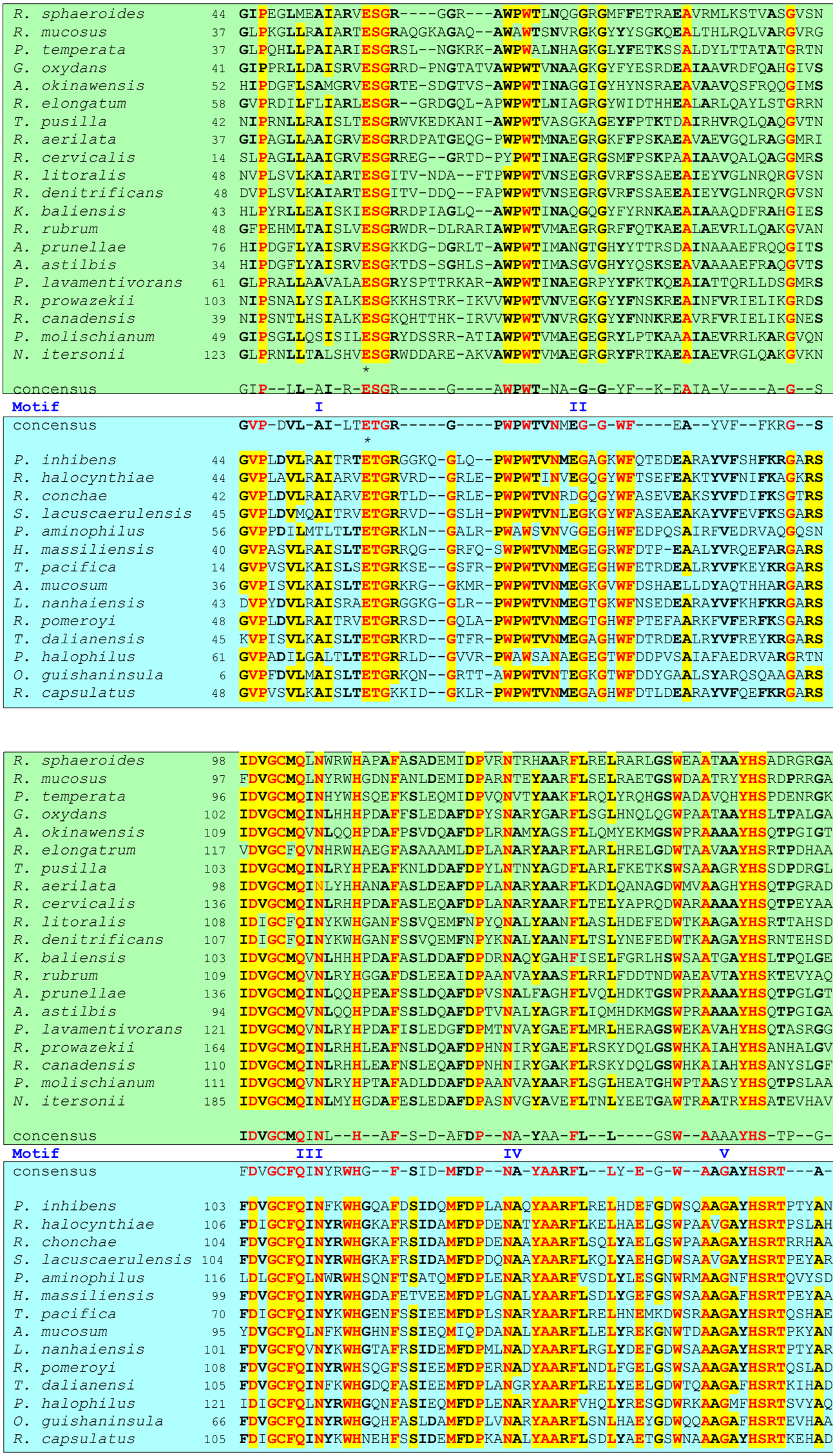
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R. mucosus 37 GLPKGLLRAIARTESGRAQGKAGAQ--AWAWTSNVRGKGYYYSGKQEALTHLRQLVARGVRG
P. temperata 37 GLPQHLLPAIARIESGRSL--NGKRK-AWPWALNHAGKGLYFETKSSALDYLTTATATGRTN
G. oxydans 41 GIPPRLLDAISRVESGRRD-PNGTATVAWPWTVNAAGKGYFYESRDEAIAAVRDFQAHGIVS
A. okinawensis 52 HIPDGFLSAMGRVESGRTE-SDGTVS-AWPWTINAGGIGYHYNSRAEAVAAVQSFRQQGIMS
R. elongatum 58 GVPRDILFLIARLESGR--GRDGQL-APWPWTLNIAGRGYWIDTHHEALARLQAYLSTGRRN
T. pusilla 42 NIPRNLLRAISLTESGRWVKEDKANI-AWPWTVASGKAGEYFPTKTDAIRHVRQLQAQGVTN
R. aerilata 37 GIPAGLLAAIGRVESGRRDPATGEQG-PWPWTMNAEGRGKFFPSKAEAVAEVGQLRAGGMRI
R. cervicalis 14 SLPAGLLAAIGRVESGRREG--GRTD-PYPWTINAEGRGSMFPSKPAAIAAVQALQAGGMRS
R. litoralis 48 NVPLSVLKAIARTESGITV-NDA--FTPWPWTVNSEGRGVRFSSAEEAIEYVGLNRQRGVSN
R. denitrificans 48 DVPLSVLKAIARTESGITV-DDQ--FAPWPWTVNSEGRGVRFSSAEEAIEYVGLNRQRGVSN
K. baliensis 43 HLPYRLLEAISKIESGRRDPIAGLQ--AWPWTINAQGQGYFYRNKAEAIAAAQDFRAHGIES
R. rubrum 48 GFPEHMLTAISLVESGRWDR-DLRARIAWPWTVMAEGRGRFFQTKAEALAEVRLLQAKGVAN
A. prunellae 76 HIPDGFLYAISRVESGKKDG-DGRLT-AWPWTIMANGTGHYYTTRSDAINAAAEFRQQGITS
A. astilbis 34 HIPDGFLYAISRVESGKTDS-SGHLS-AWPWTIMASGVGHYYQSKSEAVAAAAEFRAQGVTS
P. lavamentivorans 61 GLPRALLAAVALAESGRYSPTTRKAR-AWPWTINAEGRPYYFKTKQEAIATTQRLLDSGMRS
R. prowazekii 103 NIPSNALYSIALKESGKKHSTRK-IKVVWPWTVNVEGKGYYFNSKREAINFVRIELIKGRDS
R. canadensis 39 NIPSNTLHSIALKESGKQHTTHK-IRVVWPWTVNVRGKGYYFNNKREAVRFVRIELIKGNES
P. molischianum 49 GIPSGLLQSISILESGRYDSSRR-ATIAWPWTVMAEGEGRYLPTKAAAIAEVRRLKARGVQN
N. itersonii 123 GLPRNLLTALSHVESGRWDDARE-AKVAWPWTVMAEGRGRYFRTKAEAIAEVRGLQAKGVKN
concensus GIP--LL-AI-R-ESGR-----G----AWPWT-NA-G-G-YF--K-EAIA-V----A-G--S
Motif I II
concensus GVP-DVL-AI-LTETGR-----G----PWPWTVNMEG-G-WF----EA--YVF--FKRG--S
P. inhibens 44 GVPLDVLRAITRTETGRGGKQ-GLQ--PWPWTVNMEGAGKWFQTEDEARAYVFSHFKRGARS
