

# **Mascot Search Results**

## Protein View

Match to: **CHEB\_SALCH** Score: 30

**Chemotaxis response regulator protein-glutamate methylesterase** OS=Salmonella choleraesuis (strain SC-B67) GN=cheB PE=3 SV=1  
Found in search of 281474976711693.mgf

Nominal mass (M<sub>r</sub>): **37498**; Calculated pI value: **8.48**

NCBI BLAST search of [CHEB\\_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: **2%**

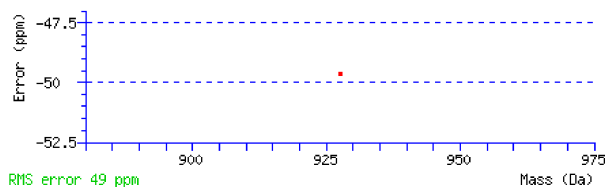
Matched peptides shown in **Bold Red**

```
1 MSKIRVLSVD DSALMRQIMT EIINSHSDME MVATAPDPLV ARDLIKKFNP
51 DVLTLDDVEMP RMDGLDFLEK LMRLRPMPPV MVSSLTGKGS EVTLRALELG
101 AIDFVTKPQL GIREGMLAYS EMIAEKVRTA ARARIAAHKP MAAPATLKAG
151 PLLSSEKLI AIGASTGGTEA IRHVLQPLPL SSPAVITQH MPPGFTRSF A
201 ERLNKLQIS VKEAEDGERV LPHGAYIAPG DKHME LARS G ANYQIKIHDG
251 PPNRHRPSV DVL FHSVAKH AGRNAVGVIL TGMGNDGAAG MLAMYQAGAW
301 TIAQNEASC VFGMPREAIN MGGVSEVVDL SQVSQQLAK ISAGQAIRI
```

Show predicted peptides also

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

Start	End	Observed	Mr (expt)	Mr (calc)	ppm	Miss	Sequence
341	349	928.5114	927.5041	927.5501	-50	1	K.ISAGQAIRI.- (Ions score 30)



ID CHEB\_SALCH Reviewed; 349 AA.  
AC Q57N81;  
DT 07-MAR-2006, integrated into UniProtKB/Swiss-Prot.  
DT 10-MAY-2005, sequence version 1.  
DT 16-MAY-2012, entry version 56.  
DE RecName: Full=Chemotaxis response regulator protein-glutamate methylesterase;  
DE EC=3.1.1.61;  
GN Name=cheB; OrderedLocusNames=SC\_1924;  
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 [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: Involved in the modulation of the chemotaxis system;  
CC catalyzes the demethylation of specific methylglutamate residues  
CC introduced into the chemoreceptors (methyl-accepting chemotaxis  
CC proteins) by CheR (By similarity).  
CC -!- CATALYTIC ACTIVITY: Protein L-glutamate O(5)-methyl ester + H(2)O  
CC = protein L-glutamate + methanol.  
CC -!- SUBCELLULAR LOCATION: Cytoplasm.  
CC -!- DOMAIN: The N-terminal regulatory domain inhibits the activity of  
CC the C-terminal effector domain.  
CC -!- PTM: Phosphorylated by CheA. Phosphorylation suppresses the  
CC inhibitory activity of the N-terminal domain (By similarity).  
CC -!- SIMILARITY: Contains 1 cheB-type methylesterase domain.  
CC -!- SIMILARITY: Contains 1 response regulatory 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; AE017220; AAX65830.1; -, Genomic\_DNA.  
DR RefSeq; YP\_216911.1; NC\_006905.1.  
DR ProteinModelPortal; Q57N81; -.  
DR SMR; Q57N81; 1-349.

DR GeneID; 3334405; -.  
 DR GenomeReviews; AE017220\_GR; SCH\_1924.  
 DR KEGG; sec:SC1924; -.  
 DR PATRIC; 32324739; VBISalEnt136302\_2357.  
 DR eggNOG; COG2201; -.  
 DR KO; K03412; -.  
 DR OMA; FVTKPKL; -.  
 DR ProtClustDB; PRK00742; -.  
 DR BioCyc; SENT321314:SCH\_1924-MONOMER; -.  
 DR GO; GO:0005737; C:cytoplasm; IEA:UniProtKB-SubCell.  
 DR GO; GO:0008984; F:protein-glutamate methyltransferase activity; IEA:EC.  
 DR GO; GO:0000156; F:two-component response regulator activity; IEA:InterPro.  
 DR GO; GO:0006935; P:chemotaxis; IEA:UniProtKB-KW.  
 DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA:InterPro.  
 DR Gene3D; G3DSA:3.40.50.180; Chemotax\_RR\_pGlu\_Me-esterase; 1.  
 DR HAMAP; MF\_00099; CheB\_methylase; 1; -.  
 DR InterPro; IPR011006; CheY-like superfamily.  
 DR InterPro; IPR008248; Sig\_transdc\_resp-reg\_CheB.  
 DR InterPro; IPR000673; Sig\_transdc\_resp-reg\_Me-esterase.  
 DR InterPro; IPR001789; Sig\_transdc\_resp-reg\_receiver.  
 DR Pfam; PF01339; CheB\_methylase; 1.  
 DR Pfam; PF00072; Response\_reg; 1.  
 DR PIRSF; PIRSF000876; RR\_chemtxs\_CheB; 1.  
 DR SMART; SM00448; REC; 1.  
 DR SUPFAM; SSF52738; Chemotax\_RR\_pGlu\_Me-esterase; 1.  
 DR SUPFAM; SSF52172; CheY\_like; 1.  
 DR PROSITE; PS50122; CHEB; 1.  
 DR PROSITE; PS50110; RESPONSE\_REGULATORY; 1.  
 PE 3: Inferred from homology;  
 KW Chemotaxis; Complete proteome; Cytoplasm; Hydrolase; Phosphoprotein.  
 FT CHAIN 1 349 Chemotaxis response regulator protein-  
 FT glutamate methyltransferase.  
 FT /FTId=PRO\_0000225483.  
 FT DOMAIN 5 122 Response regulatory.  
 FT DOMAIN 152 344 CheB-type methyltransferase.  
 FT ACT\_SITE 164 164 By similarity.  
 FT ACT\_SITE 190 190 By similarity.  
 FT ACT\_SITE 286 286 By similarity.  
 FT MOD\_RES 56 56 4-aspartylphosphate (By similarity).  
 SQ SEQUENCE 349 AA; 37522 MW; 82B408862A8F9590 CRC64;  
 MSKIRVLSVD DSALMRQIMT EIINSHSDME MVATAPDPLV ARDLIKKFNP DVLTLDVEMP  
 RMDGLDFLEK LMLRLRMPV VVSSLTGKGS EVTLRALELG AIDFVTKPQL GIREGMLAYS  
 EMIAEKVRTA ARARIAAHKP MAAPATLKAG PLLSSEKLI AIGASTGGTEA IRHVLQPLPL  
 SSPAVIITQH MPPGFTRSF AERLNKLCQIS VKEAEDGERV LPGHAYIAPG DKHMLARSG  
 ANYQIKIHG PPVNRHRPSV DVLFHSAKH AGRNAVGVIL TGMGNDGAAG MLAMYQAGAW  
 TIAQNEASCV VFGMPREAIN MGGVSEVVDL SQVSQQLAK ISAGQAIRI

Mascot: <http://www.matrixscience.com/>