Figure S1

```
CDA_Scoe        ----MSENSSVRHGLTSAQHEVWLAQQLDPR-GAHYRTGSCLEIDGPLDHAVLSRALRLT
CDA_Sliv        ----MSENSSVRHGLTSAQHEVWLAQQLDPR-GAHYRTGSCLEIDGPLDHAVLSRALRLT
Plu3535_Plum    --MLLDKVEPLVIPLNQQQKEIYLDHINRED-TAAFNIGGYVEIKQSINIKNLECAIKHT
SrfAC_Bsub      MSQFSKDQVQDMYYLSPMQEGMLFHAILNPG-QSFYLEQITMKVKGSLNIKCLEESMNVI
VibH_Vcho       ------------MSMLLAQKPFWQRHLAYPH-INLDTVAHSLRLTGPLDTTLLLRALHLT
TycC_Bpar       ----EPVQKQAYYPVSSAQKRMYILDQFEGV-GISYNMPSTMLIEGKLERTRVEAAFQRL
Dhbf_Bsub       ----MPDTKDLQYSLTGAQTGIWFAQQLDPD-NPIYNTAEYIEINGPVNIALFEEALRHV
EntF_Shyg       ---MQPAVPATRLPLSTGQSEIWFIQQLEPPESTTFKVGEYLEIQGPIDAAIFERALRQA
Gram_Bpum       ----MSIQSVDSFPLTGAQSGIWYAQQLDPS-NPIFNTAEYIDIKGPIDPVHFEAAIRKT
                             :   *  .                  : :   ::   .  ::.

                                                 "CDA-C1 specific loop"
                                                  |---------------|
CDA_Scoe        VAGTETLCSRFLTDEEGRPYRAYCPPAPEGSAAVEDPDGVPYTPVLLRHIDLSGHE--DP
CDA_Sliv        VAGTETLCSRFLTDEEGRPYRAYCPPAPEGSAAVEDPDGVPYTPVLLRHIDLSGHE--DP
Plu3535_Plum    IQEHAVLRCSI-VDKYSMPHHIDSDA---LKDTVEFAHIVQDHHFELSHLDLSGEE--EA
SrfAC_Bsub      MDRYDVFRTVFIHEKVKRPVQVVLK----------------KRQFHIEEIDLTHLTGSEQ
VibH_Vcho       VSEIDLFRARF-SAQGELYWHPFSP------------------PIDYQ--DLSIHL--EA
TycC_Bpar       IARHESLRTSF-AVVNGEPVQNIHE------------------DVPFALAY-S-----EV
Dhbf_Bsub       IKEAESLHVRF-GENMDGPWQMINP----------------SPDVQLHVIDVSSEP--DP
EntF_Shyg       VAEAEPYNVRV-GEDDGVPWQVLDP----------------VTDWDFPVLDLSGEP--DP
Gram_Bpum       VLEADSLYMRF-VEDTDGPKQWLIS----------------KKEIPFQSINLQNEK--QP
                :         .         :                                     :

CDA_Scoe        EGEAQRWMDRDRATPLPLDRPGLSSHALFTLGGGRHLYYLGVHHIVIDGTSMALFYERLA
CDA_Sliv        EGEAQRWMDRDRATPLPLDRPGLSSHALFTLGGGRHLYYLGVHHIVIDGTSMALFYERLG
Plu3535_Plum    ESKALAIVQRIFSEPFRLAQDVLYRVGLIQLATNRFWLYFISHHIIIDGVGYANWFRRIF
SrfAC_Bsub      TAKINEYKEQDKIRGFDLTRDIPMRAAIFKKAEESFEWVWSYHHIILDGWCFGIVVQDLF
VibH_Vcho       EPLAWRQIEQDLQRSSTLIDAPITSHQVYRLSHSEHLIYTRAHHIVLDGYGMMLFEQRLS
TycC_Bpar       TEQEARELVSSLVQPFDLEVAPLIRVSLLKIGEDRYVLFTDMHHSISDGVSSGILLAEWV
Dhbf_Bsub       EKTALNWMKADLAKPVDLGYAPLFNEALFIAGPDRFFWYQRIHHIAIDGFGFSLIAQRVA
EntF_Shyg       HAAAVRWMKHDLATGLELDARPLFSFALLKLSDDCFLWYQGTHHIVSDAGSAALLGRRTA
Gram_Bpum       LDAAKAWMKTDLATPVSLEKDVLFREVLFQLADDRFIWYQRIHHIAIDGFAFSLIARRVA
                                  *          :   .   .     **   *.

