

MATRIX
SCIENCE

MASCOT Search Results

Protein View: gi|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|476706170

from [Escherichia coli P0298942.1](#)

gi|476789110

from [Escherichia coli 2862600](#)

gi|476836849

from [Escherichia coli P0298942.10](#)

gi|476849850

from [Escherichia coli P0298942.11](#)

gi|476856383

from [Escherichia coli P0298942.14](#)

gi|476859283

from [Escherichia coli P0298942.12](#)

gi|476864814

from [Escherichia coli P0298942.15](#)

gi|476864995

from [Escherichia coli P0298942.6](#)

gi|476865686

from [Escherichia coli P0298942.2](#)

gi|476880445

from [Escherichia coli P0298942.8](#)

gi|476881798

from [Escherichia coli P0298942.9](#)

gi|476883093

from [Escherichia coli P0298942.7](#)

gi|477055168

from [Escherichia coli 2733950](#)

gi|477081371

from [Escherichia coli P0298942.4](#)

gi|477081788

from [Escherichia coli P0298942.3](#)

Sequence similarity is available as [an NCBI BLAST search of gi|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**.

1MATGKIVQVI

GAVVDVEFPQ

DAVPRVYDAL

EVQNGNERLV

LEVQQQLGGG

51IVR**TIAMGSS DGLRR**

101EIGEEERWAI

HRAAPSYEEL

SNSQELLETG

IKVIDLMCPF

AKGGKVGLFG

151GAGVGKTVNM

MELIRNIAIE

HSGSVFAVG

GERTREGNDF

YHEMTDSNVI

201DKVSLVYGQM

NEPPGNRLRV

ALTGLTMAEK

FRDEGRDVLL

FVDNIYRYTL

251AGTEVSALLG

RMPSAVGYQP

TLAEMGVLQ

ERITSTKTGS

ITSVQAVYVP

301ADDLTDPSPA

TTFAHLDATV

VLSRQIASLG

IYPAVDPLDS

TSRQLDPLVV

351GQEHYDTARG

VQSILQRYQE

LKDIIAILGM

DELSEEDKL

VARARKIQRF

401LSQPPFFVAEV

FTGSPGKYVS

LKDTIRGFKG

IMEGEYDHL

EQAFYMGVSI

451EEAVEKAKKL

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

R.TIAMGSSDGLRR.G + Oxidation (M)

24

360 - 367

450.9700

899.9254

899.5189

0.4066

0

38

0.71

1

R.GVQSILQR.Y

Error (Da)

0.5

0.45

0.4

900

1000

1100

1200

RMS error 433 ppm

Error (ppm)

450

440

430

420

900

1000

1100

1200

RMS error 433 ppm

LOCUSWP_001401369460 aalinearBCT 16-AUG-2017

DEFINITIONF0F1 ATP synthase subunit beta [Escherichia coli].

ACCESSIONWP_001401369

VERSIONWP_001401369.1

KEYWORDSDRefSeq.

SOURCEEscherichia coli

ORGANISMEscherichia coli

Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia.

COMMENTREFSEQ: 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

source

1..460

/organism="Escherichia coli"

/db_xref="taxon:562"

Protein

1..460

/product="F0F1 ATP synthase subunit beta"

/EC_number="3.6.3.14"

/calculated_mol_wt=50184

Region

1..460

/region_name="PRK09280"

/note="F0F1 ATP synthase subunit beta; Validated"

/db_xref="CDD:236447"

Region

6..72

/region_name="ATP-synt_ab_N"

/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"

Site

order(98,115,117..118,120,122,183..185,188,210..212,217,247,250,254,260..262,264..265,270,274,281,298,301..302,306,313,315..317,328..329,338..339,341,343)

/site_type="other"

/note="alpha subunit interaction interface [polypeptide binding]"

/db_xref="CDD:238553"

Site

151..157

/site_type="other"

/note="Walker A motif"

/db_xref="CDD:238553"

Site

order(153,156..158,182..183,186,243,247,331..332)

/site_type="other"

http://mascot/mascot/cgi/protein_view.pl?file=.%2Fdata%2F20180206%2FF004365.dat&hit=gi%7C485778118&db_idx=1&px=1&ave_thresh=49&... 1/2