

## Supplementary dataset

### Structural characterization of a soil viral auxiliary metabolic gene product – a functional chitosanase

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>OutGroup\_PhageLysozyme\_YP\_006987285.139-307  
TSLSVQEAIVQQ---EPQ---ITIQKQPPVLIQPEEATVNRKQYKVLSSG---DSLWTIANRI---KP-----HNVEDEYVVKLVV---NSDVEMH-----PGTME---EIPSADLKEVTLPDVLIHFD  
ITDETVNHHK---AEGTSEQAQLKRRLLGKVKGPSFK---N-GKPYPRDSTGHFTTGYGHYLGKSEKDAAYRNGSKRQAHDLLTDMQRMTMDNVLIIQRKRAVDLTVQDQRILYEMAFILGVDKLSRFNKMWSVENNQHFKTEIANSIWKYQMGNRVAVMLV  
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TGHVDADG-S---G---GN---PW-G-DPD---FQPRISLKR---PDG---NWLNANEERYIAYPPGVV---S---GV---RPI-----VLGQAWVLYR---  
GHCY---SA-----VVADV-----GP---AG---KLGELSACA  
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DAIMDIDG-S---PDW---QRDP-YGQADTTLH-H---N-G-KP-I-----DSESVFFVLPPEVI---K---AF---KGV---ILGCHGTHYE---GKSI---  
---DA-----VCADV-----GP---HS---KLGESPEAA  
>exp\_virus\_3300005937---Ga0081455\_10000703\_2940-129  
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GESH---DA-----VCGEI-----GP---PN---KTGEASYCLA  
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QQAS---PA-----VTGEI-----GP---DD---KTGEAAAYCLC  
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KVS---AA-----VTGEI-----GP---DD---KTGEAAVCLA  
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KLAVDIGD-D---PR---CYNP---NGRP---PG---LDFLANA---GH---PGNWWGLAC-D---GE-G-IP---FQIEASD---PAPGFVSTTSLD---HSL-A-ASN---PR---RYVNSGQIPFVLPSPK---K---FS---PAQ---  
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DKME---FG---VFGDE-----N-T-DP---YGGQTSFT---QSD---GR---P-LNAELLPWVYVPE---TPNPFYD-AT---RNI---YGEGAVVLY---N-  
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GKME---YG---VFGDE-----T-T-DP---AYGQTSFT---QSN---GE---P-LNAELLPWVYVPE---TPNPFYD-AT---RDI---HGEGAVVLY---N-  
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GQMY---YG---ILGDS-----N-Q-D---GQDQTNW  
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KKMY---YG---ILGDS-----N-Q-D---GQDQTNW  
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NMDIDCDQ-IQ SKG DG-DC AS S-G-D TQSQTRWG S-IVK-GYN KGI DDVDAIYHSHVYVFGNDG SK SGYVTFDP-RK YGV  
DPLSVAVVC-G-DKMF YG VWADT NG DDGP-P LVGEASISLIG  
ref\_fungi\_KX95726.1.Roonan2101-112  
MDIDCDQ-ATR S YDG DN-RC DG S-T-D TQSQTSFK D-ELKAKH GI DDLNAYHSHVYVFGNT GSR PGYVNFDP-RD HGI  
SPLSVMAVVC-G-DKLF YG VWGDE NG DDGERA VIGEASIALA  
ref\_fungi\_OA959425.1.Roonan25180-191  
DMVDCDQ-ATV-P IDG DT-RC NA S-Q-D TPIETFK D-NVK-QF GI DDLNAYHSHVYVFGNT GSK EGVFNPNQ-E FGM  
