



MASCOT Search Results

Protein View: gi|446651772

molecular chaperone GroEL [Escherichia coli]

Database: NCBI

Score: 377

Nominal mass (M<sub>r</sub>): 57492

Calculated pI: 4.85

Taxonomy: [Escherichia coli](#)

Sequence similarity is available as [an NCBI BLAST search of gi|446651772 against nr](#).

Search parameters

MS data file: 5-2.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: 17%

Matched peptides shown in **bold red**.

1 MAAKDVKFGN DARVKMLR**GV NVLADAVKVT** LGPKGRNVVL DKSFGAPTIT

51 **KDGVSVAREI** ELEDKFENMG AQMVKEVASK ANDAAGDGT TATVLAQAI

101 TEGLKAVAAG MNFMDLKRGI DRAVTAAVEE **LKALSVPCSD SKAIAQVGTI**

151 SANSDETGVK LIAEAMDRVG KEGVITVEDG TGLQDELDVV EGMQFDRGYL

201 SPYFINKPET GAVELESPFI LLADKKISNI **REMLPVL**EAV **AKAGKPLLI**

251 AEDVEGEALA TLVNTMRGI VKVAAV**KAPG FGDR**RRKAMLQ DIATLTGGTV

301 ISEEIGMELE **KATLEDLQGA** KRVVINKDIT TIIDGVGEEV AIQGRVAQIR

351 QQIEEATSDY DREKLQERVA **KLAGGVAVIK** VGAATEVEMK EKKAR**VEDAL**

401 **HATRAA**VEEG VVAGGGVALI RVASK**LADLR GQ**NEDQNVGI **KVALRAMEAP**

451 **LRQIV**LNCGE EPSVVANTVK GGDGNYGNA ATEEYGNMID MGILDPTKVT

501 RSALQYAASV AGIMITTECM VTDLPRNDAA DLGAAGMGGM MGGMGGM

Unformatted sequence string: **548 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="#">23</a>	19 - 28	493.5200	985.0254	984.5604	0.4651	0	79	6e-005	1	U	R.GVNVLADAVK.V
<a href="#">17</a>	52 - 58	352.3700	702.7254	702.3661	0.3594	0	22	7.5	4	U	K.DGVSVAR.E
<a href="#">38</a>	133 - 142	532.5000	1062.9854	1062.5016	0.4839	0	13	1.9e+002	1	U	K.ALSVPCSDSK.A
<a href="#">42</a>	232 - 242	608.5900	1215.1654	1214.6580	0.5074	0	18	67	2	U	R.EMLPVLEAVAK.A + Oxidation (M)
<a href="#">20</a>	278 - 284	360.3400	718.6654	718.3398	0.3256	0	30	0.93	1	U	K.APGFGDR.R
<a href="#">37</a>	312 - 321	523.5300	1045.0454	1044.5451	0.5003	0	23	30	1	U	K.ATLEDLGQAK.R
<a href="#">41</a>	312 - 322	401.4200	1201.2382	1200.6462	0.5919	1	17	79	3	U	K.ATLEDLGQAKR.V
<a href="#">24</a>	372 - 380	414.4700	826.9254	826.5276	0.3978	0	55	0.012	1	U	K.LAGGVAVIK.V
<a href="#">35</a>	396 - 404	506.5000	1010.9854	1010.5145	0.4710	0	54	0.018	1	U	R.VEDALHATR.A
<a href="#">11</a>	426 - 441	590.9100	1769.7082	1768.9068	0.8014	1	18	1.4e+002	2	U	K.LADLRGQNEQNVGIK.V
<a href="#">40</a>	431 - 441	601.5500	1201.0854	1200.5735	0.5120	0	38	0.65	1	U	R.GQNEQNVGIK.V
<a href="#">23</a>	446 - 452	402.4100	802.8054	802.4007	0.4048	0	16	1.1e+002	1	U	R.AMEAPLR.Q + Oxidation (M)





LOCUS WP\_000729118 548 aa linear BCT 22-JUL-2017

DEFINITION chaperonin GroEL [Escherichia coli].

ACCESSION WP\_000729118

VERSION WP\_000729118.1

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..548

protein 1..548

region 2..530

site order(4,8,25,36..39,41,46..47,49,59,61,69,73,76,197,229,257,384,386,459,513,516..522)

site order(31..33,87,91,150,398,415,454,493,495)

site order(109,434,452,461,463..464,467)

site order(141,186,193,375,409..410)

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