

MASCOT SCIENCE Mascot Search Results

Protein View

Match to: **FLID_SALTY** Score: **98** Expect: **1.9e-006**
Flagellar hook-associated protein 2 OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) GN=flid PE=1 SV=2

Nominal mass (M_r): **49805**; Calculated pI value: **5.27**
 NCBI BLAST search of **FLID_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: **50**
 Number of mass values matched: **13**
 Sequence Coverage: **36%**

Matched peptides shown in **Bold Red**

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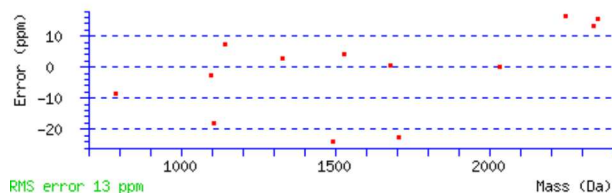
1 MASISLGLVGV SNLPLDQLLT DLTKNEKGRLL TPITKQOSAN SAKLTAYGTL
51 KSALEKFQTA NTALNKADLF KSTVASSTTE DLKVSTTAGA AAGTYKINVT
101 QLAAQSLAT KTTTFATTKEQ LGDTSVTSRT IKIEQPGRKE PLEIKLDKGD
151 TSMEAIRDAI NDADSGIAAS IVKVKENEFQ LVLTANSGTD NTMKITVEGD
201 TKLNDLLAYD STTNTGNMQE LVKAENAKLN VNGIDIERQS NTVTDAPQGI
251 TLTLTKKVTD ATVTVTKDDT KAKEAIKSWV DAYNSLVDTF SSLTKYTAVE
301 PGEEASDKNG ALLGDSVVRT IQTGIRAQFA NSGSNSAFKT MAEIGITQDG
351 TSGYKLKIDDD KLTKVLKDNT AAARELLVGD GKETGITTKI ATEVKSYLAD
401 DGIIDNAQDN VNATLKSLTK QYLSVSNSISID ETVARYKAQF TQLDTMMSKL
451 NNTSSYLTQQ FTAMNKS
    
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Show predicted peptides also

Sort Peptides By Residue Number Increasing Mass Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Sequence
57 - 66	1107.5593	1106.5520	1106.5720	-18	0	K.FQTANTALNK.A
97 - 111	1528.8756	1527.8684	1527.8620	4	0	K.INVTQLAAQSLATK.T
174 - 194	2339.1859	2338.1786	2338.1475	13	1	K.VKENEFQLVLTANSGTDNTMK.I
174 - 194	2355.1866	2354.1793	2354.1424	16	1	K.VKENEFQLVLTANSGTDNTMK.I Oxidation (M)
229 - 238	1142.6248	1141.6176	1141.6091	7	0	K.LNVNGIDIER.Q
258 - 271	1493.7333	1492.7260	1492.7621	-24	1	K.VTDATVTVTKDDTK.A
278 - 295	2032.9860	2031.9787	2031.9789	-0	0	K.SWVDAYNSLVDTFSSLTK.Y
309 - 319	1100.6029	1099.5956	1099.5986	-3	0	K.NGALLGDSVVR.T
320 - 326	788.4559	787.4487	787.4552	-8	0	R.TIQTGIR.A
327 - 339	1328.6267	1327.6194	1327.6157	3	0	R.AQFANGSGNSAFK.T
396 - 416	2250.1251	2249.1178	2249.0811	16	0	K.SYLADDGIIDNAQDNVNATLK.S
421 - 435	1681.8403	1680.8330	1680.8319	1	0	K.QYLSVNSISIDETVAR.Y
436 - 449	1707.7696	1706.7623	1706.8008	-23	1	R.YKAQFTQLDTMMSK.L Oxidation (M)

No match to: 628.0453, 644.0066, 650.0311, 662.2878, 666.0072, 832.2875, 833.0613, 855.0439, 870.5380, 871.0200, 973.5341, :



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ID FLID_SALTY Reviewed; 467 AA.
AC P16328;
DT 01-AUG-1990, integrated into UniProtKB/Swiss-Prot.
DT 23-JAN-2007, sequence version 2.
DT 16-MAY-2012, entry version 81.
DE RecName: Full=Flagellar hook-associated protein 2;
DE Short=HAP2;
DE AltName: Full=Filament cap protein;
DE AltName: Full=Flagellar cap protein;
GN Name=flid; Synonyms=flaV, flbC; OrderedLocusNames=STM1960;
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=90294298; PubMed=2193164; DOI=10.1016/S0022-2836(05)80266-9;
RA Homma M., Derosier D.J., Macnab R.M.;
RT "Flagellar hook and hook-associated proteins of Salmonella typhimurium
RT and their relationship to other axial components of the flagellum.";
RL J. Mol. Biol. 213:819-832(1990).
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.,
    
