

MATRIX SCIENCE MASCOT Search Results

Protein View: gi|928847216

universal stress protein UspD [Escherichia coli]

Database: NCBIInr
Score: 30
Nominal mass (M_r): 16396
Calculated pI: 6.64
Taxonomy: Escherichia coli

This protein sequence matches the following other entries:

- gi|922650545 from Escherichia coli

Sequence similarity is available as an NCBI BLAST search of gi|928847216 against nr.

Search parameters

MS data file: G2.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: 11%

Matched peptides shown in bold red.

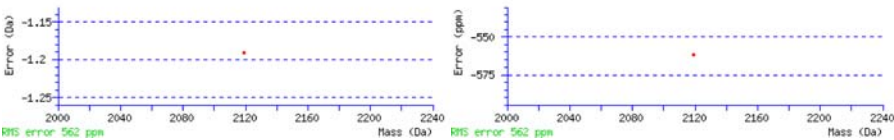
1 MAYKHIGVAI SGNEEDALLV NKALELARHN DAHLTLIHID DGLSELYPGI
51 YFPATEDILQ LLKNKSDNKL YKLTNIIQWP KTKLRIERGE MPETLLEIMQ
101 **K****EQCNLLVCG** **HHHSFINR**.L PAYRGMINKM SADLLIVPFI DK

Unformatted sequence string: 142 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
34	102 - 118	707.2700	2118.7882	2119.9792	-1.1911	0 30	3.2	1	U	K.EQCNLLVCGHHHSFINR.L



LOCUS WP_053897192 142 aa linear BCT 16-AUG-2017
DEFINITION MULTISPECIES: universal stress protein UspD [Enterobacteriaceae].
ACCESSION WP_053897192
VERSION WP_053897192.1
KEYWORDS RefSeq.
SOURCE Enterobacteriaceae
ORGANISM Enterobacteriaceae
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacterales.
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 Location/Qualifiers
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/organism="Enterobacteriaceae"
/db_xref="taxon:543"
Protein 1..142
/product="universal stress protein UspD"
/calculated_mol_wt=16161
Region 1..142
/region_name="PRK09982"
/note="universal stress protein UspD; Provisional"
/db_xref="CDD:137627"

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