

Protein View: P28825

Meprin A subunit alpha OS=Mus musculus OX=10090 GN=Mep1a PE=1 SV=4

Database: UP589_M_musculus
Score: 296
Monoisotopic mass (M_r): 84177
Calculated pI: 5.81

Sequence similarity is available as [an NCBI BLAST search of P28825 against nr](#).

Search parameters

MS data file: mas42E.tmp
Enzyme: Trypsin: cuts C-term side of KR unless next residue is P.
Variable modifications: Carbamidomethyl (C), Oxidation (M).

Protein sequence coverage: 17%

Matched peptides shown in **bold red**.

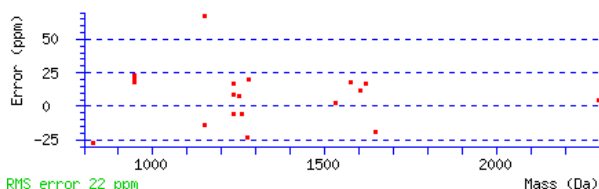
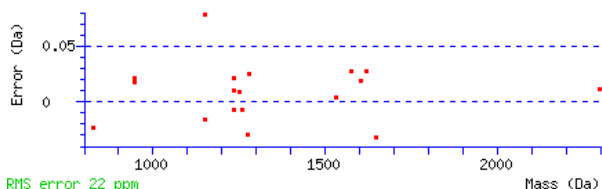
```

1 MLWIQPACLL SLIFSAHIAA VSIKHLNGS DHDTDVGEQK DIFEINLAAG
51 LNLFGQDILL PRTRNAMRDP SSRWKLPIDY ILADNLELNA KGAILHAFEM
101 FRLKSCVDFK PYEGESSYII FQKLSGCWSM IGDQQVGQNI SIGEGCDFKA
151 TIEHEILHAL GFFHEQSRTD RDDYVNIWWD QIITDYEHNF NTYDDNTITD
201 LNTPYDYESL MHYGPFSFNK NESIPTITTK IPEFNTIIGQ LPDFSALDLI
251 RLNRMYNCTA THTLLDHCDF EKTNVCGMIO GTRDDADWAH GDSSQPEQVD
301 HTLVGQCKGA GYFMFFNTSL GARGEAALLE SRILYPKRKQ QCLQFFYKMT
351 GSPADRFVW VRDDNAGKV RQLAKIQTFQ GDSDHNWKIA HVTLNEEKKF
401 RYVFLGTKGD PGNSSGGIYL DDITLTETPC PAGVWTIRNI SQILENTVKG
451 DKLVSPRFYN SEGYGVGVTI YPNGRITSNS GFLGLTFHLY SGDNDAILLEW
501 PVENRQAIMT ILDQQADTRN RMSLTLMFTT SKNQTSSAIN GSVIWDPSK
551 VGVDKDCDC FRSLDWGWGQ AISHQLLKRR NFLKGDLSII FVDFKDLTHL
601 NRTEVPASAR STMPRGLLLQ GQESPALGES SRKAMLEESL PSSLGQRHPS
651 RQKRSVENTG PMEDHNWPQY FRDPCDPNPC QNEGTCVNVK GMASCRCVSG
701 HAFYAGERC QAMHVHGSLL GLIGCIAGL IFLTFVTFTST TNGKLRQ
  