EPLSVMAVVC-G-DQMF YG VWGDT NG DDQPPA AIGEASLSLA  
DMVDCDQ-ALG PGS DC-N S G-G-D TQSQTSFK N-IVS-TY GI SDDLASHSHVYVFGNDNS GNL PGFOTFRP-QD HGI  
EPLSVMAVVC-N-GKLI FG VWGDE NG NDGQHS VIGEASLIG  
ref\_fungi\_KIW55987.1.Roonan24975-184  
NMDIDCDQ-AKN PL PV-R A G-S-D TQLWTSFR D-SVR-SY GI SDDLASHSHVYVFLGNADD DHT PGYVTFNP-QD YGV  
QPLSVMAVVC-N-NKLF YG IWGDE NG SDGP-P LVGEASIALA  
ref\_fungi\_KAG9252431.1.Roonan25482-194  
NMDIDCDQ-IAN-G AGD DG-RC GN S-E-D TQYQATFQ Y-TVS-SYS NGV SDLNAYHSHVYVFGNYG SA DGYVTFDP-EQ YGV  
KPLSIGAVVC-G-DKLV YG VWGDT NG DDGN-P LVGEASIALA  
ref\_fungi\_KFH4216.1.Roonan25380-191  
NMDIDCDQ-LAD-G PGS DG-RC DS S-D-D TQYQATFQ H-IVS-SYS NGV EDLNSYHSHVYVFGNYG GG D-YINFHP-ED HNI  
HPLSVMAVVC-G-DQLV YG VWGDS NG DDGP-P LIGEASLSLA  
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NMDIDCDQ-IQPNR PGD DG-RC AS S-T-D TQATTSFQ D-VVQ-TYG I EDLNAFVSHVYVFLGNVND AGGK PPKYVTFHP-EE HGV  
EPLSVAVVC-N-NKLI YG VWGDA NG DDGP-P LVGEASIALA  
ref\_fungi\_OAF55565.1.Roonan39681-195  
DMIDCDGHIKS PYS DG-RC EA S-Q-D TQPSYSY E-QIA-RYN VGI KDVSYHSHVYVFLGNAD QGK PGYVTFHP-TD YGI  
EPLSVAVVC-N-NKLF YG VWADQ NG DDGP-P MVGEASIALA  
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NMDIDCDQ-AQ THG DG-RC GS S-T-D TQSQTSFK S-EIQ-GYK AGI KDLNAYHSHVYVFGNDG SK PGWPTDFP-KK HGI  
EPLSVMAVVC-N-NKVI YG VWGDT NG DDGNQA MVGEASIALA  
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NMDIDCDQ-AQ SSG DG-RC AS S-T-D TQSQTSFK S-RLS-SWG YG DLSNYHSHVYVFGNEG SK PNWPTDFP-KE HGI  
EPLSVMAVVC-N-NKLF YG IWGDT NG DDGQDP MVGEASIALA  
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EPLSVAVVC-G-DKLV YG VWGDT NG DDGK-P LVGEASLATG  
ref\_fungi\_EAW89861.1.Roonan30384-191  
NMDIDCDQ-EQ SGG DG-RC KS S-T-D TQGGITFS T-NLH-KF EI GDNLNANHPPYVFLGNAG NY SP-TFDP-RS VGV QPLSVAVVC  
-R-DQLV YG IWGDT NG DDGEPH MVGEASIALA  
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NMDIDCDQ-EQ SGG DG-RC KS S-T-D TQGGTRWG LR-HPE-KY GV GDNLNANHPPYVFLGNAG NY SP-TFDP-RT AGV  
EPLGIVAVVC-G-DELV YG IWGDT NG DDNEHP MVGEASIALA  
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NMDIDCDQ-EQ SRG DG-RC KS S-T-D TQGGTRWG LK-HLE-KH GV RDLNANHPPYVFLGNAG NY SP-TFDP-RT VGV  
EPLSVAVVC-A-DELV YG VWGDT NG DDNEHP MVGEASIALA  
ref\_fungi\_EEA26294.1.Roonan107083-189  
DMIDCDQ-NQH GV DS-RC HL S-G-D TQPTAFK D-QLP-KYG I SDRADHPPYVFLGNAG NY S-PTFHP-ED HNI KPLSVAVVC  
-N-NKLI YG IWGDT NG DDGP-P LIGESSLAVG  
ref\_fungi\_EED22169.1.Roonan459293-399  
DMIDCDQ-SQK GI DH-RC KS S-D-D TQDEAFK D-QVS-KYG I SDRADHPPYVFLGNAG NY S-PTFDP-EQ HGI KPLSVAVVC  
