



MASCOT Search Results

Protein View: Q6PIC6

Sodium/potassium-transporting ATPase subunit alpha-3 OS=Mus musculus OX=10090 GN=Atp1a3 PE=1 SV=1

Database: UP589_M_musculus
Score: 76
Monoisotopic mass (M_r): 111620
Calculated pI: 5.26

Sequence similarity is available as [an NCBI BLAST search of Q6PIC6 against nr.](#)

Search parameters

MS data file: masA79.tmp
Enzyme: Trypsin: cuts C-term side of KR unless next residue is P.
Variable modifications: [Carbamidomethyl \(C\)](#), [Oxidation \(M\)](#)

Protein sequence coverage: 5%

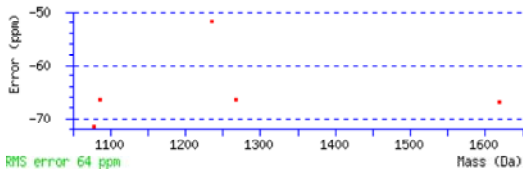
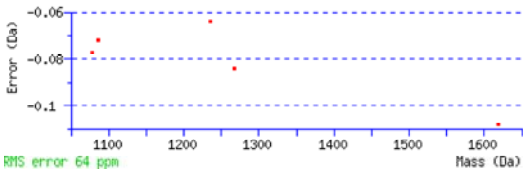
Matched peptides shown in **bold red**.

1 MGDKKDDKSS PKKSKAKERR DLDDLKKEVA MTEHKMSVEE VCRKYNTDCV
51 QGLTHSKAQE ILARDGPNAL TPPPTTPEWV KFCRQLFGGF SILLWIGAIL
101 CFLAYGIQAG TEDDPSPGDNL YLGIVLAAVV IITGCFSYQY EAKSSKIMES
151 **FKNMVFPQQAL VIREGEKMQV** NAEVVVVGDL VEIKGGDRVP ADLRIISAHG
201 **CKVDNSSLTG ESEPPQTRSPD** CTHDNPLETR NITFFSTNCV EGTARGVVVA
251 TGDRTVMGRI ATLASGLEVG KTPIAIEIEH PIQLITGVAV FLGVSFFILS
301 LILGYTWLEA VIFLIGIIVA NVPEGLLATV TVCLTLTAKR MARKNCLVKV
351 LEAVETLGST STICSDKTGT LTQNRMTVAH MWFNQIHEA DTTEDQSGTS
401 FDKSSHTWVA LSHIAGLCNR AVFKGGQDNI PVLKRDVAGD ASESALLK**CI**
451 **ELSSGSVVKLM** RERNKKVAEI PFNSTNKYQL SIHETEDPND NRYLLVMKGA
501 PERILDRCAT ILLQGKEQPL DEEMKEAFQN AYLELGGLGE RVLGFCHYYL
551 PEEQFPKGFA FDCDDVNFTT DNLCFVGLMS MIDPPRAAVP DAVGKCRSAG
601 IKVIMVTGDH PITAKAIAKG VGIISEGNET VEDIAAR**LNI** **PVSQVNPRDA**
651 KACVIHGTDL KDFTSEQIDE ILQNHTEIVF ARTSPQQK**LI** **IIVEGCQRQGA**
701 IVAVTGSGVN DSPALKKADI GVAMGIAGSD VSKQAADMIL LDDNFASIVT
751 GVEEGRLIFD NLKKSIAITL TSNIPETIPF LLFIMANIPL PLGTITILCI
801 DLGTDMPAI SLAYEAAESD IMKRQPRNPR TDKLVNERLI SMAYGQIGMI
851 QALGGFFSYF VILAENGFLP GNLVGIRLNV DDRTVNDLED SYGQQWTYEQ
901 RKVVEFTCHT AFFVSIVVVQ WADLIICKTR RNSVFQQGMK NKILIFGLFE
951 ETALAAFLSY CPGMDVALRM YPLKPSWWFC AFPYSFLIFV YDEIRKLILR
1001 RNPGGWVEKE TTY

