

Phyre2

Job Description	sven0925_	Date	Tue Aug 12 16:31:53 BST 2014
Confidence	97.96%	Aligned Residues	77
Rank	1	Template	c2lkiA_
% Identity	19%	PDB info	PDB header: lipid transport
		Chain: A: PDB Molecule:	putative uncharacterized protein;
		Resolution	UNK
Model Dimensions (Å)	X:47.623 Y:30.804 Z:31.761		
PDBTitle: solution nmr structure of holo acyl carrier protein ne2163 from2 nitrosomonas europaea. northeast structural genomics consortium3 target net1.			

Show / Hide SS confidence

Show / Hide Conservation and Alignment quality

- Insertion relative to template
- Deletion relative to template
- Catalytic residue from the CSA

[Detailed help on interpreting your alignment](#)

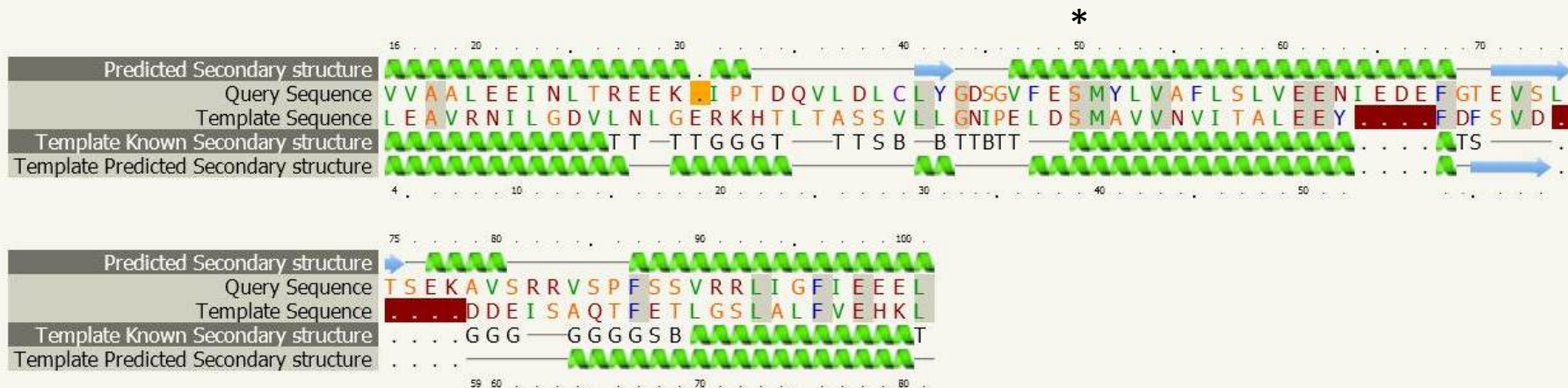


FIG. S1. Phyre² alignment of Sven0925 to the holo acyl carrier protein ne2163 from *Nitrosomonas europaea*. 77 residues of Sven0925 (71% of its sequence) were modelled with 98% confidence to the structure of the holo acyl carrier protein (output from Phyre2; <http://www.sbg.bio.ic.ac.uk/phyre2>). *, conserved serine at position 50 of Sven0925 that is predicted to be the catalytic residue needed for addition of the 4'-phosphopantetheine moiety .

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Bacillus_cereus      -----MEDTNKEKIIQVVLCCVEEVNENLENKIDLEKGLKAHLYDW 41
Bacillus_bombysepticus -----MEDTNKEKIIQIVLCCVEEVNENLENKIDLEKGLKAHLYDW 41
Bacillus_thuringiensis MICKKECIYLEDTKKKEKIIQIVLCCVEEVNENLENKIDLEKGLKAHLYDW 50
Pelosinus            -----MEQKIIGIILHEVSELNEQLDHKVAIENGENAGLYGL 37
Sven0925             -----MLDGGLKVTERIQGVVVAAL EEINLTREEKIPTDQVLDLCLYGD 44
Desulfovibrio        -----MPLRQQVKQALIEDLN-LQSITPEDI EDDAP-----LFG- 33
                    :::  ::  :.  ::  ..:  :  *:.