-N-NKLI YG IWGDT NG DDGP-P LIGESSLAVG  
ref\_fungi\_OJ80140.1.Roonan24379-184  
NTDIDCDQ-DQO NA DP-RC LG S-S-D TQPATFR R-QVQ-R LSNL TDLNASHPPYVFLGNAG NY VTFDP-RD HGI EPLSVAVVC  
G-QLI YG IWGDT NG NDGM-A LVGEASIALA  
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NMDVDCDQ-IQN-ST GSG DG-RC TG L-P-D TQQAATFR S-ILQ-A GYGI PDLNAYHSHVYVFLGNAG NY PYWRTFDP-RT ADI  
YPLSVAVVC-G-NKLV YG VWGDT NG DDGP-P LVGEASIALA  
ref\_fungi\_PLN86131.1.Roonan32087-194  
NMDIDCDQ-QEK DSN D-RC GG D-D-D TQYETRYK D-EVK-K MGI PDLTYHSHVYVFLGNAG NY DGKATFLP-EK ANI  
EPLSVAVVC-N-DRLV YG VWGDT NG DDGP-P LIGEASIALA  
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NMDVDCDQ-VQG-G SQD DG-RCS LGR S-P-D YQDATAFR D-LIQ-SFK VGI SDLNAYHSHVYVFGNSG SK PGWRTFDP-TD YGV  
RPLSVMAVVC-G-NKLV YG IWGDT NG DDGDKP MVGEASIALA  
ref\_fungi\_KAF4471231.1.Roonan51479-192  
NMDVDCDQ-AQG-G POD DG-RC GE S-T-T TPTTAIK S-IIE-GYN VGI SDLNPHSHVYVFGNSG TK AGWKTDFP-RE YGV  
QKASIMAVVC-G-DRVF YG IWSDS NG DHGDRP SVGEASIALA  
ref\_fungi\_AE09828.1.Roonan30683-210  
NMDVDCDQ-ANG-GGGGGA AVAAD DG-RCRP STA N-S-D TQGITAFR D-AVA-GYNR NI TDLNAYHSHVYVFGNAG NY GTR-RR-RGWRAFDP-TA YGV  
-RPLSVAVVC-G-YRLV FG VWGDT NG DDGPKP MVGEASIALA  
ref\_fungi\_AE059530.1.Roonan497272-403  
NLDVDCDQ-SSE-G PSD DG-RCR REL S-P-D LQNTSFR D-VLA-SYGRA GV AELNPPYHSHVYVFGNAG NY ATKTITASTGRGAKSGAWRAFDP-SE YGM  
-RPLSVAVVCPT-S-RKLV YG VWGDM NG DDGARP MVGEASIALA  
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NLDVDCDQ-TVG-G PSD DG-RCR REL S-P-D LOGATFR D-TLA-GYGHG NAT ADLNAYHSHVYVFGNAG NY GTR-GR-AGWRAFDP-SA HGM  
RPLSVAVVC-D-RRLV YG VWGDT NG DDGPKP MVGEASIALA  
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NMDVDCDQ-VQG-G ASD DG-RCS VGV S-A-D YQSTAFQ D-MVA-AYN VGV RDLNAYHSHVYVFGNEVKNDNDN DK DLRWVFDP-RA YLV  
-RPLSVMAVVC-DG-SKLV YG VWGDT NG DDGDKS MVGEASIALA

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DMVDVDCG-AQR-A---GSD---DG-RC---NS---S-T-D---TQETAFR---S-TVA-GYG---RGL---ADLDPFVHPVYVFNEG---SK---PGWKTFFD-RA---YGV---  
EPLSVMAVC---G-DQLL---YA---IWGDT---NG---DDGAKP---MVGESIALA  
ref\_fungi\_PHH68142.1Ruonan283/80-192  
NMIDICDG-DASTP---FTN---DT-RC---RS---S-L-D---TQQTFR---D-QLL-PYG---I---PDLNANIHTYVVFNGTA---SK---PGWPTFFD-AS---HGL---  
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ref\_fungi\_KA8908972.1Ruonan266/96-203  
NMVDVDCG-GIS---GKN---DK-RC---AS---S-K-D---TQIDTAFQ---D-QVS-RH---GL---NDLPTIHPYVVFNGTN---DKL---EFDPTK---HGL---  
KPLSVMAVC---N-NKLI---YG---VWGDY---NG---EED-EP---KVGEASILA  