R. halocynthiae 44 GVPLAVLRAIARVETGRVRD--GRLE-PWPWTINVEGQGYWFTSEFEAKTYVFNIFKAGKRS
R. conchae 42 GVPLDVLRAIARVETGRTLD--GRLE-PWPWTVNRDGQGYWFASEVEAKSYVFDIFKSGTRS
S. lacuscaerulensis 45 GVPLDVMQAITRVETGRRVD--GSLH-PWPWTVNLEGKGYWFASEAEAKAYVFEVFKSGARS
P. aminophilus 56 GVPPDILMTLTLTETGRKLN--GALR-PWAWSVNVGGEGHWFEDPQSAIRFVEDRVAQGQSN
H. massiliensis 40 GVPASVLRAISLTETGRRQG--GRFQ-SWPWTVNMEGEGRWFDTP-EAALYVRQEFARGARS
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A. mucosum 36 GVPISVLKAISLTETGRKRG--GKMR-PWPWTVNMEGKGVWFDSHAELLDYAQTHHARGARS
L. nanhaiensis 43 DVPYDVLRAISRAETGRGGKG-GLR--PWPWTVNMEGTGKWFNSEDEARAYVFKHFKRGARS
R. pomeroyi 48 GVPLDVLRAITRVETGRRSD--GQLA-PWPWTVNMEGTGHWFPTEFAARKFVFERFKSGARS
T. dalianensis 45 KVPISVLKAISLTETGRKRD--GTFR-PWPWTVNMEGAGHWFDTRDEALRYVFREYKRGARS
P. halophilus 61 GVPADILGALTLTETGRRLD--GVVR-PWAWSANAEGEGTWFDDPVSAIAFAEDRVARGRTN
O. guishaninsula 6 GVPFDVLMAISLTETGRKQN--GRTT-AWPWTVNTEGKGTWFDDYGAALSYARQSQAAGARS
R. capsulatus 48 GVPVSVLKAISLTETGKKID--GKLR-PWPWTVNMEGAGHWFDTLDEARAYVFQEFKRGARS
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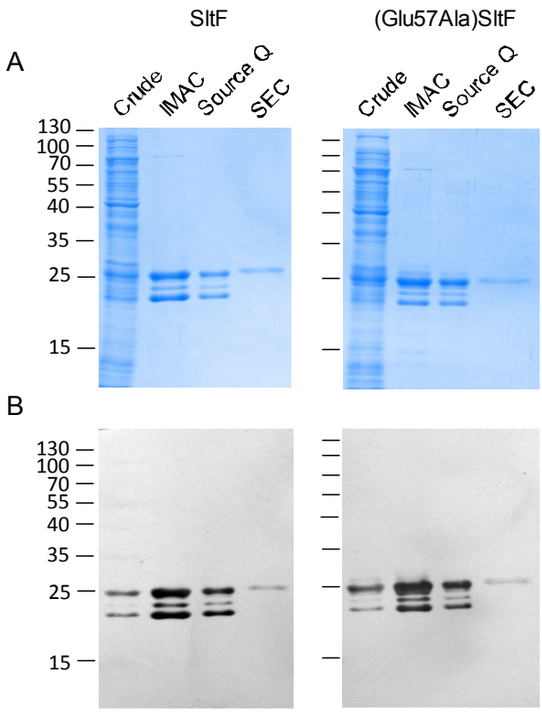
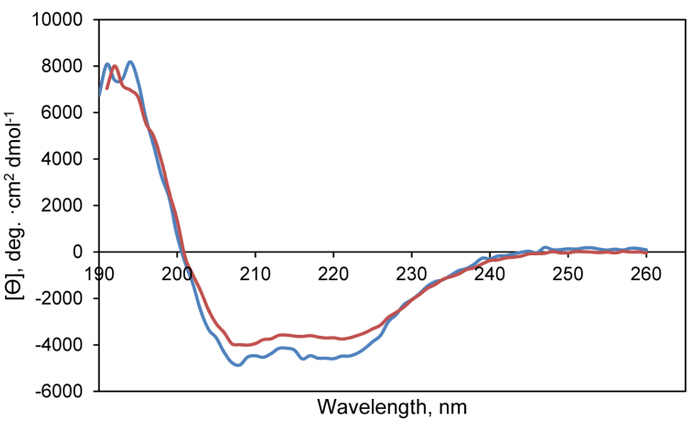
R. mucosus 97 FDVGCMQLNYRWHGDNFANLDEMIDPARNTEYAARFLSELRAETGSWDAATRYYHSRDPRRGAAY
P. temperata 96 IDVGCMQINHYWHSQEFKSLEQMIDPVQNVTYAAKFLRQLYRQHGSWADAVQHYHSPDENRGKRY
G. oxydans 102 IDVGCMQINLHHHPDAFFSLEDAFDPYSNARYGARFLSGLHNQLQGWPAATAAYHSLTPALGADY
A. okinawensis 109 IDVGCMQVNLQQHPDAFPSVDQAFDPLRNAMYAGSFLLQMYEKMGSWPRAAAAYHSQTPGIGTPY
R. elongatrum 117 VDVGCFQVNHRWHAEGFASAAAMLDPLANARYAARFLARLHRELGDWTAAVAAYHSRTPDHAARY
T. pusilla 103 IDVGCMQINLRYHPEAFKNLDDAFDPYLNTNYAGDFLARLFKETKSWSAAAGRYHSSDPDRGLYY
R. aerilata 98 IDVGCMQINLYHHANAFASLDEAFDPLANARYAARFLKDLQANAGDWMVAAGHYHSQTPGRADAY
R. cervicalis 136 IDVGCMQINLRHHPDAFASLEQAFDPLANARYAARFLTELYAPRQDWARAAAAYHSQTPEYAAPY
