

MASCOT Search Results

Protein View: gi|485723954

malate dehydrogenase [Escherichia coli]

Database: NCBItr

Score: 207

Nominal mass (M<sub>r</sub>): 32532

Calculated pI: 5.62

Taxonomy: [Escherichia coli](#)

This protein sequence matches the following other entries:

- [gi|323966415](#) from [Escherichia coli M863](#)
- [gi|327251329](#) from [Escherichia coli STEC 7v](#)
- [gi|386140017](#) from [Escherichia coli 1.2741](#)
- [gi|914355797](#) from [Escherichia coli](#)

Sequence similarity is available as [an NCBI BLAST search of gi|485723954 against nr](#).

Search parameters

MS data file: 20.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: 20%

Matched peptides shown in **bold red**.

1 MKVAVLGAAG GIGQALALL KTQLPSGSEL SLYDIAPVTP GVAVDLSHIP

51 TAVKIKGFSG EDATPALEGA DVVLISAGVA RKPMDRSDL FNVNAGIVK**N**

101 **LVQQVAK**TCP KACIGIITNP VNTTVAIAAE VLKKAGVYDK NKLFGVTTLD

151 IIR**SNTFVAE LK**GRQPGGEV VPVIGGHSV TILPLLSQVP GVSFTEQEVA

201 ELTKR**IQNAG TEVVEAKAGG GSATLSMGQA AARFGLSLVR** ALQGEQGVVE

251 CAYVEGDGQY ARFFSQPLLL GKNGVEERKS IGTLTSTFEQN ALEGMLDTLK

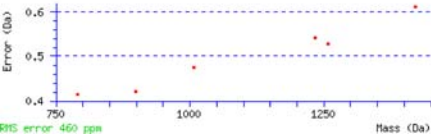
301 **KDIALGEEFV NK**

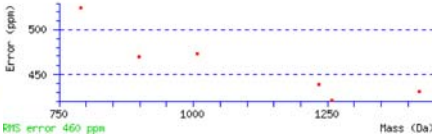
Unformatted sequence string: **312 residues** (for pasting into other applications).

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="#">28</a>	100 - 107	450.4800	898.9454	898.5236	0.4218	0	40	0.47	<a href="#">1</a>	<b>U K.NLVQQVAK.T</b>
<a href="#">30</a>	154 - 162	505.0100	1008.0054	1007.5287	0.4767	0	23	19	<a href="#">1</a>	<b>R.SNTFVAELK.G</b>
<a href="#">41</a>	206 - 217	630.1000	1258.1854	1257.6565	0.5290	0	36	1.1	<a href="#">1</a>	<b>R.IQNAGTEVVEAK.A</b>
<a href="#">48</a>	218 - 233	711.6500	1421.2854	1420.6729	0.6126	0	52	0.024	<a href="#">1</a>	<b>K.AGGGSATLSMGQAAAR.F + Oxidation (M)</b>
<a href="#">23</a>	234 - 240	396.4500	790.8854	790.4701	0.4153	0	17	66	<a href="#">1</a>	<b>R.FGLSLVR.A</b>
<a href="#">28</a>	302 - 312	618.0900	1234.1654	1233.6241	0.5413	0	39	0.45	<a href="#">1</a>	<b>K.DIALGEEFVNK.-</b>





LOCUS WP\_001354992 312 aa linear BCT 11-MAY-2013

DEFINITION malate dehydrogenase [Escherichia coli].

ACCESSION WP\_001354992

VERSION WP\_001354992.1

KEYWORDS RefSeq.

SOURCE Escherichia coli

ORGANISM Escherichia coli

Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacterales; 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.

FEATURES Location/Qualifiers

source

1..312

/organism="Escherichia coli"

/db\_xref="taxon:562"

Protein

1..312

/product="malate dehydrogenase"

/calculated\_mol\_wt=32250

Region

1..312

/region\_name="PRK05086"

/note="malate dehydrogenase; Provisional"

/db\_xref="CDD:235340"

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