```

Unformatted sequence string: **747 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
337	105 - 123	766.3684	2296.0834	2296.0722	0.0112 0	44	0.0035	1	U	K.SCVDFKPYEGESSYIIFQK.L + Carbamidomethyl (C)
238	273 - 283	618.7913	1235.5681	1235.5751	-0.0070 0	56	0.00035	1	U	K.TNVCGMIOGTR.D + Carbamidomethyl (C)
239	273 - 283	618.7999	1235.5853	1235.5751	0.0102 0	62	9.7e-05	1	U	K.TNVCGMIOGTR.D + Carbamidomethyl (C)
240	273 - 283	618.8056	1235.5966	1235.5751	0.0215 0	44	0.0056	1	U	K.TNVCGMIOGTR.D + Carbamidomethyl (C)
244	273 - 283	626.7967	1251.5789	1251.5700	0.0089 0	26	0.37	1	U	K.TNVCGMIOGTR.D + Carbamidomethyl (C); Oxidation (M)
183	324 - 332	473.2621	944.5096	944.4927	0.0169 0	39	0.023	1	U	R.GEAALLES.R
184	324 - 332	473.2630	944.5115	944.4927	0.0188 0	39	0.026	1	U	R.GEAALLES.R
185	324 - 332	473.2637	944.5129	944.4927	0.0202 0	40	0.019	1	U	R.GEAALLES.R
186	324 - 332	473.2643	944.5141	944.4927	0.0214 0	41	0.015	1	U	R.GEAALLES.R
246	340 - 348	631.3019	1260.5893	1260.5961	-0.0069 0	42	0.011	1	U	K.QCCLQFFYK.M + Carbamidomethyl (C)
312	349 - 362	550.9294	1649.7664	1649.7984	-0.0320 1	24	0.53	1	U	K.MTGSPADRFVWVR.R
307	376 - 388	525.9203	1574.7391	1574.7114	0.0277 0	24	0.61	1	U	K.IQTFQGDSDHNWK.I
216	389 - 398	577.3063	1152.5980	1152.6139	-0.0158 0	17	3.1	1	U	K.IAHVTLNEEK.K
217	389 - 398	577.3530	1152.6915	1152.6139	0.0776 0	39	0.018	1	U	K.IAHVTLNEEK.K
258	389 - 399	427.9187	1280.7344	1280.7088	0.0256 1	2	80	5	U	K.IAHVTLNEEKK.F
94	402 - 408	414.2252	826.4359	826.4589	-0.0229 0	9	14	7	U	R.YVFLGTK.G
310	506 - 519	802.9107	1603.8068	1603.7876	0.0192 0	72	9e-06	1	U	R.QAIMTILDQADTR.N
311	506 - 519	810.9123	1619.8101	1619.7825	0.0276 0	73	6.7e-06	1	U	R.QAIMTILDQADTR.N + Oxidation (M)
254	522 - 532	638.3050	1274.5955	1274.6250	-0.0296 0	11	14	1	U	R.MSLTLMFTTSK.N + Oxidation (M)
303	551 - 562	511.8884	1532.6433	1532.6388	0.0045 1	34	0.054	1	U	K.VGVYDKDCDCFR.S + 2 Carbamidomethyl (C)



ID MEP1A MOUSE Reviewed; 747 AA.

AC P28825; B0V2P9; Q91WH9;

DT 01-DEC-1992, integrated into UniProtKB/Swiss-Prot.

DT 13-JUL-2010, sequence version 4.

DT 02-JUN-2021, entry version 191.

DE RecName: Full=Meprin A subunit alpha;

DE EC=3.4.24.18;

DE AltName: Full=Endopeptidase-2;

DE AltName: Full=MEP-1;

DE Flags: Precursor;

GN Name=Mepla;

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], AND PROTEIN SEQUENCE OF 65-103; 107-122;

RP 273-292; 314-348; 370-375; 377-386; 389-398 AND 527-557.

RC STRAIN=C3H/He, and C57BL/6J; TISSUE=Kidney;

RX PubMed=1374387;

RA Jiang W., Gorbea C.M., Flannery A.V., Beynon R.J., Grant G.A., Bond J.S.;

RT "The alpha subunit of meprin A. Molecular cloning and sequencing,

RT differential expression in inbred mouse strains, and evidence for divergent

RT evolution of the alpha and beta subunits.";

RL J. Biol. Chem. 267:9185-9193(1992).

RN [2]

RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].

RC STRAIN=C57BL/6J;

RX PubMed=19468303; DOI=10.1371/journal.pbio.1000112;

RA Church D.M., Goodstadt L., Hillier L.W., Zody M.C., Goldstein S., She X.,

RA Bult C.J., Agarwala R., Cherry J.L., DiCuccio M., Hlavina W., Kapustin Y.,

RA Meric P., Maglott D., Birtle Z., Marques A.C., Graves T., Zhou S.,

RA Teague B., Potamoudis K., Churas C., Place M., Herschleb J., Runnheim R.,

RA Forrest D., Amos-Landgraf J., Schwartz D.C., Cheng Z., Lindblad-Toh K.,

RA Eichler E.E., Ponting C.P.;

RT "Lineage-specific biology revealed by a finished genome assembly of the

RT mouse.";

RL PLoS Biol. 7:E1000112-E1000112(2009).

RN [3]

RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].

RC STRAIN=FVB/N; TISSUE=Kidney;

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 [4]

RP PROTEIN SEQUENCE OF 21-25 AND 65-69.

RX PubMed=8615815; DOI=10.1042/bj3150461;

RA Beynon R.J., Oliver S., Robertson D.H.L.;

RT "Characterization of the soluble, secreted form of urinary meprin.";

RL Biochem. J. 315:461-465(1996).