R. litoralis 108 IDIGCFQINYKWHGANFSSVQEMFNPYQNALYAANFLASLHDEFEDWTKAAGAYHSRTTAHSDLY
R. denitrificans 107 IDIGCFQINYKWHGANFSSVQEMFNPYKNALYAANFLTSLYNEFEDWTKAAGAYHSRNTEHSDLY
K. baliensis 103 IDVGCMQVNLHHHPDAFASLDDAFDPDRNAQYGAHFISELFGRLHSWSAATGAYHSLTPQLGEEY
R. rubrum 109 IDVGCMQVNLRYHGGAFDSLEEAIDPAANVAYAASFLRRLFDDTNDWAEAVTAYHSKTEVYAQRY
A. prunellae 136 IDVGCMQINLQQHPEAFSSLDQAFDPVSNALFAGHFLVQLHDKTGSWPRAAAAYHSQTPGLGTPY
A. astilbis 94 IDVGCMQVNLQQHPDAFSSLDQAFDPTVNALYAGRFLIQMHDKMGSWPRAAAAYHSQTPGIGAPY
P. lavamentivorans 121 IDVGCMQVNLRYHPDAFISLEDGFDPMTNVAYGAEFLMRLHERAGSWEKAVAHYHSQTASRGGRY
R. prowazekii 164 IDVGCMQINLRHHLEAFNSLDQAFDPHNNIRYGAEFLRSKYDQLGSWHKAIAHYHSANHALGVKY
R. canadensis 110 IDVGCMQINLRHHLEAFNSLEQAFDPNHNIRYGAKFLRSKYDQLGSWHKAIAHYHSANYSLGFQY
P. molischianum 111 IDVGCMQVNLRYHPTAFADLDDAFDPAANVAYAARFLSGLHEATGHWPTAASYYHSQTPSLAAAY
N. itersonii 185 IDVGCMQINLMYHGDAFESLEDAFDPASNVGYAVEFLTNLYEETGAWTRAATRYHSATEVHAVRY
concensus IDVGCMQINL--H--AF-S-D-AFDP--NA-YAA-FL--L----GSW--AAAAYHS-TP--G--Y
Motif III IV V
consensus FDVGCFQINYRWHG--F-SID-MFDP--NA-YAARFL--LY-E-G-W--AAGAYHSRT---A-RY
P. inhibens 103 FDVGCFQINFKWHGQAFDSIDQMFDPLANAQYAARFLRELHDEFGDWSQAAGAYHSRTPTYANRY
R. halocynthiae 106 FDIGCFQINYRWHGKAFRSIDAMFDPDENATYAARFLKELHAELGSWPAAVGAYHSRTPSLAHAY
R. chonchae 104 FDVGCFQINYRWHGKAFRSIDAMFDPDENAAYAARFLSQLYAELGSWPAAAGAYHSRTRRHAAAY
S. lacuscaerulensis 104 FDVGCFQINYRWHGKAFRSIDAMFDPDQNAAYAARFLKQLYAEHGDWSAAVGAYHSRTPEYARRY
P. aminophilus 116 LDLGCFQLNWRWHSQNFTSATQMFDPLENARYAARFVSDLYLESGNWRMAAGNFHSRTQVYSDRY
H. massiliensis 99 FDVGCFQINYRWHGDAFETVEEMFDPLGNALYAARFLSDLYGEFGSWSAAGAFHSRTPEYAARY
T. pacifica 70 FDIGCFQINYKWHGENFSSIEEMFDPLSNARYAARFLRELHNEMKDWSRAAGAYHSRTQSHAERY
A. mucosum 95 YDVGCFQLNFKWHGHNFSSIEQMIQPDANALYAARFLLELYREKGNWTDAAGAYHSRTPKYANKY
L. nanhaiensis 101 FDVGCFQVNYKWHGTAFRSIDEMFDPMLNADYAARFLRGLYDEFGDWSAAGAYHSRTPTYARSY