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NMIDICDG-DRS-K---N-D---DG-RC---DD---A-H-S---VQSATAMR---D-YVS-AYK---NGV---PDLNPFVHDYVVFNGSG---DK---DGWITFFD-RD---HGM---  
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NMIDICDG-DRT-G---FLD---DT-RC---GS---H-P-T---TQSMTAMK---R-YVS-SYS---NGV---PDLNPFVHDYVVFNGTG---ST---PGWVTFD-RR---YGM---  
EPLSLMAIVC---N-DKLI---YG---VWGDY---NG---DDGDS---RIGESSISA  
ref\_fungi\_GAM83196.1Ruonan319/78-188  
NMIDICDG-DQK---GNG---PG-TAC---AS---S-S-D---TQSETAFK---D-TVS-QYG---I---RDLNANIHPYVVFNGQG---SK---AGYKNFDP-QA---HGV---  
RPLSVMAVC---N-NKVV---YG---IWGDT---NG---DDGP-P---LVGEAALSVG  
ref\_bact\_APR80523.1Ruonan244/95-190  
DMVDVDCG---KS---T-AEC---NP---S-T-DP---AYQSETSAT---DSN---GA---P-LDAAKLPVYVVP---LPSKFDY-GA---GGL---ALGSVIAVIY---K---  
KGLA---YG---VFGDE---GP---KD---IIGESYAMA  
ref\_bact\_APR82716.1Ruonan283/134-229  
DMVDVDCG---KM---S-AQC---NI---D-V-DP---AYQDQTSAT---DSN---GD---P-LDAATLPVYVVP---LPSNKLDY-QA---VGL---DLGSVIAVIY---  
K-GKLA---YG---VFGDE---GP---KD---IIGESYAMA  
ref\_bact\_TRU57399.1Ruonan369/221-313  
DMIDICDG---GS---T-DTC---K-A-DR---TYQETSC---QSS---GK---P-LDASYLPYVLP---KDSNGLAL-NN---LGL---RCGSIAAVIY---N---  
KGVY---YG---VLGDR---GP---AG---VIGESYAMA  
ref\_bact\_APR86004.1Ruonan419/272-365  
DLVDVDCG---GK---G-AAK---K---A-DP---YYQETAAT---DSK---GN---P-LDASTLPVYVVP---MASNGFDY-KQ---AGL---KLGSVVAVIY---G---  
GKIS---YG---ILGDV---GP---AG---VIGESYAMA  
ref\_bact\_TKC9219.1Ruonan231/84-177  
DMIDICDG---GR---G-AAK---K---A-DP---YYQETAAT---DAR---GK---P-LDASTLPVYVVP---KPSHGFDK-KA---QGL---KMGSVVAVIY---  
K-GNVE---YG---ILGDV---GP---AG---IIGESYAMA  
ref\_bact\_SDN22910.1Ruonan373/89-184  
DMIDICDG---VT---T-SHC---NS---S-T-DP---WYQDQTSFQ---TST---GN---W-FTSDVTRYFVIP---LPSRSFY-QN---AGI---TPGSVAAVY---N---  
KQVA---YA---VFADE---GP---ST---IIGESYALA  
ref\_bact\_WP\_168115188.1Ruonan225/78-173  
DMIDICDG---YS---T-SNC---NS---R-T-DP---WYQQTAYR---TSK---GG---Y-FQSDATHFVIP---ASSRSFY-SS---AGI---RPGTVAVIY---R---  
GAVV---YA---VADV---GP---SN---VIGESYATA  
ref\_bact\_TML25165.1Ruonan230/79-174  
DMVDVDCG---VK---T-SHC---NS---H-T-DC---CYQDQTSFH---TSK---GK---P-FQADLTHFVIP---LPSRSFY-TK---AGI---KPGSIAALVY---N---  
NKVL---YA---VFADE---GP---SN---IIGESYATN  
ref\_bact\_WP\_030441780.1Ruonan219/73-168  
DMIDICDG---VR---T-SNC---NE---N-T-DP---WYQQTSEF---TSA---GK---S-FQADKTHFVIP---LPSRSFY-SS---NGI---KPGSVAIY---H---  
NKVV---YA---VFADE---GP---SN---IIGESYATA  
ref\_bact\_WP\_168079847.1Ruonan218/73-168  
