MATRIX SCIENCE MASCOT Search Results

Protein View: P05064

Fructose-bisphosphate aldolase A OS=Mus musculus OX=10090 GN=Aldoa PE=1 SV=2

Database:	UP589_M_musculus
Score:	36
Monoisotopic mass (M_r):	39331
Calculated pI:	8.31

Sequence similarity is available as an NCBI BLAST search of P05064 against nr.

Search parameters

MS data file:	masA7A.tmp
Enzyme:	Trypsin: cuts C-term side of KR unless next residue is P.
Variable modifications:	Carbamidomethyl (C), Oxidation (M)

Protein sequence coverage: 7%

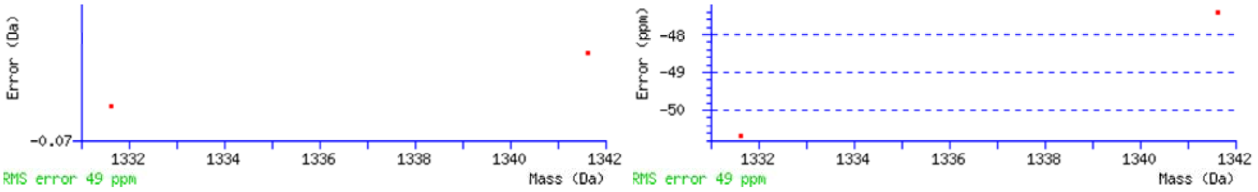
Matched peptides shown in ***bold red***.

1 MPHPYPALTP EQKKELSDIA HRIVAPGK**GI** **LAADESTGSI** **AK**RLQSIGTE
51 NTEENRRFYR QLLLTADDRV NPCIGGVILF HETLYQK**ADD** **GRPFPQVIK**S
101 KGGVVGIKVD KGVVPLAGTN GETTTQGLDG LSERCAQYKK DGADFAKWRC
151 VLKIGEHTPS ALAIMENANV LARYASICQQ NGIVPIVEPE ILPDGDHDLK
201 RCQYVTEKVL AAVYKALSDH HVYLEGTLLK PNMVTPGHAC TQKFSNEEIA
251 MATVTALRRT VPPAVTGVTF LSGGQSEEEA SINLNAINKC PLLKPWALTF
301 SYGRALQASA LKAWGGKKEN LKAAQEEYIK RALANSLACQ GKYTPSGQSG
351 AAASESLFIS NHAY

Unformatted sequence string: 364 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
410	29 – 42	666.8202	1331.6258	1331.6932	-0.0675	0	36	0.044	1	U	K.GILAADESTGSIAK.R
416	88 – 99	448.2208	1341.6405	1341.7041	-0.0636	0	10	15	1	U	K.ADDGRPFPQVIK.S