R. pomeroyi 108 FDVGCFQINYRWHSQGFSSIEEMFDPERNADYAARFLNDLFGELGSWSAAGAYHSRTQSLADAY
T. dalianensi 105 FDVGCFQINFKWHGDQFASIEEMFDPLANGRYAARFLRELYEELGDWTQAAGAFHSRTKIHADRY
P. halophilus 121 IDIGCFQLNYRWHGQNFASIEQMFDPLENARYAARFVHQLYRESGDWRKAAGMFHSRTSVYAQRY
O. guishaninsula 66 FDVGCFQINYRWHGQHFASLDAMFDPLVNARYAARFLSNLHAEYGDWQQAAGAFHSRTEVHAARY
R. capsulatus 105 FDIGCFQINYKWHNEHFSSIDEMFDPKANALYAARFLSDLYAETGSWNAAGAYHSRTKEHADRY

Supplemental FIG 1. Identification of consensus motifs in the alignment of known and hypothetical SltF homologs. The known and hypothetical amino acid sequences of the LT domains of SltF and its homologs identified in the genome database for the α-Protoeobacteria were aligned. Residues in bold, and highlighted in yellow denote over 50% and 80% identity, respectively; red font denotes invariant residues, and the asterisks identify the putative catalytic Glu residues. The consensus motifs are presented below and above the two subsets of aligned sequences, respectively. Abbreviations for bacteria and sequence accession numbers in parentheses) are: *Rhodbacter sphaeroides* (NC_007493), *Roseovarius mucosus* (NZ_KN293980), *Planktomarina temperata* (WP_052377022), *Gluconobacter oxydans* (NC_006677), *Acetobacter okinawensis* (NZ_BAJU01000118), *Roseibacterium elongatum* (NZ_CP004372), *Terasakiella pusilla* (NZ_JHYO01000012), *Roseomonas aerilata* (NZ_JONP01000009), *Roseomonas cervicalis* (NZ_GG771252), *Roseobacter litoralis* (NC_015730), *Roseobacter denitrificans* (NC_008209), *Kozakia baliensis* (NZ_JNAB01000023), *Rhodospirillum rubrum* (NC_007643), *Asaia prunellae* (NZ_BAJV01000004), *Asaia astilbis* (NZ_BAJT01000016), *Parvibaculum lavamentivorans* (NC_009719), *Rickettsia prowazekii* (NC_000963) *Rickettsia canadensis* (NC_009879), *Phaeospirillum