GMSIDCG---YA---T-PRC---NA---G-T-DP---AYQALTYR---GAD---GR---Y-LTADAEARYFVIP---LPSRFDY-RS---AGI---APGNVGAIVY---D---  
KGVY---YG---IFADV---GP---ET---AIGESYATA  
ref\_bact\_WP\_203916775.1Ruonan563/106-201  
DMAIDCG---EV---T-DEC---NP---D-T-DS---TFSEGNFK---TST---GK---Y-FTADVTHFVIP---LPSRFDY-QN---AGI---KPGNVGAVIY---N---  
CKLY---YA---VFDL---GP---SD---SIGESYATA  
ref\_bact\_OLY91822.1Ruonan455/239-383  
HAKICADG-A---PD---AYKI---GN---KG---TDDLRNA---GKPPSPNASTKLNDRWSWVALV---DEH---N-NP---VIQTSQD---SNPGYVSTTAHVN---POF-K-KTD---PR---AYVNAEPIYVLPKK---N---  
-AGSA---KLGDFAYVDRK---T-GTIC---IYSEV---GP---KD---ALGEISIAA  
ref\_bact\_CCT2542.1Ruonan319/23-258  
KMSIDADG-A---PN---AYHP---DN---IG---LDDLKNA---GY---PNTSWWKNLVPD---PONP-N-RA---YEQPSG---PYQGVFVSMTALQD---GTK-A-KTD---PS---RYVDSTRIPYVLPGG---G---  
SAGA---KLGDFAVFNGK---N-KGVY---NG---IYADV---GP---SN---KIGESIALA  
ref\_bact\_TCT02366.1Ruonan230/29-167  
VYSLDADG-T---PR---AYHP---DN---TG---LDDLANA---GY---PHKG-WRGLVTD---PADP-A-RP---LVREGG---PYAGFYFSKTSLHD---PDR-E-ETD---PL---KYVDETIPIYVLPGA---FY---AQ---  
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ref\_bact\_VXC90397.1Ruonan226/30-168  
HVTLADG-S---PR---AYHP---OD---IG---IDANANA---GY---PHRG-WRGLVVD---PADS-D-RP---YVQPTG---DYAGYFVSMTSLRN---NSG-A-ATA---PS---TYVNAETIPIYVFPGA---FY---GV---  
KGTG---RYDLAMVRSIA---N-GRVT---AA---IVADV---GP---FKA---PLGEMSIALL  
ref\_bact\_PHS66042.1Ruonan268/51-201  
EVRVDADG-A---PN---AYHP---DDVGLNCTQEGFGK---LDCPANG---GY---PKHSWRSVAIVAG---PDNP-A-QA---YVQPEG---TFKGLVSRSLQD---EQK-A-VTD---PQ---RYVDSRSPYVLPFGD---FY---  
KK---KGTG---ALGDFGALNLS---N-GQSS---PF---IIADI---GP---ARA---MLGEMSIALL  
ref\_bact\_AE195071.1Ruonan269/51-201  
HAKVDADG-A---PN---AYHP---DDVGLNCTQEGFGK---LDCPANG---GY---PSQDWRSVAIVPD---PHNK-N-VG---YVQPEG---EFKGFVSQTSKLD---AQK-S-DLD---PT---KYVNAATPYVLPFGD---FN---  
RL---SGTG---TLGDAGYAFNLD---N-GKVS---PF---IVAEI---GP---SDA---TLGEMSIALL  
ref\_bact\_AUT48628.1Ruonan269/51-201  
HAQVDADG-A---PN---AYHP---DDVGLNCTQEGFGK---LDCPANG---GY---PNGDWWPSVAIVPD---PKNK-K-KG---YVQPEG---EFKGFVSQTSKLD---GAR-S-DLD---PA---KYVNAATPYVLPFGA---FH---  
QK---AGTG---TLGLDGYAVNLD---N-GKTS---AF---IVAEV---GP---SDA---KLGEMSIALL  
ref\_bact\_PXM0977.1Ruonan270/57-206  
KFLSDVDG-A---PN---AYHP---QDKGNCKSDTFLG---LDLQNA---GY---KNGN-WKSHIPA---PINS-D-EG---YVQPSG---EYKGFVSQTSKLD---HSK-I-NTD---IN---KYVNSKIPYVLPST---LY---SM---  
KGTG---MLGDVGYAVNVT---N-GLES---PF---IIAET---GP---KKS---NLGEISFLA  
ref\_bact\_WP\_145339878.1Ruonan269/56-205  
SFLSDVDG-A---PN---AYHP---QDKGNCKRTKNFNG---VDLQNA---GY---KGGDWKSLVPD---PKKP-D-EG---YVQPEG---IYEGFVSQTSKLD---NKK-R-DTD---IS---KYVNPPIYVVAIGE---FY---KR---  