CDA_Scoe        E-VYRALRDGRAV-PAAAFGDTDRMVAGEEAYRASARYERDRAYWTGLFTDRPEPVSLTG
CDA_Sliv        RGVPRAAGTGVPC-PRPPFGDTDRMVAGEEAYRASARYERDRAYWTGLFADRPEPVSLTG
Plu3535_Plum    DAYQQLSLGNAPK--ENTGVRFLDLAAQPLPENYSQQFAKAAKYWKELLHHLPDVPFQCR
SrfAC_Bsub      KVYNALREQ-KPY-SLPPVKPYKDYIKWLEKQDKQ----ASLRYWREYLEGFEGQTTFAE
VibH_Vcho       QHYQSLLSGQTP---TAAFKPYQSYLEEEAAYLTSHRYWQDKQFWQGYLREAPDLTLTSA
TycC_Bpar       QLYQGD-----VL-PELR-IQYKDFAVWQQEFSQSAAFHKQEAYWLQTFADDIPVLNLPT
Dhbf_Bsub       STYTAL-IKGQTA-KSRSFGSLQAILEEDTDYRGSEQYEKDRQFWLDRFADAPEVVSLAD
EntF_Shyg       EIYTALTESGDPVAGETVFGSLRTMLDRDEEYRSSEDFAKDRAYWTEHFADSPEPARLSG
Gram_Bpum       EVYSAL-SKGTPV-PPQTFGSLHDVVQEEITYQQSNRYEDDRVFWKNRFADQPEIVSLAE
                                                  .        :*   :

CDA_Scoe        RGGGRAL---APTVRSLGLPPERTEVLGRAAEATGAHWARVVIAGVAAFLHRTTGARDVV
CDA_Sliv        RGGGRAL---APTVRNLGLPPERTEVLGRAAEATGAHWARVVIAGVAAFLHRTTGARDVV
Plu3535_Plum    KEGPGTADSRKNSRLVHFIKPDRYKSFLTKASQCNLPISPLFITAIASLVNRINQSDGVL
SrfAC_Bsub      QRK-KQKDGYEPKELLFSLSEAETKAFTELAKSQHTTLSTALQAVWSVLISRYQQSGDLA
VibH_Vcho       TYDPQLS---HAVSLSYTLNSQLNHLLLKLANANQIGWPDALVALCALYLESAE-PDAPW
TycC_Bpar       DFTRPSTQSFAGDQCTIGAGKALTEGLHQLAQATGTTLYMVLLAAYNVLLAKYAGQEDII
Dhbf_Bsub       RAPRTSN---SFLRHTAYLPPSDVNALKEAARYFSGSWHEVMIAVSAVYVHRMTGSEDVV
EntF_Shyg       RPGDELS---SVLRETAYLTEAEAVELRAAARKYATHWSAMIIAATATYLHRLTGKSDII
Gram_Bpum       LAPRTSD---HFIRKTASFDAEKVSKMKKNAQFFGGTWHEMILAASALYMHRMIGAHDIV
                                          :   *          . :     :

CDA_Scoe        VSVPVTGRYGA--NARITPGMVSNRLPLRLAVRPGESFARVVETVSEAMSGLLAHSRFRG
CDA_Sliv        VSVPVTGRYGA--NARITPGMVSNRLPLRLAVRPGESFARVVETVSEAMSGLLAHSRFRG
Plu3535_Plum    IGTPLHNRTTS--AQRNMVGSFISMLPVMCVQNEQMSVAESVAMTARTIKSGYRYRSYPS
SrfAC_Bsub      FGTVVSGRPAEIKGVEHMVGLFINVVPRRVKLSEGITFNGLLKRLQEQSLQSEPHQYVPL
VibH_Vcho       LWLPFMNRWGS--VAANVPGLMVNSLPLLRLSAQQTSLGNYLKQSGQAIRSLYLHGRYRI
TycC_Bpar       VGTPITGRSHA--DLEPIVGMFVNTLAMRNKPQREKTFSEFLQEVKQNALDAYGHQDYPF
Dhbf_Bsub       LGLPMMGRIGS--ASLNVPAMVMNLLPLRLTVSSSMSFSELIQQISREIRSIRRHHKYRH
