

MATRIX SCIENCE MASCOT Search Results

Protein View: gi|446211927

fructose-bisphosphate aldolase [Escherichia coli]

Database: NCBInr
Score: 129
Nominal mass (M_r): 31062
Calculated pI: 5.93
Taxonomy: Escherichia coli

Sequence similarity is available as an NCBI BLAST search of gi|446211927 against nr.

Search parameters

MS data file: ii.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.

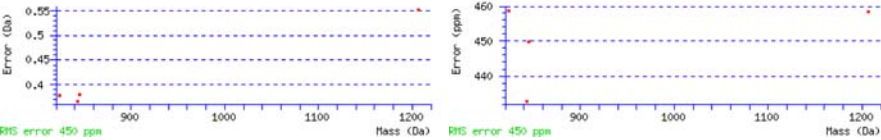
1 MYVVSTKQML NNAQRGGYAV PAFNIHNLET MQVVVETAAN LHAPVIIAGT
51 PGTFTHAGTE NLLALVSAMA KHYHHPLAIH LDHHTKFDDI AQKVRSGVRS
101 VMXDASHLPF AQNISRVKEV VDFCHRFDSV VEAELGQLGG QEDDVQVNEA
151 DAFYTNPAQA REFPAETGID SLAVAIGTAH GMYASAPALD FSRLENIRQW
201 VNLPLVLHGA SGLSTKDIQQ TIKLGICKIN VATELKNAFS QALKNYLTEH
251 PEATDPRDYL QSAKSAMRDV VSKVIADCGC EGRA

Unformatted sequence string: 284 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
28	1 - 7	422.4000	842.7854	842.4208	0.3647	0	23	26	1	U -_MYVVSTK.Q + Oxidation (M)
29	217 - 223	423.4300	844.8454	844.4654	0.3800	0	37	1.1	1	U K.DIQQTIK.L
27	258 - 264	412.9000	823.7854	823.4076	0.3779	0	20	28	1	U R.DYLGSAK.S
15	274 - 284	604.5400	1207.0654	1206.5121	0.5533	1	50	0.071	1	U K.VIADCGCEGRA.-



LOCUS WP_000289782 284 aa linear BCT 23-JUL-2017
DEFINITION tagatose bisphosphate family class II aldolase [Escherichia coli].
ACCESSION WP_000289782
VERSION WP_000289782.1
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
Location/Qualifiers
source 1..284
/organism="Escherichia coli"
/db_xref="taxon:562"
Protein 1..284
/product="tagatose bisphosphate family class II aldolase"
Region 1..284
/region_name="gatY"
/note="Tagatose-bisphosphate aldolase; Reviewed; PRK09195"
/db_xref="CDD:181690"
Site order(27..29,32,52,55..57,61,65,68..69,142,233..234,236..237,240,244,247)
/site_type="other"
/note="intersubunit interface [polypeptide binding]"
/db_xref="CDD:238477"
Site order(82..83,179..181,183,208..209,211,230,232..233)
/site_type="active"
/db_xref="CDD:238477"
Site order(83,180,208)
/site_type="other"
/note="zinc binding site [ion binding]"
/db_xref="CDD:238477"
Site order(179,181,183,209,211)
/site_type="other"
/note="Na+ binding site [ion binding]"
/db_xref="CDD:238477"

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