

Protein View: P97449

Aminopeptidase N OS=Mus musculus OX=10090 GN=Anpep PE=1 SV=4

Database: UP589_M_musculus
Score: 588
Monoisotopic mass (M_r): 109582
Calculated pI: 5.62

Sequence similarity is available as [an NCBI BLAST search of P97449 against nr.](#)

Search parameters

MS data file: mas3E2.tmp
Enzyme: Trypsin: cuts C-term side of KR unless next residue is P.
Variable modifications: [Carbamidomethyl \(C\)](#), [Oxidation \(M\)](#)

Protein sequence coverage: 27%

Matched peptides shown in **bold red**.

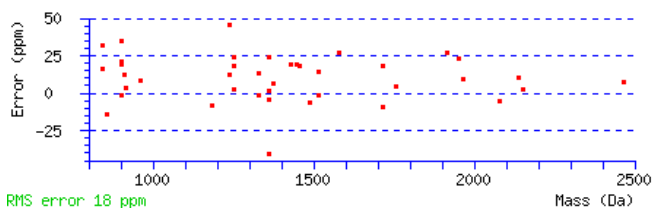
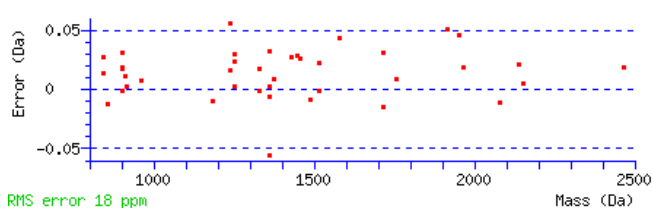
1 MAKGFYISK T LGILGILLGV AAVCTIIALS VVYAQEKNRN AENSATAPTL
51 PGSTSATTAT TTPAVDESKP WNQYRLPK**TL IPDSYR**VILR PYLTPNNQGL
101 YIFQGNSTVR FTCNQTTDVI IHSKKLNYT LKGNHRVVL**R TLDGTPAPNI**
151 **DKTELVERTE** YLVVHLQGS L VEGRQYEMDS QFQGE LADDL AGFYR**SEYME**
201 **GDVKKVVATT QMQAADARKS FPCFDEPAMK** AMFNITLIYP>NNLIALSNML
251 **PKESKPYPED PSCTMTEFHS TPKMSTYLLA** YIVSEFKNIS SVSANGVQIG
301 IWARPSAIDE GQGDYALNVT GPILNFFAQH YNTSYPLPKS DQIALPDFNA
351 GAMENWGLVT Y**RESSLVFDS QSSSISNKER** VVTVIAHELA HQWFGNLVTV
401 AWWNDLWLNE GFASYVEYLG ADYAEPTWNL **KDLMVLNDVY RVMAVDALAS**
451 **SHPLSSPADE IKTPDQIMEL** FDSITYSKGA SVIR**MLSSFL TEDLFFKGLS**
501 SYLHTYQYSN TVYLDLWEHL **QKAVNQQTAV QPPATV**RTIM DRWILQMGFP
551 VITVNTNTGE ISQ**KHFLDLS KSNVTRPSEF** NYIWIPIPF LKSGQEDHYW
601 LDVEKNQSAK FQTSSNEWIL LNINVTGYL VNYDENNW**KK LQNQLQTDLS**
651 **VIPVINRAQI IHDSFNLASA KMIPITLALD** NTLFLVKAEAE YMPWQAALSS
701 LNYFTLMFDR **SEVYGPMKRY** LKKQVTPLFF YFQNRNTNNWV NRPPTLMEQY
751 NEINAISTAC SSGLKECRDL VVELYSQWMK NPNNNTIHPN LRSTVYCNAI
801 AFGGEEENWF AWEQFRNATL VNEADKLRS A LACSK**DVWIL NRYLSYTLNP**
851 **DYIRKQDITS TIISIASNVA** GHPLVWDFVR SNWKKLFENY GGSFSSFANL
901 IQGVTR**RFSS EFELQQLQF KADNSATGFG TGTRALEQAL EKTRANIDWV**
951 **KENKDAVFKW FTENSS**

Unformatted sequence string: **966 residues** (for pasting into other applications).

