTDTVDTVLEKN 40
gi|229598896|gb|ACQ83310.1|      ----------MKAILVVLLYTFATANADTLCIGYHANNSTDTVDTVLEKN 40
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gi|238914614|gb|ACR78156.1|      ----------MKAILVVLLYTFATANADTLCIGYHANNSTDTVDTVLEKN 40
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gi|238914630|gb|ACR78164.1|      ----------MKAILVVLLYTFATANADTLCIGYHANNSTDTVDTVLEKN 40
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gi|237769986|gb|ACR18989.1|      ----------MKAILVVLLYTFATANADTLCIGYHANNSTDTVDTVLEKN 40
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gi|238623290|gb|ACR47006.1|      ----------MKAILVVLLYTFATANADTLCIGYHANNSTDTVDTVLEKN 40
gi|239812963|gb|ACS27770.1|      ----------MKAILVVLLYTFATANADTLCIGYHANNSTDTVDTVLEKN 40
gi|238627878|gb|ACR49284.1|      ----------MKAILVVLLYTFATANADTLCIGYHANNSTDTVDTVLEKN 40
gi|238627888|gb|ACR49289.1|      ----------MKAILVVLLYTFATANADTLCIGYHANNSTDTVDTVLKKN 40
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gi|237847682|gb|ACR23302.1|      ----------MKAILVVLLYTFATANADTLCIGYHANNSTDTVDTVLEKN 40
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gi|237689834|gb|ACR15748.1|      ------------------LYTFTTANADTLCIGYHANNSTDTVDTVLEKN 32
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gi|237651252|gb|ACR08500.1|      VTVTHSVNLLEDKHNGKLCKLRGVAPLHLGKCNIAGWILGNPECESLSTA 90
gi|238914622|gb|ACR78160.1|      VTVTHSVNLLEDKHNGKLCKLRGVAPLHLGKCNIAGWILGNPECESLSTA 90
gi|239504534|gb|ACR78585.1|      VTVTHSVNLLEDKHNGKLCKLRGVAPLHLGKCNIAGWILGNPECESLSTA 90
gi|228860929|gb|ACQ45338.1|      VTVTHSVNLLEDKHNGKLCKLRGVAPLHLGKCNIAGWILGNPECESLSTA 90
gi|229783367|gb|ACQ84451.1|      VTVTHSVNLLEDKHNGKLCKLRGVAPLHLGKCNIAGWILGNPECESLSTA 90
gi|238695727|gb|ACR55004.1|      VTVTHSVNLLEDKHNGKLCKLRGVAPLHLGKCNIAGWILGNPECESLSTA 90
gi|229536049|gb|ACQ76362.1|      VTVTHSVDLLEDKHNGKLCKLRGVAPLHLGKCNIAGWILGNPECESLSTA 90
gi|237769990|gb|ACR18991.1|      VTVTHSVNLLEDKHNRKLCKLRGVAPLHLGKCNIAGWILGNPECESLSTA 90
gi|238505424|gb|ACR43939.1|      VTVTHSVNLLEDKHNGKLCKLRGVAPLHLGKCNIAGWILGNPECESLSTA 90
gi|237769863|gb|ACR18920.1|      VTVTHSVNLLEDKHNGKLCKLRGVAPLHLGKCNIAGWILGNPECESLSTA 90
gi|229598896|gb|ACQ83310.1|      VTVTHSVNLLEDKHNGKLCKLRGVAPLHLGKCNIAGWILGNPECESLSTA 90
gi|238618451|gb|ACR46992.1|      VTVTHSVNLLEDKHNGKLCKLRGVAPLHLGKCNIAGWILGNPECESLSTA 90
gi|237651248|gb|ACR08498.1|      VTVTHSVNLLEDKHNGKLCKLRGVAPLHLGKCNIAGWILGNPECESLSTA 90
gi|238914614|gb|ACR78156.1|      VTVTHSVNLLEDKHNGKLCKLRGVAPLHLGKCNIAGWILGNPECESLSTA 90
gi|238695673|gb|ACR54974.1|      VTVTHSVNLLEDKHNGKLCKLRGVAPLHLGKCNIAGWILGNPECESLSTA 90
gi|238914630|gb|ACR78164.1|      VTVTHSVNLLEDKHNGKLCKLRGVAPLHLGKCNIAGWILGNPECESLSTA 90
gi|238867295|gb|ACR67244.1|      VTVTHSVNLLEDKHNGKLCKLRGVAPLHLGKCNIAGWILGNPECESLSTA 90
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gi|238568508|gb|ACR46671.1|      VTVTHSVNILEDKHNGKLCKLRGVAPLHLGKCNIAGWILGNPECESLSTA 90
gi|238623290|gb|ACR47006.1|      VTVTHSVNILEDKHNGKLCKLRGVAPLHLGKCNIAGWILGNPECESLSTA 90
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gi|238801242|gb|ACR56352.1|      VTVTHSVNLLEDKHNGKLCKLRGVAPLHLGKCNIAGWILGNPECESLSTA 90
gi|223551672|gb|ACM90863.1|      VTVTHSVNLLENSHNGKLCLLKGIAPLQLGNCSVAGWILGNPECELLISK 90
gi|237688901|gb|ACR15238.1|      VTVTHSVNLLENSHNGKLCLLKGIAPLQLGNCSVAGWILGNPECELLISK 90
gi|237689340|gb|ACR15491.1|      VTVTHSVNLLENSHNGKLCLLKGIAPLQLGNCSVAGWILGNPECELLISK 100
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gi|238695727|gb|ACR55004.1|      SSWSYIVETSSSDNGTCYPGDFIDYEELREQLSSVSSFERFEIFPKTSSW 140
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gi|238505424|gb|ACR43939.1|      DCNTTCQTPKGAINTSLPFQNIHPITIGKCPKYVKSTKLRLATGLRNVPS 340
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gi|229598896|gb|ACQ83310.1|      DCNTTCQTPKGAINTSLPFQNIHPITIGKCPKYVKSTKLRLATGLRNVPS 340
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gi|237689340|gb|ACR15491.1|      ECMESVKNGTYDYPKYSEESKLNREKIDGIKLESMGVYQILAIYSTVASS 549
                                  ********** *******:**** :***:****  :*************

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gi|237689852|gb|ACR15758.1|      LVLVVSLGAISFWMCSNGSLQC---- 554
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Tabel Skor

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SeqA Name                         Len(aa)  SeqB Name                         Len(aa)  Score
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1    gi|223551672|gb|ACM90863.1|  565      3    gi|238695727|gb|ACR55004.1|  566      79
1    gi|223551672|gb|ACM90863.1|  565      4    gi|238914630|gb|ACR78164.1|  562      79
1    gi|223551672|gb|ACM90863.1|  565      5    gi|238695673|gb|ACR54974.1|  566      79
1    gi|223551672|gb|ACM90863.1|  565      6    gi|238867295|gb|ACR67244.1|  566      79
1    gi|223551672|gb|ACM90863.1|  565      7    gi|237688901|gb|ACR15238.1|  565      99
1    gi|223551672|gb|ACM90863.1|  565      8    gi|229783367|gb|ACQ84451.1|  566      79
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1    gi|223551672|gb|ACM90863.1|  565      16   gi|238867287|gb|ACR67262.1|  566      79
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4.2. Protein HA Inang Babi

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gi|4585155|gb|AAD25301.1|AF091      -------------MKAILLVLLCTFAATNADTLCIGYHANNSTDTVDTIL 37
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gi|197344172|gb|ACH69547.1|         -------------MKAILVVLLYTFTTANADTLCIGYHANNSTDTVDTVL 37
gi|237872683|gb|ACR26701.1|         -------------MKAILVVLLHTLTTTNADTLCIGYHANNSTETVDTVL 37
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gi|52078155|gb|AAU25851.1|          EKNITVTHSVNLLEDSHNGKLCSLNGIAPLQLGKCNVAGWLLGNPECDLL 87
gi|4585155|gb|AAD25301.1|AF091      EKNVTVTHSVNLLEDKHNGKLCKLGGIAPLHLGKCNIAGWLLGNPECELL 87
gi|163676476|gb|ABY40409.1|         EKNVTVTHSVNLLEDRHNGKLCNLRGKAPLHLGKCNIAGWLLGNPECELL 87
gi|82622903|gb|ABB86907.1|          EKNVTVTHSVNLLEDKHNGKLCRLGGIAPLHLGKCNIAGWLLGNPECDLL 87
gi|82622957|gb|ABB86937.1|          EKNVTVTHSVNLLEDKHNGRLCKLGGIAPLHLGKCNIAGWLLGNPECELL 87
gi|190403701|gb|ACE77928.1|         EKNVTVTHSVNLLENKHNGKLCKLRGIAPLHLGKCNIAGWLLGNPECESL 87
gi|157168458|gb|ABV25643.1|         EKNVTVTHSVNLLENKHDGKLCKLRGIAPLHLGKCNIAGWLLGNPECESL 87
gi|157168452|gb|ABV25640.1|         EKNVTVTHSVNLLENKHNGKLCKLRGVAPLHLGKCNIAGWLLGNPECESL 87
gi|237624328|gb|ACR01025.1|         EKNVTVTHSVNLLEDKHNGKLCKLRGVAPLHLGKCNIAGWILGNPECESL 87
gi|197344172|gb|ACH69547.1|         EKNVTVTHSVNLLENRHNGKLCKLRGVAPLHLGKCNIAGWLLGNPECESL 87
gi|237872683|gb|ACR26701.1|         EKNVTVTHSVNLLEDRHNGKLCKLRGVAPLHLGKCNIAGWLLGNPECESL 87
gi|221327007|gb|ACM17276.1|         EKNVTVTHSVNLLEDSHNGKLCLLKGIAPLQLGNCSVAGWILGNPECELL 87
gi|221326988|gb|ACM17265.1|         EKNVTVTHSVNLLEDSHNGKLCLLKGIAPLQLGNCSVAGWILGNPECELL 87
gi|151335575|gb|ABS00315.1|         EKNVTVTHSVNLLEDSHNGKLCRLKGIAPLQLGNCSVAGWILGNPECESL 100
                                    ***:**********: *:*:** * *  **:**:*.:** :****:*: *

gi|224979377|gb|ACN72617.1|         LTANSWSYIIETSDSKNGACYPGEFADYEELREQLSTVSSFERFEIFPKA 137
gi|91177888|gb|ABE27153.1|          LTANSWSYIIETSNSKNGACYPGEFADYEELREQLSTVSSFERFEIFPKA 137
gi|238057035|gb|ACR39188.1|         LTANSWSYIIETSNSKNGTCYPGEFADNEELREQLSTVSSFERFEIFPKA 137
gi|20068267|emb|CAC86337.1|         LTANSWSYIIETSNSKNGACYPGEFADYEELREQLSTVSSFERFEIFPKA 123
gi|210076637|gb|ACJ06667.1|         LTANSWSYIIETSNSKNGACYPGEFADYEELKEQLSTVSSFERFEIFPKA 137
gi|224923729|gb|ACN67524.1|         LTANSWSYIIETSNSKNGKCYPGEFADYEELREQLSTVSSFERFEIFPKA 137
gi|238867285|gb|ACR67261.1|         LTANSWSYIIETSNSENGTCYPGEFIDYEELREQLSSVSSFERFEIFPKA 137
gi|52078155|gb|AAU25851.1|          LTANSWSYIIETSNSENGTCYPGEFIDYEELREQLSSVSSFEKFEIFPKA 137
gi|4585155|gb|AAD25301.1|AF091      FTVSSWSYIVETSNSDNGTCYPGDFINYEELREQLSSVSSFERFEIFPKT 137
gi|163676476|gb|ABY40409.1|         FAVNSWSYIVETSNSDNGTCYPGDFTSYEELREQLSSVSSFERFEIFPKA 137
gi|82622903|gb|ABB86907.1|          LTVSSWSYIVETSNSYNGTCYPGDFTNYEELREQLSSVSSFERFEIFPKA 137
gi|82622957|gb|ABB86937.1|          FTVSSWSYIVETSNSYNGTCYPGDFINYEELREQLSSVSSFERFEIFPKA 137
gi|190403701|gb|ACE77928.1|         FTASSWSYIVETPNSDNGTCYPGDFINYEELREHLSSVSSFERFEIFPKA 137
gi|157168458|gb|ABV25643.1|         FTASSWSYIVETPNSDNGTCYPGDFINYEELREHLSSVSSFERFEIFPKA 137
gi|157168452|gb|ABV25640.1|         FTASSWSYIVETSNSDNGTCYPGDFINYEELREHLSSVSSFERFEIFPKA 137
gi|237624328|gb|ACR01025.1|         STASSWSYIVETSSSDNGTCYPGDFIDYEELREQLSSVSSFERFEIFPKT 137
gi|197344172|gb|ACH69547.1|         STASSWSYIVETSNSDNGTCYPGDFINYEELREQLSSVSSFERFEIFPKT 137
gi|237872683|gb|ACR26701.1|         FTASSWSYIVETSNSDNGTCYPGDFINYEELREQLSSVSSFERFEIFPNA 137
gi|221327007|gb|ACM17276.1|         ISKESWSYIVETPNPENGACYPGYFTDYEELREQLSSVSSFERFEIFPKE 137
gi|221326988|gb|ACM17265.1|         ISKESWSYIVETPNPENGTCYPGYFTDYEELREQLSSVSSFERFEIFPKE 137
gi|151335575|gb|ABS00315.1|         FSKKSWSYIAETPNSENGTCYPGYFADYEELREQLSSVSSFERFEIFPKE 150
                                     : .***** **... ** **** * . ***:*:**:*****:*****:

gi|224979377|gb|ACN72617.1|         TSWPNHETTKGTTVACSHSGANSFYRNLLWIVKKGNSYPKLSKSYTNNKG 187
gi|91177888|gb|ABE27153.1|          TSWPNHETTKGTTVACSHSGANSFYRNLLWIVKKGNSYPKLSKSYTNNKG 187
gi|238057035|gb|ACR39188.1|         TSWPNHETTKGTTVSCSHSGANSFYRNLLWIVKKGNSYPKLSKSYTNNKG 187
gi|20068267|emb|CAC86337.1|         TSWPNHDTTRGTTVSCSHSGANSFYRNLLWIVKKGNSYPKLSKSYTNNKG 173
gi|210076637|gb|ACJ06667.1|         TSWPNHDTTRGTTVACPHSGANSFYRNLLWIVKKGNSYPKLSKSYTNNKG 187
gi|224923729|gb|ACN67524.1|         TSWPNHETTKGTTTACSHSGASSFYRNLLWIVKKGNSYPKLSKSYTNNKG 187
gi|238867285|gb|ACR67261.1|         NSWPNHETTKGVTAACSYSGAHSFYRNLLWIVKKGNSYPKLSKSYTNNKG 187
gi|52078155|gb|AAU25851.1|          NSWPNHETTKGVTAACSYSGASSFYRNLLWITKKGTSYPKLSKSYTNNKG 187
gi|4585155|gb|AAD25301.1|AF091      SSWPDHETNRGVTAACPYAGANSFYRNLIWLVKKGNSYPKLSKSYVNNKG 187
gi|163676476|gb|ABY40409.1|         SSWPNHETNRGVTAACPYAGTNDFYRNLIWLVKKGNSYPKLRKSYVNNKK 187
gi|82622903|gb|ABB86907.1|          SSWPNHETNRGVTAACPHAGTNSFYRNLIWLVKKGNTYPKLSKSYVNNKG 187
gi|82622957|gb|ABB86937.1|          SSWPNHETNRGVTAACPHAGTNSFYRNLIWLVKKGNTYPKISKSYVNNKG 187
gi|190403701|gb|ACE77928.1|         NSWPNHDTDKGVTAACPYAGANSFYRNLIWLVKKGNSYPKLSKSYINNKK 187
gi|157168458|gb|ABV25643.1|         NSWPNHDTNKGVTAACPYAGASSFYRNLIWLVKKGNSYPKLSKSYINNKK 187
gi|157168452|gb|ABV25640.1|         NSWPNHDTDKGVTAACPYAGANSFYRNLIWLVKKGNSYPKLSKSYINNKK 187
gi|237624328|gb|ACR01025.1|         SSWPNHDSNKGVTAACPHAGAKSFYKNLIWLVKKGNSYPKLSKSYINDKG 187
gi|197344172|gb|ACH69547.1|         SSWPNHDTNRGVTAACPHAGTNSFYRNLIWLVKKGNSYPKINKSYINNKE 187
gi|237872683|gb|ACR26701.1|         SSWPDHETNKGVTAACSHXGAKSFYRNLLWLVKRKNSYPKLSKSYINNKG 187
gi|221327007|gb|ACM17276.1|         SSWPNHTVT-GVSASCSHNGKSSFYRNLLWLTGKNGLYPNLSKSYTNNKE 186
gi|221326988|gb|ACM17265.1|         SSWPNHTVT-GVSASCSHNGKSSFYRNLLWLTGKNGLYPNLSKSYTNNKE 186
gi|151335575|gb|ABS00315.1|         SSWPNHTVTKGVSASCSHKGRSSFYRNLLWLTEKNGSYPNLSKSYVNNKE 200
                                    .***:*    *.:.:*.: *  .**:**:*:. :   **:: *** *:*

gi|224979377|gb|ACN72617.1|         KEVLVIWGVHHPPTDSDQQTLYQNKHTYVSVGSSKYYQRFTPEIVTRPKV 237
gi|91177888|gb|ABE27153.1|          KEVLVIWGVHHPPTDSNQQTLYQNNHTYVSVGSSKYYQRFTPEIVARPKV 237
gi|238057035|gb|ACR39188.1|         KEVLVIWGVHHPPTDSDQQTLYQNNHTYVSVGSSKYYQRFTPEIVARPKV 237
gi|20068267|emb|CAC86337.1|         KEVLVIWGVHHPPTDSDQQTLYQNNHTYVSVGSSKYYQRFTPEIVARPKV 223
gi|210076637|gb|ACJ06667.1|         KEVLVIWGVHHPPTDSDQQTLYQNNHTYVSVGSSKYYKRFTPEIVARPKV 237
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gi|224923729|gb|ACN67524.1|         KEVLVIWGVHHPPTNSDQQTLYQNAYTYVSVESSKYYRRFTPEIAARPKV 237
gi|238867285|gb|ACR67261.1|         KEVLVIWGVHHPPTTNDQQSLYQNADAYVSVGSSKYNRRFTPEIAARPKV 237
gi|52078155|gb|AAU25851.1|          KEVLVLWGVHHPPTTSDQQSIYQNTDAYVSVGSSKYNRRFTPEIAARPKV 237
gi|4585155|gb|AAD25301.1|AF091      KEVLVLWGIHHPPTSTDQQSLYQNADAYIFVGSSKYNRKFKPEIAERPKV 237
gi|163676476|gb|ABY40409.1|         KEVLVLWGIHHPPTNTDQQSLYQNADAYVFVGSSKYSRKFKPEIAERPKV 237
gi|82622903|gb|ABB86907.1|          KEVLVLWGIHHPSTSTDQQSLYQNADTYVFVGTSKYNKKFKPEIAVRPKV 237
gi|82622957|gb|ABB86937.1|          KEVLVLWGIHHPSTSNDQQSLYQNADTYVFVGPSKYNKKFKPEIATRPKV 237
gi|190403701|gb|ACE77928.1|         KEVLVIWGIHHPPTSTDQQTLYQNADAYVFVGSSKYSKRFKPEIAARPKV 237
gi|157168458|gb|ABV25643.1|         KEVLVIWGIHHPPTSTDQQTLYQNADAYVFVGSSKYSKRFKPEIAARPKV 237
gi|157168452|gb|ABV25640.1|         KEVLVIWGIHHPPTSTDQQTLYQNADAYVFVGSSKYSKEFKPEIAARPKV 237
gi|237624328|gb|ACR01025.1|         KEVLVLWGIHHPSTSADQQSLYQNADANVFVGSSRYSKKFKPEIAIRPKV 237
gi|197344172|gb|ACH69547.1|         KEVLVLWAIHHPSTSADQQSLYQNADAYVFVGSSRYSRKFEPEIATRPKV 237
gi|237872683|gb|ACR26701.1|         KEVLVLWGIHHPSTNQDQETLYQNTDAYVFVGSSKYSKKFKPEIATRPKV 237
gi|221327007|gb|ACM17276.1|         KEVLVLWGVHHPSNIGDQRALYHTENAYVSVVSSHCSRRFTPEIAKRPKV 236
gi|221326988|gb|ACM17265.1|         KEVLVLWGVHHPPNIGNQRALYHTENAYVSVVSSHYSRRFTPEIAKRPKV 236
gi|151335575|gb|ABS00315.1|         REVLVLWGVHHPSNIGEQRAIYHTENAYVSVVSSHYNRRFTPEIAKRPKV 250
                                    :****:*.:***..  :*.::*:.  : : * .*:  :.* ***. ****

gi|224979377|gb|ACN72617.1|         REQAGRMNYYWTLLDQGDTITFEATGNLIAPWHAFALNKGSNSGIMMSDA 287
gi|91177888|gb|ABE27153.1|          REQAGRMNYYWTLLDQGDTITFEATGNLIAPWHAFALNKGSSSGIMMSDA 287
gi|238057035|gb|ACR39188.1|         RGQAGRMNYYWTLLDQGDTITFEATGNLIAPWHAFALNKGSSSGIMMSDA 287
gi|20068267|emb|CAC86337.1|         RKQAGRINYYWTLLDQGDTITFEATGNLIAPWHAFALNKGSSSGIMMSDA 273
gi|210076637|gb|ACJ06667.1|         REQAGRMNYYWTLLDQGDTITFEATGNLIVPWHAFALKKGSNSGIMMSDA 287
gi|224923729|gb|ACN67524.1|         RGQAGRMNYYWTLLDQGDTITFEATGNLIAPWYAFALNKGSNSGIMMSDA 287
gi|238867285|gb|ACR67261.1|         KGQAGRMNYYWTLLDQGDTIRFEATGNLIAPWYAFALNKGSGSGIITSDA 287
gi|52078155|gb|AAU25851.1|          RGQAGRMNYYWTLLDQGDTITFEATGNLIAPWYAFALNKGSDSGIITSDA 287
gi|4585155|gb|AAD25301.1|AF091      RGQAGRMNYYWTLIEPGDTIKFEATGNLVVPRYAFAMNRDPGSGIITSDA 287
gi|163676476|gb|ABY40409.1|         RGQAGRMNYYWTLIEPGDTITFEATGNLVAPRYAFAMNRGPVSGIITSDA 287
gi|82622903|gb|ABB86907.1|          KDQAGRMNYYWTLVEPGDTITFEATGNLVVPRYAFAMNRGHGSGIIISDT 287
gi|82622957|gb|ABB86937.1|          RDQAGRMNYYWTLVEPGDTITFEATGNLVVPRYAFAMNRGSESGIIISDT 287
gi|190403701|gb|ACE77928.1|         RDQAGRMNYYWTLIEPGDTITFEATGNLVVPRYAFPMKRGSGSGIIVSDA 287
gi|157168458|gb|ABV25643.1|         RDQAGRMDYYWTLIEPGDTITFEATGNLVVPRYAFAMKRGSGSGIIVSDA 287
gi|157168452|gb|ABV25640.1|         RDQAGRMNYYWTLIEPGDTITFEATGNLVVPRYAFAMKRGSGSGIIISDK 287
gi|237624328|gb|ACR01025.1|         RDQEGRMNYYWTLVEPGDKITFEATGNLVVPRYAFAMERNAGSGIIISDT 287
gi|197344172|gb|ACH69547.1|         RDQAGRMNYYWTLVEPGDKITFEATGNLVVPRYAFALKRNSGSGIIISDT 287
gi|237872683|gb|ACR26701.1|         RDQTGRMNYYWTLIEPGDTITFEATGNLVVPRYAFAMERGSGSGIIISDA 287
gi|221327007|gb|ACM17276.1|         RDQEGRINYYWTLLEPGDTIIFEANGNLIAPRYAFALSRGFGSGIITSNA 286
gi|221326988|gb|ACM17265.1|         RDQEGRINYYWTLLEPGDTIIFEANGNLIAPRYAFALSRGFGSGIITSNA 286
gi|151335575|gb|ABS00315.1|         RGQEGRINYYWTLLEPGDTIIFEANGNLIAPWYAFALSRGFGSGIITSNA 300
                                    : * **::*****:: **.* ***.***:.* :**.:.:.  ***: *:

gi|224979377|gb|ACN72617.1|         HVHNCTTKCQTPHGALKGNLPFQNVHPITIGECPKYVKSTQLRMATGLRN 337
gi|91177888|gb|ABE27153.1|          HVHNCTTKCQTPHGALKSNLPFQNVHPITIGECPKYVKSTQLRMATGLRN 337
gi|238057035|gb|ACR39188.1|         HVHNCTTKCQTPHGALKSNLPFQNVHPITIGECPKYVKSTQLRMATGLRN 337
gi|20068267|emb|CAC86337.1|         HVHNCTTKCQTPHGALKSNLPFQNVHPVTIGECPKYVKSTQLRMATGLRN 323
gi|210076637|gb|ACJ06667.1|         QVHNCTTKCQTPHGALKSNLPFQNVHPVTIGECPKYVKSTQLRMATGLRN 337
gi|224923729|gb|ACN67524.1|         HVHNCTTKCQTPHGALKSNLPFQNVHPITIGECPKYVKSTQLRMATGLRN 337
gi|238867285|gb|ACR67261.1|         PVHNCDTKCQTPHGALNSSLPFQNVHPITIGECPKYVKSTKLRMATGLRN 337
gi|52078155|gb|AAU25851.1|          PVHNCDTRCQTPHGALNSSLPFQNVHPITIGECPKYVKSTKLRMATGLRN 337
gi|4585155|gb|AAD25301.1|AF091      PVHDCNTTCQTPKGAINTSLPFQNIHPVTIGECPKYVKSTKLRMATGLRN 337
gi|163676476|gb|ABY40409.1|         PVHDCNATCQTPKGAINTSLPFQNIHPITIGECPKYVKSTRLRMATGLRN 337
gi|82622903|gb|ABB86907.1|          PVHDCNTTCQTPKGAINTSLPFQNVHPVTIGKCPKYVKSTRLRMATGLRN 337
gi|82622957|gb|ABB86937.1|          PVHDCNTTCQTPKGAINTSLPFQNVHPVTIGECPKYVKSTRLRMATGLRN 337
gi|190403701|gb|ACE77928.1|         PVHDCNTTCQTPKGAINTSLPFQNIHPVTIGECPKYVKSTKLRMATGLRN 337
gi|157168458|gb|ABV25643.1|         PVHDCNTTCQTPKGAINTSLPFQNIHPVTIGECPKYVKSTKLRMATGLRN 337
gi|157168452|gb|ABV25640.1|         PVHDCNTTCQTPKGAINTSLPFQNIHPVTIGECPKYVKSTKLRMATGLRN 337
gi|237624328|gb|ACR01025.1|         PVHDCNTTCQTPKGAINTSLPFQNIHPITIGKCPKYVKSTKLRLATGLRN 337
gi|197344172|gb|ACH69547.1|         SVHDCDTTCQTPNGAINTSLPFQNIHPVTIGECPKYVKSTKLRMATGLRN 337
gi|237872683|gb|ACR26701.1|         TVHDCNATCQTPKGAINTSLPFQNIHPVTIGECPKYVKSTKLRMATGLRN 337
gi|221327007|gb|ACM17276.1|         PMDECNAKCQTPQGAINSSLPFQNVHPVTIGECPKYVRSAKLRMVTGLRN 336
gi|221326988|gb|ACM17265.1|         PMDECNAKCQTPQGAINSSLPFQNVHPVTIGECPKYVRSAKLRMVTGLRN 336
gi|151335575|gb|ABS00315.1|         SMDECDAKCQTPQGAINSSLPFQNVHPVTIGECPKYVRSTKLRMVTGLRN 350
                                     :.:* : ****:**:: .*****:**:***:*****:*::**:.*****

gi|224979377|gb|ACN72617.1|         IPSIQSRGLFGAIAGFIEGGWTGMIDGWYGYHHQNEQGSGYAADRKSTQI 387
gi|91177888|gb|ABE27153.1|          IPSTQSRGLFGAIAGFIEGGWTGMIDGWYGYHHQNEQGSGYAADQKSTQI 387
gi|238057035|gb|ACR39188.1|         IPSIPSRGLFGAIAGFIEGGWTGMIDGWYGYHHQNEQGSGYAADQKSTQI 387
gi|20068267|emb|CAC86337.1|         IPSIQSRGLFGAIAGFIEGGWTGMIDGWYGYHHQNEQGSGYAADQKSTQI 373
gi|210076637|gb|ACJ06667.1|         IPSIQSRGLFGAIAGFIEGGWTGMIDGWYGYHHQNEQGSGYAADQKSTQI 387
gi|224923729|gb|ACN67524.1|         VPSIQSRGLFGAIAGFIEGGWTGMIDGWYGYHHQNEQGSGYAADQKSTQI 387
gi|238867285|gb|ACR67261.1|         VPSIQSRGLFGAIAGFIEGGWTGMIDGWYGYHHQNEQGSGYAADQKSTQN 387
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gi|52078155|gb|AAU25851.1|          VPSIQSRGLFGAIAGFIEGGWTGMIDGWYGYHHQNEQGSGYAADQKSTQN 387
gi|4585155|gb|AAD25301.1|AF091      IPSIQSRGLFGAIAGFIEGGWTGMIDGWYGYHHQNEQGSGYAADQKSTQN 387
gi|163676476|gb|ABY40409.1|         IPSIQSRGLFGAIAGFIEGGWTGMIDGWYGYHHQNGQGSGYAADQKSTQN 387
gi|82622903|gb|ABB86907.1|          IPSIQSRGLFGAIAGFIEGGWTGMIDGWYGYHHQNGQGSGYAADQKSTQN 387
gi|82622957|gb|ABB86937.1|          IPSIQSRGLFGAIAGFIEEGWTGMIDGWYGYHHQNGQGSGYAADQKSTQN 387
gi|190403701|gb|ACE77928.1|         IPSIQSRGLFGAIAGFIEGGWTGMIDGWYGYHHQNEQGSGYAADQKSTQN 387
gi|157168458|gb|ABV25643.1|         IPSIQSRGLFGAIAGFIEGGWTGMIDGWYGYHHQNEQGSGYAADQKSTQN 387
gi|157168452|gb|ABV25640.1|         IPSIQSRGLFGAIAGFIEGGWTGMIDGWYGYHHQNEQGSGYAADQKSTQN 387
gi|237624328|gb|ACR01025.1|         VPSIQSRGLFGAIVGFIEGGWTGMVDGWYGYHHQNEQGSGYAADLKSTQN 387
gi|197344172|gb|ACH69547.1|         IPSIQSRGLFGAIAGFIEGGWTGMIDGWYGYHHQNEQGSGYAADLKSTQN 387
gi|237872683|gb|ACR26701.1|         VPSIQSRGLFGAIAGFIEGGWTGMIDGWYGYHHQNEQGSGYAADRKSTQN 387
gi|221327007|gb|ACM17276.1|         TPSIQSRGLFGAIAGFIEGGWTGMVDGWYGYHHQNEQGSGYAADQKSTQN 386
gi|221326988|gb|ACM17265.1|         TPSIQSRGLFGAIAGFIEGGWTGMVDGWYGYHHQNEQGSGYAADQKSTQN 386
gi|151335575|gb|ABS00315.1|         IPSIQSRGLFGAIAGFIEGGWTGMIDGWYGYHHQNEQGSGYAADQKSTQN 400
                                     **  ********.**** *****:********** ******** ****

gi|224979377|gb|ACN72617.1|         AIDGISNKVNSVIEKMNIQFTSVGKEFNNLEKRIENLNKKVDDGFLDVWT 437
gi|91177888|gb|ABE27153.1|          AIDGISNKVNSVIEKMNIQFTSVGKEFNNLEKRIENLNKKVDDGFLDVWT 437
gi|238057035|gb|ACR39188.1|         AIDGISNKVNSVIEKMNIQFTSVGKEFNNLEKRIENLNKKVDDGFLDVWT 437
gi|20068267|emb|CAC86337.1|         AIDGISNKVNSVIEKMNIQFTSVGKEFNDLEKRIENLNKKVDDGFLDVWT 423
gi|210076637|gb|ACJ06667.1|         AIDGISNKVNSVIEKMNIQFTSMGKEFNNLEKRMENLNKKVDDGFLDVWT 437
gi|224923729|gb|ACN67524.1|         AIDGISNKVNSVIEKMNIQFTSVGKEFNNLEKRIENLNKKVDDGFLDIWT 437
gi|238867285|gb|ACR67261.1|         AIDGISNKVNSVIEKMNTQFTAVGKEFNDLEKRIENLNKKVDDGFLDVWT 437
gi|52078155|gb|AAU25851.1|          AIDGITNKVNSVIEKMNTQFTAVGKEFNNLERRIENLNRKVDDGFLDVWT 437
gi|4585155|gb|AAD25301.1|AF091      AVDGITNKVNSVIKKMNTQFAAVGKEFNHLEKRIENLNKKVDDGFLDVWT 437
gi|163676476|gb|ABY40409.1|         AIDRITNKVNSVIEKMNIQFTAVGKEFNHLERRIENLNKKVDDGFLDVWT 437
gi|82622903|gb|ABB86907.1|          AIDGITNKVNSVIEKMNTQFTAVGKEFNHLEKRIENLNKKVDDGFLDVWT 437
gi|82622957|gb|ABB86937.1|          AIDGITNKVNSVIEKMNTQFTAVGKEFNHLEKRIENLNKKVDDGFLDVWT 437
gi|190403701|gb|ACE77928.1|         AIDGITNKVNSIIEKMNTQFTAVGKEFSQLEKRIESLNNKVDDGFLDIWT 437
gi|157168458|gb|ABV25643.1|         AIDGITNKVNSIIEKMNTQFTAVGKEFSQLEKRIESLNNKVDDGFLDIWT 437
gi|157168452|gb|ABV25640.1|         AIDGITNKVNSVIEKMNTQFTAVGKEFNQLEKRIESLNNKVDDGFLDIWT 437
gi|237624328|gb|ACR01025.1|         AIDEITNKVNSVIEKMNTQFTAVGKEFNHLEKRIENLNKKVDDGFLDIWT 437
gi|197344172|gb|ACH69547.1|         AIDGITNKVNSVIEKMNTQFTAVGKEFSHLERRIENLNKKVDDGFLDIWT 437
gi|237872683|gb|ACR26701.1|         AIDGITNKVNSVIEKMNTQFTAVGKEFNHLEKRIENLNKKVDDGFLDVWT 437
gi|221327007|gb|ACM17276.1|         AINGITNKVNSVIEKMNTQFTAVGKEFNKLERRMENLNKKVDDGFLDIWT 436
gi|221326988|gb|ACM17265.1|         AINGITNKVNSVIEKMNTQFTAVGKEFNKLERRMENLNKKVDDGFLDIWT 436
gi|151335575|gb|ABS00315.1|         AINGITNKVNSVIEKMNTQFTAVGKEFNKLERRMENLNKKVDDGFLDIWT 450
                                    *:: *:*****:*:*** **:::****..**:*:*.**.********:**

gi|224979377|gb|ACN72617.1|         YNAELLILLENERTLDFHDFNVKNLYEKVKSQLRNNAKEIGNGCFEFYHK 487
gi|91177888|gb|ABE27153.1|          YNAELLILLENERTLDFHDFNVKNLYEKVKSQLRNNAKEIGNGCFEFYHK 487
gi|238057035|gb|ACR39188.1|         YNAELLILLENERTLDFHDFNVKNLYEKVKSQLRNNAKEIGNGCFEFYHK 487
gi|20068267|emb|CAC86337.1|         YNAELLILLENERTLDFHDFNVKNLYEKVKSQLRNNAKEIGNGCFEFYHK 473
gi|210076637|gb|ACJ06667.1|         YNAELLILLENERTLDFHDLNVKNLYEKVKSQLRNNAKEIGNGCFEFYHK 487
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gi|238867285|gb|ACR67261.1|         YNAELLVLLENERTLDFHDFNVRNLYEKVKSQLRNNAKEIGNGCFEFYHK 487
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gi|157168452|gb|ABV25640.1|         YNAELLVLLENERTLDYHDSNVKNLYEKVRSQLKNNAKEIGNGCFEFYHK 487
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gi|197344172|gb|ACH69547.1|         YNAELLVLLENERTLDYHDSNVKNLYEKVRSQLKNNAKEIGNGCFEFYHK 487
gi|237872683|gb|ACR26701.1|         YNAELLVLLENERTLDYHDSNVKNLYEKVRSQLKNNAKEIGNGCFEFYHK 487
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gi|221326988|gb|ACM17265.1|         YNAELLVLLENERTLDFHDSNVKNLYEKVKSQLKNNAKEIGNGCFEFYHK 486
gi|151335575|gb|ABS00315.1|         YNAELLVLLENERTLDFHDSNVKNLYEKVKSQLKNNAKEIGNGCFEFYHK 500
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gi|224979377|gb|ACN72617.1|         CDNECMESVKNGTYNYPRYSEESKLNREEIDGVKLESVGVHQILAIYSTV 537
gi|91177888|gb|ABE27153.1|          CDNECMESVKNGTYNYPRYSEESKLNREEIDGVKLESVGVHQILAIYSTV 537
gi|238057035|gb|ACR39188.1|         CDNECMESVKNGTYNYPRYXEESKLNREEIDGVKLESVGVHQILAIYSTV 537
gi|20068267|emb|CAC86337.1|         CDNECMESVKNGTYNYPKYSEESKLNREEIDGVKLESMGIHQILAIYSTV 523
gi|210076637|gb|ACJ06667.1|         CDNECMESVKNGTYNYPKYSEESKLNREEIDGVKLESMGIHQILAIYSTV 537
gi|224923729|gb|ACN67524.1|         CDNECMESVKNGTYNYPKYSEESKLNREEIDGVKLESMGVHQILAIYSTV 537
gi|238867285|gb|ACR67261.1|         CDDECMESVKNGTYNYPKYSEESKLNREEIDGVKLESMGVYQILAIYSTV 537
gi|52078155|gb|AAU25851.1|          CDDECMESVKNGTYDYPKYSEESKLNREEIDGVRLESMGVYQILAIYSTV 537
gi|4585155|gb|AAD25301.1|AF091      CDDTCMESVKNGTYDYPRYSEESKLNREEIDGVKLESTRIYQILAIYSTA 537
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gi|82622957|gb|ABB86937.1|          CDDACMESVKNGTYDYPKYSEESRLNREEINGIKLDSTRIYQILAIYSTV 537
gi|190403701|gb|ACE77928.1|         CDDTCMESVKNGTYDYPKYSEEAKLNREEIDGVKLESTRIYQILAIYSTV 537
gi|157168458|gb|ABV25643.1|         CDNTCMESVKNGTYDYPKYSEEAKLNREEIDGVKLESARIYQILAIYSTV 537
gi|157168452|gb|ABV25640.1|         CDDTCMESVKNGTYDYPKYSEEAKLNREEIDGVKLESTRIYQILAIYSTV 537
gi|237624328|gb|ACR01025.1|         CDNTCMESVKNGTYDYPKYSEEAKLNREEIDGVKLESTRIYQILAIYSTV 537
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gi|237872683|gb|ACR26701.1|         CDDTCMESVKNGTYDYPKYSEEAKLNREEIDGVKLESTRIYQILAIYSTV 537
gi|221327007|gb|ACM17276.1|         CNDECMESVKNGTYDYPKYSEESKLNREKIDGVKLESMGVYQILAIYSTV 536
gi|221326988|gb|ACM17265.1|         CNDECMESVKNGTYDYPKYSEESKLNREKIDGVKLESMGVYQILAIYSTV 536
gi|151335575|gb|ABS00315.1|         CNNECMESVKNGTYDYPKYSEESKLNREKIDGVKLESMGVYQILAIYSTV 550
                                    *:: ****:*****:**:* **::****:*:*::*:*  ::********.

gi|224979377|gb|ACN72617.1|         ASSLVLLVSLGAISFWMCSNGSLQCRICI 566
gi|91177888|gb|ABE27153.1|          ASSLVLLVSLGAISFWMCSNGSLQCRICI 566
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gi|20068267|emb|CAC86337.1|         ASSLVLLVSLGAISFWMCSNGSLQCRICI 552
gi|210076637|gb|ACJ06667.1|         ASSLVLLVSLGAISFWMCSNGSLQCRVCI 566
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Tabel Skor

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SeqA Name                             Len(aa)  SeqB Name                             Len(aa)  Score
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1    gi|4585155|gb|AAD25301.1|AF091   566      2    gi|163676476|gb|ABY40409.1|       566      92
1    gi|4585155|gb|AAD25301.1|AF091   566      3    gi|210076637|gb|ACJ06667.1|       566      80
1    gi|4585155|gb|AAD25301.1|AF091   566      4    gi|190403701|gb|ACE77928.1|       566      91
1    gi|4585155|gb|AAD25301.1|AF091   566      5    gi|151335575|gb|ABS00315.1|       579      80
1    gi|4585155|gb|AAD25301.1|AF091   566      6    gi|238867285|gb|ACR67261.1|       566      85
1    gi|4585155|gb|AAD25301.1|AF091   566      7    gi|238057035|gb|ACR39188.1|       566      81
1    gi|4585155|gb|AAD25301.1|AF091   566      8    gi|224923729|gb|ACN67524.1|       566      81
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1    gi|4585155|gb|AAD25301.1|AF091   566      11   gi|91177888|gb|ABE27153.1|        566      80
1    gi|4585155|gb|AAD25301.1|AF091   566      12   gi|52078155|gb|AAU25851.1|        566      84
1    gi|4585155|gb|AAD25301.1|AF091   566      13   gi|157168452|gb|ABV25640.1|       566      91
1    gi|4585155|gb|AAD25301.1|AF091   566      14   gi|157168458|gb|ABV25643.1|       566      90
1    gi|4585155|gb|AAD25301.1|AF091   566      15   gi|237624328|gb|ACR01025.1|       566      89
1    gi|4585155|gb|AAD25301.1|AF091   566      16   gi|197344172|gb|ACH69547.1|       566      90
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1    gi|4585155|gb|AAD25301.1|AF091   566      20   gi|82622957|gb|ABB86937.1|        566      92
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2    gi|163676476|gb|ABY40409.1|      566      4    gi|190403701|gb|ACE77928.1|       566      89
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2	gi|163676476|gb|ABY40409.1|	566	15	gi|237624328|gb|ACR01025.1|	566	87
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4.3. Protein NA Inang Manusia

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CLUSTAL 2.0.10 multiple sequence alignment