RN [5]

RP NUCLEOTIDE SEQUENCE [GENOMIC DNA] OF 62-258.

RC STRAIN=129;

RX PubMed=9161413; DOI=10.1016/s0378-1119(96)00834-7;

RA Jiang W., Flannery A.V.;

RT "Correlation of the exon/intron organization to the secondary structures of

RT the protease domain of mouse meprin alpha subunit.";

RL Gene 189:65-71(1997).

RN [6]

RP NUCLEOTIDE SEQUENCE [MRNA] OF 64-262.

RX PubMed=1939172;

RA Dumermuth E., Sterchi E.E., Jiang W., Wolz R.L., Bond J.S., Flannery A.V.,

RA Beynon R.J.;

RT "The astacin family of metalloendopeptidases.";

RL J. Biol. Chem. 266:21381-21385(1991).

RN [7]

RP PROTEIN SEQUENCE OF 65-72; 315-348 AND 529-546, ACTIVITY REGULATION,

RP BIOPHYSICOCHEMICAL PROPERTIES, AND GLYCOSYLATION.

RC STRAIN=ICR; TISSUE=Kidney;

RX PubMed=1894622;

RA Kounnas M.Z., Wolz R.L., Gorbea C.M., Bond J.S.;

RT "Meprin-A and -B. Cell surface endopeptidases of the mouse kidney.";

RL J. Biol. Chem. 266:17350-17357(1991).

RN [8]

RP SUBUNIT.

RX PubMed=1929422; DOI=10.1016/0003-9861(91)90580-c;

RA Gorbea C.M., Flannery A.V., Bond J.S.;

RT "Homo- and heterotetrameric forms of the membrane-bound

RT metalloendopeptidases meprin A and B.";

RL Arch. Biochem. Biophys. 290:549-553(1991).

RN [9]

RP CATALYTIC ACTIVITY, ACTIVITY REGULATION, AND BIOPHYSICOCHEMICAL PROPERTIES.

RX PubMed=1883833; DOI=10.1021/bi00098a029;

RA Wolz R.L., Harris R.B., Bond J.S.;

RT "Mapping the active site of meprin-A with peptide substrates and

RT inhibitors.";

RL Biochemistry 30:8488-8493(1991).

RN [10]

RP CATALYTIC ACTIVITY.

RX PubMed=11278902; DOI=10.1074/jbc.m011414200;

RA Bertenshaw G.P., Turk B.E., Hubbard S.J., Matters G.L., Bylander J.E.,

RA Crisman J.M., Cantley L.C., Bond J.S.;

RT "Marked differences between metalloproteases meprin A and B in substrate

RT and peptide bond specificity.";

RL J. Biol. Chem. 276:13248-13255(2001).

RN [11]

RP INTERACTION WITH MBL2.