Sort by ☒ residue number ☐ increasing mass ☐ decreasing mass
Show ☒ matched peptides only ☐ predicted peptides also

Query	Start - End	Observed	Mr (expt)	Mr (calc)	Delta M	Score	Expect	Rank	U	Peptide
272	79 - 86	482.7625	963.5105	963.5025	0.0080	0	20	1.7	1	U K.TLIPDSYR.V
361	141 - 152	621.3301	1240.6457	1240.6299	0.0158	0	29	0.18	1	U R.TLDGTPAPNIDK.T
528	141 - 158	657.0187	1968.0344	1968.0164	0.0180	1	32	0.066	1	U R.TLDGTPAPNIDKTELVER.T
327	196 - 205	593.2718	1184.5290	1184.5383	-0.0093	1	12	11	1	U R.SEYMEGDVKK.V
434	206 - 218	681.3178	1360.6211	1360.6769	-0.0558	0	32	0.1	1	U K.VVATTQMQAADAR.K
435	206 - 218	681.3429	1360.6712	1360.6769	-0.0056	0	93	7.4e-08	1	U K.VVATTQMQAADAR.K
436	206 - 218	681.3468	1360.6790	1360.6769	0.0021	0	63	8.2e-05	1	U K.VVATTQMQAADAR.K
437	206 - 218	681.3619	1360.7092	1360.6769	0.0323	0	40	0.017	1	U K.VVATTQMQAADAR.K
445	206 - 218	689.3477	1376.6808	1376.6718	0.0090	0	27	0.32	1	U K.VVATTQMQAADAR.K + Oxidation (M)
471	206 - 219	497.2615	1488.7628	1488.7719	-0.0090	1	18	2.4	1	U K.VVATTQMQAADARK.S
466	219 - 230	486.2336	1455.6789	1455.6526	0.0263	1	16	3.5	1	U R.KSFPCFDEPAMK.A + Carbamidomethyl (C)
424	220 - 230	664.7852	1327.5559	1327.5577	-0.0018	0	11	12	1	U K.SFPCFDEPAMK.A + Carbamidomethyl (C)
425	220 - 230	664.7951	1327.5756	1327.5577	0.0179	0	50	0.0015	1	U K.SFPCFDEPAMK.A + Carbamidomethyl (C)
554	253 - 273	617.7786	2467.0853	2467.0672	0.0182	0	25	0.22	1	U K.ESKPYPEDPSCTMTEFHSTPK.M + Carbamidomethyl (C)
504	363 - 378	857.9025	1713.7904	1713.8057	-0.0153	0	13	6.6	1	U R.ESSLVFDSQSSSISNK.E
505	363 - 378	857.9253	1713.8361	1713.8057	0.0304	0	63	6.4e-05	1	U R.ESSLVFDSQSSSISNK.E
360	432 - 441	619.3439	1236.6733	1236.6172	0.0561	0	54	0.00062	1	U K.DLMVLNDVYR.V
365	432 - 441	627.3147	1252.6149	1252.6122	0.0027	0	22	0.96	1	U K.DLMVLNDVYR.V + Oxidation (M)
545	442 - 462	713.3719	2137.0938	2137.0725	0.0213	0	49	0.0013	1	U R.VMAVDALASSHPLSSPADEIK.T
547	442 - 462	718.6981	2153.0726	2153.0674	0.0052	0	15	3.1	1	U R.VMAVDALASSHPLSSPADEIK.T + Oxidation (M)
460	485 - 496	715.8791	1429.7437	1429.7163	0.0274	0	59	0.00018	1	U R.MLSSFLTEDLFFK.K

