

MATRIX SCIENCE MASCOT Search Results

Protein View: gi|723058084

molecular chaperone HtpG [Escherichia coli]

Database: NCBIInr
Score: 131
Nominal mass (M_r): 71418
Calculated pI: 5.06
Taxonomy: Escherichia coli

Sequence similarity is available as an NCBI BLAST search of gi|723058084 against nr.

Search parameters

MS data file: 4-2.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: 9%

Matched peptides shown in bold red.

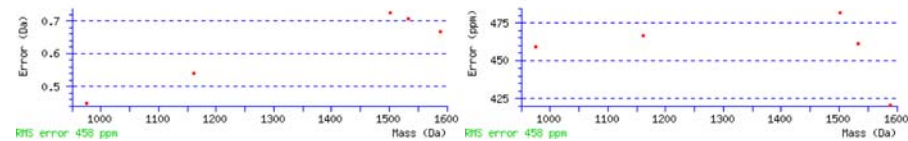
1 MKGQETRGFQ SEVKQLLYLM IHSLYSNKEI FLRE**ELISNAS DAADKLR**FRA
51 LSNPDLYEGD GELRVVVSFD KDKRTLISD NGVGMTRDEV IDHLGTIAKS
101 GTKSPLESGL SDQAKDSQLI GQFGVGFYSA FIVADKVTVR TRAAGEKPEN
151 GVFWESAGEG EYTVADITKE DRGTEITLHL REGEDEFLDD WVRVSIISKY
201 SDHIALPVEI EKREKDGDET IISWEKINKA QALWTRNKSE ITDEEYKEFY
251 KHIAHDFNDP LTWSHNRVEG KQEYTSLLYI PSQAPWDMWN RDHKHGLKLY
301 VQRVPIMDDA EQFMPNYLRF VRGLIDSSDL PLNVSR**EILQ DSTVTR**NLRN
351 ALTKRVLQML EKLAKDAAEK YQTFWQQFGL VLK**EGPAEDF ANQEAI**AKLL
401 RFASTHTDSS AQTVSLEDYV SRMKEGQEKI YYITADSYAA AKSSPHLELL
451 RKKGIEVLLI SDRIDEWMNN YLTFDFGKPF QSVSKVDES**L**E**LADEVDES**
501 **AKAEAK**LTP FIDRVKALLG ERVKDVRLLH RLTDTPAIVS TDAEMSTQM
551 AKLFAAAGQK VPEVKYIFEL NPDHVLVKRA ADTEDEAKFS EWWELLLDQA
601 LLAERGTLTD PNLFIR**RMNQ L**LV**S**

Unformatted sequence string: 624 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
43	34 - 47	501.8400	1502.4982	1501.7736	0.7246	1	24	19	1	U R.ELISNASDAADKLR.F
41	337 - 346	581.5800	1161.1454	1160.6037	0.5417	0	46	0.098	1	U R.EILQDSTVTR.N
45	384 - 398	795.7100	1589.4054	1588.7369	0.6686	0	14	1.6e+002	1	U K.EGPAEDFANQEAIK.L
44	493 - 506	512.1500	1533.4282	1532.7206	0.7076	1	24	15	1	U K.LADEVDESAAEK.A
35	617 - 624	488.9900	975.9654	975.5171	0.4483	1	24	21	1	U R.RMNQLLV.S - + Oxidation (M)



LOCUS WP_033552820 624 aa linear BCT 27-OCT-2015
DEFINITION molecular chaperone HtpG [Escherichia coli].
ACCESSION WP_033552820
VERSION WP_033552820.1
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
source 1..624
/organism="Escherichia coli"
/db_xref="taxon:562"
Protein 1..624
/product="molecular chaperone HtpG"
/calculated_mol_wt=71332
Region 4..623
/region_name="PRK05218"
/note="heat shock protein 90; Provisional"
/db_xref="CDD:235366"
Region 27..154
/region_name="HATPase_c"
/note="Histidine kinase-like ATPases; smart00387"
/db_xref="CDD:214643"
Site order(34,38,41,78,80,82,84..85,124..127,164,168,173..174,176)
/site_type="other"
/note="ATP binding site [chemical binding]"
/db_xref="CDD:238030"
Site 38
/site_type="other"
/note="Mg2+ binding site [ion binding]"
/db_xref="CDD:238030"
Site order(82,84,124,126)
/site_type="other"
/note="G-X-G motif"
/db_xref="CDD:238030"
Region 186..622
/region_name="HSP90"
/note="Hsp90 protein; pfam00183"
/db_xref="CDD:278607"