Unformatted sequence string: **1013 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
371	153 - 163	634.8187	1267.6229	1267.7071	-0.0842	0 30	0.15	1	U	K.NMVPQQALVIR.E
413	203 - 217	810.3249	1618.6353	1618.7435	-0.1081	0 46	0.0027	1	U	K.VDNSSLTGESEPPQTR.S
331	449 - 458	540.2351	1078.4557	1078.5329	-0.0772	0 19	2.2	5	U	K.CIELSSGSVK.L + Carbamidomethyl (C)
356	638 - 648	618.8247	1235.6349	1235.6986	-0.0637	0 52	0.00099	1	U	R.LNIPVSVQNPR.D
334	689 - 697	544.2639	1086.5133	1086.5856	-0.0723	0 27	0.35	1	U	K.LIIVEGCQR.Q + Carbamidomethyl (C)



ID AT1A3_MOUSE Reviewed; 1013 AA.
AC Q6PIC6;
DT 13-SEP-2004, integrated into UniProtKB/Swiss-Prot.
DT 05-JUL-2004, sequence version 1.
DT 08-NOV-2023, entry version 163.
DE RecName: Full=Sodium/potassium-transporting ATPase subunit alpha-3;
DE Short=Na(+)/K(+) ATPase alpha-3 subunit;
DE EC=7.2.2.13;
DE AltName: Full=Na(+)/K(+) ATPase alpha(III) subunit;
DE AltName: Full=Sodium pump subunit alpha-3;
GN Name=Atp1a3;
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 [LARGE SCALE MRNA].
RC TISSUE=Eye;
RX PubMed=15489334; DOI=10.1101/gr.2596504;
RG The MGC Project Team;