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ID   ALDOA_MOUSE             Reviewed;         364 AA.
AC   P05064;
DT   13-AUG-1987, integrated into UniProtKB/Swiss-Prot.
DT   23-JAN-2007, sequence version 2.
DT   08-NOV-2023, entry version 207.
DE   RecName: Full=Fructose-bisphosphate aldolase A;
DE            EC=4.1.2.13 {ECO:0000250|UniProtKB:P04075};
DE   AltName: Full=Aldolase 1;
DE   AltName: Full=Muscle-type aldolase;
GN   Name=Aldoa; Synonyms=Aldo1;
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].
RC   STRAIN=129;
RX   PubMed=3697100; DOI=10.1093/nar/15.24.10595;
RA   Mestek A., Stauffer J., Tolan D.R., Ciejek-Baez E.;
RT   "Sequence of a mouse brain aldolase A cDNA.";
RL   Nucleic Acids Res. 15:10595-10595(1987).
RN   [2]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC   STRAIN=C57BL/6J; TISSUE=Brain;
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).";
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RL   Genome Res. 14:2121-2127(2004).
RN   [3]
RP   NUCLEOTIDE SEQUENCE [GENOMIC DNA] OF 1-266 AND 295-364.
RX   PubMed=2365699; DOI=10.1016/s0021-9258(19)38465-0;
RA   Stauffer J.K., Colbert M.C., Ciejek-Baez E.;
RT   "Nonconservative utilization of aldolase A alternative promoters.";
RL   J. Biol. Chem. 265:11773-11782(1990).
RN   [4]
RP   PROTEIN SEQUENCE OF 2-22; 29-57; 61-109; 112-134; 154-258; 260-312 AND
RP   323-364, AND IDENTIFICATION BY MASS SPECTROMETRY.
RC   STRAIN=C57BL/6J, and OF1; TISSUE=Brain, and Hippocampus;
RA   Lubec G., Kang S.U., Klug S., Yang J.W., Zigmond M., Sunyer B., Chen W.-Q.;
RL   Submitted (JAN-2009) to UniProtKB.
RN   [5]
RP   NUCLEOTIDE SEQUENCE [MRNA] OF 99-355.
RX   PubMed=3009179; DOI=10.1111/j.1432-1033.1986.tb09572.x;
RA   Paolella G., Buono P., Mancini P., Izzo P., Salvatore F.;
RT   "Structure and expression of mouse aldolase genes. Brain-specific aldolase
RT   C amino acid sequence is closely related to aldolase A.";
RL   Eur. J. Biochem. 156:229-235(1986).
RN   [6]
RP   IDENTIFICATION BY MASS SPECTROMETRY [LARGE SCALE ANALYSIS].
RC   TISSUE=Brain, Brown adipose tissue, Heart, Kidney, Liver, Lung,
RC   Pancreas, 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).
CC   -!- FUNCTION: Catalyzes the reversible conversion of beta-D-fructose 1,6-
CC       bisphosphate (FBP) into two triose phosphate and plays a key role in
CC       glycolysis and gluconeogenesis (By similarity). In addition, may also
CC       function as scaffolding protein (By similarity). {ECO:0000250,
CC       ECO:0000250|UniProtKB:P04075}.
CC   -!- CATALYTIC ACTIVITY:
CC       Reaction=beta-D-fructose 1,6-bisphosphate = D-glyceraldehyde 3-
CC         phosphate + dihydroxyacetone phosphate; Xref=Rhea:RHEA:14729,
CC         ChEBI:CHEBI:32966, ChEBI:CHEBI:57642, ChEBI:CHEBI:59776; EC=4.1.2.13;
CC         Evidence={ECO:0000250|UniProtKB:P04075};
CC       PhysiologicalDirection=left-to-right; Xref=Rhea:RHEA:14730;
CC         Evidence={ECO:0000250|UniProtKB:P04075};
CC   -!- PATHWAY: Carbohydrate degradation; glycolysis; D-glyceraldehyde 3-
CC       phosphate and glycerone phosphate from D-glucose: step 4/4.
CC   -!- SUBUNIT: Homotetramer. Interacts with SNX9 and WAS. Interacts with
CC       FBP2; the interaction blocks FBP2 inhibition by physiological
CC       concentrations of AMP and reduces inhibition by Ca(2+) (By similarity).
