

MASCOT Search Results

Protein View: gi|345351497

phosphoglycerate kinase [Escherichia coli 3030-1]

Database: NCBI

Score: 75

Nominal mass (M_r): 40719

Calculated pI: 5.02

Taxonomy: [Escherichia coli 3030-1](#)

Sequence similarity is available as [an NCBI BLAST search of gi|345351497 against nr](#).

Search parameters

MS data file: 14-4.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 MTDLDLAGKR VFIR**ADLNVP VKDGK**VTSDA RIRASLPTIE LALKQGAKVM

51 VTSHLGRPTE GEYNEEFSLL PVVNYLKDKL SNPVLVKDY LDGVDVAEGE

101 LVVLENVRFN KGEKKDDETL SKKYAALCDV FVMDFGTAH RAQASTHGIG

151 KFADVACAGP LLAAELDALG KALKEPARFM VAIVGGSKVS **TKLTVLDSLS**

201 K~~I~~ADQLIVGG GIANTFIAAQ GHDVGKSLYE ADLVDEAKRL LTTCNIPVPS

251 D~~V~~R**VATEFSE TAPATL**KSVN DVKADEQILD IGDAQAQELA EILKNAKTIL

301 WNGPVGVEFEF PNFRKGTIV ANAIADSEAF SIAGGDTLA AIELFGIADK

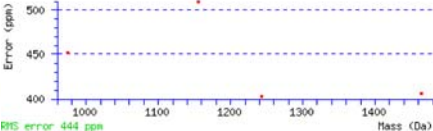
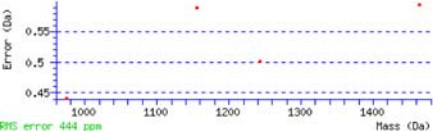
351 ISYISTGGGA FLEFVEGR**KVL PAVAMLEER**A KK

Unformatted sequence string: **382 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
35	15 - 25	386.0800	1155.2182	1154.6295	0.5886	1	11	2.9e+002	6	U	R.ADLNVFVKDGK.V
33	193 - 201	488.5100	975.0054	974.5648	0.4406	0	25		15	1	K.LTVLDSLSK.I
39	254 - 267	733.1800	1464.3454	1463.7508	0.5947	0	26		9.8	1	R.VATEFSETAPATLK.S
37	369 - 379	622.5900	1243.1654	1242.6642	0.5013	0	15	1.2e+002	1	1	K.VLPAVAMLEER.A + Oxidation (M)



LOCUS EGW83758 382 aa linear BCT 01-SEP-2011

DEFINITION phosphoglycerate kinase [Escherichia coli 3030-1].

ACCESSION EGW83758

VERSION EGW83758.1

DBLINK BioProject: PRJNA48253

BioSample: SAMN00016548

accession AFDT01000049.1

DBSOURCE .

KEYWORDS .

SOURCE Escherichia coli 3030-1

ORGANISM Escherichia coli 3030-1

Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Escherichia.

REFERENCE 1 (residues 1 to 382)

AUTHORS Rasko,D., Redman,J., Daugherty,S.C., Tallon,L., Sadzewicz,L., Jones,K., Santana-Cruz,I. and Liu,X.

TITLE Direct Submission

JOURNAL Submitted (31-AUG-2011) Institute for Genome Sciences, The University of Maryland School of Medicine, 801 W. Baltimore St, Baltimore, MD 21201, USA

COMMENT Bacteria and DNA available from the STEC Center at Michigan State, East Lansing, MI, USA.

##Genome-Assembly-Data-START##

Assembly Method :: Celera v. 6.0

Genome Coverage :: 15x

Sequencing Technology :: 454

##Genome-Assembly-Data-END##

Method: conceptual translation.

FEATURES Location/Qualifiers

source 1..382

/organism="Escherichia coli 3030-1"

/strain="3030-1"

/db_xref="taxon:754080"

Protein 1..382

/product="phosphoglycerate kinase"

/EC_number="2.7.2.3"

CDS 1..382

/locus_tag="EC30301_3424"

/coded_by="complement (AFDT01000049.1:152735..153883)"

/transl_table=11

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