

Protein View: Q61847

Meprin A subunit beta OS=Mus musculus OX=10090 GN=Mep1b PE=1 SV=2

Database: UP589_M_musculus
Score: 131
Monoisotopic mass (M_r): 79450
Calculated pI: 5.59

Sequence similarity is available as [an NCBI BLAST search of Q61847 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: 10%

Matched peptides shown in **bold red**.

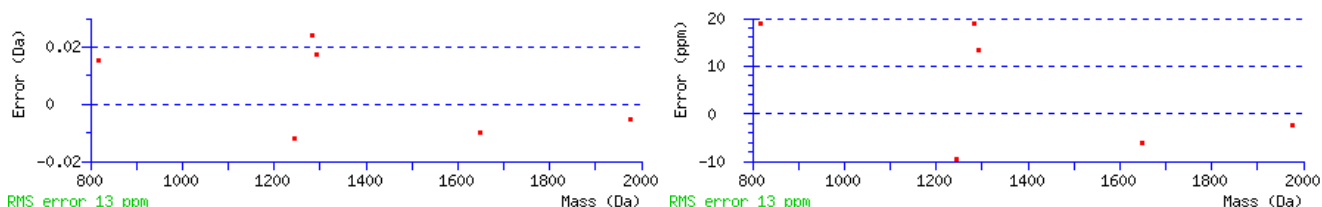
```

1 MDARHQPWFL VFATFLLVSG LPAPEKFVKD IDGGIDQDIF DINQGLGLDL
51 FEGDIKLEAN GKNSIIGDHK RWPHTIPYVL EDSLEMNAKG VILNAFERYR
101 LKTCIDFKPW SGEANYISVF KGSGCWSSVG NIHAGKQELS IGTNCDRIAT
151 VQHEFLHALG FWHQSRADR DDYVIVWDR IQPGKEHNFN IYNDVSDSL
201 NVPYDYTSVM HYSKTAFQNG TESTIVTRIS EFEDVIGQRM DFDSDYDLKL
251 NQLYNTSSL SFMDSCDFEL ENICGMIQSS GDSADWQVRS QVLSGPESDH
301 SKMGQCKDSG FFMHFNTSIL NEGATAMLES RLLYPKRGFQ CLEFYLYNSG
351 SGNDQLNIYT REYTTGQGG VLTLQRQIKE VPIGSWQLHY VTLQVTKKFR
401 VVFEGRLGPG TSSGGLSIDD INLSETRCPH HIWHIQNFTQ ILGGQDTSVY
451 SPPFYSSKGY AFQIYMDLRS STNVGIYFHL ISGANDDQLQ WPCPWQQATM
501 TLLDQNPDIR QRMFNQRSIT TDPTMTSDNG SYFWDPRSKV GVTDFVPNGT
551 QFSRGIGYGT TVFITRERLK SREFIKGDDI YILLTVEDIS HLNSTSAVPD
601 PVPTLAVHNA CSEVVCQNGG ICVVQDGRAE CKCPAGEDWW YMGRKCEKRG
651 STRDTVIIAV SSTVTVFAVM LIITLVSVYC TRRKYRKKAR ANTAAMTLEN
701 QHAF
  
```

Unformatted sequence string: **704 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
☒ 264	229 - 239	646.8363	1291.6580	1291.6408	0.0172	0	59	0.00022	1	U R.ISEFEDVIGQR.M
☒ 242	240 - 249	623.7807	1245.5468	1245.5587	-0.0119	0	11	12	1	U R.MDFSDYDLK.L
☒ 313	362 - 376	825.9209	1649.8273	1649.8373	-0.0100	0	59	0.00018	1	U R.EYTTGQQGGVLTQLR.Q
☒ 89	401 - 407	410.2475	818.4804	818.4650	0.0154	0	6	38	2	U R.VVFEGRLR.G
☒ 329	408 - 427	988.4795	1974.9444	1974.9494	-0.0051	0	39	0.014	1	U R.GPGTSSGGLSIDDINLSETR.C
☒ 261	555 - 566	642.8631	1283.7117	1283.6874	0.0243	0	47	0.0028	1	U R.GIGYGTTFVITR.E