#
Bacillus_cereus      EGY-LDSLGLVSLVLSIEQGLEDELGLSVDLVNLDTMSQHNSPFKTI EAL 90
Bacillus_bombysepticus EGY-LDSLGLVSLVLSIEQGLEDELGLSVDLVNLDTMSQHNSPFKTI EAL 90
Bacillus_thuringiensis EGY-LDSLGLVSLVLSIEQGLEDELGLSVDLVNLDTMSQHNSPFKTI ETL 99
Pelosinus            TGV-LDSLGLVTLIVAVEQAIEDELGLAISLADERAMSKNSPFRTIGTL 86
Sven0925             SGV-FESMYLVAFSLVEENIEDEFGTEVSLTSEKAVSRVSPFSSVRRLL 93
Desulfovibrio        DGLGLDSLDAVELVVLVQK----RFGVEIKNMDEGRVA-----FASVTAL 74
                    *  ::*:  *  ::  :::  .*  :.  .  ::  *  ::  *

Bacillus_cereus      VAYILECQEQLKSLT 105
Bacillus_bombysepticus VAYILECQEQLKSLT 105
Bacillus_thuringiensis VAYIIECQETLKSLLT 114
Pelosinus            ADYIVKVSQEEA--- 98
Sven0925             IGFIEEELVGVGRG 108
Desulfovibrio        AGFIEERR----- 82
                    :*  :

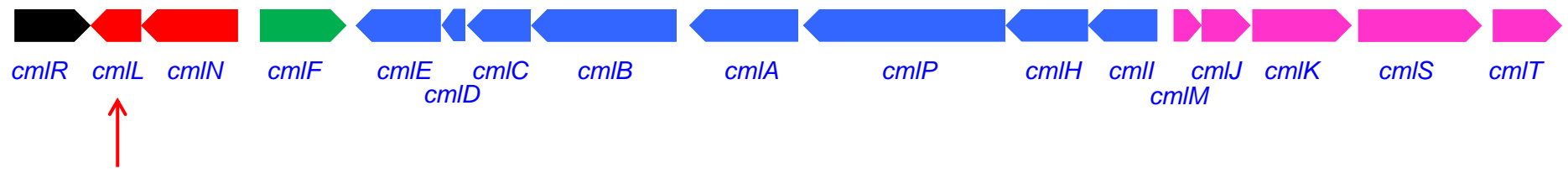
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Percent amino acid sequence identity

	Sven0925
Desulfovibrio	34.15
Pelosinus fermentans	30.61
Bacillus thuringiensis	29.63
Bacillus cereus	31.43
Bacillus bombysepticus	30.48

FIG. S2. Clustal Omega alignment of Sven0925 to homologous proteins identified in a blastP search of the NCBI database as acyl carrier proteins. #, conserved serine at position 50 of Sven0925 that is predicted to be the site of addition of the 4'-phosphopantetheine moiety. Percentage amino acid sequence identities to Sven0925 are given below the alignment.

Streptomyces venezuelae



Micromonospora sp. ATCC 39149



FIG. S3. Comparison of the CHL biosynthetic gene clusters of *S. venezuelae* and *Micromonospora* sp. ATCC 39149. Note the absence of a *cmlL* homologue in the *Micromonospora* gene cluster. The different colours represent potential transcription units.

Table S1. Oligonucleotides used in this study.