Query	Start - End	Observed	Mr(expt)	Mr(calc)	Delta M	Score	Expect	Rank	U	Peptide
463	485 - 496	723.8769	1445.7392	1445.7112	0.0280	0	65	5.1e-05	1	U R.MLSSFLTEDLFFK.K + Oxidation (M)
491	523 - 537	790.4527	1578.8909	1578.8478	0.0431	0	42	0.0084	1	U K.AVNQQTAVQPPATVR.T
492	523 - 537	790.4528	1578.8911	1578.8478	0.0433	0	35	0.037	1	U K.AVNQQTAVQPPATVR.T
191	565 - 571	430.2312	858.4479	858.4599	-0.0120	0	6	54	3	U K.HFLLDISK.S
538	640 - 657	693.7317	2078.1734	2078.1848	-0.0114	1	24	0.28	1	U K.KLQNQLQTDLSVIPVINR.A
526	641 - 657	976.0748	1950.1351	1950.0898	0.0453	0	70	6e-06	1	U K.LQNQLQTDLSVIPVINR.A
476	658 - 671	505.6108	1513.8107	1513.7889	0.0218	0	52	0.00082	1	U R.AQIIHDSFNLASAK.M
251	711 - 718	455.7259	909.4373	909.4266	0.0108	0	9	19	1	U R.SEVYGPMK.R
254	836 - 842	458.2574	914.5002	914.4974	0.0028	0	16	4.6	2	U K.DVWILNR.Y
477	843 - 854	759.3846	1516.7547	1516.7562	-0.0015	0	54	0.00056	1	U R.YLSYTLNPDYIR.K
519	907 - 921	639.3401	1914.9983	1914.9476	0.0508	1	21		1	U R.RFSSEFELQQLQLEQFK.A
507	908 - 921	880.4347	1758.8549	1758.8465	0.0085	0	22	0.68	1	U R.FSSEFELQQLQLEQFK.A
368	922 - 934	627.8008	1253.5870	1253.5637	0.0234	0	34	0.062	1	U K.ADNSATGFGTGTR.A
369	922 - 934	627.8041	1253.5937	1253.5637	0.0301	0	29	0.21	1	U K.ADNSATGFGTGTR.A
243	935 - 942	451.2523	900.4901	900.4916	-0.0015	0	4	77	6	U R.ALEQALEK.T
245	935 - 942	451.2616	900.5086	900.4916	0.0170	0	41	0.017	1	U R.ALEQALEK.T
246	935 - 942	451.2624	900.5103	900.4916	0.0187	0	48	0.0033	1	U R.ALEQALEK.T
248	935 - 942	451.2688	900.5230	900.4916	0.0314	0	47	0.0039	1	U R.ALEQALEK.T
166	945 - 951	423.2363	844.4580	844.4443	0.0137	0	1	1.6e+02	1	U R.ANIDWVK.E
168	945 - 951	423.2428	844.4710	844.4443	0.0267	0	19	2.5	1	U R.ANIDWVK.E



