

LAMPIRAN A

Jenis dan Singkatan Asam amino penyusun protein/Enzim

<p style="text-align: center;"><i>Asam amino alifatik sederhana</i></p> <p><u>Glisin</u> (Gly, G)</p> <p><u>Alanin</u> (Ala, A)</p> <p><u>Valin</u> (Val, V)</p> <p><u>Leusin</u> (Leu, L)</p> <p><u>Isoleusin</u> (Ile, I)</p>	<p style="text-align: center;"><i>Asam amino hidroksi-alifatik</i></p> <p><u>Serin</u> (Ser, S)</p> <p><u>Treonin</u> (Thr, T)</p>	<p style="text-align: center;"><i>Asam amino dikarboksilat (asam)</i></p> <p><u>Asam aspartat</u> (Asp, D)</p> <p><u>Asam glutamat</u> (Glu, E)</p>	<p style="text-align: center;"><i>Amida</i></p> <p><u>Asparagin</u> (Asn, N)</p>
<p style="text-align: center;"><i>Asam amino basa</i></p> <p><u>Lisin</u> (Lys, K)</p> <p><u>Arginin</u> (Arg, R)</p> <p><u>Histidin</u> (His, H) (memiliki gugus siklik)</p>	<p style="text-align: center;"><i>Asam amino dengan sulfur</i></p> <p><u>Sistein</u> (Cys, C)</p> <p><u>Metionin</u> (Met, M)</p>	<p style="text-align: center;"><i>Prolin</i></p> <p><u>Prolin</u> (Pro, P) (memiliki gugus siklik)</p>	<p style="text-align: center;"><i>Asam amino aromatik</i></p> <p><u>Fenilalanin</u> (Phe, F)</p> <p><u>Tirosin</u> (Tyr, Y)</p> <p><u>Triptofan</u> (Trp, W)</p>





LAMPIRAN B

DATA SET SEQUENCE PROTEIN DARI NCBI

Data Sequence Protein Shble

LOCUS 2104260B 122 aa linear BCT 10-JUL-1992
DEFINITION bleomycin-binding protein.
ACCESSION 2104260B
VERSION 2104260B GI:1093569
DBSOURCE prf: locus 2104260B;
state: osteosarcoma;
taxonomy: Prokaryota.
KEYWORDS blmA/blmB Gene; Streptomyces verticillus; Mol Cloning; Seq
Determination; Acc.No.L26955; 663/1019bp; 122/301AAs; Bleomycin
Binding Protein; Bleomycin Acetyltransferase; Expression in E.coli;
Resistance Marker in Gene Transfer.
SOURCE Streptomyces verticillus
ORGANISM [Streptomyces verticillus](#)
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Streptomycineae; Streptomycetaceae; Streptomyces.
REFERENCE 1 (residues 1 to 122)
AUTHORS Sugiyama,M., Thompson,C.J., Kumagai,T., Suzuki,K., Deblaere,R.,
Villarroel,R. and Davies,J.
TITLE Characterisation by molecular cloning of two genes from
Streptomyces verticillus encoding resistance to bleomycin
JOURNAL Gene 151(1/2), 11-16 (1994)
COMMENT EC=1.1.99.5:GENE=blmA.
FEATURES Location/Qualifiers
source 1..122
/organism="Streptomyces verticillus"
/db_xref="taxon:[29309](#)"
ORIGIN

1 mvkflgavpv ltavdvpanv sfwvdtlgfe kdfgdrdfag vrrgdirhli srtehqvad
61 ntsawievtd pdalheewar avstadyadts gpamtpvges pagrefavrd pagncvvhfta
121 ge

Data Sequence Protein Dmeh

LOCUS NP_725059 552 aa linear INV 04-November-2008
DEFINITION engrailed CG9015-PB, isoform B [Drosophila melanogaster].
ACCESSION NP_725059
VERSION NP_725059.1 GI:24652772
DBSOURCE REFSEQ: accession [NM_165841.1](#)
KEYWORDS .
SOURCE Drosophila melanogaster (fruit fly)
ORGANISM [Drosophila melanogaster](#)
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila; Sophophora.
REFERENCE 1 (residues 1 to 552)
AUTHORS Hoskins,R.A., Carlson,J.W., Kennedy,C., Acevedo,D., Evans-Holm,M.,
Frise,E., Wan,K.H., Park,S., Mendez-Lago,M., Rossi,F.,
Villasante,A., Dimitri,P., Karpen,G.H. and Celniker,S.E.
TITLE Sequence Finishing and Mapping of Drosophila melanogaster
Heterochromatin
JOURNAL Science 316 (5831), 1625-1628 (2007)
PUBMED [17569867](#)
REFERENCE 2 (residues 1 to 552)
AUTHORS Smith,C.D., Shu,S., Mungall,C.J. and Karpen,G.H.
TITLE The Release 5.1 Annotation of Drosophila melanogaster
Heterochromatin

JOURNAL Science 316 (5831), 1586-1591 (2007)
 PUBMED [17569856](#)

REFERENCE 3 (residues 1 to 552)
 AUTHORS Quesneville,H., Bergman,C.M., Andrieu,O., Autard,D., Nouaud,D.,
 Ashburner,M. and Anxolabehere,D.
 TITLE Combined evidence annotation of transposable elements in genome
 sequences

JOURNAL PLoS Comput. Biol. 1 (2), e22 (2005)
 PUBMED [16110336](#)

REFERENCE 4 (residues 1 to 552)
 AUTHORS Hoskins,R.A., Smith,C.D., Carlson,J.W., de Carvalho,A.B.,
 Halpern,A., Kaminker,J.S., Kennedy,C., Mungall,C.J., Sullivan,B.A.,
 Sutton,G.G., Yasuhara,J.C., Wakimoto,B.T., Myers,E.W.,
 Celniker,S.E., Rubin,G.M. and Karpen,G.H.
 TITLE Heterochromatic sequences in a Drosophila whole-genome shotgun
 assembly

JOURNAL Genome Biology 3 (12), RESEARCH0085 (2002)
 PUBMED [12537574](#)

REFERENCE 5 (residues 1 to 552)
 AUTHORS Kaminker,J.S., Bergman,C.M., Kronmiller,B., Carlson,J.,
 Svirskas,R., Patel,S., Frise,E., Wheeler,D.A., Lewis,S.E.,
 Rubin,G.M., Ashburner,M. and Celniker,S.E.
 TITLE The transposable elements of the Drosophila melanogaster
 euchromatin: a genomics perspective

JOURNAL Genome Biol. 3 (12), RESEARCH0084 (2002)
 PUBMED [12537573](#)

REFERENCE 6 (residues 1 to 552)
 AUTHORS Misra,S., Crosby,M.A., Mungall,C.J., Matthews,B.B., Campbell,K.S.,
 Hradecky,P., Huang,Y., Kaminker,J.S., Millburn,G.H., Prochnik,S.E.,
 Smith,C.D., Tupy,J.L., Whitfield,E.J., Bayraktaroglu,L.,

Berman,B.P., Bettencourt,B.R., Celniker,S.E., de Grey,A.D., Drysdale,R.A., Harris,N.L., Richter,J., Russo,S., Schroeder,A.J., Shu,S.Q., Stapleton,M., Yamada,C., Ashburner,M., Gelbart,W.M., Rubin,G.M. and Lewis,S.E.

TITLE Annotation of the *Drosophila melanogaster* euchromatic genome: a systematic review

JOURNAL Genome Biol. 3 (12), RESEARCH0083 (2002)

PUBMED [12537572](#)

REFERENCE 7 (residues 1 to 552)

AUTHORS Celniker,S.E., Wheeler,D.A., Kronmiller,B., Carlson,J.W., Halpern,A., Patel,S., Adams,M., Champe,M., Dugan,S.P., Frise,E., Hodgson,A., George,R.A., Hoskins,R.A., Lavery,T., Muzny,D.M., Nelson,C.R., Pacleb,J.M., Park,S., Pfeiffer,B.D., Richards,S., Sodergren,E.J., Svirskas,R., Tabor,P.E., Wan,K., Stapleton,M., Sutton,G.G., Venter,C., Weinstock,G., Scherer,S.E., Myers,E.W., Gibbs,R.A. and Rubin,G.M.