RX PubMed=16116208; DOI=10.4049/jimmunol.175.5.3177;
RA Hirano M., Ma B.Y., Kawasaki N., Okimura K., Baba M., Nakagawa T., Miwa K.,
RA Kawasaki N., Oka S., Kawasaki T.;
RT "Mannan-binding protein blocks the activation of metalloproteases meprin
RT alpha and beta.";
RL J. Immunol. 175:3177-3185(2005).
RN [12]
RP SUBUNIT, GLYCOSYLATION AT ASN-28; ASN-139; ASN-221; ASN-257; ASN-317;
RP ASN-413; ASN-439; ASN-533 AND ASN-540, AND MUTAGENESIS OF ASN-139; SER-141;
RP ASN-221; ASN-257 AND THR-259.
RX PubMed=17040911; DOI=10.1074/jbc.m602769200;
RA Ishmael S.S., Ishmael F.T., Jones A.D., Bond J.S.;
RT "Protease domain glycans affect oligomerization, disulfide bond formation,
RT and stability of the meprin A metalloprotease homo-oligomer.";
RL J. Biol. Chem. 281:37404-37415(2006).
RN [13]
RP ACTIVITY REGULATION, AND BIOPHYSICOCHEMICAL PROPERTIES.
RX PubMed=17976009; DOI=10.1515/bc.2007.156;
RA Bylander J.E., Bertenshaw G.P., Matters G.L., Hubbard S.J., Bond J.S.;
RT "Human and mouse homo-oligomeric meprin A metalloendopeptidase: substrate
RT and inhibitor specificities.";
RL Biol. Chem. 388:1163-1172(2007).
RN [14]
RP IDENTIFICATION BY MASS SPECTROMETRY [LARGE SCALE ANALYSIS].
RC TISSUE=Kidney;
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 [15]
RP 3D-STRUCTURE MODELING.
RX PubMed=8508794; DOI=10.1111/j.1432-1033.1993.tb17915.x;
RA Stoecker W., Gomis-Rueth F.-X., Bode W., Zwilling R.;
RT "Implications of the three-dimensional structure of astacin for the
RT structure and function of the astacin family of zinc-endopeptidases.";
RL Eur. J. Biochem. 214:215-231(1993).
CC -!- CATALYTIC ACTIVITY:
CC Reaction=Hydrolysis of protein and peptide substrates preferentially on
CC carboxyl side of hydrophobic residues.; EC=3.4.24.18;
CC Evidence={ECO:0000269|PubMed:11278902, ECO:0000269|PubMed:1883833};
CC -!- COFACTOR:
CC Name=Zn(2+); Xref=ChEBI:CHEBI:29105;
CC Evidence={ECO:0000255|PROSITE-ProRule:PRU01211};
CC Note=Binds 1 zinc ion per subunit. {ECO:0000255|PROSITE-
CC ProRule:PRU01211};
CC -!- ACTIVITY REGULATION: Inhibited by metal ion chelators EDTA and 1,10-
CC phenanthroline, bradykinin analogs, cysteine, CONA65, and several
CC hydroxamate compounds, particularly tyrosine hydroxamate. Not inhibited
CC by 3,4-dichloroisocoumarin, soybean trypsin inhibitor, or the cysteine
CC proteinase inhibitors iodoacetic acid and E-64.
CC {ECO:0000269|PubMed:17976009, ECO:0000269|PubMed:1883833,
CC ECO:0000269|PubMed:1894622}.