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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
 RT LT2.";
 RL Nature 413:852-856(2001).
 RN [3]
 RP NUCLEOTIDE SEQUENCE [GENOMIC DNA] OF 441-467.
 RC STRAIN=SJW1103;
 RX MEDLINE=92407478; PubMed=1527488;
 RA Kawagishi I., Mueller V., Williams A.W., Irikura V.M., Macnab R.M.;
 RT "Subdivision of flagellar region III of the Escherichia coli and
 RT Salmonella typhimurium chromosomes and identification of two
 RT additional flagellar genes.";
 RL J. Gen. Microbiol. 138:1051-1065(1992).
 RN [4]
 RP SUBUNIT.
 RX MEDLINE=99096876; PubMed=9878359; DOI=10.1006/jmbi.1998.2274;
 RA Vonderviszt F., Imada K., Furukawa Y., Uedaira H., Taniguchi H.,
 RA Namba K.;
 RT "Mechanism of self-association and filament capping by flagellar
 RT HAP2.";
 RL J. Mol. Biol. 284:1399-1416(1998).
 RN [5]
 RP SUBUNIT.
 RX MEDLINE=20568409; PubMed=11118149; DOI=10.1126/science.290.5499.2148;
 RA Yonekura K., Maki S., Morgan D.G., DeRosier D.J., Vonderviszt F.,
 RA Imada K., Namba K.;
 RT "The bacterial flagellar cap as the rotary promoter of flagellin self-
 RT assembly.";
 RL Science 290:2148-2152(2000).
 CC -!- FUNCTION: Required for the morphogenesis and for the elongation of
 CC the flagellar filament by facilitating polymerization of the
 CC flagellin monomers at the tip of growing filament. Forms a capping
 CC structure, which prevents flagellin subunits (transported through
 CC the central channel of the flagellum) from leaking out without
 CC polymerization at the distal end.
 CC -!- SUBUNIT: Homopentamer.
 CC -!- SUBCELLULAR LOCATION: Secreted. Bacterial flagellum.
 CC -!- SIMILARITY: Belongs to the flid family.
 CC -----
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 CC -----
 DR EMBL; X51740; CAA36030.1; -; Genomic_DNA.
 DR EMBL; AE006468; AAL20872.1; -; Genomic_DNA.
 DR EMBL; M85241; AAA27076.1; -; Genomic_DNA.
 DR PIR; S10364; S10364.
 DR RefSeq; NP_460913.1; NC_003197.1.
 DR ProteinModelPortal; P16328; -.
 DR PRIDE; P16328; -.
 DR GeneID; 1253481; -.
 DR GenomeReviews; AE006468_GR; STM1960.
 DR KEGG; stm:STM1960; -.
 DR PATRIC; 32382481; VBISalEnt20916_2076.
 DR eggNOG; COG1345; -.
 DR HOGENOM; HOG000254632; -.
 DR KO; K02407; -.
 DR OMA; FRTQISA; -.
 DR ProtClustDB; PRK08032; -.
 DR BioCyc; STYP99287:STM1960-MONOMER; -.
 DR GO; GO:0009288; C:bacterial-type flagellum; IEA:UniProtKB-SubCell.
 DR GO; GO:0005576; C:extracellular region; IEA:UniProtKB-SubCell.
 DR GO; GO:0007155; P:cell adhesion; IEA:InterPro.
 DR GO; GO:0006928; P:cellular component movement; IEA:InterPro.
 DR GO; GO:0009296; P:flagellum assembly; IEA:InterPro.
 DR InterPro; IPR010810; Flagellin_hook_IN_motif.
 DR InterPro; IPR010809; Flid_C.
 DR InterPro; IPR003481; Flid_N.
 DR Pfam; PF07196; Flagellin_IN; 1.
 DR Pfam; PF07195; Flid_C; 1.
 DR Pfam; PF02465; Flid_N; 1.
 PE 1: Evidence at protein level;
 KW Bacterial flagellum; Coiled coil; Complete proteome;
 KW Reference proteome; Secreted.
 FT INIT_MET 1 1 Removed.
 FT CHAIN 2 467 Flagellar hook-associated protein 2.
 FT /FTid=PRO_0000177024.
 FT COILED 411 439 Potential.
 SQ SEQUENCE 467 AA; 49835 MW; 5C1BD69A1F233BEA CRC64;
 MASISLGVG SNLPLDQLLT DLTKNEKGR L TPITKQQSAN SAKLTAYGTL KSALEKFQTA
 NTALNKADLF KSTVASSTTE DLKVSTTAGA AAGTYKINVT QLAAAQSLAT KTFATTKEQ
 LGDTSVTSRT IKIEQPGRKE PLEIKLDRGD TSMEAIRDAI NDADSGIAAS IVKVKENEFO
 LVLVTANSSTD NTKMITVEGD TKLNDLLAYD STTNTGNMQE LVKAENAKLN VNGIDIERQS
 NTVTDAPQGI TLTLTKKVD ATVTVTKDDT KAKEAIKSW DAYNSLVDTF SSLTKYTAVE
 PGEASDKNG ALLGDSVVRT IQTGIRAQFA NSGSNSAFKT MAEIGITQDG TSGKLIKDD
 KLTKVLKDNT AAARELLVGD GKETGITTKI ATEVKSYLEAD DGIIDNAQDN VNATLKSLLTK
 QYLSVSN SID ETVARYKAQF TQLDTMMSKL NNTSSYLTOQ FTAMNKS