ID AMPN_MOUSE Reviewed; 966 AA.
AC P97449; Q91YH8; Q99K63;
DT 01-NOV-1997, integrated into UniProtKB/Swiss-Prot.
DT 23-JAN-2007, sequence version 4.
DT 02-JUN-2021, entry version 197.
DE RecName: Full=Aminopeptidase N {ECO:0000305};
DE Short=AP-N;
DE Short=mAPN;
DE EC=3.4.11.2 {ECO:0000269|PubMed:8691132};
DE AltName: Full=Alanyl aminopeptidase;
DE AltName: Full=Aminopeptidase M;
DE Short=AP-M;
DE AltName: Full=Membrane protein p161;
DE AltName: Full=Microsomal aminopeptidase;
DE AltName: CD_antigen=CD13;
GN Name=Anpep; Synonyms=Lap-1, Lap1;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
OC Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae;
OC Murinae; Mus; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE [MRNA], PROTEIN SEQUENCE OF 538-564; 886-908; 922-942
RP AND 961-965, SUBCELLULAR LOCATION, GLYCOSYLATION, AND TISSUE SPECIFICITY.
RX PubMed=8805662;
RA Chen H., Kinzer C.A., Paul W.E.;
RT "p161, a murine membrane protein expressed on mast cells and some
RT macrophages, is mouse CD13/aminopeptidase N.";
RL J. Immunol. 157:2593-2600 (1996).
RN [2]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC STRAIN=Czech II, and FVB/N; TISSUE=Mammary tumor;
RX PubMed=15489334; DOI=10.1101/gr.2596504;
RG The MGC Project Team;
RT "The status, quality, and expansion of the NIH full-length cDNA project:
RT the Mammalian Gene Collection (MGC).";
RL Genome Res. 14:2121-2127 (2004).
RN [3]
RP TISSUE SPECIFICITY.
RX PubMed=8103749; DOI=10.1002/eji.1830230946;
RA Hansen A.S., Noren O., Sjostrom H., Werdelin O.;
RT "A mouse aminopeptidase N is a marker for antigen-presenting cells and
RT appears to be co-expressed with major histocompatibility complex class II
RT molecules.";
RL Eur. J. Immunol. 23:2358-2364 (1993).
RN [4]
RP FUNCTION IN ENZYMATIC CLEAVAGE OF ANTIGEN PEPTIDES BOUND TO CLASS II MHC,
RP AND CATALYTIC ACTIVITY.
RX PubMed=8691132; DOI=10.1084/jem.184.1.183;
RA Larsen S.L., Pedersen L.O., Buus S., Stryhn A.;
RT "T cell responses affected by aminopeptidase N (CD13)-mediated trimming of
RT major histocompatibility complex class II-bound peptides.";
RL J. Exp. Med. 184:183-189 (1996).
RN [5]
RP PHOSPHORYLATION [LARGE SCALE ANALYSIS] AT TYR-852, AND IDENTIFICATION BY
RP MASS SPECTROMETRY [LARGE SCALE ANALYSIS].
RC TISSUE=Mast cell;