CC -!- BIOPHYSICOCHEMICAL PROPERTIES:
CC Kinetic parameters:
CC KM=29.6 uM for GRP {ECO:0000269|PubMed:17976009,
CC ECO:0000269|PubMed:1883833, ECO:0000269|PubMed:1894622};
CC KM=67.2 uM for PTH 12-34 {ECO:0000269|PubMed:17976009,
CC ECO:0000269|PubMed:1883833, ECO:0000269|PubMed:1894622};
CC KM=111 uM for secretin {ECO:0000269|PubMed:17976009,
CC ECO:0000269|PubMed:1883833, ECO:0000269|PubMed:1894622};
CC KM=30.6 uM for substance P {ECO:0000269|PubMed:17976009,
CC ECO:0000269|PubMed:1883833, ECO:0000269|PubMed:1894622};
CC KM=156 uM for LHRH {ECO:0000269|PubMed:17976009,
CC ECO:0000269|PubMed:1883833, ECO:0000269|PubMed:1894622};
CC KM=22.3 uM for alpha-MSH {ECO:0000269|PubMed:17976009,
CC ECO:0000269|PubMed:1883833, ECO:0000269|PubMed:1894622};
CC KM=101 uM for bradykinin {ECO:0000269|PubMed:17976009,
CC ECO:0000269|PubMed:1883833, ECO:0000269|PubMed:1894622};
CC KM=290 uM for Arg-Pro-Pro-Gly-Npa-Ser-Pro-Phe-Arg
CC {ECO:0000269|PubMed:17976009, ECO:0000269|PubMed:1883833,
CC ECO:0000269|PubMed:1894622};
CC KM=331 uM for Arg-Pro-Pro-Gly-Npa-Ala-Pro-Phe-Arg
CC {ECO:0000269|PubMed:17976009, ECO:0000269|PubMed:1883833,
CC ECO:0000269|PubMed:1894622};
CC KM=174 uM for Arg-Pro-Pro-Gly-Npa-Arg-Pro-Phe-Arg
CC {ECO:0000269|PubMed:17976009, ECO:0000269|PubMed:1883833,
CC ECO:0000269|PubMed:1894622};
CC KM=226 uM for Arg-Pro-Pro-Gly-Npa-Phe-Pro-Phe-Arg
CC {ECO:0000269|PubMed:17976009, ECO:0000269|PubMed:1883833,
CC ECO:0000269|PubMed:1894622};
CC KM=182 uM for Arg-Pro-Pro-Gly-Npa-Lys-Pro-Phe-Arg
CC {ECO:0000269|PubMed:17976009, ECO:0000269|PubMed:1883833,
CC ECO:0000269|PubMed:1894622};
CC KM=339 uM for Arg-Pro-Pro-Gly-Npa-Glu-Pro-Phe-Arg
CC {ECO:0000269|PubMed:17976009, ECO:0000269|PubMed:1883833,
CC ECO:0000269|PubMed:1894622};
CC KM=366 uM for 2ABz-Arg-Pro-Gly-Phe-Ser-Pro-Npa-Arg
CC {ECO:0000269|PubMed:17976009, ECO:0000269|PubMed:1883833,
CC ECO:0000269|PubMed:1894622};
CC KM=296 uM for 2ABz-Arg-Pro-Ile-Phe-Ser-Pro-Npa-Arg
CC {ECO:0000269|PubMed:17976009, ECO:0000269|PubMed:1883833,
CC ECO:0000269|PubMed:1894622};
CC KM=183 uM for 2ABz-Arg-Hyp-Gly-Phe-Ser-Pro-Npa-Arg
CC {ECO:0000269|PubMed:17976009, ECO:0000269|PubMed:1883833,
CC ECO:0000269|PubMed:1894622};
CC KM=220 uM for 2ABz-Arg-Gly-Pro-Phe-Ser-Pro-Npa-Arg
CC {ECO:0000269|PubMed:17976009, ECO:0000269|PubMed:1883833,
CC ECO:0000269|PubMed:1894622};
CC KM=1380 uM for 2ABz-Arg-Pro-Gly-Ala-Ser-Pro-Npa-Arg
CC {ECO:0000269|PubMed:17976009, ECO:0000269|PubMed:1883833,

