

# MATRIX SCIENCE MASCOT Search Results

## Protein View: gi|445923422

### elongation factor Tu, partial [Escherichia coli]

**Database:** NCBInr  
**Score:** 271  
**Nominal mass (Mr):** 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 K/R unless next residue is P.  
**Fixed modifications:** Carbamidomethyl (C)  
**Variable modifications:** Oxidation (M)

#### Protein sequence coverage: 18%

Matched peptides shown in **bold red**.

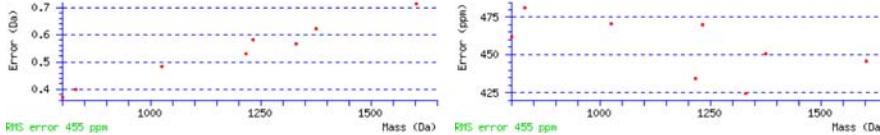
```
1 DHGKTTLTAA ITTVLAKTYG GAARAFDQID NAPEEKARGI TINTSHVEYD
51 TPTRHYAHVD CPGHADYVKN MITGAAQMVG AILVVATDG PMPQTREHIL
101 LGRQVGVPI IVPFLNKCDMV DDEELLELVE MEVRELLSQY DFPGGDDTPIV
151 RGSALKALEG DAEWEAKILE LAGFLDSYIP EPERAIDKPF LLPIEDVFSI
201 SGRGTVVTR VERGIIKVGE EVEIVGKET QKSTCTGVEM FRKLLDEGRA
251 GENVGVLRLR IKREEIERGQ VLAKPGTIKP HTKFESEVYI LSKDEGGRH
301 PFFKGYRPQF YFRTTDVGT IELPEGVEMV MPGDNIKMVV TLIHPIAMDD
351 GLRFAIREGG RTVGAGVVAK 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
<b>44</b> 25 - 36	689.1300	1376.2454	1375.6255	0.6199	0	23	20	<b>1</b>	R.AFDQIDNAPEEK.A
<b>46</b> 25 - 38	535.5000	1603.4782	1602.7638	0.7144	1	18	62	<b>3</b>	R.AFDQIDNAPEEKAR.G
<b>37</b> 157 - 167	610.0500	1218.0854	1217.5564	0.5291	0	55	0.014	<b>1</b> U	K.ALEGDAEWEAK.I
<b>43</b> 233 - 243	666.5900	1331.1654	1330.6010	0.5645	1	15	1.2e+002	<b>2</b>	K.STCTGVEMFRK.L + Oxidation (M)
<b>21</b> 243 - 249	415.9400	829.8654	829.4657	0.3997	1	40	0.58	<b>1</b>	R.KLLDEGR.R
<b>30</b> 250 - 259	514.5400	1027.0654	1026.5822	0.4833	0	62	0.0027	<b>1</b>	R.AGENGVVLLR.G
<b>40</b> 305 - 313	412.0700	1233.1882	1232.6091	0.5791	0	19	60	<b>2</b>	K.GYRPQFYFR.T
<b>19</b> 362 - 370	401.4300	800.8454	800.4756	0.3698	0	43	0.23	<b>1</b>	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:
  Location/Qualifiers
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            /organism="Escherichia coli"
            /db_xref="taxon:562"
  Protein   1..373
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            /calculated_mol_wt=40907
  Region    1..372
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            /note="elongation factor Tu; Reviewed"
            /db_xref="CDD:234596"
  Region    1..182
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            /note="Elongation Factor Tu (EF-Tu) GTP-binding proteins;
cd01884"
            /db_xref="CDD:206671"
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           128,132,158..159)
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            /note="GTP interaction site [polypeptide binding]"
            /db_xref="CDD:206671"
  Site      order(1..6,26,115..116,118,153..155)
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            /note="GTP/Mg2+ binding site [chemical binding]"
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            /db_xref="CDD:206671"
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            /note="G3 box"
            /db_xref="CDD:206671"
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            /db_xref="CDD:206671"
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            /note="G4 box"
            /db_xref="CDD:206671"
  Site      153..155
            /site_type="other"
            /note="G5 box"
            /db_xref="CDD:206671"
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