CC       {ECO:0000250}.
CC   -!- SUBCELLULAR LOCATION: Cytoplasm, myofibril, sarcomere, I band
CC       {ECO:0000250|UniProtKB:P00883}. Cytoplasm, myofibril, sarcomere, M line
CC       {ECO:0000250|UniProtKB:P00883}. Note=In skeletal muscle, accumulates
CC       around the M line and within the I band, colocalizing with FBP2 on both
CC       sides of the Z line in the absence of Ca(2+).
CC       {ECO:0000250|UniProtKB:P00883}.
CC   -!- MISCELLANEOUS: In vertebrates, three forms of this ubiquitous
CC       glycolytic enzyme are found, aldolase A in muscle, aldolase B in liver
CC       and aldolase C in brain.
CC   -!- SIMILARITY: Belongs to the class I fructose-bisphosphate aldolase
CC       family. {ECO:0000305}.
CC   ---------------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see https://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution (CC BY 4.0) License
CC   ---------------------------------------------------------------------------
DR   EMBL; X03797; CAA27423.1; -; mRNA.
DR   EMBL; BC043026; AAH43026.1; -; mRNA.
DR   EMBL; BC050896; AAH50896.1; -; mRNA.
DR   EMBL; J05517; AAA37210.2; -; Genomic_DNA.
DR   EMBL; Y00516; CAA68571.1; -; mRNA.
DR   CCDS; CCDS21845.1; -.
DR   PIR; S06323; ADMSA.
DR   RefSeq; NP_001170779.1; NM_001177308.1.
DR   RefSeq; NP_031464.1; NM_007438.4.
DR   RefSeq; XP_006507273.1; XM_006507210.2.
DR   RefSeq; XP_006507274.1; XM_006507211.3.
DR   AlphaFoldDB; P05064; -.
DR   SMR; P05064; -.
DR   BioGRID; 198067; 35.
DR   IntAct; P05064; 22.
DR   STRING; 10090.ENSMUSP00000084846; -.
DR   MoonProt; P05064; -.
DR   GlyGen; P05064; 2 sites, 1 O-linked glycan (2 sites).
DR   iPTMnet; P05064; -.
DR   PhosphoSitePlus; P05064; -.
DR   SwissPalm; P05064; -.
DR   COMPLUYEAST-2DPAGE; P05064; -.
DR   REPRODUCTION-2DPAGE; IPI00221402; -.
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DR   SWISS-2DPAGE; P05064; -.
DR   EPD; P05064; -.
DR   jPOST; P05064; -.
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DR   PeptideAtlas; P05064; -.
DR   ProteomicsDB; 296171; -.
DR   Pumba; P05064; -.
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DR   GeneID; 11674; -.
DR   KEGG; mmu:11674; -.
DR   UCSC; uc009jsu.2; mouse.
DR   AGR; MGI:87994; -.
DR   CTD; 226; -.
DR   MGI; MGI:87994; Aldoa.
DR   VEuPathDB; HostDB:ENSMUSG00000030695; -.
DR   eggNOG; KOG1557; Eukaryota.
DR   GeneTree; ENSGT00950000182987; -.
DR   HOGENOM; CLU_031243_0_0_1; -.
DR   InParanoid; P05064; -.
DR   OMA; WRAVITI; -.
DR   OrthoDB; 3664741at2759; -.
DR   PhylomeDB; P05064; -.
DR   Reactome; R-MMU-114608; Platelet degranulation.
DR   Reactome; R-MMU-6798695; Neutrophil degranulation.
DR   Reactome; R-MMU-70171; Glycolysis.
DR   Reactome; R-MMU-70263; Gluconeogenesis.
DR   SABIO-RK; P05064; -.
DR   UniPathway; UPA00109; UER00183.
DR   BioGRID-ORCS; 11674; 34 hits in 80 CRISPR screens.
DR   ChiTaRS; Aldoa; mouse.
DR   PRO; PR:P05064; -.
DR   Proteomes; UP000000589; Chromosome 7.
DR   RNAct; P05064; Protein.
DR   Bgee; ENSMUSG00000030695; Expressed in gastrocnemius medialis and 276 other tissues.
DR   ExpressionAtlas; P05064; baseline and differential.
DR   Genevisible; P05064; MM.
DR   GO; GO:0015629; C:actin cytoskeleton; ISO:MGI.
DR   GO; GO:0005737; C:cytoplasm; IDA:MGI.
DR   GO; GO:0005829; C:cytosol; IDA:MGI.
DR   GO; GO:0070062; C:extracellular exosome; ISO:MGI.
