



MASCOT Search Results

Protein View: gi|446438286

molecular chaperone DnaK [Escherichia coli]

Database: NCBInr

Score: 75

Nominal mass (M<sub>r</sub>): 69160

Calculated pI: 4.83

Taxonomy: [Escherichia coli](#)

This protein sequence matches the following other entries:

- [gi|386233828](#) from [Escherichia coli 2.4168](#)
- [gi|1651772638](#) from [Escherichia coli 2-210-07 S1 C3](#)
- [gi|1651816353](#) from [Escherichia coli 2-210-07 S1 C2](#)
- [gi|1652168877](#) from [Escherichia coli 2-474-04 S1 C1](#)

Sequence similarity is available as [an NCBI BLAST search of gi|446438286 against nr](#).

Search parameters

MS data file: 3-1.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: 4%

Matched peptides shown in **bold red**.

1 MGKIIIGIDLG TNSCVAIMD GTTPRVLENA EGDRTTPSII AYTQDGETLV

51 GQPAKRQAVT NPQNTLFAIK RLIGRRFQDE EVQRDVSIMP FKIIAADNGD

101 AWVEVKGQKM APPQISAELV KMMKKTAEYD LGPEPVTEAVI TVPAYFNDAQ

151 RQATKDAGRI AGLEVKRIIN EPTAALAYG LDKGTGNRTI AVYDLGGGTF

201 DISIIEIDEV DGEKTFEVL A TNGDTHLGE DFDRLINYL VEEFKKDQGI

251 **DLRNDPLAMQ** **RLKEAAEKAK** IELSSAQQT D VNLPLYTADA TGPKHMKIV

301 TRAKLESIVE DLVNRSIEPL KVALQDAGLS VSDIDDVLV GGQTRMPMVQ

351 KKVAEFFGKE PRKDVNPDEA VAIGAAVOGG VLTGDKVDL LLDVTPLSLG

401 IETMGVMTT LIAKNTTIPT KHSQVFSTAE DNQSAVTIHV LQGERKRAAD

451 NKSLGGFNLD GINPAPRGMP QIEVTFDIDA DGILHVSAD KNSGKEQKIT

501 **IKASSGLNED** **EIQK**MVRDAE ANAEADRFKE ELVQTRNQGD HLLHSTRKQV

551 EEAGDKLPAD DKTAIESALT ALETALKGED KATIEAK**MQE** **LAQVSQKLME**

601 IAQQQHAQQQ TAGADASANN AKDDDVVD AE FEEVKDKK

Unformatted sequence string: **638 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="#">32</a>	254 - 261	480.9600	959.9054	959.4494	0.4560	0	31	5.1	<a href="#">1</a>	U	<b>R</b> .ND <b>PLAMQR</b> .L + Oxidation (M)
<a href="#">36</a>	503 - 514	646.1200	1290.2254	1289.6099	0.6156	0	17	89	<a href="#">2</a>	U	<b>K</b> .ASSGLN <b>EDIQK</b> .M
<a href="#">35</a>	588 - 597	589.5900	1177.1654	1176.5809	0.5846	0	27	9.2	<a href="#">1</a>	U	<b>K</b> . <b>MQE</b> LAQVSQ <b>K</b> .L + Oxidation (M)



RMS error 483 ppm



RMS error 483 ppm

LOCUS WP\_000516141 638 aa linear BCT 19-MAY-2015

DEFINITION molecular chaperone DnaK [Escherichia coli].

ACCESSION WP\_000516141

VERSION WP\_000516141.1

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.

COMPLETENESS: full length.

FEATURES Location/Qualifiers

source 1..638

Protein 1..638

Region 1..638

Region 1..382

Site order(10..13,70,171,196..197,199,229,267,270,274,341..343,345)

Site order(28,31,49,53,56..57,59..60,129..132,257,260..261,264,282,284..285)

Site order(148..149,151..152,167..168,170,216..219)

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

http://mascot/mascot/cgi/protein\_view.pl?file=.%2Fdata%2F20180206%2FF004355.dat&hit=gi%7C446438286&db\_idx=1&px=1&ave\_thresh=50&... 1/1