TITLE Finishing a whole-genome shotgun: release 3 of the *Drosophila melanogaster* euchromatic genome sequence

JOURNAL Genome Biol. 3 (12), RESEARCH0079 (2002)

PUBMED [12537568](#)

REFERENCE 8 (residues 1 to 552)

AUTHORS Adams,M.D., Celniker,S.E., Holt,R.A., Evans,C.A., Gocayne,J.D., Amanatides,P.G., Scherer,S.E., Li,P.W., Hoskins,R.A., Galle,R.F., George,R.A., Lewis,S.E., Richards,S., Ashburner,M., Henderson,S.N., Sutton,G.G., Wortman,J.R., Yandell,M.D., Zhang,Q., Chen,L.X., Brandon,R.C., Rogers,Y.H., Blazej,R.G., Champe,M., Pfeiffer,B.D., Wan,K.H., Doyle,C., Baxter,E.G., Helt,G., Nelson,C.R., Gabor,G.L., Abril,J.F., Agbayani,A., An,H.J., Andrews-Pfannkoch,C., Baldwin,D., Ballew,R.M., Basu,A., Baxendale,J., Bayraktaroglu,L., Beasley,E.M., Beeson,K.Y., Benos,P.V., Berman,B.P., Bhandari,D., Bolshakov,S.,

Borkova,D., Botchan,M.R., Bouck,J., Brokstein,P., Brottier,P.,
Burtis,K.C., Busam,D.A., Butler,H., Cadieu,E., Center,A.,
Chandra,I., Cherry,J.M., Cawley,S., Dahlke,C., Davenport,L.B.,
Davies,P., de Pablos,B., Delcher,A., Deng,Z., Mays,A.D., Dew,I.,
Dietz,S.M., Dodson,K., Doup,L.E., Downes,M., Dugan-Rocha,S.,
Dunkov,B.C., Dunn,P., Durbin,K.J., Evangelista,C.C., Ferraz,C.,
Ferriera,S., Fleischmann,W., Fosler,C., Gabrielian,A.E., Garg,N.S.,
Gelbart,W.M., Glasser,K., Glodek,A., Gong,F., Gorrell,J.H., Gu,Z.,
Guan,P., Harris,M., Harris,N.L., Harvey,D., Heiman,T.J.,
Hernandez,J.R., Houck,J., Hostin,D., Houston,K.A., Howland,T.J.,
Wei,M.H., Ibegwam,C., Jalali,M., Kalush,F., Karpen,G.H., Ke,Z.,
Kennison,J.A., Ketchum,K.A., Kimmel,B.E., Kodira,C.D., Kraft,C.,
Kravitz,S., Kulp,D., Lai,Z., Lasko,P., Lei,Y., Levitsky,A.A.,
Li,J., Li,Z., Liang,Y., Lin,X., Liu,X., Mattei,B., McIntosh,T.C.,
McLeod,M.P., McPherson,D., Merkulov,G., Milshina,N.V., Mobarry,C.,
Morris,J., Moshrefi,A., Mount,S.M., Moy,M., Murphy,B., Murphy,L.,
Muzny,D.M., Nelson,D.L., Nelson,D.R., Nelson,K.A., Nixon,K.,
Nusskern,D.R., Pacleb,J.M., Palazzolo,M., Pittman,G.S., Pan,S.,
Pollard,J., Puri,V., Reese,M.G., Reinert,K., Remington,K.,
Saunders,R.D., Scheeler,F., Shen,H., Shue,B.C., Siden-Kiamos,I.,
Simpson,M., Skupski,M.P., Smith,T., Spier,E., Spradling,A.C.,
Stapleton,M., Strong,R., Sun,E., Svirskas,R., Tector,C., Turner,R.,
Venter,E., Wang,A.H., Wang,X., Wang,Z.Y., Wassarman,D.A.,
Weinstock,G.M., Weissenbach,J., Williams,S.M., WoodageT,
Worley,K.C., Wu,D., Yang,S., Yao,Q.A., Ye,J., Yeh,R.F.,
Zaveri,J.S., Zhan,M., Zhang,G., Zhao,Q., Zheng,L., Zheng,X.H.,
Zhong,F.N., Zhong,W., Zhou,X., Zhu,S., Zhu,X., Smith,H.O.,
Gibbs,R.A., Myers,E.W., Rubin,G.M. and Venter,J.C.

TITLE The genome sequence of *Drosophila melanogaster*
JOURNAL Science 287 (5461), 2185-2195 (2000)

PUBMED [10731132](#)
 REFERENCE 9 (residues 1 to 552)
 AUTHORS Celniker,S., Carlson,J., Wan,K., Pfeiffer,B., Frise,E., George,R.,
 Hoskins,R., Stapleton,M., Pacleb,J., Park,S., Svirskas,R.,
 Smith,E., Yu,C. and Rubin,G.
 CONSRTM Berkeley Drosophila Genome Project
 TITLE Drosophila melanogaster release 4 sequence
 JOURNAL Unpublished
 REFERENCE 10 (residues 1 to 552)
 AUTHORS Celniker,S., Carlson,J., Kennedy,C., Wan,K., Frise,E., Hoskins,R.,
 Park,S., Svirskas,R. and Karpen,G.
 TITLE Direct Submission
 JOURNAL Submitted (10-AUG-2006) Berkeley Drosophila Genome Project,
 Lawrence Berkeley National Laboratory, One #Cyclotron RoadOne
 Cyclotron Road, MS 64-121, Berkeley, CA 94720, USA
 REMARK Direct Submission
 REFERENCE 11 (residues 1 to 552)
 AUTHORS Celniker,S., Carlson,J., Wan,K., Frise,E., Hoskins,R., Park,S.,
 Svirskas,R. and Rubin,G.
 TITLE Direct Submission
 JOURNAL Submitted (10-AUG-2006) Berkeley Drosophila Genome Project,
 Lawrence Berkeley National Laboratory, One Cyclotron Road, MS
 64-121, Berkeley, CA 94720, USA
 REMARK Direct Submission
 REFERENCE 12 (residues 1 to 552)
 AUTHORS Smith,C.D., Shu,S., Yandell,M.D. and Karpen,G.H.
 CONSRTM Drosophila Heterochromatin Genome Project
 TITLE Direct Submission
 JOURNAL Submitted (01-AUG-2006) Drosophila Heterochromatin Genome Project,
 Ernest Orlando Lawrence Berkeley National Laboratory, 1 Cyclotron

Road, Mailstop 64-121, Berkeley, CA 94720, USA

REFERENCE 13 (residues 1 to 552)

AUTHORS Adams,M.D., Celniker,S.E., Gibbs,R.A., Rubin,G.M. and Venter,C.J.

TITLE Direct Submission

JOURNAL Submitted (21-MAR-2000) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA

COMMENT REVIEWED [REFSEQ](#): This record has been curated by FlyBase. The reference sequence was derived from [AAM68711](#).
Method: conceptual translation.

FEATURES Location/Qualifiers

source 1..552
/organism="Drosophila melanogaster"
/db_xref="taxon:[7227](#)"
/chromosome="2R"
/map="2-62.0"

[Protein](#) 1..552
/product="engrailed CG9015-PB, isoform B"
/name="CG9015 gene product from transcript CG9015-RB"
/note="Apigmented abdomen; Erased; spermatheca; transcript group V"
/calculated_mol_wt=59280

[Region](#) 455..512
/region_name="homeodomain"
/note="Homeodomain; DNA binding domains involved in the transcriptional regulation of key eukaryotic developmental processes; may bind to DNA as monomers or as homo- and/or heterodimers, in a sequence-specific manner; cd00086"
/db_xref="CDD:[28970](#)"

[Site](#) order(455..459,461,478,484,497,499..500,503..504,506..508,510..511)

Site

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/db_xref="CDD:28970"  
order(457,460,500,503..504,507)  
/site_type="other"  
/note="specific DNA base contacts"
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CDS

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1..552  
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/gene_synonym="153867_at"  
/gene_synonym="Apa"  
/gene_synonym="CG9015"  
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/gene_synonym="Eng"  
/gene_synonym="Engrailed"  
/gene_synonym="Engrailed/Invected"  
/gene_synonym="Es"  
/gene_synonym="V"  
/gene_synonym="spt"  
/coded_by="NM_165841.1:541..2199"  
/db_xref="FLYBASE:FBgn0000577"  
/db_xref="GeneID:36240"
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ORIGIN

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1 maledrcspq sapspitlqm qhlhhqqqqq qqqqqmqhl hqlqqlqqlh qqqlaagvfh  
61 hpamafdaaa aaaaaaaaaa ahahaaalq rlsqsgspas cstpasstpl tikeeesdsv  
121 igdmsfhnqt httneeeae eddidvdvd dtsaggrlpp pahqqqstak pslafsisni  
181 lsdrfgdvqk pgksmenqas ifrpfearsr qtatpsaftr vdllfstrqq qaataataa
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241 mmleranfln cfnpaaypri heeivqsrlr rsaanavipp pmsskmsdan peksalgslc
301 kavsqigqpa aptmtqppls ssasslaspp pasnastiss tssvatssss sssgcssaas
361 slnsspssrl gasgsgvnas spqpppippp savsrdsgme ssddtrsetg sttteggkne
421 mwpawvyctr ysdrpssgpr yrrpkqpkdk tndekrprta fsseqlark refnenrylt
481 errrqlsse lglneaqiki wfgnkrakik kstgsknpla lqlmaqglyn httvpltkee
541 eelemrmngq ip
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//

Data Sequence Protein B-GUS

LOCUS AAB30197 603 aa linear BCT 23-SEP-1994
DEFINITION beta-glucuronidase; GUS [Escherichia coli].
ACCESSION AAB30197
VERSION AAB30197.1 GI:545894
DBSOURCE accession [S69414.1](#)
KEYWORDS .
SOURCE Escherichia coli
ORGANISM [Escherichia coli](#)
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
REFERENCE 1 (residues 1 to 603)
AUTHORS Schlaman,H.R., Risseeuw,E., Franke-van Dijk,M.E. and Hooykaas,P.J.
TITLE Nucleotide sequence corrections of the uidA open reading frame
encoding beta-glucuronidase
JOURNAL Gene 138 (1-2), 259-260 (1994)
PUBMED [8125312](#)

REMARK GenBank staff at the National Library of Medicine created this entry [NCBI gibbsq 145980] from the original journal article.