RX PubMed=17947660; DOI=10.4049/jimmunol.179.9.5864;
RA Cao L., Yu K., Banh C., Nguyen V., Ritz A., Raphael B.J., Kawakami Y.,
RA Kawakami T., Salomon A.R.;
RT "Quantitative time-resolved phosphoproteomic analysis of mast cell
RT signaling.";
RL J. Immunol. 179:5864-5876(2007).
RN [6]
RP GLYCOSYLATION [LARGE SCALE ANALYSIS] AT ASN-106; ASN-128; ASN-606; ASN-784
RP AND ASN-817.
RC TISSUE=Myoblast;
RX PubMed=19656770; DOI=10.1074/mcp.m900195-mcp200;
RA Gundry R.L., Raginski K., Tarasova Y., Tchernyshyov I., Bausch-Fluck D.,
RA Elliott S.T., Boheler K.R., Van Eyk J.E., Wollscheid B.;
RT "The mouse C2C12 myoblast cell surface N-linked glycoproteome:
RT identification, glycosite occupancy, and membrane orientation.";
RL Mol. Cell. Proteomics 8:2555-2569(2009).
RN [7]
RP GLYCOSYLATION [LARGE SCALE ANALYSIS] AT ASN-106; ASN-114; ASN-332; ASN-606;
RP ASN-784 AND ASN-817.
RX PubMed=19349973; DOI=10.1038/nbt.1532;
RA Wollscheid B., Bausch-Fluck D., Henderson C., O'Brien R., Bibel M.,
RA Schiess R., Aebersold R., Watts J.D.;
RT "Mass-spectrometric identification and relative quantification of N-linked
RT cell surface glycoproteins.";
RL Nat. Biotechnol. 27:378-386(2009).
RN [8]
RP IDENTIFICATION BY MASS SPECTROMETRY [LARGE SCALE ANALYSIS].
RC TISSUE=Brain, Brown adipose tissue, Heart, Kidney, Liver, Lung, Pancreas,
RC Spleen, and Testis;
RX PubMed=21183079; DOI=10.1016/j.cell.2010.12.001;
RA Huttlin E.L., Jedrychowski M.P., Elias J.E., Goswami T., Rad R.,
RA Beausoleil S.A., Villen J., Haas W., Sowa M.E., Gygi S.P.;
RT "A tissue-specific atlas of mouse protein phosphorylation and expression.";
RL Cell 143:1174-1189(2010).
RN [9]
RP FUNCTION, INTERACTION WITH SLC6A19, TISSUE SPECIFICITY, AND MUTAGENESIS OF
RP GLU-354; GLU-388; GLU-410 AND TYR-476.
RX PubMed=22677001; DOI=10.1042/bj20120307;
RA Fairweather S.J., Broeer A., O'Mara M.L., Broeer S.;
RT "Intestinal peptidases form functional complexes with the neutral amino
RT acid transporter B(0)AT1.";
RL Biochem. J. 446:135-148(2012).
CC -!- FUNCTION: Broad specificity aminopeptidase which plays a role in the
CC final digestion of peptides generated from hydrolysis of proteins by
CC gastric and pancreatic proteases. Also involved in the processing of
CC various peptides including peptide hormones, such as angiotensin III
CC and IV, neuropeptides, and chemokines (By similarity). May also be
CC involved the cleavage of peptides bound to major histocompatibility
CC complex class II molecules of antigen presenting cells
CC (PubMed:8691132). May have a role in angiogenesis and promote
CC cholesterol crystallization (By similarity). May have a role in amino
CC acid transport by acting as binding partner of amino acid transporter
CC SLC6A19 and regulating its activity (PubMed:22677001).
CC {ECO:0000250|UniProtKB:P15144, ECO:0000269|PubMed:22677001,
CC ECO:0000269|PubMed:8691132}.
CC -!- CATALYTIC ACTIVITY:
CC Reaction=Release of an N-terminal amino acid, Xaa-|-Yaa- from a
CC peptide, amide or arylamide. Xaa is preferably Ala, but may be most
CC amino acids including Pro (slow action). When a terminal hydrophobic
CC residue is followed by a prolyl residue, the two may be released as
CC an intact Xaa-Pro dipeptide.; EC=3.4.11.2;
CC Evidence={ECO:0000269|PubMed:8691132};
CC -!- COFACTOR:
CC Name=Zn(2+); Xref=ChEBI:CHEBI:29105;
CC Evidence={ECO:0000250|UniProtKB:P15144};
CC Note=Binds 1 zinc ion per subunit. {ECO:0000250|UniProtKB:P15144};
CC -!- SUBUNIT: Homodimer (By similarity). Interacts with SLC6A19
CC (PubMed:22677001). {ECO:0000250|UniProtKB:P15144,
CC ECO:0000269|PubMed:22677001}.
CC -!- SUBCELLULAR LOCATION: Cell membrane {ECO:0000269|PubMed:8805662};
CC Single-pass type II membrane protein {ECO:0000250|UniProtKB:P15144}.
CC Note=Also found as a soluble form. {ECO:0000250|UniProtKB:P15144}.
CC -!- TISSUE SPECIFICITY: Expressed in the intestinal brush border (at
CC protein level) (PubMed:22677001). Highly expressed in intestinal tract
CC and kidney, present in liver, lymph node, spleen, and brain
CC (PubMed:8805662, PubMed:8103749). Found as well in monocytes,
CC macrophages, dendritic cells, veiled cells and B-cells but not on T-
CC cells and thymocytes (PubMed:8103749). {ECO:0000269|PubMed:22677001,
CC ECO:0000269|PubMed:8103749, ECO:0000269|PubMed:8805662}.
CC -!- PTM: N- and O-glycosylated. {ECO:0000269|PubMed:8805662}.
CC -!- PTM: Sulfated. {ECO:0000250|UniProtKB:P15144}.
CC -!- PTM: May undergo proteolysis and give rise to a soluble form.
CC {ECO:0000250|UniProtKB:P15144}.
CC -!- SIMILARITY: Belongs to the peptidase M1 family. {ECO:0000305}.
CC -----
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CC -----
DR EMBL; U77083; AAB19065.1; -; mRNA.
DR EMBL; BC005431; AAH05431.1; -; mRNA.
DR EMBL; BC017011; AAH17011.1; -; mRNA.
DR EMBL; BC040792; AAH40792.1; -; mRNA.
DR CCDS; CCDS21388.1; -.
DR RefSeq; NP_032512.2; NM_008486.2.
DR RefSeq; XP_006540741.1; XM_006540678.3.

