

Mascot Search Results

Protein View

Match to: **OMPA_SALTY** Score: **85** Expect: **4.3e-005**
Outer membrane protein A OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) GN=ompA PE=3 SV=2

Nominal mass (M_r): **37492**; Calculated pI value: **5.60**
 NCBI BLAST search of [OMPA_SALTY](#) against nr
 Unformatted [sequence string](#) for pasting into other applications

Taxonomy: [Salmonella enterica subsp. enterica serovar Typhimurium str. LT2](#)

Variable modifications: Carbamidomethyl (C), Oxidation (M)
 Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
 Number of mass values searched: **38**
 Number of mass values matched: **10**
 Sequence Coverage: **30%**

Matched peptides shown in **Bold Red**

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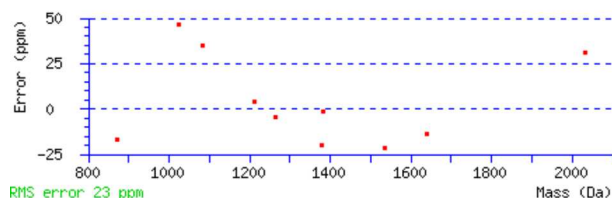
1 MKKTAIAIAV ALAGFATVAQ AAPKDNTWYA GAKLGWSQYH DTGFIHNDGP
51 THENQLGAGA FGGYQVNPYV GFEMGYDWLG RMPYKGDNIN GAYKAQGVQL
101 TAKLGYPITD DLDVYTRLGG MVWRADTKSN VPGGPSTKDH DTGVSVPVAFG
151 GIEYAITPEI ATRLEYQWTN NIGDANTIGT RPDNGLLSVG VSYRFGQQEA
201 APVVAPAPAP APEVQTKHFT LKSDVLFNFK KSTLKPEGQQ ALDQLYSQLS
251 NLDPKDGSVV VLGFTDRIGS DAYNQGLSEK RAQSVVDYLI SKGIPSDKIS
301 ARGMGESNPV TGNTCDNVKP RAALIDCLAP DRRVEIEVKG VKDVVTQPQA
351
    