Name	Sequence	Notes
HygF0909_PCR_T1	TCAGTCGCCTCGGGCCGTGGCTGCCGCGTGG GCGGTCGGCTGACGCCGTTGGATACACC	HYG ^R cassette for PCR-Targeting <i>sven0909- sven0912</i>
HygR0912_PCR_T1	TGCACGACGGCTGGCTCCGGAGCCGTACGGG GCACGGCGTCAGGCGCCGGGGGCGGTGT	HYG ^R cassette for PCR-Targeting <i>sven0909- sven0913</i>
HygF0913_PCR_T2	ATGTCCACGATTTCCGGATCTACGACAGGCGTC GACCTTCCTGACGCCGTTGGATACACC	HYG ^R cassette for PCR-Targeting <i>sven0913- sven0915</i>
HygR0915_PCR_T2	ATGACGACCCACCAGACAGCCATGATCATGAT GGGGCTCTCAGGCGCCGGGGGCGGTGT	HYG ^R cassette for PCR-Targeting <i>sven0913- sven0915</i>
Hyg0913_F_KO	CTTTCCTGTCATCGATGACGTGCGTTCCTGGAG GCATTGCTGACGCCGTTGGATACACC	HYG ^R cassette for PCR-Targeting <i>sven0913</i>
Hyg0913_R_KO	GAGCGGGCGCCGCCGCTACGGCGGGGCGGC GGTAGGGGATCAGGCGCCGGGGGCGGTGT	HYG ^R cassette for PCR-Targeting <i>sven0913</i>
Hyg0914_F_KO	GAAGCGAGCGGCGGCCGACGCGGGCCCGG CCTGATCCCTGACGCCGTTGGATACACC	HYG ^R cassette for PCR-Targeting <i>sven0914</i>
Hyg0914_R_KO	CGCCCGCGCCGGCGGGGAAGCCGTCCGGG GGCGAAGCGTCAGGCGCCGGGGGCGGTGT	HYG ^R cassette for PCR-Targeting <i>sven0914</i>
Hyg0915_F_KO	GCGCCGCTTCCGGTACGAGCCCGGTCAGGAG CGTCGGCGCTGACGCCGTTGGATACACC	HYG ^R cassette for PCR-Targeting <i>sven0915</i>
Hyg0915_R_KO	TAACGACTTGGACACCCCGGCGCGGAGAAGG AGTGTTCCTCAGGCGCCGGGGGCGGTGT	HYG ^R cassette for PCR-Targeting <i>sven0915</i>
Compl13_SpeI_F	CCGTA TAGTCTGACCCGGCGCCGCCTTCC	Complementation of <i>sven0913</i>
Compl13_BamHI_R	CGGTGGATCCTCAGGCCGGGCCCGCTCCG	Complementation of <i>sven0913</i>
Compl14_NdeI_F	GGGCGAACATATGACGCCGACGCTCCTGAC	Complementation of <i>sven0913</i>
Compl14_SacII_R	CCTCCGCGGCTACCGCCGCCCGCCGTAG	Complementation of <i>sven0913</i>
Compl15_SpeI_F	CGAAACTAGTGAAAAAGCTCCA ACTACATC	Complementation of <i>sven0913</i>
Compl15_BamHI_R	AGCGGGATCCTCACCGCTTCGCCCCGACG	Complementation of <i>sven0913</i>
F0913_OE_NdeI	AAATATACATATGTCCACGATTTCCGGATC	Overexpression of <i>sven0913</i>
R0913_OE_HindIII	AAAAGCTTTCAGGCCGGGCCCGGTCC	Overexpression of <i>sven0913</i>
Cm_0912_RT_F	CACCGTCTCGGTGTCA	RT-PCR <i>sven0912</i>
Cm_0912_RT_R	TCGCCATCCCTCGAAAG	RT-PCR <i>sven0912</i>
Cm_0913_RT_F	GTCATCGACGGCATGCAC	RT-PCR <i>sven0913</i>
Cm_0913_RT_R	GTACGTAATATCCGCAGCGC	RT-PCR <i>sven0913</i>
Cm_0915_RT_F	ATGACGACCCACCAGACAG	RT-PCR <i>sven0915</i>
Cm_0915_RT_R	CCGACGAGGAACATGAACAG	RT-PCR <i>sven0915</i>
Cm_0916_RT_F	GTCGGAATTCATGCTGTCCG	RT-PCR <i>sven0916</i>
Cm_0916_RT_R	GAGGAGGAACGTGATGAGGA	RT-PCR <i>sven0916</i>
Cm_0920_RT_F	GTACGAGATCTGCCTGACCA	RT-PCR <i>sven0920</i>
Cm_0920_RT_R	CTTGATGGGCTTGGACTCGA	RT-PCR <i>sven0920</i>
Cm_0924_RT_F	TCTCCATCAACGCCTACCTC	RT-PCR <i>sven0924</i>
Cm_0924_RT_R	GACCTGCTTCATCATCTCGC	RT-PCR <i>sven0924</i>
Cm_0927_RT_F	CTGCGAAGGTTGAGGACT	RT-PCR <i>sven0927</i>
Cm_0927_RT_R	CACCGAGTCCAGCGAGTAGT	RT-PCR <i>sven0927</i>
Cm_0929_RT_F	GACCACATCGACCTCTGCTA	RT-PCR <i>sven0929</i>
Cm_0929_RT_R	AGGGAGTACTCGGACTGGAC	RT-PCR <i>sven0929</i>
Cm_0930_RT_F	GCATCACCGAGGAACAGC	RT-PCR <i>sven0930</i>
Cm_0930_RT_R	CCAGTCGAAGTACTCCACCA	RT-PCR <i>sven0930</i>