COMMENT Glu-279 in previously reported sequence is replaced by Gln; the codon for Leu-301 contains a silent mutation.
Method: conceptual translation supplied by author.

FEATURES Location/Qualifiers

source 1..603
/organism="Escherichia coli"
/db_xref="taxon:[562](#)"

[Protein](#) 1..603
/product="beta-glucuronidase"
/note="GUS"

[Region](#) 1..598
/region_name="PRK10150"
/note="beta-D-glucuronidase; Provisional; PRK10150"
/db_xref="CDD:[104351](#)"

[Region](#) 9..180
/region_name="Glyco_hydro_2_N"
/note="Glycosyl hydrolases family 2, sugar binding domain. This family contains beta-galactosidase, beta-mannosidase and beta-glucuronidase activities and has a jelly-roll fold; pfam02837"
/db_xref="CDD:[89970](#)"

[Region](#) 182..272
/region_name="Glyco_hydro_2"
/note="Glycosyl hydrolases family 2, immunoglobulin-like beta-sandwich domain. This family contains beta-galactosidase, beta-mannosidase and beta-glucuronidase activities; pfam00703"
/db_xref="CDD:[89059](#)"

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Region      274..593
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            /note="Glycosyl hydrolases family 2, TIM barrel domain.
            This family contains beta-galactosidase, beta-mannosidase
            and beta-glucuronidase activities; pfam02836"
            /db_xref="CDD:89969"

CDS         1..603
            /gene="uidA"
            /coded_by="S69414.1:1..1812"

ORIGIN
1  mlrpvetptr eikkldglwa fsldrencgi dqrwwesalq esraiaavpgs fndqfadadi
61 rnyagnvwyq revfipkgwa gqrivlrfda vthygkvwvn nqevmehqgg ytpfeadvtp
121 yviagksvri tvcvnnelnw qtippgmvit dengkkkqsy fhdffnyagi hrsvmlyttp
181 ntwvdditvv thvaqdcnha svdqvvang dvsvelrdad qqvvatgqgt sgtlqvvnph
241 lwqpgegyly elcvtaksqt ecdiyplrvg irsvavkgeq flinhkpfyf tgfgrhedad
301 lrgkgfdnvl mvhdhalmdw igansyrtsy ypyaeemldw adehgivvid etaavgfnls
361 lgigfeagnk pkelyseeav ngetqqahlq aikeliardk nhpsvwmwsi anepdtrpqq
421 areyfaplae atrkldptrp itcvnvmfcd ahtdtisdlf dvlclnryyg wyvqsgdlet
481 aekvlekell awqeklhqpi iiteygvdtl aglshmytdm wseeyqcawl dmyhrvfdrv
541 savvgeqvwv fadfatsqgi lrvggkkgi ftrdrkpkksa aflqkrwtg mnfgekpqqg
601 gkq

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Data sequence Protein FAOX

LOCUS	BAB91123	372 aa	linear	BCT 07-JUN-2003
DEFINITION	fructosyl-amino acid oxidase [Corynebacterium sp. 2-4-1].			
ACCESSION	BAB91123			
VERSION	BAB91123.1 GI:20302586			
DBSOURCE	accession AB073548.1			
KEYWORDS	.			
SOURCE	Corynebacterium sp. 2-4-1			
ORGANISM	Corynebacterium sp. 2-4-1 Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacteriineae; Corynebacteriaceae; Corynebacterium.			
REFERENCE	1			
AUTHORS	Horiuchi,T., Kurokawa,T. and Saito,N.			
TITLE	Purification and Properties of Fructosyl-amino Acid Oxidase from Corynebacterium sp. 2-4-1			
JOURNAL	Agric. Biol. Chem. 53, 103-110 (1989)			
REFERENCE	2			
AUTHORS	Sakaue,R., Hiruma,M., Kajiyama,N. and Koyama,Y.			
TITLE	Cloning and expression of fructosyl-amino acid oxidase gene from Corynebacterium sp. 2-4-1 in Escherichia coli			
JOURNAL	Biosci. Biotechnol. Biochem. 66 (6), 1256-1261 (2002)			
PUBMED	12162546			
REFERENCE	3 (residues 1 to 372)			
AUTHORS	Sakaue,R., Hiruma,M., Kajiyama,N. and Koyama,Y.			
TITLE	Direct Submission			

JOURNAL Submitted (24-OCT-2001) Ryoichi Sakaue, Kikkoman Corporation,
 Research and Development Division; Noda399, Noda, Chida 278-0037,
 Japan (E-mail:rsakaue@mail.kikkoman.co.jp, Tel:81-471-23-5569,
 Fax:81-471-23-5968)

FEATURES Location/Qualifiers

source 1..372
 /organism="Corynebacterium sp. 2-4-1"
 /strain="2-4-1"
 /db_xref="taxon:[175533](#)"

[Protein](#) 1..372
 /product="fructosyl-amino acid oxidase"
 /EC_number="[1.5.3.-](#)"
 /function="oxidoreductase"

[Region](#) 6..372
 /region_name="DadA"
 /note="Glycine/D-amino acid oxidases (deaminating) [Amino
 acid transport and metabolism]; COG0665"
 /db_xref="CDD:[31009](#)"

[Region](#) 7..>53
 /region_name="Pyr_redox"
 /note="Pyridine nucleotide-disulphide oxidoreductase. This
 family includes both class I and class II oxidoreductases
 and also NADH oxidases and peroxidases. This domain is
 actually a small NADH binding domain within a larger FAD
 binding domain; cl10024"
 /db_xref="CDD:[108649](#)"

[Region](#) 96..>221
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and also NADH oxidases and peroxidases. This domain is actually a small NADH binding domain within a larger FAD binding domain; cl10024"

Region

/db_xref="CDD:[108649](#)"
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/region_name="Pyr_redox"
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CDS

/db_xref="CDD:[108649](#)"
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/standard_name="FAOX-C"
/coded_by="AB073548.1:1..1119"
/note="The fructosyl-amino acid oxidase(FAOX-C) shows high activity toward D-fructosyl-L-valine, but no activity toward epsilon-fructosyl-lysine"
/transl_table=[11](#)

ORIGIN

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1 msstatkhva vigggilgvs tavhllrqga tvtllteqgl aseatgrsls wlmsagerst
61 pyhqlriagv dryrtlfaad psrewlqfgg glmwnaages evtkarhaye ksigydsqll
121 apeeigsvtp gidasavpen aifnpegewv slpdlvnflm eefhalggql vlnagkasvm
181 veggratave tatgetypad avlvacgaat pavvkplgve ipngspvsml vvtkpvehqv
241 aavmntpraa vrpnpngtfa ldhdwyeghi tehadsfti pddvvelad esskliagnp
301 elkpaswkig ykpihgdep vfgelgrvpg cfvafthsga tlgliagell sgeiltgdkh
361 pmfatfrpgr fs
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//

Data Sequence Protein EcHPH

LOCUS NP_623328 66 aa linear BCT 23-JUL-2008
DEFINITION cold shock proteins [Thermoanaerobacter tengcongensis MB4].
ACCESSION NP_623328
VERSION NP_623328.1 GI:20808157
DBSOURCE REFSEQ: accession [NC_003869.1](#)
KEYWORDS .
SOURCE Thermoanaerobacter tengcongensis MB4
ORGANISM [Thermoanaerobacter tengcongensis MB4](#)
Bacteria; Firmicutes; Clostridia; Thermoanaerobacterales;
Thermoanaerobacteraceae; Thermoanaerobacter.
REFERENCE 1 (residues 1 to 66)
AUTHORS Bao,Q., Tian,Y., Li,W., Xu,Z., Xuan,Z., Hu,S., Dong,W., Yang,J.,
Chen,Y., Xue,Y., Xu,Y., Lai,X., Huang,L., Dong,X., Ma,Y., Ling,L.,
Tan,H., Chen,R., Wang,J., Yu,J. and Yang,H.