DR SMR; P97449; -.
 DR IntAct; P97449; 10.
 DR MINT; P97449; -.
 DR STRING; 10090.ENSMUSP00000103015; -.
 DR BindingDB; P97449; -.
 DR ChEMBL; ChEMBL2189140; -.
 DR DrugCentral; P97449; -.
 DR GuidetoPHARMACOLOGY; 1560; -.
 DR MEROPS; M01.001; -.
 DR GlyConnect; 2126; 6 N-Linked glycans (3 sites).
 DR GlyGen; P97449; 13 sites.
 DR iPTMnet; P97449; -.
 DR PhosphoSitePlus; P97449; -.
 DR jPOST; P97449; -.
 DR MaxQB; P97449; -.
 DR PaxDb; P97449; -.
 DR PeptideAtlas; P97449; -.
 DR PRIDE; P97449; -.
 DR ProteomicsDB; 281971; -.
 DR Antibodypedia; 3713; 1911 antibodies.
 DR DNASU; 16790; -.
 DR Ensembl; ENSMUST00000049004; ENSMUSP00000035943; ENSMUSG00000039062.
 DR Ensembl; ENSMUST00000107392; ENSMUSP00000103015; ENSMUSG00000039062.
 DR GeneID; 16790; -.
 DR KEGG; mmu:16790; -.
 DR UCSC; uc009hzd.1; mouse.
 DR CTD; 290; -.
 DR MGI; MGI:5000466; Anpep.
 DR eggNOG; KOG1046; Eukaryota.
 DR GeneTree; ENSGT00940000154876; -.
 DR HOGENOM; CLU_003705_2_2_1; -.
 DR InParanoid; P97449; -.
 DR OMA; TAKWFIF; -.
 DR OrthoDB; 110058at2759; -.
 DR PhylomeDB; P97449; -.
 DR TreeFam; TF300395; -.
 DR Reactome; R-MMU-6798695; Neutrophil degranulation.
 DR BioGRID-ORCS; 16790; 0 hits in 53 CRISPR screens.
 DR ChiTaRS; Anpep; mouse.
 DR PRO; PR:P97449; -.
 DR Proteomes; UP000000589; Chromosome 7.
 DR RNAct; P97449; protein.
 DR Bgee; ENSMUSG00000039062; Expressed in jejunum and 225 other tissues.
 DR Genevisible; P97449; MM.
 DR GO; GO:0031526; C:brush border membrane; ISO:MGI.
 DR GO; GO:0005737; C:cytoplasm; IBA:GO_Central.
 DR GO; GO:0005793; C:endoplasmic reticulum-Golgi intermediate compartment; ISO:MGI.
 DR GO; GO:0009897; C:external side of plasma membrane; IDA:MGI.
 DR GO; GO:0070062; C:extracellular exosome; ISO:MGI.
 DR GO; GO:0005615; C:extracellular space; ISO:MGI.
 DR GO; GO:0016021; C:integral component of membrane; IEA:UniProtKB-KW.
 DR GO; GO:0005886; C:plasma membrane; ISO:MGI.
 DR GO; GO:0004177; F:aminopeptidase activity; ISO:MGI.
 DR GO; GO:0070006; F:metalloaminopeptidase activity; IBA:GO_Central.
 DR GO; GO:0042277; F:peptide binding; ISO:MGI.
 DR GO; GO:0008270; F:zinc ion binding; IBA:GO_Central.
 DR GO; GO:0001525; P:angiogenesis; IEA:UniProtKB-KW.
 DR GO; GO:0030154; P:cell differentiation; IEA:UniProtKB-KW.
 DR GO; GO:0035814; P:negative regulation of renal sodium excretion; ISO:MGI.
 DR GO; GO:0043171; P:peptide catabolic process; ISO:MGI.
 DR GO; GO:0006508; P:proteolysis; ISO:MGI.
 DR GO; GO:0008217; P:regulation of blood pressure; IBA:GO_Central.
 DR GO; GO:0007165; P:signal transduction; IBA:GO_Central.
 DR CDD; cd09601; M1_APN-Q_like; 1.
 DR Gene3D; 2.60.40.1730; -; 1.
 DR InterPro; IPR042097; Aminopeptidase_N-like_N.
 DR InterPro; IPR024571; ERAP1-like_C_dom.
 DR InterPro; IPR034016; M1_APN-tyr.
 DR InterPro; IPR001930; Peptidase_M1.
 DR InterPro; IPR014782; Peptidase_M1_dom.
 DR Pfam; PF11838; ERAP1_C; 1.
 DR Pfam; PF01433; Peptidase_M1; 1.
 DR PRINTS; PRO0756; ALADIPTASE.
 DR SUPFAM; SSF63737; SSF63737; 1.
 DR PROSITE; PS00142; ZINC_PROTEASE; 1.
 PE 1: Evidence at protein level;
 KW Aminopeptidase; Angiogenesis; Cell membrane; Developmental protein;
 KW Differentiation; Direct protein sequencing; Disulfide bond; Glycoprotein;
 KW Hydrolase; Membrane; Metal-binding; Metalloprotease; Phosphoprotein;
 KW Protease; Reference proteome; Signal-anchor; Sulfation; Transmembrane;
 KW Transmembrane helix; Zinc.
 FT CHAIN 1..966
 FT /note="Aminopeptidase N"
 FT /id="PRO_0000095082"
 FT TOPO_DOM 1..8
 FT /note="Cytoplasmic"
 FT /evidence="ECO:0000250|UniProtKB:P15144"
 FT TRANSMEM 9..32
 FT /note="Helical; Signal-anchor for type II membrane protein"
 FT /evidence="ECO:0000255"
 FT TOPO_DOM 33..966
 FT /note="Extracellular"
 FT /evidence="ECO:0000250|UniProtKB:P15144"
 FT REGION 33..68
 FT /note="Cytosolic Ser/Thr-rich junction"