KGTG---KLGDFGYANIK---T-GKSS---PF---IIADI---GP---KNA---SLGEMSLRLA  
ref\_bact\_WP\_027993824.1Ruonan270/54-202  
RTAIDADG-A---PK---AYHP---DDVGLNCTQEGFGK---LDCPANA---GY---PNKSWPTVLASD---PTNP-S-KA---FVQPSG---PAKGFVSQTSKLD---SANGN-ERD---TA---RYVDASTIPIYVLPFRP---FF---QL---  
---VGTG---KPDGLMAFHLE---T-QRQT---AF---IVADI---GP---DE---PLGESSIALF  
ref\_bact\_QBM74628.1Ruonan283/84-202  
HKLVDADG-A---PN---AYHP---ADVPNTPEGTG---RG---IDCLAA---GY---PDGWSQWTLVAD---PADP-T-RP---AIQDQG---PYKGFVSMTSLRN---TAFAG-PAS---TA---SYVDAAIPIYVLPAP---IY---RT---  
---DGMG---EMGDIGFATNLD---T-GQTT---PF---VIADY---GP---VE---RLGEASVAFW  
ref\_bact\_PTI05158.1Ruonan232/31-171  
HAAYDADG-A---PN---AYHP---DD---IG---LDLALANA---GY---PHTNWRDVLVVD---PDHP-A-RA---YVQPSG---EYEGYFVAMTSLRA---PSG-A-RTD---PA---TYVDATRPYVLPVPTG---FE---RL---  
PHVA---RAGDVGFAVHP---T-GVTS---TF---IVGDA---GGG---SAA---RLGESSIALF  
ref\_bact\_KQN25083.1Ruonan266/52-201  
HSRVVDADG-A---PD---AYHP---DD---RMRSPYPLG---LDNPQNA---GW---PQTGWPDVLTRD---PANP-K-VP---YRQSG---PYRGYFVSHTALRV---RGG-S-ETD---PA---TFDASRTIPIYVLPDSD---FP---RR---  
---RTG---AFCDVGYAVNLA---T-GKGT---AF---VIGDT---GGG---AGA---RLGEASIAFF  
ref\_bact\_WP\_168605515.1Ruonan269/53-205  
HSRIDADG-A---PN---AYHP---AD---LQRKAPYLG---LDNPANA---GWG---LNASHWPDVVLVD---PEHP-S-RP---YVQPSG---PFAGYFVSQTSKLD---RGG-V-PTD---PK---TYDNTIPIYVLPDPSA---FP---  
KL---KGTG---AGDVGIVNLA---N-GKST---PF---VIGDT---VGG---ADA---NLGESSIALF  
ref\_bact\_EX136305.1Ruonan297/92-231  
HKAVDADG-A---PN---AYHP---KN---KG---LDYLANA---GY---PKNSWRSVLED---PKNP-G-RA---YVQPEG---PEGYSFVSQTSKLD---SSK-E-ETD---SS---RYVDATSIPIYVLPES---FY---LR---  
KGTG---RLGDLGVFNVA---T-GDAS---PF---VIADI---GP---RKA---KLGESIALA  
ref\_bact\_GAC14840.1Ruonan259/52-191  
HKAIDADG-A---PN---AYHP---EN---IG---LDNYLANA---GY---PDSDWPSVLED---PNHP-N-KP---YVQPEG---EFKGFVSQTSKLD---KQK-S-KLD---PS---RYVDATHFPIYVLPYK---FY---SK---  
KGTG---RLGDFGAINLE---T-NDQ---SF---VVADY---GP---SNA---SLGEMSMALA  
ref\_bact\_PME88446.1Ruonan249/47-185  
YKAIADG-A---PN---AYHP---DN---IG---LDHLANA---GY---PNKG-WKNVLVVD---PKQP-Q-KP---FVQTTG---DFKGYFLSKTILED---KSK-P-PTD---SK---RYVNSVEIPIYVFPGN---FY---SL---  
KGTG---KLGDFGYAYNAK---T-KKSS---AF---VFADI---GP---KSA---PLGEMSIALL  
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KGTG---RLGDFGAKNMT---T-GVTS---SE---IIADV---GP---PNH---PLAEVSIALA  
ref\_bact\_ASQ90483.1Ruonan282/63-202  
HMTDADG-A---PD---AYHP---DN---TG---LDHLKHA---GY---PGTSWKNVLVTD---PKDP-E-KP---YVVPDQ---PYQGYLSMTSLRD---MTR-K-PTD---PS---RYVDASRPYVLPFST---FS---RL---  
