

Mascot Search Results

Protein View

Match to: **FLIC_SALCH** Score: **101**

Flagellin OS=Salmonella choleraesuis (strain SC-B67) GN=fliC PE=3 SV=3

Found in search of 281474976711690.mgf

Nominal mass (M_r): **52081**; Calculated pI value: **4.85**

NCBI BLAST search of [FLIC_SALCH](#) against nr

Unformatted [sequence string](#) for pasting into other applications

Taxonomy: [Salmonella enterica subsp. enterica serovar Choleraesuis str. SC-B67](#)

Variable modifications: Carboxymethyl (C), Oxidation (M)

Cleavage by Trypsin: cuts C-term side of KR unless next residue is P

Sequence Coverage: **6%**

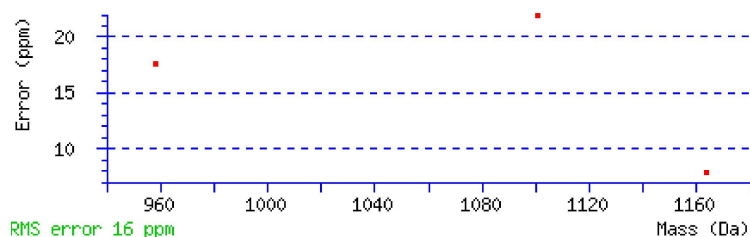
Matched peptides shown in **Bold Red**

1 MAQVINTNSL SLTQNNLNK SQSALGTAIE RLSSGLRINS **AKDDAAGQAI**
51 **ANR**FTANIKG LTQASRNAND GISIAQTTEG ALNEINNNLQ RVRELAVQSA
101 NSTNSQSDLD SIQAEITQRL NEIDR**VSGQT QFNGVK**VLAQ DNTLTIQVGA
151 NDGETIDIDL KQINSQTLGL DTLNVQKKYD VSDTAVAASY SDSKQNIAVP
201 DKTAITAKIG AATSGGAGIK ADISFKDGKY YATVSGYDDA ADTDKNGTYE
251 VTVAADTGAV TFATTPTVVD LPTDAKAVSK VQQNDTEIAA TNAKAALKAA
301 GVADAEADTA TLVKMSYTDN NGKVIDGGFA FKTSGGYAA SVDKSGAASL
351 KVTSYVDATT GTEKTAANKL GGADGKTEVV TIDGKTYNAS KAAGHNFKAQ
401 PELAEAAATT TENPLQKIDA ALAQVDALRS **DLGAVQNR**FN SAITNLGNTV
451 NNLSSARSRI EDSYATEVS NMSRAQILQQ AGTSVLAQAN QVPQNVLSLL
501 R

Show predicted peptides also

Sort Peptides By ☒ Residue Number ☐ Increasing Mass ☐ Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Sequence	
43 - 53	1101.5524	1100.5451	1100.5210	22	0	K.DDAAGQAIANR.F	(Ions score 58)
126 - 136	1164.6100	1163.6027	1163.5935	8	0	R.VSGQTQFNGVK.V	(Ions score 18)
430 - 438	959.5074	958.5001	958.4832	18	0	R.SDLGAVQNR.F	(Ions score 25)



ID FLIC_SALCH Reviewed; 501 AA.
AC P06176; Q57N43;
DT 01-JAN-1988, integrated into UniProtKB/Swiss-Prot.
DT 23-JAN-2007, sequence version 3.
DT 16-MAY-2012, entry version 86.
DE RecName: Full=Flagellin;
DE AltName: Full=Phase 1-C flagellin;
GN Name=fliC; OrderedLocusNames=SCH_1962;
OS Salmonella choleraesuis (strain SC-B67).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Salmonella;
OC Salmonella enterica subsp. enterica serovar Choleraesuis.
OX NCBI_TaxID=321314;
RN [1]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RC STRAIN=ATCC 7001;
RX MEDLINE=86143833; PubMed=4093985; DOI=10.1016/0022-2836(85)90397-3;

