



MASCOT Search Results

Protein View: gi|41936

tryptophanase [Escherichia coli]

Database: NCBI

Score: 298

Nominal mass (M_r): 53098

Calculated pI: 5.88

Taxonomy: [Escherichia coli](#)

This protein sequence matches the following other entries:

- [gi|147997](#) from [Escherichia coli](#)

Sequence similarity is available as [an NCBI BLAST search of gi|41936 against nr](#).

Search parameters

MS data file: P.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: 14%

Matched peptides shown in **bold red**.

1 MENFKHLPEP FRIR**VIEPVK** RTTRAYREEA IIKSGMNPFL LQSEDFVIDL

51 LTDSGTGAVT QSMQAAMMRG DEAYSGSR**SY YALAESVK**NI FGQYTIPTH

101 QGRGAEQIYI PVLIKKREQE KGLDRSKMVA FSNYFFDTTQ GHSQINGCTV

151 RNVVIKE**AFD T**GVRYDFK**GN F**DLEGLERGI EVGPNNVVPY IVATITSNSA

201 GGQFPVSLANL **K**AMYSIA**K**KY DIPVMDSAR **F**AE**N**AV**F**IKQ REAEYKDWTI

251 EQITRETYKY **A**D**M**L**A**MSAKK DAMVPMGGLL CMKDDSFDDV YTECRSLCVV

301 GGQFPYTGGL EGGAMERLAV GLYDGMNLWD LAYRIAQVQY LVDGLEEIGV

351 VCQQAAGHAA FVDAGKLLPH IPADQFPATG LACELYKVAG IRAVEIGSFL

401 LGRDPKTKGQ LPCPAELLRL TIPRATYQTG HMDFIIEAFK HVKENAANIK

451 **GLTFTTYEPK**V LRHFTAKLKE V

Unformatted sequence string: **471 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
24	15 - 21	420.9400	839.8654	839.5229	0.3426	1	30	3.3	3	..	R.VIEPVKR.T
36	79 - 88	566.0200	1130.0254	1129.5655	0.4599	0	64	0.0016	1	1	R.SYYALAESVK.N
32	157 - 164	447.9200	893.8254	893.4243	0.4011	0	22	27	2	2	K.EAFDTGVR.Y
39	169 - 178	575.5200	1149.0254	1148.5462	0.4793	0	65	0.0014	1	1	K.GNFDLEGLER.G
21	212 - 218	400.3800	798.7454	798.3945	0.3509	0	35	1	1	1	K.AMYSIAK.K + Oxidation (M)
35	231 - 239	552.0100	1102.0054	1101.5495	0.4560	0	27	8.4	1	1	R.FAENAVFIK.Q
37	260 - 269	567.0000	1131.9854	1131.4940	0.4914	0	42	0.28	1	U	K.YADMLAMSAK.K + 2 Oxidation (M)
34	451 - 459	528.5000	1054.9854	1054.5335	0.4519	0	15	1.3e+002	1	1	K.GLTFTTYEPK.V





LOCUS CAA34096 471 aa linear BCT 18-APR-2005

DEFINITION tryptophanase [Escherichia coli].

ACCESSION CAA34096

VERSION CAA34096.1

DBSOURCE embl accession X15974.1

KEYWORDS .

SOURCE Escherichia coli

ORGANISM Escherichia coli

Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia.

REFERENCE 1 (residues 1 to 471)

AUTHORS Tokushige,M., Tsujimoto,N., Oda,T., Honda,T., Yumoto,N., Ito,S., Yamamoto,M., Kim,E.H. and Hiragi,Y.

TITLE Role of cysteine residues in tryptophanase for monovalent cation-induced activation

JOURNAL Biochimie 71 (6), 711-720 (1989)

PUBMED 2502187

FEATURES

source

1..471

/organism="Escherichia coli"

/strain="B/1t7-A"

/db_xref="taxon:562"

Protein

1..471

/product="tryptophanase"

/EC_number="4.1.99.1"

Region

1..471

/region_name="TnaA"

/note="Tryptophanase [Amino acid transport and metabolism]; COG3033"

/db_xref="CDD:225576"

Region

5..471

/region_name="tnaA_trp_ase"

/note="Tryptophanase, leader peptide-associated; TIGR02617"

/db_xref="CDD:131666"

Site

order(102..103,106,194,227,230,267,270)

/site_type="other"

/note="pyridoxal 5'-phosphate binding pocket [chemical binding]"

/db_xref="CDD:99742"

Site

270

/site_type="active"

/note="catalytic residue [active]"

/db_xref="CDD:99742"

CDS

1..471

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/transl_table=11

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/db_xref="PDB:2QXQ"

/db_xref="PDB:2V0Y"

http://mascot/mascot/cgi/protein_view.pl?file=.%2Fdata%2F20180213%2FF004453.dat&hit=gi%7C41936&db_idx=1&px=1&ave_thresh=50&ign... 1/2