TITLE	A complete sequence of the <i>T. tengcongensis</i> genome
JOURNAL	Genome Res. 12 (5), 689-700 (2002)
PUBMED	11997336
REFERENCE	2 (residues 1 to 66)
CONSRM	NCBI Genome Project
TITLE	Direct Submission
JOURNAL	Submitted (16-MAY-2002) National Center for Biotechnology Information, NIH, Bethesda, MD 20894, USA
REFERENCE	3 (residues 1 to 66)
AUTHORS	Bao,Q., Xu,Z., Hu,S., Dong,W., Chen,Y., Wang,J., Yu,J. and Yang,H.
TITLE	Direct Submission
JOURNAL	Submitted (07-OCT-2001) Beijing Genomics Institute/Genomics and Bioinformatics Center, Institute of Genetics and Development, Chinese Academy of Sciences, Beijing Airport Industrial Zone B6, Beijing 101300, China
REFERENCE	4 (residues 1 to 66)
AUTHORS	Li,W., Xuan,Z., Yang,J., Ling,L. and Chen,R.
TITLE	Direct Submission
JOURNAL	Submitted (07-OCT-2001) Institute of Biophysics, Chinese Academy of Sciences, Beijing 100101, China
REFERENCE	5 (residues 1 to 66)
AUTHORS	Tian,Y., Xue,Y., Xu,Y., Lai,X., Huang,L., Dong,X., Ma,Y. and Tan,H.
TITLE	Direct Submission
JOURNAL	Submitted (07-OCT-2001) Institute of Microbiology, Chinese Academy of Sciences, Beijing 100080, China
COMMENT	PROVISIONAL REFSEQ : This record has not yet been subject to final NCBI review. The reference sequence was derived from AAM24932 . Method: conceptual translation.
FEATURES	Location/Qualifiers
source	1..66

Protein	<pre> /organism="Thermoanaerobacter tengcongensis MB4" /strain="MB4T" /db_xref="taxon:273068" /note="type strain of Thermoanaerobacter tengcongensis MB4" </pre>
Region	<pre> 1..66 /product="cold shock proteins" /calculated_mol_wt=7262 2..65 /region_name="CSP_CDS" /note="Cold-Shock Protein (CSP) contains an S1-like cold-shock domain (CSD) that is found in eukaryotes, prokaryotes, and archaea. CSP's include the major cold-shock proteins CspA and CspB in bacteria and the eukaryotic gene regulatory factor Y-box protein...; cd04458" </pre>
Site	<pre> /db_xref="CDD:88424" order(8,17,27,56) /site_type="DNA binding" </pre>
Site	<pre> /db_xref="CDD:88424" order(14..20,26..29) /site_type="other" /note="RNA-binding motif" </pre>
CDS	<pre> /db_xref="CDD:88424" 1..66 /gene="CspC" /locus_tag="TTE1738" /coded_by="complement(NC_003869.1:1684038..1684238)" /note="Best Blastp hit = gi 10176234 dbj BAB07329.1 (AP001519) cold-shock protein [Bacillus halodurans], score </pre>

```
106, E-value 3.00E-23"
/transl_table=11
/db_xref="GeneID:996748"
ORIGIN
  1 mvrqkvwfn aekgygfier edgtdvfvhy saiegegftk leegqavefe vvqaakgpqa
  61 skvrkl
//
```

