



MASCOT Search Results

Protein View: gi|446366641

isocitrate dehydrogenase [Escherichia coli]

Database: NCBInr

Score: 100

Nominal mass (M_r): 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 gi|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 LNVPENPIIP YIEGDGIGVD VTPAMLKVVD

51 AAVEKAYKGE RKISWMEIYT GEKSTQVYQQ DVWLPAETLD LIREYRVAIK

101 GPLTTPVGGG IRSLNVALRQ ELDLYICLRP VRYQGTSPSP VKHPELTDV

151 IFRENSEDIY AGIEWKADSA DAEKVINFLR EEMGVKKIRF PEHCIGIGIKP

201 CSEEGTKRLV RAAIEYAIAN DRDSVTLVHK GNIMKFTEGA FKDWGYQLAR

251 EEPGGELIDG GPWLKVKNPN TGKEIVIKDV IADAFLLQIL LRPAEYDVIA

301 CMNLNGDIYS DALAAQVGGI GIAPGANIGD ECALFEATHG TAPKYAGQDK

351 VNPGSILISA EMMLRHMGWT EAADLIVKGM EGAINAKTVT YDFERLMEGA

401 KLLKCEFGD 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
17	5 - 12	399.4300	796.8454	796.4807	0.3648	0	16	47	3	U	K.VVVPAQGK.K
26	5 - 13	463.5000	924.9854	924.5757	0.4098	1	14	1.4e+002	4	U	K.VVVPAQGRK.I
20	48 - 55	415.9200	829.8254	829.4545	0.3709	0	36	1.3	1	U	K.VVDAAVEK.A
30	101 - 112	563.0800	1124.1454	1123.6350	0.5105	0	34	1.5	1	U	K.GPLTTPVGGGIR.S



Mass error 450 ppm



Mass error 450 ppm

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/>