KGTG---ALGDLGYAVNLD---T-GVYS---PF---IIADI---GP---EKH---PLGESSIOLA  
ref\_bact\_ABB23846.1Ruonan286/63-202  
FMTDADG-A---PN---AYHP---NN---SG---LDDLANA---GY---PRHSWNTVLVVD---PADG-S-RP---YIMKSG---PYAGYISMTLKD---LRY-A-ETD---SR---RYVDASRPYVVPET---FA---AM---  
DGVG---QKGDYGYAVNLD---N-GSSG---GF---VVADI---GP---RRH---PLGESSIALA  
ref\_bact\_TCD48936.1Ruonan285/62-201  
FMTDADG-A---PE---AYHP---KN---TG---LDDLANA---GY---PRTSWNTVLVVD---PADN-S-RP---YILKSG---PHAGYVVSMTALKD---LRW-A-DTD---SR---RYVDASRPYVVPET---FA---AL---  
EGVG---QIGDYGAVNLA---S-GCSS---GF---VVADI---GP---RRH---PLGESSIALA  
ref\_bact\_KA6232620.1Ruonan275/70-209  
FMTDADG-A---PT---AYHP---GD---EG---LDMLKHS---GY---PKMWKWTVLVVD---PADR-Q-RP---FVMPG---PYAGYVVSMTALKN---MKK-A-KTD---PL---RYVDASKVPIYVFPVT---FA---RK---  
RDVG---ALGDFGAVNLD---N-GMKS---PF---VVADI---GP---ERH---KLGESIALA  
ref\_bact\_PWB83328.1Ruonan269/56-198  
KMSIDADG-A---PD---AYHP---NSPKSG---WG---RDYLANA---GF---GRNCNVIC---KTE-K-HPEKGYKTEEG---PYAGYVVSASSLKD---SSV-EDRGD---YR---RYVDARVPIYVPAIGSA---A---KK---  
-MGA---QIGDYGAVNLD---N-GERS---PA---IFADI---GT---EG---TLGESSIALA  
ref\_bact\_RYY9046.1Ruonan444/43-569  
KAIADG-S---AR---AYHP---DAGNP---DA---LDDIGNAN---SY---SKYIQQQR-NN---HV-G-K---QPRDGYVSATSLQR---GD-DWD---AD---AYVDAPYVLPDPA---P---GY---R---  
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ref\_bact\_RAZ89077.1Ruonan242/48-172  
KLAIDAG-S---PT---AYHP---GD---IG---SYDILANVS---KNDLH---GI---QEGD-G-AV---GPAFGYVVSATSLSN---PAY-K-PSD---TR---HWVDAATPYVLPVTRQEPQ---FNV---  
PLCGVATVVDLQ-S-RKRT---GA---ILADT---GR---AVGESSIALA  
ref\_bact\_WP\_089837271.1Ruonan229/37-175  
FLHVDVDCG-A---PN---AYGP---PG-KKALDFEKNH---EGAKLSGVVGY---G---LTKHS-R-KP---VLQPNP---PYPGYISTGTIFYD---RSV-DDET---PR---RYVNAKINYVLPDGFRR---  
PHV---KLGDFVAVYSR---T-KKSV---YA---IVDE---G---NP---SGCEGSLALV  
ref\_bact\_QD08867.1Ruonan252/55-192  
RMSVDVDCG-A---PN---AYGP---KN-KKTLDYELNAH---VGAKKSAGVAY---G---LVDMDG-N-P---IIQKSD---PAPGYISQTYVD---VKN-NNKFD---PR---RYVNAATEINTLADSACK---  
KGV---KTGDFCVHSVN---N-NKTV---FA---IVGDT---G---NS---NKEGESSIALL  
ref\_bact\_AE138989.1Ruonan246/39-178  
RMDVDVDCG-A---PT---AYGP---PS-KPTLDYLRNH---RIGPGAIVGY---G---LTDDNP-IP---YVQPGH---PAPGYISQTYVD---PAL-TNARD---LR---RYVDATRIYVLPGREATR---  
KGA---RLGDFVAHSQR---T-GHSV---YG---IVGDD---G---NP---SNEGESSLHL  
ref\_bact\_ADW70543.1Ruonan259/67-207  
KMNVDVDCG-A---PN---AYGP---PG-KKALDIDAHARAPKEHPGAVGY---G---MTEYEG-G-PP---TKOQPHD---PYPGYVVSQTFAD---LSN-KRMD---PR---RYVDAARINYLQVGRVAKQ---  
