

Mascot Search Results

Protein View

Match to: BAMA_SALTI Score: 67 Expect: 0.0025
Outer membrane protein assembly factor BamA OS=Salmonella typhi GN=bamA PE=3 SV=1

Nominal mass (M_r): 89525; Calculated pI value: 4.92
NCBI BLAST search of BAMA_SALTI against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Salmonella enterica subsp. enterica serovar Typhi

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Number of mass values searched: 50
Number of mass values matched: 10
Sequence Coverage: 19%

Matched peptides shown in Bold Red

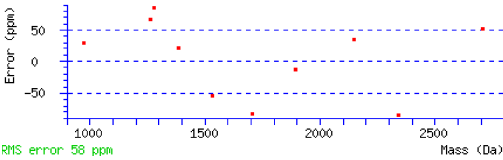
1 MAMKKLIAS LLFSSATVYG AEGFVVKDIH FEGLQRVAVG AALLSMPVRT
51 GDTVNDEDIS NTIRALFATG NFEDVRVLRD GNTLLVQVKE RPTIASITFS
101 GNKSVKDDML KQNLEASGVR VGESLDRTTL SDIEKGLEDF YYSVGKYSAS
151 VKAVVTPLPR NRVDLKLIVFO EGVSAKIQI NIVGNHAFST EELISHFQLR
201 DEVPPWNNVVG DRKYQKQKLA GDLETLRSYY LDRGYARFNI DSTQVSLTPD
251 KKGIIYITVNI TEGDQYKLSG VQVSGNLAGH SAEIEKLTKI EPGELYNGTK
301 VTKMEDDIKK LLGRYGYAYP RVQSQPEIND ADKTVKLRVN VDAGNRFYVR
351 KIRFEGNDTS KDSVLRREMR QMEGAWLGSD LVDQGKERLN RLGFETVDT
401 DTQRVPGSPD QVDVVYKVE RNTGSFNFI GYGESGVSF QAGVQDNDWL
451 GTQSVGNGING TKNDQTYSE LSVTNPFYFTV DGVSLGGRIF YNDFEADDAD
501 LSDYTNKSYG TDVTLGFPIN EYNTLRAGLG YVHNKLSNMQ PQIAMDRIY
551 SMGDDPDASDF AADDTFFNYG WTYNKLDRGY FPTDGSRVNL TGKVTIPGSD
601 NEYYKVS LDT ATVPIDNDH KVVVLGRTRW GYDGLGCKE MPFYENFYAG
651 GSSTVRGFSQ NTIGPKAVYK NGAHTSWDDD DDYEDCTQES GCKSDDAVGG
701 NAMAVASLEF ITPTPFISEK YANSVRTSFF WDMGTVDWDTN WDPSSAFSDV
751 PDYSDPGNIR MSAGIALQWM SPLGPLVFSY AQPFKKYDGD KAEQFQFNIG
801 KTW

Show predicted peptides also

Sort Peptides By Residue Number Increasing Mass Decreasing Mass

Start	End	Observed	Mr (expt)	Mr (calc)	ppm	Miss	Sequence
65	79	1707.7742	1706.7670	1706.9104	-84	1	R.ALFATGNFEDVRVLR.D
112	120	973.5347	972.5274	972.4988	29	0	K.QNLEASGVR.V
136	146	1277.7129	1276.7056	1276.5976	85	0	K.GLEDFYYSVGK.Y
163	176	1532.7870	1531.7797	1531.8610	-53	1	R.VDLKLIVFQEGVSAK.I
228	237	1263.6956	1262.6883	1262.6044	67	1	R.SYILDRGYAR.F
268	286	1895.9570	1894.9497	1894.9748	-13	0	K.LSGVQVSGNLAGHSAEIEK.L
368	386	2150.0771	2149.0698	2148.9932	36	1	R.EMRQMEGAWLGSDLVQCK.E
527	547	2342.9698	2341.9625	2342.1623	-85	1	R.AGLGYVHNKLSNMQFPQIAMDRI.Y
576	587	1383.6925	1382.6852	1382.6579	20	1	K.LDRGYFPTDGSR.V
671	693	2705.1059	2704.0986	2703.9562	53	0	K.NGAHTSWDDDDYEDCTQESGCK.S

No match to: 601.4593, 856.5298, 870.5436, 1107.5504, 1128.5691, 1140.5835, 1157.5879, 1193.6068, 1219.6164, 1233.6807, 1235.6313, 1259.6806,



ID BAMA_SALTI Reviewed; 803 AA.
AC Q8Z9A3; Q7CBP9;
DT 20-DEC-2005, integrated into UniProtKB/Swiss-Prot.
DT 01-MAR-2002, sequence version 1.
DT 13-JUN-2012, entry version 59.
DE RecName: Full=Outer membrane protein assembly factor BamA;
DE Flags: Precursor;
GN Name=bamA; Synonyms=yaeT; OrderedLocusNames=STY0247, t0225;
OS Salmonella typhi.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Salmonella.
OX NCBI_TaxID=90370;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=CT18;
RX MEDLINE=21534947; PubMed=11677608; DOI=10.1038/35101607;
RA Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J.,
RA Churcher C.M., Mungall K.L., Bentley S.D., Holden M.T.G., Sebahia M.,
RA Baker S., Basham D., Brooks K., Chillingworth T., Connerton P.,
RA Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,
RA Feltham T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K.,
RA Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C.,
RA Quail M.A., Rutherford K.M., Simmonds M., Skelton J., Stevens K.,
RA Whitehead S., Barrell B.G.;
RT "Complete genome sequence of a multiple drug resistant Salmonella
RT enterica serovar Typhi CT18.";
RL Nature 413:848-852(2001).
RN [2]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=ATCC 700931 / Ty2;
RX MEDLINE=22531367; PubMed=12644504;
RX DOI=10.1128/JB.185.7.2330-2337.2003;
RA Deng W., Liou S.-R., Plunkett G. III, Mayhew G.F., Rose D.J.,

