



MASCOT Search Results

Protein View: gi|486356887

chaperone protein ClpB [Escherichia coli]

Database: NCBI

Score: 103

Nominal mass (M_r): 95712

Calculated pI: 5.37

Taxonomy: [Escherichia coli](#)

This protein sequence matches the following other entries:

- [gi|431347921](#) from [Escherichia coli KTE84](#)
- [gi|660050098](#) from [Escherichia coli 6-175-07 S1 C1](#)
- [gi|1921464780](#) from [Escherichia coli](#)
- [gi|1921474406](#) from [Escherichia coli](#)
- [gi|1921478964](#) from [Escherichia coli](#)

Sequence similarity is available as [an NCBI BLAST search of gi|486356887 against nr](#).

Search parameters

MS data file: 2-2.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: 2%

Matched peptides shown in **bold red**.

1 MRLDRLTNKF QIALADAQSL ALGHDNQFIE PLHLMSALLN QEGGSVSPLL

51 TSAGINAGQL RTDINQALNR LPQVEGTGGD VQPSQDLVRV LNLCDKLAQK

101 RGDNFISSEL FVLAALESRG TLADILKAAG ATTANITQAI EQMRGGESVN

151 DQGAEDQRQA LKKYTIDLTE RAEQGLDPV IGRDEIRRT IQVLQRRTKN

201 NPVLIGEPGV GK**TAIVEGLA QRI**INGEVPE GLKGRRV**LAL DMGALVAGAK**

251 YRGEFEERLK GVLNDLARQE GNVILFIDEL HTMVGAGKAD GAMDAGNMLK

301 PALARGELHC VGATTLDEYR QYIEKDAALE RRFQKVFVAE PSVEDTIAIL

351 RGLKERYELH HHVQITDPAI VAAATLSHRY IADRQLPDKA IDLIDEAASS

401 IRMQIDSKPE ELDRLDRII QLKLEQQALM KESDEASKKR LDMLENEELSD

451 KERQYSELEE EWKAEEKASLS GTQTIKAELE QAKIAIEQAR RVGDLARMSE

501 LQYGKIPLEE KQLEAATQLE GKTMRLLRNK VTDAEIAEVL ARWTGIPVSR

551 MMESEREKLL RMEQELHHRV IGQNEAVDAV SNAIRRSRAG LADPNRPIGS

601 FLFLGPTGVG KTELCKALAN FMFDSDEAMV RIDMSEFMEK HSVSRLVGAP

651 PGYVGYEEGG YLTEAVRRRP YSVILLDEVE KAHPDVFNIL LQVLDDGRLT

701 DQGGRTVDFR NTVVIMTSNL GSDLIQERFG ELDYAHMKEL VLGVVSHNFR

751 PEFINRIDEV VVEHPLGEQH IASIAQIQLK RLYKRLEERG YEIHISDEAL

801 KQLSENGYDP VYGARPLKRA IQQIQIENPLA QQILSGELVP GKVIRLEVNE

851 DRIVAVQ

Unformatted sequence string: **857 residues** (for pasting into other applications).

Sort peptides by

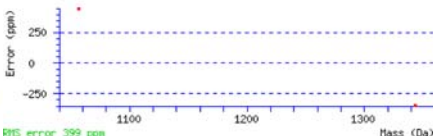

☒ Residue Number

☐ Increasing Mass

☐ Decreasing Mass

Show predicted peptides also

Query	Start - End	Observed	Mr (expt)	Mr (calc)	Delta	M	Score	Expect	Rank	U	Peptide
27	213 - 222	529.5400	1057.0654	1056.5927	0.4727	0	69	0.0005	1	..	K.TAIVEGLAQR.I
29	237 - 250	672.6500	1343.2854	1343.7483	-0.4628	0	33	1.9	1	U	R.VLALDMGALVAGAK.Y + Oxidation (M)



LOCUS WP_001592512 857 aa linear BCT 05-AUG-2017

DEFINITION ATP-dependent chaperone ClpB [Escherichia coli].

ACCESSION WP_001592512

VERSION WP_001592512.1

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..857

/organism="Escherichia coli"

/db_xref="taxon:562"

Protein

1..857

/product="ATP-dependent chaperone ClpB"

/calculated_mol_wt=95469

Region

1..857

/region_name="PRK10865"

/note="protein disaggregation chaperone; Provisional"

/db_xref="CDD:182791"

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