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gi|229598898|gb|ACQ83302.1|      SKDNSVRIGSKGDVFVIREPFISCSPLECRTFFLTQGALLNDKHSNGTIK 142
gi|229892732|gb|ACQ89919.1|      SKDNSVRIGSKGDVFVIREPFISCSPLECRTFFLTQGALLNDKHSNGTIK 150
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gi|237604392|gb|ACR01016.1|      SKDNSVRIGSKGDVFVIREPFISCSPLECRTFFLTQGALLNDKHSNGTIK 150
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gi|227831797|gb|ACP41947.1|      SKDNSVRIGSKGDVFVIREPFISCSPLECRTFFLTQGALLNDKHSNGTIK 150
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gi|238623294|gb|ACR47008.1|      SKDNSVRIGSKGDVFVIREPFISCSPLECRTFFLTQGALLNDKHSNGTIK 150
gi|195661083|gb|ACG50708.1|      TKDNSIRIGSKGDVFVIREPFISCSHLECRTFFLTQGALLNDKHSNGTVK 146
gi|237689231|gb|ACR15428.1|      TKDNSIRIGSKGDVFVIREPFISCSHLECRTFFLTKGALLNDKHSNGTVK 150
gi|31096413|emb|CAD57261.1|      TKDNSIRIGSKGDVFVIREPFISCSHLECRTFFLTQGALLNDKHSNGTVK 146
gi|148276812|gb|ABQ53690.1|      TKDNSIRIGSKGDVFVIREPFISCSHLECRTFFLTQGALLNDKHSNGTVK 150
gi|60811|emb|CAA33354.1|         SKDNSIRIGSKGDVFVIREPFISCSHLECRTFFLTQGALLNDKHSNGTVK 150
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gi|237651246|gb|ACR08497.1|      DRSPYRTLMSCPIGEVPSPYNSRFESVAWSASACHDGINWLTIGISGPDN 200
gi|238627784|gb|ACR49231.1|      DRSPYRTLMSCPIGEVPSPYNSRFESVAWSASACHDGINWLTIGISGPDN 200
gi|237604390|gb|ACR01015.1|      DRSPYRTLMSCPIGEVPSPYNSRFESVAWSASACHDGINWLTIGISGPDN 200
gi|237681728|gb|ACR10226.1|      DRSPYRTLMSCPIGEVPSPYNSRFESVAWSASACHDGINWLTIGISGPDN 200
gi|227977158|gb|ACP44181.1|      DRSPYRTLMSCPIGEVPSPYNSRFESVAWSASACHDGINWLTIGISGPDN 200
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gi|229396353|gb|ACQ63207.1|      DRSPYRTLMSCPIGEVPSPYNSRFESVAWSASACHDGINWLTIGISGPDN 200
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gi|238231184|gb|ACR40331.1|      DRSPYRTLMSCPIGEVPSPYNSRFESVAWSASACHDGINWLTIGISGPDN 200
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gi|229609553|gb|ACQ83396.1|      DRSPYRTLMSCPIGEVPSPYNSRFESVAWSASACHDGINWLTIGISGPDN 190
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gi|237681744|gb|ACR10236.1|      DRSPYRTLMSCPIGEVPSPYNSRFESVAWSASACHDGINWLTIGISGPDN 200
gi|237689829|gb|ACR15745.1|      DRSPYRTLMSCPIGEVPSPYNSRFESVAWSASACHDGINWLTIGISGPDN 199
gi|229598898|gb|ACQ83302.1|      DRSPYRTLMSCPIGEVPSPYNSRFESVAWSASACHDGINWLTIGISGPDN 192
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gi|238914612|gb|ACR78155.1|      GAVAVLKYNGIITDTIKSWRNNILRTQESECACVNGSCFTVMTDGPSDGQ 250
gi|237651246|gb|ACR08497.1|      GAVAVLKYNGIITDTIKSWRNNILRTQESECACVNGSCFTVMTDGPSDGQ 250
gi|238627784|gb|ACR49231.1|      GAVAVLKYNGIITDTIKSWRNNILRTQESECACVNGSCFTVMTDGPSDGQ 250
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gi|237681728|gb|ACR10226.1|      GAVAVLKYNGIITDTIKSWRNNILRTQESECACVNGSCFTVMTDGPSDGQ 250
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gi|31096413|emb|CAD57261.1|      GAVAVLKYNGIITETIKSWKKRILRTQESECVCVNGSCFTIMTDGPSNGA 246
gi|148276812|gb|ABQ53690.1|      GAVAVLKYNGIITETIKSWKKQILRTQESECVCVNGSCFTIMTDGPSDRA 250
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gi|237651246|gb|ACR08497.1|      ASYKIFRIEKGKIVKSVEMNAPNYHYEECSCYPDSSEITCVCRDNWHGSN 300
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gi|239812998|gb|ACS27784.1|      ASNKIFRIEKGKIVKSVEMNAPNYHYEECSCYPDSSEITCVCRDNWHGSN 300
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gi|60811|emb|CAA33354.1|         ASYRIFKIEKGKITKSIELDAPNSHYEECSCYPDTGTVMCVCRDNWHGSN 300
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gi|237604390|gb|ACR01015.1|      RPWVSFNQNLEYQIGYICSGIFGDNPRPNDKTGSCGPVSSNGANGVKGFS 350
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gi|239812998|gb|ACS27784.1|      RPWVSFNQNLEYQIGYICSGIFGDNPRPNDKTGSCGPVSSNGANGVKGFS 350
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gi|238627784|gb|ACR49231.1|      FKYGNGVWIGRTKSISSRNGFEMIWDPNGWTGTDNNFSIKQDIVGINEWS 400
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gi|60811|emb|CAA33354.1|         YRYGNGVWIGRTKSNSSRKGFEMIWDPNGWTDTDSNFLVKQDVVAMTDWS 400
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gi|238914612|gb|ACR78155.1|      GYSGSFVQHPELTGLDCIRPCFWVELIRGRPKEN-TIWTSGSSISFCGVN 449
gi|237651246|gb|ACR08497.1|      GYSGSFVQHPELTGLDCIRPCFWVELIRGRPKEN-TIWTSGSSISFCGVN 449
gi|238627784|gb|ACR49231.1|      GYSGSFVQHPELTGLDCIRPCFWVELIRGRPKEN-TIWTSGSSISFCGVN 449
gi|237604390|gb|ACR01015.1|      GYSGSFVQHPELTGLDCIRPCFWVELIRGRPKEN-TIWTSGSSISFCGVN 449
gi|237681728|gb|ACR10226.1|      GYSGSFVQHPELTGLDCIRPCFWVELIRGRPKEN-TIWTSGSSISFCGVN 449
gi|227977158|gb|ACP44181.1|      GYSGSFVQHPELTGLDCIRPCFWVELIRGRPKEN-TIWTSGSSISFCGVN 449
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gi|229892682|gb|ACQ89891.1|      GYSGSFVQHPELTGLDCIRPCFWVELIRGRPKEN-TIWTSGSSISFCGVN 449
gi|229609553|gb|ACQ83396.1|      GYSGSFVQHPELTGLDCIRPCFWVELIRGRPKEN-TIWTSGSSISFCGVN 439
gi|237511840|gb|ACQ99631.1|      GYSGSFVQHPELTGLDCIRPCFWVELIRGRPKEN-TIWTSGSSISFCGVN 439
gi|237681744|gb|ACR10236.1|      GYSGSFVQHPELTGLDCIRPCFWVELIRGRPKEN-TIWTSGSSISFCGVN 449
gi|237689829|gb|ACR15745.1|      GYSGSFVQHPELTGLDCIRPCFWVELIRGRPKEN-TIWTSGSSISFCGVN 448
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gi|229892732|gb|ACQ89919.1|      GYSGSFVQHPELTGLDCIRPCFWVELIRGRPKEN-TIWTSGSSISFCGVN 449
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gi|238914612|gb|ACR78155.1|      SDTVGWSWPDGAELPF---- 465
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gi|238627784|gb|ACR49231.1|      SDTVGWSWPDGAELPFT--- 466
gi|237604390|gb|ACR01015.1|      SDTVGWSWPDGAELPFTIDK 469
gi|237681728|gb|ACR10226.1|      SDTVGWSWPDGAELPFTIDK 469
gi|227977158|gb|ACP44181.1|      SDTVGWSWPDGAELPFTIDK 469
gi|238635095|gb|ACR40321.2|      SDTVGWSWPDGAELPFTIDK 469
gi|229396353|gb|ACQ63207.1|      SDTVGWSWPDGAELPFTIDK 469
gi|239812998|gb|ACS27784.1|      SDTVGWSWPDGAELPFTIDK 469
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gi|237681744|gb|ACR10236.1|      SDTVGWSWPDGAELPFTIDK 469
gi|237689829|gb|ACR15745.1|      SDTVGWSWPDGAELPFTID- 467
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gi|227831797|gb|ACP41947.1|      SDTVGWSWPDGAELPFTI-- 467
gi|238914624|gb|ACR78161.1|      SDTVGWSWPDGAELPF---- 465
gi|238623294|gb|ACR47008.1|      SDTVGWSWPDGAELPFTIDK 469
gi|195661083|gb|ACG50708.1|      SDTANWSWPDGAELPFTIDK 466
gi|237689231|gb|ACR15428.1|      SDTANWSWPDGAELPFTIDK 470
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Tabel Skor

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SeqA Name                        Len(aa)  SeqB Name                        Len(aa)  Score
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1    gi|195661083|gb|ACG50708.1|   466      3    gi|237681744|gb|ACR10236.1|   469      80
1    gi|195661083|gb|ACG50708.1|   466      4    gi|237689850|gb|ACR15757.1|   457      79
1    gi|195661083|gb|ACG50708.1|   466      5    gi|238914612|gb|ACR78155.1|   465      80
1    gi|195661083|gb|ACG50708.1|   466      6    gi|239812998|gb|ACS27784.1|   469      80
1    gi|195661083|gb|ACG50708.1|   466      7    gi|237604390|gb|ACR01015.1|   469      80
1    gi|195661083|gb|ACG50708.1|   466      8    gi|229892682|gb|ACQ89891.1|   469      80
1    gi|195661083|gb|ACG50708.1|   466      9    gi|228860931|gb|ACQ45339.1|   469      80
1    gi|195661083|gb|ACG50708.1|   466      10   gi|229609553|gb|ACQ83396.1|   452      80
1    gi|195661083|gb|ACG50708.1|   466      11   gi|238618427|gb|ACR46980.1|   469      80
1    gi|195661083|gb|ACG50708.1|   466      12   gi|238627784|gb|ACR49231.1|   466      79
1    gi|195661083|gb|ACG50708.1|   466      13   gi|237689829|gb|ACR15745.1|   467      80
1    gi|195661083|gb|ACG50708.1|   466      14   gi|237681728|gb|ACR10226.1|   469      80
1    gi|195661083|gb|ACG50708.1|   466      15   gi|229368679|gb|ACQ59196.1|   467      80
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1    gi|195661083|gb|ACG50708.1|   466      17   gi|229396353|gb|ACQ63207.1|   469      80
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1    gi|195661083|gb|ACG50708.1|   466      19   gi|238623294|gb|ACR47008.1|   469      80
1    gi|195661083|gb|ACG50708.1|   466      20   gi|227977158|gb|ACP44181.1|   469      80
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4.4. Protein NA Inang Babi

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CLUSTAL 2.0.10 multiple sequence alignment


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gi|1212736|dbj|BAA06717.1|      -----------------MNPNQKIITIGSISMAIGIISLILQIGNIISIWA 34
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gi|190403802|gb|ACE77988.1|     -----------------MNTNQRIITIGTVCLIVGIISLLLQIGNIVSLWI 34
gi|188572592|gb|ACD65204.1|     -----------------MNTNQRIITIGTVCLIVGIVSLLLQIGNIVSLWI 34
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gi|168487842|gb|ACA25342.1|      LAGNSSLCPVNGWAIYSKDNSIRIGSKGDIFVIREPFISCSHLECRTFFL 134
                                 *.*.*.***:  ***::***.:****:**:**:***** ** :***:***

gi|163676450|gb|ABY40396.1|      TQGALLNDKHSNGTIKDRSPYRTLMSCLVGEVPSPYNSRFESVAWSASAC 184
gi|163676452|gb|ABY40397.1|      TQGALLNDKHSNGTIKDRSPYRTLMSCLVGEVPSPYNSRFESVAWSASAC 184
gi|210076639|gb|ACJ06668.1|      TQGALLNDKHSNGTIKDRSPYRTLMSCPIGEVPSPYNSRFESVAWSASAC 184
gi|89789284|gb|ABD78107.1|       TQGALLNDKHSNGTIKDRSPYRTLMSCPIGEVPSPYNSRFESVAWSASAC 184
gi|237624332|gb|ACR01027.1|      TQGALLNDKHSNGTIKDRSPYRTLMSCPIGEVPSPYNSRFESVAWSASAC 184
gi|224979384|gb|ACN72621.1|      TQGALLNDKHSNGTVKDRSPYRTLMSCPIGEVPSPYNSRFESVAWSASAC 184
gi|91177893|gb|ABE27156.1|       TQGALLNDKHSNGTVKDRSPYRTLMSCPIGEVPSPYNSRFESVAWSASAC 184
gi|195933633|gb|ABS50330.2|      TQGALLNDKHSNGTVKDRSPYRTLMSCPIGEVPSPYNSRFESVAWSASAC 184
gi|238057618|gb|ACR39305.1|      TQGALLNDKHSNGTIKDRSPYRTLMSCPIGEVPSPYNSRFESVAWSASAC 184
gi|52078153|gb|AAU25850.1|       TQGALLNDKHSNGTVKDRSPYRTLMSCPVGEAPSPYNSRFESVAWSASAC 184
gi|1212736|dbj|BAA06717.1|       TQGALLNDKHSNGTVKDRSPYRALMSCPLGEAPSPYNSRFESVAWSASAC 184
gi|190403800|gb|ACE77987.1|      TQGALLNDKHSNGTVKDRSPYRTLMSCPIGEAPSPYNSRFESVAWSASAC 200
gi|190403802|gb|ACE77988.1|      TQGALLNDKHSNGTVKDRSPYRTLMSCPIGEAPSPYNSRFESVAWSASAC 184
gi|188572592|gb|ACD65204.1|      TQGALLNDRHSNGTVKDRSPYRTLMSCPIGEAPSPYNSRFESVAWSASAC 184
gi|197344174|gb|ACH69548.1|      TQGALLNDRHSNGTVKDRSPYRTLMSCPIGEAPSPYNSRFESVAWSASAC 184
gi|237872673|gb|ACR26696.1|      TQGALLNDRHSNGTVKDRSPYRTLMSCPIGEAPSPYNSRFESVAWSASAC 183
gi|168487842|gb|ACA25342.1|      TQGALLNDRHSNGTVKDRSPYRTLMSCPIGEAPSPYNSKFESVAWSASAC 184
                                 ********:*****:*******:**** :**.******:***********

gi|163676450|gb|ABY40396.1|      HDGISWLTIGISGPDNEAVAVLKYNGIITDTIKSWRKNILRTQESECACV 234
gi|163676452|gb|ABY40397.1|      HDGISWLTIGISGPDNEAVAVLKYNGIITDTIKSWRKNILRTQESECACV 234
gi|210076639|gb|ACJ06668.1|      HDGTSWLTIGISGPDNGAVAVLKYNGIITDTIKSWRKNILRTQESECACV 234
gi|89789284|gb|ABD78107.1|       HDGTSWLTIGISGPDNGAVAVLKYNGIITDTIKSWRNNILRTQESECACV 234
gi|237624332|gb|ACR01027.1|      HDGINWLTIGISGPDNGAVAVLKYNGIITDTIKSWRNNILRTQESECACV 234
gi|224979384|gb|ACN72621.1|      HDGSSWLTIGISGPDNGAVAVLKYNDIITDTIKSWKNNILRTQESECACL 234
gi|91177893|gb|ABE27156.1|       HDGTSWLTIGISGPDNGAVAVLKYNDIITDTIKSWKNNILRTQESECACL 234
gi|195933633|gb|ABS50330.2|      HDGTSWLTIGISGPDNGAVAVLKYNGIITDTIKSWKNNILRTQESECACL 234
gi|238057618|gb|ACR39305.1|      HDGTSWLTIGISGPDNGAVAVLKYNDIITDTIKSWRNNILRTQESECACM 234
gi|52078153|gb|AAU25850.1|       HDGISWLTIGISGPDNGAVAVLKYNGIITDTVKSWRNNILRTQESECACI 234
gi|1212736|dbj|BAA06717.1|       HDGMGWLTIGISGPDDGAVAVLKYNGIITETIKSWRKQILRTQESECVCV 234
gi|190403800|gb|ACE77987.1|      HDGMGWLTIGISGPDNGAVAVLKYNGIITDTIKSWRNKILRTQESECVCM 250
gi|190403802|gb|ACE77988.1|      HDGMGWLTIGISGPDNGAVAVLKYNGIITDTIKSWRNKILRTQESECVCM 234
gi|188572592|gb|ACD65204.1|      HDGMGWLTIGISGPDNGAVAVLKYNGIITDTIKSWRNKILRTQESECVCI 234
gi|197344174|gb|ACH69548.1|      HDGMGWLTIGISGPDNGAVAVLKYNGIITDTIKSWRNKILRTQESECVCI 234
gi|237872673|gb|ACR26696.1|      HDGMGWLTIGISGPDNGAVAVLKYNGIITDTIKSWRNKILRTQESECVCI 233
gi|168487842|gb|ACA25342.1|      HDGMGWLTIGISGPDNGAVAVLKYNGIITDTIKSWRNRILRTQESECVCI 234
                                 *** .**********: ********.***:*:***::.*********.*:

gi|163676450|gb|ABY40396.1|      NGSCFTVMTDGPSNGQASYKIFKIEKGKVVKSVELNAPNYHYEECSCYPE 284
gi|163676452|gb|ABY40397.1|      NGSCFTVMTDGPSNGQASYKIFKIEKGKVVKSVELNAPNYHYEECSCYPE 284
gi|210076639|gb|ACJ06668.1|      NGSCFTVMTDGPSNGQASYKVFKIERGKVVKSVELNAPNYHYEECSCYPE 284
gi|89789284|gb|ABD78107.1|       NGSCFTVMTDGPSNGQASYKIFKIEKGKVVKSVELNAPNYHYEECSCYPE 284
gi|237624332|gb|ACR01027.1|      NGSCFTVMTDGPSNGQASYKIFRIEKGKIVKSVEMNAPNYHYEECSCYPD 284
gi|224979384|gb|ACN72621.1|      NGSCFTVMTDGPSNGQASYKIFKIEKGKVVKSVELNAPNYHYEECSCYPD 284
gi|91177893|gb|ABE27156.1|       NGSCFTVMTDGPSNGQASYKIFKIEKGKVVKSVELNAPNYHYEECSCYPD 284
gi|195933633|gb|ABS50330.2|      NGSCFTVMTDGPSNGQASYKIFKIEKGKVVKSVELNAPNYHYEECSCYPD 284
gi|238057618|gb|ACR39305.1|      NGSCFTVMTDGPSNGQASYKIFKIEKGKVVKSVELNAPNYHYEECSCYPD 284
gi|52078153|gb|AAU25850.1|       NGSCFTIMTDGPSNGQASYKIFKIEKGKVVKSVELNAPNYHYEECSCYPD 284
gi|1212736|dbj|BAA06717.1|       NGSCFTIMTDGPSDGPASYRIFKIEKGKVTKSIELDAPNYHYEECSCYPD 284
gi|190403800|gb|ACE77987.1|      NGSCFTVLTDGPSNGQASYKIFKVEKGKIIKSIELDAPNYHYEECSCYPD 300
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gi|190403802|gb|ACE77988.1|      NGSCFTVLTDGPSNGQASYKIFKVEKGKIIKSIELDAPNYHYEECSCYPD 284
gi|188572592|gb|ACD65204.1|      NGSCFTIMTDGPSNGQASYKIFKMEKGKIIKSVELDAPNYHYEECSCYPD 284
gi|197344174|gb|ACH69548.1|      NGSCFTIMTDGPSNGQASYKIFKMEKGKIIKSVELDAPNYHYEECSCYPD 284
gi|237872673|gb|ACR26696.1|      NGSCFTIMTDGPSNGQASYKIFKMEKGKIIKSVELDAPNYHYEECSCYPD 283
gi|168487842|gb|ACA25342.1|      NGSCFTIMTDGPSNGQASYKIFKMERGKIIKSVELDAPNYHYEECSCYPD 284
                                 ******::*****:* ***::*::*:**: **:*::*************:

gi|163676450|gb|ABY40396.1|      SGKITCVCRDNWHGSNRPWVSFNQNLEYQIGYICSGIFGDNPRPNDRTGS 334
gi|163676452|gb|ABY40397.1|      SGKITCVCRDNWHGSNRPWVSFNQNLEYQIGYICSGIFGDNPRPNDRTGS 334
gi|210076639|gb|ACJ06668.1|      SGEITCVCRDNWHGSNRPWVSFNQNLEYQMGYICSGIFGDNPRPNDKTGS 334
gi|89789284|gb|ABD78107.1|       SGEITCVCRDNWHGSNRPWVSFNQNLEYQIGYICSGIFGDNPRPNDRTGS 334
gi|237624332|gb|ACR01027.1|      SSEITCVCRDNWHGSNRPWVSFNQNLEYQIGYICSGIFGDNPRPNDKTGC 334
gi|224979384|gb|ACN72621.1|      SGEIICVCRDNWHGSNRPWVSFNQNLEYQIGYICSGVLGDNPRPNDRTGN 334
gi|91177893|gb|ABE27156.1|       SGEIICVCRDNWHGSNRPWVTFNQNLEYQIGYICSGVLGDNPRPNDRTGS 334
gi|195933633|gb|ABS50330.2|      SGEIICVCRDNWHGSNRPWVSFNQNLEYQIGYICSGVLGDNPRPNDRTGS 334
gi|238057618|gb|ACR39305.1|      SGEIICVCRDNWHGSNRPWVSFNQNLEYQIGYICSGVLGDNPRPNDRTGS 334
gi|52078153|gb|AAU25850.1|       ASEVMCVCRDNWHGSNRPWVSFNQNLEYQIGYICSGVFGDNPRPNDGTGS 334
gi|1212736|dbj|BAA06717.1|       TGTVMCVCRDNWHGSNRPWVSFNQNLDYQIGYICSGVFGDNPRPKDGEGS 334
gi|190403800|gb|ACE77987.1|      TGKVMCVCRDNWHASNRPWVSFDQNLDYQMGYICSGVFGDNPRSNDGKGN 350
gi|190403802|gb|ACE77988.1|      TGKVMCVCRDNWHASNRPWVSFDQNLDYQMGYICSGVFGDNPRSNDGKGN 334
gi|188572592|gb|ACD65204.1|      TGKVVCVCRDNWHASNRPWVTFDQNLNYQIGYICSGVFGDNPRSNDGKGN 334
gi|197344174|gb|ACH69548.1|      TGKVVCVCRDNWHASNRPWVTFDQNLNYQIGYICSGVFGDNPRSNDGKGN 334
gi|237872673|gb|ACR26696.1|      TGKVVCVCRDNWHASNRPWVSFDQNXNYQIGYICSGVFGDNPRSNDGKGN 333
gi|168487842|gb|ACA25342.1|      TGKVVCVCRDNWHASNRPWVSFDQNLDYQIGYICSGVFGDNPRSNDGKGN 334
                                 :. : ********.******:*:** :**:******::*****.:*  *

gi|163676450|gb|ABY40396.1|      CGPVSSNGANGVKGFSFKYGNGVWIGRTKSTSLRSGFEMIWDPNGWTGTD 384
gi|163676452|gb|ABY40397.1|      CGPVSSYGANGVKGFSFKYGNGVWIGRTKSTSLRSGFEMIWDPNGWTGTD 384
gi|210076639|gb|ACJ06668.1|      CGPVFSNGANGVKGFSFKYGNGVWIGRTKSTSSRRGFEMIWDPDGWTRTD 384
gi|89789284|gb|ABD78107.1|       CGPVFSNGANGVKGFSFKYGNGVWIGRTKSTSSRSGFEMIWDPNGWTRTD 384
gi|237624332|gb|ACR01027.1|      CGPVSSNGANGVKGFSFKYGNGVWIGRTKSISSRNGFEMIWDPNGWTGTD 384
gi|224979384|gb|ACN72621.1|      CGPVSSHGANGVKGFSFKYGDGIWIGRTKSTSSRSGFEMIWDPNGWTGTD 384
gi|91177893|gb|ABE27156.1|       CGPVSSHGANGVKGFSFKYGNGIWIGRTKSTSSRSGFEMIWDPNGWTGTD 384
gi|195933633|gb|ABS50330.2|      CGPVSSHGANGVKGFSFKYGNGIWIGRTKSTSTRSGFEMIWDPNGWTGTD 384
gi|238057618|gb|ACR39305.1|      CGPVSSNGANGVKGFSFKYGNGVWIGRTKSTSSRSGFEMIWDPNGWTGTD 384
gi|52078153|gb|AAU25850.1|       CGPVSSNGAYGVKGFSFKYGNGVWIGRTKSTSSRSGFEMIWDPNGWTETD 384
gi|1212736|dbj|BAA06717.1|       CNPVTVDGADGVKGFSYRYGNGVWIGRTKSNRLRKGFEMIWDPNGWTDTD 384
gi|190403800|gb|ACE77987.1|      CGPVLSNGANGVKGFSYRYGNGVWIGRTKSIDSRSGFEMIWDPNGWTETD 400
gi|190403802|gb|ACE77988.1|      CGPVLSNGANGVKGFSYRYGNGVWIGRTKSTDSRSGFEMIWDPNGWTETD 384
gi|188572592|gb|ACD65204.1|      CGPVPSNGANGVKGFSFRYGNGVWIGRTKSISSRSGFEMIWDPNGWTETD 384
gi|197344174|gb|ACH69548.1|      CGPVPSNGANGVKGFSFRYGNGVWIGRTKSISSRSGFEMIWDPNGWTETD 384
gi|237872673|gb|ACR26696.1|      CGPVLSNGANGVKGFSFRYGNGVWIGRTKSISSRSGFEMIWDPNGWTETD 383
gi|168487842|gb|ACA25342.1|      CGPVLSNGANGVKGFSFRYGNGVWIGRTKSTNSRSGFEMIWDPNGWTETD 384
                                 *.**   ** ******::**:*:*******   * ********:*** **

gi|163676450|gb|ABY40396.1|      NNFSAKQDIIGINDWSGYSGSFVQHPELTGLDCMRPCFWVELIRGRPKE- 433
gi|163676452|gb|ABY40397.1|      NNFSAKQDIIGINDWSGYSGSFVQHPELTGLDCMRPCFWVELIRGRPKE- 433
gi|210076639|gb|ACJ06668.1|      DKFSVKQDIIGITDWSGYSGSFVQHPELTGLDCMRPCFWVELIRGRPKE- 433
gi|89789284|gb|ABD78107.1|       DNFSVKQDIIGMTDWSGYSGSFVQHPELTGLDCMRPCFWVELIRGRPKE- 433
gi|237624332|gb|ACR01027.1|      NNFSIKQDIVGINEWSGYSGSFVQHPELTGLDCIRPCFWVELIRGRPKE- 433
gi|224979384|gb|ACN72621.1|      NNFSVKQDIVGITDWTGYSGSFVQHPELTGLDCIRPCFWVELIRGRPKE- 433
gi|91177893|gb|ABE27156.1|       NNFSVKQDIVGITDWSGYSGSFVQHPELTGLDCIRPCFWVELIRGRPKE- 433
gi|195933633|gb|ABS50330.2|      NKFSVKQDIVGITDWSGYSGSFVQHPELTGLDCIRPCFWVELIRGRPKE- 433
gi|238057618|gb|ACR39305.1|      NNFSVKQDIVGITDWSGYSGSFVQHPELTGLSCMRPCFWVELIRGRPKE- 433
gi|52078153|gb|AAU25850.1|       NSFSVKQDIVAITDWSGYSGSFVQHPELTGLDCMRPCFWVELIRGRPKE- 433
gi|1212736|dbj|BAA06717.1|       SDFSVKQDVVAMTDWSGYSGSFVQHPELTGLDCMRPCFWVELIRGRPREK 434
gi|190403800|gb|ACE77987.1|      SSFSMKQDIIALTDWSGYSGSFVQHPELTGMNCIRPCFWVELIRGQPKE- 449
gi|190403802|gb|ACE77988.1|      SSFSMKQDIIALTDWSGYSGSFVQHPELTGMNCIRPCFWVELIRGQPKE- 433
gi|188572592|gb|ACD65204.1|      SSFSIKQDIIALTDWSGYSGSFVQHPELTGMNCIKPCFWVELIRGQPKE- 433
gi|197344174|gb|ACH69548.1|      SSFSIKQDIIALTDWSGYSGSFVQHPELTGMNCIKPCFWVELIRGQPKE- 433
gi|237872673|gb|ACR26696.1|      SSFXTKQDIIALTDWSGYSGSFVQHPELTGMNCIKPCFWVELIRGQPKE- 432
gi|168487842|gb|ACA25342.1|      SNFSMKQDIIALTDWSGYSGSFVQHPELTGMNCIRPCFWVELIRGQPKE- 433
                                 ..*  ***::.:.:*:**************:.*::**********:*:*

gi|163676450|gb|ABY40396.1|      NTIWTSGSSISFCGVNSDTVGWSWPDGAELPFN-----------YDK 469
gi|163676452|gb|ABY40397.1|      NTIWTSGSSISFCGVNSDTVGWSWPDGAELPFT-----------IDK 469
gi|210076639|gb|ACJ06668.1|      NTIWTSGSSISFCGVNSDTVGWSWPDGAELPFT-----------IDK 469
gi|89789284|gb|ABD78107.1|       NTIWTSGSSISFCGVNSDTVSWSWPDGAELPFT-----------IDK 469
gi|237624332|gb|ACR01027.1|      NTIWTSGSSISFCGVNSDTVGWSWPDGAELPFT-----------IDK 469
gi|224979384|gb|ACN72621.1|      NTIWTSGSSISFCGVNSDTVGWSWPDGAELPFT-----------IDK 469
gi|91177893|gb|ABE27156.1|       NTIWTSGSSISFCGVNSDTVGWSWPDGAELPFT-----------IDK 469
```

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gi|195933633|gb|ABS50330.2|      NTIWTSGSSISFCGVNSDTVDW------------------------- 455
gi|238057618|gb|ACR39305.1|      NTIWTSGSSISFCGVNSDTVGWSWPDGAELPFT-----------IDK 469
gi|52078153|gb|AAU25850.1|       NTIWTSGSSISFCGVNSDTVGWSWPDGAELPFT-----------IDK 469
gi|1212736|dbj|BAA06717.1|       TTIWTSGSSISFCGVNSDTANWSWPDGAELPFT-----------IDK 470
gi|190403800|gb|ACE77987.1|      STIWASGSSISFCGVNSETASWSWPDGADLPFT-----------IDK 485
gi|190403802|gb|ACE77988.1|      STIWASGSSISFCGVNSETASWSWPDGADLPFT-----------IDK 469
gi|188572592|gb|ACD65204.1|      STIWTSGSSISFCGVDSETVSWSWPDGADLPFT-----------IDK 469
gi|197344174|gb|ACH69548.1|      STIWTSGSSISFCGVDSETVSWSWPDGADLPFT-----------IDK 469
gi|237872673|gb|ACR26696.1|      STIWTSGSSISFCGVDSETASWSWPDGADLPFTSWPDGAELPFTIDK 479
gi|168487842|gb|ACA25342.1|      STIWTSGSSISFCGVDSETASWSWPDGADLPFT-----------IDK 469
                                 .***:**********:*:*..*
```

Tabel Skor

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SeqA Name                        Len(aa)  SeqB Name                        Len(aa)  Score
=========================================================================================
1    gi|1212736|dbj|BAA06717.1|    470      2    gi|190403800|gb|ACE77987.1|  485        82
1    gi|1212736|dbj|BAA06717.1|    470      3    gi|190403802|gb|ACE77988.1|  469        82
1    gi|1212736|dbj|BAA06717.1|    470      4    gi|163676450|gb|ABY40396.1|  469        82
1    gi|1212736|dbj|BAA06717.1|    470      5    gi|163676452|gb|ABY40397.1|  469        83
1    gi|1212736|dbj|BAA06717.1|    470      6    gi|168487842|gb|ACA25342.1|  469        81
1    gi|1212736|dbj|BAA06717.1|    470      7    gi|210076639|gb|ACJ06668.1|  469        84
1    gi|1212736|dbj|BAA06717.1|    470      8    gi|224979384|gb|ACN72621.1|  469        81
1    gi|1212736|dbj|BAA06717.1|    470      9    gi|89789284|gb|ABD78107.1|   469        84
1    gi|1212736|dbj|BAA06717.1|    470      10   gi|91177893|gb|ABE27156.1|   469        82
1    gi|1212736|dbj|BAA06717.1|    470      11   gi|238057618|gb|ACR39305.1|  469        82
1    gi|1212736|dbj|BAA06717.1|    470      12   gi|195933633|gb|ABS50330.2|  455        82
1    gi|1212736|dbj|BAA06717.1|    470      13   gi|237872673|gb|ACR26696.1|  479        80
1    gi|1212736|dbj|BAA06717.1|    470      14   gi|52078153|gb|AAU25850.1|   469        85
1    gi|1212736|dbj|BAA06717.1|    470      15   gi|237624332|gb|ACR01027.1|  469        81
1    gi|1212736|dbj|BAA06717.1|    470      16   gi|188572592|gb|ACD65204.1|  469        81
1    gi|1212736|dbj|BAA06717.1|    470      17   gi|197344174|gb|ACH69548.1|  469        81
2    gi|190403800|gb|ACE77987.1|   485      3    gi|190403802|gb|ACE77988.1|  469        99
2    gi|190403800|gb|ACE77987.1|   485      4    gi|163676450|gb|ABY40396.1|  469        81
2    gi|190403800|gb|ACE77987.1|   485      5    gi|163676452|gb|ABY40397.1|  469        82
2    gi|190403800|gb|ACE77987.1|   485      6    gi|168487842|gb|ACA25342.1|  469        92
2    gi|190403800|gb|ACE77987.1|   485      7    gi|210076639|gb|ACJ06668.1|  469        83
2    gi|190403800|gb|ACE77987.1|   485      8    gi|224979384|gb|ACN72621.1|  469        81
2    gi|190403800|gb|ACE77987.1|   485      9    gi|89789284|gb|ABD78107.1|   469        82
2    gi|190403800|gb|ACE77987.1|   485      10   gi|91177893|gb|ABE27156.1|   469        82
2    gi|190403800|gb|ACE77987.1|   485      11   gi|238057618|gb|ACR39305.1|  469        82
2    gi|190403800|gb|ACE77987.1|   485      12   gi|195933633|gb|ABS50330.2|  455        81
2    gi|190403800|gb|ACE77987.1|   485      13   gi|237872673|gb|ACR26696.1|  479        90
2    gi|190403800|gb|ACE77987.1|   485      14   gi|52078153|gb|AAU25850.1|   469        83
2    gi|190403800|gb|ACE77987.1|   485      15   gi|237624332|gb|ACR01027.1|  469        82
2    gi|190403800|gb|ACE77987.1|   485      16   gi|188572592|gb|ACD65204.1|  469        92
2    gi|190403800|gb|ACE77987.1|   485      17   gi|197344174|gb|ACH69548.1|  469        92
3    gi|190403802|gb|ACE77988.1|   469      4    gi|163676450|gb|ABY40396.1|  469        81
3    gi|190403802|gb|ACE77988.1|   469      5    gi|163676452|gb|ABY40397.1|  469        82
3    gi|190403802|gb|ACE77988.1|   469      6    gi|168487842|gb|ACA25342.1|  469        92
3    gi|190403802|gb|ACE77988.1|   469      7    gi|210076639|gb|ACJ06668.1|  469        83
3    gi|190403802|gb|ACE77988.1|   469      8    gi|224979384|gb|ACN72621.1|  469        81
3    gi|190403802|gb|ACE77988.1|   469      9    gi|89789284|gb|ABD78107.1|   469        83
3    gi|190403802|gb|ACE77988.1|   469      10   gi|91177893|gb|ABE27156.1|   469        82
3    gi|190403802|gb|ACE77988.1|   469      11   gi|238057618|gb|ACR39305.1|  469        82
3    gi|190403802|gb|ACE77988.1|   469      12   gi|195933633|gb|ABS50330.2|  455        82
3    gi|190403802|gb|ACE77988.1|   469      13   gi|237872673|gb|ACR26696.1|  479        92
3    gi|190403802|gb|ACE77988.1|   469      14   gi|52078153|gb|AAU25850.1|   469        83
3    gi|190403802|gb|ACE77988.1|   469      15   gi|237624332|gb|ACR01027.1|  469        81
3    gi|190403802|gb|ACE77988.1|   469      16   gi|188572592|gb|ACD65204.1|  469        92
3    gi|190403802|gb|ACE77988.1|   469      17   gi|197344174|gb|ACH69548.1|  469        92
4    gi|163676450|gb|ABY40396.1|   469      5    gi|163676452|gb|ABY40397.1|  469        98
4    gi|163676450|gb|ABY40396.1|   469      6    gi|168487842|gb|ACA25342.1|  469        81
4    gi|163676450|gb|ABY40396.1|   469      7    gi|210076639|gb|ACJ06668.1|  469        93
4    gi|163676450|gb|ABY40396.1|   469      8    gi|224979384|gb|ACN72621.1|  469        90
4    gi|163676450|gb|ABY40396.1|   469      9    gi|89789284|gb|ABD78107.1|   469        94
4    gi|163676450|gb|ABY40396.1|   469      10   gi|91177893|gb|ABE27156.1|   469        91
4    gi|163676450|gb|ABY40396.1|   469      11   gi|238057618|gb|ACR39305.1|  469        92
4    gi|163676450|gb|ABY40396.1|   469      12   gi|195933633|gb|ABS50330.2|  455        91
4    gi|163676450|gb|ABY40396.1|   469      13   gi|237872673|gb|ACR26696.1|  479        80
4    gi|163676450|gb|ABY40396.1|   469      14   gi|52078153|gb|AAU25850.1|   469        89
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4	gi|163676450|gb|ABY40396.1|	469	15	gi|237624332|gb|ACR01027.1|	469	91
4	gi|163676450|gb|ABY40396.1|	469	16	gi|188572592|gb|ACD65204.1|	469	82
4	gi|163676450|gb|ABY40396.1|	469	17	gi|197344174|gb|ACH69548.1|	469	82
5	gi|163676452|gb|ABY40397.1|	469	6	gi|168487842|gb|ACA25342.1|	469	81
5	gi|163676452|gb|ABY40397.1|	469	7	gi|210076639|gb|ACJ06668.1|	469	94
5	gi|163676452|gb|ABY40397.1|	469	8	gi|224979384|gb|ACN72621.1|	469	91
5	gi|163676452|gb|ABY40397.1|	469	9	gi|89789284|gb|ABD78107.1|	469	94
5	gi|163676452|gb|ABY40397.1|	469	10	gi|91177893|gb|ABE27156.1|	469	92
5	gi|163676452|gb|ABY40397.1|	469	11	gi|238057618|gb|ACR39305.1|	469	92
5	gi|163676452|gb|ABY40397.1|	469	12	gi|195933633|gb|ABS50330.2|	455	91
5	gi|163676452|gb|ABY40397.1|	469	13	gi|237872673|gb|ACR26696.1|	479	80
5	gi|163676452|gb|ABY40397.1|	469	14	gi|52078153|gb|AAU25850.1|	469	89
5	gi|163676452|gb|ABY40397.1|	469	15	gi|237624332|gb|ACR01027.1|	469	92
5	gi|163676452|gb|ABY40397.1|	469	16	gi|188572592|gb|ACD65204.1|	469	82
5	gi|163676452|gb|ABY40397.1|	469	17	gi|197344174|gb|ACH69548.1|	469	82
6	gi|168487842|gb|ACA25342.1|	469	7	gi|210076639|gb|ACJ06668.1|	469	82
6	gi|168487842|gb|ACA25342.1|	469	8	gi|224979384|gb|ACN72621.1|	469	81
6	gi|168487842|gb|ACA25342.1|	469	9	gi|89789284|gb|ABD78107.1|	469	82
6	gi|168487842|gb|ACA25342.1|	469	10	gi|91177893|gb|ABE27156.1|	469	81
6	gi|168487842|gb|ACA25342.1|	469	11	gi|238057618|gb|ACR39305.1|	469	82
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6	gi|168487842|gb|ACA25342.1|	469	13	gi|237872673|gb|ACR26696.1|	479	93
6	gi|168487842|gb|ACA25342.1|	469	14	gi|52078153|gb|AAU25850.1|	469	83
6	gi|168487842|gb|ACA25342.1|	469	15	gi|237624332|gb|ACR01027.1|	469	81
6	gi|168487842|gb|ACA25342.1|	469	16	gi|188572592|gb|ACD65204.1|	469	94
6	gi|168487842|gb|ACA25342.1|	469	17	gi|197344174|gb|ACH69548.1|	469	94
7	gi|210076639|gb|ACJ06668.1|	469	8	gi|224979384|gb|ACN72621.1|	469	91
7	gi|210076639|gb|ACJ06668.1|	469	9	gi|89789284|gb|ABD78107.1|	469	95
7	gi|210076639|gb|ACJ06668.1|	469	10	gi|91177893|gb|ABE27156.1|	469	92
7	gi|210076639|gb|ACJ06668.1|	469	11	gi|238057618|gb|ACR39305.1|	469	92
7	gi|210076639|gb|ACJ06668.1|	469	12	gi|195933633|gb|ABS50330.2|	455	91
7	gi|210076639|gb|ACJ06668.1|	469	13	gi|237872673|gb|ACR26696.1|	479	81
7	gi|210076639|gb|ACJ06668.1|	469	14	gi|52078153|gb|AAU25850.1|	469	90
7	gi|210076639|gb|ACJ06668.1|	469	15	gi|237624332|gb|ACR01027.1|	469	91
7	gi|210076639|gb|ACJ06668.1|	469	16	gi|188572592|gb|ACD65204.1|	469	83
7	gi|210076639|gb|ACJ06668.1|	469	17	gi|197344174|gb|ACH69548.1|	469	83
8	gi|224979384|gb|ACN72621.1|	469	9	gi|89789284|gb|ABD78107.1|	469	91
8	gi|224979384|gb|ACN72621.1|	469	10	gi|91177893|gb|ABE27156.1|	469	98
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8	gi|224979384|gb|ACN72621.1|	469	12	gi|195933633|gb|ABS50330.2|	455	96
8	gi|224979384|gb|ACN72621.1|	469	13	gi|237872673|gb|ACR26696.1|	479	80
8	gi|224979384|gb|ACN72621.1|	469	14	gi|52078153|gb|AAU25850.1|	469	89
8	gi|224979384|gb|ACN72621.1|	469	15	gi|237624332|gb|ACR01027.1|	469	90
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8	gi|224979384|gb|ACN72621.1|	469	17	gi|197344174|gb|ACH69548.1|	469	81
9	gi|89789284|gb|ABD78107.1|	469	10	gi|91177893|gb|ABE27156.1|	469	93
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9	gi|89789284|gb|ABD78107.1|	469	13	gi|237872673|gb|ACR26696.1|	479	81
9	gi|89789284|gb|ABD78107.1|	469	14	gi|52078153|gb|AAU25850.1|	469	89
9	gi|89789284|gb|ABD78107.1|	469	15	gi|237624332|gb|ACR01027.1|	469	91
9	gi|89789284|gb|ABD78107.1|	469	16	gi|188572592|gb|ACD65204.1|	469	83
9	gi|89789284|gb|ABD78107.1|	469	17	gi|197344174|gb|ACH69548.1|	469	83
10	gi|91177893|gb|ABE27156.1|	469	11	gi|238057618|gb|ACR39305.1|	469	97
10	gi|91177893|gb|ABE27156.1|	469	12	gi|195933633|gb|ABS50330.2|	455	98
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10	gi|91177893|gb|ABE27156.1|	469	14	gi|52078153|gb|AAU25850.1|	469	89
10	gi|91177893|gb|ABE27156.1|	469	15	gi|237624332|gb|ACR01027.1|	469	91
10	gi|91177893|gb|ABE27156.1|	469	16	gi|188572592|gb|ACD65204.1|	469	82
10	gi|91177893|gb|ABE27156.1|	469	17	gi|197344174|gb|ACH69548.1|	469	82
11	gi|238057618|gb|ACR39305.1|	469	12	gi|195933633|gb|ABS50330.2|	455	96
11	gi|238057618|gb|ACR39305.1|	469	13	gi|237872673|gb|ACR26696.1|	479	81
11	gi|238057618|gb|ACR39305.1|	469	14	gi|52078153|gb|AAU25850.1|	469	89
11	gi|238057618|gb|ACR39305.1|	469	15	gi|237624332|gb|ACR01027.1|	469	91
11	gi|238057618|gb|ACR39305.1|	469	16	gi|188572592|gb|ACD65204.1|	469	82
11	gi|238057618|gb|ACR39305.1|	469	17	gi|197344174|gb|ACH69548.1|	469	82
12	gi|195933633|gb|ABS50330.2|	455	13	gi|237872673|gb|ACR26696.1|	479	81
12	gi|195933633|gb|ABS50330.2|	455	14	gi|52078153|gb|AAU25850.1|	469	89
12	gi|195933633|gb|ABS50330.2|	455	15	gi|237624332|gb|ACR01027.1|	469	90
12	gi|195933633|gb|ABS50330.2|	455	16	gi|188572592|gb|ACD65204.1|	469	82
12	gi|195933633|gb|ABS50330.2|	455	17	gi|197344174|gb|ACH69548.1|	469	82