FT	REGION	42..64
FT		/note="Disordered"
FT		/evidence="ECO:0000256 SAM:MobiDB-lite"
FT	REGION	69..966
FT		/note="Metalloprotease"
FT	REGION	351..355
FT		/note="Substrate binding"
FT		/evidence="ECO:0000250 UniProtKB:P15144"
FT	ACT_SITE	388
FT		/note="Proton acceptor"
FT		/evidence="ECO:0000255 PROSITE-ProRule:PRU10095"
FT	METAL	387
FT		/note="Zinc; catalytic"
FT		/evidence="ECO:0000255 PROSITE-ProRule:PRU10095"
FT	METAL	391
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FT	SITE	476
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FT		/evidence="ECO:0000250 UniProtKB:P15144"
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FT		/evidence="ECO:0007744 PubMed:17947660"
FT	CARBOHYD	106
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FT		/evidence="ECO:0000269 PubMed:19349973,
FT		ECO:0000269 PubMed:19656770"
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FT		/evidence="ECO:0000269 PubMed:19349973"
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FT	CARBOHYD	817
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FT		amino acid transport."
FT		/evidence="ECO:0000269 PubMed:22677001"
FT	MUTAGEN	388
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FT		mediated amino acid transport."
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FT		amino acid transport."
FT		/evidence="ECO:0000269 PubMed:22677001"
FT	MUTAGEN	476

