

MATRIX SCIENCE MASCOT Search Results

Protein View: gi|828163674

uridine phosphorylase [Moellerella wisconsensis]

Database: NCBI
Score: 158
Nominal mass (M_r): 27264
Calculated pI: 5.64
Taxonomy: Moellerella wisconsensis

This protein sequence matches the following other entries:

- gi|827595280 from Moellerella wisconsensis
- gi|1928454144 from Moellerella wisconsensis ATCC 35017

Sequence similarity is available as an NCBI BLAST search of gi|828163674 against nr.

Search parameters

MS data file: 190.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: 8%

Matched peptides shown in bold red.

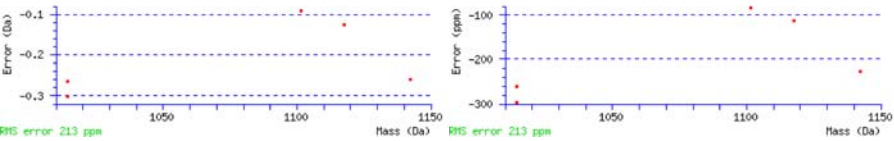
1 M**SDVFHLGLK** KSDLQGATLA IVPGDPKRVE KIARLMDNPV HLASLREFTS
51 WRGEVDGKAV IVCSTGIGGP STSIAVEELA QLGINTFLRI GTTGAIQENI
101 NVGDLVLTAA SVRLDGASQH FAPLEYPAVA DPECTNALYA AAKDAGAVVH
151 VGVTAASDTF YPGQERYDTY TGRVVSFRFG SMKENQQMGV MNYEMESATL
201 LTMCSQGLR **SGMVAGIVNV** RTQQEIPNEE LLKKTESNVL GIVVDAARRL
251 LK

Unformatted sequence string: 252 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
69	2 - 10	339.0900	1014.2482	1014.5498	-0.3017	0	36	25	1	..	M.SDV FHLGLK .K
70	2 - 10	508.1500	1014.2854	1014.5498	-0.2644	0	57	0.18	1		M.SDV FHLGLK .K
83	2 - 11	572.2000	1142.3854	1142.6448	-0.2593	1	31	80	2		M.SDV FHLGLK .S
78	211 - 221	551.7600	1101.5054	1101.5965	-0.0910	0	70	0.012	5	U	R.SGM VAGIVNV .T
80	211 - 221	559.7400	1117.4654	1117.5914	-0.1259	0	29	1.6e+002	1	U	R.SGM VAGIVNV .T + Oxidation (M)



LOCUS WP_047254674 252 aa linear BCT 08-JUN-2015
DEFINITION uridine phosphorylase [Moellerella wisconsensis].
ACCESSION WP_047254674
VERSION WP_047254674.1
KEYWORDS RefSeq.
SOURCE Moellerella wisconsensis
ORGANISM Moellerella wisconsensis
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacterales; Morganellaceae; Moellerella.
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="Moellerella wisconsensis"
/db_xref="taxon:158849"
Protein 1..252
/product="uridine phosphorylase"
/EC_number="2.4.2.3"
/calculated_mol_wt=26979
Region 1..251
/region_name="PRK11178"
/note="uridine phosphorylase; Provisional"
/db_xref="CDD:183018"

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