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13   gi|237872673|gb|ACR26696.1|   479      14   gi|52078153|gb|AAU25850.1|    469      82
13   gi|237872673|gb|ACR26696.1|   479      15   gi|237624332|gb|ACR01027.1|   469      80
13   gi|237872673|gb|ACR26696.1|   479      16   gi|188572592|gb|ACD65204.1|   469      96
13   gi|237872673|gb|ACR26696.1|   479      17   gi|197344174|gb|ACH69548.1|   469      96
14   gi|52078153|gb|AAU25850.1|    469      15   gi|237624332|gb|ACR01027.1|   469      88
14   gi|52078153|gb|AAU25850.1|    469      16   gi|188572592|gb|ACD65204.1|   469      85
14   gi|52078153|gb|AAU25850.1|    469      17   gi|197344174|gb|ACH69548.1|   469      85
15   gi|237624332|gb|ACR01027.1|   469      16   gi|188572592|gb|ACD65204.1|   469      82
15   gi|237624332|gb|ACR01027.1|   469      17   gi|197344174|gb|ACH69548.1|   469      82
16   gi|188572592|gb|ACD65204.1|   469      17   gi|197344174|gb|ACH69548.1|   469      99
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4.5. Protein M2 Inang Manusia

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CLUSTAL 2.0.10 multiple sequence alignment


gi|229783371|gb|ACQ84453.1|       MSLLTEVETPTRSEWECRCSDSSDPLVIAANIIGILHLILWITDRLFFKC 50
gi|238058512|gb|ACR39405.1|       MSLLTEVETPTRSEWECRCSDSSDPLVIAANIIGILHLILWITDRLFFKC 50
gi|229462687|gb|ACQ66059.1|       MSLLTEVETPTRSEWECRCSDSSDPLVIAANIIGILHLILWITDRLFFKC 50
gi|239586243|gb|ACR83533.1|       MSLLTEVETPTRSEWECRCSDSSDPLVIAANIIGILHLILWITDRLFFKC 50
gi|237769932|gb|ACR18961.1|       MSLLTEVETPTRSEWECRCSDSSDPLVIAANIIGILHLILWITDRLFFKC 50
gi|237659610|gb|ACR09359.1|       MSLLTEVETPTRSEWECRCSDSSDPLVIAANIIGILHLILWITDRLFFKC 50
gi|229536073|gb|ACQ76375.1|       MSLLTEVETPTRSEWECRCSDSSDPLVIAANIIGILHLILWITDRLFFKC 50
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gi|237681732|gb|ACR10228.1|       MSLLTEVETPTRSEWECRCSDSSDPLVIAANIIGILHLILWITDRLFFKC 50
gi|239812968|gb|ACS27773.1|       MSLLTEVETHTRSEWECRCSDSSDPLVIAANIIGILHLILWITDRLFFKC 50
gi|228481037|gb|ACQ42237.1|       MSLLTEVETPTRSEWECRCSDSSDPLVIAANIIGILHLILWITDRLFFKC 50
gi|237769935|gb|ACR18963.1|       MSLLTEVETPTXSEWECRCSDSSDPLVIAANIIGILHLILWITDRLFFKC 50
gi|224021238|gb|ACN32514.1|       MSLLTEVETPIRNEWGCRCNDSSDPLVVAASIIGIVHLILWIIDRLFSKS 50
gi|187935967|gb|ACD37491.1|       MSLLTEVETPIRNEWGCRCNDSSDPLVVAASIIGIVHLILWIIDRLFSKS 50
gi|187935959|gb|ACD37486.1|       MSLLTEVETPIRNEWGCRCNDSSDPLVVAASIIGIVHLILWIIDRLFFKS 50
gi|187935874|gb|ACD37435.1|       MSLLTEVETPIRNEWGCRCNDSSDPLVVAASIIGIVHLILWIIDRLFSKS 50
gi|148356909|dbj|BAF63137.1|      MSLLTEVETPIRNEWGCRCNDSSDPLVVAANIIGIVHLILWIIDRLFSKS 50
gi|187935899|gb|ACD37450.1|       MSLLTEVETPIRNEWGCRCNDSSDPLVVAANIIGIVHLILWIIDRLFSKS 50
gi|187936002|gb|ACD37512.1|       MSLLTEVETPIKNEWGCRCNDSSDPLVVAANIIGIVHLILWIIDRLFSKS 50
gi|133754211|gb|ABO38397.1|       MSLLTEVETPIRNEWGCRCNDSSDPLVVAASIIGILHLILWILDRLFFKC 50
                                  *********   .** ***.*******:**.****:****** **** *.

gi|229783371|gb|ACQ84453.1|       IYRRFKYGLKRGPSTEGVPESMREEYQQEQQSAVDVDDGHFVNIELE- 97
gi|238058512|gb|ACR39405.1|       IYRRFKYGLKRGPSTEGVPESMREEYQQEQQSAVDVDDGHFVNIEL-- 96
gi|229462687|gb|ACQ66059.1|       IYRRFKYGLKRGPSTEGVPESMREEYQQEQQSAVDVDDGHFVNIELE- 97
gi|239586243|gb|ACR83533.1|       IYRRFKYGLKRGPSTEGVPESMREEYQQEQQSAVDVDDGHFVNIELE- 97
gi|237769932|gb|ACR18961.1|       IYRRFKYGLKRGPSTEGVPESLREEYQQEQQSAVDVDDGHFVNIELE- 97
gi|237659610|gb|ACR09359.1|       IYRRFKYGLKRGPFTEGVPESMREEYQQEQQSAVDVDDGHFVNIELE- 97
gi|229536073|gb|ACQ76375.1|       IYRRFKYGLKRGPSMEGVPESMREEYQQEQQSAVDVDDGHFVNIELE- 97
gi|238867514|gb|ACR67216.1|       IYRRFKYGLKRGPSTEGVPESMREEYQQEQQSAVDVDDGHFVNRELE- 97
gi|237681732|gb|ACR10228.1|       IYRRFKYGLKRGPSTEGVPESMREEYQQEQQSAVDVDDGHFVNIDLE- 97
gi|239812968|gb|ACS27773.1|       IYRRFKYGLKRGPSTEGVPESMREEYQQEQQSAVDVDDGHFVNIELE- 97
gi|228481037|gb|ACQ42237.1|       IYRRFKYGLKRGPSTEGVPESMREEYQQEQQSAVDVDDGHFVNIELE- 97
gi|237769935|gb|ACR18963.1|       IYRRFKYGLKRGPSTEGVPESMREEYQQEQQSAVDVDDGHFVNIELE- 97
gi|224021238|gb|ACN32514.1|       IYRIFKHGLKRGPSTEGVPESMREEYREEQQNAVDADDDHFVSIELE- 97
gi|187935967|gb|ACD37491.1|       IYRIFKHGLKRGPSTEGVPESMREEYREEQQNAVDADDDHFVSIELEG 98
gi|187935959|gb|ACD37486.1|       IYRIFKHGLKRGPSTEGVPESMREEYREEQQNAVDADDDHFVSIELE- 97
gi|187935874|gb|ACD37435.1|       IYRIFKHGLKGGPSTEGVPESMREEYREEQQNAVDADDGHFVSIEQ-- 96
gi|148356909|dbj|BAF63137.1|      IYRIFKHGLKRGPSTEGVPESMREEYREEQQNAVDADDGHFVSIELE- 97
gi|187935899|gb|ACD37450.1|       IYRIFKHGLKRGPSTEGVPESMREEYREEQQNAVDADDGHFVSIELE- 97
gi|187936002|gb|ACD37512.1|       IYRIFKHGLKRGPSTEGVPESMREEYREEQQNAVDADDGHFVSIELE- 97
gi|133754211|gb|ABO38397.1|       IYRLLKRGLKRGPSTEGVPESMREEYREEQQNAVDADDGHFVSIEL-- 96
                                  *** :* *** **  ******:****::***.***.**.***. :
```

Tabel Skor

```
SeqA Name                        Len(aa)  SeqB Name                         Len(aa)  Score
==========================================================================================
1    gi|229783371|gb|ACQ84453.1|    97       2    gi|224021238|gb|ACN32514.1|     97       81
1    gi|229783371|gb|ACQ84453.1|    97       3    gi|148356909|dbj|BAF63137.1|    97       83
1    gi|229783371|gb|ACQ84453.1|    97       4    gi|187935874|gb|ACD37435.1|     96       80
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1	gi|229783371|gb|ACQ84453.1|	97	5	gi|133754211|gb|ABO38397.1|	96	84
1	gi|229783371|gb|ACQ84453.1|	97	6	gi|239812968|gb|ACS27773.1|	97	98
1	gi|229783371|gb|ACQ84453.1|	97	7	gi|237681732|gb|ACR10228.1|	97	98
1	gi|229783371|gb|ACQ84453.1|	97	8	gi|229462687|gb|ACQ66059.1|	97	100
1	gi|229783371|gb|ACQ84453.1|	97	9	gi|238867514|gb|ACR67216.1|	97	98
1	gi|229783371|gb|ACQ84453.1|	97	10	gi|238058512|gb|ACR39405.1|	96	100
1	gi|229783371|gb|ACQ84453.1|	97	11	gi|229536073|gb|ACQ76375.1|	97	98
1	gi|229783371|gb|ACQ84453.1|	97	12	gi|237769932|gb|ACR18961.1|	97	98
1	gi|229783371|gb|ACQ84453.1|	97	13	gi|237659610|gb|ACR09359.1|	97	98
1	gi|229783371|gb|ACQ84453.1|	97	14	gi|237769935|gb|ACR18963.1|	97	98
1	gi|229783371|gb|ACQ84453.1|	97	15	gi|228481037|gb|ACQ42237.1|	97	100
1	gi|229783371|gb|ACQ84453.1|	97	16	gi|187936002|gb|ACD37512.1|	97	82
1	gi|229783371|gb|ACQ84453.1|	97	17	gi|187935899|gb|ACD37450.1|	97	83
1	gi|229783371|gb|ACQ84453.1|	97	18	gi|187935967|gb|ACD37491.1|	98	81
1	gi|229783371|gb|ACQ84453.1|	97	19	gi|187935959|gb|ACD37486.1|	97	82
1	gi|229783371|gb|ACQ84453.1|	97	20	gi|239586243|gb|ACR83533.1|	97	100
2	gi|224021238|gb|ACN32514.1|	97	3	gi|148356909|dbj|BAF63137.1|	97	97
2	gi|224021238|gb|ACN32514.1|	97	4	gi|187935874|gb|ACD37435.1|	96	96
2	gi|224021238|gb|ACN32514.1|	97	5	gi|133754211|gb|ABO38397.1|	96	91
2	gi|224021238|gb|ACN32514.1|	97	6	gi|239812968|gb|ACS27773.1|	97	80
2	gi|224021238|gb|ACN32514.1|	97	7	gi|237681732|gb|ACR10228.1|	97	80
2	gi|224021238|gb|ACN32514.1|	97	8	gi|229462687|gb|ACQ66059.1|	97	81
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2	gi|224021238|gb|ACN32514.1|	97	10	gi|238058512|gb|ACR39405.1|	96	81
2	gi|224021238|gb|ACN32514.1|	97	11	gi|229536073|gb|ACQ76375.1|	97	80
2	gi|224021238|gb|ACN32514.1|	97	12	gi|237769932|gb|ACR18961.1|	97	80
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3	gi|148356909|dbj|BAF63137.1|	97	4	gi|187935874|gb|ACD37435.1|	96	96
3	gi|148356909|dbj|BAF63137.1|	97	5	gi|133754211|gb|ABO38397.1|	96	91
3	gi|148356909|dbj|BAF63137.1|	97	6	gi|239812968|gb|ACS27773.1|	97	82
3	gi|148356909|dbj|BAF63137.1|	97	7	gi|237681732|gb|ACR10228.1|	97	82
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3	gi|148356909|dbj|BAF63137.1|	97	10	gi|238058512|gb|ACR39405.1|	96	83
3	gi|148356909|dbj|BAF63137.1|	97	11	gi|229536073|gb|ACQ76375.1|	97	82
3	gi|148356909|dbj|BAF63137.1|	97	12	gi|237769932|gb|ACR18961.1|	97	82
3	gi|148356909|dbj|BAF63137.1|	97	13	gi|237659610|gb|ACR09359.1|	97	82
3	gi|148356909|dbj|BAF63137.1|	97	14	gi|237769935|gb|ACR18963.1|	97	82
3	gi|148356909|dbj|BAF63137.1|	97	15	gi|228481037|gb|ACQ42237.1|	97	83
3	gi|148356909|dbj|BAF63137.1|	97	16	gi|187936002|gb|ACD37512.1|	97	98
3	gi|148356909|dbj|BAF63137.1|	97	17	gi|187935899|gb|ACD37450.1|	97	100
3	gi|148356909|dbj|BAF63137.1|	97	18	gi|187935967|gb|ACD37491.1|	98	97
3	gi|148356909|dbj|BAF63137.1|	97	19	gi|187935959|gb|ACD37486.1|	97	96
3	gi|148356909|dbj|BAF63137.1|	97	20	gi|239586243|gb|ACR83533.1|	97	83
4	gi|187935874|gb|ACD37435.1|	96	5	gi|133754211|gb|ABO38397.1|	96	90
4	gi|187935874|gb|ACD37435.1|	96	6	gi|239812968|gb|ACS27773.1|	97	79
4	gi|187935874|gb|ACD37435.1|	96	7	gi|237681732|gb|ACR10228.1|	97	79
4	gi|187935874|gb|ACD37435.1|	96	8	gi|229462687|gb|ACQ66059.1|	97	80
4	gi|187935874|gb|ACD37435.1|	96	9	gi|238867514|gb|ACR67216.1|	97	79
4	gi|187935874|gb|ACD37435.1|	96	10	gi|238058512|gb|ACR39405.1|	96	80
4	gi|187935874|gb|ACD37435.1|	96	11	gi|229536073|gb|ACQ76375.1|	97	79
4	gi|187935874|gb|ACD37435.1|	96	12	gi|237769932|gb|ACR18961.1|	97	79
4	gi|187935874|gb|ACD37435.1|	96	13	gi|237659610|gb|ACR09359.1|	97	79
4	gi|187935874|gb|ACD37435.1|	96	14	gi|237769935|gb|ACR18963.1|	97	79
4	gi|187935874|gb|ACD37435.1|	96	15	gi|228481037|gb|ACQ42237.1|	97	80
4	gi|187935874|gb|ACD37435.1|	96	16	gi|187936002|gb|ACD37512.1|	97	95
4	gi|187935874|gb|ACD37435.1|	96	17	gi|187935899|gb|ACD37450.1|	97	96
4	gi|187935874|gb|ACD37435.1|	96	18	gi|187935967|gb|ACD37491.1|	98	96
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4	gi|187935874|gb|ACD37435.1|	96	20	gi|239586243|gb|ACR83533.1|	97	80
5	gi|133754211|gb|ABO38397.1|	96	6	gi|239812968|gb|ACS27773.1|	97	83
5	gi|133754211|gb|ABO38397.1|	96	7	gi|237681732|gb|ACR10228.1|	97	83
5	gi|133754211|gb|ABO38397.1|	96	8	gi|229462687|gb|ACQ66059.1|	97	84
5	gi|133754211|gb|ABO38397.1|	96	9	gi|238867514|gb|ACR67216.1|	97	83

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6	gi|239812968|gb|ACS27773.1|	97	14	gi|237769935|gb|ACR18963.1|	97	97
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7	gi|237681732|gb|ACR10228.1|	97	8	gi|229462687|gb|ACQ66059.1|	97	98
7	gi|237681732|gb|ACR10228.1|	97	9	gi|238867514|gb|ACR67216.1|	97	97
7	gi|237681732|gb|ACR10228.1|	97	10	gi|238058512|gb|ACR39405.1|	96	98
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7	gi|237681732|gb|ACR10228.1|	97	12	gi|237769932|gb|ACR18961.1|	97	97
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8	gi|229462687|gb|ACQ66059.1|	97	9	gi|238867514|gb|ACR67216.1|	97	98
8	gi|229462687|gb|ACQ66059.1|	97	10	gi|238058512|gb|ACR39405.1|	96	100
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8	gi|229462687|gb|ACQ66059.1|	97	13	gi|237659610|gb|ACR09359.1|	97	98
8	gi|229462687|gb|ACQ66059.1|	97	14	gi|237769935|gb|ACR18963.1|	97	98
8	gi|229462687|gb|ACQ66059.1|	97	15	gi|228481037|gb|ACQ42237.1|	97	100
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9	gi|238867514|gb|ACR67216.1|	97	13	gi|237659610|gb|ACR09359.1|	97	97
9	gi|238867514|gb|ACR67216.1|	97	14	gi|237769935|gb|ACR18963.1|	97	97
9	gi|238867514|gb|ACR67216.1|	97	15	gi|228481037|gb|ACQ42237.1|	97	98
9	gi|238867514|gb|ACR67216.1|	97	16	gi|187936002|gb|ACD37512.1|	97	81
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10	gi|238058512|gb|ACR39405.1|	96	11	gi|229536073|gb|ACQ76375.1|	97	98
10	gi|238058512|gb|ACR39405.1|	96	12	gi|237769932|gb|ACR18961.1|	97	98
10	gi|238058512|gb|ACR39405.1|	96	13	gi|237659610|gb|ACR09359.1|	97	98
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10	gi|238058512|gb|ACR39405.1|	96	15	gi|228481037|gb|ACQ42237.1|	97	100
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10	gi|238058512|gb|ACR39405.1|	96	17	gi|187935899|gb|ACD37450.1|	97	83
10	gi|238058512|gb|ACR39405.1|	96	18	gi|187935967|gb|ACD37491.1|	98	81
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10	gi|238058512|gb|ACR39405.1|	96	20	gi|239586243|gb|ACR83533.1|	97	100

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11   gi|229536073|gb|ACQ76375.1|    97       13   gi|237659610|gb|ACR09359.1|    97       97
11   gi|229536073|gb|ACQ76375.1|    97       14   gi|237769935|gb|ACR18963.1|    97       97
11   gi|229536073|gb|ACQ76375.1|    97       15   gi|228481037|gb|ACQ42237.1|    97       98
11   gi|229536073|gb|ACQ76375.1|    97       16   gi|187936002|gb|ACD37512.1|    97       81
11   gi|229536073|gb|ACQ76375.1|    97       17   gi|187935899|gb|ACD37450.1|    97       82
11   gi|229536073|gb|ACQ76375.1|    97       18   gi|187935967|gb|ACD37491.1|    98       80
11   gi|229536073|gb|ACQ76375.1|    97       19   gi|187935959|gb|ACD37486.1|    97       81
11   gi|229536073|gb|ACQ76375.1|    97       20   gi|239586243|gb|ACR83533.1|    97       98
12   gi|237769932|gb|ACR18961.1|    97       13   gi|237659610|gb|ACR09359.1|    97       97
12   gi|237769932|gb|ACR18961.1|    97       14   gi|237769935|gb|ACR18963.1|    97       97
12   gi|237769932|gb|ACR18961.1|    97       15   gi|228481037|gb|ACQ42237.1|    97       98
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12   gi|237769932|gb|ACR18961.1|    97       18   gi|187935967|gb|ACD37491.1|    98       80
12   gi|237769932|gb|ACR18961.1|    97       19   gi|187935959|gb|ACD37486.1|    97       81
12   gi|237769932|gb|ACR18961.1|    97       20   gi|239586243|gb|ACR83533.1|    97       98
13   gi|237659610|gb|ACR09359.1|    97       14   gi|237769935|gb|ACR18963.1|    97       97
13   gi|237659610|gb|ACR09359.1|    97       15   gi|228481037|gb|ACQ42237.1|    97       98
13   gi|237659610|gb|ACR09359.1|    97       16   gi|187936002|gb|ACD37512.1|    97       81
13   gi|237659610|gb|ACR09359.1|    97       17   gi|187935899|gb|ACD37450.1|    97       82
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13   gi|237659610|gb|ACR09359.1|    97       19   gi|187935959|gb|ACD37486.1|    97       81
13   gi|237659610|gb|ACR09359.1|    97       20   gi|239586243|gb|ACR83533.1|    97       98
14   gi|237769935|gb|ACR18963.1|    97       15   gi|228481037|gb|ACQ42237.1|    97       98
14   gi|237769935|gb|ACR18963.1|    97       16   gi|187936002|gb|ACD37512.1|    97       82
14   gi|237769935|gb|ACR18963.1|    97       17   gi|187935899|gb|ACD37450.1|    97       82
14   gi|237769935|gb|ACR18963.1|    97       18   gi|187935967|gb|ACD37491.1|    98       80
14   gi|237769935|gb|ACR18963.1|    97       19   gi|187935959|gb|ACD37486.1|    97       81
14   gi|237769935|gb|ACR18963.1|    97       20   gi|239586243|gb|ACR83533.1|    97       98
15   gi|228481037|gb|ACQ42237.1|    97       16   gi|187936002|gb|ACD37512.1|    97       82
15   gi|228481037|gb|ACQ42237.1|    97       17   gi|187935899|gb|ACD37450.1|    97       83
15   gi|228481037|gb|ACQ42237.1|    97       18   gi|187935967|gb|ACD37491.1|    98       81
15   gi|228481037|gb|ACQ42237.1|    97       19   gi|187935959|gb|ACD37486.1|    97       82
15   gi|228481037|gb|ACQ42237.1|    97       20   gi|239586243|gb|ACR83533.1|    97       100
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16   gi|187936002|gb|ACD37512.1|    97       18   gi|187935967|gb|ACD37491.1|    98       96
16   gi|187936002|gb|ACD37512.1|    97       19   gi|187935959|gb|ACD37486.1|    97       95
16   gi|187936002|gb|ACD37512.1|    97       20   gi|239586243|gb|ACR83533.1|    97       82
17   gi|187935899|gb|ACD37450.1|    97       18   gi|187935967|gb|ACD37491.1|    98       97
17   gi|187935899|gb|ACD37450.1|    97       19   gi|187935959|gb|ACD37486.1|    97       96
17   gi|187935899|gb|ACD37450.1|    97       20   gi|239586243|gb|ACR83533.1|    97       83
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18   gi|187935967|gb|ACD37491.1|    98       20   gi|239586243|gb|ACR83533.1|    97       81
19   gi|187935959|gb|ACD37486.1|    97       20   gi|239586243|gb|ACR83533.1|    97       82
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4.6. Protein M2 Inang Babi

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CLUSTAL 2.0.10 multiple sequence alignment


gi|216409292|dbj|BAH02073.1|      MSLLTEVETLTKNGWECRYSDSSDPLVIAANIIGILHLILWILDRLFFKC 50
gi|186898584|gb|ACC94103.1|       MSLLTEVETSTRNGWECRYSDSSNPLVIAANIIGILHLILWILDRLFFKC 50
gi|210076642|gb|ACJ06670.1|       MSLLTEVETPTRNGWECRYSDSSDPLVIAANIIGILHLILWILDRLFFKC 50
gi|89789282|gb|ABD78106.1|        MSLLTEVETPTRNGWECRYSGSSDPLVIAANIIGILHLILWILDRLFFKC 50
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gi|237624335|gb|ACR01029.1|       MSLLTEVETPTRSEWECRCSDSSDPLVIAANIIGILHLILWITDRLFFKC 50
gi|168487838|gb|ACA25340.1|       MSLLTEVETPIRNEWECKCNDSSDPLIAAASIIGTLHLILWILDRLFFKC 50
gi|1912399|gb|AAB50983.1|         MSLLTEVETPIRNEWGCKCNDSSDPLIAAASIIGILHLILWILDRLFFKC 50
gi|82622852|gb|ABB86879.1|        MSLLTEVETPIRNEWGCRCNGSSDPLVAVASIIGILHLILWILDRLFFKC 50
gi|216409436|dbj|BAH02153.1|      MSLLTEVETPIRSEWGCRCNDSSDPLVAAASIIGILHLILWTLDRLFFKC 50
gi|188572567|gb|ACD65189.1|       MSLLTEVETPIRNGWECKCNDSSDPLIDAASIIGILHLILWIFDRLFFKC 50
                                  *********  :. * *: ..**: :  .*.*** ******  *******

gi|216409292|dbj|BAH02073.1|      IYRRLKYGLKRGPSTEGVPESMREEYQQEQQSAVDVDDGHFVNIELE 97
gi|186898584|gb|ACC94103.1|       IYRRLRYGLKRGPSTEGVPESMREEYQQEQQSAVDVDDGHFVNIELE 97
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gi|210076642|gb|ACJ06670.1|       IYRRLKYGLKRGPSTEGVPESMREEYQQEQQSAVDVDDGHFVNIELE 97
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gi|224979382|gb|ACN72620.1|       IYRRLKYGLKRGPSTEGVPESMREEYQQEQQISVDVDDGHFVNIELE 97
gi|237624335|gb|ACR01029.1|       IYRRFKYGLKRGPSTEGVPESMREEYQQEQQSAVDVDDGHFVNIELE 97
gi|168487838|gb|ACA25340.1|       IYHHFKYGRKRGPSTEGVPESMREEYRQKQQSAVDVDDGHFVNIVLE 97
gi|1912399|gb|AAB50983.1|         IYHHFKYGLKRGPSTEGVPESMREEYRQKQQSAVDVDDGHFVNIVLE 97
gi|82622852|gb|ABB86879.1|        IYRHFKYGLKWGPSTEGVPESMREEYRQKQQNAVDVDDGHFVNIVLE 97
gi|216409436|dbj|BAH02153.1|      IYRRFKYGLKRGPSTEGVPESMREEYRQKQQSAVDVDDGHFVNIVLE 97
gi|188572567|gb|ACD65189.1|       IYRRFKYGLQRGPSTEGVPESMREEYRQKQQSAVDVDDGHFVNIVL- 96
                                  **::::** : ***************:*:** :*********** *
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Tabel Skor

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SeqA Name                           Len(aa)  SeqB Name                          Len(aa)  Score
=============================================================================================
1    gi|216409292|dbj|BAH02073.1|   97       2    gi|216409436|dbj|BAH02153.1|  97       84
1    gi|216409292|dbj|BAH02073.1|   97       3    gi|168487838|gb|ACA25340.1|   97       81
1    gi|216409292|dbj|BAH02073.1|   97       4    gi|210076642|gb|ACJ06670.1|   97       97
1    gi|216409292|dbj|BAH02073.1|   97       5    gi|1912399|gb|AAB50983.1|     97       82
1    gi|216409292|dbj|BAH02073.1|   97       6    gi|224979382|gb|ACN72620.1|   97       88
1    gi|216409292|dbj|BAH02073.1|   97       7    gi|89789282|gb|ABD78106.1|    97       96
1    gi|216409292|dbj|BAH02073.1|   97       8    gi|186898584|gb|ACC94103.1|   97       95
1    gi|216409292|dbj|BAH02073.1|   97       9    gi|237624335|gb|ACR01029.1|   97       92
1    gi|216409292|dbj|BAH02073.1|   97       10   gi|188572567|gb|ACD65189.1|   96       84
1    gi|216409292|dbj|BAH02073.1|   97       11   gi|82622852|gb|ABB86879.1|    97       81
2    gi|216409436|dbj|BAH02153.1|   97       3    gi|168487838|gb|ACA25340.1|   97       90
2    gi|216409436|dbj|BAH02153.1|   97       4    gi|210076642|gb|ACJ06670.1|   97       86
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2    gi|216409436|dbj|BAH02153.1|   97       7    gi|89789282|gb|ABD78106.1|    97       85
2    gi|216409436|dbj|BAH02153.1|   97       8    gi|186898584|gb|ACC94103.1|   97       83
2    gi|216409436|dbj|BAH02153.1|   97       9    gi|237624335|gb|ACR01029.1|   97       89
2    gi|216409436|dbj|BAH02153.1|   97       10   gi|188572567|gb|ACD65189.1|   96       90
2    gi|216409436|dbj|BAH02153.1|   97       11   gi|82622852|gb|ABB86879.1|    97       92
3    gi|168487838|gb|ACA25340.1|    97       4    gi|210076642|gb|ACJ06670.1|   97       83
3    gi|168487838|gb|ACA25340.1|    97       5    gi|1912399|gb|AAB50983.1|     97       96
3    gi|168487838|gb|ACA25340.1|    97       6    gi|224979382|gb|ACN72620.1|   97       78
3    gi|168487838|gb|ACA25340.1|    97       7    gi|89789282|gb|ABD78106.1|    97       82
3    gi|168487838|gb|ACA25340.1|    97       8    gi|186898584|gb|ACC94103.1|   97       80
3    gi|168487838|gb|ACA25340.1|    97       9    gi|237624335|gb|ACR01029.1|   97       84
3    gi|168487838|gb|ACA25340.1|    97       10   gi|188572567|gb|ACD65189.1|   96       91
3    gi|168487838|gb|ACA25340.1|    97       11   gi|82622852|gb|ABB86879.1|    97       89
4    gi|210076642|gb|ACJ06670.1|    97       5    gi|1912399|gb|AAB50983.1|     97       84
4    gi|210076642|gb|ACJ06670.1|    97       6    gi|224979382|gb|ACN72620.1|   97       90
4    gi|210076642|gb|ACJ06670.1|    97       7    gi|89789282|gb|ABD78106.1|    97       98
4    gi|210076642|gb|ACJ06670.1|    97       8    gi|186898584|gb|ACC94103.1|   97       96
4    gi|210076642|gb|ACJ06670.1|    97       9    gi|237624335|gb|ACR01029.1|   97       94
4    gi|210076642|gb|ACJ06670.1|    97       10   gi|188572567|gb|ACD65189.1|   96       86
4    gi|210076642|gb|ACJ06670.1|    97       11   gi|82622852|gb|ABB86879.1|    97       83
5    gi|1912399|gb|AAB50983.1|      97       6    gi|224979382|gb|ACN72620.1|   97       79
5    gi|1912399|gb|AAB50983.1|      97       7    gi|89789282|gb|ABD78106.1|    97       83
5    gi|1912399|gb|AAB50983.1|      97       8    gi|186898584|gb|ACC94103.1|   97       81
5    gi|1912399|gb|AAB50983.1|      97       9    gi|237624335|gb|ACR01029.1|   97       85
5    gi|1912399|gb|AAB50983.1|      97       10   gi|188572567|gb|ACD65189.1|   96       92
5    gi|1912399|gb|AAB50983.1|      97       11   gi|82622852|gb|ABB86879.1|    97       92
6    gi|224979382|gb|ACN72620.1|    97       7    gi|89789282|gb|ABD78106.1|    97       91
6    gi|224979382|gb|ACN72620.1|    97       8    gi|186898584|gb|ACC94103.1|   97       87
6    gi|224979382|gb|ACN72620.1|    97       9    gi|237624335|gb|ACR01029.1|   97       86
6    gi|224979382|gb|ACN72620.1|    97       10   gi|188572567|gb|ACD65189.1|   96       83
6    gi|224979382|gb|ACN72620.1|    97       11   gi|82622852|gb|ABB86879.1|    97       78
7    gi|89789282|gb|ABD78106.1|     97       8    gi|186898584|gb|ACC94103.1|   97       95
7    gi|89789282|gb|ABD78106.1|     97       9    gi|237624335|gb|ACR01029.1|   97       93
7    gi|89789282|gb|ABD78106.1|     97       10   gi|188572567|gb|ACD65189.1|   96       85
7    gi|89789282|gb|ABD78106.1|     97       11   gi|82622852|gb|ABB86879.1|    97       84
8    gi|186898584|gb|ACC94103.1|    97       9    gi|237624335|gb|ACR01029.1|   97       91
8    gi|186898584|gb|ACC94103.1|    97       10   gi|188572567|gb|ACD65189.1|   96       83
8    gi|186898584|gb|ACC94103.1|    97       11   gi|82622852|gb|ABB86879.1|    97       80
9    gi|237624335|gb|ACR01029.1|    97       10   gi|188572567|gb|ACD65189.1|   96       86
9    gi|237624335|gb|ACR01029.1|    97       11   gi|82622852|gb|ABB86879.1|    97       84
10   gi|188572567|gb|ACD65189.1|    96       11   gi|82622852|gb|ABB86879.1|    97       87
=============================================================================================
```

Lampiran 5. Hasil *Proteasomal Cleavage Protein* HA Menggunakan *Server* NetChop 3.0

5.1. Protein HA Inang Manusia

```
NetChop 3.0 predictions using version C-term. Threshold 0.500000

566 Sequence

MKAILVVLLYTFATANADTLCIGYHANNSTDTVDTVLEKNVTVTHSVNLLEDKHNGKLCKLRGVAPLHLGKCNIAGWILG
......SS.S.S..S.S..S...S.S......S..SS.S...S.S.S.SS......SS..S.....S.S.S..S..S...
NPECESLSTASSWSYIVETSSSDNGTCYPGDFIDYEELREQLSSVSSFERFEIFPKTSSWPNHDSNKGVTAACPHAGAKS
......S.....S.S.S.S........S......S..S...S..S..S..S.SS.SS..S........S.SS........
FYKNLIWLVKKGNSYPKLSKSYINDKGKEVLVLWGIHHPSTSADQQSLYQNADAYVFVGSSRYSKKFKPEIAIRPKVRDQ
S.....SSSSS...S.SS...SS.......S.SS.S..SS..S....SS.....SSS....SS.SSS...S.SS.SS...
EGRMNYYWTLVEPGDKITFEATGNLVVPRYAFAMERNAGSGIIISDTPVHDCNTTCQTPKGAINTSLPFQNIHPITIGKC
.....SSS.SS.....S.S.S...S....S.S.S.S......S.....S.S...S..........SS.S.....S.S.S.
PKYVKSTKLRLATGLRNVPSIQSRGLFGAIAGFIEGGWTGMVDGWYGYHHQNEQGSGYAADLKSTQNAIDEITNKVNSVI
..S.S..SSSS...SS....S....S......S........S.....SSS.......S...S............SS..S.
EKMNTQFTAVGKEFNHLEKRIENLNKKVDDGFLDIWTYNAELLVLLENERTLDYHDSNVKNLYEKVRSQLKNNAKEIGNG
.SS...S..S.S....S.S....S..S.......S..S.S.S.SSS...S.S.S.....S.SS.SS...SS...S.S...
CFEFYHKCDNTCMESVKNGTYDYPKYSEEAKLNREEIDGVKLESTRIYQILAIYSTVASSLVLVVSLGAISFWMCSNGSL
.S.SS.S.....S.......S.S..S...SSS........SS.....S..S..S..SS..SSS.S.S..S.SSS.....S
QCRICI
......
```

5.2. Protein HA Inang Babi

```
NetChop 3.0 predictions using version C-term. Threshold 0.500000

497 Sequence

MKAILLVLLCTFAATNADTLCIGYHANNSTDTVDTILEKNVTVTHSVNLLEDKHNGKLCKLGGIAPLHLGKCNIAGWLLG
......SSS..S.......S...S.S......S...S.S...S.S.S.SS......SS..S.....S.S.S..S..S...
NPECELLFTVSSWSYIVETSNSDNGTCYPGDFINYEELREQLSSVSSFERFEIFPKTSSWPDHETNRGVTAACPYAGANS
.....S.S.S..S.SSS.S........S......SS.S...S..S..S..S.SS.SS..S..........SS..S.....
FYRNLIWLVKKGNSYPKLSKSYVNNKGKEVLVLWGIHHPPTSTDQQSLYQNADAYIFVGSSKYNRKFKPEIAERPKVRGQ
SS.....SSSS...S.SS...SS.......S.SS.S..SS...SSS.SS.....S......SS..SS....S.S.S....
AGRMNYYWTLIEPGDTIKFEATGNLVVPRYAFAMNRDPGSGIITSDAPVHDCNTTCQTPKGAINTSLPFQNIHPVTIGEC
.....SSS.S......SSS.....S....S.SSS.S......S.S.........S..........SS.S..S..S.S...
PKYVKSTKLRMATGLRNIPSIQSRGLFGAIAGFIEGGWTGMIDGWYGYHHQNEQGSGYAADQKSTQNAVDGITNKVNSVI
.SS.S..SSSS....S....S....S......S........S.....S.S.......S................SS..S.
KKMNTQFAAVGKEFNHLEKRIENLNKKVDDGFLDVWTYNAELLVLLENERTLDFHDSNVKNLYEKVRSQLRNNAKEIGNG
.SS...S..S.S....S.S....S..S.......S..S.S.S.SSS...S.S.S....SS.SS.SS...SS.........
CFEFYHKCDDTCMESVK
.S.SS.S.....S....
```

5.3. Protein NA Inang Manusia

```
NetChop 3.0 predictions using version C-term. Threshold 0.500000

457 Sequence

MNPNQKIITIGSVCMTIGMANLILQIGNIISIWISHSIQLGNQNQIETCNQSVITYENNTWVNQTYVNISNTNFAAGQSV
.........S..S.S......S.S.......SSS...S.S.....S.........S.....S...SS.....SS......
VSVKLAGNSSLCPVSGWAIYSKDNSVRIGSKGDVFVIREPFISCSPLECRTFFLTQGALLNDKHSNGTIKDRSPYRTLMS
S.SSS.....S.....S..S.S...SSS........SS..S.....S....SSS..SSSS.........S....SS.SS.
```

```
CPIGEVPSPYNSRFESVAWSASACHDGINWLTIGISGPDNGAVAVLKYNGIITDTIKSWRNNILRTQESECACVNGSCFT
..S..S...S..SS..S.S.S.S.......S.S.S.........SS.S..........S...SSS...............
VMTDGPSNGQASYKIFRIEKGKIVKSVEMNAPNYHYEECSCYPDSSEITCVCRDNWHGSNRPWVSFNQNLEYQIGYICSG
S...........S....S.S...SS...S....S.S.S...S.....S..S.S............S.SSS.S...SS...
IFGDNPRPNDKTGSCGPVSSNGANGVKGFSFKYGNGVWIGRTKSISSRNGFEMIWDPNGWTGTDNNFSIKQDIVGINEWS
..........S.S....S.......SS.S...S....S....SSS..S....SSS....S......S.S......S..S.
GYSGSFVQHPELTGLDCIRPCFWVELIRGRPKENTIWTSGSSISFCGVNSDTVGWSW
.S...S..S..S..S......S...SS........SSS....S.S..S......S.S
```

5.4. Protein NA Inang Babi

```
NetChop 3.0 predictions using version C-term. Threshold 0.500000

469 Sequence

MNTNQRIITIGTVCLIVGIISLLLQIGNIVSLWISHSIQTGGKNHTEMCNQNVITYVNNTWVNRTYVNISNTNIAAVQDV
S...........S.S......SSS....SS.SSS...SS...S....S............SS...SS......S......
TSVILAGNSSLCPVSGWAIYSKDNSIRIGSKGDIFVIREPFISCSQLECRTFFLTQGALLNDKHSNGTVKDRSPYRTLMS
..SSS.....S.....S..S.S...SSS........S...SS....S......S..SSSS........SS....SS.SS.
CPIGEAPSPYNSRFESVAWSASACHDGMGWLTIGISGPDNGAVAVLKYNGIITDTIKSWRNKILRTQESECVCMNGSCFT
..S......S..SS..S.S.S.S.........S.S.........SS.S..........S...SS.......S........
VLTDGPSNGQASYKIFKVEKGKIIKSIELDAPNYHYEECSCYPDTGKVMCVCRDNWHASNRPWVSFDQNLDYQMGYICSG
SS..........S.S..S.S....S.S.S....S.S.S...S.....SS.S..............S.S...S...S....
VFGDNPRSNDGKGNCGPVLSNGANGVKGFSYRYGNGVWIGRTKSIDSRSGFEMIWDPNGWTETDSSFSMKQDIIALTDWS
SS....S..........SS......SS.S.S.S....SS...S.S..S....S.S....S......S.S......S..S.
GYSGSFVQHPELTGMNCIRPCFWVELIRGQPKESTIWASGSSISFCGVNSETASWSWPDGADLPFTIDK
.S...S.....S.............SS....S...SSS....S.S..S......S.S.....S.S.S.S
```

5.5. Protein M2 Inang Manusia

```
NetChop 3.0 predictions using version C-term. Threshold 0.500000

97 Sequence

MSLLTEVETPTRSEWECRCSDSSDPLVIAANIIGILHLILWITDRLFFKCIYRRFKYGLKRGPSTEGVPESMREEYQQEQ
S.SS..S....S..S.S..................S.S.S....SS.....SS.S.S.SSS......S...SS..S....
QSAVDVDDGHFVNIELE
...S.......S.S.S.
```

5.6. Protein M2 Inang Babi