```

Show predicted peptides also

Sort Peptides By Residue Number Increasing Mass Decreasing Mass

Start - End	Observed	Mr (expt)	Mr (calc)	ppm	Miss	Sequence
25 - 33	1025.5163	1024.5091	1024.4614	47	0	K.DNTWYAGAK.L
104 - 117	1640.7939	1639.7866	1639.8094	-14	0	K.LGYPI^TDDLDVYTR.L
223 - 231	1083.5850	1082.5778	1082.5397	35	0	K.SDVLFNFK.S
256 - 267	1264.6474	1263.6401	1263.6460	-5	0	K.DGSVVVLGFTDR.I
268 - 280	1381.6572	1380.6499	1380.6521	-2	0	R.IGSDAYNQGLSEK.R
268 - 281	1537.7272	1536.7200	1536.7532	-22	1	R.IGSDAYNQGLSEKR.A
281 - 292	1378.7417	1377.7344	1377.7616	-20	1	K.RAQSVVDYLISK.G
303 - 321	2032.9803	2031.9731	2031.9102	31	0	R.GMGESNPVTGNTCDNVKPR.A Carbamidomethyl (C)
322 - 332	1214.6249	1213.6176	1213.6125	4	0	R.AALIDCLAPDR.R Carbamidomethyl (C)
333 - 339	872.5051	871.4978	871.5127	-17	1	R.RVEIEVK.G

No match to: 644.1343, 662.4507, 818.5446, 832.3867, 833.0637, 842.6634, 855.0318, 870.6121, 870.9993, 1059.9536, 1106.6079



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ID OMPA_SALTY Reviewed; 350 AA.
AC P02936;
DT 21-JUL-1986, integrated into UniProtKB/Swiss-Prot.
DT 23-JAN-2002, sequence version 2.
DT 16-MAY-2012, entry version 100.
DE RecName: Full=Outer membrane protein A;
DE AltName: Full=Outer membrane major heat-modifiable protein;
DE AltName: Full=Outer membrane protein 33K;
DE Flags: Precursor;
GN Name=ompA; OrderedLocusNames=STM1070;
OS Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Salmonella;
OC Salmonella enterica subsp. enterica serovar Typhimurium.
OX NCBI_TaxID=99287;
RN [1]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RX MEDLINE=83287368; PubMed=6349993;
RX DOI=10.1111/j.1432-1033.1983.tb07594.x;
RA Freudl R., Cole S.T.;
RT "Cloning and molecular characterization of the ompA gene from
RT Salmonella typhimurium.";
RL Eur. J. Biochem. 134:497-502(1983).
RN [2]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=LT2 / SGSC1412 / ATCC 700720;
RX MEDLINE=21534948; PubMed=11677609; DOI=10.1038/35101614;
RA McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,
RA Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D.,
RA Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,
RA Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,
RA Waterston R., Wilson R.K.;
RT "Complete genome sequence of Salmonella enterica serovar Typhimurium
    
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RT      LT2.";
RL      Nature 413:852-856(2001).
CC      !- FUNCTION: Required for the action of colicins K and L and for the
CC      stabilization of mating aggregates in conjugation. Serves as a
CC      receptor for a number of T-even like phages. Also acts as a porin
CC      with low permeability that allows slow penetration of small
CC      solutes (By similarity).
CC      !- SUBUNIT: Monomer (Probable).
CC      !- SUBCELLULAR LOCATION: Cell outer membrane; Multi-pass membrane
CC      protein.
CC      !- SIMILARITY: Belongs to the OmpA family.
CC      !- SIMILARITY: Contains 1 OmpA-like domain.
CC      -----
CC      Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC      Distributed under the Creative Commons Attribution-NoDerivs License
CC      -----
DR      EMBL; X02006; CAA26037.1; -; Genomic_DNA.
DR      EMBL; AE006468; AAL20003.1; -; Genomic_DNA.
DR      PIR; A03436; MMEBAT.
DR      RefSeq; NP_460044.1; NC_003197.1.
DR      ProteinModelPortal; P02936; -.
DR      SMR; P02936; 22-196.
DR      PRIDE; P02936; -.
DR      GeneID; 1252588; -.
DR      GenomeReviews; AE006468_GR; STM1070.
DR      KEGG; stm:STM1070; -.
DR      PATRIC; 32380577; VBISalEnt20916_1135.
DR      eggNOG; COG2885; -.
DR      HOGENOM; HOG000274199; -.
DR      KO; K03286; -.
DR      OMA; DDNEAQQ; -.
DR      ProtClustDB; PRK10808; -.
DR      BioCyc; STYP99287:STM1070-MONOMER; -.
DR      GO; GO:0009279; C:cell outer membrane; IEA:UniProtKB-SubCell.
DR      GO; GO:0005886; C:plasma membrane; IEA:UniProtKB-KW.
DR      GO; GO:0046930; C:pore complex; IEA:UniProtKB-KW.
DR      GO; GO:0015288; F:porin activity; IEA:UniProtKB-KW.
DR      GO; GO:0005198; F:structural molecule activity; IEA:InterPro.
DR      GO; GO:0000746; P:conjugation; IEA:UniProtKB-KW.
DR      GO; GO:0006811; P:ion transport; IEA:UniProtKB-KW.
DR      Gene3D; G3DSA:2.40.160.20; OMP_b-brl; 1.
DR      Gene3D; G3DSA:3.30.1330.60; OmpA/MotB_C; 1.
DR      InterPro; IPR011250; OMP_b-brl.
DR      InterPro; IPR006664; OMP_bac.
DR      InterPro; IPR002368; OmpA.
DR      InterPro; IPR006690; OMPA-like_CS.
DR      InterPro; IPR000498; OmpA-like_TM_dom.
DR      InterPro; IPR006665; OmpA/MotB_C.
DR      Pfam; PF00691; OmpA; 1.
DR      Pfam; PF01389; OmpA_membrane; 1.
DR      PRINTS; PR01021; OMPADOMAIN.
DR      PRINTS; PR01022; OUTRMBRANEA.
DR      SUPFAM; SSF103088; OmpA/MotB_C; 1.
DR      PROSITE; PS01068; OMPA_1; 1.
DR      PROSITE; PS51123; OMPA_2; 1.
PE      3: Inferred from homology;
KW      Cell membrane; Cell outer membrane; Complete proteome; Conjugation;
KW      Disulfide bond; Ion transport; Membrane; Porin; Reference proteome;
KW      Repeat; Signal; Transmembrane; Transmembrane beta strand; Transport.
FT      SIGNAL          1      21      By similarity.
FT      CHAIN           22     350     Outer membrane protein A.
FT                                     /FTId=PRO_0000020099.
FT      TRANSMEM       27     40      Beta stranded; (Potential).
FT      TRANSMEM       55     67      Beta stranded; (Potential).
FT      TRANSMEM       70     85      Beta stranded; (Potential).
FT      TRANSMEM       97    107     Beta stranded; (Potential).
FT      TRANSMEM      111    126     Beta stranded; (Potential).
FT      TRANSMEM      146    157     Beta stranded; (Potential).
FT      TRANSMEM      163    179     Beta stranded; (Potential).
FT      TRANSMEM      185    196     Beta stranded; (Potential).
FT      REPEAT         205    206     1.
FT      REPEAT         207    208     2.
FT      REPEAT         209    210     3.
FT      REPEAT         211    212     4.
FT      DOMAIN         214    342     OmpA-like.
FT      REGION         205    212     4 X 2 AA tandem repeats of A-P.
FT      DISULFID       315    327     By similarity.
FT      CONFLICT       114    114     V -> F (in Ref. 1; CAA26037).
FT      CONFLICT       247    247     S -> I (in Ref. 1; CAA26037).
SQ      SEQUENCE       350 AA; 37515 MW; B4AC52C8C5DF54FE CRC64;
MKTATAIAIV ALAGFATVAQ AAPKDNTWYA GAKLGWSQYH DTGFIHNDGP THENQLGAGA
FGGYQVNPYV GFEMGYDWLG RMPYKGDNIN GAYKAQGVQL TAKLGYPTD DLDVYTRLGG
MVWRADTKSN VPGGPSTKDH DTGVSFVFAG GIEYAITPEI ATRLEYQWTN NIGDANTIGT
RPDNGLLSVG VSYRFGQGEA APVVAPAPAP APEVQTKHFT LKSDVLFNFN KSTLKPGEQQ
ALDQLYSQLS NLDPKDGSVV VLGFTDRIGS DAYNQGLSEK RAQSVVDYLI SKGIPSDKIS
ARGMGESNPV TGNTCDNVKP RAALIDCLAP DRRVEIEVKG VKDVTVPQQA
    
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