ID MEPIB_MOUSE Reviewed; 704 AA.
 AC Q61847; Q059K0;
 DT 01-NOV-1997, integrated into UniProtKB/Swiss-Prot.
 DT 13-JUL-2010, sequence version 2.
 DT 02-JUN-2021, entry version 184.
 DE RecName: Full=Meprin A subunit beta;
 DE EC=3.4.24.63;
 DE AltName: Full=Endopeptidase-2;
 DE AltName: Full=Meprin B;
 DE Flags: Precursor;
 GN Name=Mep1b; Synonyms=Mep-1b;
 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] (ISOFORM 1), AND PROTEIN SEQUENCE OF 65-88;
 RP 96-109; 329-345 AND 541-549.
 RC TISSUE=Kidney;
 RX PubMed=8407940;
 RA Gorbea C.M., Marchand P., Jiang W., Copeland N.G., Gilbert D.J.,
 RA Jenkins N.A., Bond J.S.;
 RT "Cloning, expression, and chromosomal localization of the mouse meprin beta
 RT subunit.";
 RL J. Biol. Chem. 268:21035-21043(1993).
 RN [2]
 RP NUCLEOTIDE SEQUENCE [MRNA] (ISOFORM 2).
 RC TISSUE=Kidney;
 RX PubMed=8567689; DOI=10.1074/jbc.271.4.2271;
 RA Dietrich J.M., Bond J.S., Jiang W.;
 RT "A novel meprin beta' mRNA in mouse embryonal and human colon carcinoma
 RT cells.";
 RL J. Biol. Chem. 271:2271-2278(1996).
 RN [3]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA] (ISOFORM 1).
 RA Mural R.J., Adams M.D., Myers E.W., Smith H.O., Venter J.C.;
 RL Submitted (JUL-2005) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 1).
 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 [5]
 RP PROTEIN SEQUENCE OF 21-30 (ISOFORM 1), CATALYTIC ACTIVITY, ACTIVITY
 RP REGULATION, BIOPHYSICOCHEMICAL PROPERTIES, AND GLYCOSYLATION.
 RC STRAIN=C3H/He; 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 [6]
 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 [7]
 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 [8]
 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 [9]
 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).
 CC -!- FUNCTION: Membrane metallopeptidase that sheds many membrane-bound
 CC proteins. Exhibits a strong preference for acidic amino acids at the
 CC P1' position (PubMed:11278902). Known substrates include: FGF19, VGFA,
 CC IL1B, IL18, procollagen I and III, E-cadherin, KLK7, gastrin, ADAM10,
 CC tenascin-C. The presence of several pro-inflammatory cytokine among
 CC substrates implicate MEP1B in inflammation. It is also involved in
 CC tissue remodeling due to its capability to degrade extracellular matrix
 CC components (By similarity). {ECO:0000250|UniProtKB:Q16820,
 CC ECO:0000269|PubMed:11278902}.
 CC -!- CATALYTIC ACTIVITY:
 CC Reaction=Hydrolysis of proteins, including azocasein, and peptides.
 CC Hydrolysis of 5-His-|-Leu-6, 6-Leu-|-Cys-7, 14-Ala-|-Leu-15 and 19-
 CC Cys-|-Gly-20 bonds in insulin B chain.; EC=3.4.24.63;
 CC Evidence={ECO:0000269|PubMed:11278902, ECO:0000269|PubMed:1894622};
 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: Strongly inhibited by fetuin-A/AHSG (By
 CC similarity). Inhibited by cysteine and by the metal ion chelators EDTA
 CC and 1,10-phenanthroline. Not inhibited by 3,4-dichloroisocoumarin,
 CC soybean trypsin inhibitor, or the cysteine proteinase inhibitors
 CC iodoacetic acid and E-64. {ECO:0000250, ECO:0000269|PubMed:1894622}.
 CC -!- BIOPHYSICOCHEMICAL PROPERTIES:
 CC Temperature dependence:
 CC The half-life at 58 degrees Celsius is less than 3 minutes.