Data Sequence PTDH

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LOCUS       O69054                336 aa           linear   BCT 25-NOV-2008
DEFINITION  RecName: Full=Phosphonate dehydrogenase; AltName:
            Full=NAD-dependent phosphite dehydrogenase.
ACCESSION   O69054
VERSION     O69054.1  GI:21362789
DBSOURCE    swissprot: locus PTXD_PSEST, accession O69054;
            class: standard.
```

created: Jun 6, 2002.
 sequence updated: Aug 1, 1998.
 annotation updated: Nov 25, 2008.
 xrefs: [AF061070.1](#), [AAC71709.1](#)
 xrefs (non-sequence databases): HSSP:[P36234](#), GO:[0051287](#),
 GO:[0016616](#), GO:[0050609](#), GO:[0055114](#), GO:[0006950](#), InterPro:[IPR006139](#),
 InterPro:[IPR006140](#), InterPro:[IPR016040](#), Gene3D:G3DSA:3.40.50.720,
 Pfam:[PF00389](#), Pfam:[PF02826](#), PROSITE:PS00065, PROSITE:PS00670,
 PROSITE:PS00671

KEYWORDS Direct protein sequencing; NAD; Oxidoreductase; Stress response.

SOURCE Pseudomonas stutzeri

ORGANISM [Pseudomonas stutzeri](#)
 Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
 Pseudomonadaceae; Pseudomonas.

REFERENCE 1 (residues 1 to 336)

AUTHORS Metcalf,W.W. and Wolfe,R.S.

TITLE Molecular genetic analysis of phosphite and hypophosphite oxidation
 by Pseudomonas stutzeri WM88

JOURNAL J. Bacteriol. 180 (21), 5547-5558 (1998)

PUBMED [9791102](#)

REMARK NUCLEOTIDE SEQUENCE [GENOMIC DNA].
 STRAIN=WM88

REFERENCE 2 (residues 1 to 336)

AUTHORS Costas,A.M., White,A.K. and Metcalf,W.W.

TITLE Purification and characterization of a novel phosphorus-oxidizing
 enzyme from Pseudomonas stutzeri WM88

JOURNAL J. Biol. Chem. 276 (20), 17429-17436 (2001)

PUBMED [11278981](#)

REMARK PROTEIN SEQUENCE OF 1-15, FUNCTION, CATALYTIC ACTIVITY, COFACTOR,
 ENZYME REGULATION, SUBUNIT, INDUCTION, AND MASS SPECTROMETRY.

STRAIN=WM88

COMMENT [FUNCTION] Catalyzes phosphite (phosphonate) oxidation.
 [CATALYTIC ACTIVITY] Phosphonate + NAD(+) + H(2)O = phosphate + NADH.
 [ENZYME REGULATION] Inhibited by NaCl, NADH and sulfite.
 [BIOPHYSICOCHEMICAL PROPERTIES] pH dependence: Optimum pH is 7.25-7.75; Temperature dependence: Optimum temperature is 35 degrees Celsius.
 [SUBUNIT] Homodimer.
 [INDUCTION] By phosphate starvation.
 [MASS SPECTROMETRY] Mass=36413; Mass_error=18; Method=MALDI; Range=1-336; Source=PubMed:11278981.
 [SIMILARITY] Belongs to the D-isomer specific 2-hydroxyacid dehydrogenase family.

FEATURES Location/Qualifiers

source 1..336
 /organism="Pseudomonas stutzeri"
 /db_xref="taxon:[316](#)"

[gene](#) 1..336
 /gene="ptxD"

[Protein](#) 1..336
 /gene="ptxD"
 /product="Phosphonate dehydrogenase"
 /EC_number="[1.20.1.1](#)"
 /note="NAD-dependent phosphite dehydrogenase"

[Region](#) 1..336
 /gene="ptxD"
 /region_name="Mature chain"
 /experiment="experimental evidence, no additional details recorded"

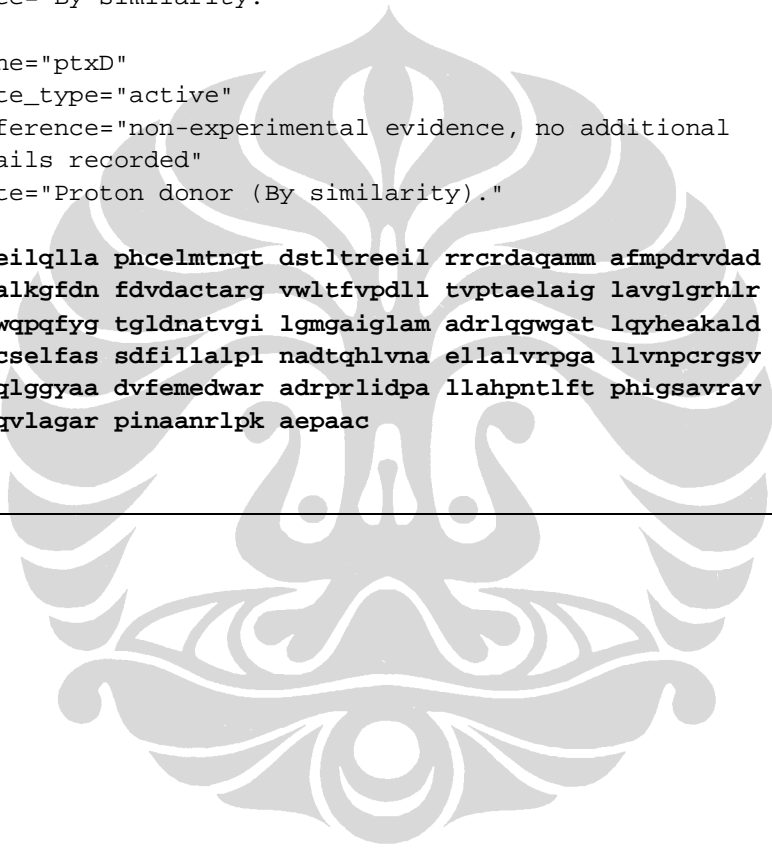
[Region](#) /note="Phosphonate dehydrogenase. /FTId=PRO_0000076033."
 6..326
 /gene="ptxD"
 /region_name="2-Hacid_dh"
 /note="D-isomer specific 2-hydroxyacid dehydrogenase, catalytic domain. This family represents the largest portion of the catalytic domain of 2-hydroxyacid dehydrogenases as the NAD binding domain is inserted within the structural domain; pfam00389"
 /db_xref="CDD:[88878](#)"

[Region](#) 109..294
 /gene="ptxD"
 /region_name="AdoHcyase"
 /note="S-adenosyl-L-homocysteine hydrolase (AdoHycase) catalyzes the hydrolysis of S-adenosyl-L-homocysteine (AdoHyc) to form adenosine (Ado) and homocysteine (Hcy). The equilibrium lies far on the side of AdoHyc synthesis, but in nature the removal of Ado...; cl09931"
 /db_xref="CDD:[108621](#)"

[Site](#) 237
 /gene="ptxD"
 /site_type="active"
 /inference="non-experimental evidence, no additional details recorded"
 /note="By similarity."

[Site](#) 266
 /gene="ptxD"
 /site_type="active"
 /inference="non-experimental evidence, no additional details recorded"


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Site /note="By similarity."  
292  
/gene="ptxD"  
/site_type="active"  
/inference="non-experimental evidence, no additional  
details recorded"  
/note="Proton donor (By similarity)."  
ORIGIN  
1 mlpklvithr vhdeilqla phcelmntqt dstltreeil rrcrdaqamm afmpdrvdad  
61 flqacpelrv vgcalkgfdn fdvdactarg vwltfvpdl1 tvptaelaig lavglgrh1r  
121 aadafvrsge fggwppqfyg tgldnatvgi lmggaiglam adrlqgwgat lqyheakald  
181 tqteqrlglr qvacselfas sdfillalpl nadtqhlvna ellalvrpga llvnpgrgsv  
241 vdeaavlaal ergqlggyaa dvfemedwar adrprlidpa llahpntlft phigsavrav  
301 rleiercaaq niiqvlagar pinaanrlpk aepaac  
//
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Data Sequence Cbadh

LOCUS P25984 351 aa linear BCT 25-NOV-2008
DEFINITION RecName: Full=NADP-dependent alcohol dehydrogenase; AltName: Full=CbADH.
ACCESSION P25984
VERSION P25984.2 GI:166228784
DBSOURCE swissprot: locus ADH_CLOBE, accession [P25984](#);
class: standard.
extra accessions:Q9R559
created: May 1, 1992.
sequence updated: Dec 4, 2007.
annotation updated: Nov 25, 2008.
xrefs: [AF157307.2](#), [AAA23199.2](#), [1JQB_A](#), [1JQB_B](#), [1JQB_C](#), [1JQB_D](#),
[1KEV_A](#), [1KEV_B](#), [1KEV_C](#), [1KEV_D](#), [1PED_A](#), [1PED_B](#), [1PED_C](#), [1PED_D](#),
[2B83_A](#), [2B83_B](#), [2B83_C](#), [2B83_D](#)
xrefs (non-sequence databases): PDBsum:1JQB, PDBsum:1KEV,
PDBsum:1PED, PDBsum:2B83, LinkHub:P25984, GO:[0008106](#), GO:[0008270](#),
GO:[0055114](#), InterPro:[IPR013154](#), InterPro:[IPR002085](#),
InterPro:[IPR013149](#), InterPro:[IPR002328](#), PANTHER:PTHR11695,
Pfam:[PF08240](#), Pfam:[PF00107](#), PROSITE:PS00059
KEYWORDS 3D-structure; Direct protein sequencing; Metal-binding; NADP;
Oxidoreductase; Zinc.
SOURCE Clostridium beijerinckii
ORGANISM [Clostridium beijerinckii](#)
Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;

Clostridium.

REFERENCE 1 (residues 1 to 351)
 AUTHORS Rifaat,M.M. and Chen,J.S.
 TITLE Direct Submission
 JOURNAL Submitted (??-SEP-1999)
 REMARK NUCLEOTIDE SEQUENCE [GENOMIC DNA].
 STRAIN=NRRL B-593

REFERENCE 2 (residues 1 to 351)
 AUTHORS Ismaiel,A.A., Zhu,C.X., Colby,G.D. and Chen,J.S.
 TITLE Purification and characterization of a primary-secondary alcohol
 dehydrogenase from two strains of Clostridium beijerinckii
 JOURNAL J. Bacteriol. 175 (16), 5097-5105 (1993)
 PUBMED [8349550](#)
 REMARK PROTEIN SEQUENCE OF 1-21.
 STRAIN=NESTE 255, and NRRL B-593

REFERENCE 3 (residues 1 to 351)
 AUTHORS Korkhin,Y., Kalb(Gilboa),A.J., Peretz,M., Bogin,O., Burstein,Y. and
 Frolow,F.
 TITLE NADP-dependent bacterial alcohol dehydrogenases: crystal structure,
 cofactor-binding and cofactor specificity of the ADHs of
 Clostridium beijerinckii and Thermoanaerobacter brockii
 JOURNAL J. Mol. Biol. 278 (5), 967-981 (1998)
 PUBMED [9836873](#)
 REMARK X-RAY CRYSTALLOGRAPHY (2.05 ANGSTROMS).

REFERENCE 4 (residues 1 to 351)
 AUTHORS Bogin,O., Levin,I., Hacham,Y., Tel-Or,S., Peretz,M., Frolow,F. and
 Burstein,Y.
 TITLE Structural basis for the enhanced thermal stability of alcohol
 dehydrogenase mutants from the mesophilic bacterium Clostridium
 beijerinckii: contribution of salt bridging

JOURNAL Protein Sci. 11 (11), 2561-2574 (2002)
 PUBMED [12381840](#)
 REMARK X-RAY CRYSTALLOGRAPHY (1.97 ANGSTROMS).
 COMMENT On Jan 29, 2008 this sequence version replaced gi:[113414](#).
 [CATALYTIC ACTIVITY] An alcohol + NADP(+) = an aldehyde + NADPH.
 [COFACTOR] Binds 1 zinc ion per subunit.
 [SUBUNIT] Homotetramer.
 [SIMILARITY] Belongs to the zinc-containing alcohol dehydrogenase family.

FEATURES Location/Qualifiers
 source 1..351
 /organism="Clostridium beijerinckii"
 /db_xref="taxon:[1520](#)"
 1..351
 /gene="adh"
 1..351
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 /product="NADP-dependent alcohol dehydrogenase"
 /EC_number="[1.1.1.2](#)"
 /note="CbADH"
 1..351
 /gene="adh"
 /region_name="Mature chain"
 /experiment="experimental evidence, no additional details recorded"
 /note="NADP-dependent alcohol dehydrogenase."
 /FTId=PRO_0000160739."
 1..349
 /gene="adh"
 /region_name="Tdh"

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/feature "Region" /note="Threonine dehydrogenase and related Zn-dependent
dehydrogenases [Amino acid transport and metabolism /
General function prediction only]; COG1063"
/db_xref="CDD:31263"
2..8
/gene="adh"
/region_name="Beta-strand region"
/experiment="experimental evidence, no additional details
recorded"
/feature "Region"
11..16
/gene="adh"
/region_name="Beta-strand region"
/experiment="experimental evidence, no additional details
recorded"
/feature "Region"
26..126
/gene="adh"
/region_name="ADH_N"
/note="Alcohol dehydrogenase GroES-like domain. This is
the catalytic domain of alcohol dehydrogenases. Many of
them contain an inserted zinc binding domain. This domain
has a GroES-like structure; pfam08240"
/db_xref="CDD:90373"
/feature "Region"
27..34
/gene="adh"
/region_name="Beta-strand region"
/experiment="experimental evidence, no additional details
recorded"
/feature "Site"
37
/gene="adh"
/site_type="metal-binding"

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[Region](#)

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/experiment="experimental evidence, no additional details  
recorded"  
/note="Zinc; catalytic."  
38..46  
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/region_name="Helical region"
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[Region](#)

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/experiment="experimental evidence, no additional details  
recorded"  
53..56  
/gene="adh"  
/region_name="Beta-strand region"
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[Site](#)

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/experiment="experimental evidence, no additional details  
recorded"  
59  
/gene="adh"  
/site_type="metal-binding"  
/experiment="experimental evidence, no additional details  
recorded"
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[Site](#)

```
/note="Zinc; catalytic."  
60  
/gene="adh"  
/site_type="metal-binding"  
/experiment="experimental evidence, no additional details  
recorded"
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[Region](#)

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/note="Zinc; catalytic."  
61..68  
/gene="adh"  
/region_name="Beta-strand region"  
/experiment="experimental evidence, no additional details  
recorded"
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[Region](#) 80..83
/gene="adh"
/region_name="Beta-strand region"
/experiment="experimental evidence, no additional details recorded"

