

MATRIX SCIENCE MASCOT Search Results

Protein View: ATPB_HUMAN

ATP synthase subunit beta, mitochondrial OS=Homo sapiens GN=ATP5B
PE=1 SV=3

Database: SwissProt
Score: 117
Expect: 4e-08
Monoisotopic mass (M_r): 56525
Calculated pI: 5.26
Taxonomy: Homo sapiens

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

Search parameters

Enzyme: Trypsin: cuts C-term side of KR unless next residue is P.
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Mass values searched: 15
Mass values matched: 11

Protein sequence coverage: 28%

Matched peptides shown in **bold red**.

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1  MLGFVGRVAA APASGALRRL TPSASLPPAQ LLLRAAPTAV HPVRDYAAQT
51  SPSPKAGAAAT GRIVAVIGAV VDVQFDEGLP PILNALEVQG RETRLVLEVA
101 QHLGESTVRT IAMDGTEGLV RGQKVLDSGA PIKIPVGPET LGRIMNVIGE
151 PIDERGPIKT KQFAPIHAEA PEFMEMSVEQ EILVTGIKVV DLLAPYAKGG
201 KIGLFGGAGV GKTVLIMELI NNVAKAHGGY SVFAGVGERT REGNDLYHEM
251 IESGVINLKD ATSKVALVYG QMNEPPGARA RVALTGLTVA EYFRDQEGQD
301 VLLFIDNIFR FTQAGSEVSA LLGRIPSAVG YQPTLATDMG TMQERITTTK
351 KGSITSVQAI YVPADDLTD PATTTFAPHL ATTVALSRAIA ELGIYPAVDP
401 LDSTSRIMDP NIVGSEHYDV ARGVQKILQD YKSLQDIIAI LGMDELSEED
451 KLTVSRARKI QRFLSQPFQV AEVFTGHMGK LVPLKETIKG FQQILAGEYD
501 HLPEQAFYMV GPIEEAVAKA DKLAEEHSS

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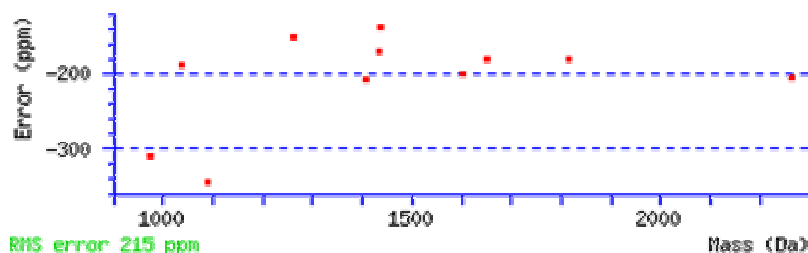
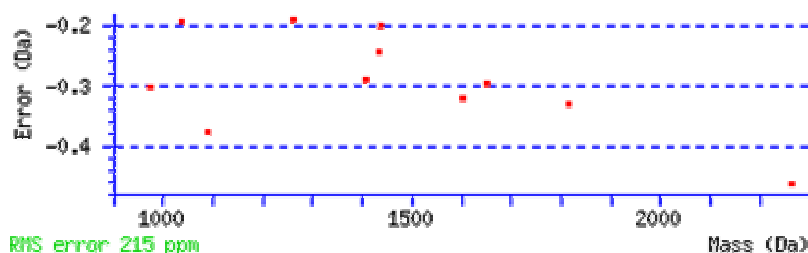
Unformatted sequence string: **529 residues** (for pasting into other applications).

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

Start - End	Observed	Mr (expt)	Mr (calc)	Delta M	Peptide
95 - 109	1650.6200	1649.6127	1649.9101	-0.2973 0	R.LVLEVAQHLGESTVR.T
110 - 121	1262.4500	1261.4427	1261.6336	-0.1909 0	R.TIAMDGTEGLVR.G
134 - 143	1038.4000	1037.3927	1037.5869	-0.1942 0	K.IPVGPETLGR.I
189 - 198	1088.2600	1087.2527	1087.6277	-0.3750 0	K.VVDLLAPYAK.G
202 - 212	975.2600	974.2527	974.5549	-0.3022 0	K.IGLFGGAGVGK.T
226 - 239	1406.3900	1405.3827	1405.6739	-0.2912 0	K.AHGGYSVFAGVGER.T
265 - 279	1601.4900	1600.4827	1600.8031	-0.3204 0	K.VALVYGQMNEPPGAR.A
282 - 294	1439.5900	1438.5827	1438.7820	-0.1993 0	R.VALTGLTVAEYFR.D
311 - 324	1435.5100	1434.5027	1434.7467	-0.2440 0	R.FTQAGSEVSALLGR.I
325 - 345	2265.6200	2264.6127	2265.0770	-0.4642 0	R.IPSAVGYQPTLATDMGMTMQER.I

Start - End	Observed	Mr (expt)	Mr (calc)	Delta M	Peptide
407 - 422	1815.5400	1814.5327	1814.8621	-0.3294 0	R.IMDPNIVGSEHYDVAR.G

No match to: 621.7400, 860.7400, 1920.9700, 1990.5700



ID ATPB_HUMAN Reviewed; 529 AA.
AC P06576; A8K4X0; Q14283;
DT 01-JAN-1988, integrated into UniProtKB/Swiss-Prot.
DT 01-APR-1990, sequence version 3.
DT 25-OCT-2017, entry version 212.
DE RecName: Full=ATP synthase subunit beta, mitochondrial;
DE EC=3.6.3.14;
DE Flags: Precursor;
GN Name=ATP5B; Synonyms=ATPMB, ATPSB;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
OC Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RX PubMed=2687158; DOI=10.1016/0888-7543(89)90125-0;
RA Neckelmann N., Warner C.K., Chung A., Kudoh J., Minoshima S.,
RA Fukuyama R., Maekawa M., Shimizu Y., Shimizu N., Liu J.D.,
RA Wallace D.C.;
RT "The human ATP synthase beta subunit gene: sequence analysis,
RT chromosome assignment, and differential expression.";
RL Genomics 5:829-843(1989).
RN [2]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA], AND VARIANT GLN-274.
RX PubMed=2900241;
RA Ohta S., Tomura H., Matsuda K., Kagawa Y.;
RT "Gene structure of the human mitochondrial adenosine triphosphate
RT synthase beta subunit.";
RL J. Biol. Chem. 263:11257-11262(1988).
RN [3]
RP NUCLEOTIDE SEQUENCE [MRNA], AND VARIANT GLN-274.
RX PubMed=2870059;
RA Ohta S., Kagawa Y.;
RT "Human F1-ATPase: molecular cloning of cDNA for the beta subunit.";
RL J. Biochem. 99:135-141(1986).
RN [4]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RX PubMed=14702039; DOI=10.1038/ng1285;
RA Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,
RA Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,
RA Sekine M., Obayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,