DR   GO; GO:0005615; C:extracellular space; HDA:BHF-UCL.
DR   GO; GO:0000792; C:heterochromatin; ISO:MGI.
DR   GO; GO:0031430; C:M band; IEA:UniProtKB-SubCell.
DR   GO; GO:0016020; C:membrane; IDA:UniProtKB.
DR   GO; GO:0043209; C:myelin sheath; HDA:UniProtKB.
DR   GO; GO:0005886; C:plasma membrane; IDA:MGI.
DR   GO; GO:0032991; C:protein-containing complex; IDA:UniProtKB.
DR   GO; GO:0035686; C:sperm fibrous sheath; IDA:MGI.
DR   GO; GO:0061827; C:sperm head; ISO:MGI.
DR   GO; GO:0030018; C:Z disc; IDA:UniProtKB.
DR   GO; GO:0008092; F:cytoskeletal protein binding; ISO:MGI.
DR   GO; GO:0070061; F:fructose binding; ISO:MGI.
DR   GO; GO:0004332; F:fructose-bisphosphate aldolase activity; IDA:MGI.
DR   GO; GO:0042802; F:identical protein binding; ISO:MGI.
DR   GO; GO:0002020; F:protease binding; IPI:UniProtKB.
DR   GO; GO:0006754; P:ATP biosynthetic process; ISO:MGI.
DR   GO; GO:0007339; P:binding of sperm to zona pellucida; ISO:MGI.
DR   GO; GO:0061621; P:canonical glycolysis; IDA:MGI.
DR   GO; GO:0030388; P:fructose 1,6-bisphosphate metabolic process; ISO:MGI.
DR   GO; GO:0006000; P:fructose metabolic process; ISO:MGI.
DR   GO; GO:0006096; P:glycolytic process; ISS:UniProtKB.
DR   GO; GO:0061615; P:glycolytic process through fructose-6-phosphate; IC:MGI.
DR   GO; GO:0019242; P:methylglyoxal biosynthetic process; ISO:MGI.
DR   GO; GO:0046716; P:muscle cell cellular homeostasis; ISO:MGI.
DR   GO; GO:0030335; P:positive regulation of cell migration; IMP:CAFA.
DR   GO; GO:0051289; P:protein homotetramerization; ISS:UniProtKB.
DR   GO; GO:0008360; P:regulation of cell shape; ISO:MGI.
DR   GO; GO:0006941; P:striated muscle contraction; ISO:MGI.
DR   CDD; cd00948; FBP_aldolase_I_a; 1.
DR   Gene3D; 3.20.20.70; Aldolase class I; 1.
DR   InterPro; IPR029768; Aldolase_I_AS.
DR   InterPro; IPR013785; Aldolase_TIM.
DR   InterPro; IPR000741; FBA_I.
DR   NCBIfam; NF033379; FrucBisAld_I; 1.
DR   PANTHER; PTHR11627; FRUCTOSE-BISPHOSPHATE ALDOLASE; 1.
DR   PANTHER; PTHR11627:SF1; FRUCTOSE-BISPHOSPHATE ALDOLASE A; 1.
DR   Pfam; PF00274; Glycolytic; 1.
DR   SUPFAM; SSF51569; Aldolase; 1.
DR   PROSITE; PS00158; ALDOLASE_CLASS_I; 1.
PE   1: Evidence at protein level;
KW   Acetylation; Cytoplasm; Direct protein sequencing; Glycolysis;
KW   Hydroxylation; Isopeptide bond; Lyase; Phosphoprotein; Reference proteome;
KW   Schiff base; Ubl conjugation.
FT   INIT_MET        1
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FT                   /note="Proton acceptor"
FT                   /evidence="ECO:0000250"
FT   ACT_SITE        230
FT                   /note="Schiff-base intermediate with dihydroxyacetone-P"
FT   BINDING         56
FT                   /ligand="substrate"
FT   BINDING         147
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FT   SITE            364
FT                   /note="Necessary for preference for fructose 1,6-
FT                   bisphosphate over fructose 1-phosphate"
FT   MOD_RES         5
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     GETTTQGLDG LSERCAQYKK DGADFAKWRC VLKIGEHTPS ALAIMENANV LARYASICQQ
     NGIVPIVEPE ILPDGDHDLK RCQYVTEKVL AAVYKALSDH HVYLEGTLLK PNMVTPGHAC
     TQKFSNEEIA MATVTALRRT VPPAVTGVTF LSGGQSEEEA SINLNAINKC PLLKPWALTF
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     NHAY
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