[Region](#) 90..92
/gene="adh"
/region_name="Beta-strand region"
/experiment="experimental evidence, no additional details recorded"

[Region](#) 93..96
/gene="adh"
/region_name="Helical region"
/experiment="experimental evidence, no additional details recorded"

[Region](#) 100..102
/gene="adh"
/region_name="Helical region"
/experiment="experimental evidence, no additional details recorded"

[Region](#) 106..109
/gene="adh"
/region_name="Hydrogen bonded turn"
/experiment="experimental evidence, no additional details recorded"

[Region](#) 113..115
/gene="adh"
/region_name="Hydrogen bonded turn"
/experiment="experimental evidence, no additional details recorded"

[Region](#) 119..128
/gene="adh"
/region_name="Beta-strand region"
/experiment="experimental evidence, no additional details recorded"

[Region](#) 129..132
/gene="adh"
/region_name="Helical region"
/experiment="experimental evidence, no additional details recorded"

[Region](#) 142..146
/gene="adh"
/region_name="Helical region"
/experiment="experimental evidence, no additional details recorded"

[Region](#) 147..150
/gene="adh"
/region_name="Hydrogen bonded turn"
/experiment="experimental evidence, no additional details recorded"

[Site](#) 150
/gene="adh"
/site_type="metal-binding"
/experiment="experimental evidence, no additional details recorded"
/note="Zinc; catalytic."

[Region](#) 151..161
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/region_name="Helical region"
/experiment="experimental evidence, no additional details recorded"

[Region](#) recorded"
170..173
/gene="adh"
/region_name="Beta-strand region"
/experiment="experimental evidence, no additional details
recorded"

[Region](#) 177..187
/gene="adh"
/region_name="Helical region"
/experiment="experimental evidence, no additional details
recorded"

[Region](#) 187..309
/gene="adh"
/region_name="ADH_zinc_N"
/note="Zinc-binding dehydrogenase; pfam00107"
/db_xref="CDD:[88701](#)"

[Region](#) 188..190
/gene="adh"
/region_name="Hydrogen bonded turn"
/experiment="experimental evidence, no additional details
recorded"

[Region](#) 194..197
/gene="adh"
/region_name="Beta-strand region"
/experiment="experimental evidence, no additional details
recorded"

[Region](#) 201..210
/gene="adh"
/region_name="Helical region"
/experiment="experimental evidence, no additional details



[Region](#) recorded"
213..216
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/region_name="Beta-strand region"
/experiment="experimental evidence, no additional details
recorded"

[Region](#) 218..220
/gene="adh"
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/experiment="experimental evidence, no additional details
recorded"

[Region](#) 223..230
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/experiment="experimental evidence, no additional details
recorded"

[Region](#) 231..233
/gene="adh"
/region_name="Hydrogen bonded turn"
/experiment="experimental evidence, no additional details
recorded"

[Region](#) 236..241
/gene="adh"
/region_name="Beta-strand region"
/experiment="experimental evidence, no additional details
recorded"

[Region](#) 248..255
/gene="adh"
/region_name="Helical region"
/experiment="experimental evidence, no additional details
recorded"



[Region](#) recorded"
256..264
/gene="adh"
/region_name="Beta-strand region"
/experiment="experimental evidence, no additional details
recorded"

[Region](#) 270..277
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/experiment="experimental evidence, no additional details
recorded"

[Region](#) 278..281
/gene="adh"
/region_name="Hydrogen bonded turn"
/experiment="experimental evidence, no additional details
recorded"

[Region](#) 282..284
/gene="adh"
/region_name="Helical region"
/experiment="experimental evidence, no additional details
recorded"

[Region](#) 289..293
/gene="adh"
/region_name="Beta-strand region"
/experiment="experimental evidence, no additional details
recorded"

[Region](#) 298..310
/gene="adh"
/region_name="Helical region"
/experiment="experimental evidence, no additional details
recorded"

[Region](#) recorded"
 316..319
 /gene="adh"
 /region_name="Helical region"
 /experiment="experimental evidence, no additional details recorded"

[Region](#) recorded"
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 /experiment="experimental evidence, no additional details recorded"

[Region](#) recorded"
 327..329
 /gene="adh"
 /region_name="Helical region"
 /experiment="experimental evidence, no additional details recorded"

[Region](#) recorded"
 330..339
 /gene="adh"
 /region_name="Helical region"
 /experiment="experimental evidence, no additional details recorded"

[Region](#) recorded"
 345..350
 /gene="adh"
 /region_name="Beta-strand region"
 /experiment="experimental evidence, no additional details recorded"

ORIGIN

1 mkgfamlgin klgwiekerp vagsydaivr plavspctsd ihtvfegalg drknmilghe
 61 avgevvvevgs evkdfkpgdr vivpcttpdw rslevqagfq qhsngmlagw kfsnfkdgvf
 121 geyfhvndad mnlailpkdm plenavmitd mmttgfhgae ladiqmgssv vvigigavgl

```
181 mgiagaklrg agriigvgsr picveaakfy gatdilnykn ghivdqvmkl tngkgvdrvi
241 magggsetls qavsmvkpgg iisninyhgs gdalliprve wgcgmahkti kggllcpggrl
301 raemlrnmv ynrvdlsklv thvyhgfdhi eealllmkdk pkdlikavvi l
```

//

Data sequence Pdao

```
LOCUS      P00371                347 aa          linear      MAM 25-NOV-2008
DEFINITION RecName: Full=D-amino-acid oxidase; Short=DAMOX; Short=DAAO;
            Short=DAO.
ACCESSION  P00371
VERSION    P00371.2  GI:129305
DBSOURCE   swissprot: locus OXDA_PIG, accession P00371;
            class: standard.
            created: Jul 21, 1986.
            sequence updated: Jul 1, 1989.
            annotation updated: Nov 25, 2008.
            xrefs: M16972.1, AAA30985.1, M18447.1, AAA31025.1, M18444.1,
            M18445.1, M18446.1, M18448.1, AAA31026.1, OXPGDA, A33798,
            NP\_999231.1, 1AN9\_A, 1AN9\_B, 1DAO\_A, 1DAO\_B, 1DAO\_C, 1DAO\_D,
            1DAO\_E, 1DAO\_F, 1DAO\_G, 1DAO\_H, 1DDO\_A, 1DDO\_B, 1DDO\_C, 1DDO\_D,
```

[1DDO_E](#), [1DDO_F](#), [1DDO_G](#), [1DDO_H](#), [1EVI_A](#), [1EVI_B](#), [1KIF_A](#), [1KIF_B](#),
[1KIF_C](#), [1KIF_D](#), [1KIF_E](#), [1KIF_F](#), [1KIF_G](#), [1KIF_H](#), [1VE9_A](#), [1VE9_B](#)
xrefs (non-sequence databases): UniGene:[Ssc.232](#), PDBsum:1AN9,
PDBsum:1DAO, PDBsum:1DDO, PDBsum:1EVI, PDBsum:1KIF, PDBsum:1VE9,
GeneID:[397134](#), KEGG:ssc:397134, HOVERGEN:P00371, LinkHub:P00371,
GO:[0005777](#), GO:[0005488](#), GO:[0003884](#), GO:[0055114](#), InterPro:[IPR006181](#),
InterPro:[IPR006076](#), InterPro:[IPR016040](#), Gene3D:G3DSA:3.40.50.720,
Pfam:[PF01266](#), PROSITE:PS00677

KEYWORDS 3D-structure; Direct protein sequencing; FAD; Flavoprotein;
Oxidoreductase; Peroxisome.

SOURCE Sus scrofa (pig)
ORGANISM [Sus scrofa](#)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
Sus.