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FT      /note="Y->F: No impact on substrate affinity of SLC6A19-
FT      mediated amino acid transport."
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FT  CONFLICT 62
FT      /note="T -> TATTTATTT (in Ref. 2; AAH17011/AAH40792)"
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FT  CONFLICT 84
FT      /note="S -> A (in Ref. 1; AAB19065)"
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FT  CONFLICT 106
FT      /note="N -> S (in Ref. 2; AAH17011/AAH40792)"
FT      /evidence="ECO:0000305"
FT  CONFLICT 181
FT      /note="Q -> E (in Ref. 2; AAH17011/AAH40792)"
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FT  CONFLICT 202
FT      /note="D -> G (in Ref. 2; AAH17011/AAH40792)"
FT      /evidence="ECO:0000305"
FT  CONFLICT 532
FT      /note="P -> L (in Ref. 2; AAH17011/AAH40792)"
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FT  CONFLICT 557
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FT  CONFLICT 557
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FT  CONFLICT 689
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FT  CONFLICT 726
FT      /note="T -> M (in Ref. 2; AAH17011/AAH40792)"
FT      /evidence="ECO:0000305"
FT  CONFLICT 966
FT      /note="S -> G (in Ref. 2; AAH17011/AAH40792)"
FT      /evidence="ECO:0000305"
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TTPAVDESKP WNQYRLPKTL IPDSYRVILR PYLTPNNQGL YIFQGNSTVR FTCNQTTDVI
IIHSSKLNLT LKGNHRVVLRL TLDGTPAPNI DKTELVERTE YLVVHLQGS L VEGRQYEMDS
QQQGE LADDL AGFYRSEYME GDVKKVVATT QMQAADARKS FPCFDEPAMK AMFNITLIYP
NNLIALSNML PKESKPYPED PSCTMTEFHS TPKMSTYLLA YIVSEFKNIS SVSANGVQIG
IWARPSAIDE GQGDYALNVT GPILNFFAQH YNTSYPLPKS DQIALPDFNA GAMENWGLVT
YRESSLVFDS QSSSISNKER VVTVIAHELA HQWFGNLVTV AWWNDLWLNE GFASYVEYLG
ADYAEPTWNL KDLMLNDVY RVMAVDALAS SHPLSSPADE IKTPDQIMEL FDSITYSKGA
SVIRMLSSFL TEDLFKKGLS SYLHTYQYSN TVYLDLWEHL QKAVNQQTAV QPPATVRTIM
DRWILQMGGP VITVNTNTGE ISQKHFLDLS KSNVTRPSEF NYIWIAPIPF LKSGQEDHYW
LDVEKNQSAK FQTSSNEWIL LNINVTGYLL VNYDENNNWKK LQNQLQTDLS VIPVINRAQI
IHDSFNLASA KMIPITLALD NTLFLVKAE YMPWQAALSS LNYFTLMFDR SEVYGPMKRY
LKKQVTPLEF YFQNRNTNNWV NRPPTLMEQY NEINAISTAC SSGLKECRDL VVELYSQWMK
NPNNNNTIHPN LRSTVYCNAI AFGGEEENWF AWEQFRNATL VNEADKLRS LACSKDVWIL
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FTENSS

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