

# MATRIX SCIENCE 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|65172638 from **Escherichia coli** 2-210-07 S1 C3
- gi|651816353 from **Escherichia coli** 2-210-07 S1 C2
- gi|652168877 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**.

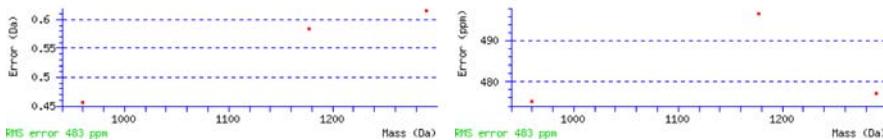
```
1 MOKIIGIDLG TTNSCAVAIMD GTTPRLVLENA EGDRTTPSII AYTQDGGETLV
55 QQPARKQAVT NPPNTLFAIK RLIGRRFQDE EVQRDWSIMP FKIIAADNGD
101 AWVEVKGQKM APPQISAEV LKKMKTAEVDY LGEPVTTEAVI TVPAYFNDAQ
151 RQATKDAGRI AGLEVKRIN EPTAAALAYG LDKGTRGNRTI AVYDLCGGTF
201 DISIIIEDEV DGEEKTFEVLA TNGDTHLGE DFDSRSLINYV VEEFKKDQGI
251 DLRNDPLAMQ RLKEAAEKAK IELSSAQTD VNLPYITADA TGPKHHNNIKV
301 TRAKLESIVE DLVNRNSIEPL KVALQDAGLS VSDIDDVILV GGQTRMPMVQ
351 KKVAEFFGKE PRKDVPNDEA VAIGAAVQGG VLTDGVKDVL LLDVTPLSLG
401 IETMGGVMTT LIAKNNTIPT KHSQVFSTAE DNQSAVTHV LQGERRKRAAD
451 NKSLLQQFNLD GINPAPRGMQ QIEVTFDIDA DGILHVSAKD KNSGKEQKIT
501 IKAASSGLNED EIQKMRDAB ANAAEADRKFELVQTRNQGD HLLHSTRKQV
551 EAAGDKLPAD DTKTAIESALT ALETALKGED KATIEAKMQE LAQVSQKLME
601 IAQQQHAAQOO TAGADASANN AKDDVVDAE 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
<b>32</b>	254 - 261	480.9600	959.9054	959.4494	0.4560	0	31	5.1	<u>1</u>	<b>U R.NDPLAMQ.R</b> L + Oxidation (M)
<b>36</b>	503 - 514	646.1200	1290.2254	1289.6099	0.6156	0	17	89	<u>2</u>	<b>U K.ASSGLNED<b>EIQK</b>.M</b>
<b>35</b>	588 - 597	589.5900	1177.1654	1176.5809	0.5846	0	27	9.2	<u>1</u>	<b>U K.MQELAQVSQK.L</b> + Oxidation (M)



```
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; 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..638
/organism="Escherichia coli"
/db_xref="taxon:562"
Protein 1..638
/product="molecular chaperone DnaK"
/calculated_mol_wt=69014
Region 1..638
/region_name="dnaK"
/note="molecular chaperone DnaK; Provisional; PRK00290"
/db_xref="CDD:234715"
Region 1..382
/region_name="HSP90-like_NBD"
/note="Nucleotide-binding domain of human HSP90,
Escherichia coli DnaK, and similar proteins; cdd11733"
/db_xref="CDD:212683"
Site order(10..13,70,171,196..197,199,229,267,270,274,341..343,
345)
/site_type="other"
/note="nucleotide binding site [chemical binding]"
/db_xref="CDD:212683"
Site order(28,31,49,53,56..57,59..60,129..132,257,260..261,264,
282,284..285)
/site_type="other"
/note="NBF interaction site [polypeptide binding]"
/db_xref="CDD:212683"
Site order(148..149,151..152,167..168,170,216..219)
/site_type="other"
/note="SBD interface [polypeptide binding]"
/db_xref="CDD:212683"
```

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