

MATRIX SCIENCE MASCOT Search Results

Protein View: gi|41936

tryptophanase [Escherichia coli]

Database: NCBInr
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 FRIVRIEPKV RTRRAYREAA IIKSGMNPFL LDSEDVFIDL
51 LTDSTGTAVT QSMQAAMMRG DEAYSGSRSY YALAESVKNI FGYQYTIPHT
101 QGRGAEQIYI PVLIKKREQE KGLDRSKMVA FSNYFFDTTQ GHSQINGCTV
151 RNVYKEAFD TGVRDFKGN FDLEGLERGI EEVGVNNVPY IVATITSNSA
201 GGQPVSLANL KAMYSIAKKY DIPVPMDSAR FAENAYFIKQ REAEYKDWTI
251 EQITRETYKY ADMILAMSAKK DAMVPMGGLL CMKDDSFEDV YTECRTLCVV
301 QEGFPETYGGL EGGAMERLAV GLYDGMMNLW LAYRIAQVQY LVVGLEEIGV
351 VCQQAGGHHAA FVDAGKLPH IPADQPFATG LACELYKVAG IRAVEIGSFL
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451 GLTFTYEPKV LRHFTAKLKE V

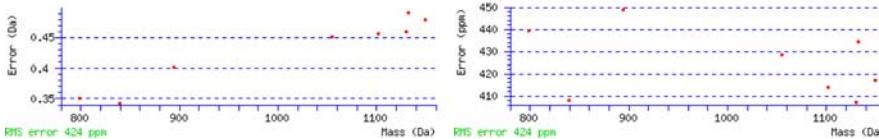
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Unformatted sequence string: [471 residues](#) (for pasting into other applications).

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	R.VIEPVKR.T	
36	79 - 88	566.0200	1130.0254	1129.5655	0.4599	0	64	0.0016	I	R.SYYALAESVK.N
32	157 - 164	447.9200	893.8254	893.4243	0.4011	0	22	27	2	K.EAFDTGVR.Y
39	169 - 178	575.5200	1149.0254	1148.5462	0.4793	0	65	0.0014	I	K.GNFDFLEGLER.G
21	212 - 218	400.3800	798.7454	798.3945	0.3509	0	35	1	I	K.AMYSIAK.K + Oxidation (M)
35	231 - 239	552.0100	1102.0054	1101.5495	0.4560	0	27	8.4	I	R.FAENAYFIK.Q
37	260 - 269	567.0000	1131.9854	1131.4940	0.4914	0	42	0.28	I	U K.YADMILAMSA.K + 2 Oxidation (M)
34	451 - 459	528.5000	1054.9854	1054.5335	0.4519	0	15	1.3e+002	I	K.GLTFTYEPK.V



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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; Enterobacteriales;
           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
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           /note="catalytic residue [active]"
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