

**MATRIX SCIENCE MASCOT Search Results**

**Protein View: gj|446366641**

**isocitrate dehydrogenase [Escherichia coli]**

**Database:** NCBInr  
**Score:** 100  
**Nominal mass (M<sub>r</sub>):** 46069  
**Calculated pI:** 5.21  
**Taxonomy:** [Escherichia coli](#)

This protein sequence matches the following other entries:

- [gi|1215264462](#) from [Escherichia coli O127:H6 str. E2348/69](#)
- [gi|1312288845](#) from [Escherichia coli 2362-75](#)
- [gi|1377846921](#) from [Escherichia coli DEC1A](#)
- [gi|1377848771](#) from [Escherichia coli DEC1C](#)
- [gi|1377851752](#) from [Escherichia coli DEC1B](#)
- [gi|1377860568](#) from [Escherichia coli DEC1D](#)
- [gi|1377864181](#) from [Escherichia coli DEC1E](#)
- [gi|1377866555](#) from [Escherichia coli DEC2A](#)
- [gi|1377877100](#) from [Escherichia coli DEC2B](#)
- [gi|1377881273](#) from [Escherichia coli DEC2D](#)
- [gi|1377883097](#) from [Escherichia coli DEC2C](#)
- [gi|1606539341](#) from [Escherichia coli O86:H34 str. 99-3124](#)
- [gi|1921445946](#) from [Escherichia coli](#)

Sequence similarity is available as [an NCBI BLAST search of gj|446366641 against nr.](#)

**Search parameters**

**MS data file:** 10-1.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: 6%**

Matched peptides shown in **bold red**.

```

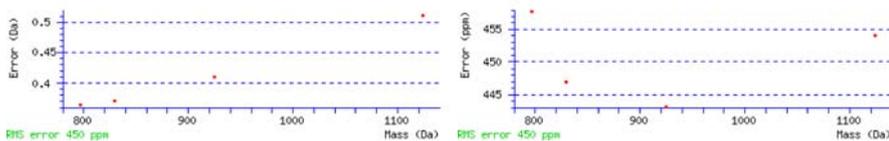
1 MESKVVVPAQ GKKITLQNGK LNVPEPIIP YIEGDGIGVD VTPAMLKVVD
51 AAVEKAYKGE RRISWMEIYT GEKSTQVYQG DVWLPARTLD LIREYRVAIK
101 GPLTFVGGG IRSLNVALRQ ELDLYICLRP VRYQGTSPS VKHPELTMV
151 IFRENSEDIY AGIEWKADSA DAEKVINFLR EEMGVKKIRF PEHCIGIKP
201 CSEEGTKRLV RAAIEYAIAN DRDSVTLVHK GNIMKFTEGA FKDWGYQLAR
251 EEPGGELIDG GPWLKVKKNPN TGKEIVIKDV IADAFLOQIL LRPAEYDVIA
301 CMNLNGDYSIS DALAAQVGGI GIAPGANIGD ECALFEATHG TAPKYAGQDK
351 VNPGSIIISA EMMLRHMGWT EAADLIVKGM EGAINAKTVT YDFERLMEGA
401 KLLKCSEFGD AIIKNM
    
```

Unformatted sequence string: **416 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="#">17</a>	5 - 12	399.4300	796.8454	796.4807	0.3648	16	47	3	U	K.VVVPAQGK.K
<a href="#">26</a>	5 - 13	463.5000	924.9854	924.5757	0.4098	14	1.4e+002	4	U	K.VVVPAQGKK.I
<a href="#">20</a>	48 - 55	415.9200	829.8254	829.4545	0.3709	36	1.3	1	U	K.VVDAAVEK.A
<a href="#">30</a>	101 - 112	563.0800	1124.1454	1123.6350	0.5105	34	1.5	1	U	K.GPLTFVGGGIR.S



LOCUS WP\_000444496 416 aa linear BCT 27-DEC-2017  
 DEFINITION NADP-dependent isocitrate dehydrogenase [Escherichia coli].  
 ACCESSION WP\_000444496  
 VERSION WP\_000444496.1  
 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 Location/Qualifiers  
 source 1..416  
 /organism="Escherichia coli"  
 /db\_xref="taxon:562"  
 Protein 1..416  
 /product="NADP-dependent isocitrate dehydrogenase"  
 /calculated\_mol\_wt=45625  
 Region 8..416  
 /region\_name="PRK07006"  
 /note="Isocitrate dehydrogenase; Reviewed"  
 /db\_xref="CDD:180792"

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