CC ECO:0000269|PubMed:1894622};
 CC KM=1220 uM for 2ABz-Arg-Pro-Gly-Glu-Ser-Pro-Npa-Arg
 CC {ECO:0000269|PubMed:17976009, ECO:0000269|PubMed:1883833,
 CC ECO:0000269|PubMed:1894622};
 CC KM=402 uM for 2ABz-Arg-Pro-Gly-Lys-Ser-Pro-Npa-Arg
 CC {ECO:0000269|PubMed:17976009, ECO:0000269|PubMed:1883833,
 CC ECO:0000269|PubMed:1894622};
 CC KM=2460 uM for 2ABz-Arg-Pro-Gly-Leu-Ser-Pro-Npa-Arg
 CC {ECO:0000269|PubMed:17976009, ECO:0000269|PubMed:1883833,
 CC ECO:0000269|PubMed:1894622};
 CC Temperature dependence:
 CC The half-life at 58 degrees Celsius is 50 minutes.
 CC {ECO:0000269|PubMed:17976009, ECO:0000269|PubMed:1883833,
 CC ECO:0000269|PubMed:1894622};
 CC -!- SUBUNIT: Homotetramer consisting of disulfide-linked alpha subunits,
 CC homooligomer consisting of disulfide-linked alpha subunit homodimers,
 CC or heterotetramer of two alpha and two beta subunits formed by non-
 CC covalent association of two disulfide-linked heterodimers. Genetic
 CC factors determine which oligomer(s) will be formed (strain-specific).
 CC Interacts with MBL2 through its carbohydrate moiety. This interaction
 CC may inhibit its catalytic activity. {ECO:0000269|PubMed:16116208,
 CC ECO:0000269|PubMed:17040911, ECO:0000269|PubMed:1929422}.
 CC -!- SUBCELLULAR LOCATION: Membrane; Single-pass type I membrane protein.
 CC -!- TISSUE SPECIFICITY: Kidney, intestinal brush borders and salivary
 CC ducts.
 CC -!- PTM: N-glycosylated; contains GlcNAc, galactose, mannose and a small
 CC amount of fucose. {ECO:0000269|PubMed:17040911,
 CC ECO:0000269|PubMed:1894622}.
 CC -!- SEQUENCE CAUTION:
 CC Sequence=AAA75354.1; Type=Erroneous initiation; Note=Extended N-terminus.; Evidence={ECO:0000305};
 CC Sequence=AAH15258.1; Type=Erroneous initiation; Note=Extended N-terminus.; Evidence={ECO:0000305};
 CC -----
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 CC -----
 DR EMBL; M74897; AAA75354.1; ALT_INIT; mRNA.
 DR EMBL; CT010585; -; NOT_ANNOTATED_CDS; Genomic_DNA.
 DR EMBL; BC015258; AAH15258.1; ALT_INIT; mRNA.
 DR EMBL; U62765; AAC53194.1; -; Genomic_DNA.
 DR PIR; A40195; A40195.
 DR RefSeq; NP_032611.2; NM_008585.2.
 DR RefSeq; XP_006523814.1; XM_006523751.3.
 DR PDB; 1IAF; Model; -; A=65-261.
 DR PDBsum; 1IAF; -.
 DR SMR; P28825; -.
 DR BioGRID; 201396; 2.
 DR IntAct; P28825; 4.
 DR MINT; P28825; -.
 DR STRING; 10090.ENSMUSP00000024707; -.
 DR MEROPS; M12.002; -.
 DR GlyGen; P28825; 9 sites.
 DR iPTMnet; P28825; -.
 DR PhosphoSitePlus; P28825; -.
 DR jPOST; P28825; -.
 DR MaxQB; P28825; -.
 DR PaxDb; P28825; -.
 DR PeptideAtlas; P28825; -.
 DR PRIDE; P28825; -.
 DR ProteomicsDB; 295924; -.
 DR DNASU; 17287; -.
 DR Ensembl; ENSMUST00000117137; ENSMUSP00000113838; ENSMUSG00000023914.
 DR GeneID; 17287; -.
 DR KEGG; mmu:17287; -.
 DR UCSC; uc008cpc.1; mouse.
 DR CTD; 4224; -.
 DR MGI; MGI:96963; Mep1a.
 DR eggNOG; KOG3714; Eukaryota.
 DR GeneTree; ENSGT00950000183111; -.
 DR HOGENOM; CLU_021966_1_0_1; -.
 DR InParanoid; P28825; -.
 DR OMA; VKFRYAF; -.
 DR OrthoDB; 241999at2759; -.
 DR PhylomeDB; P28825; -.
 DR TreeFam; TF315280; -.
 DR BRENDA; 3.4.24.18; 3474.
 DR SABIO-RK; P28825; -.
 DR BioGRID-ORCS; 17287; 1 hit in 46 CRISPR screens.
 DR ChiTaRS; Mep1a; mouse.
 DR PRO; PR:P28825; -.
 DR Proteomes; UP000000589; Chromosome 17.
 DR RNAct; P28825; protein.
 DR Bgee; ENSMUSG00000023914; Expressed in proximal tubule and 81 other tissues.
 DR ExpressionAtlas; P28825; baseline and differential.
 DR Genevisible; P28825; MM.
 DR GO; GO:0016020; C:membrane; IDA:MGI.
 DR GO; GO:0017090; C:mep1a complex; ISO:MGI.
 DR GO; GO:0004222; F:metalloendopeptidase activity; IBA:GO_Central.
 DR GO; GO:0008270; F:zinc ion binding; IEA:InterPro.
 DR CDD; cd06263; MAM; 1.
 DR Gene3D; 2.60.210.10; -; 1.
 DR Gene3D; 3.40.390.10; -; 1.
 DR InterPro; IPR013320; ConA-like_dom_sf.
 DR InterPro; IPR000742; EGF-like_dom.
 DR InterPro; IPR000998; MAM_dom.
 DR InterPro; IPR002083; MATH/TRAF_dom.
 DR InterPro; IPR008294; Mep1a.
 DR InterPro; IPR034301; Mep1a_alpha.
 DR InterPro; IPR024079; MetalloPept_cat_dom_sf.
 DR InterPro; IPR001506; Peptidase_M12A.
 DR InterPro; IPR006026; Peptidase_Metallo.
 DR InterPro; IPR008974; TRAF-like.