```
NetChop 3.0 predictions using version C-term. Threshold 0.500000

97 Sequence

MSLLTEVETLTKNGWECRYSDSSDPLVIAANIIGILHLILWILDRLFFKCIYRRLKYGLKRGPSTEGVPESMREEYQQEQ
S.SS.....S.S..S..SS......S.........S.S....S.S......SS.S.S.SSS......S...SS..S....
QSAVDVDDGHFVNIELE
...S.......S.S.S.
```

Lampiran 6. Hasil *TAP Binding Protein* Menggunakan *Server* TAPPred

6.1. Protein HA Inang Manusia

Prediction Approach	Cascade SVM
Antigen Name	HA Inang Manusia
Scanned on	Mon Sept 15 14:34:52 2008
Length of input sequence	566 amino acids
Number of nonamers from input sequence	559

Peptide Rank	Start Position	Sequence	Score	Predicted Affinity
1	340	SIQSRGLFG	8.645	High
2	110	GDFIDYEEL	8.643	High
3	289	VHDCNTTCQ	8.642	High
4	454	YHDSNVKNL	8.637	High
5	418	EKRIENLNK	8.637	High
6	402	KMNTQFTAV	8.636	High
7	186	KGKEVLVLW	8.636	High
8	479	NGCFEFYHK	8.633	High
9	439	NAELLVLLE	8.632	High
10	518	DGVKLESTR	8.628	High
11	326	STKLRLATG	8.621	High
12	10	YTFATANAD	8.618	High
.	.	.	.	.
.	.	.	.	.
.	.	.	.	.
198	222	RYSKKFKPE	6.136	High
199	266	VVPRYAFAM	6.082	High
200	128	FERFEIFPK	6.076	High
201	271	AFAMERNAG	6.043	High
202	490	NTCMESVKN	6.012	High

6.2. Protein HA Inang Babi

Prediction Approach	Cascade SVM
Antigen Name	HA Inang Babi
Scanned on	Mon Sept 15 14:35:56 2008
Length of input sequence	566 amino acids
Number of nonamers from input sequence	559

Peptide Rank	Start Position	Sequence	Score	Predicted Affinity
1	307	LPFQNIHPV	8.653	High
2	340	SIQSRGLFG	8.645	High
3	289	VHDCNTTCQ	8.642	High
4	418	EKRIENLNK	8.637	High
5	186	KGKEVLVLW	8.636	High
6	209	YQNADAYIF	8.635	High
7	216	IFVGSSKYN	8.634	High
8	479	NGCFEFYHK	8.633	High
9	439	NAELLVLLE	8.632	High
10	518	DGVKLESTR	8.628	High
11	176	PKLSKSYVN	8.624	High
12	334	GLRNIPSIQ	8.623	High
.	.	.	.	.
.	.	.	.	.
.	.	.	.	.
187	499	GTYDYPRYS	6.115	High
188	200	PTSTDQQSL	6.114	High
189	266	VVPRYAFAM	6.082	High
190	128	FERFEIFPK	6.076	High
191	217	FVGSSKYNR	6.004	High

6.3. Protein NA Inang Manusia

Prediction Approach	Cascade SVM
Antigen Name	NA Inang Manusia
Scanned on	Mon Sept 15 14:46:37 2008
Length of input sequence	390 amino acids
Number of nonamers from input sequence	383

Peptide Rank	Start Position	Sequence	Score	Predicted Affinity
1	134	LTQGALLND	8.645	High
2	297	HGSNRPWVS	8.642	High
3	138	ALLNDKHSN	8.641	High
4	344	NGVKGFSFK	8.641	High
5	90	SLCPVSGWA	8.639	High
6	106	VRIGSKGDV	8.636	High
7	79	SVVSVKLAG	8.633	High
8	74	FAAGQSVVS	8.631	High
9	12	SVCMTIGMA	8.624	High
10	382	GTDNNFSIK	8.619	High

11	293	RDNWHGSNR	8.619	High
12	168	SPYNSRFES	8.618	High
.	.	.	.	.
.	.	.	.	.
.	.	.	.	.
148	361	RTKSISSRN	6.111	High
149	117	IREPFISCS	6.090	High
150	6	KIITIGSVC	6.068	High
151	170	YNSRFESVA	6.032	High
152	313	QIGYICSGI	6.008	High

6.4. Protein NA Inang Babi

Prediction Approach	Cascade SVM
Antigen Name	NA Inang Babi
Scanned on	Mon Sept 15 14:47:15 2008
Length of input sequence	469 amino acids
Number of nonamers from input sequence	462

Peptide Rank	Start Position	Sequence	Score	Predicted Affinity
1	419	RPCFWVELI	8.645	High
2	35	SHSIQTGGK	8.645	High
3	134	LTQGALLND	8.645	High
4	426	LIRGQPKES	8.644	High
5	255	IFKVEKGKI	8.642	High
6	138	ALLNDKHSN	8.641	High
7	109	GSKGDIFVI	8.639	High
8	90	SLCPVSGWA	8.639	High
9	283	PDTGKVMCV	8.634	High
10	262	KIIKSIELD	8.631	High
11	333	GNCGPVLSN	8.631	High
12	220	RNKILRTQE	8.629	High
.	.	.	.	.
.	.	.	.	.
.	.	.	.	.
172	117	IREPFISCS	6.090	High
173	162	PIGEAPSPY	6.088	High
174	265	KSIELDAPN	6.085	High
175	170	YNSRFESVA	6.032	High
176	316	YICSGVFGD	6.007	High

6.5. Protein M2 Inang Manusia

Prediction Approach	Cascade SVM
Antigen Name	M2 Inang Manusia
Scanned on	Mon Sept 15 14:55:37 2008
Length of input sequence	97 amino acids
Number of nonamers from input sequence	90

Peptide Rank	Start Position	Sequence	Score	Predicted Affinity
1	70	ESMREEYQQ	8.641	High
2	17	CRCSDSSDP	8.596	High
3	69	PESMREEYQ	8.570	High
4	12	RSEWECRCS	8.508	High
5	78	QEQQSAVDV	8.482	High
6	21	DSSDPLVIA	8.377	High
7	86	VDDGHFVNI	8.243	High
8	73	REEYQQEQQ	8.175	High
9	9	TPTRSEWEC	8.046	High
10	90	HFVNIELE	8.026	High
11	74	EEYQQEQQS	7.934	High
12	82	SAVDVDDGH	7.751	High
.	.	.	.	.
.	.	.	.	.
.	.	.	.	.
21	4	LTEVETPTR	6.614	High
22	54	RFKYGLKRG	6.407	High
23	43	TDRLFFKCI	6.398	High
24	22	SSDPLVIAA	6.168	High
25	85	DVDDGHFVN	6.107	High

6.6. Protein M2 Inang Babi

Prediction Approach	Cascade SVM
Antigen Name	M2 Inang Babi
Scanned on	Mon Sept 15 14:55:59 2008
Length of input sequence	97 amino acids
Number of nonamers from input sequence	90

Peptide Rank	Start Position	Sequence	Score	Predicted Affinity
1	70	ESMREEYQQ	8.641	High
2	54	RLKYGLKRG	8.574	High
3	69	PESMREEYQ	8.570	High
4	15	WECRYSDSS	8.539	High
5	78	QEQQSAVDV	8.482	High
6	21	DSSDPLVIA	8.377	High
7	2	SLLTEVETL	8.245	High
8	86	VDDGHFVNI	8.243	High
9	73	REEYQQEQQ	8.175	High
10	90	HFVNIELE	8.026	High
11	74	EEYQQEQQS	7.934	High
12	82	SAVDVDDGH	7.751	High
.	.	.	.	.
.	.	.	.	.
.	.	.	.	.
20	4	LTEVETLTK	6.671	High
21	9	TLTKNGWEC	6.493	High
22	22	SSDPLVIAA	6.168	High
23	43	LDRLFFKCI	6.149	High
24	85	DVDDGHFVN	6.107	High

Lampiran 7. Hasil MHC Kelas I dan MHC Kelas II Menggunakan *Server* MHCPred

7.1. Protein HA Inang Manusia

MHC Kelas I

Allele: A0201

Amino acid groups	Predicted -logIC$_{50}$ (M)	Predicted IC$_{50}$ Value (nM)	Confidence of prediction (Max = 1)
YYWTLVEPG	8.266	5.42	0.78
KNVTVTHSV	7.906	12.42	0.89
YSKKFKPEI	7.829	14.83	0.89
GCFEFYHKC	7.775	16.79	0.89
DIWTYNAEL	7.767	17.10	1.00
YNAELLVLL	7.66	21.88	0.89
FYKNLIWLV	7.622	23.88	0.89
AIAGFIEGG	7.607	24.72	0.89
YDYPKYSEE	7.583	26.12	0.78
GLFGAIAGF	7.557	27.73	1.00
.	.	.	.
.	.	.	.
.	.	.	.
NGSLQCRIC	-	-	-
DQEGRMNYY	-	-	-

Allele: A0101

Amino acid groups	Predicted -logIC$_{50}$ (M)	Predicted IC$_{50}$ Value (nM)	Confidence of prediction (Max = 1)
ISDTPVHDC	7.824	15.00	1.00
STDTVDTVL	7.69	20.42	0.89
ATANADTLC	7.538	28.97	1.00
DQEGRMNYY	7.52	30.20	1.00
YEELREQLS	7.459	34.75	0.78
KAILVVLLY	7.356	44.06	1.00
YSTVASSLV	7.33	46.77	1.00
WTGMVDGWY	7.184	65.46	0.89
DKGKEVLVL	7.124	75.16	0.78
LLEDKHNGK	7.108	77.98	0.89
.	.	.	.
.	.	.	.
.	.	.	.
KVRDQEGRM	-	-	-

KVRSQLKNN	-	-	-

Allele: A0202

Amino acid groups	Predicted -logIC_{50} (M)	Predicted IC_{50} Value (nM)	Confidence of prediction (Max = 1)
KNVTVTHSV	8.078	8.36	0.89
AIDEITNKV	7.954	11.12	0.89
PEIAIRPKV	7.763	17.26	0.78
KHNGKLCKL	7.726	18.79	0.89
WLVKKGNSY	7.72	19.05	0.89
RLATGLRNV	7.691	20.37	0.89
LFGAIAGFI	7.684	20.70	0.89
QNADAYVFV	7.67	21.38	0.78
NDKGKEVLV	7.496	31.92	0.67
LLEDKHNGK	7.461	34.59	0.56
.	.	.	.
.	.	.	.
.	.	.	.
GAINTSLPF	-	-	-
IVETSSSDN	-	-	-

Allele: A0203

Amino acid groups	Predicted -logIC_{50} (M)	Predicted IC_{50} Value (nM)	Confidence of prediction (Max = 1)
ILVVLLYTF	8.839	1.45	0.78
HLEKRIENL	8.624	2.38	0.78
WLVKKGNSY	8.564	2.73	0.89
KHNGKLCKL	8.488	3.25	0.89
KLESTRIYQ	8.449	3.56	0.67
VLLENERTL	8.437	3.66	0.78
RLATGLRNV	8.435	3.67	0.89
FQNIHPITI	8.414	3.85	0.78
TLVEPGDKI	8.395	4.03	0.89
ELLVLLENE	8.393	4.05	0.56
.	.	.	.
.	.	.	.
.	.	.	.
GVTAACPHA	-	-	-
LVLVVSLGA	-	-	-

Allele: A0206

Amino acid groups	Predicted -logIC_{50} (M)	Predicted IC_{50} Value (nM)	Confidence of prediction (Max = 1)
KIFKVEKGK	7.959	10.99	0.67
ISLLLQIGN	7.7	19.95	0.78
VAVLKYNGI	7.629	23.50	1.00

KSIDSRSGF	7.591	25.64	0.67
AIYSKDNSI	7.571	26.85	1.00
YICSGVFGD	7.514	30.62	0.89
KQDIIALTD	7.504	31.33	0.67
AWSASACHD	7.501	31.55	0.78
NDKHSNGTV	7.5	31.62	0.56
NIVSLWISH	7.481	33.04	0.78
.	.	.	.
.	.	.	.
.	.	.	.
SGPDNGAVA	-	-	-
GNGVWIGRT	-	-	-

Allele: A0301

Amino acid groups	Predicted -logIC_{50} (M)	Predicted IC_{50} Value (nM)	Confidence of prediction (Max = 1)
KIFKVEKGK	8.366	4.31	1.00
GIITDTIKS	7.886	13.00	0.89
VELIRGQPK	7.787	16.33	0.78
SIDSRSGFE	7.636	23.12	0.89
SIQTGGKNH	7.617	24.15	1.00
VIREPFISC	7.532	29.38	0.89
VLKYNGIIT	7.528	29.65	0.78
GIISLLLQI	7.494	32.06	0.89
RIITIGTVC	7.484	32.81	0.89
TIGTVCLIV	7.482	32.96	0.89
.	.	.	.
.	.	.	.
.	.	.	.
LMSCPIGEA	-	-	-
IQTGGKNHT	-	-	-

Allele: A1101

Amino acid groups	Predicted -logIC_{50} (M)	Predicted IC_{50} Value (nM)	Confidence of prediction (Max = 1)
STRIYQILA	8.298	5.04	0.67
EKMNTQFTA	8.175	6.68	0.78
NKVNSVIEK	7.994	10.14	0.78
FERFEIFPK	7.982	10.42	0.78
SWPNHDSNK	7.974	10.62	0.67
NIHPITIGK	7.907	12.39	0.78
KKVDDGFLD	7.86	13.80	0.78
SVNLLEDKH	7.842	14.39	0.89
TVTHSVNLL	7.836	14.59	0.89
NTQFTAVGK	7.82	15.14	0.89
.	.	.	.
.	.	.	.

.	.	.	.
LRGVAPLHL	6.378	418.79	0.67
LENERTLDY	6.356	440.55	0.78

Allele: A3101

Amino acid groups	Predicted -logIC_{50} (M)	Predicted IC_{50} Value (nM)	Confidence of prediction (Max = 1)
TVKDRSPYR	7.404	39.45	0.67
GDNPRSNDG	7.111	77.45	0.56
NTNQRIITI	7.015	96.61	0.78
ISGPDNGAV	6.942	114.29	0.33
RSPYRTLMS	6.912	122.46	0.44
IFVIREPFI	6.868	135.52	0.33
ELIRGQPKE	6.868	135.52	0.78
SGVFGDNPR	6.84	144.54	0.67
GMNCIRPCF	6.827	148.94	0.67
FLTQGALLN	6.81	154.88	0.67
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.	.	.	.

Allele: A6801

Amino acid groups	Predicted -logIC_{50} (M)	Predicted IC_{50} Value (nM)	Confidence of prediction (Max = 1)
SEEAKLNRE	7.744	18.03	0.67
YAFAMERNA	7.65	22.39	0.56
KSFYKNLIW	7.528	29.65	0.44
IAIRPKVRD	7.513	30.69	0.78
SADQQSLYQ	7.512	30.76	0.78
FAMERNAGS	7.471	33.81	0.67
SSFERFEIF	7.449	35.56	0.44
FEFYHKCDN	7.413	38.64	0.44
DKITFEATG	7.377	41.98	0.67
SKKFKPEIA	7.372	42.46	0.56
.	.	.	.
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.	.	.	.
CYPGDFIDY	6.551	281.19	0.33
SDTPVHDCN	6.543	286.42	0.44

Allele: A6802

Amino acid groups	Predicted -logIC_{50} (M)	Predicted IC_{50} Value (nM)	Confidence of prediction (Max = 1)
FEIFPKTSS	7.77	16.98	0.67
YQILAIYST	7.76	17.38	0.78

TVASSLVLV	7.746	17.95	1.00
IAIRPKVRD	7.691	20.37	0.78
QNIHPITIG	7.667	21.53	0.56
PEIAIRPKV	7.651	22.34	0.78
FVGSSRYSK	7.633	23.28	0.78
SIIISDTPV	7.619	24.04	0.89
SVIEKMNTQ	7.553	27.99	0.89
STQNAIDEI	7.533	29.31	0.89
.	.	.	.
.	.	.	.
.	.	.	.
	6.027	939.72	0.78
GNPECESLS	6.026	941.89	0.56

Allele: B3501

Amino acid groups	Predicted -logIC$_{50}$ (M)	Predicted IC$_{50}$ Value (nM)	Confidence of prediction (Max = 1)
FWMCSNGSL	6.961	109.40	0.67
FAMERNAGS	6.957	110.41	0.67
GAINTSLPF	6.921	119.95	0.89
FPKTSSWPN	6.855	139.64	0.78
FIEGGWTGM	6.802	157.76	0.67
FVGSSRYSK	6.79	162.18	0.67
FATANADTL	6.79	162.18	0.89
FEFYHKCDN	6.778	166.72	0.67
SSFERFEIF	6.76	173.78	0.89
PSIQSRGLF	6.714	193.20	0.56
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.	.	.	.
.	.	.	.
LVLLENERT	5.693	2027.68	0.89
TGLRNVPSI	5.682	2079.70	1.00

MHC Kelas II

Allele: DRB0101

Amino acid groups	Predicted -logIC$_{50}$ (M)	Predicted IC$_{50}$ Value (nM)	Confidence of prediction (Max = 1)
FYKNLIWLV	9.359	0.44	0.78
YVKSTKLRL	9.285	0.52	0.89
YTFATANAD	9.215	0.61	1.00
NSYPKLSKS	8.959	1.10	1.00
YIVETSSSD	8.947	1.13	0.89
IYQILAIYS	8.856	1.39	1.00
NYYWTLVEP	8.856	1.39	0.78
DLKSTQNAI	8.819	1.52	1.00
YQNADAYVF	8.68	2.09	0.89

EITNKVNSV	8.677	2.10	0.78
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.	.	.	.
.	.	.	.
HHPSTSADQ	7.171	67.45	0.89
SSSDNGTCY	7.17	67.61	0.89

Allele: DRB0401

Amino acid groups	**Predicted -logIC_{50} (M)**	**Predicted IC_{50} Value (nM)**	**Confidence of prediction (Max = 1)**
YSTVASSLV	7.312	48.75	0.89
VSLGAISFW	7.308	49.20	0.89
TGLRNVPSI	7.266	54.20	0.78
VKKGNSYPK	7.241	57.41	1.00
KGAINTSLP	7.208	61.94	0.89
KNLIWLVKK	7.164	68.55	0.89
GVTAACPHA	7.143	71.94	0.67
RGVAPLHLG	7.062	86.70	0.78
WMCSNGSLQ	7.051	88.92	0.78
VKNGTYDYP	7.027	93.97	0.89
.	.	.	.
.	.	.	.
.	.	.	.
LRGVAPLHL	5.841	1442.12	1.00
IRPKVRDQE	5.84	1445.44	0.78

Allele: DRB0701

Amino acid groups	**Predicted -logIC_{50} (M)**	**Predicted IC_{50} Value (nM)**	**Confidence of prediction (Max = 1)**
YPKLSKSYI	7.656	22.08	1.00
EAKLNREEI	7.626	23.66	1.00
FATANADTL	7.529	29.58	0.89
YAFAMERNA	7.475	33.50	1.00
QLKNNAKEI	7.416	38.37	1.00
LVVLLYTFA	7.396	40.18	1.00
IYQILAIYS	7.393	40.46	1.00
KSTQNAIDE	7.391	40.64	0.89
EKMNTQFTA	7.368	42.85	1.00
DEITNKVNS	7.347	44.98	1.00
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.	.	.	.
ADQQSLYQN	-	-	-
IGYHANNST	-	-	-

7.2. Protein HA Inang Babi

MHC Kelas I

Allele: A0201

Amino acid groups	Predicted -logIC_{50} (M)	Predicted IC_{50} Value (nM)	Confidence of prediction (Max = 1)
YYWTLIEPG	8.511	3.08	0.78
KNVTVTHSV	7.906	12.42	0.89
GCFEFYHKC	7.775	16.79	0.89
YNAELLVLL	7.66	21.88	0.89
AIAGFIEGG	7.607	24.72	0.89
VLWGIHHPP	7.602	25.00	0.89
GLFGAIAGF	7.557	27.73	1.00
GWYGYHHQN	7.55	28.18	0.78
DVWTYNAEL	7.547	28.38	1.00
FEATGNLVV	7.515	30.55	0.89
.	.	.	.
.	.	.	.
.	.	.	.
TNADTLCIG	-	-	-
REQLSSVSS	-	-	-

Allele: A0101

Amino acid groups	Predicted -logIC_{50} (M)	Predicted IC_{50} Value (nM)	Confidence of prediction (Max = 1)
STDTVDTIL	7.637	23.07	0.89
YEELREQLS	7.459	34.75	0.78
YIFVGSSKY	7.424	37.67	1.00
DTCMESVKN	7.33	46.77	0.89
ECELLFTVS	7.243	57.15	0.78
ILEKNVTVT	7.127	74.64	0.89
DHETNRGVT	7.124	75.16	0.89
LLEDKHNGK	7.108	77.98	0.89
LLENERTLD	7.073	84.53	1.00
IVETSNSDN			
.	.	.	.
.	.	.	.
.	.	.	.
DQKSTQNAV	-	-	-
TYNAELLVL	-	-	-

Allele: A0202

Amino acid groups	Predicted -logIC_{50} (M)	Predicted IC_{50} Value (nM)	Confidence of prediction (Max = 1)
KNVTVTHSV	8.078	8.36	0.89
QNADAYIFV	7.896	12.71	0.78
KHNGKLCKL	7.726	18.79	0.89

WLVKKGNSY	7.72	19.05	0.89
LFGAIAGFI	7.684	20.70	0.89
AVDGITNKV	7.642	22.80	0.89
KFEATGNLV	7.593	25.53	0.78
TIGECPKYV	7.575	26.61	0.78
NNKGKEVLV	7.496	31.92	0.67
LLEDKHNGK	7.461	34.59	0.56
.	.	.	.
.	.	.	.
.	.	.	.
DAPVHDCNT	5.651	2233.57	0.67
DKHNGKLCK	5.647	2254.24	0.56

Allele: A0203

Amino acid groups	Predicted -logIC$_{50}$ (M)	Predicted IC$_{50}$ Value (nM)	Confidence of prediction (Max = 1)
WLLGNPECE	8.844	1.43	0.78
KMNTQFAAV	8.751	1.77	1.00
ILLVLLCTF	8.713	1.94	0.78
HLEKRIENL	8.624	2.38	0.78
WLVKKGNSY	8.564	2.73	0.89
FQNIHPVTI	8.521	3.01	0.78
KHNGKLCKL	8.488	3.25	0.89
KLSKSYVNN	8.465	3.43	0.89
KLESTRIYQ	8.449	3.56	0.67
ELLFTVSSW	8.439	3.64	0.78
.	.	.	.
.	.	.	.
.	.	.	.
PKYVKSTKL	6.954	111.17	0.67
INTSLPFQN	6.952	111.69	0.78

Allele: A0206

Amino acid groups	Predicted -logIC$_{50}$ (M)	Predicted IC$_{50}$ Value (nM)	Confidence of prediction (Max = 1)
KEVLVLWGI	8.278	5.27	0.89
AILLVLLCT	8.068	8.55	1.00
PECELLFTV	7.872	13.43	0.78
AELLVLLEN	7.829	14.83	0.78
AASSLVLLV	7.743	18.07	1.00
KAILLVLLC	7.724	18.88	0.89
QILAIYSTA	7.705	19.72	1.00
KNVTVTHSV	7.69	20.42	0.89
YPKLSKSYV	7.672	21.28	0.56
LIWLVKKGN	7.619	24.04	0.67
.	.	.	.
.	.	.	.

.	.	.	.
GQAGRMNYY	6.396	401.79	0.78
VGKEFNHLE	6.394	403.65	0.67

Allele: A0301

Amino acid groups	Predicted -logIC_{50} (M)	Predicted IC_{50} Value (nM)	Confidence of prediction (Max = 1)
GIAPLHLGK	8.173	6.71	1.00
SIQSRGLFG	7.855	13.96	0.89
LLFTVSSWS	7.756	17.54	0.78
GIITSDAPV	7.65	22.39	0.78
VVPRYAFAM	7.574	26.67	0.78
GSGYAADQK	7.574	26.67	0.78
NTQFAAVGK	7.531	29.44	0.89
KLNREEIDG	7.518	30.34	0.78
FERFEIFPK	7.502	31.48	0.89
FINYEELRE	7.451	35.40	0.78
.	.	.	.
.	.	.	.
.	.	.	.
FEIFPKTSS	5.732	1853.53	0.78
GYHHQNEQG	5.721	1901.08	0.78

Allele: A1101

Amino acid groups	Predicted -logIC_{50} (M)	Predicted IC_{50} Value (nM)	Confidence of prediction (Max = 1)
STRIYQILA	8.298	5.04	0.67
NKVNSVIKK	8.061	8.69	0.78
FERFEIFPK	7.982	10.42	0.78
KKMNTQFAA	7.953	11.14	0.89
AYIFVGSSK	7.86	13.80	0.89
KKVDDGFLD	7.86	13.80	0.78
SVNLLEDKH	7.842	14.39	0.89
SFYRNLIWL	7.842	14.39	0.56
TVTHSVNLL	7.836	14.59	0.89
SNVKNLYEK	7.819	15.17	0.89
.	.	.	.
.	.	.	.
.	.	.	.
NGTYDYPRY	6.514	306.20	0.89
LGGIAPLHL	6.423	377.57	0.67

Allele: A3101

Amino acid groups	Predicted -logIC_{50} (M)	Predicted IC_{50} Value (nM)	Confidence of prediction (Max = 1)
YEKVRSQLR	7.131	73.96	0.67
LLVLLENER	7.017	96.16	0.56

YDYPRYSEE	7.003	99.31	0.44
ATGLRNIPS	6.974	106.17	0.67
LENERTLDF	6.952	111.69	0.56
EIAERPKVR	6.903	125.03	0.67
LWGIHHPPT	6.856	139.32	0.56
HLEKRIENL	6.837	145.55	0.56
GSLQCRICI	6.836	145.88	0.78
LLGNPECEL	6.824	149.97	0.56
.	.	.	.
.	.	.	.
.	.	.	.
YRNLIWLVK	5.956	1106.62	0.44
GVKLESTRI	5.955	1109.17	0.67

Allele: A6801

Amino acid groups	Predicted -logIC$_{50}$ (M)	Predicted IC$_{50}$ Value (nM)	Confidence of prediction (Max = 1)
YAFAMNRDP	7.656	22.08	0.33
FINYEELRE	7.622	23.88	0.78
SSFERFEIF	7.449	35.56	0.44
SEESKLNRE	7.443	36.06	0.67
FEFYHKCDD	7.413	38.64	0.44
KAILLVLLC	7.377	41.98	0.78
IAERPKVRG	7.373	42.36	0.67
NSFYRNLIW	7.37	42.66	0.44
QKSTQNAVD	7.358	43.85	0.44
KEFNHLEKR	7.307	49.32	0.78
.	.	.	.
.	.	.	.
.	.	.	.
VNLLEDKHN	5.336	4613.18	0.67
APLHLGKCN	-	-	-

Allele: A6802

Amino acid groups	Predicted -logIC$_{50}$ (M)	Predicted IC$_{50}$ Value (nM)	Confidence of prediction (Max = 1)
FEIFPKTSS	7.77	16.98	0.67
YQILAIYST	7.76	17.38	0.78
PEIAERPKV	7.608	24.66	0.67
SVIKKMNTQ	7.596	25.35	0.78
DTILEKNVT	7.514	30.62	0.78
AVDGITNKV	7.485	32.73	0.78
FYRNLIWLV	7.448	35.65	0.78
GVKLESTRI	7.311	48.87	0.78
TGLRNIPSI	7.302	49.89	0.78
LVLWGIHHP	7.302	49.89	0.78
.	.	.	.

.	.	.	.
.	.	.	.
KKVDDGFLD	-	-	-
LLVSLGAIS	-	-	-

Allele: B3501

Amino acid groups	Predicted -logIC_{50} (M)	Predicted IC_{50} Value (nM)	Confidence of prediction (Max = 1)
FWMCSNGSL	6.961	109.40	0.67
GAINTSLPF	6.921	119.95	0.89
FAATNADTL	6.869	135.21	0.78
FPKTSSWPD	6.855	139.64	0.78
FAMNRDPGS	6.837	145.55	0.67
FIEGGWTGM	6.802	157.76	0.67
FVGSSKYNR	6.792	161.44	0.67
FEFYHKCDD	6.778	166.72	0.67
SSFERFEIF	6.76	173.78	0.89
PSIQSRGLF	6.714	193.20	0.56
.	.	.	.
.	.	.	.
.	.	.	.
LVLLENERT	5.693	2027.68	0.89
TGLRNIPSI	5.63	2344.23	1.00

MHC Kelas II

Allele: DRB0101

Amino acid groups	Predicted -logIC_{50} (M)	Predicted IC_{50} Value (nM)	Confidence of prediction (Max = 1)
YVKSTKLRM	9.379	0.42	0.89
YIVETSNSD	9.164	0.69	0.89
FYRNLIWLV	9.052	0.89	0.67
IYSTAASSL	9.035	0.92	1.00
NSYPKLSKS	8.959	1.10	1.00
IYQILAIYS	8.856	1.39	1.00
IITSDAPVH	8.789	1.63	1.00
YSTAASSLV	8.762	1.73	1.00
NYYWTLIEP	8.716	1.92	0.78
FLDVWTYNA	8.713	1.94	1.00
.	.	.	.
.	.	.	.
.	.	.	.
GIHHPPTST	6.963	108.89	1.00
NGKLCKLGG	6.959	109.90	0.78

Allele: DRB0401

Amino acid groups	Predicted -logIC_{50} (M)	Predicted IC_{50} Value (nM)	Confidence of prediction (Max = 1)
YSTAASSLV	7.596	25.35	0.89
VSLGAISFW	7.308	49.20	0.89
GVTAACPYA	7.305	49.55	0.67
VKKGNSYPK	7.241	57.41	1.00
KGAINTSLP	7.208	61.94	0.89
RNLIWLVKK	7.164	68.55	0.89
VRGQAGRMN	7.088	81.66	1.00
GGIAPLHLG	7.051	88.92	0.78
WMCSNGSLQ	7.051	88.92	0.78
VETSNSDNG	7.041	90.99	0.78
.	.	.	.
.	.	.	.
.	.	.	.
DGVKLESTR	5.809	1552.39	0.67
VSSFERFEI	5.805	1566.75	0.89

Allele: DRB0701

Amino acid groups	Predicted -logIC_{50} (M)	Predicted IC_{50} Value (nM)	Confidence of prediction (Max = 1)
YPKLSKSYV	7.873	13.40	1.00
YAGANSFYR	7.621	23.93	1.00
PEIAERPKV	7.477	33.34	1.00
DGITNKVNS	7.455	35.08	1.00
KKMNTQFAA	7.409	38.99	1.00
IYQILAIYS	7.393	40.46	1.00
FAATNADTL	7.372	42.46	1.00
LLVLLCTFA	7.357	43.95	0.89
KSTQNAVDG	7.356	44.06	0.89
QLRNNAKEI	7.243	57.15	1.00
.	.	.	.
.	.	.	.
.	.	.	.
IGYHANNST	-	-	-
SEESKLNRE	-	-	-

7.3. Protein NA Inang Manusia

MHC Kelas I

Allele: A0201

Amino acid groups	Predicted -logIC_{50} (M)	Predicted IC_{50} Value (nM)	Confidence of prediction (Max = 1)
FFLTQGALL	7.396	40.18	0.89
YICSGIFGD	7.394	40.36	0.89

FSFKYGNGV	7.335	46.24	0.89
FNQNLEYQI	7.322	47.64	0.89
GMANLILQI	7.315	48.42	1.00
GIFGDNPRP	7.286	51.76	0.89
FKYGNGVWI	7.28	52.48	0.89
LKYNGIITD	7.273	53.33	0.78
YHYEECSCY	7.125	74.99	0.78
FLTQGALLN	7.079	83.37	0.89
.	.	.	.
.	.	.	.
.	.	.	.
IFRIEKGKI	-	-	-
TDTIKSWRN	-	-	-

Allele: A0202

Amino acid groups	Predicted -logIC_{50} (M)	Predicted IC_{50} Value (nM)	Confidence of prediction (Max = 1)
PLECRTFFL	8.652	2.23	0.78
FRIEKGKIV	7.704	19.77	0.67
WTGTDNNFS	7.61	24.55	0.78
LILQIGNII	7.38	41.69	0.89
FVIREPFIS	7.365	43.15	0.78
EMIWDPNGW	7.323	47.53	0.56
VFVIREPFI	7.275	53.09	0.67
FSFKYGNGV	7.249	56.36	0.89
FFLTQGALL	7.199	63.24	0.89
AIYSKDNSV	7.197	63.53	1.00
.	.	.	.
.	.	.	.
.	.	.	.
IYSKDNSVR	-	-	-
GRTKSISSR	-	-	-

Allele: A0203

Amino acid groups	Predicted -logIC_{50} (M)	Predicted IC_{50} Value (nM)	Confidence of prediction (Max = 1)
NPNQKIITI	8.373	4.24	0.78
WLTIGISGP	8.356	4.41	0.78
IKSWRNNIL	8.304	4.97	0.67
GFSFKYGNG	8.277	5.28	0.78
PLECRTFFL	8.277	5.28	0.78
NLEYQIGYI	8.215	6.10	0.56
LMSCPIGEV	8.212	6.14	1.00
SISSRNGFE	8.2	6.31	0.89
KLAGNSSLC	8.178	6.64	0.89
GINWLTIGI	8.175	6.68	0.89
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GKIVKSVEM	6.806	156.31	0.78
AVAVLKYNG	6.806	156.31	0.67

Allele: A0206

Amino acid groups	Predicted -logIC_{50} (M)	Predicted IC_{50} Value (nM)	Confidence of prediction (Max = 1)
ANLILQIGN	7.917	12.11	0.67
AIYSKDNSV	7.898	12.65	1.00
KGFSFKYGN	7.709	19.54	0.67
KSISSRNGF	7.689	20.46	0.78
KIFRIEKGK	7.669	21.43	0.67
VAVLKYNGI	7.629	23.50	1.00
KIVKSVEMN	7.626	23.66	0.67
ASYKIFRIE	7.542	28.71	0.56
AWSASACHD	7.501	31.55	0.78
ECRTFFLTQ	7.459	34.75	0.56
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GSNRPWVSF	-	-	-
GNGVWIGRT	-	-	-

Allele: A0301

Amino acid groups	Predicted -logIC_{50} (M)	Predicted IC_{50} Value (nM)	Confidence of prediction (Max = 1)
KIFRIEKGK	8.502	3.15	1.00
GIFGDNPRP	7.968	10.76	0.89
GIITDTIKS	7.886	13.00	0.89
GTDNNFSIK	7.833	14.69	1.00
KIITIGSVC	7.75	17.78	0.89
TIKDRSPYR	7.72	19.05	1.00
GINWLTIGI	7.684	20.70	0.78
KSWRNNILR	7.542	28.71	1.00
VIREPFISC	7.532	29.38	0.89
VLKYNGIIT	7.528	29.65	0.78
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LNDKHSNGT	-	-	-
INWLTIGIS	-	-	-

Allele: A1101

Amino acid groups	Predicted -logIC_{50} (M)	Predicted IC_{50} Value (nM)	Confidence of prediction (Max = 1)
DTIKSWRNK	8.032	9.29	0.67

ETDSSFSMK	8.002	9.95	0.56
AVQDVTSVI	7.957	11.04	0.89
SHSIQTGGK	7.913	12.22	0.78
FVIREPFIS	7.9	12.59	0.89
KIFKVEKGK	7.875	13.34	0.89
WVSFDQNLD	7.861	13.77	0.78
WVNRTYVNI	7.846	14.26	0.78
SGSSISFCG	7.842	14.39	0.78
TETDSSFSM	7.841	14.42	0.78
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LLLQIGNIV	6.563	273.53	0.89
NGAVAVLKY	6.346	450.82	0.89

Allele: A3101

Amino acid groups	Predicted -logIC$_{50}$ (M)	Predicted IC$_{50}$ Value (nM)	Confidence of prediction (Max = 1)
TIKDRSPYR	7.363	43.35	0.67
ISGPDNGAV	6.942	114.29	0.33
RSPYRTLMS	6.912	122.46	0.44
VFVIREPFI	6.845	142.89	0.44
FLTQGALLN	6.81	154.88	0.67
SGIFGDNPR	6.806	156.31	0.78
HSNGTIKDR	6.786	163.68	0.67
LGNQNQIET	6.78	165.96	0.89
WHGSNRPWV	6.772	169.04	0.56
PLECRTFFL	6.768	170.61	0.56
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.	.	.	.
SVVSVKLAG	5.682	2079.70	0.67
KDRSPYRTL	5.671	2133.04	0.67

Allele: B6801

Amino acid groups	Predicted -logIC$_{50}$ (M)	Predicted IC$_{50}$ Value (nM)	Confidence of prediction (Max = 1)
QASYKIFRI	7.919	12.05	0.78
SEITCVCRD	7.613	24.38	0.67
RTFFLTQGA	7.607	24.72	0.67
GIFGDNPRP	7.599	25.18	0.67
SCFTVMTDG	7.568	27.04	0.56
SRFESVAWS	7.524	29.92	0.67
SGIFGDNPR	7.484	32.81	0.89
MANLILQIG	7.459	34.75	0.56
CRTFFLTQG	7.427	37.41	0.44
QIETCNQSV	7.418	38.19	0.67

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ANGVKGFSF	5.338	4591.98	0.78
ALLNDKHSN	-	-	-

Allele: A6802

Amino acid groups	Predicted -logIC$_{50}$ (M)	Predicted IC$_{50}$ Value (nM)	Confidence of prediction (Max = 1)
QKIITIGSV	8.03	9.33	0.78
LQIGNIISI	7.88	13.18	0.78
FVIREPFIS	7.669	21.43	0.67
SVCMTIGMA	7.662	21.78	0.78
WVNQTYVNI	7.513	30.69	1.00
YQIGYICSG	7.51	30.90	0.67
TVMTDGPSN	7.502	31.48	0.78
SGIFGDNPR	7.492	32.21	0.78
SVITYENNT	7.482	32.96	0.89
DVFVIREPF	7.478	33.27	0.67
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.	.	.	.
CMTIGMANL	-	-	-
PWVSFNQNL	-	-	-

Allele: B3501

Amino acid groups	Predicted -logIC$_{50}$ (M)	Predicted IC$_{50}$ Value (nM)	Confidence of prediction (Max = 1)
FISCSPLEC	6.93	117.49	0.78
FESVAWSAS	6.924	119.12	0.78
FVIREPFIS	6.81	154.88	0.78
FAAGQSVVS	6.792	161.44	0.89
CACVNGSCF	6.768	170.61	0.89
ANGVKGFSF	6.767	171.00	0.78
FFLTQGALL	6.763	172.58	0.78
FTVMTDGPS	6.694	202.30	0.56
GKIVKSVEM	6.661	218.27	0.78
FLTQGALLN	6.657	220.29	0.78
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IGSKGDVFV	5.598	2523.48	1.00
LGNQNQIET	5.573	2673.01	1.00

MHC Kelas II

Allele: DRB0101

Amino acid groups	Predicted -logIC_{50} (M)	Predicted IC_{50} Value (nM)	Confidence of prediction (Max = 1)
TIKSWRNNI	8.846	1.43	0.89
PYRTLMSCP	8.78	1.66	0.78
FLTQGALLN	8.757	1.75	1.00
FTVMTDGPS	8.682	2.08	0.89
FESVAWSAS	8.655	2.21	1.00
IITDTIKSW	8.655	2.21	0.89
YRTLMSCPI	8.632	2.33	0.89
YSKDNSVRI	8.572	2.68	1.00
FISCSPLEC	8.489	3.24	0.89
NQIETCNQS	8.438	3.65	0.67
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.	.	.	.
VKGFSFKYG	-	-	-
APNYHYEEC	-	-	-

Allele: DRB0401

Amino acid groups	Predicted -logIC_{50} (M)	Predicted IC_{50} Value (nM)	Confidence of prediction (Max = 1)
WVSFNQNLE	7.258	55.21	0.89
WVNQTYVNI	7.251	56.10	0.78
VNISNTNFA	7.096	80.17	1.00
SSLCPVSGW	7.077	83.75	0.67
GSCGPVSSN	6.982	104.23	0.78
YSKDNSVRI	6.973	106.41	1.00
NGAVAVLKY	6.957	110.41	0.78
IGMANLILQ	6.948	112.72	0.78
FLTQGALLN	6.937	115.61	0.89
VKLAGNSSL	6.922	119.67	0.89
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.	.	.	.
.	.	.	.
NQNLEYQIG	-	-	-
IKDRSPYRT	-	-	-

Allele: DRB0701

Amino acid groups	Predicted -logIC_{50} (M)	Predicted IC_{50} Value (nM)	Confidence of prediction (Max = 1)
PVSGWAIYS	7.825	14.96	1.00
GPDNGAVAV	7.759	17.42	1.00
VSVKLAGNS	7.674	21.18	1.00
YENNTWVNQ	7.449	35.56	1.00
FAAGQSVVS	7.264	54.45	1.00

GALLNDKHS	7.244	57.02	1.00
WIGRTKSIS	7.24	57.54	1.00
GQSVVSVKL	7.204	62.52	1.00
FGDNPRPND	7.203	62.66	1.00
WVNQTYVNI	7.167	68.08	1.00
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.	.	.	.
.	.	.	.
SSNGANGVK	-	-	-
VSGWAIYSK	-	-	-

7.4. Protein NA Inang Babi

MHC Kelas I

Allele: A0201

Amino acid groups	Predicted -logIC_{50} (M)	Predicted IC_{50} Value (nM)	Confidence of prediction (Max = 1)
KIFKVEKGK	7.505	31.26	0.89
YRYGNGVWI	7.47	33.88	0.89
CLIVGIISL	7.455	35.08	1.00
FFLTQGALL	7.396	40.18	0.89
GIISLLLQI	7.366	43.05	1.00
LKYNGIITD	7.273	53.33	0.78
FSYRYGNGV	7.259	55.08	0.89
KSIELDAPN	7.218	60.53	0.78
GMGWLTIGI	7.169	67.76	1.00
ADLPFTIDK	7.167	68.08	0.78
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.	.	.	.
EMCNQNVIT	-	-	-
DGKGNCGPV	-	-	-

Allele: A0101

Amino acid groups	Predicted -logIC_{50} (M)	Predicted IC_{50} Value (nM)	Confidence of prediction (Max = 1)
ETDSSFSMK	7.871	13.46	0.89
GADLPFTID	7.861	13.77	1.00
ELDAPNYHY	7.315	48.42	1.00
HTEMCNQNV	7.236	58.08	1.00
LECRTFFLT	7.184	65.46	0.89
WTETDSSFS	7.049	89.33	0.78
YHYEECSCY	7.022	95.06	0.89
ILAGNSSLC	7.008	98.17	1.00
LTDGPSNGQ	6.982	104.23	1.00
DTGKVMCVC			

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IRIGSKGDI	-	-	-
WDPNGWTET	-	-	-

Allele: A0202

Amino acid groups	Predicted -logIC$_{50}$ (M)	Predicted IC$_{50}$ Value (nM)	Confidence of prediction (Max = 1)
QLECRTFFL	8.733	1.85	0.89
LLLQIGNIV	8.109	7.78	0.89
NLDYQMGYI	7.533	29.31	0.67
NCIRPCFWV	7.506	31.19	0.78
CLIVGIISL	7.393	40.46	0.89
FKVEKGKII	7.39	40.74	0.67
FVIREPFIS	7.365	43.15	0.78
DGADLPFTI	7.349	44.77	0.67
QASYKIFKV	7.335	46.24	0.89
EMIWDPNGW	7.323	47.53	0.56
.	.	.	.
.	.	.	.
.	.	.	.
ASWSWPDGA	5.553	2798.98	0.78
NPRSNDGKG	5.55	2818.38	0.56

Allele: A0203

Amino acid groups	Predicted -logIC$_{50}$ (M)	Predicted IC$_{50}$ Value (nM)	Confidence of prediction (Max = 1)
ISNTNIAAV	8.594	2.55	0.89
WISHSIQTG	8.427	3.74	0.78
CLIVGIISL	8.396	4.02	0.89
WLTIGISGP	8.356	4.41	0.78
GMGWLTIGI	8.344	4.53	0.89
GTVCLIVGI	8.337	4.60	1.00
QRIITIGTV	8.287	5.16	0.78
NTNQRIITI	8.277	5.28	0.89
WRNKILRTQ	8.272	5.35	0.67
SISFCGVNS	8.245	5.69	0.78
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.	.	.	.
.	.	.	.
CVCRDNWHA	-	-	-
LTDWSGYSG	-	-	-

Allele: A0206

Amino acid groups	Predicted -logIC$_{50}$ (M)	Predicted IC$_{50}$ Value (nM)	Confidence of prediction (Max = 1)
KIFKVEKGK	7.959	10.99	0.67
ISLLLQIGN	7.7	19.95	0.78
VAVLKYNGI	7.629	23.50	1.00
KSIDSRSGF	7.591	25.64	0.67
AIYSKDNSI	7.571	26.85	1.00
YICSGVFGD	7.514	30.62	0.89
KQDIIALTD	7.504	31.33	0.67
AWSASACHD	7.501	31.55	0.78
NDKHSNGTV	7.5	31.62	0.56
NIVSLWISH	7.481	33.04	0.78
.	.	.	.
.	.	.	.
.	.	.	.
WSWPDGADL	5.952	1116.86	0.78
MGYICSGVF	5.949	1124.60	0.56

Allele: A0301

Amino acid groups	Predicted -logIC$_{50}$ (M)	Predicted IC$_{50}$ Value (nM)	Confidence of prediction (Max = 1)
KIFKVEKGK	8.366	4.31	1.00
GIITDTIKS	7.886	13.00	0.89
VELIRGQPK	7.787	16.33	0.78
SIDSRSGFE	7.636	23.12	0.89
SIQTGGKNH	7.617	24.15	1.00
VIREPFISC	7.532	29.38	0.89
VLKYNGIIT	7.528	29.65	0.78
GIISLLLQI	7.494	32.06	0.89
RIITIGTVC	7.484	32.81	0.89
TIGTVCLIV	7.482	32.96	0.89
.	.	.	.
.	.	.	.
.	.	.	.
ISCSQLECR	5.588	2582.26	0.89
TDWSGYSGS	5.587	2588.21	0.78

Allele: A1101

Amino acid groups	Predicted -logIC$_{50}$ (M)	Predicted IC$_{50}$ Value (nM)	Confidence of prediction (Max = 1)
DTIKSWRNK	8.032	9.29	0.67
ETDSSFSMK	8.002	9.95	0.56
AVQDVTSVI	7.957	11.04	0.89
SHSIQTGGK	7.913	12.22	0.78
FVIREPFIS	7.9	12.59	0.89
KIFKVEKGK	7.875	13.34	0.89
WVSFDQNLD	7.861	13.77	0.78

WVNRTYVNI	7.846	14.26	0.78
SGSSISFCG	7.842	14.39	0.78
TETDSSFSM	7.841	14.42	0.78
.	.	.	.
.	.	.	.
.	.	.	.
LLLQIGNIV	6.563	273.53	0.89
NGAVAVLKY	6.346	450.82	0.89

Allele: A3101

Amino acid groups	Predicted -logIC$_{50}$ (M)	Predicted IC$_{50}$ Value (nM)	Confidence of prediction (Max = 1)
TVKDRSPYR	7.404	39.45	0.67
GDNPRSNDG	7.111	77.45	0.56
NTNQRIITI	7.015	96.61	0.78
ISGPDNGAV	6.942	114.29	0.33
RSPYRTLMS	6.912	122.46	0.44
IFVIREPFI	6.868	135.52	0.33
ELIRGQPKE	6.868	135.52	0.78
SGVFGDNPR	6.84	144.54	0.67
GMNCIRPCF	6.827	148.94	0.67
FLTQGALLN	6.81	154.88	0.67
.	.	.	.
.	.	.	.
.	.	.	.
KIFKVEKGK	-	-	-
QDVTSVILA	-	-	-

Allele: A6801

Amino acid groups	Predicted -logIC$_{50}$ (M)	Predicted IC$_{50}$ Value (nM)	Confidence of prediction (Max = 1)
SCFTVLTDG	7.798	15.92	0.67
RTFFLTQGA	7.607	24.72	0.67
SGFEMIWDP	7.552	28.05	0.56
SRFESVAWS	7.524	29.92	0.67
SWRNKILRT	7.502	31.48	0.67
QDVTSVILA	7.444	35.97	0.67
QASYKIFKV	7.437	36.56	0.78
CRTFFLTQG	7.427	37.41	0.44
QDIIALTDW	7.417	38.28	0.67
DIFVIREPF	7.4	39.81	0.56
.	.	.	.
.	.	.	.
.	.	.	.
TQGALLNDK	6.648	224.91	0.67
FKVEKGKII	6.646	225.94	0.56

Allele: A6802

Amino acid groups	Predicted -logIC$_{50}$ (M)	Predicted IC$_{50}$ Value (nM)	Confidence of prediction (Max = 1)
QRIITIGTV	7.756	17.54	0.78
SVILAGNSS	7.752	17.70	0.89
WVNRTYVNI	7.681	20.84	1.00
FVIREPFIS	7.669	21.43	0.67
STIWASGSS	7.645	22.65	0.67
WVELIRGQP	7.563	27.35	0.78
FVQHPELTG	7.552	28.05	0.67
ASNRPWVSF	7.468	34.04	0.78
TVKDRSPYR	7.444	35.97	0.56
LTIGISGPD	7.431	37.07	0.78
.	.	.	.
.	.	.	.
.	.	.	.
RSPYRTLMS	6.077	837.53	0.44
ALLNDKHSN	6.074	843.33	0.67

Allele: B3501

Amino acid groups	Predicted -logIC$_{50}$ (M)	Predicted IC$_{50}$ Value (nM)	Confidence of prediction (Max = 1)
FESVAWSAS	6.924	119.12	0.78
FISCSQLEC	6.868	135.52	0.78
FDQNLDYQM	6.835	146.22	0.89
WASGSSISF	6.817	152.41	1.00
FVIREPFIS	6.81	154.88	0.78
FFLTQGALL	6.763	172.58	0.78
APSPYNSRF	6.732	185.35	0.78
TETDSSFSM	6.732	185.35	0.89
KSIDSRSGF	6.718	191.43	0.56
IDSRSGFEM	6.711	194.54	0.89
.	.	.	.
.	.	.	.
.	.	.	.
DGKGNCGPV	5.654	2218.20	0.78
IGSKGDIFV	5.555	2786.12	1.00

MHC Kelas II

Allele: DRB0101

Amino acid groups	Predicted -logIC$_{50}$ (M)	Predicted IC$_{50}$ Value (nM)	Confidence of prediction (Max = 1)
SIELDAPNY	8.827	1.49	0.89
TIKSWRNKI	8.813	1.54	0.89
PYRTLMSCP	8.78	1.66	0.78
FLTQGALLN	8.757	1.75	1.00

FISCSQLEC	8.722	1.90	0.89
YVNNTWVNR	8.696	2.01	0.89
FTVLTDGPS	8.667	2.15	0.89
FESVAWSAS	8.655	2.21	1.00
IITDTIKSW	8.655	2.21	0.89
YRTLMSCPI	8.632	2.33	0.89
.	.	.	.
.	.	.	.
.	.	.	.
APNYHYEEC	-	-	-
VKGFSYRYG	-	-	-

Allele: DRB0401

Amino acid groups	Predicted -logIC$_{50}$ (M)	Predicted IC$_{50}$ Value (nM)	Confidence of prediction (Max = 1)
IGEAPSPYN	7.169	67.76	1.00
GNCGPVLSN	7.102	79.07	0.78
WVNRTYVNI	7.094	80.54	0.67
VSLWISHSI	7.083	82.60	0.78
SSLCPVSGW	7.077	83.75	0.67
FVQHPELTG	7.062	86.70	0.89
MCNQNVITY	6.963	108.89	0.56
NGAVAVLKY	6.957	110.41	0.78
VGIISLLLQ	6.954	111.17	1.00
FLTQGALLN	6.937	115.61	0.89
.	.	.	.
.	.	.	.
.	.	.	.
IISLLLQIG	-	-	-
LTDWSGYSG	-	-	-

Allele: DRB0701

Amino acid groups	Predicted -logIC$_{50}$ (M)	Predicted IC$_{50}$ Value (nM)	Confidence of prediction (Max = 1)
TSVILAGNS	7.974	10.62	1.00
YVNNTWVNR	7.909	12.33	1.00
PVSGWAIYS	7.825	14.96	1.00
GPDNGAVAV	7.759	17.42	1.00
HASNRPWVS	7.439	36.39	0.89
FTVLTDGPS	7.325	47.32	1.00
MCNQNVITY	7.284	52.00	0.78
YPDTGKVMC	7.27	53.70	1.00
GALLNDKHS	7.244	57.02	1.00
QRIITIGTV	7.215	60.95	1.00
.	.	.	.
.	.	.	.
.	.	.	.

VSGWAIYSK	-	-	-
AIYSKDNSI	-	-	-

7.5. Protein M2 Inang Manusia

MHC Kelas I

Allele: A0101

Amino acid groups	Predicted -logIC$_{50}$ (M)	Predicted IC$_{50}$ Value (nM)	Confidence of prediction (Max = 1)
ITDRLFFKC	7.869	13.52	1.00
DDGHFVNIE	7.432	36.98	0.78
IIGILHLIL	7.039	91.41	0.89
LTEVETPTR	6.918	120.78	1.00
DVDDGHFVN	6.88	131.83	0.89
STEGVPESM	6.347	449.78	0.89
SLLTEVETP	6.246	567.54	0.89
AANIIGILH	6.201	629.51	0.89
CSDSSDPLV	6.198	633.87	1.00
ILHLILWIT	6.16	691.83	0.89
.	.	.	.
.	.	.	.
.	.	.	.
FFKCIYRRF	-	-	-
FKYGLKRGP	-	-	-

Allele: A0202

Amino acid groups	Predicted -logIC$_{50}$ (M)	Predicted IC$_{50}$ Value (nM)	Confidence of prediction (Max = 1)
VDVDDGHFV	8.006	9.86	0.67
KCIYRRFKY	7.724	18.88	0.67
NIIGILHLI	7.625	23.71	0.89
WITDRLFFK	7.616	24.21	0.78
PLVIAANII	7.534	29.24	0.67
LILWITDRL	7.365	43.15	0.78
LWITDRLFF	7.355	44.16	0.67
LVIAANIIG	7.003	99.31	0.78
FKCIYRRFK	6.943	114.02	0.56
STEGVPESM	6.94	114.82	0.78
.	.	.	.
.	.	.	.
.	.	.	.
HLILWITDR	-	-	-
CRCSDSSDP	-	-	-

Allele: A0203

Amino acid groups	Predicted -logIC$_{50}$ (M)	Predicted IC$_{50}$ Value (nM)	Confidence of prediction (Max = 1)
SLLTEVETP	8.449	3.56	0.67
GLKRGPSTE	8.342	4.55	0.89
GPSTEGVPE	7.978	10.52	0.67
VIAANIIGI	7.758	17.46	1.00
PLVIAANII	7.755	17.58	0.67
IIGILHLIL	7.747	17.91	0.78
PESMREEYQ	7.714	19.32	0.33
GILHLILWI	7.707	19.63	0.89
IAANIIGIL	7.681	20.84	0.89
FKYGLKRGP	7.644	22.70	0.56
.	.	.	.
.	.	.	.
.	.	.	.
CSDSSDPLV	-	-	-
DVDDGHFVN	-	-	-

Allele: A0206

Amino acid groups	Predicted -logIC$_{50}$ (M)	Predicted IC$_{50}$ Value (nM)	Confidence of prediction (Max = 1)
LHLILWITD	7.612	24.43	0.67
KCIYRRFKY	7.583	26.12	0.67
WITDRLFFK	7.58	26.30	0.78
VIAANIIGI	7.42	38.02	1.00
KRGPSTEGV	7.408	39.08	0.78
TDRLFFKCI	7.341	45.60	0.67
ILHLILWIT	7.329	46.88	0.89
FKYGLKRGP	7.228	59.16	0.56
NIIGILHLI	7.211	61.52	0.89
ITDRLFFKC	7.139	72.61	0.78
.	.	.	.
.	.	.	.
.	.	.	.
TRSEWECRC	5.36	4365.16	0.67
TEVETPTRS	-	-	-

Allele: A3101

Amino acid groups	Predicted -logIC$_{50}$ (M)	Predicted IC$_{50}$ Value (nM)	Confidence of prediction (Max = 1)
WITDRLFFK	8.415	3.85	0.89
CIYRRFKYG	8.073	8.45	0.78
RLFFKCIYR	7.763	17.26	1.00
ITDRLFFKC	7.451	35.40	0.89
YRRFKYGLK	7.44	36.31	0.78
RRFKYGLKR	7.328	46.99	0.89
VIAANIIGI	7.307	49.32	0.89

ETPTRSEWE	7.243	57.15	0.56
IIGILHLIL	7.162	68.87	0.78
GPSTEGVPE	7.093	80.72	0.78
.	.	.	.
.	.	.	.
.	.	.	.
EYQQEQQSA	-	-	-
ANIIGILHL	-	-	-

Allele: A1101

Amino acid groups	Predicted -logIC_{50} (M)	Predicted IC_{50} Value (nM)	Confidence of prediction (Max = 1)
ITDRLFFKC	8.026	9.42	0.78
AANIIGILH	7.934	11.64	0.78
WITDRLFFK	7.893	12.79	0.89
YRRFKYGLK	7.855	13.96	0.67
GVPESMREE	7.812	15.42	0.67
DVDDGHFVN	7.781	16.56	0.67
SAVDVDDGH	7.73	18.62	0.78
SMREEYQQE	7.719	19.10	0.78
GHFVNIELE	7.71	19.50	0.78
EVETPTRSE	7.701	19.91	0.78
.	.	.	.
.	.	.	.
.	.	.	.
VPESMREEY	6.599	251.77	0.67
LWITDRLFF	6.548	283.14	0.78

Allele: A3101

Amino acid groups	Predicted -logIC_{50} (M)	Predicted IC_{50} Value (nM)	Confidence of prediction (Max = 1)
LTEVETPTR	7.144	71.78	0.78
RLFFKCIYR	6.921	119.95	0.89
TEGVPESMR	6.852	140.60	0.44
PSTEGVPES	6.848	141.91	0.67
VETPTRSEW	6.826	149.28	0.44
PESMREEYQ	6.726	187.93	0.33
KCIYRRFKY	6.704	197.70	0.67
MREEYQQEQ	6.685	206.54	0.56
KYGLKRGPS	6.678	209.89	0.67
YGLKRGPST	6.648	224.91	0.78
.	.	.	.
.	.	.	.
.	.	.	.
SAVDVDDGH	5.594	2546.83	0.33
QQSAVDVDD	5.516	3047.89	0.56

Allele: B6801

Amino acid groups	Predicted -logIC$_{50}$ (M)	Predicted IC$_{50}$ Value (nM)	Confidence of prediction (Max = 1)
RLFFKCIYR	7.974	10.62	0.78
LFFKCIYRR	7.76	17.38	0.78
NIIGILHLI	7.52	30.20	0.78
QQEQQSAVD	7.481	33.04	0.44
YRRFKYGLK	7.258	55.21	0.56
GHFVNIELE	7.24	57.54	0.56
IGILHLILW	7.154	70.15	0.67
QEQQSAVDV	7.111	77.45	0.56
RRFKYGLKR	7.092	80.91	0.56
ETPTRSEWE	7.04	91.20	0.44
.	.	.	.
.	.	.	.
.	.	.	.
YGLKRGPST	5.779	1663.41	0.67
VETPTRSEW	5.714	1931.97	0.67

Allele: A6802

Amino acid groups	Predicted -logIC$_{50}$ (M)	Predicted IC$_{50}$ Value (nM)	Confidence of prediction (Max = 1)
LVIAANIIG	7.626	23.66	0.78
EVETPTRSE	7.492	32.21	0.44
AVDVDDGHF	7.304	49.66	0.56
IGILHLILW	7.236	58.08	0.67
NIIGILHLI	7.217	60.67	0.89
QEQQSAVDV	7.148	71.12	0.78
FFKCIYRRF	7.089	81.47	0.67
GVPESMREE	7.032	92.90	0.78
CSDSSDPLV	6.992	101.86	0.78
DVDDGHFVN	6.981	104.47	0.67
.	.	.	.
.	.	.	.
.	.	.	.
WITDRLFFK	5.451	3539.97	0.78
IIGILHLIL	5.399	3990.25	0.78

Allele: B3501

Amino acid groups	Predicted -logIC$_{50}$ (M)	Predicted IC$_{50}$ Value (nM)	Confidence of prediction (Max = 1)
FFKCIYRRF	6.9	125.89	0.56
FKYGLKRGP	6.658	219.79	0.56
ILWITDRLF	6.628	235.50	0.78
FKCIYRRFK	6.628	235.50	0.44
KCIYRRFKY	6.603	249.46	0.67
IIGILHLIL	6.551	281.19	0.89
TPTRSEWEC	6.528	296.48	0.78

IAANIIGIL	6.515	305.49	0.78
RCSDSSDPL	6.487	325.84	0.67
LWITDRLFF	6.485	327.34	0.67
.	.	.	.
.	.	.	.
.	.	.	.
LLTEVETPT	5.79	1621.81	0.67
VIAANIIGI	5.665	2162.72	0.78

MHC Kelas II

Allele: DRB0101

Amino acid groups	Predicted -logIC$_{50}$ (M)	Predicted IC$_{50}$ Value (nM)	Confidence of prediction (Max = 1)
GILHLILWI	8.518	3.03	0.89
PLVIAANII	8.35	4.47	1.00
WITDRLFFK	8.327	4.71	0.89
YQQEQQSAV	8.319	4.80	0.78
NIIGILHLI	8.22	6.03	0.89
ITDRLFFKC	8.202	6.28	1.00
SSDPLVIAA	8.2	6.31	1.00
KYGLKRGPS	8.133	7.36	1.00
DPLVIAANI	8.128	7.45	0.89
TEVETPTRS	8.055	8.81	0.78
.	.	.	.
.	.	.	.
.	.	.	.
LVIAANIIG	5.914	1218.99	1.00
LKRGPSTEG	5.648	2249.05	0.78

Allele: DRB0401

Amino acid groups	Predicted -logIC$_{50}$ (M)	Predicted IC$_{50}$ Value (nM)	Confidence of prediction (Max = 1)
VIAANIIGI	6.883	130.92	0.89
EQQSAVDVD	6.845	142.89	0.89
YRRFKYGLK	6.792	161.44	0.89
WECRCSDSS	6.772	169.04	0.67
CRCSDSSDP	6.751	177.42	0.78
YGLKRGPST	6.723	189.23	0.89
GHFVNIELE	6.714	193.20	0.78
PSTEGVPES	6.664	216.77	0.67
YQQEQQSAV	6.55	281.84	1.00
NIIGILHLI	6.526	297.85	0.78
.	.	.	.
.	.	.	.
.	.	.	.
LFFKCIYRR	-	-	-

ITDRLFFKC	-	-	-

Allele: DRB0701

Amino acid groups	Predicted -logIC$_{50}$ (M)	Predicted IC$_{50}$ Value (nM)	Confidence of prediction (Max = 1)
QQSAVDVDD	7.114	76.91	1.00
VIAANIIGI	7.114	76.91	1.00
KYGLKRGPS	7.02	95.50	1.00
MSLLTEVET	7.004	99.08	0.89
QEQQSAVDV	6.998	100.46	1.00
DPLVIAANI	6.965	108.39	1.00
LHLILWITD	6.903	125.03	1.00
KCIYRRFKY	6.896	127.06	0.78
YQQEQQSAV	6.875	133.35	1.00
GPSTEGVPE	6.865	136.46	1.00
.	.	.	.
.	.	.	.
.	.	.	.
LFFKCIYRR	-	-	-
STEGVPESM	-	-	-

7.6. Protein M2 Inang Babi

MHC Kelas I

Allele: A0201

Amino acid groups	Predicted -logIC$_{50}$ (M)	Predicted IC$_{50}$ Value (nM)	Confidence of prediction (Max = 1)
YSDSSDPLV	7.735	18.41	0.89
SLLTEVETL	7.201	62.95	1.00
GILHLILWI	7.176	66.68	1.00
KRGPSTEGV	7.17	67.61	0.89
NIIGILHLI	7.056	87.90	1.00
ILDRLFFKC	6.869	135.21	1.00
VDVDDGHFV	6.86	138.04	0.89
GHFVNIELE	6.857	139.00	0.78
LFFKCIYRR	6.715	192.75	0.89
ESMREEYQQ	6.701	199.07	0.67
.	.	.	.
.	.	.	.
.	.	.	.
RGPSTEGVP	-	-	-
GWECRYSDS	-	-	-

Allele: A0101

Amino acid groups	Predicted -logIC$_{50}$ (M)	Predicted IC$_{50}$ Value (nM)	Confidence of prediction (Max = 1)
LTEVETLTK	7.552	28.05	0.89
ILDRLFFKC	7.528	29.65	1.00
DDGHFVNIE	7.432	36.98	0.78
YSDSSDPLV	7.165	68.39	1.00
IIGILHLIL	7.039	91.41	0.89
DVDDGHFVN	6.88	131.83	0.89
GWECRYSDS	6.531	294.44	0.78
ETLTKNGWE	6.527	297.17	0.89
STEGVPESM	6.347	449.78	0.89
SLLTEVETL	6.246	567.54	0.89
.	.	.	.
.	.	.	.
.	.	.	.
FFKCIYRRL	-	-	-
IYRRLKYGL	-	-	-

Allele: A0202

Amino acid groups	Predicted -logIC$_{50}$ (M)	Predicted IC$_{50}$ Value (nM)	Confidence of prediction (Max = 1)
WILDRLFFK	8.021	9.53	0.78
VDVDDGHFV	8.006	9.86	0.67
NIIGILHLI	7.625	23.71	0.89
PLVIAANII	7.534	29.24	0.67
LILWILDRL	7.425	37.58	0.78
FFKCIYRRL	7.34	45.71	0.78
ILDRLFFKC	7.144	71.78	0.78
ILHLILWIL	7.143	71.94	0.89
LWILDRLFF	7.119	76.03	0.67
KCIYRRLKY	7.056	87.90	0.67
.	.	.	.
.	.	.	.
.	.	.	.
HLILWILDR	-	-	-
CRYSDSSDP	-	-	-

Allele: A0203

Amino acid groups	Predicted -logIC$_{50}$ (M)	Predicted IC$_{50}$ Value (nM)	Confidence of prediction (Max = 1)
SLLTEVETL	8.757	1.75	0.78
GLKRGPSTE	8.342	4.55	0.89
GPSTEGVPE	7.978	10.52	0.67
VIAANIIGI	7.758	17.46	1.00
PLVIAANII	7.755	17.58	0.67
IIGILHLIL	7.747	17.91	0.78
PESMREEYQ	7.714	19.32	0.33

GILHLILWI	7.707	19.63	0.89
IAANIIGIL	7.681	20.84	0.89
TEVETLTKN	7.649	22.44	0.78
.	.	.	.
.	.	.	.
.	.	.	.
YSDSSDPLV	-	-	-
DVDDGHFVN	-	-	-

Allele: A0206

Amino acid groups	Predicted -logIC_{50} (M)	Predicted IC_{50} Value (nM)	Confidence of prediction (Max = 1)
LDRLFFKCI	7.46	34.67	0.67
VIAANIIGI	7.42	38.02	1.00
KRGPSTEGV	7.408	39.08	0.78
YSDSSDPLV	7.315	48.42	0.78
ILHLILWIL	7.279	52.60	0.89
KCIYRRLKY	7.245	56.89	0.67
ILDRLFFKC	7.243	57.15	0.78
NIIGILHLI	7.211	61.52	0.89
LHLILWILD	7.194	63.97	0.67
LDRLFFKCI	7.46	34.67	0.67
.	.	.	.
.	.	.	.
.	.	.	.
EGVPESMRE	5.396	4017.91	0.56
TKNGWECRY	5.31	4897.79	0.67

Allele: A3101

Amino acid groups	Predicted -logIC_{50} (M)	Predicted IC_{50} Value (nM)	Confidence of prediction (Max = 1)
WILDRLFFK	8.168	6.79	0.89
CIYRRLKYG	7.867	13.58	0.78
RLFFKCIYR	7.763	17.26	1.00
ILDRLFFKC	7.515	30.55	0.89
VIAANIIGI	7.307	49.32	0.89
IIGILHLIL	7.162	68.87	0.78
FKCIYRRLK	7.123	75.34	0.78
GPSTEGVPE	7.093	80.72	0.78
GILHLILWI	7.087	81.85	0.78
AANIIGILH	7.064	86.30	0.89
.	.	.	.
.	.	.	.
.	.	.	.
EYQQEQQSA	-	-	-
ANIIGILHL	-	-	-

Allele: A3101

Amino acid groups	Predicted -logIC$_{50}$ (M)	Predicted IC$_{50}$ Value (nM)	Confidence of prediction (Max = 1)
LTKNGWECR	7.05	89.13	0.44
RLFFKCIYR	6.921	119.95	0.89
TEGVPESMR	6.852	140.60	0.44
PSTEGVPES	6.848	141.91	0.67
HLILWILDR	6.762	172.98	0.56
PESMREEYQ	6.726	187.93	0.33
KCIYRRLKY	6.701	199.07	0.67
MREEYQQEQ	6.685	206.54	0.56
KYGLKRGPS	6.678	209.89	0.67
YGLKRGPST	6.648	224.91	0.78
.	.	.	.
.	.	.	.
.	.	.	.
SAVDVDDGH	5.594	2546.83	0.33
QQSAVDVDD	5.516	3047.89	0.56

Allele: A6801

Amino acid groups	Predicted -logIC$_{50}$ (M)	Predicted IC$_{50}$ Value (nM)	Confidence of prediction (Max = 1)
RLFFKCIYR	7.974	10.62	0.78
LFFKCIYRR	7.76	17.38	0.78
NIIGILHLI	7.52	30.20	0.78
QQEQQSAVD	7.481	33.04	0.44
GHFVNIELE	7.24	57.54	0.56
IGILHLILW	7.154	70.15	0.67
FKCIYRRLK	7.147	71.29	0.67
QEQQSAVDV	7.111	77.45	0.56
HLILWILDR	7.048	89.54	0.56
FFKCIYRRL	7.009	97.95	0.67
.	.	.	.
.	.	.	.
.	.	.	.
VPESMREEY	5.801	1581.25	0.56
YGLKRGPST	5.779	1663.41	0.67

Allele: B6802

Amino acid groups	Predicted -logIC$_{50}$ (M)	Predicted IC$_{50}$ Value (nM)	Confidence of prediction (Max = 1)
LVIAANIIG	7.626	23.66	0.78
AVDVDDGHF	7.304	49.66	0.56
IGILHLILW	7.236	58.08	0.67
NIIGILHLI	7.217	60.67	0.89
YSDSSDPLV	7.203	62.66	0.78
QEQQSAVDV	7.148	71.12	0.78
GVPESMREE	7.032	92.90	0.78

DVDDGHFVN	6.981	104.47	0.67
ESMREEYQQ	6.891	128.53	0.33
STEGVPESM	6.88	131.83	0.78
.	.	.	.
.	.	.	.
.	.	.	.
RRLKYGLKR	-	-	-
SLLTEVETL	-	-	-

Allele: B3501

Amino acid groups	Predicted -logIC_{50} (M)	Predicted IC_{50} Value (nM)	Confidence of prediction (Max = 1)
FFKCIYRRL	6.706	196.79	0.56
FKCIYRRLK	6.677	210.38	0.44
ILWILDRLF	6.609	246.04	0.78
KCIYRRLKY	6.558	276.69	0.67
IIGILHLIL	6.551	281.19	0.89
IAANIIGIL	6.515	305.49	0.78
ILHLILWIL	6.5	316.23	0.78
RYSDSSDPL	6.487	325.84	0.67
AVDVDDGHF	6.485	327.34	0.56
LWILDRLFF	6.459	347.54	0.78
.	.	.	.
.	.	.	.
.	.	.	.
REEYQQEQQ	5.803	1573.98	0.78
VIAANIIGI	5.665	2162.72	0.78

MHC Kelas II

Allele: DRB0101

Amino acid groups	Predicted -logIC_{50} (M)	Predicted IC_{50} Value (nM)	Confidence of prediction (Max = 1)
ILDRLFFKC	8.528	2.96	1.00
GILHLILWI	8.518	3.03	0.89
PLVIAANII	8.35	4.47	1.00
YQQEQQSAV	8.319	4.80	0.78
RYSDSSDPL	8.248	5.65	0.78
NIIGILHLI	8.22	6.03	0.89
LILWILDRL	8.211	6.15	0.67
SSDPLVIAA	8.2	6.31	1.00
HLILWILDR	8.167	6.81	0.89
KYGLKRGPS	8.133	7.36	1.00
.	.	.	.
.	.	.	.
.	.	.	.
LVIAANIIG	5.914	1218.99	1.00

LKRGPSTEG	5.648	2249.05	0.78

Allele: DRB0401

Amino acid groups	Predicted -logIC$_{50}$ (M)	Predicted IC$_{50}$ Value (nM)	Confidence of prediction (Max = 1)
VIAANIIGI	6.883	130.92	0.89
EQQSAVDVD	6.845	142.89	0.89
WECRYSDSS	6.772	169.04	0.67
RRLKYGLKR	6.761	173.38	0.67
YGLKRGPST	6.723	189.23	0.89
GHFVNIELE	6.714	193.20	0.78
CRYSDSSDP	6.714	193.20	0.89
PSTEGVPES	6.664	216.77	0.67
WILDRLFFK	6.61	245.47	1.00
YQQEQQSAV	6.55	281.84	1.00
.	.	.	.
.	.	.	.
.	.	.	.
ILHLILWIL	-	-	-
ILDRLFFKC	-	-	-

Allele: DRB0701

Amino acid groups	Predicted -logIC$_{50}$ (M)	Predicted IC$_{50}$ Value (nM)	Confidence of prediction (Max = 1)
QQSAVDVDD	7.114	76.91	1.00
VIAANIIGI	7.114	76.91	1.00
KYGLKRGPS	7.02	95.50	1.00
MSLLTEVET	7.004	99.08	0.89
QEQQSAVDV	6.998	100.46	1.00
DPLVIAANI	6.965	108.39	1.00
YQQEQQSAV	6.875	133.35	1.00
KNGWECRYS	6.869	135.21	0.89
GPSTEGVPE	6.865	136.46	1.00
LWILDRLFF	6.852	140.60	0.89
.	.	.	.
.	.	.	.
.	.	.	.
LFFKCIYRR	-	-	-
STEGVPESM	-	-	-

Lampiran 8. Hasil Penentuan *Epitope* Sel B Menggunakan *Server* BepiPred dan DiscoTope

6.1. HA Host Human

BepiPred

Average:0.061 **Minimum:**-2.655 **Maximum:**1.709 **Threshold:**0.350

Predicted epitopes:

```
No.    Start  End    Peptide                     Peptide Length
1      15     15     A                                 1
2      26     34     ANNSTDTVD                         9
3      55     55     N                                 1
4      83     91     ECESLSTAS                         9
5      99     111    TSSSDNGTCYPGD                     13
6      113    114    ID                                2
7      137    161    TSSWPNHDSNKGVTAACPHAGAKSF         25
8      174    180    SYPKLSK                           7
9      183    188    INDKGK                            6
10     200    213    STSADQQSLYQNAD                    14
11     225    231    KKFKPEI                           7
12     235    235    P                                 1
13     239    246    DQEGRMNY                          8
14     254    262    GDKITFEAT                         9
15     279    283    GSGII                             5
16     291    308    DCNTTCQTPKGAINTSLP                18
17     326    328    STK                               3
18     344    345    RG                                2
19     364    366    GWY                               3
20     373    396    EQGSGYAADLKSTQNAIDEITNKV          24
21     399    399    V                                 1
22     432    434    FLD                               3
23     457    463    SNVKNLY                           7
24     476    483    EIGNGCFE                          8
25     503    522    YPKYSEEAKLNREEIDGVKL              20
26     524    524    S                                 1
27     529    529    Q                                 1
```

IEDB Analysis Resource

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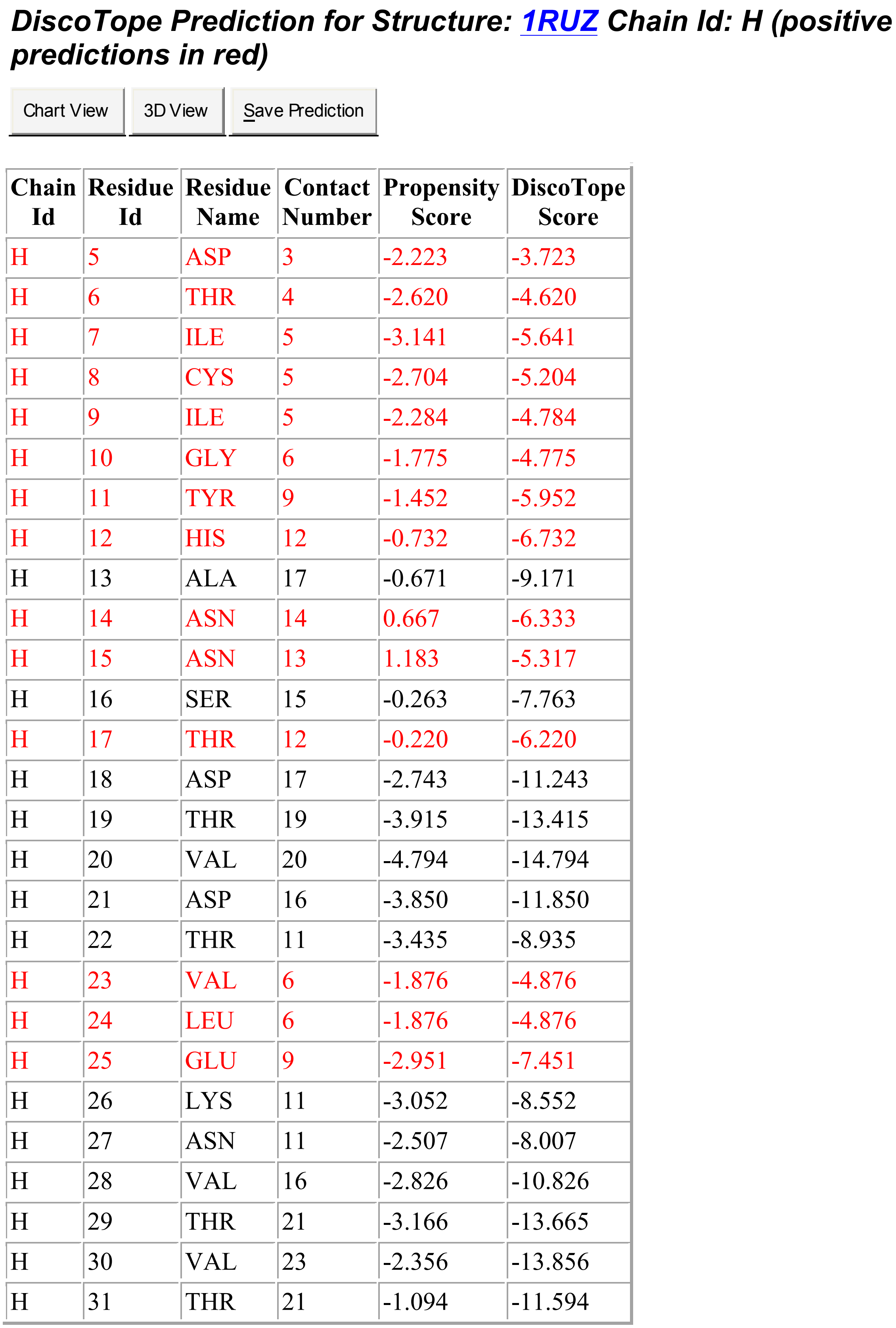
DiscoTope: Structure-based Antibody Prediction



DiscoTope Prediction for Structure: 1RUZ Chain Id: H (positive predictions in red)

Chain Id	Residue Id	Residue Name	Contact Number	Propensity Score	DiscoTope Score
H	5	ASP	3	-2.223	-3.723
H	6	THR	4	-2.620	-4.620
H	7	ILE	5	-3.141	-5.641
H	8	CYS	5	-2.704	-5.204
H	9	ILE	5	-2.284	-4.784
H	10	GLY	6	-1.775	-4.775
H	11	TYR	9	-1.452	-5.952
H	12	HIS	12	-0.732	-6.732
H	13	ALA	17	-0.671	-9.171
H	14	ASN	14	0.667	-6.333
H	15	ASN	13	1.183	-5.317
H	16	SER	15	-0.263	-7.763
H	17	THR	12	-0.220	-6.220
H	18	ASP	17	-2.743	-11.243
H	19	THR	19	-3.915	-13.415
H	20	VAL	20	-4.794	-14.794
H	21	ASP	16	-3.850	-11.850
H	22	THR	11	-3.435	-8.935
H	23	VAL	6	-1.876	-4.876
H	24	LEU	6	-1.876	-4.876
H	25	GLU	9	-2.951	-7.451
H	26	LYS	11	-3.052	-8.552
H	27	ASN	11	-2.507	-8.007
H	28	VAL	16	-2.826	-10.826
H	29	THR	21	-3.166	-13.665
H	30	VAL	23	-2.356	-13.856
H	31	THR	21	-1.094	-11.594

H	32	HIS	19	-2.111	-11.611
H	33	SER	18	-3.476	-12.476
H	34	VAL	15	-3.255	-10.755
H	35	ASN	15	-2.831	-10.331
H	36	LEU	17	-2.283	-10.783
H	37	LEU	25	-1.908	-14.408
H	38	GLU	23	-1.054	-12.554
H	39	ASP	16	-0.069	-8.069
H	40	SER	15	0.305	-7.195
H	41	HIS	16	-0.038	-8.038
H	42	ASN	17	-1.051	-9.551
H	44	GLY	18	-1.259	-10.259
H	45	LYS	22	-2.863	-13.863
H	46	LEU	27	-5.655	-19.155
H	47	CYS	28	-6.447	-20.447
H	48	LYS	23	-6.793	-18.293
H	49	LEU	22	-6.407	-17.407
H	49A	LYS	12	-4.755	-10.755
H	50	GLY	14	-5.562	-12.562
H	51	ILE	14	-5.826	-12.826
H	52	ALA	21	-7.839	-18.339
H	53	PRO	21	-6.967	-17.467
H	54	LEU	19	-7.706	-17.206
H	55	GLN	22	-9.293	-20.293
H	56	LEU	22	-8.363	-19.363
H	57	GLY	20	-6.537	-16.537
H	58	LYS	17	-5.045	-13.545
H	59	CYS	28	-11.479	-25.479
H	60	ASN	24	-7.642	-19.642
H	61	ILE	23	-6.037	-17.537
H	62	ALA	21	-4.770	-15.270
H	63	GLY	24	-10.025	-22.025
H	64	TRP	24	-12.444	-24.444

H	65	LEU	23	-12.423	-23.923
H	66	LEU	26	-11.238	-24.238
H	67	GLY	23	-11.934	-23.434
H	68	ASN	27	-12.588	-26.088
H	69	PRO	22	-11.569	-22.569
H	70	GLU	20	-12.328	-22.328
H	71	CYS	22	-11.543	-22.543
H	72	ASP	14	-9.220	-16.220
H	73	LEU	14	-9.472	-16.472
H	74	LEU	18	-11.453	-20.453
H	75	LEU	14	-8.980	-15.980
H	76	THR	9	-6.960	-11.460
H	77	ALA	14	-8.602	-15.602
H	78	SER	15	-8.061	-15.561
H	79	SER	18	-7.452	-16.452
H	80	TRP	21	-8.532	-19.032
H	81	SER	26	-7.619	-20.619
H	82	TYR	25	-7.077	-19.577
H	83	ILE	23	-7.390	-18.890
H	84	VAL	26	-6.702	-19.702
H	85	GLU	21	-5.141	-15.641
H	86	THR	18	-4.011	-13.011
H	87	SER	11	-1.522	-7.022
H	88	ASN	13	-2.562	-9.062
H	89	SER	18	-4.796	-13.796
H	90	GLU	18	-4.580	-13.580
H	91	ASN	20	-6.958	-16.958
H	92	GLY	23	-9.081	-20.581
H	93	THR	25	-8.003	-20.503
H	94	CYS	23	-9.541	-21.041
H	95	TYR	23	-4.559	-16.059
H	96	PRO	19	-0.134	-9.634
H	97	GLY	18	0.763	-8.237

H	98	ASP	16	-0.751	-8.751
H	99	PHE	17	-1.978	-10.478
H	100	ILE	13	-0.514	-7.014
H	101	ASP	13	-0.506	-7.006
H	102	TYR	16	-2.040	-10.040
H	103	GLU	11	-0.497	-5.997
H	104	GLU	11	-0.782	-6.282
H	105	LEU	19	-3.226	-12.726
H	106	ARG	15	-2.958	-10.458
H	107	GLU	13	-1.889	-8.389
H	108	GLN	14	-2.243	-9.243
H	109	LEU	21	-4.376	-14.876
H	110	SER	20	-3.146	-13.146
H	111	SER	19	-3.884	-13.384
H	112	VAL	22	-5.709	-16.709
H	113	SER	21	-6.014	-16.514
H	114	SER	19	-7.411	-16.911
H	115	PHE	21	-8.098	-18.598
H	116	GLU	16	-5.504	-13.504
H	117	LYS	19	-8.565	-18.065
H	118	PHE	15	-4.725	-12.225
H	119	GLU	14	-4.283	-11.283
H	120	ILE	20	-3.235	-13.235
H	121	PHE	21	-2.402	-12.902
H	122	PRO	14	-0.886	-7.886
H	123	LYS	22	-1.009	-12.009
H	124	THR	11	2.896	-2.604
H	125	SER	9	2.176	-2.324
H	126	SER	15	2.553	-4.947
H	127	TRP	16	3.522	-4.478
H	128	PRO	12	3.705	-2.295
H	129	ASN	15	3.905	-3.595
H	130	HIS	19	3.677	-5.823

H	131	GLU	19	2.016	-7.484
H	132	THR	19	2.086	-7.414
H	132A	THR	14	-0.610	-7.610
H	133	LYS	14	-2.782	-9.782
H	134	GLY	17	-3.297	-11.797
H	135	VAL	17	-8.296	-16.796
H	136	THR	16	-8.348	-16.348
H	137	ALA	17	-7.926	-16.426
H	138	ALA	18	-6.800	-15.800
H	139	CYS	22	-11.117	-22.117
H	140	SER	19	-12.023	-21.523
H	141	TYR	15	-10.592	-18.092
H	142	ALA	9	-6.192	-10.692
H	143	GLY	9	-6.858	-11.358
H	144	ALA	11	-8.495	-13.995
H	145	SER	15	-10.311	-17.811
H	146	SER	19	-12.079	-21.579
H	147	PHE	24	-11.989	-23.989
H	148	TYR	26	-11.406	-24.406
H	149	ARG	19	-9.313	-18.813
H	150	ASN	26	-10.536	-23.536
H	151	LEU	25	-9.245	-21.745
H	152	LEU	24	-7.630	-19.630
H	153	TRP	25	-6.367	-18.867
H	154	LEU	24	-2.196	-14.196
H	155	THR	24	0.101	-11.899
H	156	LYS	23	1.276	-10.224
H	157	LYS	18	2.920	-6.080
H	158	GLY	14	2.432	-4.568
H	159	SER	14	1.253	-5.747
H	160	SER	15	1.964	-5.536
H	161	TYR	22	0.267	-10.733
H	162	PRO	17	0.370	-8.130

H	163	LYS	15	-1.424	-8.924
H	164	LEU	17	-0.669	-9.169
H	165	SER	15	-2.055	-9.555
H	166	LYS	14	-0.200	-7.200
H	167	SER	16	-0.256	-8.256
H	168	TYR	15	0.589	-6.911
H	169	VAL	17	-0.176	-8.676
H	170	ASN	18	-0.459	-9.459
H	171	ASN	15	-0.224	-7.724
H	172	LYS	14	-0.924	-7.924
H	173	GLY	12	-0.954	-6.954
H	174	LYS	20	-3.369	-13.369
H	175	GLU	21	-3.892	-14.392
H	176	VAL	26	-5.004	-18.004
H	177	LEU	20	-6.905	-16.905
H	178	VAL	21	-8.443	-18.943
H	179	LEU	22	-9.081	-20.081
H	180	TRP	24	-8.577	-20.577
H	181	GLY	23	-5.350	-16.850
H	182	VAL	24	-2.695	-14.695
H	183	HIS	23	0.399	-11.101
H	184	HIS	21	2.504	-7.996
H	185	PRO	23	4.774	-6.726
H	186	PRO	19	4.562	-4.938
H	187	THR	15	4.007	-3.493
H	188	GLY	14	2.680	-4.320
H	189	THR	13	2.976	-3.524
H	190	ASP	16	3.996	-4.004
H	191	GLN	22	1.861	-9.139
H	192	GLN	17	2.227	-6.273
H	193	SER	15	1.739	-5.761
H	194	LEU	21	0.037	-10.463
H	195	TYR	25	-0.818	-13.318

H	196	GLN	22	0.152	-10.848
H	197	ASN	18	-0.780	-9.780
H	198	ALA	17	-0.407	-8.907
H	199	ASP	14	-1.487	-8.487
H	200	ALA	19	-3.479	-12.979
H	201	TYR	19	-3.963	-13.463
H	202	VAL	23	-3.845	-15.345
H	203	SER	17	-2.353	-10.853
H	204	VAL	18	-1.644	-10.644
H	205	GLY	16	0.309	-7.691
H	206	SER	19	0.254	-9.246
H	207	SER	13	-0.289	-6.789
H	208	LYS	13	-0.073	-6.573
H	209	TYR	13	0.058	-6.442
H	210	ASN	12	0.705	-5.295
H	211	ARG	10	0.363	-4.637
H	212	ARG	13	-1.224	-7.724
H	213	PHE	16	-1.977	-9.977
H	214	THR	17	-2.255	-10.755
H	215	PRO	20	-1.870	-11.870
H	216	GLU	15	3.524	-3.976
H	217	ILE	18	3.954	-5.046
H	218	ALA	14	3.187	-3.813
H	219	ALA	12	2.183	-3.817
H	220	ARG	12	2.198	-3.802
H	221	PRO	11	2.680	-2.820
H	222	LYS	12	2.278	-3.722
H	223	VAL	15	0.765	-6.735
H	224	ARG	13	-1.596	-8.096
H	225	ASP	12	-0.044	-6.044
H	226	GLN	17	0.186	-8.314
H	227	ALA	17	4.120	-4.380
H	228	GLY	23	3.552	-7.948

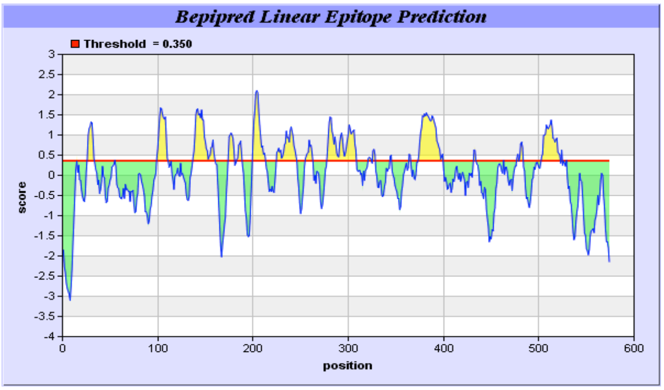
H	229	ARG	21	2.121	-8.379
H	230	MET	21	-0.465	-10.965
H	231	ASN	18	-0.914	-9.914
H	232	TYR	20	-3.250	-13.250
H	233	TYR	17	-2.586	-11.086
H	234	TRP	16	-3.633	-11.633
H	235	THR	18	-4.070	-13.070
H	236	LEU	20	-4.594	-14.594
H	237	LEU	23	-2.282	-13.782
H	238	GLU	21	-0.742	-11.242
H	239	PRO	15	-0.390	-7.890
H	240	GLY	15	0.332	-7.168
H	241	ASP	14	0.640	-6.360
H	242	THR	17	0.233	-8.267
H	243	ILE	23	-0.853	-12.353
H	244	THR	17	-0.480	-8.980
H	245	PHE	20	-4.005	-14.005
H	246	GLU	18	-3.762	-12.762
H	247	ALA	23	-3.736	-15.236
H	248	THR	21	-4.534	-15.034
H	249	GLY	30	-4.408	-19.408
H	250	ASN	26	-3.470	-16.470
H	251	LEU	29	-6.779	-21.279
H	252	ILE	23	-7.109	-18.609
H	253	ALA	22	-7.894	-18.894
H	254	PRO	23	-8.130	-19.630
H	255	TRP	22	-6.892	-17.892
H	256	TYR	24	-8.840	-20.840
H	257	ALA	23	-9.218	-20.718
H	258	PHE	22	-7.939	-18.939
H	259	ALA	22	-4.672	-15.672
H	260	LEU	23	-6.800	-18.300
H	261	ASN	17	-5.000	-13.500

H	262	ARG	17	-4.208	-12.708
H	263	GLY	14	-3.340	-10.340
H	264	SER	12	-2.469	-8.469
H	265	GLY	15	-3.360	-10.860
H	266	SER	22	-5.610	-16.610
H	267	GLY	20	-4.255	-14.255
H	268	ILE	20	-4.537	-14.537
H	269	ILE	17	-2.881	-11.381
H	270	THR	16	-1.663	-9.663
H	271	SER	20	-3.504	-13.504
H	272	ASP	17	-2.228	-10.728
H	273	ALA	18	-2.580	-11.580
H	274	PRO	13	-2.533	-9.033
H	275	VAL	19	-4.462	-13.962
H	276	HIS	14	-3.561	-10.561
H	277	ASP	11	-3.556	-9.056
H	278	CYS	15	-4.439	-11.939
H	279	ASN	17	-4.877	-13.377
H	280	THR	19	-4.470	-13.970
H	281	LYS	17	-4.343	-12.843
H	282	CYS	20	-4.164	-14.164
H	283	GLN	28	-4.497	-18.497
H	284	THR	26	-2.167	-15.167
H	285	PRO	21	-1.441	-11.941
H	286	HIS	21	-1.434	-11.934
H	287	GLY	23	-1.735	-13.235
H	288	ALA	27	-4.612	-18.112
H	289	ILE	27	-2.494	-15.994
H	290	ASN	17	-1.822	-10.322
H	291	SER	18	-1.113	-10.113
H	292	SER	12	-1.523	-7.523
H	293	LEU	16	-1.966	-9.966
H	294	PRO	14	-1.691	-8.691

H	295	PHE	21	-1.162	-11.662
H	296	GLN	24	-0.446	-12.446
H	297	ASN	18	0.219	-8.781
H	298	ILE	23	-0.179	-11.679
H	299	HIS	17	0.334	-8.166
H	300	PRO	14	-0.280	-7.280
H	301	VAL	14	-1.184	-8.184
H	302	THR	23	-2.108	-13.608
H	303	ILE	20	-3.596	-13.596
H	304	GLY	17	-3.687	-12.187
H	305	GLU	14	-2.338	-9.338
H	306	CYS	22	-2.389	-13.389
H	307	PRO	22	-2.160	-13.160
H	308	LYS	17	-1.002	-9.502
H	309	TYR	18	-0.428	-9.428
H	310	VAL	14	0.246	-6.754
H	311	ARG	12	0.620	-5.380
H	312	SER	11	-0.090	-5.590
H	313	THR	11	0.047	-5.453
H	314	LYS	15	-1.893	-9.393
H	315	LEU	16	-2.538	-10.538
H	316	ARG	15	-3.515	-11.015
H	317	MET	18	-4.655	-13.655
H	318	ALA	21	-4.412	-14.912
H	319	THR	12	-2.910	-8.910
H	320	GLY	15	-2.777	-10.277
H	321	LEU	16	-2.323	-10.322
H	322	ARG	18	-2.281	-11.281
H	323	ASN	21	-0.269	-10.769
H	324	ILE	16	0.619	-7.381
H	325	PRO	12	1.087	-4.913
H	326	ALA	7	1.394	-2.106
H	327	ARG	6	1.431	-1.569

6.2. HA Host Swine

BepiPred



Average:0.064 **Minimum:**-3.093 **Maximum:**2.093 **Threshold:** 0.350

Predicted epitopes:

```
No.     Start   End     Peptide                         Peptide Length
1       15      15      T                                       1
2       26      33      ANNSTDTV                                8
3       55      55      N                                       1
4       99      110     TSNSDNGTCYPG                            12
5       137     160     TSSWPDHETNRGVTAACPYAGANS                24
6       174     180     SYPKLSK                                 7
7       183     188     VNNKGK                                  6
8       200     213     PTSTDQQSLYQNAD                          14
9       225     246     RKFKPEIAERPKVRGQAGRMNY                  22
10      255     262     DTIKFEAT                                8
11      278     308     PGSGIITSDAPVHDCNTTCQTPKGAINTSLP         31
12      321     324     PKYV                                    4
13      326     328     STK                                     3
14      344     345     RG                                      2
15      364     365     GW                                      2
16      374     399     QGSGYAADQKSTQNAVDGITNKVNSV              26
17      432     434     FLD                                     3
18      463     463     Y                                       1
19      477     478     IG                                      2
20      480     483     GCFE                                    4
21      503     522     YPRYSEESKLNREEIDGVKL                    20
22      524     524     S                                       1
23      529     529     Q                                       1
```

DiscoTope Prediction for Structure: 1RUY Chain Id: H (positive predictions in red)

Threshold: -7.7

Chain Id	Residue Id	Residue Name	Contact Number	Propensity Score	DiscoTope Score
H	5	ASP	3	-2.796	-4.296
H	6	THR	4	-3.332	-5.332
H	7	LEU	6	-4.563	-7.563
H	8	CYS	5	-3.441	-5.941

H	9	ILE	5	-2.959	-5.459
H	10	GLY	7	-3.060	-6.560
H	11	TYR	9	-1.827	-6.327
H	12	HIS	12	-0.981	-6.981
H	13	ALA	17	-0.920	-9.420
H	14	ASN	13	0.397	-6.103
H	15	ASN	12	1.154	-4.846
H	16	SER	15	-0.263	-7.763
H	17	THR	12	-0.220	-6.220
H	18	ASP	19	-3.209	-12.709
H	19	THR	19	-3.915	-13.415
H	20	VAL	18	-4.086	-13.086
H	21	ASP	15	-3.695	-11.195
H	22	THR	10	-3.114	-8.114
H	23	VAL	6	-1.876	-4.876
H	24	LEU	6	-1.876	-4.876
H	25	GLU	9	-2.951	-7.451
H	26	LYS	11	-3.052	-8.552
H	27	ASN	11	-2.507	-8.007
H	28	VAL	16	-2.826	-10.826
H	29	THR	19	-3.380	-12.880
H	30	VAL	23	-2.356	-13.856
H	31	THR	21	-1.094	-11.594
H	32	HIS	19	-2.111	-11.611
H	33	SER	18	-3.476	-12.476
H	34	VAL	14	-2.788	-9.788
H	35	ASN	15	-2.197	-9.697
H	36	LEU	17	-2.298	-10.798
H	37	LEU	25	-1.947	-14.447
H	38	GLU	23	-1.083	-12.583
H	39	ASP	17	0.025	-8.475
H	40	SER	16	0.175	-7.825
H	41	HIS	18	-0.014	-9.014
H	42	ASN	15	-0.891	-8.391
H	44	GLY	19	-1.509	-11.009
H	45	LYS	23	-3.389	-14.889
H	46	LEU	27	-5.957	-19.457
H	47	CYS	26	-6.387	-19.387
H	48	ARG	24	-7.806	-19.806
H	49	LEU	23	-7.704	-19.204
H	49A	GLY	12	-5.601	-11.601
H	50	GLY	14	-6.449	-13.449
H	51	ILE	14	-6.622	-13.622
H	52	ALA	21	-8.468	-18.968

H	53	PRO	20	-7.320	-17.320
H	54	LEU	20	-8.037	-18.037
H	55	GLN	24	-8.563	-20.563
H	56	LEU	21	-7.146	-17.646
H	57	GLY	20	-5.117	-15.117
H	58	LYS	17	-3.759	-12.259
H	59	CYS	28	-10.182	-24.182
H	60	ASN	24	-5.738	-17.738
H	61	ILE	24	-5.049	-17.049
H	62	ALA	21	-4.104	-14.604
H	63	GLY	25	-9.655	-22.155
H	64	TRP	24	-12.167	-24.167
H	65	LEU	25	-12.946	-25.446
H	66	LEU	26	-11.209	-24.209
H	67	GLY	25	-11.808	-24.308
H	68	ASN	27	-11.991	-25.491
H	69	PRO	25	-11.595	-24.095
H	70	GLU	20	-11.475	-21.475
H	71	CYS	22	-11.305	-22.305
H	72	ASP	15	-9.663	-17.163
H	73	LEU	14	-9.445	-16.445
H	74	LEU	18	-11.421	-20.421
H	75	LEU	14	-8.943	-15.943
H	76	THR	9	-6.918	-11.418
H	77	VAL	14	-8.540	-15.540
H	78	SER	15	-7.861	-15.361
H	79	SER	18	-7.566	-16.566
H	80	TRP	21	-9.627	-20.127
H	81	SER	25	-8.231	-20.731
H	82	TYR	27	-7.896	-21.396
H	83	ILE	23	-7.227	-18.727
H	84	VAL	25	-5.553	-18.053
H	85	GLU	21	-3.746	-14.246
H	86	THR	18	-2.762	-11.762
H	87	PRO	12	-0.978	-6.978
H	88	ASN	15	-1.755	-9.255
H	89	SER	19	-4.007	-13.507
H	90	ASP	17	-2.784	-11.284
H	91	ASN	21	-6.566	-17.066
H	92	GLY	23	-7.707	-19.207
H	93	THR	27	-8.183	-21.683
H	94	CYS	25	-8.466	-20.966
H	95	TYR	23	-2.825	-14.325
H	96	PRO	20	-0.139	-10.139

H	97	GLY	19	0.883	-8.617
H	98	ASP	15	-0.754	-8.254
H	99	PHE	17	-1.940	-10.440
H	100	ILE	13	-0.514	-7.014
H	101	ASP	13	-0.506	-7.006
H	102	TYR	16	-2.040	-10.040
H	103	GLU	12	-1.042	-7.042
H	104	GLU	11	-0.782	-6.282
H	105	LEU	19	-3.226	-12.726
H	106	ARG	15	-3.003	-10.503
H	107	GLU	13	-1.935	-8.435
H	108	GLN	14	-2.296	-9.296
H	109	LEU	21	-4.621	-15.121
H	110	SER	20	-3.086	-13.086
H	111	SER	19	-3.973	-13.473
H	112	VAL	22	-5.639	-16.639
H	113	SER	21	-5.940	-16.440
H	114	SER	20	-7.366	-17.366
H	115	PHE	21	-7.632	-18.132
H	116	GLU	15	-5.106	-12.606
H	117	ARG	19	-8.041	-17.541
H	118	PHE	15	-4.168	-11.668
H	119	GLU	14	-3.959	-10.959
H	120	ILE	20	-2.773	-12.773
H	121	PHE	20	-1.716	-11.716
H	122	PRO	14	-0.744	-7.744
H	123	LYS	18	0.002	-8.998
H	124	THR	10	3.111	-1.889
H	125	SER	9	2.643	-1.857
H	126	SER	14	3.474	-3.526
H	127	TRP	17	4.358	-4.142
H	128	PRO	12	4.974	-1.026
H	129	ASN	16	5.451	-2.549
H	130	HIS	21	5.720	-4.780
H	131	ASN	17	4.022	-4.478
H	132	THR	20	3.104	-6.896
H	133	ASN	13	0.730	-5.770
H	133A	LYS	15	-0.673	-8.173
H	134	GLY	18	-2.334	-11.334
H	135	VAL	18	-6.096	-15.096
H	136	THR	19	-6.871	-16.371
H	137	ALA	17	-6.563	-15.063
H	138	ALA	19	-6.087	-15.587
H	139	CYS	21	-9.640	-20.140

H	140	PRO	18	-10.193	-19.193
H	141	TYR	15	-9.119	-16.619
H	142	ALA	9	-5.465	-9.965
H	143	GLY	9	-5.839	-10.339
H	144	ALA	12	-7.938	-13.938
H	145	SER	15	-8.907	-16.407
H	146	SER	19	-9.916	-19.416
H	147	PHE	23	-10.797	-22.297
H	148	TYR	28	-12.083	-26.083
H	149	ARG	20	-10.297	-20.297
H	150	ASN	25	-11.100	-23.600
H	151	LEU	25	-9.144	-21.644
H	152	LEU	25	-6.723	-19.223
H	153	TRP	24	-5.187	-17.187
H	154	LEU	24	-0.299	-12.299
H	155	VAL	25	2.812	-9.688
H	156	LYS	23	3.633	-7.867
H	157	LYS	18	4.897	-4.103
H	158	GLY	11	3.054	-2.446
H	159	ASN	15	3.427	-4.073
H	160	SER	18	4.072	-4.928
H	161	TYR	24	1.992	-10.008
H	162	PRO	17	1.855	-6.645
H	163	LYS	16	-0.513	-8.513
H	164	LEU	17	0.404	-8.096
H	165	SER	14	-1.135	-8.135
H	166	LYS	15	-0.436	-7.936
H	167	SER	16	-0.327	-8.327
H	168	TYR	16	0.326	-7.674
H	169	VAL	16	0.260	-7.740
H	170	ASN	19	-0.185	-9.685
H	171	ASN	15	-0.086	-7.586
H	172	LYS	15	-0.917	-8.417
H	173	GLY	12	-0.815	-6.815
H	174	LYS	19	-2.761	-12.261
H	175	GLU	22	-3.807	-14.807
H	176	VAL	26	-5.119	-18.119
H	177	LEU	20	-6.427	-16.427
H	178	VAL	22	-8.162	-19.162
H	179	LEU	22	-8.674	-19.674
H	180	TRP	24	-8.530	-20.530
H	181	GLY	24	-5.323	-17.323
H	182	VAL	23	-3.117	-14.617
H	183	HIS	26	-1.030	-14.030

H	184	HIS	24	2.646	-9.354
H	185	PRO	25	5.723	-6.777
H	186	PRO	19	4.350	-5.150
H	187	THR	16	4.665	-3.335
H	188	SER	19	3.659	-5.841
H	189	THR	14	4.101	-2.899
H	190	ASP	16	4.839	-3.161
H	191	GLN	23	2.604	-8.896
H	192	GLN	19	4.060	-5.440
H	193	ASN	16	3.769	-4.231
H	194	LEU	22	2.875	-8.125
H	195	TYR	26	1.550	-11.450
H	196	GLN	23	2.395	-9.105
H	197	ASN	21	1.046	-9.454
H	198	ALA	16	0.282	-7.718
H	199	ASP	14	-0.997	-7.997
H	200	ALA	19	-2.791	-12.291
H	201	TYR	19	-3.854	-13.354
H	202	VAL	23	-3.702	-15.202
H	203	SER	17	-2.384	-10.884
H	204	VAL	19	-1.521	-11.021
H	205	GLY	17	0.180	-8.320
H	206	SER	20	0.009	-9.991
H	207	SER	13	-0.289	-6.789
H	208	LYS	13	-0.073	-6.573
H	209	TYR	14	0.104	-6.896
H	210	ASN	12	0.705	-5.295
H	211	ARG	10	0.363	-4.637
H	212	ARG	12	-0.907	-6.907
H	213	PHE	16	-2.008	-10.008
H	214	THR	16	-2.027	-10.027
H	215	PRO	23	-0.666	-12.166
H	216	GLU	17	3.398	-5.102
H	217	ILE	18	4.008	-4.992
H	218	ALA	15	2.791	-4.709
H	219	ALA	15	2.707	-4.793
H	220	ARG	13	2.062	-4.438
H	221	PRO	11	1.960	-3.540
H	222	LYS	12	1.776	-4.224
H	223	VAL	15	0.447	-7.053
H	224	ARG	13	-1.512	-8.012
H	225	GLY	13	-0.704	-7.204
H	226	GLN	20	0.138	-9.862
H	227	ALA	17	3.470	-5.030

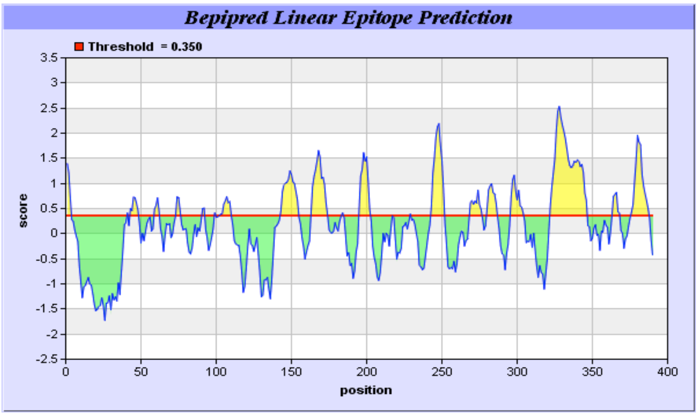
H	228	GLY	23	3.075	-8.425
H	229	ARG	24	1.598	-10.402
H	230	MET	22	-0.158	-11.158
H	231	ASN	18	-0.915	-9.915
H	232	TYR	21	-2.858	-13.358
H	233	TYR	16	-2.857	-10.857
H	234	TRP	17	-4.065	-12.565
H	235	THR	19	-4.292	-13.792
H	236	LEU	21	-4.405	-14.905
H	237	LEU	23	-2.144	-13.644
H	238	GLU	22	-0.987	-11.987
H	239	PRO	16	-0.635	-8.635
H	240	GLY	15	0.626	-6.874
H	241	ASP	16	-0.076	-8.076
H	242	THR	18	0.624	-8.376
H	243	ILE	22	-0.580	-11.580
H	244	THR	17	-0.480	-8.980
H	245	PHE	19	-4.389	-13.889
H	246	GLU	18	-3.723	-12.723
H	247	ALA	22	-3.533	-14.533
H	248	THR	22	-3.343	-14.343
H	249	GLY	30	-2.482	-17.482
H	250	ASN	28	-3.209	-17.209
H	251	LEU	28	-6.598	-20.598
H	252	VAL	23	-7.282	-18.782
H	253	ALA	23	-7.614	-19.114
H	254	PRO	24	-8.296	-20.296
H	255	ARG	23	-7.116	-18.616
H	256	TYR	24	-8.601	-20.601
H	257	ALA	23	-8.746	-20.246
H	258	PHE	23	-7.168	-18.668
H	259	ALA	24	-4.707	-16.707
H	260	LEU	23	-6.355	-17.855
H	261	ASN	18	-5.029	-14.029
H	262	ARG	18	-3.967	-12.967
H	263	GLY	13	-3.048	-9.548
H	264	SER	11	-2.145	-7.645
H	265	GLY	15	-3.250	-10.750
H	266	SER	21	-5.402	-15.902
H	267	GLY	21	-3.945	-14.445
H	268	ILE	22	-4.321	-15.321
H	269	ILE	18	-2.122	-11.122
H	270	ILE	18	-0.943	-9.943
H	271	SER	21	-2.489	-12.989

H	272	ASN	18	-1.376	-10.376
H	273	ALA	19	-2.176	-11.676
H	274	PRO	15	-2.874	-10.374
H	275	VAL	19	-4.664	-14.164
H	276	HIS	14	-3.925	-10.925
H	277	ASP	11	-3.544	-9.044
H	278	CYS	15	-4.919	-12.419
H	279	ASN	19	-5.974	-15.474
H	280	THR	19	-5.203	-14.703
H	281	LYS	18	-5.489	-14.489
H	282	CYS	21	-4.372	-14.872
H	283	GLN	29	-5.148	-19.648
H	284	THR	25	-2.238	-14.738
H	285	PRO	23	-1.806	-13.306
H	286	HIS	22	-1.387	-12.387
H	287	GLY	24	-2.262	-14.262
H	288	ALA	28	-4.587	-18.587
H	289	ILE	25	-2.034	-14.534
H	290	ASN	18	-2.215	-11.215
H	291	SER	19	-1.459	-10.959
H	292	SER	12	-1.528	-7.528
H	293	LEU	16	-1.975	-9.975
H	294	PRO	14	-1.705	-8.705
H	295	PHE	21	-1.196	-11.696
H	296	GLN	26	-0.552	-13.552
H	297	ASN	18	0.180	-8.820
H	298	ILE	23	0.027	-11.473
H	299	HIS	17	0.315	-8.185
H	300	PRO	15	-0.524	-8.024
H	301	VAL	15	-1.161	-8.661
H	302	THR	23	-2.122	-13.622
H	303	ILE	22	-3.850	-14.850
H	304	GLY	17	-4.437	-12.937
H	305	GLU	16	-3.419	-11.419
H	306	CYS	21	-2.505	-13.005
H	307	PRO	23	-2.395	-13.895
H	308	LYS	16	-1.264	-9.264
H	309	TYR	18	-0.457	-9.457
H	310	VAL	14	0.211	-6.789
H	311	LYS	12	0.591	-5.409
H	312	SER	12	-0.014	-6.014
H	313	THR	12	-0.114	-6.114
H	314	LYS	15	-1.288	-8.788
H	315	LEU	16	-2.557	-10.557

H	316	ARG	16	-3.517	-11.517
H	317	MET	17	-4.400	-12.900
H	318	ALA	21	-4.417	-14.917
H	319	THR	12	-2.910	-8.910
H	320	GLY	14	-2.807	-9.807
H	321	LEU	16	-2.447	-10.447
H	322	ARG	19	-2.234	-11.734
H	323	ASN	21	-0.394	-10.894
H	324	ILE	16	0.494	-7.506
H	325	PRO	12	1.087	-4.913
H	326	ALA	7	1.394	-2.106
H	327	ARG	5	1.143	-1.357

6.3. NA Host Human

Bepipred



Average:0.161 Minimum:-1.731 Maximum:2.543 Threshold: 0.34

Predicted epitopes:

No.	Start	End	Peptide	Peptide Length
1	1	3	MNP	3

2	41	41	G	1
3	43	48	QNQIET	6
4	59	62	NTWV	4
5	73	76	NFAA	4
6	91	92	LC	2
7	99	99	I	1
8	102	110	KDNSVRIGS	9
9	143	154	KHSNGTIKDRSP	12
10	163	174	IGEVPSPYNSRF	12
11	184	184	C	1
12	195	202	ISGPDNGA	8
13	217	217	K	1
14	229	229	S	1
15	243	251	TDGPSNGQA	9
16	269	276	MNAPNYHY	8
17	280	286	SCYPDSS	7
18	296	304	WHGSNRPWV	9
19	322	346	FGDNPRPNDKTGSCGPVSSNGANGV	25
20	363	368	KSISSR	6
21	376	387	DPNGWTGTDNNF	12

DiscoTope Prediction for Structure: 2HTY Chain Id: A (positive predictions in red)

Threshold: -7.7

Chain Id	Residue Id	Residue Name	Contact Number	Propensity Score	DiscoTope Score
A	83	VAL	12	-6.919	-12.919
A	84	LYS	17	-11.368	-19.868
A	85	LEU	22	-13.851	-24.851
A	86	ALA	20	-12.358	-22.358
A	87	GLY	27	-16.880	-30.380
A	88	ASN	19	-10.726	-20.226
A	89	SER	18	-8.484	-17.484
A	90	SER	19	-9.673	-19.173
A	91	LEU	24	-10.357	-22.357
A	92	CYS	18	-9.553	-18.553
A	93	PRO	15	-8.487	-15.987
A	94	ILE	17	-7.695	-16.195
A	95	ASN	14	-4.909	-11.909
A	96	GLY	23	-6.517	-18.017
A	97	TRP	25	-10.061	-22.561
A	98	ALA	20	-7.337	-17.337
A	99	VAL	19	-6.494	-15.994

A	100	TYR	16	-6.685	-14.685
A	101	SER	16	-4.923	-12.923
A	102	LYS	21	-4.844	-15.344
A	103	ASP	21	-3.771	-14.271
A	104	ASN	22	-1.052	-12.052
A	105	SER	28	-1.523	-15.523
A	106	ILE	29	-1.029	-15.529
A	107	ARG	20	-0.090	-10.090
A	108	ILE	15	1.062	-6.438
A	109	GLY	21	0.159	-10.341
A	110	SER	20	-1.738	-11.738
A	111	LYS	13	-0.790	-7.290
A	112	GLY	16	0.577	-7.423
A	113	ASP	20	0.073	-9.927
A	114	VAL	25	0.765	-11.735
A	115	PHE	28	-3.983	-17.983
A	116	VAL	29	-4.224	-18.724
A	117	ILE	30	-7.605	-22.605
A	118	ARG	25	-9.141	-21.641
A	119	GLU	29	-13.516	-28.016
A	120	PRO	32	-14.567	-30.567
A	121	PHE	32	-16.294	-32.294
A	122	ILE	32	-17.197	-33.197
A	123	SER	29	-16.133	-30.633
A	124	CYS	23	-11.336	-22.836
A	125	SER	21	-9.463	-19.963
A	126	HIS	20	-9.037	-19.037
A	127	LEU	12	-5.962	-11.962
A	128	GLU	12	-7.086	-13.086
A	129	CYS	21	-10.740	-21.240
A	130	ARG	21	-11.368	-21.868
A	131	THR	26	-11.720	-24.720
A	132	PHE	32	-14.814	-30.814
A	133	PHE	29	-12.136	-26.636
A	134	LEU	28	-11.979	-25.979
A	135	THR	25	-8.016	-20.516
A	136	GLN	26	-1.135	-14.135
A	137	GLY	17	-1.910	-10.410
A	138	ALA	22	-0.948	-11.948
A	139	LEU	23	-2.629	-14.129
A	140	LEU	29	-1.069	-15.569
A	141	ASN	24	-1.920	-13.920
A	142	ASP	17	-1.444	-9.944
A	143	LYS	13	0.488	-6.012

A	144	HIS	17	0.008	-8.492
A	145	SER	23	-2.140	-13.640
A	146	ASN	17	0.311	-8.189
A	147	GLY	19	1.984	-7.516
A	148	THR	12	3.084	-2.916
A	149	VAL	13	3.448	-3.052
A	150	LYS	10	1.786	-3.214
A	151	ASP	13	1.325	-5.175
A	152	ARG	18	0.569	-8.431
A	153	SER	15	1.302	-6.198
A	154	PRO	16	-0.123	-8.123
A	155	HIS	18	-2.340	-11.340
A	156	ARG	25	-6.217	-18.717
A	157	THR	24	-7.588	-19.588
A	158	LEU	30	-12.139	-27.139
A	159	MET	25	-7.652	-20.152
A	160	SER	25	-8.474	-20.974
A	161	CYS	23	-5.988	-17.488
A	162	PRO	18	-5.724	-14.724
A	163	VAL	25	-10.745	-23.245
A	164	GLY	21	-6.419	-16.919
A	165	GLU	19	-3.211	-12.711
A	166	ALA	27	-1.822	-15.322
A	167	PRO	32	-5.145	-21.145
A	168	SER	22	-1.060	-12.060
A	169	PRO	17	-1.188	-9.688
A	169A	TYR	11	0.750	-4.750
A	170	ASN	14	-0.633	-7.633
A	171	SER	22	-4.414	-15.414
A	172	ARG	16	-1.880	-9.880
A	173	PHE	15	-2.489	-9.989
A	174	GLU	24	-7.210	-19.210
A	175	SER	25	-7.355	-19.855
A	176	VAL	23	-6.923	-18.423
A	177	ALA	28	-8.392	-22.392
A	178	TRP	27	-4.738	-18.238
A	179	SER	27	-7.329	-20.829
A	180	ALA	31	-14.586	-30.086
A	181	SER	32	-16.310	-32.310
A	182	ALA	30	-15.733	-30.733
A	183	CYS	26	-14.644	-27.644
A	184	HIS	26	-15.834	-28.834
A	185	ASP	27	-16.024	-29.524
A	186	GLY	23	-14.102	-25.602

A	187	THR	16	-7.866	-15.866
A	188	SER	19	-7.644	-17.144
A	189	TRP	21	-7.974	-18.474
A	190	LEU	29	-9.163	-23.663
A	191	THR	29	-11.107	-25.607
A	192	ILE	33	-13.707	-30.207
A	193	GLY	27	-10.196	-23.696
A	194	ILE	30	-5.634	-20.634
A	195	SER	26	-3.731	-16.731
A	196	GLY	20	-0.455	-10.455
A	197	PRO	17	2.206	-6.294
A	198	ASP	17	1.933	-6.567
A	199	ASN	16	1.533	-6.467
A	200	GLY	18	1.244	-7.756
A	201	ALA	24	-0.487	-12.487
A	202	VAL	24	-1.633	-13.633
A	203	ALA	26	-6.564	-19.564
A	204	VAL	23	-6.076	-17.576
A	205	LEU	27	-6.585	-20.085
A	206	LYS	24	-5.456	-17.456
A	207	TYR	22	-4.892	-15.892
A	208	ASN	16	-3.143	-11.143
A	209	GLY	15	-3.514	-11.014
A	210	ILE	15	-3.351	-10.851
A	211	ILE	17	-3.529	-12.029
A	212	THR	19	-2.367	-11.867
A	213	ASP	17	-2.217	-10.717
A	214	THR	17	-2.953	-11.453
A	215	ILE	18	-2.069	-11.069
A	216	LYS	16	-0.205	-8.205
A	217	SER	23	0.876	-10.624
A	218	TRP	17	1.533	-6.967
A	219	ARG	18	2.521	-6.479
A	220	ASN	17	2.113	-6.387
A	221	ASN	20	2.882	-7.118
A	222	ILE	25	2.025	-10.475
A	223	LEU	29	0.602	-13.898
A	224	ARG	27	-6.302	-19.802
A	225	THR	28	-9.630	-23.630
A	226	GLN	28	-14.029	-28.029
A	227	GLU	29	-13.879	-28.379
A	228	SER	33	-16.670	-33.170
A	229	GLU	31	-16.382	-31.882
A	230	CYS	32	-17.526	-33.526

A	231	ALA	29	-18.011	-32.511
A	232	CYS	30	-17.677	-32.677
A	233	VAL	24	-15.359	-27.359
A	234	ASN	18	-11.466	-20.466
A	235	GLY	18	-10.456	-19.456
A	236	SER	24	-10.316	-22.316
A	237	CYS	27	-12.830	-26.330
A	238	PHE	28	-12.903	-26.903
A	239	THR	28	-13.222	-27.222
A	240	VAL	28	-8.514	-22.514
A	241	MET	24	-4.584	-16.584
A	242	THR	27	0.072	-13.428
A	243	ASP	27	2.689	-10.811
A	244	GLY	20	4.444	-5.556
A	245	PRO	18	3.559	-5.441
A	246	SER	20	2.457	-7.543
A	247	ASN	14	2.235	-4.765
A	248	GLY	14	3.236	-3.764
A	249	GLN	18	3.742	-5.258
A	250	ALA	21	2.804	-7.696
A	251	SER	22	1.770	-9.230
A	252	TYR	24	-0.715	-12.715
A	253	LYS	19	-2.382	-11.882
A	254	ILE	21	-2.414	-12.914
A	255	PHE	21	-3.430	-13.930
A	256	LYS	23	-5.386	-16.886
A	257	MET	21	-5.560	-16.060
A	258	GLU	19	-6.462	-15.962
A	259	LYS	21	-5.572	-16.072
A	260	GLY	26	-5.136	-18.136
A	261	LYS	21	-2.916	-13.416
A	262	VAL	19	-2.476	-11.976
A	263	VAL	12	-0.618	-6.618
A	264	LYS	15	-0.760	-8.260
A	265	SER	17	-2.530	-11.030
A	266	VAL	16	-1.301	-9.301
A	267	GLU	15	-2.425	-9.925
A	268	LEU	19	-1.362	-10.862
A	269	ASP	14	-0.976	-7.976
A	270	ALA	17	-0.106	-8.606
A	271	PRO	10	0.811	-4.189
A	272	ASN	14	1.999	-5.001
A	273	TYR	25	0.441	-12.059
A	274	HIS	27	2.107	-11.393

A	275	TYR	30	-3.702	-18.702
A	276	GLU	29	-5.854	-20.354
A	277	GLU	30	-12.446	-27.446
A	278	CYS	33	-12.959	-29.459
A	279	SER	33	-14.932	-31.432
A	280	CYS	31	-13.640	-29.140
A	281	TYR	31	-16.230	-31.730
A	282	PRO	31	-16.755	-32.255
A	283	ASN	24	-13.701	-25.701
A	284	ALA	16	-9.235	-17.235
A	285	GLY	17	-9.894	-18.394
A	286	GLU	25	-11.539	-24.039
A	287	ILE	25	-11.718	-24.218
A	288	THR	24	-8.284	-20.284
A	289	CYS	30	-10.704	-25.704
A	290	VAL	32	-8.221	-24.221
A	291	CYS	31	-7.801	-23.301
A	292	ARG	30	-3.461	-18.461
A	293	ASP	32	-1.102	-17.102
A	294	ASN	27	1.809	-11.691
A	295	TRP	24	1.810	-10.190
A	296	HIS	23	2.035	-9.465
A	297	GLY	30	2.228	-12.772
A	298	SER	33	1.272	-15.228
A	299	ASN	35	-2.648	-20.148
A	300	ARG	37	-6.847	-25.347
A	301	PRO	27	-4.316	-17.816
A	302	TRP	25	-5.892	-18.392
A	303	VAL	22	-6.227	-17.227
A	304	SER	21	-5.857	-16.357
A	305	PHE	19	-4.193	-13.693
A	306	ASN	16	-4.216	-12.216
A	308	GLN	18	-7.473	-16.473
A	309	ASN	13	-0.726	-7.226
A	310	LEU	21	-2.448	-12.948
A	311	GLU	13	-0.283	-6.783
A	312	TYR	18	-2.727	-11.727
A	313	GLN	15	-0.836	-8.336
A	314	ILE	18	-3.137	-12.137
A	315	GLY	20	-2.503	-12.503
A	316	TYR	25	-3.256	-15.756
A	317	ILE	31	-3.833	-19.333
A	318	CYS	25	-4.068	-16.568
A	319	SER	31	-1.333	-16.833

A	320	GLY	27	-0.562	-14.062
A	321	VAL	28	1.654	-12.346
A	322	PHE	29	2.627	-11.873
A	323	GLY	33	1.889	-14.611
A	324	ASP	33	2.642	-13.858
A	325	ASN	32	4.900	-11.100
A	326	PRO	25	6.385	-6.115
A	327	ARG	26	5.974	-7.026
A	328	PRO	22	4.397	-6.603
A	329	ASN	16	3.147	-4.853
A	330	ASP	16	0.988	-7.012
A	331	GLY	14	-0.591	-7.591
A	332	THR	17	-2.656	-11.156
A	333	GLY	24	-4.141	-16.141
A	335	SER	20	-4.597	-14.597
A	336	CYS	19	-3.712	-13.212
A	339	GLY	18	-1.742	-10.742
A	340	PRO	25	-1.799	-14.299
A	341	VAL	24	-0.959	-12.959
A	342	SER	15	2.355	-5.145
A	343	SER	16	4.045	-3.955
A	344	ASN	20	5.787	-4.213
A	345	GLY	28	3.835	-10.165
A	346	ALA	22	3.322	-7.678
A	347	TYR	19	3.382	-6.118
A	348	GLY	27	2.324	-11.176
A	349	VAL	25	-1.972	-14.472
A	350	LYS	29	-7.957	-22.457
A	351	GLY	30	-6.551	-21.551
A	352	PHE	30	-6.944	-21.944
A	353	SER	31	-5.826	-21.326
A	354	PHE	24	-6.004	-18.004
A	355	LYS	21	-1.837	-12.337
A	356	TYR	20	-0.826	-10.826
A	357	GLY	12	1.840	-4.160
A	358	ASN	13	2.199	-4.301
A	359	GLY	20	1.484	-8.516
A	360	VAL	23	1.457	-10.043
A	361	TRP	24	0.648	-11.352
A	362	ILE	28	-0.015	-14.015
A	363	GLY	29	-2.536	-17.036
A	364	ARG	31	0.041	-15.459
A	365	THR	33	2.094	-14.406
A	366	LYS	25	0.617	-11.883

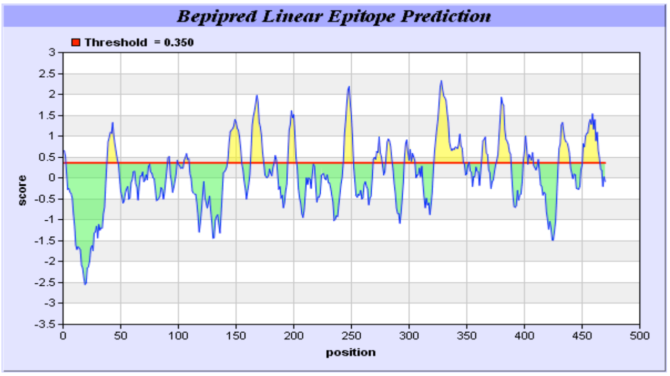
A	367	SER	21	4.596	-5.904
A	368	THR	22	7.045	-3.955
A	369	ASN	17	5.683	-2.817
A	370	SER	18	3.994	-5.006
A	371	ARG	26	1.827	-11.173
A	372	SER	23	0.836	-10.664
A	373	GLY	25	-0.674	-13.174
A	374	PHE	28	-1.950	-15.950
A	375	GLU	21	-0.848	-11.348
A	376	MET	23	-0.691	-12.191
A	377	ILE	22	-0.595	-11.595
A	378	TRP	25	-0.509	-13.009
A	379	ASP	24	-0.063	-12.063
A	380	PRO	21	1.782	-8.718
A	381	ASN	20	0.528	-9.472
A	382	GLY	27	-1.296	-14.796
A	383	TRP	27	-2.024	-15.524
A	384	THR	19	-1.888	-11.388
A	385	GLU	20	-1.836	-11.836
A	386	THR	19	-3.025	-12.525
A	387	ASP	20	-1.138	-11.138
A	388	SER	17	-0.587	-9.087
A	389	SER	18	-0.445	-9.445
A	390	PHE	19	-0.827	-10.327
A	391	SER	9	0.612	-3.888
A	392	VAL	15	-1.254	-8.754
A	394	LYS	17	-0.811	-9.311
A	395	GLN	18	-1.747	-10.747
A	396	ASP	22	-1.380	-12.380
A	397	ILE	29	-4.330	-18.830
A	398	VAL	26	-3.594	-16.594
A	399	ALA	21	-1.108	-11.608
A	400	ILE	20	-0.727	-10.727
A	401	THR	13	-0.667	-7.167
A	402	ASP	20	-1.416	-11.416
A	403	TRP	26	-0.576	-13.576
A	404	SER	30	-3.747	-18.747
A	405	GLY	26	-3.615	-16.615
A	406	TYR	27	-8.019	-21.519
A	407	SER	30	-10.036	-25.036
A	408	GLY	30	-13.227	-28.227
A	409	SER	30	-13.545	-28.545
A	410	PHE	29	-14.869	-29.369
A	411	VAL	25	-13.203	-25.703

A	412	GLN	26	-13.337	-26.337
A	412A	HIS	28	-13.565	-27.565
A	412B	PRO	20	-8.636	-18.636
A	412C	GLU	20	-9.663	-19.663
A	412D	LEU	18	-9.369	-18.369
A	413	THR	14	-6.637	-13.637
A	414	GLY	11	-4.216	-9.716
A	415	LEU	14	-6.071	-13.071
A	416	ASP	15	-7.647	-15.147
A	417	CYS	21	-10.123	-20.623
A	418	ILE	27	-12.635	-26.135
A	419	ARG	24	-10.603	-22.603
A	420	PRO	26	-11.080	-24.080
A	421	CYS	24	-9.467	-21.467
A	422	PHE	27	-9.257	-22.757
A	423	TRP	30	-11.772	-26.772
A	424	VAL	32	-9.167	-25.167
A	425	GLU	27	-8.156	-21.656
A	426	LEU	31	-5.825	-21.325
A	427	ILE	28	-2.445	-16.445
A	428	ARG	27	-1.196	-14.696
A	429	GLY	19	0.409	-9.091
A	430	ARG	15	2.638	-4.862
A	431	PRO	12	2.069	-3.931
A	432	LYS	13	2.309	-4.191
A	433	GLU	14	1.259	-5.741
A	435	SER	13	0.881	-5.619
A	436	THR	18	0.552	-8.448
A	437	ILE	19	2.000	-7.500
A	438	TRP	25	2.054	-10.446
A	439	THR	21	2.114	-8.386
A	440	SER	23	-2.087	-13.587
A	441	GLY	27	-4.658	-18.158
A	442	SER	30	-4.436	-19.436
A	443	SER	33	-8.383	-24.883
A	444	ILE	27	-8.625	-22.125
A	445	SER	27	-9.580	-23.080
A	446	PHE	21	-8.696	-19.196
A	447	CYS	21	-8.358	-18.858
A	448	GLY	25	-10.903	-23.403
A	449	VAL	18	-9.161	-18.161
A	450	ASN	13	-5.314	-11.814
A	451	SER	11	-4.608	-10.108
A	452	ASP	12	-4.609	-10.609

A	453	THR	15	-4.343	-11.843
A	454	VAL	13	-2.076	-8.576
A	455	GLY	18	-2.548	-11.548
A	456	TRP	13	-1.484	-7.984
A	457	SER	17	-2.164	-10.664
A	458	TRP	20	-3.809	-13.809
A	459	PRO	27	-5.154	-18.654
A	460	ASP	25	-2.523	-15.023
A	461	GLY	16	-0.545	-8.545
A	462	ALA	17	-0.160	-8.660
A	463	GLU	11	-0.983	-6.483
A	464	LEU	15	-1.059	-8.559
A	465	PRO	15	-1.619	-9.119
A	466	PHE	19	-1.516	-11.016
A	467	THR	11	-2.252	-7.752
A	468	ILE	15	-1.334	-8.834

6.4. NA Host Swine

BepiPred



Average:0.095 **Minimum:**-2.549 **Maximum:**2.317 **Threshold:**0.350

Predicted epitopes:

No.	Start	End	Peptide	Peptide Length
1	1	2	MN	2
2	38	47	IQTGGKNHTE	10
3	91	92	LC	2
4	99	99	I	1

5	105	109	SIRIG	5
6	143	154	KHSNGTVKDRSP	12
7	163	174	IGEAPSPYNSRF	12
8	183	185	ACH	3
9	195	202	ISGPDNGA	8
10	243	251	TDGPSNGQA	9
11	269	276	LDAPNYHY	8
12	280	285	SCYPDT	6
13	296	305	WHASNRPWVS	10
14	322	347	FGDNPRSNDGKGNCGPVLSNGANGVK	26
15	352	352	R	1
16	363	368	KSIDSR	6
17	376	388	DPNGWTETDSSFS	13
18	399	402	WSGY	4
19	404	407	GSFV	4
20	412	412	L	1
21	430	439	QPKESTIWAS	10
22	451	465	ETASWSWPDGADLPF	15

DiscoTope Prediction for Structure: 2HUO Chain Id: A (positive predictions in red)

Threshold: -7.7

Chain Id	Residue Id	Residue Name	Contact Number	Propensity Score	DiscoTope Score
A	28	PHE	8	0.637	-3.363
A	29	ARG	12	0.709	-5.291
A	30	ASN	13	0.572	-5.928
A	31	TYR	15	-2.654	-10.154
A	32	THR	7	0.182	-3.318
A	33	SER	11	-0.361	-5.861
A	34	GLY	12	-0.141	-6.141
A	35	PRO	10	-1.043	-6.043
A	36	LEU	18	-0.796	-9.796
A	37	LEU	18	-1.595	-10.595
A	38	ASP	16	-2.677	-10.677
A	39	ARG	16	-2.758	-10.758
A	40	VAL	19	-2.866	-12.366
A	41	PHE	19	-4.339	-13.839
A	42	THR	16	-2.595	-10.595
A	43	THR	23	-3.345	-14.845
A	44	TYR	26	-7.898	-20.898
A	45	LYS	22	-4.138	-15.138
A	46	LEU	20	-1.227	-11.227
A	47	MET	27	-3.210	-16.710
A	48	HIS	27	-5.363	-18.863
A	49	THR	19	2.421	-7.079
A	50	HIS	20	1.650	-8.350
A	51	GLN	26	-0.217	-13.217
A	52	THR	25	1.282	-11.218

A	53	VAL	21	-0.100	-10.600
A	54	ASP	13	0.294	-6.206
A	55	PHE	15	-0.142	-7.642
A	56	VAL	21	0.069	-10.431
A	57	SER	15	0.340	-7.160
A	58	ARG	14	0.955	-6.045
A	59	LYS	16	1.379	-6.621
A	60	ARG	17	1.410	-7.090
A	61	ILE	11	1.692	-3.808
A	62	GLN	13	1.964	-4.536
A	63	TYR	17	1.725	-6.775
A	64	GLY	16	2.369	-5.631
A	65	SER	14	1.626	-5.374
A	66	PHE	18	0.994	-8.006
A	67	SER	11	0.579	-4.921
A	68	TYR	12	-0.046	-6.046
A	69	LYS	11	-1.445	-6.945
A	70	LYS	14	-2.016	-9.016
A	71	MET	15	-3.724	-11.224
A	72	THR	18	-4.256	-13.256
A	73	ILE	21	-6.217	-16.717
A	74	MET	17	-4.290	-12.790
A	75	GLU	13	-3.591	-10.091
A	76	ALA	21	-6.195	-16.695
A	77	VAL	23	-6.970	-18.470
A	78	GLY	18	-4.794	-13.794
A	79	MET	19	-4.977	-14.477
A	80	LEU	24	-6.463	-18.463
A	81	ASP	15	-4.000	-11.500
A	82	ASP	15	-3.878	-11.378
A	83	LEU	18	-3.237	-12.237
A	84	VAL	18	-1.853	-10.853
A	85	ASP	23	-2.394	-13.894
A	86	GLU	23	-3.459	-14.959
A	87	SER	24	-3.990	-15.990
A	88	ASP	20	-2.294	-12.294
A	89	PRO	21	-0.336	-10.836
A	90	ASP	21	-0.364	-10.864
A	91	VAL	17	-0.029	-8.529
A	92	ASP	15	0.200	-7.300
A	93	PHE	17	-0.937	-9.437
A	94	PRO	17	-2.252	-10.752
A	95	ASN	23	-4.262	-15.762
A	96	SER	24	-6.938	-18.938

A	97	PHE	23	-5.576	-17.076
A	98	HIS	25	-5.340	-17.840
A	99	ALA	26	-8.229	-21.229
A	100	PHE	26	-6.247	-19.247
A	101	GLN	26	-5.270	-18.270
A	102	THR	27	-6.772	-20.272
A	103	ALA	24	-5.180	-17.180
A	104	GLU	22	-2.909	-13.909
A	105	GLY	20	-1.560	-11.560
A	106	ILE	26	-1.511	-14.511
A	107	ARG	19	0.716	-8.784
A	108	LYS	11	1.942	-3.558
A	109	ALA	12	2.449	-3.551
A	110	HIS	14	2.815	-4.185
A	111	PRO	11	2.757	-2.743
A	112	ASP	11	2.790	-2.710
A	113	LYS	12	1.699	-4.301
A	114	ASP	17	-0.339	-8.839
A	115	TRP	20	-2.744	-12.744
A	116	PHE	23	-2.855	-14.355
A	117	HIS	25	-1.277	-13.777
A	118	LEU	28	-5.517	-19.517
A	119	VAL	22	-6.115	-17.115
A	120	GLY	26	-6.448	-19.448
A	121	LEU	26	-7.417	-20.417
A	122	LEU	24	-7.593	-19.593
A	123	HIS	25	-6.048	-18.548
A	124	ASP	27	-6.345	-19.845
A	125	LEU	24	-6.419	-18.419
A	126	GLY	24	-4.797	-16.797
A	127	LYS	28	-6.244	-20.244
A	128	ILE	23	-5.871	-17.371
A	129	MET	21	-3.477	-13.977
A	130	ALA	22	-4.806	-15.806
A	131	LEU	15	-4.270	-11.770
A	132	TRP	10	-2.027	-7.027
A	133	GLY	9	-2.070	-6.570
A	134	GLU	14	-2.760	-9.760
A	135	PRO	15	-2.440	-9.940
A	136	GLN	22	-3.440	-14.440
A	137	TRP	27	-3.309	-16.809
A	138	ALA	23	-2.612	-14.112
A	139	VAL	26	-3.869	-16.869
A	140	VAL	26	-4.338	-17.338

A	141	GLY	26	-4.239	-17.239
A	142	ASP	21	-3.563	-14.063
A	143	THR	27	-3.226	-16.726
A	144	PHE	28	-6.623	-20.623
A	145	PRO	24	-4.686	-16.686
A	146	VAL	25	-1.731	-14.231
A	147	GLY	29	-0.383	-14.883
A	148	CYS	25	-0.891	-13.391
A	149	ARG	19	-1.418	-10.918
A	150	PRO	25	-5.884	-18.384
A	151	GLN	19	-5.841	-15.341
A	152	ALA	15	-5.666	-13.166
A	153	SER	18	-5.544	-14.544
A	154	VAL	21	-7.129	-17.629
A	155	VAL	23	-8.804	-20.304
A	156	PHE	15	-6.548	-14.048
A	157	CYS	16	-7.179	-15.179
A	158	ASP	13	-7.055	-13.555
A	159	SER	11	-4.169	-9.669
A	160	THR	20	-4.585	-14.585
A	161	PHE	22	-1.142	-12.142
A	162	GLN	15	0.861	-6.639
A	163	ASP	14	3.386	-3.614
A	164	ASN	18	4.164	-4.836
A	165	PRO	16	4.112	-3.888
A	166	ASP	23	3.683	-7.817
A	167	LEU	22	3.455	-7.545
A	168	GLN	12	4.664	-1.336
A	169	ASP	14	3.755	-3.245
A	170	PRO	13	3.279	-3.221
A	171	ARG	15	3.119	-4.381
A	172	TYR	22	2.306	-8.694
A	173	SER	18	2.927	-6.073
A	174	THR	16	1.125	-6.875
A	175	GLU	17	-1.615	-10.115
A	176	LEU	19	-1.138	-10.638
A	177	GLY	19	0.783	-8.717
A	178	MET	19	-0.948	-10.448
A	179	TYR	21	-2.361	-12.861
A	180	GLN	13	-1.763	-8.263
A	181	PRO	15	-1.186	-8.686
A	182	HIS	18	-4.071	-13.071
A	183	CYS	15	-3.778	-11.278
A	184	GLY	19	-4.668	-14.168

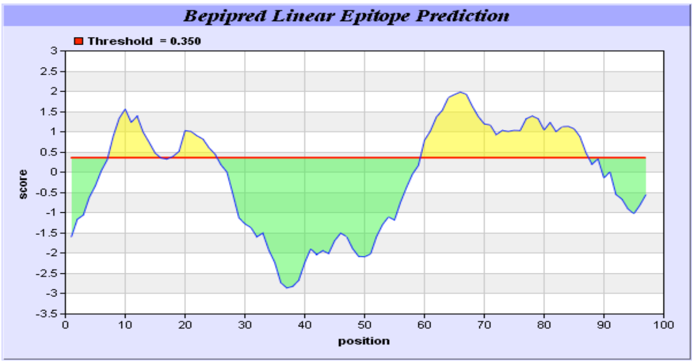
A	185	LEU	21	-5.623	-16.123
A	186	GLU	16	-4.540	-12.540
A	187	ASN	14	-3.600	-10.600
A	188	VAL	20	-4.792	-14.792
A	189	LEU	21	-4.264	-14.764
A	190	MET	24	-4.509	-16.509
A	191	SER	30	-3.135	-18.135
A	192	TRP	28	-2.309	-16.309
A	193	GLY	29	-3.387	-17.887
A	194	HIS	27	-3.767	-17.267
A	195	ASP	31	-3.363	-18.863
A	196	GLU	27	-0.278	-13.778
A	197	TYR	26	-0.973	-13.973
A	198	LEU	23	-1.654	-13.154
A	199	TYR	20	-0.182	-10.182
A	200	GLN	21	1.729	-8.771
A	201	MET	22	0.631	-10.369
A	202	MET	21	-0.825	-11.325
A	203	LYS	13	1.311	-5.189
A	204	PHE	16	0.639	-7.361
A	205	ASN	16	-1.116	-9.116
A	206	LYS	13	-0.397	-6.897
A	207	PHE	18	-2.138	-11.138
A	208	SER	16	-2.061	-10.061
A	209	LEU	18	-3.504	-12.504
A	210	PRO	12	-2.482	-8.482
A	211	SER	9	-2.294	-6.794
A	212	GLU	16	-3.654	-11.654
A	213	ALA	22	-4.900	-15.900
A	214	PHE	22	-2.562	-13.562
A	215	TYR	21	-4.077	-14.577
A	216	MET	26	-3.300	-16.300
A	217	ILE	28	-3.631	-17.631
A	218	ARG	24	-2.043	-14.043
A	219	PHE	25	-2.896	-15.396
A	220	HIS	24	-1.854	-13.854
A	221	SER	25	-2.009	-14.509
A	222	PHE	25	-2.000	-14.500
A	223	TYR	21	-1.882	-12.382
A	224	PRO	22	-3.853	-14.853
A	225	TRP	24	-0.973	-12.973
A	226	HIS	21	1.615	-8.885
A	227	THR	15	1.513	-5.987
A	228	GLY	15	-1.206	-8.706

A	229	GLY	13	-0.118	-6.618
A	230	ASP	19	-1.312	-10.812
A	231	TYR	22	-2.669	-13.669
A	232	ARG	17	-1.423	-9.923
A	233	GLN	16	-2.013	-10.013
A	234	LEU	22	-4.344	-15.344
A	235	CYS	20	-4.252	-14.252
A	236	SER	17	-3.884	-12.384
A	237	GLN	12	-1.826	-7.826
A	238	GLN	12	-2.708	-8.708
A	239	ASP	18	-3.661	-12.661
A	240	LEU	15	-1.776	-9.276
A	241	ASP	11	-1.689	-7.189
A	242	MET	15	-2.005	-9.505
A	243	LEU	18	-0.768	-9.768
A	244	PRO	14	-0.588	-7.588
A	245	TRP	17	-1.174	-9.674
A	246	VAL	24	-1.531	-13.531
A	247	GLN	18	0.065	-8.935
A	248	GLU	13	-0.610	-7.110
A	249	PHE	24	-3.780	-15.780
A	250	ASN	22	-1.424	-12.424
A	251	LYS	14	-1.171	-8.171
A	252	PHE	19	-2.157	-11.657
A	253	ASP	24	-4.164	-16.164
A	254	LEU	16	-1.299	-9.299
A	255	TYR	15	-1.871	-9.371
A	256	THR	18	-3.211	-12.211
A	257	LYS	18	-2.618	-11.618
A	258	CYS	16	-1.861	-9.861
A	259	PRO	13	-0.979	-7.479
A	260	ASP	9	-2.116	-6.616
A	261	LEU	13	-2.447	-8.947
A	262	PRO	16	-2.330	-10.330
A	263	ASP	12	-1.673	-7.673
A	264	VAL	15	-1.635	-9.135
A	265	GLU	8	-0.288	-4.288
A	266	SER	10	-0.383	-5.383
A	267	LEU	13	-0.500	-7.000
A	268	ARG	14	-0.135	-7.135
A	269	PRO	12	0.225	-5.775
A	270	TYR	11	-0.247	-5.747
A	271	TYR	22	-2.418	-13.418
A	272	GLN	18	-2.030	-11.030

A	273	GLY	13	-1.488	-7.988
A	274	LEU	18	-1.928	-10.928
A	275	ILE	21	-3.754	-14.254
A	276	ASP	12	-1.844	-7.844
A	277	LYS	15	-1.181	-8.681
A	278	TYR	18	-2.448	-11.448
A	279	CYS	20	-3.595	-13.595
A	280	PRO	17	-2.925	-11.425
A	281	GLY	13	-2.897	-9.397
A	282	THR	14	-2.741	-9.741
A	283	LEU	20	-1.967	-11.967
A	284	SER	17	-0.531	-9.031
A	285	TRP	25	-1.187	-13.687

6.5. M2 Host Human

Bepipred



Average:-0.088 **Minimum:**-2.858 **Maximum:**1.983 **Threshold:** 0.350

Predicted epitopes:

No.	Start	End	Peptide	Peptide Length
1	8	16	ETPTRSEWE	9
2	18	25	RCSDSSDP	8
3	60	87	KRGPSTEGVPESMREEYQQEQQSAVDVD	28

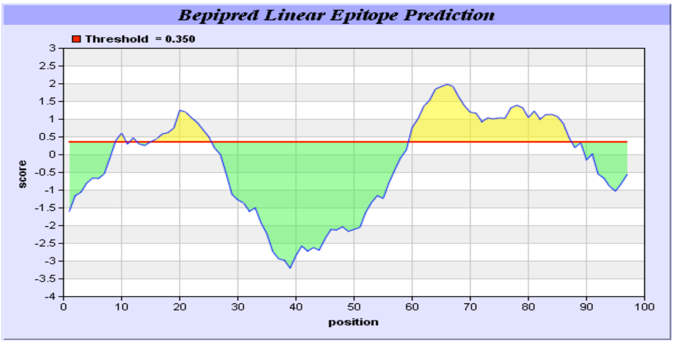
DiscoTope Prediction for Structure: 1MP6 Chain Id: A (positive predictions in red)

Threshold: -7.7

Chain Id	Residue Id	Residue Name	Contact Number	Propensity Score	DiscoTope Score
A	22	SER	6	-2.789	-5.789
A	23	SER	7	-3.548	-7.048
A	24	ASP	8	-4.463	-8.463
A	25	PRO	10	-6.385	-11.385
A	26	LEU	10	-6.385	-11.385
A	27	VAL	12	-7.977	-13.977
A	28	VAL	11	-7.923	-13.423
A	29	ALA	11	-8.320	-13.820
A	30	ALA	11	-8.458	-13.958
A	31	SER	12	-9.244	-15.244
A	32	ILE	11	-8.669	-14.169
A	33	ILE	12	-9.383	-15.383
A	34	GLY	11	-8.867	-14.367
A	35	ILE	11	-8.735	-14.235
A	36	LEU	11	-8.159	-13.659
A	37	HIS	11	-8.034	-13.534
A	38	LEU	12	-8.367	-14.367
A	39	ILE	11	-7.714	-13.214
A	40	LEU	11	-7.455	-12.955
A	41	TRP	11	-7.360	-12.860
A	42	ILE	10	-6.574	-11.574
A	43	LEU	9	-5.861	-10.361
A	44	ASP	9	-5.861	-10.361
A	45	ARG	7	-4.208	-7.708
A	46	LEU	6	-3.425	-6.425

6.6. M2 Host Swine

Bepipred



Average:-0.224 **Minimum:**-3.202 **Maximum:**1.983 **Threshold:**0.350

DiscoTope Prediction for Structure: 1NYJ Chain Id: A (positive predictions in red)

Chain Id	Residue Id	Residue Name	Contact Number	Propensity Score	DiscoTope Score
A	1	SER	6	-2.789	-5.789
A	2	SER	7	-3.548	-7.048
A	3	ASP	8	-4.463	-8.463
A	4	PRO	10	-6.385	-11.385
A	5	LEU	10	-6.385	-11.385
A	6	VAL	11	-7.324	-12.824
A	7	VAL	11	-7.923	-13.423
A	8	ALA	11	-8.320	-13.820
A	9	ALA	11	-8.458	-13.958
A	10	SER	12	-9.244	-15.244
A	11	ILE	12	-9.383	-15.383
A	12	ILE	11	-8.687	-14.187
A	13	GLY	11	-8.867	-14.367
A	14	ILE	12	-9.182	-15.182
A	15	LEU	11	-8.159	-13.659
A	16	HIS	11	-8.034	-13.534
A	17	LEU	13	-9.305	-15.805
A	18	ILE	11	-7.714	-13.214
A	19	LEU	11	-7.455	-12.955
A	20	TRP	12	-7.958	-13.958
A	21	ILE	10	-6.574	-11.574
A	22	LEU	9	-5.861	-10.361
A	23	ASP	9	-5.861	-10.361
A	24	ARG	7	-4.208	-7.708
A	25	LEU	6	-3.425	-6.425

Lampiran 9. Hasil Pencarian *Template* Vaksin Pada *Database* PDB Menggunakan *server* CPHModels 3.0

1. HA Host Human

CPHmodels-3.0 Server - prediction results

Technical University of Denmark

