



MASCOT Search Results

Protein View: gi|445923422

elongation factor Tu, partial [Escherichia coli]

Database: NCBI

Score: 271

Nominal mass (M<sub>r</sub>): 41052

Calculated pI: 5.07

Taxonomy: [Escherichia coli](#)

This protein sequence matches the following other entries:

- [gi|378195286](#) from [Escherichia coli DEC13D](#)

Sequence similarity is available as [an NCBI BLAST search of gi|445923422 against nr](#).

Search parameters

MS data file: 13-1.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: 18%

Matched peptides shown in **bold red**.

1 DHGKTTLTAA ITTVLAKTYG GAAR**AFDQID** **NAPEEK**ARGI TINTSHVEYD

51 TPTRHYAHVD CPGHADYVKN MITGAAQMDG AILVVAATDG PMPQTRHIL

101 LGRQVGVPYI IVFLNKCMMV DDEELLELVE MEVRELLSQY DFPGDDTPIV

151 RGSALK**ALEG** **DAEWEA**KILE LAGFLDSVIP EPERAIDKPF LLPIEDVFISI

201 SGRGTVVTGR VERGIHKVGE EVEIVGIKET QK**STCTGVEM** **FRKLLDEGRA**

251 **GENVGVLLRG** IKREEIERGQ VLAKPGTIKP HTKFESEVYI LSKDEGGRHT

301 PFFK**GYRQPF** **YFR**TTDVTGT IELPEGVEMV MPGDNIKMVV TLIHPIAMDD

351 GLRFAIREGG **RTVGAGV**VAK VLG

Unformatted sequence string: **373 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
<a href="#">44</a>	25 - 36	689.1300	1376.2454	1375.6255	0.6199	0	23	20	1	R.AFDQIDNAPEEK.A
<a href="#">46</a>	25 - 38	535.5000	1603.4782	1602.7638	0.7144	1	18	62	1	R.AFDQIDNAPEEKAR.G
<a href="#">37</a>	157 - 167	610.0500	1218.0854	1217.5564	0.5291	0	55	0.014	1	U K.ALEGDAEWEAK.I
<a href="#">43</a>	233 - 243	666.5900	1331.1654	1330.6010	0.5645	1	15	1.2e+002	2	K.STCTGVEMFRK.L + Oxidation (M)
<a href="#">21</a>	243 - 249	415.9400	829.8654	829.4657	0.3997	1	40	0.58	1	R.KLLDEGR.A
<a href="#">30</a>	250 - 259	514.5400	1027.0654	1026.5822	0.4833	0	62	0.0027	1	R.AGENVGVLLR.G
<a href="#">40</a>	305 - 313	412.0700	1233.1882	1232.6091	0.5791	0	19	60	2	K.GYRQPFYFR.T
<a href="#">19</a>	362 - 370	401.4300	800.8454	800.4756	0.3698	0	43	0.23	1	R.TVGAGVVAK.V





LOCUS WP\_000001277 373 aa linear BCT 14-MAY-2013

DEFINITION elongation factor Tu, partial [Escherichia coli].

ACCESSION WP\_000001277

VERSION WP\_000001277.1

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: incomplete on the amino end.

FEATURES

source 1..373

/organism="Escherichia coli"

/db\_xref="taxon:562"

Protein 1..373

/product="elongation factor Tu"

/calculated\_mol\_wt=40907

Region 1..372

/region\_name="PRK00049"

/note="elongation factor Tu; Reviewed"

/db\_xref="CDD:234596"

Region 1..182

/region\_name="EF\_Tu"

/note="Elongation Factor Tu (EF-Tu) GTP-binding proteins; cd01884"

Site

order(1,5..6,9,12..13,17,45..46,64..65,88..89,91..94,97,128,132,158..159)

/site\_type="other"

/note="GEF interaction site [polypeptide binding]"

/db\_xref="CDD:206671"

Site

order(1..6,26,115..116,118,153..155)

/site\_type="other"

/note="GTP/Mg2+ binding site [chemical binding]"

/db\_xref="CDD:206671"

Site 35..45

/site\_type="other"

/note="Switch I region"

/db\_xref="CDD:206671"

Site 41

/site\_type="other"

/note="G2 box"

/db\_xref="CDD:206671"

Site 60..63

/site\_type="other"

/note="G3 box"

/db\_xref="CDD:206671"

Site 62..80

/site\_type="other"

/note="Switch II region"

/db\_xref="CDD:206671"

Site 115..118

/site\_type="other"

/note="G4 box"

/db\_xref="CDD:206671"

Site 153..155

/site\_type="other"

/note="G5 box"

/db\_xref="CDD:206671"

http://mascot/mascot/cgi/protein\_view.pl?file=.%2Fdata%2F20180206%2FF004374.dat&hit=gi%7C445923422&db\_idx=1&px=1&ave\_thresh=49&... 1/2