DR PANTHER; PTHR10127:SF824; PTHR10127:SF824; 1.
 DR Pfam; PF01400; Astacin; 1.
 DR Pfam; PF00008; EGF; 1.
 DR Pfam; PF00629; MAM; 1.
 DR PIRSF; PIRSF001196; Mepirin; 1.
 DR PRINTS; PR00480; ASTACIN.
 DR PRINTS; PR00020; MAMDOMAIN.
 DR SMART; SM00137; MAM; 1.
 DR SMART; SM00061; MATH; 1.
 DR SMART; SM00235; ZnMc; 1.
 DR SUPFAM; SSF49599; SSF49599; 1.
 DR SUPFAM; SSF49899; SSF49899; 1.
 DR PROSITE; PS51864; ASTACIN; 1.
 DR PROSITE; PS50026; EGF_3; 1.
 DR PROSITE; PS00740; MAM_1; 1.
 DR PROSITE; PS50060; MAM_2; 1.
 DR PROSITE; PS50144; MATH; 1.
 DR PROSITE; PS00142; ZINC_PROTEASE; 1.
 PE 1: Evidence at protein level;
 KW 3D-structure; Direct protein sequencing; Disulfide bond; EGF-like domain;
 KW Glycoprotein; Hydrolase; Membrane; Metal-binding; Metalloprotease;
 KW Protease; Reference proteome; Signal; Transmembrane; Transmembrane helix;
 KW Zinc; Zymogen.
 FT SIGNAL 1..20
 FT /evidence="ECO:0000269|PubMed:8615815"
 FT PROPEP 21..64
 FT /evidence="ECO:0000269|PubMed:1374387,
 FT ECO:0000269|PubMed:1894622, ECO:0000269|PubMed:8615815"
 FT /id="PRO_0000028879"
 FT CHAIN 65..747
 FT /note="Mepirin A subunit alpha"
 FT /id="PRO_0000028880"
 FT TOPO_DOM 65..713
 FT /note="Extracellular"
 FT /evidence="ECO:0000255"
 FT TRANSMEM 714..741
 FT /note="Helical"
 FT /evidence="ECO:0000255"
 FT TOPO_DOM 742..747
 FT /note="Cytoplasmic"
 FT /evidence="ECO:0000255"
 FT DOMAIN 65..259
 FT /note="Peptidase M12A"
 FT /evidence="ECO:0000255|PROSITE-ProRule:PRU01211"
 FT DOMAIN 263..432
 FT /note="MAM"
 FT /evidence="ECO:0000255|PROSITE-ProRule:PRU00128"
 FT DOMAIN 433..594
 FT /note="MATH"
 FT /evidence="ECO:0000255|PROSITE-ProRule:PRU00129"
 FT DOMAIN 671..711
 FT /note="EGF-like"
 FT /evidence="ECO:0000255|PROSITE-ProRule:PRU00076"
 FT REGION 638..663
 FT /note="Disordered"
 FT /evidence="ECO:0000256|SAM:MobiDB-lite"
 FT ACT_SITE 155
 FT /evidence="ECO:0000255|PROSITE-ProRule:PRU01211"
 FT METAL 154
 FT /note="Zinc; via tele nitrogen; catalytic"
 FT /evidence="ECO:0000255|PROSITE-ProRule:PRU01211"
 FT METAL 158
 FT /note="Zinc; via tele nitrogen; catalytic"
 FT /evidence="ECO:0000255|PROSITE-ProRule:PRU01211"
 FT METAL 164
 FT /note="Zinc; via tele nitrogen; catalytic"
 FT /evidence="ECO:0000255|PROSITE-ProRule:PRU01211"
 FT SITE 601
 FT /note="Not glycosylated"
 FT CARBOHYD 28
 FT /note="N-linked (GlcNAc...) asparagine"
 FT /evidence="ECO:0000269|PubMed:17040911"
 FT CARBOHYD 139
 FT /note="N-linked (GlcNAc...) asparagine"
 FT /evidence="ECO:0000269|PubMed:17040911"
 FT CARBOHYD 221
 FT /note="N-linked (GlcNAc...) asparagine"
 FT /evidence="ECO:0000269|PubMed:17040911"
 FT CARBOHYD 257
 FT /note="N-linked (GlcNAc...) asparagine"
 FT /evidence="ECO:0000269|PubMed:17040911"
 FT CARBOHYD 317
 FT /note="N-linked (GlcNAc...) asparagine"
 FT /evidence="ECO:0000269|PubMed:17040911"
 FT CARBOHYD 413
 FT /note="N-linked (GlcNAc...) asparagine"
 FT /evidence="ECO:0000269|PubMed:17040911"
 FT CARBOHYD 439
 FT /note="N-linked (GlcNAc...) asparagine"
 FT /evidence="ECO:0000269|PubMed:17040911"
 FT CARBOHYD 533
 FT /note="N-linked (GlcNAc...) asparagine"
 FT /evidence="ECO:0000269|PubMed:17040911"
 FT CARBOHYD 540
 FT /note="N-linked (GlcNAc...) asparagine"
 FT /evidence="ECO:0000269|PubMed:17040911"
 FT DISULFID 106..258
 FT /evidence="ECO:0000255|PROSITE-ProRule:PRU01211"
 FT DISULFID 127..146
 FT /evidence="ECO:0000255|PROSITE-ProRule:PRU01211"
 FT DISULFID 268..430