RA Wei L.-N., Joys T.M.;
 RT "Covalent structure of three phase-1 flagellar filament proteins of
 RT Salmonella.";
 RL J. Mol. Biol. 186:791-803(1985).
 RN [2]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RC STRAIN=SC-B67;
 RX PubMed=15781495; DOI=10.1093/nar/gki297;
 RA Chiu C.-H., Tang P., Chu C., Hu S., Bao Q., Yu J., Chou Y.-Y.,
 RA Wang H.-S., Lee Y.-S.;
 RT "The genome sequence of Salmonella enterica serovar Choleraesuis, a
 RT highly invasive and resistant zoonotic pathogen.";
 RL Nucleic Acids Res. 33:1690-1698(2005).
 CC -!- FUNCTION: Flagellin is the subunit protein which polymerizes to
 CC form the filaments of bacterial flagella.
 CC -!- SUBCELLULAR LOCATION: Secreted. Bacterial flagellum.
 CC -!- MISCELLANEOUS: Individual Salmonella serotypes usually alternate
 CC between the production of 2 antigenic forms of flagella, termed
 CC phase 1 and phase 2, each specified by separate structural genes.
 CC -!- SIMILARITY: Belongs to the bacterial flagellin family.
 CC -!- SEQUENCE CAUTION:
 CC Sequence=CAA27129.1; Type=Erroneous initiation;
 CC -----
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 CC -----
 DR EMBL; X03394; CAA27129.1; ALT_INIT; Genomic_DNA.
 DR EMBL; AE017220; AAX65868.1; -; Genomic_DNA.
 DR PIR; S09637; S09637.
 DR RefSeq; YP_216949.1; NC_006905.1.
 DR ProteinModelPortal; P06176; -.
 DR GeneID; 3334444; -.
 DR GenomeReviews; AE017220_GR; SCH_1962.
 DR KEGG; sec:SC1962; -.
 DR PATRIC; 32324831; VBISalEnt136302_2400.
 DR eggNOG; COG1344; -.
 DR KO; K02406; -.
 DR OMA; NSTEDRE; -.
 DR ProtClustDB; PRK08026; -.
 DR BioCyc; SENT321314:SCH_1962-MONOMER; -.
 DR GO; GO:0009420; C:bacterial-type flagellum filament; IEA:InterPro.
 DR GO; GO:0005576; C:extracellular region; IEA:UniProtKB-SubCell.
 DR GO; GO:0005198; F:structural molecule activity; IEA:InterPro.
 DR GO; GO:0001539; P:ciliary or flagellar motility; IEA:InterPro.
 DR Gene3D; G3DSA:2.30.220.10; G3DSA:2.30.220.10; 1.
 DR InterPro; IPR001492; Flagellin.
 DR InterPro; IPR001029; Flagellin_D0/D1.
 DR InterPro; IPR014981; Flagellin_D3.
 DR InterPro; IPR023357; Flagellin_f41_beta-roll_dom.
 DR Pfam; PF00700; Flagellin_C; 1.
 DR Pfam; PF08884; Flagellin_D3; 1.
 DR Pfam; PF00669; Flagellin_N; 1.
 DR PRINTS; PR00207; FLAGELLIN.
 PE 3: Inferred from homology;
 KW Bacterial flagellum; Complete proteome; Secreted.
 FT INIT_MET 1 1 Removed (By similarity).
 FT CHAIN 2 501 Flagellin.
 FT /FTId=PRO_0000182565.
 FT CONFLICT 265 265 T -> R (in Ref. 1; CAA27129).
 FT CONFLICT 296 307 Missing (in Ref. 1).
 FT CONFLICT 348 348 A -> R (in Ref. 1; CAA27129).
 FT CONFLICT 406 406 A -> R (in Ref. 1; CAA27129).
 SQ SEQUENCE 501 AA; 52112 MW; 69F85666ADD866D3 CRC64;
 MAQVINTNSL SLLTQNNLNK SQSALGTAIE RLSSGLRINS AKDDAAGQAI ANRFTANIKG
 LTQASRNAND GISIAQTTEG ALNEINNNLQ RVRELAVQSA NSTNSQSDLD SIQAEITQRL
 NEIDRVSGQT QFNGVKVLAQ DNTLTIQVGA NDGETIDIDL KQINSQTLGL DTLNVQKKYD
 VSDTAVAASY SDSKQNIQAVP DKTAITAKIG AATSGGAGIK ADISFKDGKY YATVSGYDDA
 ADTDKNGTYE VTVAADTGAV TFATPTTVVD LPTDAKAVSK VQQNDTEIAA TNAKAALKAA
 GVADAEADTA TLVKMSYTDN NGKVIDGGFA FKTSGGYYAA SVDKSGAASL KVTSYVDATT
 GTEKTAANKL GGADGKTEVV TIDGKTYNAS KAAGHNFKAQ PELAEAAAATT TENPLQKIDA
 ALAQVDALRS DLGAVQNRFN SAITNLGNTV NNLSSARSRI EDSYATEVS NMSRAQILQQ
 AGTSVLAQAN QVPQNVLSLL R