```
Query sequence:
```

```
>gi_238695727_gb_ACR55004.1_
MKAILVVLLYTFATANADTLCIGYHANNSTDTVDTVLEKNVTVTHSVNLLEDKHNGKLCK
LRGVAPLHLGKCNIAGWILGNPECESLSTASSWSYIVETSSSDNGTCYPGDFIDYEELRE
QLSSVSSFERFEIFPKTSSWPNHDSNKGVTAACPHAGAKSFYKNLIWLVKKGNSYPKLSK
SYINDKGKEVLVLWGIHHPSTSADQQSLYQNADAYVFVGSSRYSKKFKPEIAIRPKVRDQ
EGRMNYYWTLVEPGDKITFEATGNLVVPRYAFAMERNAGSGIIISDTPVHDCNTTCQTPK
GAINTSLPFQNIHPITIGKCPKYVKSTKLRLATGLRNVPSIQSRGLFGAIAGFIEGGWTG
MVDGWYGYHHQNEQGSGYAADLKSTQNAIDEITNKVNSVIEKMNTQFTAVGKEFNHLEKR
IENLNKKVDDGFLDIWTYNAELLVLLENERTLDYHDSNVKNLYEKVRSQLKNNAKEIGNG
CFEFYHKCDNTCMESVKNGTYDYPKYSEEAKLNREEIDGVKLESTRIYQILAIYSTVASS
LVLVVSLGAISFWMCSNGSLQCRICI

Searching for template ...

Round   0. All hits:
entry: 1RUY chain: H score: 597 E: 1e-170
entry: 1RUY chain: J score: 597 E: 1e-170
entry: 1RUY chain: L score: 597 E: 1e-170
entry: 1RD8 chain: A score: 597 E: 1e-170
entry: 1RD8 chain: C score: 597 E: 1e-170
entry: 1RD8 chain: E score: 597 E: 1e-170
entry: 1RVT chain: H score: 594 E: 1e-170
entry: 1RVT chain: J score: 594 E: 1e-170
entry: 1RVT chain: L score: 594 E: 1e-170
entry: 1RV0 chain: H score: 594 E: 1e-170
entry: 1RV0 chain: J score: 594 E: 1e-170
entry: 1RV0 chain: L score: 594 E: 1e-170
entry: 3GBN chain: A score: 590 E: 1e-168
entry: 1RUZ chain: H score: 588 E: 1e-168
entry: 1RUZ chain: J score: 588 E: 1e-168
entry: 1RUZ chain: L score: 588 E: 1e-168
entry: 1RVX chain: A score: 529 E: 1e-150
entry: 1RVX chain: C score: 529 E: 1e-150
entry: 1RVX chain: E score: 529 E: 1e-150
entry: 1RVX chain: G score: 529 E: 1e-150
entry: 1RVX chain: I score: 529 E: 1e-150
entry: 1RVX chain: K score: 529 E: 1e-150
entry: 1RVZ chain: A score: 529 E: 1e-150
entry: 1RVZ chain: C score: 529 E: 1e-150
entry: 1RVZ chain: E score: 529 E: 1e-150
entry: 1RVZ chain: G score: 529 E: 1e-150
entry: 1RVZ chain: I score: 529 E: 1e-150
entry: 1RVZ chain: K score: 529 E: 1e-150
entry: 1RU7 chain: A score: 529 E: 1e-150
entry: 1RU7 chain: C score: 529 E: 1e-150
entry: 1RU7 chain: E score: 529 E: 1e-150
entry: 1RU7 chain: G score: 529 E: 1e-150
entry: 1RU7 chain: I score: 529 E: 1e-150
entry: 1RU7 chain: K score: 529 E: 1e-150
entry: 1HA0 chain: A score: 454 E: 1e-127
entry: 1JSO chain: A score: 402 E: 1e-112
entry: 1JSN chain: A score: 402 E: 1e-112
entry: 1JSM chain: A score: 402 E: 1e-112
entry: 2FK0 chain: A score: 394 E: 1e-109
entry: 2FK0 chain: C score: 394 E: 1e-109
entry: 2FK0 chain: E score: 394 E: 1e-109
entry: 2FK0 chain: G score: 394 E: 1e-109
entry: 2FK0 chain: I score: 394 E: 1e-109
entry: 2FK0 chain: K score: 394 E: 1e-109
entry: 2FK0 chain: M score: 394 E: 1e-109
entry: 2FK0 chain: O score: 394 E: 1e-109
entry: 2FK0 chain: Q score: 394 E: 1e-109
entry: 3FKU chain: A score: 394 E: 1e-109
entry: 3FKU chain: C score: 394 E: 1e-109
entry: 3FKU chain: E score: 394 E: 1e-109
entry: 3FKU chain: G score: 394 E: 1e-109
entry: 3FKU chain: I score: 394 E: 1e-109
entry: 3FKU chain: K score: 394 E: 1e-109
entry: 3GBM chain: C score: 394 E: 1e-109
entry: 3GBM chain: A score: 394 E: 1e-109
```

```
entry: 2IBX chain: A score: 392 E: 1e-109
entry: 2IBX chain: C score: 392 E: 1e-109
entry: 2IBX chain: E score: 392 E: 1e-109
entry: 1RD8 chain: B score: 349 E: 6e-96
entry: 1RD8 chain: D score: 349 E: 6e-96
entry: 1RD8 chain: F score: 349 E: 6e-96
entry: 3GBN chain: B score: 345 E: 1e-94
entry: 3FKU chain: B score: 326 E: 5e-89
entry: 3FKU chain: D score: 326 E: 5e-89
entry: 3FKU chain: F score: 326 E: 5e-89
entry: 3GBM chain: B score: 321 E: 1e-87
entry: 2FK0 chain: B score: 321 E: 1e-87
entry: 2FK0 chain: D score: 321 E: 1e-87
entry: 2FK0 chain: F score: 321 E: 1e-87
entry: 2FK0 chain: H score: 321 E: 1e-87
entry: 2FK0 chain: J score: 321 E: 1e-87
entry: 2FK0 chain: L score: 321 E: 1e-87
entry: 2FK0 chain: N score: 321 E: 1e-87
entry: 2FK0 chain: P score: 321 E: 1e-87
entry: 2FK0 chain: R score: 321 E: 1e-87
entry: 3FKU chain: H score: 321 E: 2e-87
entry: 3FKU chain: J score: 321 E: 2e-87
entry: 3FKU chain: L score: 321 E: 2e-87
entry: 1RUY chain: I score: 320 E: 2e-87
entry: 1RUY chain: K score: 320 E: 2e-87
entry: 1RUY chain: M score: 320 E: 2e-87
entry: 1RUZ chain: I score: 320 E: 2e-87
entry: 1RUZ chain: K score: 320 E: 2e-87
entry: 1RUZ chain: M score: 320 E: 2e-87
entry: 3GBM chain: D score: 320 E: 2e-87
entry: 1RVT chain: I score: 317 E: 3e-86
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entry: 1RVT chain: M score: 317 E: 3e-86
entry: 1RV0 chain: I score: 317 E: 3e-86
entry: 1RV0 chain: K score: 317 E: 3e-86
entry: 1RV0 chain: M score: 317 E: 3e-86
entry: 1RVX chain: B score: 316 E: 5e-86
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entry: 1RVX chain: J score: 316 E: 5e-86
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entry: 1RU7 chain: F score: 313 E: 3e-85
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entry: 1JSO chain: B score: 300 E: 3e-81
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entry: 1HGJ chain: B score: 235 E: 8e-62
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entry: 4HMG chain: F score: 235 E: 8e-62
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entry: 1MQM chain: H score: 231 E: 2e-60
entry: 1MQN chain: B score: 231 E: 2e-60
entry: 1MQN chain: E score: 231 E: 2e-60
entry: 1MQN chain: H score: 231 E: 2e-60
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entry: 4HMG chain: A score: 226 E: 6e-59
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entry: 1MQL chain: A score: 225 E: 1e-58
entry: 1MQL chain: D score: 225 E: 1e-58
entry: 1MQL chain: G score: 225 E: 1e-58
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```

```
entry: 1HGH chain: E score: 223 E: 4e-58
entry: 1HGF chain: A score: 223 E: 4e-58
entry: 1HGF chain: C score: 223 E: 4e-58
entry: 1HGF chain: E score: 223 E: 4e-58
entry: 5HMG chain: A score: 223 E: 4e-58
entry: 5HMG chain: C score: 223 E: 4e-58
entry: 5HMG chain: E score: 223 E: 4e-58
entry: 2HMG chain: A score: 223 E: 4e-58
entry: 2HMG chain: C score: 223 E: 4e-58
entry: 2HMG chain: E score: 223 E: 4e-58
entry: 1KEN chain: A score: 223 E: 5e-58
entry: 1KEN chain: C score: 223 E: 5e-58
entry: 1KEN chain: E score: 223 E: 5e-58
entry: 1HGD chain: A score: 223 E: 6e-58
entry: 1HGD chain: C score: 223 E: 6e-58
entry: 1HGD chain: E score: 223 E: 6e-58
entry: 1HGE chain: A score: 223 E: 6e-58
entry: 1HGE chain: C score: 223 E: 6e-58
entry: 1HGE chain: E score: 223 E: 6e-58
entry: 1EO8 chain: A score: 223 E: 6e-58
entry: 2VIU chain: A score: 222 E: 7e-58
entry: 1QFU chain: A score: 222 E: 1e-57
entry: 3EYM chain: C score: 222 E: 1e-57
entry: 3EYM chain: E score: 222 E: 1e-57
entry: 3EYM chain: A score: 222 E: 1e-57
entry: 1JSD chain: B score: 220 E: 3e-57
entry: 1JSH chain: B score: 220 E: 3e-57
entry: 1JSI chain: B score: 220 E: 3e-57
entry: 3EYJ chain: A score: 217 E: 2e-56
entry: 3EYK chain: A score: 217 E: 2e-56
entry: 1TI8 chain: B score: 214 E: 2e-55
entry: 1TI8 chain: A score: 202 E: 7e-52
entry: 2VIT chain: C score: 178 E: 1e-44
entry: 1QU1 chain: F score: 177 E: 2e-44
entry: 2VIR chain: C score: 177 E: 3e-44
entry: 2VIS chain: C score: 177 E: 3e-44
entry: 1QU1 chain: D score: 175 E: 1e-43
entry: 1QU1 chain: E score: 175 E: 1e-43
entry: 1QU1 chain: B score: 173 E: 4e-43
entry: 1QU1 chain: C score: 170 E: 4e-42
entry: 1HTM chain: D score: 154 E: 3e-37
entry: 1HTM chain: F score: 154 E: 3e-37
entry: 1QU1 chain: A score: 150 E: 3e-36
entry: 1HTM chain: B score: 142 E: 7e-34
entry: 2RFT chain: B score: 138 E: 2e-32
entry: 2RFU chain: B score: 138 E: 2e-32
entry: 3BT6 chain: B score: 138 E: 2e-32
entry: 2RFT chain: A score: 64 E: 5e-10
entry: 2RFU chain: A score: 64 E: 5e-10
entry: 3BT6 chain: A score: 64 E: 5e-10
entry: 1IBN chain: A score: 44 E: 5e-04
entry: 1IBO chain: A score: 44 E: 5e-04
entry: 1XOP chain: A score: 41 E: 0.003
entry: 1XOO chain: A score: 41 E: 0.003
entry: 2JRD chain: A score: 40 E: 0.006
entry: 2DCI chain: A score: 38 E: 0.024
entry: 2DMB chain: A score: 30 E: 6.8
entry: 1G5I chain: A score: 30 E: 7.4
entry: 1G5I chain: C score: 30 E: 7.4
entry: 1G5I chain: D score: 30 E: 8.1
entry: 1G5I chain: B score: 30 E: 8.8

Round   0. Hits better than threshold: 0.000010:
entry: 1RUY chain: H score: 597 E: 1e-170
entry: 1RUY chain: J score: 597 E: 1e-170
entry: 1RUY chain: L score: 597 E: 1e-170
entry: 1RD8 chain: A score: 597 E: 1e-170
entry: 1RD8 chain: C score: 597 E: 1e-170
entry: 1RD8 chain: E score: 597 E: 1e-170
entry: 1RVT chain: H score: 594 E: 1e-170
entry: 1RVT chain: J score: 594 E: 1e-170
```

```
entry: 1RVT chain: L score: 594 E: 1e-170
entry: 1RV0 chain: H score: 594 E: 1e-170
entry: 1RV0 chain: J score: 594 E: 1e-170
entry: 1RV0 chain: L score: 594 E: 1e-170
entry: 3GBN chain: A score: 590 E: 1e-168
entry: 1RUZ chain: H score: 588 E: 1e-168
entry: 1RUZ chain: J score: 588 E: 1e-168
entry: 1RUZ chain: L score: 588 E: 1e-168
entry: 1RVX chain: A score: 529 E: 1e-150
entry: 1RVX chain: C score: 529 E: 1e-150
entry: 1RVX chain: E score: 529 E: 1e-150
entry: 1RVX chain: G score: 529 E: 1e-150
entry: 1RVX chain: I score: 529 E: 1e-150
entry: 1RVX chain: K score: 529 E: 1e-150
entry: 1RVZ chain: A score: 529 E: 1e-150
entry: 1RVZ chain: C score: 529 E: 1e-150
entry: 1RVZ chain: E score: 529 E: 1e-150
entry: 1RVZ chain: G score: 529 E: 1e-150
entry: 1RVZ chain: I score: 529 E: 1e-150
entry: 1RVZ chain: K score: 529 E: 1e-150
entry: 1RU7 chain: A score: 529 E: 1e-150
entry: 1RU7 chain: C score: 529 E: 1e-150
entry: 1RU7 chain: E score: 529 E: 1e-150
entry: 1RU7 chain: G score: 529 E: 1e-150
entry: 1RU7 chain: I score: 529 E: 1e-150
entry: 1RU7 chain: K score: 529 E: 1e-150
entry: 1HA0 chain: A score: 454 E: 1e-127
entry: 1JSO chain: A score: 402 E: 1e-112
entry: 1JSN chain: A score: 402 E: 1e-112
entry: 1JSM chain: A score: 402 E: 1e-112
entry: 2FK0 chain: A score: 394 E: 1e-109
entry: 2FK0 chain: C score: 394 E: 1e-109
entry: 2FK0 chain: E score: 394 E: 1e-109
entry: 2FK0 chain: G score: 394 E: 1e-109
entry: 2FK0 chain: I score: 394 E: 1e-109
entry: 2FK0 chain: K score: 394 E: 1e-109
entry: 2FK0 chain: M score: 394 E: 1e-109
entry: 2FK0 chain: O score: 394 E: 1e-109
entry: 2FK0 chain: Q score: 394 E: 1e-109
entry: 3FKU chain: A score: 394 E: 1e-109
entry: 3FKU chain: C score: 394 E: 1e-109
entry: 3FKU chain: E score: 394 E: 1e-109
entry: 3FKU chain: G score: 394 E: 1e-109
entry: 3FKU chain: I score: 394 E: 1e-109
entry: 3FKU chain: K score: 394 E: 1e-109
entry: 3GBM chain: C score: 394 E: 1e-109
entry: 3GBM chain: A score: 394 E: 1e-109
entry: 2IBX chain: A score: 392 E: 1e-109
entry: 2IBX chain: C score: 392 E: 1e-109
entry: 2IBX chain: E score: 392 E: 1e-109
entry: 1RD8 chain: B score: 349 E: 6e-96
entry: 1RD8 chain: D score: 349 E: 6e-96
entry: 1RD8 chain: F score: 349 E: 6e-96
entry: 3GBN chain: B score: 345 E: 1e-94
entry: 3FKU chain: B score: 326 E: 5e-89
entry: 3FKU chain: D score: 326 E: 5e-89
entry: 3FKU chain: F score: 326 E: 5e-89
entry: 3GBM chain: B score: 321 E: 1e-87
entry: 2FK0 chain: B score: 321 E: 1e-87
entry: 2FK0 chain: D score: 321 E: 1e-87
entry: 2FK0 chain: F score: 321 E: 1e-87
entry: 2FK0 chain: H score: 321 E: 1e-87
entry: 2FK0 chain: J score: 321 E: 1e-87
entry: 2FK0 chain: L score: 321 E: 1e-87
entry: 2FK0 chain: N score: 321 E: 1e-87
entry: 2FK0 chain: P score: 321 E: 1e-87
entry: 2FK0 chain: R score: 321 E: 1e-87
entry: 3FKU chain: H score: 321 E: 2e-87
entry: 3FKU chain: J score: 321 E: 2e-87
entry: 3FKU chain: L score: 321 E: 2e-87
entry: 1RUY chain: I score: 320 E: 2e-87
```

```
entry: 1RUY chain: K score: 320 E: 2e-87
entry: 1RUY chain: M score: 320 E: 2e-87
entry: 1RUZ chain: I score: 320 E: 2e-87
entry: 1RUZ chain: K score: 320 E: 2e-87
entry: 1RUZ chain: M score: 320 E: 2e-87
entry: 3GBM chain: D score: 320 E: 2e-87
entry: 1RVT chain: I score: 317 E: 3e-86
entry: 1RVT chain: K score: 317 E: 3e-86
entry: 1RVT chain: M score: 317 E: 3e-86
entry: 1RV0 chain: I score: 317 E: 3e-86
entry: 1RV0 chain: K score: 317 E: 3e-86
entry: 1RV0 chain: M score: 317 E: 3e-86
entry: 1RVX chain: B score: 316 E: 5e-86
entry: 1RVX chain: D score: 316 E: 5e-86
entry: 1RVX chain: H score: 316 E: 5e-86
entry: 1RVX chain: J score: 316 E: 5e-86
entry: 1RVZ chain: B score: 316 E: 5e-86
entry: 1RVZ chain: D score: 316 E: 5e-86
entry: 1RVZ chain: F score: 316 E: 5e-86
entry: 1RVZ chain: H score: 316 E: 5e-86
entry: 1RVZ chain: J score: 316 E: 5e-86
entry: 1RVZ chain: L score: 316 E: 5e-86
entry: 1RU7 chain: B score: 316 E: 5e-86
entry: 1RU7 chain: D score: 316 E: 5e-86
entry: 1RU7 chain: H score: 316 E: 5e-86
entry: 1RU7 chain: J score: 316 E: 5e-86
entry: 1RVX chain: F score: 313 E: 3e-85
entry: 1RVX chain: L score: 313 E: 3e-85
entry: 1RU7 chain: F score: 313 E: 3e-85
entry: 1RU7 chain: L score: 313 E: 3e-85
entry: 1JSO chain: B score: 300 E: 3e-81
entry: 1JSN chain: B score: 300 E: 3e-81
entry: 1JSM chain: B score: 300 E: 3e-81
entry: 2IBX chain: B score: 299 E: 4e-81
entry: 2IBX chain: D score: 299 E: 4e-81
entry: 2IBX chain: F score: 299 E: 4e-81
entry: 1JSD chain: A score: 276 E: 3e-74
entry: 1JSH chain: A score: 276 E: 3e-74
entry: 1JSI chain: A score: 276 E: 3e-74
entry: 1HGD chain: B score: 235 E: 8e-62
entry: 1HGD chain: D score: 235 E: 8e-62
entry: 1HGD chain: F score: 235 E: 8e-62
entry: 1EO8 chain: B score: 235 E: 8e-62
entry: 1HGI chain: B score: 235 E: 8e-62
entry: 1HGI chain: D score: 235 E: 8e-62
entry: 1HGI chain: F score: 235 E: 8e-62
entry: 1HGJ chain: B score: 235 E: 8e-62
entry: 1HGJ chain: D score: 235 E: 8e-62
entry: 1HGJ chain: F score: 235 E: 8e-62
entry: 1HGG chain: B score: 235 E: 8e-62
entry: 1HGG chain: D score: 235 E: 8e-62
entry: 1HGG chain: F score: 235 E: 8e-62
entry: 1HGH chain: B score: 235 E: 8e-62
entry: 1HGH chain: D score: 235 E: 8e-62
entry: 1HGH chain: F score: 235 E: 8e-62
entry: 1HGF chain: B score: 235 E: 8e-62
entry: 1HGF chain: D score: 235 E: 8e-62
entry: 1HGF chain: F score: 235 E: 8e-62
entry: 1HGE chain: B score: 235 E: 8e-62
entry: 1HGE chain: D score: 235 E: 8e-62
entry: 1HGE chain: F score: 235 E: 8e-62
entry: 1KEN chain: B score: 235 E: 8e-62
entry: 1KEN chain: D score: 235 E: 8e-62
entry: 1KEN chain: F score: 235 E: 8e-62
entry: 3HMG chain: B score: 235 E: 8e-62
entry: 3HMG chain: D score: 235 E: 8e-62
entry: 3HMG chain: F score: 235 E: 8e-62
entry: 4HMG chain: B score: 235 E: 8e-62
entry: 4HMG chain: D score: 235 E: 8e-62
entry: 4HMG chain: F score: 235 E: 8e-62
entry: 2HMG chain: B score: 235 E: 8e-62
```

```
entry: 2HMG chain: D score: 235 E: 8e-62
entry: 2HMG chain: F score: 235 E: 8e-62
entry: 2VIU chain: B score: 235 E: 8e-62
entry: 1QFU chain: B score: 233 E: 3e-61
entry: 5HMG chain: B score: 233 E: 6e-61
entry: 5HMG chain: D score: 233 E: 6e-61
entry: 5HMG chain: F score: 233 E: 6e-61
entry: 3EYM chain: B score: 232 E: 8e-61
entry: 3EYM chain: D score: 232 E: 8e-61
entry: 3EYM chain: F score: 232 E: 8e-61
entry: 1MQL chain: B score: 231 E: 2e-60
entry: 1MQL chain: E score: 231 E: 2e-60
entry: 1MQL chain: H score: 231 E: 2e-60
entry: 1MQM chain: B score: 231 E: 2e-60
entry: 1MQM chain: E score: 231 E: 2e-60
entry: 1MQM chain: H score: 231 E: 2e-60
entry: 1MQN chain: B score: 231 E: 2e-60
entry: 1MQN chain: E score: 231 E: 2e-60
entry: 1MQN chain: H score: 231 E: 2e-60
entry: 3HMG chain: A score: 226 E: 6e-59
entry: 3HMG chain: C score: 226 E: 6e-59
entry: 3HMG chain: E score: 226 E: 6e-59
entry: 4HMG chain: A score: 226 E: 6e-59
entry: 4HMG chain: C score: 226 E: 6e-59
entry: 4HMG chain: E score: 226 E: 6e-59
entry: 1MQL chain: A score: 225 E: 1e-58
entry: 1MQL chain: D score: 225 E: 1e-58
entry: 1MQL chain: G score: 225 E: 1e-58
entry: 1MQM chain: A score: 225 E: 1e-58
entry: 1MQM chain: D score: 225 E: 1e-58
entry: 1MQM chain: G score: 225 E: 1e-58
entry: 1MQN chain: A score: 225 E: 1e-58
entry: 1MQN chain: D score: 225 E: 1e-58
entry: 1MQN chain: G score: 225 E: 1e-58
entry: 3EYJ chain: B score: 224 E: 2e-58
entry: 3EYK chain: B score: 224 E: 2e-58
entry: 1HGI chain: A score: 223 E: 4e-58
entry: 1HGI chain: C score: 223 E: 4e-58
entry: 1HGI chain: E score: 223 E: 4e-58
entry: 1HGJ chain: A score: 223 E: 4e-58
entry: 1HGJ chain: C score: 223 E: 4e-58
entry: 1HGJ chain: E score: 223 E: 4e-58
entry: 1HGG chain: A score: 223 E: 4e-58
entry: 1HGG chain: C score: 223 E: 4e-58
entry: 1HGG chain: E score: 223 E: 4e-58
entry: 1HGH chain: A score: 223 E: 4e-58
entry: 1HGH chain: C score: 223 E: 4e-58
entry: 1HGH chain: E score: 223 E: 4e-58
entry: 1HGF chain: A score: 223 E: 4e-58
entry: 1HGF chain: C score: 223 E: 4e-58
entry: 1HGF chain: E score: 223 E: 4e-58
entry: 5HMG chain: A score: 223 E: 4e-58
entry: 5HMG chain: C score: 223 E: 4e-58
entry: 5HMG chain: E score: 223 E: 4e-58
entry: 2HMG chain: A score: 223 E: 4e-58
entry: 2HMG chain: C score: 223 E: 4e-58
entry: 2HMG chain: E score: 223 E: 4e-58
entry: 1KEN chain: A score: 223 E: 5e-58
entry: 1KEN chain: C score: 223 E: 5e-58
entry: 1KEN chain: E score: 223 E: 5e-58
entry: 1HGD chain: A score: 223 E: 6e-58
entry: 1HGD chain: C score: 223 E: 6e-58
entry: 1HGD chain: E score: 223 E: 6e-58
entry: 1HGE chain: A score: 223 E: 6e-58
entry: 1HGE chain: C score: 223 E: 6e-58
entry: 1HGE chain: E score: 223 E: 6e-58
entry: 1EO8 chain: A score: 223 E: 6e-58
entry: 2VIU chain: A score: 222 E: 7e-58
entry: 1QFU chain: A score: 222 E: 1e-57
entry: 3EYM chain: C score: 222 E: 1e-57
entry: 3EYM chain: E score: 222 E: 1e-57
```

```
entry: 3EYM chain: A score: 222 E: 1e-57
entry: 1JSD chain: B score: 220 E: 3e-57
entry: 1JSH chain: B score: 220 E: 3e-57
entry: 1JSI chain: B score: 220 E: 3e-57
entry: 3EYJ chain: A score: 217 E: 2e-56
entry: 3EYK chain: A score: 217 E: 2e-56
entry: 1TI8 chain: B score: 214 E: 2e-55
entry: 1TI8 chain: A score: 202 E: 7e-52
entry: 2VIT chain: C score: 178 E: 1e-44
entry: 1QU1 chain: F score: 177 E: 2e-44
entry: 2VIR chain: C score: 177 E: 3e-44
entry: 2VIS chain: C score: 177 E: 3e-44
entry: 1QU1 chain: D score: 175 E: 1e-43
entry: 1QU1 chain: E score: 175 E: 1e-43
entry: 1QU1 chain: B score: 173 E: 4e-43
entry: 1QU1 chain: C score: 170 E: 4e-42
entry: 1HTM chain: D score: 154 E: 3e-37
entry: 1HTM chain: F score: 154 E: 3e-37
entry: 1QU1 chain: A score: 150 E: 3e-36
entry: 1HTM chain: B score: 142 E: 7e-34
entry: 2RFT chain: B score: 138 E: 2e-32
entry: 2RFU chain: B score: 138 E: 2e-32
entry: 3BT6 chain: B score: 138 E: 2e-32
entry: 2RFT chain: A score: 64 E: 5e-10
entry: 2RFU chain: A score: 64 E: 5e-10
entry: 3BT6 chain: A score: 64 E: 5e-10

Retrieving template ...

Entry: 1ruy
Chain: H

Making profile-profile alignment ...

Score:     764.0 bits
Identity:   84.5 %

Query: 1   DTLCIGYHANNSTDTVDTVLEKNVTVTHSVNLLEDKHNGKLCKLRGVAPLHLGKCNIAGW 60
           DTLCIGYHANNSTDTVDTVLEKNVTVTHSVNLLED HNGKLC+L G+APL LGKCNIAGW
Templ: 1   DTLCIGYHANNSTDTVDTVLEKNVTVTHSVNLLEDSHNGKLCRLGGIAPLQLGKCNIAGW 60

Query: 61  ILGNPECESLSTASSWSYIVETSSSDNGTCYPGDFIDYEELREQLSSVSSFERFEIFPKT 120
           +LGNPEC+ L T SSWSYIVET +SDNGTCYPGDFIDYEELREQLSSVSSFERFEIFPKT
Templ: 61  LLGNPECDLLLTVSSWSYIVETPNSDNGTCYPGDFIDYEELREQLSSVSSFERFEIFPKT 120

Query: 121 SSWPNHDSNKGVTAACPHAGAKSFYKNLIWLVKKGNSYPKLSKSYINDKGKEVLVLWGIH 180
           SSWPNH++NKGVTAACP+AGA SFY+NL+WLVKKGNSYPKLSKSY+N+KGKEVLVLWG+H
Templ: 121 SSWPNHNTNKGVTAACPYAGASSFYRNLLWLVKKGNSYPKLSKSYVNNKGKEVLVLWGVH 180

Query: 181 HPSTSADQQSLYQNADAYVFVGSSRYSKKFKPEIAIRPKVRDQEGRMNYYWTLVEPGDKI 240
           HP TS DQQ+LYQNADAYV VGSS+Y+++F PEIA RPKVR Q GRMNYYWTL+EPGD I
Templ: 181 HPPTSTDQQNLYQNADAYVSVGSSKYNRRFTPEIAARPKVRGQAGRMNYYWTLLEPGDTI 240

Query: 241 TFEATGNLVVPRYAFAMERNAGSGIIISDTPVHDCNTTCQTPKGAINTSLPFQNIHPITI 300
           TFEATGNLV PRYAFA+ R +GSGIIIS+ PVHDCNT CQTP GAIN+SLPFQNIHP+TI
Templ: 241 TFEATGNLVAPRYAFALNRGSGSGIIISNAPVHDCNTKCQTPHGAINSSLPFQNIHPVTI 300

Query: 301 GKCPKYVKSTKLRLATGLRNVPS 323
           G+CPKYVKSTKLR+ATGLRN+P+
Templ: 301 GECPKYVKSTKLRMATGLRNIPA 323
```