EntF_Shyg       LTLPVTARTDA--TLRGIPGMFANVVPLRIQVRSDMRIRDLVRQVSREVRQALRHQRYRH
Gram_Bpum       LGLPVMMRLGS--CALQTPGMVMNLVPLRLTCKPEMTLSALVRQVSDELKAIRPHQRYRH
                .   .  *           . . . :            .   :            :

CDA_Scoe        EDLDRE----LG-GAGVSGPTVNVMPYIRPVDFGGPVG---LMRSIS-----------SG
CDA_Sliv        EDLDRE----LG-GAGVSGPTVNVMPYIRPVDFGGPVG---LMRSIS-----------SG
Plu3535_Plum    SALYKDLSLRAQGRERLFDIVFNYQQIDFDFSASGLDT---ETHYLSH----------GR
SrfAC_Bsub      YDIQSQADQP-----KLIDHIIV--FENYPLQDAKNEESSENGFDMV--DVH------VF
VibH_Vcho       EQIEQDQGLNAE-QSYFMSPFINILPFESPHFADCQTE----LKVLA-----------SG
TycC_Bpar       EELVEKLAIARD-LSR--N-----PLFDTVFTFQNSTE---EVMTLPECTLAPFMTDETG
Dhbf_Bsub       EELRRDLKLIGE-NHRLFGPQINLMPFDYGLDFAGVRG---TTHNLS-----------AG
EntF_Shyg       IDLARDLHLPDG-GNGFLGPHVNIMTYDYDFDFAGHRV---IGHNLS-----------NG
Gram_Bpum       EDMRRDFKLIGR-NQRLFGPQINIMPFDYDLMFDQSIG---QAHNLS-----------AG
                  :  .                                        :

CDA_Scoe        PTTDLNIVLT-GTPESGLRVDFEGNPQVYGGQDLTVLQERFVRFLAELAA--DPAATVDE
CDA_Sliv        PTTDLNIVLT-GTPESGLRVDFEGNPQVYGGQDLTVLQERFVRFLAELAA--DPAATVDE
Plu3535_Plum    EDIPLTVILCDYGDKQSTQLQLDYRHDYFSSHQAEHLLQSIMTLVEQMVA--QPEALLTS
SrfAC_Bsub      EKSNYDLNLM-ASPGDEMLIKLAYNENVFDEAFILRLKSQLLTAIQQLIQ--NPDQPVST
VibH_Vcho       SAEGINFTFR-GSPQHELCLDITADLASYPQSHWQSHCERFPRFFEQLLAR--FQQVEQD
TycC_Bpar       QHAKFDLTFSATEEREEMTIGVEYSTSLFTRETMERFSRHFLTIAASIVQ--NPHIRLGE
Dhbf_Bsub       PVDDLSINVYDRTDGSGLRIDVDANPEVYSESDIKLHQQRILQLLQTAS-A-GEDMLIGQ
EntF_Shyg       TVEDLSIMGYDRSDGSGIRIDLNANSNLYTADSLIAHRERYLELLRTLSDTSDKERTVGA
Gram_Bpum       PVDDISINIYDRADGKGFQIDFDANPAVYKEQTVDAHQQRFLQLLEEITGL-EQDQTISQ
                       .            : .      :

CDA_Scoe        VALLT
CDA_Sliv        VALLTPD
Plu3535_Plum    LDLVGKD
SrfAC_Bsub      INLVDDR-------EREFLLTGLNPPAQAH
VibH_Vcho       VARLLAEPAALAATTSTRAIAS
TycC_Bpar       IDML
Dhbf_Bsub       MELLLPE-------EKEKVISKWNETAKSE
EntF_Shyg       IELLSAE-------ERRRAAEEWNDTAHPT
Gram_Bpum       FNLLLSE-------EKENILKHWNDTKREL
```