RA Burland V., Kodoyianni V., Schwartz D.C., Blattner F.R.;
 RT "Comparative genomics of Salmonella enterica serovar Typhi strains Ty2
 RT and CT18.";
 RL J. Bacteriol. 185:2330-2337(2003).
 CC -!- FUNCTION: Part of the outer membrane protein assembly complex,
 CC which is involved in assembly and insertion of beta-barrel
 CC proteins into the outer membrane. Constitutes, with BamD, the core
 CC component of the assembly machinery (By similarity).
 CC -!- SUBUNIT: Part of the Bam complex, which is composed of the outer
 CC membrane protein BamA, and four lipoproteins BamB, BamC, BamD and
 CC BamE (By similarity).
 CC -!- SUBCELLULAR LOCATION: Cell outer membrane (By similarity).
 CC -!- SIMILARITY: Belongs to the BamA family.
 CC -----
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 CC -----
 DR EMBL; AL627266; CAD08682.1; -; Genomic_DNA.
 DR EMBL; AE014613; AA067955.1; -; Genomic_DNA.
 DR RefSeq; NP_454831.1; NC_003198.1.
 DR RefSeq; NP_804106.1; NC_004631.1.
 DR ProteinModelPortal; Q8Z9A3; -.
 DR SMR; Q8Z9A3; 21-351.
 DR GeneID; 1067818; -.
 DR GeneID; 1246736; -.
 DR GenomeReviews; AE014613 GR; t0225.
 DR GenomeReviews; AL513382 GR; STY0247.
 DR KEGG; stt:t0225; -.
 DR KEGG; sty:STY0247; -.
 DR PATRIC; 18538311; VBISalEnt120419_0247.
 DR eggNOG; COG4775; -.
 DR HOGENOM; HOG000261766; -.
 DR KO; K07277; -.
 DR OMA; NSKTRDE; -.
 DR ProtClustDB; PRK11067; -.
 DR BioCyc; SENT209261:T0225-MONOMER; -.
 DR BioCyc; SENT220341:STY0247-MONOMER; -.
 DR GO; GO:0009279; C:cell outer membrane; IEA:UniProtKB-SubCell.
 DR GO; GO:0016021; C:integral to membrane; IEA:UniProtKB-KW.
 DR GO; GO:0005886; C:plasma membrane; IEA:UniProtKB-KW.
 DR HAMAP; MF_01430; OM_assembly_BamA; 1; -.
 DR InterPro; IPR000184; Bac_surfAg_D15.
 DR InterPro; IPR023707; OM_YaeT/YfiO_complex_suYaeT.
 DR InterPro; IPR016474; OM_YaeT/YfiO_complex_YaeT-rel.
 DR InterPro; IPR010827; Surface_Ag_variable_number.
 DR Pfam; PF01103; Bac_surface_Ag; 1.
 DR Pfam; PF07244; Surf_Ag_VNR; 5.
 DR PIRSF; PIRSF006076; OM_assembly_OMP85; 1.
 DR TIGRFAMs; TIGR03303; OM_YaeT; 1.
 PE 3: Inferred from homology;
 KW Cell membrane; Cell outer membrane; Complete proteome; Membrane;
 KW Signal; Transmembrane; Transmembrane beta strand.
 FT SIGNAL 1 20 Potential.
 FT CHAIN 21 803 Outer membrane protein assembly factor
 FT BamA.
 FT /FTid=PRO 0000045376.
 SQ SEQUENCE 803 AA; 89467 MW; BBF8670070E67628 CRC64;
 MAMKKLLIAS LLESSATVYG AEGFVVKDIH FEGLQRVAVG AALLSMPVRT GDTVNDEDIS
 NTIRALFATG NFEDVRVLRD GNTLLVQVKE RPTIASITFS GNKSVKDDML KQNLEASGVR
 VGESLDRITTL SDIEKLEDF YYSVGKYSAS VKAVVTPLPR NRVDLKLVFQ EGVSAKIQOI
 NIVGNHAFST EELISHFQLR DEVFWNNVVG DRKYQKQKLA GDLETLSRY LDRGYARFNI
 DSTQVSLTPD KKGITYITVNI TEGDQYKLSG VQVSGNLAGH SAEIEKLTKI EPGELYNGTK
 VTKMEDDIKK LLGRYGYAYP RVQSQPEIND ADKTVKLRVN VDAGNRFYVR KIRFEGNDTS
 KDSVLRREMR QMEGAWLGSD LVDQGKERLN RLGFFFVDT DTQRVPGPSD QVDVVYKVKE
 RNTGSFNFI GYGTEGVSF QAGVQDNWL GTGYSVGING TKNDYQTYSE LSVTNPYFTV
 DGVSLGGRIF YNDFEADDAD LSDYTNKSYG TDVTLGFFIN EYNTLRAGLG YVHNKLSNMQ
 PQIAMDRYLE SMGDPDASDF AADDFTFNYG WTYNKLDRGY FPTDGSRVNL TGKVTIPGSD
 NEYYKVS LDT ATYVPIDNDH KWVVLGRTRW GYGDGLGKGE MPFYENFYAG GSSTVRGFQS
 NTIGPKAVYK NGAHTSWDDD DDYEDCTQES GCKSDAVGG NAMAVASLEF ITPTPFISEK
 YANSVTSFF WDMGTVDN WDPSSAPSDV PDYSDPGNIR MSAGIALQWM SPLGPLVFSY
 AQPFPKYDGD KAEQFPQFNIG KTW