2. NA Host Human

CPHmodels-3.0 Server - prediction results

Technical University of Denmark

```
Query sequence:

>gi_237689850_gb_ACR15757.1_
MNPNQKIITIGSVCMTIGMANLILQIGNIISIWISHSIQLGNQNQIETCNQSVITYENNT
WVNQTYVNISNTNFAAGQSVVSVKLAGNSSLCPVSGWAIYSKDNSVRIGSKGDVFVIREP
FISCSPLECRTFFLTQGALLNDKHSNGTIKDRSPYRTLMSCPIGEVPSPYNSRFESVAWS
ASACHDGINWLTIGISGPDNGAVAVLKYNGIITDTIKSWRNNILRTQESECACVNGSCFT
VMTDGPSNGQASYKIFRIEKGKIVKSVEMNAPNYHYEECSCYPDSSEITCVCRDNWHGSN
RPWVSFNQNLEYQIGYICSGIFGDNPRPNDKTGSCGPVSSNGANGVKGFSFKYGNGVWIG
RTKSISSRNGFEMIWDPNGWTGTDNNFSIK

Searching for template ...

Round   0. All hits:
entry: 2HU0 chain: A score: 595 E: 1e-170
entry: 2HU0 chain: B score: 595 E: 1e-170
entry: 2HU0 chain: C score: 595 E: 1e-170
entry: 2HU0 chain: D score: 595 E: 1e-170
entry: 2HU0 chain: E score: 595 E: 1e-170
entry: 2HU0 chain: F score: 595 E: 1e-170
entry: 2HU0 chain: G score: 595 E: 1e-170
entry: 2HU0 chain: H score: 595 E: 1e-170
entry: 2HTY chain: A score: 595 E: 1e-170
entry: 2HTY chain: B score: 595 E: 1e-170
entry: 2HTY chain: C score: 595 E: 1e-170
entry: 2HTY chain: D score: 595 E: 1e-170
entry: 2HTY chain: E score: 595 E: 1e-170
entry: 2HTY chain: F score: 595 E: 1e-170
entry: 2HTY chain: G score: 595 E: 1e-170
entry: 2HTY chain: H score: 595 E: 1e-170
entry: 2HU4 chain: A score: 595 E: 1e-170
entry: 2HU4 chain: B score: 595 E: 1e-170
entry: 2HU4 chain: C score: 595 E: 1e-170
entry: 2HU4 chain: D score: 595 E: 1e-170
entry: 2HU4 chain: E score: 595 E: 1e-170
entry: 2HU4 chain: F score: 595 E: 1e-170
entry: 2HU4 chain: G score: 595 E: 1e-170
entry: 2HU4 chain: H score: 595 E: 1e-170
entry: 3CL2 chain: A score: 593 E: 1e-169
entry: 3CL2 chain: B score: 593 E: 1e-169
entry: 3CL2 chain: C score: 593 E: 1e-169
entry: 3CL2 chain: D score: 593 E: 1e-169
entry: 3CL2 chain: E score: 593 E: 1e-169
entry: 3CL2 chain: F score: 593 E: 1e-169
entry: 3CL2 chain: G score: 593 E: 1e-169
entry: 3CL2 chain: H score: 593 E: 1e-169
entry: 3CKZ chain: A score: 592 E: 1e-169
entry: 3CL0 chain: A score: 592 E: 1e-169
entry: 3CYE chain: A score: 585 E: 1e-167
entry: 3CYE chain: B score: 585 E: 1e-167
entry: 3BEQ chain: A score: 585 E: 1e-167
entry: 3BEQ chain: B score: 585 E: 1e-167
entry: 3B7E chain: A score: 585 E: 1e-167
entry: 3B7E chain: B score: 585 E: 1e-167
entry: 2HTV chain: A score: 444 E: 1e-125
entry: 2HTV chain: B score: 444 E: 1e-125
entry: 2HTW chain: A score: 444 E: 1e-125
entry: 2HT5 chain: A score: 370 E: 1e-102
entry: 2HT7 chain: A score: 370 E: 1e-102
entry: 2HT8 chain: A score: 370 E: 1e-102
entry: 2HTQ chain: A score: 370 E: 1e-102
```

```
entry: 2HTR chain: A score: 370 E: 1e-102
entry: 2HTU chain: A score: 370 E: 1e-102
entry: 6NN9 chain: A score: 299 E: 4e-81
entry: 1NNA chain: A score: 298 E: 5e-81
entry: 1NNB chain: A score: 298 E: 5e-81
entry: 1XOG chain: A score: 298 E: 5e-81
entry: 1XOE chain: A score: 298 E: 5e-81
entry: 1A14 chain: N score: 298 E: 5e-81
entry: 1F8C chain: A score: 298 E: 5e-81
entry: 1BJI chain: A score: 298 E: 5e-81
entry: 1F8E chain: A score: 298 E: 5e-81
entry: 1F8D chain: A score: 298 E: 5e-81
entry: 1F8B chain: A score: 298 E: 5e-81
entry: 2C4A chain: A score: 298 E: 5e-81
entry: 2C4L chain: A score: 298 E: 5e-81
entry: 1L7F chain: A score: 298 E: 5e-81
entry: 1MWE chain: A score: 298 E: 5e-81
entry: 1NMC chain: N score: 298 E: 5e-81
entry: 1NMC chain: A score: 298 E: 5e-81
entry: 1NNC chain: A score: 298 E: 5e-81
entry: 7NN9 chain: A score: 298 E: 5e-81
entry: 2QWI chain: A score: 298 E: 5e-81
entry: 2QWJ chain: A score: 298 E: 5e-81
entry: 2QWK chain: A score: 298 E: 5e-81
entry: 1NCA chain: N score: 298 E: 5e-81
entry: 5NN9 chain: A score: 298 E: 7e-81
entry: 3NN9 chain: A score: 297 E: 1e-80
entry: 1L7H chain: A score: 297 E: 1e-80
entry: 2QWA chain: A score: 297 E: 1e-80
entry: 2QWB chain: A score: 297 E: 1e-80
entry: 2QWC chain: A score: 297 E: 1e-80
entry: 2QWD chain: A score: 297 E: 1e-80
entry: 2QWE chain: A score: 297 E: 1e-80
entry: 2QWF chain: A score: 297 E: 1e-80
entry: 2QWG chain: A score: 297 E: 1e-80
entry: 2QWH chain: A score: 297 E: 1e-80
entry: 1NCB chain: N score: 297 E: 1e-80
entry: 1INY chain: A score: 296 E: 2e-80
entry: 1NMA chain: N score: 296 E: 3e-80
entry: 1NCC chain: N score: 296 E: 3e-80
entry: 1NCD chain: N score: 296 E: 3e-80
entry: 4NN9 chain: A score: 296 E: 3e-80
entry: 1NMB chain: N score: 296 E: 3e-80
entry: 1L7G chain: A score: 296 E: 4e-80
entry: 2B8H chain: A score: 295 E: 4e-80
entry: 2B8H chain: B score: 295 E: 4e-80
entry: 2B8H chain: C score: 295 E: 4e-80
entry: 2B8H chain: D score: 295 E: 4e-80
entry: 2CML chain: A score: 289 E: 4e-78
entry: 2CML chain: B score: 289 E: 4e-78
entry: 2CML chain: C score: 289 E: 4e-78
entry: 2CML chain: D score: 289 E: 4e-78
entry: 1V0Z chain: A score: 289 E: 4e-78
entry: 1V0Z chain: B score: 289 E: 4e-78
entry: 1V0Z chain: C score: 289 E: 4e-78
entry: 1V0Z chain: D score: 289 E: 4e-78
entry: 1W20 chain: A score: 289 E: 4e-78
entry: 1W20 chain: B score: 289 E: 4e-78
entry: 1W20 chain: C score: 289 E: 4e-78
entry: 1W20 chain: D score: 289 E: 4e-78
entry: 1W21 chain: A score: 289 E: 4e-78
entry: 1W21 chain: B score: 289 E: 4e-78
entry: 1W21 chain: C score: 289 E: 4e-78
entry: 1W21 chain: D score: 289 E: 4e-78
entry: 1W1X chain: A score: 289 E: 4e-78
entry: 1W1X chain: B score: 289 E: 4e-78
entry: 1W1X chain: C score: 289 E: 4e-78
entry: 1W1X chain: D score: 289 E: 4e-78
entry: 2AEP chain: A score: 286 E: 4e-77
entry: 2AEQ chain: A score: 286 E: 4e-77
entry: 1IVC chain: A score: 281 E: 1e-75
```

```
entry: 1IVC chain: B score: 281 E: 1e-75
entry: 1IVG chain: A score: 281 E: 1e-75
entry: 1IVG chain: B score: 281 E: 1e-75
entry: 1INX chain: A score: 281 E: 1e-75
entry: 1INH chain: A score: 281 E: 1e-75
entry: 1INH chain: B score: 281 E: 1e-75
entry: 1IVE chain: A score: 281 E: 1e-75
entry: 1IVE chain: B score: 281 E: 1e-75
entry: 1INW chain: A score: 281 E: 1e-75
entry: 1IVF chain: A score: 281 E: 1e-75
entry: 1IVF chain: B score: 281 E: 1e-75
entry: 1IVD chain: A score: 281 E: 1e-75
entry: 1IVD chain: B score: 281 E: 1e-75
entry: 1ING chain: A score: 281 E: 1e-75
entry: 1ING chain: B score: 281 E: 1e-75
entry: 2BAT chain: A score: 281 E: 1e-75
entry: 1NN2 chain: A score: 281 E: 1e-75
entry: 1INF chain: A score: 212 E: 5e-55
entry: 1VCJ chain: A score: 212 E: 5e-55
entry: 1B9S chain: A score: 212 E: 5e-55
entry: 1B9T chain: A score: 212 E: 5e-55
entry: 1B9V chain: A score: 212 E: 5e-55
entry: 1INV chain: A score: 212 E: 5e-55
entry: 1IVB chain: A score: 212 E: 5e-55
entry: 1A4G chain: A score: 211 E: 2e-54
entry: 1A4G chain: B score: 211 E: 2e-54
entry: 1A4Q chain: A score: 211 E: 2e-54
entry: 1A4Q chain: B score: 211 E: 2e-54
entry: 1NSB chain: A score: 211 E: 2e-54
entry: 1NSB chain: B score: 211 E: 2e-54
entry: 1NSD chain: A score: 211 E: 2e-54
entry: 1NSD chain: B score: 211 E: 2e-54
entry: 1NSC chain: A score: 211 E: 2e-54
entry: 1NSC chain: B score: 211 E: 2e-54
entry: 1AHP chain: A score: 32 E: 0.90
entry: 1AHP chain: B score: 32 E: 0.90
entry: 2ECP chain: A score: 32 E: 0.92
entry: 2ECP chain: B score: 32 E: 0.92
entry: 2ASV chain: A score: 32 E: 0.96
entry: 2ASV chain: B score: 32 E: 0.96
entry: 2AZD chain: A score: 32 E: 0.96
entry: 2AZD chain: B score: 32 E: 0.96
entry: 2AV6 chain: A score: 32 E: 0.96
entry: 2AV6 chain: B score: 32 E: 0.96
entry: 2AW3 chain: A score: 32 E: 0.96
entry: 2AW3 chain: B score: 32 E: 0.96
entry: 1L5V chain: A score: 32 E: 0.96
entry: 1L5V chain: B score: 32 E: 0.96
entry: 1L5W chain: A score: 32 E: 0.96
entry: 1L5W chain: B score: 32 E: 0.96
entry: 1L6I chain: A score: 32 E: 0.96
entry: 1L6I chain: B score: 32 E: 0.96
entry: 1E4O chain: A score: 32 E: 0.97
entry: 1E4O chain: B score: 32 E: 0.97
entry: 1QM5 chain: A score: 32 E: 0.97
entry: 1QM5 chain: B score: 32 E: 0.97

Round   0. Hits better than threshold: 0.000010:
entry: 2HU0 chain: A score: 595 E: 1e-170
entry: 2HU0 chain: B score: 595 E: 1e-170
entry: 2HU0 chain: C score: 595 E: 1e-170
entry: 2HU0 chain: D score: 595 E: 1e-170
entry: 2HU0 chain: E score: 595 E: 1e-170
entry: 2HU0 chain: F score: 595 E: 1e-170
entry: 2HU0 chain: G score: 595 E: 1e-170
entry: 2HU0 chain: H score: 595 E: 1e-170
entry: 2HTY chain: A score: 595 E: 1e-170
entry: 2HTY chain: B score: 595 E: 1e-170
entry: 2HTY chain: C score: 595 E: 1e-170
entry: 2HTY chain: D score: 595 E: 1e-170
entry: 2HTY chain: E score: 595 E: 1e-170
```

```
entry: 2HTY chain: F score: 595 E: 1e-170
entry: 2HTY chain: G score: 595 E: 1e-170
entry: 2HTY chain: H score: 595 E: 1e-170
entry: 2HU4 chain: A score: 595 E: 1e-170
entry: 2HU4 chain: B score: 595 E: 1e-170
entry: 2HU4 chain: C score: 595 E: 1e-170
entry: 2HU4 chain: D score: 595 E: 1e-170
entry: 2HU4 chain: E score: 595 E: 1e-170
entry: 2HU4 chain: F score: 595 E: 1e-170
entry: 2HU4 chain: G score: 595 E: 1e-170
entry: 2HU4 chain: H score: 595 E: 1e-170
entry: 3CL2 chain: A score: 593 E: 1e-169
entry: 3CL2 chain: B score: 593 E: 1e-169
entry: 3CL2 chain: C score: 593 E: 1e-169
entry: 3CL2 chain: D score: 593 E: 1e-169
entry: 3CL2 chain: E score: 593 E: 1e-169
entry: 3CL2 chain: F score: 593 E: 1e-169
entry: 3CL2 chain: G score: 593 E: 1e-169
entry: 3CL2 chain: H score: 593 E: 1e-169
entry: 3CKZ chain: A score: 592 E: 1e-169
entry: 3CL0 chain: A score: 592 E: 1e-169
entry: 3CYE chain: A score: 585 E: 1e-167
entry: 3CYE chain: B score: 585 E: 1e-167
entry: 3BEQ chain: A score: 585 E: 1e-167
entry: 3BEQ chain: B score: 585 E: 1e-167
entry: 3B7E chain: A score: 585 E: 1e-167
entry: 3B7E chain: B score: 585 E: 1e-167
entry: 2HTV chain: A score: 444 E: 1e-125
entry: 2HTV chain: B score: 444 E: 1e-125
entry: 2HTW chain: A score: 444 E: 1e-125
entry: 2HT5 chain: A score: 370 E: 1e-102
entry: 2HT7 chain: A score: 370 E: 1e-102
entry: 2HT8 chain: A score: 370 E: 1e-102
entry: 2HTQ chain: A score: 370 E: 1e-102
entry: 2HTR chain: A score: 370 E: 1e-102
entry: 2HTU chain: A score: 370 E: 1e-102
entry: 6NN9 chain: A score: 299 E: 4e-81
entry: 1NNA chain: A score: 298 E: 5e-81
entry: 1NNB chain: A score: 298 E: 5e-81
entry: 1XOG chain: A score: 298 E: 5e-81
entry: 1XOE chain: A score: 298 E: 5e-81
entry: 1A14 chain: N score: 298 E: 5e-81
entry: 1F8C chain: A score: 298 E: 5e-81
entry: 1BJI chain: A score: 298 E: 5e-81
entry: 1F8E chain: A score: 298 E: 5e-81
entry: 1F8D chain: A score: 298 E: 5e-81
entry: 1F8B chain: A score: 298 E: 5e-81
entry: 2C4A chain: A score: 298 E: 5e-81
entry: 2C4L chain: A score: 298 E: 5e-81
entry: 1L7F chain: A score: 298 E: 5e-81
entry: 1MWE chain: A score: 298 E: 5e-81
entry: 1NMC chain: N score: 298 E: 5e-81
entry: 1NMC chain: A score: 298 E: 5e-81
entry: 1NNC chain: A score: 298 E: 5e-81
entry: 7NN9 chain: A score: 298 E: 5e-81
entry: 2QWI chain: A score: 298 E: 5e-81
entry: 2QWJ chain: A score: 298 E: 5e-81
entry: 2QWK chain: A score: 298 E: 5e-81
entry: 1NCA chain: N score: 298 E: 5e-81
entry: 5NN9 chain: A score: 298 E: 7e-81
entry: 3NN9 chain: A score: 297 E: 1e-80
entry: 1L7H chain: A score: 297 E: 1e-80
entry: 2QWA chain: A score: 297 E: 1e-80
entry: 2QWB chain: A score: 297 E: 1e-80
entry: 2QWC chain: A score: 297 E: 1e-80
entry: 2QWD chain: A score: 297 E: 1e-80
entry: 2QWE chain: A score: 297 E: 1e-80
entry: 2QWF chain: A score: 297 E: 1e-80
entry: 2QWG chain: A score: 297 E: 1e-80
entry: 2QWH chain: A score: 297 E: 1e-80
entry: 1NCB chain: N score: 297 E: 1e-80
```

```
entry: 1INY chain: A score: 296 E: 2e-80
entry: 1NMA chain: N score: 296 E: 3e-80
entry: 1NCC chain: N score: 296 E: 3e-80
entry: 1NCD chain: N score: 296 E: 3e-80
entry: 4NN9 chain: A score: 296 E: 3e-80
entry: 1NMB chain: N score: 296 E: 3e-80
entry: 1L7G chain: A score: 296 E: 4e-80
entry: 2B8H chain: A score: 295 E: 4e-80
entry: 2B8H chain: B score: 295 E: 4e-80
entry: 2B8H chain: C score: 295 E: 4e-80
entry: 2B8H chain: D score: 295 E: 4e-80
entry: 2CML chain: A score: 289 E: 4e-78
entry: 2CML chain: B score: 289 E: 4e-78
entry: 2CML chain: C score: 289 E: 4e-78
entry: 2CML chain: D score: 289 E: 4e-78
entry: 1V0Z chain: A score: 289 E: 4e-78
entry: 1V0Z chain: B score: 289 E: 4e-78
entry: 1V0Z chain: C score: 289 E: 4e-78
entry: 1V0Z chain: D score: 289 E: 4e-78
entry: 1W20 chain: A score: 289 E: 4e-78
entry: 1W20 chain: B score: 289 E: 4e-78
entry: 1W20 chain: C score: 289 E: 4e-78
entry: 1W20 chain: D score: 289 E: 4e-78
entry: 1W21 chain: A score: 289 E: 4e-78
entry: 1W21 chain: B score: 289 E: 4e-78
entry: 1W21 chain: C score: 289 E: 4e-78
entry: 1W21 chain: D score: 289 E: 4e-78
entry: 1W1X chain: A score: 289 E: 4e-78
entry: 1W1X chain: B score: 289 E: 4e-78
entry: 1W1X chain: C score: 289 E: 4e-78
entry: 1W1X chain: D score: 289 E: 4e-78
entry: 2AEP chain: A score: 286 E: 4e-77
entry: 2AEQ chain: A score: 286 E: 4e-77
entry: 1IVC chain: A score: 281 E: 1e-75
entry: 1IVC chain: B score: 281 E: 1e-75
entry: 1IVG chain: A score: 281 E: 1e-75
entry: 1IVG chain: B score: 281 E: 1e-75
entry: 1INX chain: A score: 281 E: 1e-75
entry: 1INH chain: A score: 281 E: 1e-75
entry: 1INH chain: B score: 281 E: 1e-75
entry: 1IVE chain: A score: 281 E: 1e-75
entry: 1IVE chain: B score: 281 E: 1e-75
entry: 1INW chain: A score: 281 E: 1e-75
entry: 1IVF chain: A score: 281 E: 1e-75
entry: 1IVF chain: B score: 281 E: 1e-75
entry: 1IVD chain: A score: 281 E: 1e-75
entry: 1IVD chain: B score: 281 E: 1e-75
entry: 1ING chain: A score: 281 E: 1e-75
entry: 1ING chain: B score: 281 E: 1e-75
entry: 2BAT chain: A score: 281 E: 1e-75
entry: 1NN2 chain: A score: 281 E: 1e-75
entry: 1INF chain: A score: 212 E: 5e-55
entry: 1VCJ chain: A score: 212 E: 5e-55
entry: 1B9S chain: A score: 212 E: 5e-55
entry: 1B9T chain: A score: 212 E: 5e-55
entry: 1B9V chain: A score: 212 E: 5e-55
entry: 1INV chain: A score: 212 E: 5e-55
entry: 1IVB chain: A score: 212 E: 5e-55
entry: 1A4G chain: A score: 211 E: 2e-54
entry: 1A4G chain: B score: 211 E: 2e-54
entry: 1A4Q chain: A score: 211 E: 2e-54
entry: 1A4Q chain: B score: 211 E: 2e-54
entry: 1NSB chain: A score: 211 E: 2e-54
entry: 1NSB chain: B score: 211 E: 2e-54
entry: 1NSD chain: A score: 211 E: 2e-54
entry: 1NSD chain: B score: 211 E: 2e-54
entry: 1NSC chain: A score: 211 E: 2e-54
entry: 1NSC chain: B score: 211 E: 2e-54

Retrieving template ...
```

```
Entry: 2hty
Chain: A

Making profile-profile alignment ...

Score:     794.0 bits
Identity:   90.6 %

Query: 1   VKLAGNSSLCPVSGWAIYSKDNSVRIGSKGDVFVIREPFISCSPLECRTFFLTQGALLND 60
           VKLAGNSSLCP++GWA+YSKDNS+RIGSKGDVFVIREPFISCS LECRTFFLTQGALLND
Templ: 1   VKLAGNSSLCPINGWAVYSKDNSIRIGSKGDVFVIREPFISCSHLECRTFFLTQGALLND 60

Query: 61  KHSNGTIKDRSPYRTLMSCPIGEVPSPYNSRFESVAWSASACHDGINWLTIGISGPDNGA 120
           KHSNGT+KDRSP+RTLMSCP+GE PSPYNSRFESVAWSASACHDG +WLTIGISGPDNGA
Templ: 61  KHSNGTVKDRSPHRTLMSCPVGEAPSPYNSRFESVAWSASACHDGTSWLTIGISGPDNGA 120

Query: 121 VAVLKYNGIITDTIKSWRNNILRTQESECACVNGSCFTVMTDGPSNGQASYKIFRIEKGK 180
           VAVLKYNGIITDTIKSWRNNILRTQESECACVNGSCFTVMTDGPSNGQASYKIF++EKGK
Templ: 121 VAVLKYNGIITDTIKSWRNNILRTQESECACVNGSCFTVMTDGPSNGQASYKIFKMEKGK 180

Query: 181 IVKSVEMNAPNYHYEECSCYPDSSEITCVCRDNWHGSNRPWVSFNQNLEYQIGYICSGIF 240
           +VKSVE++APNYHYEECSCYP++ EITCVCRDNWHGSNRPWVSFNQNLEYQIGYICSG+F
Templ: 181 VVKSVELDAPNYHYEECSCYPNAGEITCVCRDNWHGSNRPWVSFNQNLEYQIGYICSGVF 240

Query: 241 GDNPRPNDKTGSCGPVSSNGANGVKGFSFKYGNGVWIGRTKSISSRNGFEMIWDPNGWTG 300
           GDNPRPND TGSCGPVSSNGA GVKGFSFKYGNGVWIGRTKS +SR+GFEMIWDPNGWT
Templ: 241 GDNPRPNDGTGSCGPVSSNGAYGVKGFSFKYGNGVWIGRTKSTNSRSGFEMIWDPNGWTE 300

Query: 301 TDNNFSIK 308
           TD++FS+K
Templ: 301 TDSSFSVK 308
```

3. M2 Host Human

CPHmodels-3.0 Server - prediction results

Technical University of Denmark

```
Query sequence:

>gi_229783371_gb_ACQ84453.1_
MSLLTEVETPTRSEWECRCSDSSDPLVIAANIIGILHLILWITDRLFFKCIYRRFKYGLK
RGPSTEGVPESMREEYQQEQQSAVDVDDGHFVNIELE

Searching for template ...

Round   0. All hits:
entry: 2KIH chain: A score: 69 E: 1e-12
entry: 2KIH chain: B score: 69 E: 1e-12
entry: 2KIH chain: C score: 69 E: 1e-12
entry: 2KIH chain: D score: 69 E: 1e-12
entry: 2RLF chain: A score: 67 E: 6e-12
entry: 2RLF chain: B score: 67 E: 6e-12
entry: 2RLF chain: C score: 67 E: 6e-12
entry: 2RLF chain: D score: 67 E: 6e-12
entry: 1MP6 chain: A score: 50 E: 7e-07
entry: 1NYJ chain: A score: 50 E: 7e-07
entry: 1NYJ chain: B score: 50 E: 7e-07
entry: 1NYJ chain: C score: 50 E: 7e-07
```

```
entry: 1NYJ chain: D score: 50 E: 7e-07
entry: 2KAD chain: A score: 48 E: 3e-06
entry: 2KAD chain: B score: 48 E: 3e-06
entry: 2KAD chain: C score: 48 E: 3e-06
entry: 2KAD chain: D score: 48 E: 3e-06
entry: 3C9J chain: A score: 47 E: 4e-06
entry: 3C9J chain: B score: 47 E: 4e-06
entry: 3C9J chain: C score: 47 E: 4e-06
entry: 3C9J chain: D score: 47 E: 4e-06
entry: 3BKD chain: A score: 44 E: 6e-05
entry: 3BKD chain: B score: 44 E: 6e-05
entry: 3BKD chain: C score: 44 E: 6e-05
entry: 3BKD chain: D score: 44 E: 6e-05
entry: 3BKD chain: E score: 44 E: 6e-05
entry: 3BKD chain: F score: 44 E: 6e-05
entry: 3BKD chain: G score: 44 E: 6e-05
entry: 3BKD chain: H score: 44 E: 6e-05
entry: 2H95 chain: A score: 35 E: 0.015
entry: 2H95 chain: B score: 35 E: 0.015
entry: 2H95 chain: C score: 35 E: 0.015
entry: 2H95 chain: D score: 35 E: 0.015
entry: 3BHN chain: A score: 28 E: 2.2

Round   0. Hits better than threshold: 0.000010:
entry: 2KIH chain: A score: 69 E: 1e-12
entry: 2KIH chain: B score: 69 E: 1e-12
entry: 2KIH chain: C score: 69 E: 1e-12
entry: 2KIH chain: D score: 69 E: 1e-12
entry: 2RLF chain: A score: 67 E: 6e-12
entry: 2RLF chain: B score: 67 E: 6e-12
entry: 2RLF chain: C score: 67 E: 6e-12
entry: 2RLF chain: D score: 67 E: 6e-12
entry: 1MP6 chain: A score: 50 E: 7e-07
entry: 1NYJ chain: A score: 50 E: 7e-07
entry: 1NYJ chain: B score: 50 E: 7e-07
entry: 1NYJ chain: C score: 50 E: 7e-07
entry: 1NYJ chain: D score: 50 E: 7e-07
entry: 2KAD chain: A score: 48 E: 3e-06
entry: 2KAD chain: B score: 48 E: 3e-06
entry: 2KAD chain: C score: 48 E: 3e-06
entry: 2KAD chain: D score: 48 E: 3e-06
entry: 3C9J chain: A score: 47 E: 4e-06
entry: 3C9J chain: B score: 47 E: 4e-06
entry: 3C9J chain: C score: 47 E: 4e-06
entry: 3C9J chain: D score: 47 E: 4e-06

Retrieving template ...

Entry: 2kih
Chain: A

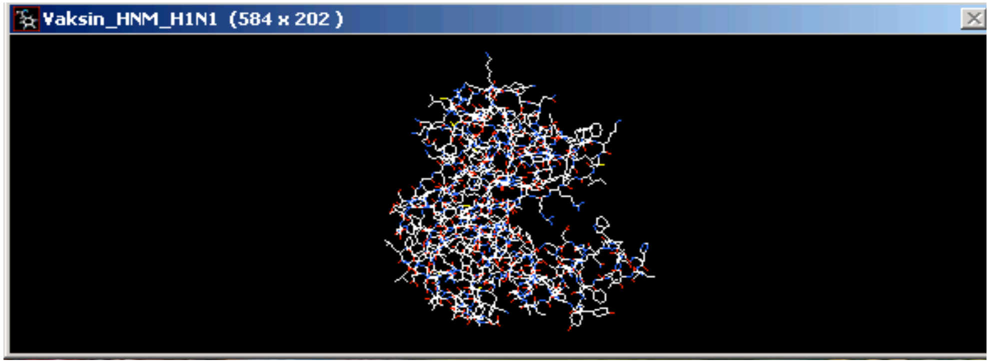
Making profile-profile alignment ...

Score:      83.0 bits
Identity:   84.2 %

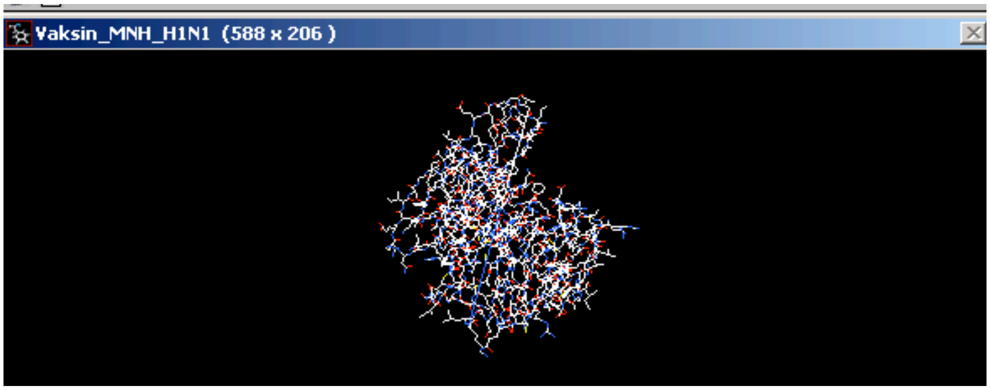
Query: 1   SDPLVIAANIIGILHLILWITDRLFFKCIYRRFKYGLK 38
           SDPLV+AANIIGILHLILWI DRLFFK IYR F++GLK
Templ: 1   SDPLVVAANIIGILHLILWILDRLFFKSIYRFFEHGLK 38
```

Lampiran 10. Visualisasi Vaksin Berdasarkan Template Menggunakan Software spdv

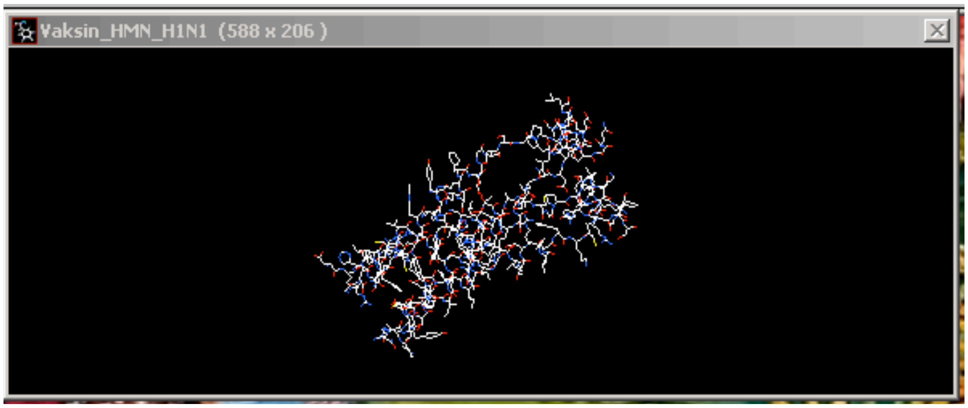
1. Vaksin HNM_H1N1



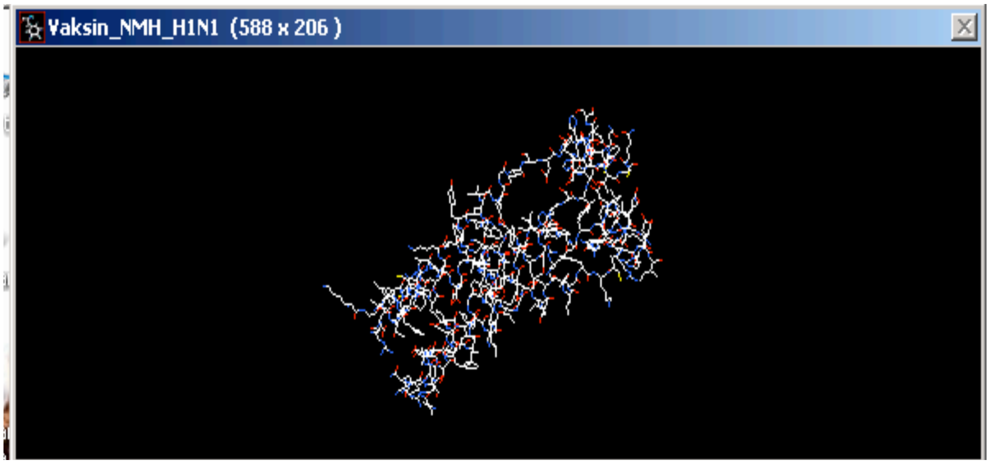
2. Vaksin MNH_H1N1



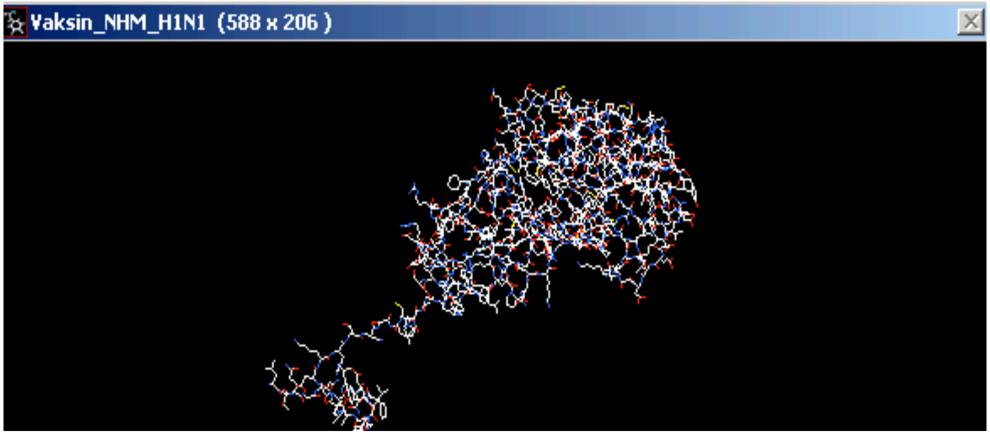
3. Vaksin HMN_H1N1



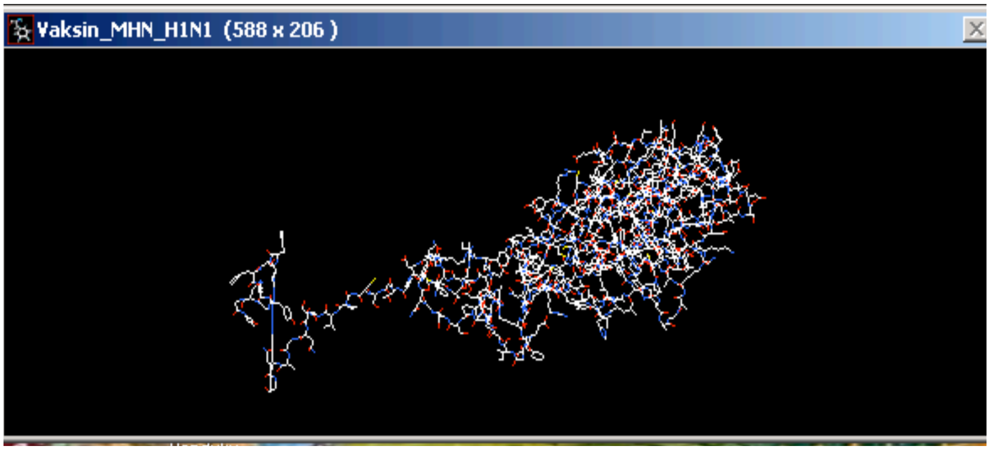
4. Vaksin NMH_H1N1



5. Vaksin NHM_HN1



6. Vaksin MHN_H1N1



Lampiran 11. Hasil *Homology Modelling* Kandidat Vaksin Pada *Server* FeatureMap3D

1. Vaksin HNM

```
Query : Vaksin__HNM.6.1 (278 aa)
Hit   : 3CKZ (molecule: NEURAMINIDASE;) (chain: a) (resolution: 1.90 ANGSTROMS.)
        Organism: INFLUENZA A VIRUS


    182 YICSGIFGDFGDNPRPNDKTGSCGPVSSNGANGV--FSFKYGNGV 224
        |||||:|||   |||||| |||||||||||| ||  |||||||||
    316 YICSGVFGD---NPRPNDGTGSCGPVSSNGAYGVKGFSFKYGNGV 360
        E   SS  S   SS   S    SS   TT SS      EEEETTEE
```

2. Vaksin MNH

```
Query : Vaksin_MNH.6.1 (279 aa)
Hit   : 3CKZ (molecule: NEURAMINIDASE;) (chain: a) (resolution: 1.90 ANGSTROMS.)
        Organism: INFLUENZA A VIRUS


    116 YICSGIFGDFGDNPRPNDKTGSCGPVSSNGANGV--FSFKYGNGV 158
        |||||:|||   |||||| |||||||||||| ||  |||||||||
    316 YICSGVFGD---NPRPNDGTGSCGPVSSNGAYGVKGFSFKYGNGV 360
        E   SS  S   SS   S    SS   TT SS      EEEETTEE
```

3. Vaksin HMN

```
Query : Vaksin_HMN.6.1 (279 aa)
Hit   : 3CKZ (molecule: NEURAMINIDASE;) (chain: a) (resolution: 1.90 ANGSTROMS.)
        Organism: INFLUENZA A VIRUS


    237 YICSGIFGDFGDNPRPNDKTGSCGPVSSNGANGV--FSFKYGNGV 279
        |||||:|||   |||||| |||||||||||| ||  |||||||||
    316 YICSGVFGD---NPRPNDGTGSCGPVSSNGAYGVKGFSFKYGNGV 360
        E   SS  S   SS   S    SS   TT SS      EEEETTEE
```

4. Vaksin NMH

```
Query : Vaksin_NHM.6.1 (279 aa)
Hit   : 3CKZ (molecule: NEURAMINIDASE;) (chain: a) (resolution: 1.90 ANGSTROMS.)
        Organism: INFLUENZA A VIRUS


     61 YICSGIFGDFGDNPRPNDKTGSCGPVSSNGANGV--FSFKYGNGV 103
        |||||:|||   |||||| |||||||||||| ||  |||||||||
```

```
    316 YICSGVFGD---NPRPNDGTGSCGPVSSNGAYGVKGFSFKYGNGV 360
        E   SS  S   SS   S    SS   TT SS     EEEETTEE
```

5. Vaksin NHM

```
Query : Vaksin_NHM.6.1 (279 aa)
Hit   : 3CKZ (molecule: NEURAMINIDASE;) (chain: a) (resolution: 1.90 ANGSTROMS.)
        Organism: INFLUENZA A VIRUS


     61 YICSGIFGDFGDNPRPNDKTGSCGPVSSNGANGV--FSFKYGNGV 103
        |||||:|||   |||||| |||||||||||| ||  |||||||||
    316 YICSGVFGD---NPRPNDGTGSCGPVSSNGAYGVKGFSFKYGNGV 360
        E   SS  S   SS   S    SS   TT SS     EEEETTEE
```

6. Vaksin MHN

```
Query : Vaksin_MHN.6.1 (279 aa)
Hit   : 3CKZ (molecule: NEURAMINIDASE;) (chain: a) (resolution: 1.90 ANGSTROMS.)
        Organism: INFLUENZA A VIRUS


    237 YICSGIFGDFGDNPRPNDKTGSCGPVSSNGANGV--FSFKYGNGV 279
        |||||:|||   |||||| |||||||||||| ||  |||||||||
    316 YICSGVFGD---NPRPNDGTGSCGPVSSNGAYGVKGFSFKYGNGV 360
        E   SS  S   SS   S    SS   TT SS     EEEETTEE
```