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RT  "The status, quality, and expansion of the NIH full-length cDNA project:
the Mammalian Gene Collection (MGC).";
RL  Genome Res. 14:2121-2127(2004).
RN  [2]
RP  PROTEIN SEQUENCE OF 21-27; 36-81; 153-163; 168-184; 203-254; 260-271;
RP  350-367; 404-420; 425-434; 436-458; 466-492; 517-557; 587-595; 603-615;
RP  620-648; 652-682; 689-764; 878-901; 931-940; 943-969 AND 1001-1009.
RC  STRAIN=C57BL/6J; TISSUE=Brain;
RA  Lubec G., Kang S.U.;
RL  Submitted (APR-2007) to UniProtKB.
RN  [3]
RP  PHOSPHORYLATION [LARGE SCALE ANALYSIS] AT SER-265, AND IDENTIFICATION BY
RP  MASS SPECTROMETRY [LARGE SCALE ANALYSIS].
RX  PubMed=15648052; DOI=10.1002/pmic.200401066;
RA  Vosseller K., Hansen K.C., Chalkley R.J., Trinidad J.C., Wells L.,
RA  Hart G.W., Burlingame A.L.;
RT  "Quantitative analysis of both protein expression and serine / threonine
RT  post-translational modifications through stable isotope labeling with
RT  dithiothreitol.";
RL  Proteomics 5:388-398(2005).
RN  [4]
RP  PHOSPHORYLATION [LARGE SCALE ANALYSIS] AT TYR-548, AND IDENTIFICATION BY
RP  MASS SPECTROMETRY [LARGE SCALE ANALYSIS].
RC  TISSUE=Brain;
RX  PubMed=18034455; DOI=10.1021/pr0701254;
RA  Ballif B.A., Carey G.R., Sunyaev S.R., Gygi S.P.;
RT  "Large-scale identification and evolution indexing of tyrosine
RT  phosphorylation sites from murine brain.";
RL  J. Proteome Res. 7:311-318(2008).
RN  [5]
RP  PHOSPHORYLATION [LARGE SCALE ANALYSIS] AT SER-56 AND SER-218, AND
RP  IDENTIFICATION BY MASS SPECTROMETRY [LARGE SCALE ANALYSIS].
RC  TISSUE=Brain, Brown adipose tissue, and Liver;
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: This is the catalytic component of the active enzyme, which
CC  catalyzes the hydrolysis of ATP coupled with the exchange of sodium and
CC  potassium ions across the plasma membrane. This action creates the
CC  electrochemical gradient of sodium and potassium ions, providing the
CC  energy for active transport of various nutrients (By similarity).
CC  {ECO:0000250}.
CC  -!- CATALYTIC ACTIVITY:
CC  Reaction=ATP + H2O + K(+)(out) + Na(+)(in) = ADP + H(+) + K(+)(in) +
CC  Na(+)(out) + phosphate; Xref=Rhea:RHEA:18353, ChEBI:CHEBI:15377,
CC  ChEBI:CHEBI:15378, ChEBI:CHEBI:29101, ChEBI:CHEBI:29103,
CC  ChEBI:CHEBI:30616, ChEBI:CHEBI:43474, ChEBI:CHEBI:456216;
CC  EC=7.2.2.13;
CC  -!- SUBUNIT: The sodium/potassium-transporting ATPase is composed of a
CC  catalytic alpha subunit, an auxiliary non-catalytic beta subunit and an
CC  additional regulatory subunit. Interacts with regulatory subunit FXYDL.
CC  {ECO:0000250|UniProtKB:P06687}.
CC  -!- SUBCELLULAR LOCATION: Cell membrane {ECO:0000250}; Multi-pass membrane
CC  protein {ECO:0000250}.
CC  -!- SIMILARITY: Belongs to the cation transport ATPase (P-type) (TC 3.A.3)
CC  family. Type IIC subfamily. {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; BC034645; AAH34645.1; -; mRNA.
DR  EMBL; BC037206; AAH37206.1; -; mRNA.
DR  EMBL; BC042894; AAH42894.1; -; mRNA.
DR  CCDS; CCDS20969.2; -.
DR  RefSeq; NP_001277398.1; NM_001290469.1.
DR  AlphaFoldDB; Q6PIC6; -.
DR  SMR; Q6PIC6; -.
DR  BioGRID; 231339; 19.
DR  IntAct; Q6PIC6; 10.
DR  MINT; Q6PIC6; -.
DR  STRING; 10090.ENSMUSP00000099922; -.
DR  GlyConnect; 2725; 1 N-Linked glycan (1 site).
DR  GlyCosmos; Q6PIC6; 1 site, 1 glycan.
DR  GlyGen; Q6PIC6; 4 sites, 1 N-linked glycan (1 site), 1 O-linked glycan (3 sites).
DR  iPTMnet; Q6PIC6; -.
DR  PhosphoSitePlus; Q6PIC6; -.
DR  SwissPalm; Q6PIC6; -.
DR  jPOST; Q6PIC6; -.
DR  MaxQB; Q6PIC6; -.
DR  PaxDb; 10090-ENSMUSP00000099922; -.
DR  PeptideAtlas; Q6PIC6; -.
DR  ProteomicsDB; 277263; -.
DR  DNASU; 232975; -.
DR  Ensembl; ENSMUST00000080882; ENSMUSP00000079691; ENSMUSG00000040907.
DR  GeneID; 232975; -.
DR  KEGG; mmu:232975; -.
DR  UCSC; uc009frf.2; mouse.
DR  AGR; MGI:88107; -.
DR  CTD; 478; -.
DR  MGI; MGI:88107; Atpla3.
DR  VEuPathDB; HostDB:ENSMUSG00000040907; -.
DR  eggNOG; KOG0203; Eukaryota.
DR  GeneTree; ENSGT00940000160476; -.
DR  HOGENOM; CLU_002360_4_3_1; -.
DR  InParanoid; Q6PIC6; -.
DR  OMA; FGIDDYI; -.
DR  OrthoDB; 203629at2759; -.
DR  Reactome; R-MMU-5578775; Ion homeostasis.
DR  Reactome; R-MMU-936837; Ion transport by P-type ATPases.
DR  BioGRID-ORCS; 232975; 3 hits in 63 CRISPR screens.
DR  ChiTaRS; Atpla3; mouse.
DR  PRO; PR:Q6PIC6; -.
DR  Proteomes; UP000000589; Chromosome 7.
DR  RNAct; Q6PIC6; Protein.
DR  Bgee; ENSMUSG00000040907; Expressed in primary visual cortex and 130 other tissues.
DR  ExpressionAtlas; Q6PIC6; baseline and differential.
DR  Genevisible; Q6PIC6; MM.

