



MASCOT Search Results

Protein View: TNAA_ECOBW

Tryptophanase OS=Escherichia coli (strain K12 / MC4100 / BW2952) GN=tnaA PE=3 SV=1

Database: SwissProt

Score: 47

Nominal mass (M_r): 53139

Calculated pI: 5.88

Taxonomy: [Escherichia coli BW2952](#)

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

Search parameters

MS data file: 12.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: 5%

Matched peptides shown in **bold red**.

1 MENFKHLPEP FRIR**VIEPVK** RTTRAYREEA IIKSGMNPFL LQSEDFVFDL

51 LTDSGTGAVT QSMQAAMMRG DEAYSGSRSY YALAESVKNI FGQYTIPTH

101 QGRGAEQIYI PVLIKKREQE KGLDRSKMVA FSNYFFDTTQ GHSQINGCTV

151 RNVYIKEAFD TGVRYDFK**GN** **FDLEGLERGI** EEVGPNNVPY IVATITSNSA

201 GGQPVSLANL KAMYSIARKY DIPVVMDSAR **FAENAYFIKQ** REAEYKDWTI

251 EQITRETYKY ADMLAMSARK DAMVPMGGLL CMKDDSFDDV YTECRTLQVV

301 QEGFPPTYGGL EGGAMERLAV GLYDGMNLDW LAYRIAQVQY LVDGLEEIGV

351 VQQAAGGHAA FVDAGKLLPH IPADQFPAQA LACELYKVAG IRAVEIGSFL

401 LGRDPKTGKQ LPCPAELLRL TIPRATYTQT HMDPIIEAFK HVKENAANIAK

451 GLTFTYPEPKV 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
22	15 - 21	420.9600	839.9054	839.5229	0.3826	1	12	25	7	U	R.VIEPVKR.T
28	169 - 178	575.5400	1149.0654	1148.5462	0.5193	0	24	2.7	2	U	K.GNFLEGLER.G
27	231 - 239	552.0300	1102.0454	1101.5495	0.4960	0	11	50	1	U	R.FAENAYFIK.Q





ID TNAA_ECOBW Reviewed; 471 AA.

AC C4ZY6;

DT 22-SEP-2009, integrated into UniProtKB/Swiss-Prot.

DT 28-JUL-2009, sequence version 1.

DT 11-NOV-2015, entry version 46.

DE RecName: Full=Tryptophanase {ECO:0000255|HAMAP-Rule:MF_00544};

DE EC=4.1.99.1 {ECO:0000255|HAMAP-Rule:MF_00544};

DE AltName: Full=L-tryptophan indole-lyase {ECO:0000255|HAMAP-Rule:MF_00544};

DE Short=TNase {ECO:0000255|HAMAP-Rule:MF_00544};

GN Name=tnaA {ECO:0000255|HAMAP-Rule:MF_00544};

GN OrderedLocusNames=BWG_3399;

OS Escherichia coli (strain K12 / MC4100 / BW2952).

OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;

OC Enterobacteriaceae; Escherichia.

OX NCBI_TaxID=595496;

RN [1]

RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].

RC STRAIN=K12 / MC4100 / BW2952;

RX PubMed=19376874; DOI=10.1128/JB.00118-09;

RA Ferenci T., Zhou Z., Betteridge T., Ren Y., Liu Y., Feng L.,

RA Reeves P.R., Wang L.;

RT "Genomic sequencing reveals regulatory mutations and recombinational

RT events in the widely used MC4100 lineage of Escherichia coli K-12."

RL J. Bacteriol. 191:4025-4029(2009).

CC -!- CATALYTIC ACTIVITY: L-tryptophan + H(2)O = indole + pyruvate +

CC NH(3). {ECO:0000255|HAMAP-Rule:MF_00544}.

CC -!- COFACTOR:

CC Name=pyridoxal 5'-phosphate; Xref=ChEBI:CHEBI:597326;

CC Evidence={ECO:0000255|HAMAP-Rule:MF_00544};

CC -!- PATHWAY: Amino-acid degradation; L-tryptophan degradation via

CC pyruvate pathway; indole and pyruvate from L-tryptophan: step 1/1.

CC {ECO:0000255|HAMAP-Rule:MF_00544}.

CC -!- SUBUNIT: Homotrimer. {ECO:0000255|HAMAP-Rule:MF_00544}.

CC -!- SIMILARITY: Belongs to the beta-eliminating lyase family.

CC {ECO:0000255|HAMAP-Rule:MF_00544}.

DR EMBL: CP001396; ACR65723.1; -; Genomic_DNA.

DR RefSeq: WP_001295247.1; NC_012759.1.

DR ProteinModelPortal; C4ZY6; -.

DR SMR; C4ZY6; 4-471.

DR BindingDB; C4ZY6; -.

DR EnsemblBacteria; ACR65723; ACR65723; BWG_3399.

DR KEGG; ebw:BWG_3399; -.

DR PATRIC; 18276448; VBIEscCol60876_3713.

DR HOGENOM; HOG000057883; -.

DR KO; K01667; -.

DR OMA; GRGAENV; -.

DR OrthoDB; EOG6K9QH6; -.

DR BioCyc; ECOL595496:G118-3530-MONOMER; -.

DR UniPathway; UPA00332; UER00452.

DR GO; GO:0009034; F:tryptophanase activity; IEA:UniProtKB-HAMAP.

DR Gene3D; 3.40.640.10; -; 1.

DR Gene3D; 3.90.1150.10; -; 1.

DR HAMAP; MF_00544; Tryptophanase; 1.

DR InterPro; IPR001597; ArAA_b-elim_lyase/Thr_aldolase.

DR InterPro; IPR011166; Beta-eliminating_lyase.

DR InterPro; IPR015424; Pyrdx1P-dep_Trfase.

DR InterPro; IPR015421; Pyrdx1P-dep_Trfase_major_sub1.

DR InterPro; IPR015422; Pyrdx1P-dep_Trfase_major_sub2.

DR InterPro; IPR013440; TNase.

DR InterPro; IPR018176; Tryptophanase_CS.

DR Pfam; PF01212; Beta_elim_lyase; 1.

DR FRSF; FRSFP001386; Trpase; 1.

DR SUPFAM; SSF53383; SSF53383; 1.

DR TIGRFAMs; TIGR02617; tnaA_trp_ase; 1.

DR PROSITE; PS00853; BETA_ELIM_LYASE; 1.

PE 3: Inferred from homology;

KW Acetylation; Lyase; Pyridoxal phosphate; Tryptophan catabolism.

FT CHAIN 1 471 Tryptophanase.

http://mascot/mascot/cgi/protein_view.pl?file=.%2Fdata%2F20180206%2FF004371.dat&hit=TNAA_ECOBW&db_idx=1&px=1&ave_thresh=41&i... 1/2