CC {ECO:0000269|PubMed:1894622};
 CC -!- SUBUNIT: Homotetramer consisting of disulfide-linked beta subunits, or
 CC heterotetramer of two alpha and two beta subunits formed by non-
 CC covalent association of two disulfide-linked heterodimers. Interacts
 CC with MBL2 through its carbohydrate moiety. This interaction may inhibit
 CC its catalytic activity. {ECO:0000269|PubMed:16116208,
 CC ECO:0000269|PubMed:1929422}.
 CC -!- SUBCELLULAR LOCATION: Cell membrane {ECO:0000250|UniProtKB:Q16820};
 CC Single-pass type I membrane protein {ECO:0000250|UniProtKB:Q16820}.
 CC Secreted {ECO:0000250|UniProtKB:Q16820}. Note=Homodimers are
 CC essentially membrane bound but may also be shed from the surface by
 CC ADAM-10 and ADAM-17. {ECO:0000250|UniProtKB:Q16820}.
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative promoter usage, Alternative splicing; Named isoforms=2;
 CC Name=1; Synonyms=Beta;
 CC IsoId=Q61847-1; Sequence=Displayed;
 CC Name=2; Synonyms=Beta';
 CC IsoId=Q61847-2; Sequence=VSP_005460;
 CC -!- TISSUE SPECIFICITY: Isoform 1 is expressed in kidney, intestinal brush
 CC borders, and salivary ducts. Isoform 2 has been found in carcinoma
 CC cells.
 CC -!- INDUCTION: By retinoic acid.
 CC -!- PTM: Proteolytically activated by trypsin in the intestinal lumen and
 CC kallikrein-related peptidases in other tissues. {ECO:0000250}.
 CC -!- PTM: N-glycosylated; contains high mannose and/or complex biantennary
 CC structures. {ECO:0000269|PubMed:1894622}.
 CC -----
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 CC -----
 DR EMBL; L15193; AAA75234.1; -; mRNA.
 DR EMBL; CH466557; EDK96962.1; -; Genomic_DNA.
 DR EMBL; BC125627; AAI25628.1; -; mRNA.
 DR EMBL; BC145979; AAI45980.1; -; mRNA.
 DR CCDS; CCDS37747.1; -. [Q61847-1]
 DR PIR; A48040; A48040.
 DR RefSeq; NP_032612.2; NM_008586.2. [Q61847-1]
 DR SMR; Q61847; -.
 DR BioGRID; 201397; 2.
 DR IntAct; Q61847; 4.
 DR MINT; Q61847; -.
 DR STRING; 10090.ENSMUSP00000080866; -.
 DR MEROPS; M12.004; -.
 DR GlyGen; Q61847; 9 sites.
 DR PhosphoSitePlus; Q61847; -.
 DR jPOST; Q61847; -.
 DR PaxDb; Q61847; -.
 DR PeptideAtlas; Q61847; -.
 DR PRIDE; Q61847; -.
 DR ProteomicsDB; 295925; -. [Q61847-1]
 DR ProteomicsDB; 295926; -. [Q61847-2]
 DR Antibodypedia; 22196; 73 antibodies.
 DR DNASU; 17288; -.
 DR Ensembl; ENSMUST00000082235; ENSMUSP00000080866; ENSMUSG00000024313. [Q61847-1]
 DR GeneID; 17288; -.
 DR KEGG; mmu:17288; -.
 DR UCSC; uc008eff.1; mouse. [Q61847-1]
 DR CTD; 4225; -.
 DR MGI; MGI:96964; Mep1b.
 DR eggNOG; KOG3714; Eukaryota.
 DR GeneTree; ENSGT00950000183111; -.
 DR HOGENOM; CLU_021966_0_0_1; -.
 DR InParanoid; Q61847; -.
 DR OMA; YVSIWD; -.
 DR OrthoDB; 241999at2759; -.
 DR PhylomeDB; Q61847; -.
 DR TreeFam; TF315280; -.
 DR BRENDA; 3.4.24.63; 3474.
 DR BioGRID-ORCS; 17288; 0 hits in 52 CRISPR screens.
 DR PRO; PR:Q61847; -.
 DR Proteomes; UP000000589; Chromosome 18.
 DR RNAct; Q61847; protein.
 DR Bgee; ENSMUSG00000024313; Expressed in jejunum and 77 other tissues.
 DR ExpressionAtlas; Q61847; baseline and differential.
 DR Genevisible; Q61847; MM.
 DR GO; GO:0005576; C:extracellular region; IEA:UniProtKB-SubCell.
 DR GO; GO:0005887; C:integral component of plasma membrane; ISO:MGI.
 DR GO; GO:0016020; C:membrane; IDA:MGI.
 DR GO; GO:0017090; C:mepripin A complex; ISO:MGI.
