

MATRIX
SCIENCE

MASCOT Search Results

Protein View: EFTS_ECOBW

Elongation factor Ts OS=Escherichia coli (strain K12 / MC4100 / BW2952) GN=tsf PE=3 SV=1

Database:SwissProt

Score:33

Nominal mass (M_r):30518

Calculated pI:5.22

Taxonomy:**Escherichia coli BW2952**

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

Search parameters

MS data file:22.mgf

Enzyme:Trypsin: cuts C-term side of KR unless next residue is P.

Fixed modifications:**Carbamidomethyl (C)**

Variable modifications:**Oxidation (HW)**

Protein sequence coverage: 2%

Matched peptides shown in **bold red**.

1 MAEITASLVK ELRERTGAGM MDCKKALTEA NGDIELAIEN MRKSGAIKAA

51 KKAGNVAADG VIKTKIDGNY GIILEVNCQT DFKVADAGFQ AFADKVLDA

101 VAGKITDVEV LKAQFEERV ALVAK**IGENI** N**IR**RVAALEG DVLGSYQHGA

151 RIGVLVAAKG ADEELVKHIA MHVAASKPEF IKPEDVSAEV VEKEYQVQLD

201 IAMQSGKPKE IAEKMEVGRM KKFTEVSLT GQPFVMEPSK TVGQLLKEHN

251 AEVTGFIREF VEGIEKIVET DFAAEVAAMS QQS

Unformatted sequence string: **283 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
22	126 - 133	464.9600	927.9054	927.5137	0.3917	0 33	0.061	1	U	K.IGENINIR.R

Error (Da)

0.4

0.38

900

925

950

975

RMS error 422 ppm

Mass (Da)

Error (ppm)

440

430

420

410

900

925

950

975

RMS error 422 ppm

Mass (Da)

ID

EFTS_ECOBW

Reviewed;

283 AA.

AC

C4ZRR2;

DT

22-SEP-2009, integrated into UniProtKB/Swiss-Prot.

DT

28-JUL-2009, sequence version 1.

DT

11-NOV-2015, entry version 43.

DE

RecName: Full=Elongation factor Ts {ECO:0000255|HAMAP-Rule:MF_00050};

DE

Short=EF-Ts {ECO:0000255|HAMAP-Rule:MF_00050};

GN

Name=tsf {ECO:0000255|HAMAP-Rule:MF_00050};

GN

OrderedLocusNames=BWG_0162;

OS

Escherichia coli (strain K12 / MC4100 / BW2952).

OC

Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;

OC

Enterobacteriaceae; Escherichia.

OX

NCBI_TaxID=595496;

RN

[1]

RP

NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].

RC

STRAIN=K12 / MC4100 / BW2952;

RX

PubMed=19376874; DOI=10.1128/JB.00118-09;

RA

Ferenci T., Zhou Z., Betteridge T., Ren Y., Liu Y., Feng L.,

RA

Reeves P.R., Wang L.;

RT

"Genomic sequencing reveals regulatory mutations and recombinational

RT

events in the widely used MC4100 lineage of Escherichia coli K-12.";

RL

J. Bacteriol. 191:4025-4029(2009).

CC

-!- FUNCTION: Associates with the EF-Tu.GDP complex and induces the

CC

exchange of GDP to GTP. It remains bound to the aminoacyl-tRNA.EF-

CC

Tu.GTP complex up to the GTP hydrolysis stage on the ribosome.

CC

{ECO:0000255|HAMAP-Rule:MF_00050}.

CC

-!- SUBCELLULAR LOCATION: Cytoplasm {ECO:0000255|HAMAP-Rule:MF_00050}.

CC

-!- SIMILARITY: Belongs to the EF-Ts family. {ECO:0000255|HAMAP-

CC

Rule:MF_00050}.

DR

EMBL; CP001396; ACR65295.1; -, Genomic_DNA.

DR

RefSeq; WP_000818114.1; NC_012759.1.

DR

ProteinModelPortal; C4ZRR2; -.

DR

SMR; C4ZRR2; 3-281.

DR

PRIDE; C4ZRR2; -.

DR

EnsemblBacteria; ACR65295; ACR65295; BWG_0162.

DR

KEGG; ebw:BWG_0162; -.

DR

PATRIC; 18269224; VBIEscCol60876_0176.

DR

HOGONOM; HOG000220986; -.

DR

KO; K02357; -.

DR

OMA; FIMEPKK; -.

DR

OrthoDB; EOG66B42N; -.

DR

BioCyc; ECOL595496:GI18-166-MONOMER; -.

DR

GO; GO:0005737; C:cytoplasm; IEA:UniProtKB-SubCell.

DR

GO; GO:0003746; F:translation elongation factor activity; IEA:UniProtKB-HAMAP.

DR

Gene3D; 3.30.479.20; -, 2.

DR

HAMAP; MF_00050; EF-Ts; 1.

DR

InterPro; IPR001816; Transl_elong_EFTs/EF1B.

DR

InterPro; IPR014039; Transl_elong_EFTs/EF1B_dimer.

DR

InterPro; IPR018101; Transl_elong_Ts_CS.

DR

InterPro; IPR009060; UBA-like.

DR

PANTHER; PTHR11741; PTHR11741; 1.

DR

Pfam; PF00889; EF_TS; 1.

DR

SUPFAM; SSF46934; SSF46934; 1.

DR

SUPFAM; SSF54713; SSF54713; 2.

DR

TIGRFAMs; TIGR00116; tsf; 1.

DR

PROSITE; PS01126; EF_TS_1; 1.

DR

PROSITE; PS01127; EF_TS_2; 1.

PE

3: Inferred from homology;

KW

Cytoplasm; Elongation factor; Protein biosynthesis.

FT

CHAIN 1 283 Elongation factor Ts.

FT

/FTId=PRO_1000202238.

FT

REGION 80 83 Involved in Mg(2+) ion dislocation from

FT

EF-Tu. {ECO:0000255|HAMAP-Rule:MF_00050}.

SQ

SEQUENCE 283 AA; 30423 MW; 0B9D21E928A5051C CRC64;

SQ

MAEITASLVK ELRERTGAGM MDCKKALTEA NGDIELAIEN MRKSGAIKAA KKAGNVAADG

SQ

VIKTKIDGNY GIILEVNCQT DFKVADAGFQ AFADKVLDA VAGKITDVEV LKAQFEERV

SQ

ALVAKIGENI NRRVAALEG DVLGSYQHGA RIGVLVAAKG ADEELVKHIA MHVAASKPEF

SQ

IKPEDVSAEV VEKEYQVQLD IAMQSGKPKE IAEKMEVGRM KKFTEVSLT GQPFVMEPSK

SQ

TVGQLLKEHN AEVTGFIREF VEGIEKIVET DFAAEVAAMS QQS

Mascot: <http://www.matrixscience.com/>