FT /evidence="ECO:0000255|PROSITE-ProRule:PRU00076"
 FT DISULFID 276
 FT /note="Interchain"
 FT /evidence="ECO:0000255|PROSITE-ProRule:PRU00076"
 FT DISULFID 307
 FT /note="Interchain"
 FT /evidence="ECO:0000255|PROSITE-ProRule:PRU00076"
 FT DISULFID 675..686
 FT /evidence="ECO:0000255|PROSITE-ProRule:PRU00076"
 FT DISULFID 680..695
 FT /evidence="ECO:0000255|PROSITE-ProRule:PRU00076"
 FT DISULFID 697..710
 FT /evidence="ECO:0000255|PROSITE-ProRule:PRU00076"
 FT MUTAGEN 139
 FT /note="N->Q: Increased susceptibility to heat-inactivation.
 FT Forms homodimers and oligomers; when associated with Q-221.
 FT Inactive, impaired ability to form homodimers or oligomers;
 FT when associated with Q-257 or Q-221 and Q-257."
 FT /evidence="ECO:0000269|PubMed:17040911"
 FT MUTAGEN 141
 FT /note="S->A: Impaired ability to form homodimers or
 FT oligomers; when associated with A-259."
 FT /evidence="ECO:0000269|PubMed:17040911"
 FT MUTAGEN 221
 FT /note="N->Q: Increased susceptibility to heat-inactivation.
 FT Forms homodimers and oligomers; when associated with Q-139
 FT or Q-257. Inactive, impaired ability to form homodimers or
 FT oligomers; when associated with Q-139 and Q-257."
 FT /evidence="ECO:0000269|PubMed:17040911"
 FT MUTAGEN 257
 FT /note="N->Q: Increased susceptibility to heat-inactivation.
 FT Forms homodimers and oligomers; when associated with Q-221.
 FT Inactive, impaired ability to form homodimers or oligomers;
 FT when associated with Q-139 or Q-139 and Q-221."
 FT /evidence="ECO:0000269|PubMed:17040911"
 FT MUTAGEN 259
 FT /note="T->A: Impaired ability to form homodimers or
 FT oligomers; when associated with A-141."
 FT /evidence="ECO:0000269|PubMed:17040911"
 FT CONFLICT 482
 FT /note="F -> L (in Ref. 1; AAA75354)"
 FT /evidence="ECO:0000305"
 FT CONFLICT 533
 FT /note="N -> I (in Ref. 7; AA sequence)"
 FT /evidence="ECO:0000305"
 FT CONFLICT 540
 FT /note="N -> S (in Ref. 7; AA sequence)"
 FT /evidence="ECO:0000305"
 FT CONFLICT 545
 FT /note="W -> T (in Ref. 7; AA sequence)"
 FT /evidence="ECO:0000305"
 SQ SEQUENCE 747 AA; 84231 MW; 2A1A268043559953 CRC64;
 MLWIQPACLL SLIFSAHIAA VSIKHLNGS DHDTDVGEQK DIFEINLAAG LNLFGQDILL
 PRTRNAMRDP SSRWKLPPIY ILADNLELNA KGAILHAFEM FRLKSCVDFK PYEGESSYII
 FQKLSGCWSM IGDQQVGQNI SIGEGCDFKA TIEHEILHAL GFFHEQSRD RDDYVNIWWD
 QIITDYEHNF NTYDDNTITD LNTPYDYESL MHYGPFSFNK NESIPTITTK IPEFNTIIGQ
 LPDFSAIDLI RLNRMYNCTA THTLLDHCDF EKTNVCGMIQ GTRDDADWAH GDSSQPEQVD
 HTLVGQCKGA GYFMFNTSL GARGEAALE SRILYPKRKQ QCLQFFYKMT GSPADRFEVW
 VRRDDNAGKV RQLAKIQTFQ GDSHDNWKIA HVTLNEEKKF RYVFLGTKGD PGNSSGGIYL
 DDITLTETPC PAGVWTIRNI SQILENTVKG DKLVSFRFYN SEGYGVTTL YPNGRITSNS
 GFLGLTFHLY SGDNDALIEW PVENRQAIMT ILDQEADTRN RMLSLTMFTT SKNQTSAIN
 GSVIWDPRPSK VGVYDKDCDC FRSLDWGWGQ AISHQLLRK NFLKGDLSII FVDFKDLTHL
 NRTEVPASAR STMPRGLLLQ QGESPALGES SRKAMLEESL PSSLGQRHPS RQKRSVENTG
 PMEDHNWPQY FRDPCDPNPC QNEGTCVNVK GMASCRCSVG HAFFYAGERC QAMHVVHGSLL
 GLLIGCIAGL IFLTFVTFTST TNGKLRQ

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