

MATRIX SCIENCE MASCOT Search Results

Protein View: gi|446058921

glycerol kinase [Escherichia coli]

Database: NCBInr
Score: 524
Nominal mass (M_r): 56496
Calculated pI: 5.36
Taxonomy: Escherichia coli

This protein sequence matches the following other entries:

- gi|323153997 from Escherichia coli EPECa14

Sequence similarity is available as [an NCBI BLAST search of gi|446058921 against nr](#).

Search parameters

MS data file: 7-1.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: 26%

Matched peptides shown in **bold red**.

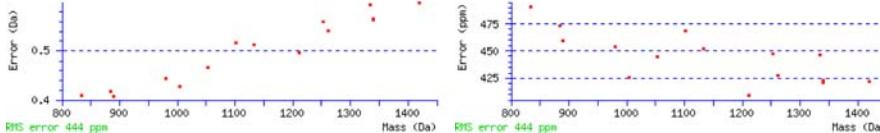
```
1 MTEKKYIVAL DQGTTSSRAV VMDHDDANIIS VSQREFPEQIY PKLGWVEHDP
51 MEIWATQSST LVEVLAKADI SSDQIAAIGI TNQREETTIVW EKETGKPIYN
101 AIVWQCRRTA EICEHLKRDG LEDYIR SNTG LVIDPYFSGT KVKWILDHIVE
151 GSRRARRG E LFGTVDTWL IWKMTQGRVH VTODYTNASR MLFNIHTLDW
201 DDKMLEVLQDI PREMLP EVR: SSEVYQQTNI GGKG GTRPI SGTAGDQQAA
251 LPFGQLCVKEG MAKNTYGTGC FMLMNTGEKA VKSENGLTT IACGPTGEVN
301 YALEGAVFMA GASIQWLRDE MKLINDAYDS EFYATKVQNT NGVYVVPAFT
351 GLGAPYWDY ARGGAI FGLTR GVNNHHIIRA TLESIA YQTR DVLEAMQADS
401 GIR LHALRVD GGA VANNFLM QFQSDILGTR VERPEVR E VT ALGAAYLAGL
451 AVGFWQNLD E LQEKAVERE FRPGIETTER NYRYAGWKKA VKRAMAWEHH
501 DE
```

Unformatted sequence string: **502 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	35 - 42	527.5000	1052.9854	1052.5178	0.4676 0	16	1.8e+002	4	U	R.EFEQIVPK.L
39	85 - 92	503.4800	1004.9454	1004.5179	0.4276 0	39	1.3	1	R.	ETTIVWEEK.E
37	119 - 126	490.9600	979.9054	979.4611	0.4444 0	46	0.2	1	R.	DGLEDYIR.S
49	144 - 153	606.5600	1211.1054	1210.6095	0.4960 0	36	2.1	1	K.	WILDHVEGS.R.E
53	179 - 189	632.0800	1262.1454	1261.6051	0.5403 0	46	0.23	1	R.	VHVTDYTNAS.R.T
47	204 - 212	551.5600	1101.1054	1100.5900	0.5155 0	65	0.0026	1	K.	MLEVLDIP.R.E + Oxidation (M)
34	213 - 219	445.4300	888.8454	888.4375	0.4080 0	23	43	7	R.	ENLPEVR.R + Oxidation (M)
57	221 - 233	670.6100	1339.2054	1338.6416	0.5639 0	45	0.22	1	R.	SSEVYQQTNIGGK.G
58	221 - 233	447.4100	1339.2082	1338.6416	0.5666 0	21	55	1	R.	SSEVYQQTNIGGK.G
26	363 - 370	417.9500	833.8854	833.4759	0.4095 0	57	0.017	1	R.	GAIIFGLTR.G
50	380 - 390	627.1100	1252.2054	1251.6459	0.5596 0	29	9.8	1	R.	ATLESIAQTR.D
62	391 - 403	711.1400	1420.2654	1419.6664	0.5991 0	45	0.24	1	R.	DVLEAMQADSGIR.L + Oxidation (M)
33	431 - 437	442.9600	883.9054	883.4875	0.4179 0	22	45	2	R.	VERPEVR.E
56	470 - 480	445.7600	1334.2582	1333.6626	0.5956 0	17	1.3e+002	4	R.	EFRPGIETTER.N
48	494 - 502	567.4700	1132.9254	1132.4131	0.5123 0	41	0.56	1	R.	AMAWEEHDE.- + Oxidation (M)



LOCUS WP_000136776 502 aa linear BCT 14-MAY-2013
DEFINITION glycerol kinase [Escherichia coli].
ACCESSION WP_000136776
VERSION WP_000136776.1
KEYWORDS RefSeq,
SOURCE Escherichia coli
ORGANISM Escherichia coli
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
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..502
/organism="Escherichia coli"
/db_xref="taxon:562"
Protein 1..502
/products="glycerol kinase"
/calculated_mol_wt=56116
Region 1..498
/region_name="glpK"
/note="glycerol kinase; Provisional; PRK00047"
/db_xref="CDD:234594"

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