molischianum* (NZ_CAHP01000001), *Novispirillum itersonii* (NZ_KB907344), *Phaeobacter inhibens* (NC_018290), *Ruegeria halocynthiae* (NZ_JQEZ01000003), *Ruegeria conchae* (NZ_AEYW01000017), *Silicibacter lacuscaerulensis* (NZ_GG704596), *Paracoccus aminophilus* (NC_022041), *Haematobacter massiliensis* (NZ_JGYG01000003), *Thioclava pacifica* (NZ_AUND01000012), *Actibacterium mucosum* (NZ_JFKE01000001), *Leisingera nanhaiensis* (NZ_KI421509), *Ruegeria pomeroyi* (NC_003911), *Thioclava dalianensis* (NZ_JHEH01000011), *Paracoccus halophilus* (NZ_JRKN01000018), *Oceaniovalibus guishaninsula* (NZ_AMGO01000047), *Rhodobacter capsulatus* (NC_014034).



Supplemental FIG 2. Purification of wild-type- and (Glu57Ala)-SltF. SDS PAGE with (A) Coomassie Brilliant Blue staining and (B) Western immunoblot analysis (using anti-His_6 primary antibody) of the respective enzymes purified by immobilized-metal affinity chromatography (IMAC) on Ni^{2+}-NTA agarose, anion-exchange chromatography on Source 15Q, and size-exclusion chromatography (SEC) on HiLoad 16/600 Superdex 200pg. The mass (kDa) of molecular weight markers are indicated on the left. The apparent mass of the recombinant SltF is 25.04 kDa, but it is susceptible to limited proteolysis within its C-terminal non-catalytic domain generating two catalytically-active, truncated forms of the enzyme (21) with apparent masses of 23 and 20.4 kDa; these can be separated by SEC.



Supplemental FIG 3. CD analysis of wild-type- (red) and (Glu57Ala)- (blue) SltF. The spectra of proteins (0.2 $mg.ml^{-1}$) in 5 mM sodium phosphate buffer, pH 7 were recorded in a 0.1 cm path length cell at an internal temperature of 25 °C. The data were recorded as an average of four accumulations at each wavelength with a scan speed of 50 $nm \cdot min^{-1}$ (bandwidth of 1 nm and data pitch of 1 nm).