 DR GO; GO:0042802; F:identical protein binding; ISO:MGI.
 DR GO; GO:0004222; F:metalloendopeptidase activity; ISO:MGI.
 DR GO; GO:0008270; F:zinc ion binding; IEA:InterPro.
 DR GO; GO:0006954; P:inflammatory response; IEA:UniProtKB-KW.
 DR GO; GO:1901998; P:toxin transport; IMP:MGI.
 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; Mepripin.
 DR InterPro; IPR034302; Mepripin_beta.
 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:SF814; PTHR10127:SF814; 1.
 DR Pfam; PF01400; Astacin; 1.
 DR Pfam; PF00008; EGF; 1.
 DR Pfam; PF00629; MAM; 1.
 DR PIRSF; PIRSF001196; Meprin; 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 Alternative promoter usage; Alternative splicing; Cell membrane;
 KW Direct protein sequencing; Disulfide bond; EGF-like domain; Glycoprotein;
 KW Hydrolase; Inflammatory response; Membrane; Metal-binding; Metalloprotease;
 KW Protease; Reference proteome; Secreted; Signal; Transmembrane;
 KW Transmembrane helix; Zinc; Zymogen.
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 FT PROPEP 21..64
 FT /evidence="ECO:0000250"
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 FT /id="PRO_0000028886"
 FT TOPO_DOM 21..654
 FT /note="Extracellular"
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 FT TRANSMEM 655..678
 FT /note="Helical"
 FT /evidence="ECO:0000255"
 FT TOPO_DOM 679..704
 FT /note="Cytoplasmic"
 FT /evidence="ECO:0000255"
 FT DOMAIN 63..257
 FT /note="Peptidase M12A"
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 FT DOMAIN 261..430
 FT /note="MAM"
 FT /evidence="ECO:0000255|PROSITE-ProRule:PRU00128"
 FT DOMAIN 431..586
 FT /note="MATH"
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 FT DOMAIN 607..647
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 FT METAL 153
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 FT METAL 157
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 FT /evidence="ECO:0000250"
 FT CARBOHYD 193
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 FT /evidence="ECO:0000303|PubMed:8567689"
 FT /id="VSP_005460"
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 FT CONFLICT 26
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 FT CONFLICT 29
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 FT /evidence="ECO:0000305"
 FT CONFLICT 470
 FT /note="S -> Y (in Ref. 1; AAA75234 and 2; no nucleotide
 FT entry)"
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 SQ SEQUENCE 704 AA; 79501 MW; 04F92C493F701525 CRC64;
 MDARHQPWFL VFATLLVSG LPAPKEKFVKD IDGGIDQDIF DINQGLGLDL FEGDIKLEAN
 GKNSIIGDHK RWPHTIPYVL EDSLEMNAKG VILNAFERYR LKTCIDFKPW SGEANYISVF
 KGSGCWSSVG NIHAGKQELS IGTNCDRIAT VQHEFLHALG FWHEQSRADR DDYVIIWDR
 IQPGKEHNFN IYNDVSVDLSL NVPYDYTSVM HYSKTAFQNG TESTIVTRIS EFEDVIGQRM
 DFDYDILLKL NQLYNCTSSL SFMDSCDFEL ENICGMIQSS GDSADWQVRV QVLSGPESDH
 SKMGQCKDSG FFMHFNTSIL NEGATAMLES RLLYPKRGFQ CLEFYLYNSG SGNDQLNIYT
 REYTTGQQGG VLTLLQRQIKE VPIGSWQLHY VTLQVTKKFR VVFEGLRGPG TSSGGLSIDD
 INLSETRCPH HIWHIQNFTQ ILGGQDTSVY SPPFYSSKGY AFQIYMDLRS STNVGIYFHL
 ISGANDDQLQ WPCPWQATM TLLDQNPDIR QRMFNQRSIT TDPTMTSDNG SYFWDPRPSKV
 GVTDFVPNGT QFSRGIGYGT TVFITRERLK SREFIKGDDI YILLTVEDIS HLNSTSAVPD
 PVPTLAVHNA CSEVVCQNGG ICSVQDGRAE CKCPAGEDWW YMGKRCEKRG STRDVTIIAV
 SSTVTVFAVM LIITLVSVYC TRRKYRKKAR ANTAAMTLEN QHAF

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