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DR GO: GO:0030424; C:axon; ISO:MGI.
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DR GO: GO:0044327; C:dendritic spine head; ISO:MGI.
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DR GO: GO:0016020; C:membrane; ISO:MGI.
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DR GO: GO:0005886; C:plasma membrane; ISS:UniProtKB.
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DR GO: GO:0001540; F:amyloid-beta binding; ISO:MGI.
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DR GO: GO:0031748; F:D1 dopamine receptor binding; ISO:MGI.
DR GO: GO:0043395; F:heparan sulfate proteoglycan binding; IPI:BHF-UCL.
DR GO: GO:0046872; F:metal ion binding; IEA:UniProtKB-KW.
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DR GO: GO:0086037; F:P-type sodium:potassium-exchanging transporter activity involved in regulation of cardiac muscle cell membrane }
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DR GO: GO:1904646; P:cellular response to amyloid-beta; ISO:MGI.
DR GO: GO:0030007; P:intracellular potassium ion homeostasis; ISO:MGI.
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DR GO: GO:0006813; P:potassium ion transport; ISO:MGI.
DR GO: GO:1902600; P:proton transmembrane transport; IBA:GO_Central.
DR GO: GO:0086036; P:regulation of cardiac muscle cell membrane potential; IGI:BHF-UCL.
DR GO: GO:0009410; P:response to xenobiotic stimulus; IMP:MGI.
DR GO: GO:0036376; P:sodium ion export across plasma membrane; IDA:BHF-UCL.
DR GO: GO:0006814; P:sodium ion transport; ISO:MGI.
DR GO: GO:0008542; P:visual learning; IMP:MGI.
DR CDD: cd02608; P-type_ATPase_Na-K_like; 1.
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DR Gene3D: 2.70.150.10; Calcium-transporting ATPase, cytoplasmic transduction domain A; 1.
DR Gene3D: 1.20.1110.10; Calcium-transporting ATPase, transmembrane domain; 1.
DR Gene3D: 3.40.50.1000; HAD superfamily/HAD-like; 1.
DR InterPro: IPR006068; ATPase_P-tyr_cation-transpstr_C.
DR InterPro: IPR004014; ATPase_P-tyr_cation-transpstr_N.
DR InterPro: IPR023299; ATPase_P-tyr_cyto_dom_N.
DR InterPro: IPR018303; ATPase_P-tyr_P_site.
DR InterPro: IPR023298; ATPase_P-tyr_TM_dom_sf.
DR InterPro: IPR008250; ATPase_P-tyr_transduc_dom_A_sf.
DR InterPro: IPR036412; HAD-like_sf.
DR InterPro: IPR023214; HAD_sf.
DR InterPro: IPR005775; P-type_ATPase_IIC.
DR InterPro: IPR001757; P-tyr_ATPase.
DR InterPro: IPR044492; P-tyr_ATPase_HD_dom.
DR NCBIfam: TIGR01106; ATPase-IIC_X-K; 1.
DR NCBIfam: TIGR01494; ATPase_P-type; 2.
DR PANTHER: PTHR43294; SODIUM/POTASSIUM-TRANSPORTING ATPASE SUBUNIT ALPHA; 1.
DR PANTHER: PTHR43294:SF15; SODIUM/POTASSIUM-TRANSPORTING ATPASE SUBUNIT ALPHA-3; 1.
DR Pfam: PF13246; Cation_ATPase; 1.
DR Pfam: PF00689; Cation_ATPase_C; 1.
DR Pfam: PF00690; Cation_ATPase_N; 1.
DR Pfam: PF00122; E1-E2_ATPase; 1.
DR PRINTS: PR00119; CATATPASE.
DR PRINTS: PR00121; NAKATPASE.
DR SFLD: SFLDG00002; C1.7: P-type_atpase_like; 1.
DR SFLD: SFLDF00027; p-type_atpase; 1.
DR SMART: SM00831; Cation_ATPase_N; 1.
DR SUPFAM: SSF81653; Calcium ATPase, transduction domain A; 1.
DR SUPFAM: SSF81665; Calcium ATPase, transmembrane domain M; 1.
DR SUPFAM: SSF56784; HAD-like; 1.
DR SUPFAM: SSF81660; Metal cation-transporting ATPase, ATP-binding domain N; 1.
DR PROSITE: PS00154; ATPASE_E1_E2; 1.
PE 1: Evidence at protein level;
KW ATP-binding; Cell membrane; Direct protein sequencing; Ion transport;
KW Magnesium; Membrane; Metal-binding; Nucleotide-binding; Phosphoprotein;
KW Potassium; Potassium transport; Reference proteome; Sodium;
KW Sodium transport; Sodium/potassium transport; Translocase; Transmembrane;
KW Transmembrane helix; Transport.
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GVAMGIAGSD VSKQAADMIL LDDNFASIVT GVEEGRILFD NLKKSIAITL TSNIPETIPF
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