REFERENCE 1 (residues 1 to 347)
AUTHORS Ronchi,S., Minchiotti,L., Galliano,M., Curti,B., Swenson,R.P.,
Williams,C.H. Jr. and Massey,V.
TITLE The primary structure of D-amino acid oxidase from pig kidney. II.
Isolation and sequence of overlap peptides and the complete
sequence
JOURNAL J. Biol. Chem. 257 (15), 8824-8834 (1982)
PUBMED [6124543](#)
REMARK PROTEIN SEQUENCE.
TISSUE=Kidney

REFERENCE 2 (residues 1 to 347)
AUTHORS Fukui,K., Watanabe,F., Shibata,T. and Miyake,Y.
TITLE Molecular cloning and sequence analysis of cDNAs encoding porcine
kidney D-amino acid oxidase
JOURNAL Biochemistry 26 (12), 3612-3618 (1987)

PUBMED [2888479](#)
 REMARK NUCLEOTIDE SEQUENCE [MRNA].
 TISSUE=Kidney
 REFERENCE 3 (residues 1 to 347)
 AUTHORS Jacobs,P., Brockly,F., Massaer,M., Loriau,R., Guillaume,J.P.,
 Ciccarelli,E., Heinderyckx,M., Cravador,A., Biemans,R., van
 Elsen,A., Herzog,A. and Bollen,A.
 TITLE Porcine D-amino acid oxidase: determination of the mRNA nucleotide
 sequence by the characterization of genomic and cDNA clones
 JOURNAL Gene 59 (1), 55-61 (1987)
 PUBMED [2893757](#)
 REMARK NUCLEOTIDE SEQUENCE [GENOMIC DNA / MRNA].
 REFERENCE 4 (residues 1 to 347)
 AUTHORS Nicholson,B.H. and Batra,S.P.
 TITLE Structural interpretation of the binding of 9-azidoacridine to
 D-amino acid oxidase
 JOURNAL Biochem. J. 255 (3), 907-912 (1988)
 PUBMED [2905598](#)
 REMARK PROTEIN SEQUENCE.
 TISSUE=Kidney
 REFERENCE 5 (residues 1 to 347)
 AUTHORS Watanabe,F., Fukui,K., Momoi,K. and Miyake,Y.
 TITLE Expression of normal and abnormal porcine kidney D-amino acid
 oxidase in Escherichia coli: purification and characterization of
 the enzymes
 JOURNAL Biochem. Biophys. Res. Commun. 165 (3), 1422-1427 (1989)
 PUBMED [2575382](#)
 REMARK NUCLEOTIDE SEQUENCE OF 1-14.
 REFERENCE 6 (residues 1 to 347)
 AUTHORS Swenson,R.P., Williams,C.H. Jr. and Massey,V.

TITLE Chemical modification of D-amino acid oxidase. Amino acid sequence of the tryptic peptides containing tyrosine and lysine residues modified by fluorodinitrobenzene
 JOURNAL J. Biol. Chem. 257 (4), 1937-1944 (1982)
 PUBMED [6120171](#)
 REMARK PRELIMINARY STUDIES ON ACTIVE SITE.
 REFERENCE 7 (residues 1 to 347)
 AUTHORS Swenson,R.P., Williams,C.H. Jr. and Massey,V.
 TITLE Identification of the histidine residue in D-amino acid oxidase that is covalently modified during inactivation by 5-dimethylaminonaphthalene-1-sulfonyl chloride
 JOURNAL J. Biol. Chem. 258 (1), 497-502 (1983)
 PUBMED [6129252](#)
 REMARK PRELIMINARY STUDIES ON ACTIVE SITE.
 REFERENCE 8 (residues 1 to 347)
 AUTHORS Watanabe,F., Fukui,K., Momoi,K. and Miyake,Y.
 TITLE Effect of site-specific mutagenesis of tyrosine-55, methionine-110 and histidine-217 in porcine kidney D-amino acid oxidase on its catalytic function
 JOURNAL FEBS Lett. 238 (2), 269-272 (1988)
 PUBMED [2901989](#)
 REMARK MUTAGENESIS OF TYR-55; MET-110 AND HIS-217.
 REFERENCE 9 (residues 1 to 347)
 AUTHORS Miyano,M., Fukui,K., Watanabe,F., Takahashi,S., Tada,M., Kanashiro,M. and Miyake,Y.
 TITLE Studies on Phe-228 and Leu-307 recombinant mutants of porcine kidney D-amino acid oxidase: expression, purification, and characterization
 JOURNAL J. Biochem. 109 (1), 171-177 (1991)
 PUBMED [1673125](#)

REMARK ACTIVE SITES TYR-228 AND HIS-307.

REFERENCE 10 (residues 1 to 347)

AUTHORS Mizutani,H., Miyahara,I., Hirotsu,K., Nishina,Y., Shiga,K., Setoyama,C. and Miura,R.

TITLE Three-dimensional structure of porcine kidney D-amino acid oxidase at 3.0 A resolution

JOURNAL J. Biochem. 120 (1), 14-17 (1996)

PUBMED [8864836](#)

REMARK X-RAY CRYSTALLOGRAPHY (3.0 ANGSTROMS).

REFERENCE 11 (residues 1 to 347)

AUTHORS Mattevi,A., Vanoni,M.A., Todone,F., Rizzi,M., Teplyakov,A., Coda,A., Bolognesi,M. and Curti,B.

TITLE Crystal structure of D-amino acid oxidase: a case of active site mirror-image convergent evolution with flavocytochrome b2

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 93 (15), 7496-7501 (1996)

PUBMED [8755502](#)

REMARK X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS).

REFERENCE 12 (residues 1 to 347)

AUTHORS Todone,F., Vanoni,M.A., Mozzarelli,A., Bolognesi,M., Coda,A., Curti,B. and Mattevi,A.

TITLE Active site plasticity in D-amino acid oxidase: a crystallographic analysis

JOURNAL Biochemistry 36 (19), 5853-5860 (1997)

PUBMED [9153426](#)

REMARK X-RAY CRYSTALLOGRAPHY (3.1 ANGSTROMS).

COMMENT On or before Jul 18, 2007 this sequence version replaced gi:[66086](#), gi:[108276](#).
 [FUNCTION] Could act as a detoxifying agent which removes D-amino acids accumulated during aging. Acts on a variety of D-amino acids with a preference for those having small hydrophobic side chains

followed by those bearing polar, aromatic, and basic groups. Does not act on acidic amino acids.
 [CATALYTIC ACTIVITY] A D-amino acid + H(2)O + O(2) = a 2-oxo acid + NH(3) + H(2)O(2).
 [COFACTOR] FAD.
 [SUBUNIT] Homodimer.
 [SUBCELLULAR LOCATION] Peroxisome.
 [SIMILARITY] Belongs to the DAMOX/DASOX family.
 [WEB RESOURCE] Name=Worthington enzyme manual;
 URL=<http://www.worthington-biochem.com/DAOFF/>'.

FEATURES	Location/Qualifiers
source	1..347 /organism="Sus scrofa" /db_xref="taxon: 9823 "
gene	1..347 /gene="DAO"
Protein	1..347 /gene="DAO" /product="D-amino-acid oxidase" /EC_number=" 1.4.3.3 " /note="DAMOX; DAAO"
Region	1..347 /gene="DAO" /region_name="Mature chain" /experiment="experimental evidence, no additional details recorded" /note="D-amino-acid oxidase. /FTId=PRO_0000162763."
Region	2..329 /gene="DAO" /region_name="DAO"

/note="FAD dependent oxidoreductase. This family includes various FAD dependent oxidoreductases: Glycerol-3-phosphate dehydrogenase EC:1.1.99.5, Sarcosine oxidase beta subunit EC:1.5.3.1, D-alanine oxidase EC:1.4.99.1, D-aspartate oxidase EC:1.4.3.1; pfam01266"
/db_xref="CDD:[89383](#)"

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Site

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/inference="non-experimental evidence, no additional details recorded"
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10..23
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Region

24..26
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/region_name="Hydrogen bonded turn"
/experiment="experimental evidence, no additional details recorded"

Region

27..29
/gene="DAO"
/region_name="Beta-strand region"

[Region](#) /experiment="experimental evidence, no additional details recorded"
31..38
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/region_name="Beta-strand region"
/experiment="experimental evidence, no additional details recorded"

[Region](#) 40..42
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/experiment="experimental evidence, no additional details recorded"

[Region](#) 44..47
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/region_name="Helical region"
/experiment="experimental evidence, no additional details recorded"

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/site_type="mutagenized"
/experiment="experimental evidence, no additional details recorded"
/note="Y->F: No effect."

[Region](#) 63..76
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[Region](#) 77..80
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Region 119..122

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141..153

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154..156

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158..161

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167..172

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176..180

[Region](#)

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183..185
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[Region](#)

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186..189
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[Region](#)

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196..206
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[Region](#)

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212..217
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[Site](#)

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217  
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/experiment="experimental evidence, no additional details  
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/note="H->L: No effect."
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/experiment="experimental evidence, no additional details recorded"

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Site 228
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Site 228
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/note="Y->F: Reduces activity."

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Region 290..296
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/experiment="experimental evidence, no additional details recorded"

Region 298..301
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Region 303..309
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Site 307
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Region    345..347
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         /region_name="Short sequence motif of biological interest"
         /experiment="experimental evidence, no additional details
         recorded"
         /note="Microbody targeting signal."
ORIGIN
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61  npqeanwnqq  tfnyllshig  spnaanmgl  pvsgynlfre  avpdpywkd  m  vlgfrkltp
121 eldmfpdyry  gwfnstlile  grkylqwlte  rltergvkff  lrkvesfeev  arggadviin
181 ctgvwagvlq  pdllqpgrg  qiikvdapwl  knfiithdle  rgiynspyii  pglqavtlgg
241 tfqvgnwnei  nniqdhntiw  egccrleptl  kdakivgeyt  gfrpvrpqvr  lereqlrfgs
301 sntevihnyg  hggylgtihw  gcalevaklf  gkvleernll  tmppshl
//
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Data Sequence PhyA

LOCUS P34752 467 aa linear PLN 25-NOV-2008

DEFINITION RecName: Full=3-phytase A; AltName: Full=3 phytase A; AltName: Full=Myo-inositol-hexaphosphate 3-phosphohydrolase A; AltName: Full=Myo-inositol hexakisphosphate phosphohydrolase A; Flags: Precursor.

