

MATRIX SCIENCE MASCOT Search Results

Protein View: gj|485778118

ATP synthase subunit beta [Escherichia coli]

Database: NCBInr
Score: 51
Nominal mass (M_r): 50341
Calculated pI: 4.90
Taxonomy: [Escherichia coli](#)

This protein sequence matches the following other entries:

- [gi|1476706170](#) from [Escherichia coli P0298942.1](#)
- [gi|1476789110](#) from [Escherichia coli 2862600](#)
- [gi|1476836849](#) from [Escherichia coli P0298942.10](#)
- [gi|1476849850](#) from [Escherichia coli P0298942.11](#)
- [gi|1476856383](#) from [Escherichia coli P0298942.14](#)
- [gi|1476859283](#) from [Escherichia coli P0298942.12](#)
- [gi|1476864814](#) from [Escherichia coli P0298942.15](#)
- [gi|1476864995](#) from [Escherichia coli P0298942.6](#)
- [gi|1476865686](#) from [Escherichia coli P0298942.2](#)
- [gi|1476880445](#) from [Escherichia coli P0298942.8](#)
- [gi|1476881798](#) from [Escherichia coli P0298942.9](#)
- [gi|1476883093](#) from [Escherichia coli P0298942.7](#)
- [gi|1477055168](#) from [Escherichia coli 2733950](#)
- [gi|1477081371](#) from [Escherichia coli P0298942.4](#)
- [gi|1477081788](#) from [Escherichia coli P0298942.3](#)

Sequence similarity is available as [an NCBI BLAST search of gj|485778118 against nr](#).

Search parameters

MS data file: 9-1.mgf
Enzyme: Trypsin: cuts C-term side of KR unless next residue is P.
Fixed modifications: [Carbamidomethyl \(C\)](#)
Variable modifications: [Oxidation \(M\)](#)

Protein sequence coverage: 4%

Matched peptides shown in **bold red**.

```

1 MATGKIVQVI GAVVDVEFPQ DAVPRVYDAL EVQNGNERLV LEVQQQLGGG
51 IVRTIAMGSS DGLRRGLDVK DLEHPVEVY GKATLGRIMN VLGESVDMKG
101 EIGEEERWAI HRAAPSYEEL SNSQELLETG IKVIDLMCPF AKGGKVLFVG
151 GAGVGTVMNM MELIRNIAIE HSGYSVFAGV GERTREGNDF YHEMTDSNVI
201 DKVSLVYQGM NEPPGNRLRV ALTGLTMAEK FRDEGRDVLV FVDNIYRYTL
251 AGTEVSALLG RMPFSAVGYQP TLAEMGVLQ ERITSTKTGS ITSVQAVYVP
301 ADDLTDPSPA TFFAHLDATV VLSRQIASLG IYFAVDPLDS TSRQLDPLVV
351 GQEHYDTARG VQSILQRYQE LKDIIALGM DELSEEDKLV VARARKIQRF
401 LSQPPFVAEV FTGSPGKYVS LKDIIRGFKG IMEGYDHLP EQAFYMGVSI
451 EEAVEKAKKL

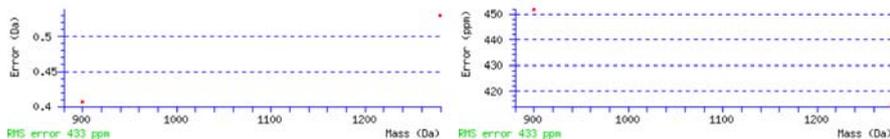
```

Unformatted sequence string: **460 residues** (for pasting into other applications).

Sort peptides by Residue Number Increasing Mass Decreasing Mass

Show predicted peptides also

Query	Start - End	Observed	Mr (expt)	Mr (calc)	Delta	M	Score	Expect	Rank	U	Peptide
30	54 - 65	640.5900	1279.1654	1278.6350	0.5304	1	13	2.2e+002	7	U	R.TIAMGSSDGLRR.G + Oxidation (M)
24	360 - 367	450.9700	899.9254	899.5189	0.4066	0	38	0.71	1	U	R.GVQSILQR.Y



LOCUS WP_001401369 460 aa linear BCT 16-AUG-2017
DEFINITION FOF1 ATP synthase subunit beta [Escherichia coli].
ACCESSION WP_001401369
VERSION WP_001401369.1
KEYWORDS RefSeq.
SOURCE Escherichia coli
ORGANISM Escherichia coli
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Escherichia.
COMMENT REFSEQ: This record represents a single, non-redundant, protein sequence which may be annotated on many different RefSeq genomes from the same, or different, species.
COMPLETENESS: full length.
FEATURES
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/note="ATP synthase alpha/beta family, beta-barrel domain; pfam02874"
/db_xref="CDD:280947"
Region 75..347
/region_name="F1-ATPase_beta"
/note="F1 ATP synthase beta subunit, nucleotide-binding domain. The F-ATPase is found in bacterial plasma membranes, mitochondrial inner membranes and in chloroplast thylakoid membranes. It has also been found in the archaea Methanosarcina barkeri. It uses a...; cd01133"
/db_xref="CDD:238553"
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/db_xref="CDD:238553"
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