

MASCOT Search Results

Protein View: OPPIA_ECOLI

Periplasmic oligopeptide-binding protein OS=Escherichia coli (strain K12) GN=oppA PE=1 SV=2

Database: SwissProt

Score: 48

Nominal mass (M_r): 60975

Calculated pI: 6.05

Taxonomy: **Escherichia coli K-12**

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

Search parameters

MS data file: 6.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: 3%

Matched peptides shown in **bold red**.

1 MTNITKRSLV AAGVLAALMA GNVALAADVP AGVTLAEKQT LVRNNGSEVQ

51 SLDPHKIEGV PESNISRDLF EGLLVSDLDG HPAPGVAESW DNKDAKVTWF

101 HLRKDAKSWD GTPVTAQDFV YSWQSRVDPN TASPYSYLQ YGHIAGIDEI

151 LEGKKPITDL GVKAIDDHTL EVTLSEPVY FYKLLVHPSF SPVPKAAIEK

201 FGKKTQPGN IVTNGAYTLK DMVVNERIVL **ERSPTYWNNK KTVINQVITYL**

251 PIASEVTDVN RYRSGEIDMT NNSMPIELFQ KLKKEIPDEV HVDPYLCTYY

301 YEINNQKPPF NDVVRVTALK LGMDRDIIVN KVKAQGNMPA YGYTPPYTDG

351 AKLTQPEWFG WSQEKRNEEA KKLAEAGYT ADKPLTINLL YNTSDLHKKL

401 AIAASSLWKK NIGVNVKLVN QEWKTFDTR **HQGTDFVARA** GWCADYNEPT

451 SFLNTMLSNS SMNTAHYKSP AFDSIMAEFL KVTDEAQRTA LYTKAEQQLD

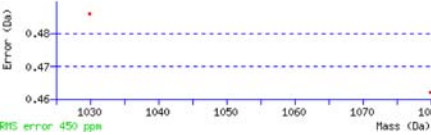
501 KDSAIVPVVY YVNARLVKFW VGGYTGKDEL DNTYTRNMYI VKH

Unformatted sequence string: **543 residues** (for pasting into other applications).

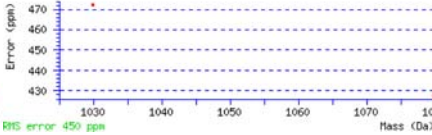
Sort peptides by ☒ Residue Number ☐ Increasing Mass ☐ Decreasing Mass

Show predicted peptides also

Query	Start	End	Observed	Mr (expt)	Mr (calc)	Delta	M	Score	Expect	Rank	U	Peptide
26	233	241	540.9900	1079.9654	1079.5036	0.4619	0	17	18	4	U	R.SPTYWNNAK.T
33	431	439	516.0000	1029.9854	1029.4992	0.4862	0	31	1	1	U	R.HQGTDFVAR.A



RMS error 450 ppm



RMS error 450 ppm

ID OPPIA_ECOLI Reviewed; 543 AA.

AC P23843; P76829;

DT 01-NOV-1991, integrated into UniProtKB/Swiss-Prot.

DT 01-OCT-1994, sequence version 2.

DT 11-NOV-2015, entry version 120.

DE RecName: Full=Periplasmic oligopeptide-binding protein;

DE Flags: Precursor;

GN Name=oppA; OrderedLocusNames=bl243, JW1235;

OS Escherichia coli (strain K12).

OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;

OC Enterobacteriaceae; Escherichia.

OX NCBI_TaxID=83333;

RN [1]

RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].

RX PubMed=2187863;

RA Kashiwagi K., Yamaguchi Y., Sakai Y., Kobayashi H., Igarashi K.;

RT "Identification of the polyamine-induced protein as a periplasmic

RT oligopeptide binding protein.";

RL J. Biol. Chem. 265:8387-8391(1990).

RN [2]

RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].

RC STRAIN=K12;

RA Pahel G., Short S.A.;

RL Submitted (JUL-1993) to the EMBL/GenBank/DDBJ databases.

RN [3]

RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].

RC STRAIN=K12 / W3110 / ATCC 27325 / DSM 5911;

RX PubMed=9097039; DOI=10.1093/dnares/3.6.363;

RA Aiba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K., Itoh T.,

RA Kasai H., Kashimoto K., Kimura S., Kitakawa M., Kitagawa M.,

RA Makino K., Miki T., Mizobuchi K., Mori H., Mori T., Motomura K.,

RA Nakade S., Nakamura Y., Nashimoto H., Nishio Y., Oshima T., Saito N.,

RA Sampei G., Seki Y., Sivasundaram S., Tagami H., Takeda J.,

RA Takemoto K., Takeuchi Y., Wada C., Yamamoto Y., Horiuchi T.;

RT "A 570-kb DNA sequence of the Escherichia coli K-12 genome

RT corresponding to the 28.0-40.1 min region on the linkage map.";

RL DNA Res. 3:363-377(1996).

RN [4]

RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].

RC STRAIN=K12 / MG1655 / ATCC 47076;

RX PubMed=9278503; DOI=10.1126/science.277.5331.1453;

RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,

RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,

RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,

RA Mau B., Shao Y.;

RT "The complete genome sequence of Escherichia coli K-12.";

RL Science 277:1453-1462(1997).

RN [5]

RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].

RC STRAIN=K12 / W3110 / ATCC 27325 / DSM 5911;

RX PubMed=16738553; DOI=10.1038/msb410049;

RA Hayashi K., Morooka N., Yamamoto Y., Fujita K., Isono K., Choi S.,

RA Ohtsubo E., Baba T., Wanner B.L., Mori H., Horiuchi T.;

RT "Highly accurate genome sequences of Escherichia coli K-12 strains

RT MG1655 and W3110.";

RL Mol. Syst. Biol. 2:E1-E5(2006).

RN [6]

RP NUCLEOTIDE SEQUENCE [GENOMIC DNA] OF 1-53.

RC STRAIN=K12;

RX PubMed=2015910; DOI=10.1016/0014-5793(91)80358-A;

RA Kessler D., Leibrecht I., Knappe J.;

RT "Pyruvate-formate-lyase-deactivase and acetyl-CoA reductase activities

RT of Escherichia coli reside on a polymeric protein particle encoded by

RT adhE.";

RL FEBS Lett. 281:59-63(1991).

RN [7]

RP NUCLEOTIDE SEQUENCE [GENOMIC DNA] OF 1-29.

RC STRAIN=DR112;

http://mascot/mascot/cgi/protein_view.pl?file=.%2Fdata%2F20180206%2FF004361.dat&hit=OPPIA_ECOLI&db_idx=1&px=1&ave_thresh=44&_ig... 1/3