ACCESSION P34752

VERSION P34752.1 GI:464382

DBSOURCE swissprot: locus PHYA_ASPNG, accession [P34752](#);
class: standard.
created: Feb 1, 1994.
sequence updated: Feb 1, 1994.
annotation updated: Nov 25, 2008.
xrefs: [Z16414.1](#), [CAA78904.1](#), [M94550.1](#), [AAA32705.1](#), [JN0482](#), [JN0656](#), [1IHP_A](#)
xrefs (non-sequence databases): PDBsum:1IHP, LinkHub:P34752, GO:[0005576](#), GO:[0016158](#), GO:[0003993](#), InterPro:[IPR000560](#), InterPro:[IPR016274](#), Pfam:[PF00328](#), PIRSF:PIRSF000894, PROSITE:PS00616, PROSITE:PS00778

KEYWORDS 3D-structure; Direct protein sequencing; Glycoprotein; Hydrolase; Secreted; Signal.

SOURCE Aspergillus niger

ORGANISM [Aspergillus niger](#)
Eukaryota; Fungi; Dikarya; Ascomycota; Pezizomycotina;
Eurotiomycetes; Eurotiomycetidae; Eurotiales; Trichocomaceae;
mitosporic Trichocomaceae; Aspergillus.

REFERENCE 1 (residues 1 to 467)

AUTHORS van Hartingsveldt,W., van Zeijl,C.M.J., Harteveld,G.M., Gouka,R.J.,
 Suykerbuyk,M.E.G., Luiten,R.G.M., van Paridon,P.A., Selten,G.C.M.,
 Veenstra,A.E., van Gorcom,R.F.M. and van den Hondel,C.A.M.J.J.
 TITLE Cloning, characterization and overexpression of the
 phytase-encoding gene (phyA) of *Aspergillus niger*
 JOURNAL Gene 127 (1), 87-94 (1993)
 PUBMED [8387447](#)
 REMARK NUCLEOTIDE SEQUENCE [GENOMIC DNA], AND PARTIAL PROTEIN SEQUENCE.
 STRAIN=NRRL 3135 / Van Tieghem / Ficum
 REFERENCE 2 (residues 1 to 467)
 AUTHORS Mullaney,E.J.
 TITLE Direct Submission
 JOURNAL Submitted (??-JUN-1992)
 REMARK NUCLEOTIDE SEQUENCE [GENOMIC DNA].
 REFERENCE 3 (residues 1 to 467)
 AUTHORS Ullah,A.H. and Dischinger,H.C. Jr.
 TITLE *Aspergillus ficuum* phytase: complete primary structure elucidation
 by chemical sequencing
 JOURNAL Biochem. Biophys. Res. Commun. 192 (2), 747-753 (1993)
 PUBMED [8387289](#)
 REMARK PROTEIN SEQUENCE OF 24-464.
 STRAIN=NRRL 3135 / Van Tieghem / Ficum
 REFERENCE 4 (residues 1 to 467)
 AUTHORS Ullah,A.H., Cummins,B.J. and Dischinger,H.C. Jr.
 TITLE Cyclohexanedione modification of arginine at the active site of
Aspergillus ficuum phytase
 JOURNAL Biochem. Biophys. Res. Commun. 178 (1), 45-53 (1991)
 PUBMED [1648914](#)
 REMARK PROTEIN SEQUENCE OF 71-93.
 STRAIN=NRRL 3135 / Van Tieghem / Ficum

REFERENCE 5 (residues 1 to 467)
 AUTHORS Ullah,A.H.
 TITLE Aspergillus ficuum phytase: partial primary structure, substrate selectivity, and kinetic characterization
 JOURNAL Prep. Biochem. 18 (4), 459-471 (1988)
 PUBMED [2852807](#)
 REMARK CHARACTERIZATION, AND PARTIAL PROTEIN SEQUENCE.
 STRAIN=NRRL 3135 / Van Tieghem / Ficuum
 REFERENCE 6 (residues 1 to 467)
 AUTHORS Kostrewa,D., Gruninger-Leitch,F., D'Arcy,A., Broger,C., Mitchell,D. and van Loon,A.P.
 TITLE Crystal structure of phytase from Aspergillus ficuum at 2.5 A resolution
 JOURNAL Nat. Struct. Biol. 4 (3), 185-190 (1997)
 PUBMED [9164457](#)
 REMARK X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).
 STRAIN=NRRL 3135 / Van Tieghem / Ficuum
 COMMENT On or before Oct 11, 2005 this sequence version replaced gi:[419906](#), gi:[484414](#).
 [FUNCTION] Catalyzes the hydrolysis of inorganic orthophosphate from phytate.
 [CATALYTIC ACTIVITY] Myo-inositol hexakisphosphate + H(2)O = 1D-myo-inositol 1,2,4,5,6-pentakisphosphate + phosphate.
 [SUBCELLULAR LOCATION] Secreted.
 [BIOTECHNOLOGY] Is used as a food and feed additive. It can facilitate the degradation of phytin in soybean and other seeds used as food for monogastric animals. Sold by Novo Nordisk under the name Phytase Novo.
 [SIMILARITY] Belongs to the histidine acid phosphatase family.
 FEATURES Location/Qualifiers

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source      1..467
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gene      1..467
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            /EC_number="3.1.3.8"
            /note="3 phytase A; Myo-inositol-hexaphosphate
            3-phosphohydrolase A; Myo-inositol hexakisphosphate
            phosphohydrolase A"
Region   1..23
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Region   24..467
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            /note="3-phytase A. /FTId=PRO_0000023970."
Site     27
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            /experiment="experimental evidence, no additional details
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Bond     bond(31,40)

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34..36
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[Region](#) 42..45
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[Region](#) 49..51
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[Region](#) 58..60
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[Site](#) 59
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/experiment="experimental evidence, no additional details recorded"
/note="N-linked (GlcNAc...)."

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<u>Region</u>	71..81 /gene="phyA" /region_name="Beta-strand region" /experiment="experimental evidence, no additional details recorded"
<u>Region</u>	72..427 /gene="phyA" /region_name="Acid_phosphat_A" /note="Histidine acid phosphatase; cl09484" /db_xref="CDD: 108600 "
<u>Site</u>	82 /gene="phyA" /site_type="active" /inference="non-experimental evidence, no additional details recorded" /note="Nucleophile (By similarity)."
<u>Region</u>	89..105 /gene="phyA" /region_name="Helical region" /experiment="experimental evidence, no additional details recorded"
<u>Site</u>	105 /gene="phyA" /site_type="glycosylation" /experiment="experimental evidence, no additional details recorded"

[Region](#) recorded"
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recorded"

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126..128
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recorded"

[Region](#) 130..146
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/region_name="Helical region"
/experiment="experimental evidence, no additional details
recorded"

[Region](#) 148..151
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/experiment="experimental evidence, no additional details
recorded"

[Region](#) 157..162
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164..182
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196..200
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bond(215,465)
/gene="phyA"
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[Region](#) 216..220
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[Region](#) 223..233

[Site](#)
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[Region](#)
254..269
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[Bond](#)
bond(264,282)
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/experiment="experimental evidence, no additional details recorded"

[Region](#)
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[Region](#) 310..312
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[Region](#) 317..328
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[Region](#) 346..348
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[Region](#) 362..371
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/region_name="Helical region"
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[Site](#) 362
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/site_type="active"

[Region](#)

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details recorded"
/note="Proton donor (By similarity)."  
372..377  
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[Site](#)

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376  
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recorded"
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383..385  
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[Site](#)

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388  
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recorded"
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[Region](#)

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Region      401..403
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              recorded"
Region      406..416
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              /experiment="experimental evidence, no additional details
              recorded"
Region      421..426
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              /experiment="experimental evidence, no additional details
              recorded"
Region      434..436
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            /experiment="experimental evidence, no additional details
            recorded"
Region      458..461
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            /experiment="experimental evidence, no additional details
            recorded"
Region      462..465
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            recorded"
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  61 svispevpag crvtfaqvls rhgaryptds kgkksyalie eiqqnattfd gkyafllkty
 121 yslgaddltp fgeqelvnsg ikfyqryesl trnivpfirs sgssrviasg kkfiiegfst
 181 klkdpraqpg qsspkidvvi seasssnt1 dpgtctvfed seladtvean ftatfvpsir
 241 qrlendlsgv tltdtevt1l mdmcsfdtis tstvdtklsp fcdlfthdew inydlqslk
 301 kyyghgagnp lgptqgvgya neliarlths pvhddtssnh tldsspatfp lntlyadfs
 361 hdngiisilf alglyngtkp lstttvenit qtdgfssawt vpfasrlyve mmqcaeqep
 421 lvr1lvndrv vplhgcpvda lgrctrdsfv rglsfarsgg dwaecfa
//

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