-IGV---ALGDFATYVCR---T-GRTA---FA---IVGDS---G---NE---SGEGSLALV  
ref\_bact\_SNT33139.1Ruonan269/76-216

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---SGV---TMDGFATVYVSCR-TGKSV-YA-IVADS-G-NE-SGAEGSLALV  
ref\_bact\_PHM10734.1Roonan28699-234  
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---KLGDFAVVYNTN-N-EKLA-FA-IYADV-GP-KN-QIGEGSIALS  
ref\_bact\_BBM83306.1Roonan536743-474  
GMSVDADG-A-PK-AYH-REKG-KG-LDYLANA-GY-PGNWWGLV-T-KN-G-VP-VVQKSSD-PAPGYVYSQTAMFS-SAK-S-YID-PR-RYVNSTIPYVFLPA-R-KS-MGA-  
---KLGDAAVVTRT-S-GKVA-YA-MYSDV-GP-KN-HIGEGSIALA  
ref\_bact\_WP\_085986336.1Roonan308117-244  
GMSIDADG-S-PR-AYHP-KN-TG-IDDLKHA-GK-GGKWWALV-KN-G-KP-VVQKS-GYVYSMTSLQD-FRY-A-PWD-QR-RYVNAETIPYVLPKVK-K-VVQS-QS-GRV-  
---KLGDAVYVYNTN-N-KRVA-YA-IYADT-GA-NT-RIGEGSIALA  
GMITDADG-S-PH-AYHP-SN-IG-IDD-NEN-GK-DEQGNVWGLV-AN-KK-P-YIQNSTD-PAPGYVYSATSLYD-MTK-R-RTD-PR-RYVDSEKIPYVLPQVMPHD-GRQC-RD-  
AKA-CLGDITVIRNIE-N-GRYA-FA-ILADQ-AP-SS-GIGEGSIALA  
ref\_bact\_WP\_079914689.1Roonan24246-178  
IMDIDADG-S-PR-AYNP-QN-TG-LDDLSHA-GR-PGHVVGIPTV-HN-GKPS-G-PP-VIOKRTD-PAPGYVYSQTALSD-FNK-R-FTD-PN-AYVNSEKIPYVLPQ-R-RS-FGA-  
---VLGDMAVVYNIK-N-GRLA-FA-VYADT-DV-GIGEGSIALA  
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TST---QKGDGYVYNNR-T-KKGC-YA-IFGDV-GG-YG-KLGEYSIYA  
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TGA---KVGDGYVYNEK-T-GKGS-FA-IFGDV-GN-QN-KLGEYSIYA  
ref\_bact\_PFK28999.1Roonan23030-165  
LGA---KLGDAVAVIRSV-T-GAYD-YA-SG-LDYLANA-GH-PGNWWALV-DN-QQPS-G-TP-VIQDSTD-PAPGYVYSTSLD-ANC-D-PKD-PR-RYVNAEAINVPLG-R-LG-  
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GMAIDADG-A-AH-AYH-PQIT-MG-LDYLGNA-GV-HGNWWALV-DN-GMPS-G-KP-LQKASD-PAPGYYSKTSLED-KDR-A-LQD-PR-RYVDAEIPVPLVLP-K-LK-FK-  
FGA---KLGIDGIAINTG-KKIC-YA-GC-HBADN-GP-SG-KIGEASIALA  
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IPM---KIGDGFVNNRS-N-NAGS-GC-IFADV-GP-ED-SIGEGSIALA  
ref\_bact\_WP\_083634555.1Roonan30696-231  
TMOQNDG-A-PT-AYH-KNLD-LG-LDYLANA-GS-KGNWWGLV-DT-GDGH-G-KP-ITQAGD-PAPGYVYSGLTLDQD-STK-E-HGD-QN-RYVSETIPVPLVLP-K-IN-  
IPH---QKGDGFVNNR-N-KTCS-YA-GC-IFADV-GP-ED-SIGEGSIALA  
ref\_bact\_RZK58430.1Roonan23747-179  
GMAIDADG-A-PK-AYH-QNST-LA-LDYLANA-GK-PGKWWALV-D-RK-G-QP-LLQKESD-PAPGYYSKTSLFY-LNK-P-TTD-PS-RYINSETPVPIAPS-G-WA-SDF-  
---QTGDIALVINK-N-GKRS-YA-IVADI-GP-RD-KIGEGSIFLA  
ref\_bact\_WP\_13848473.1Roonan23747-182  
GMITDADG-A-PK-AYH-KDNR-MA-LDPLANA-GK-PGNWWALV-DT-QKRD-G-QP-VTQSSD-PAPGYYSMTSLAN-GAK-K-TTD-PAL-RYVNSGVPYIAPP-K-FS-  
ASE---KLGDIALVNNK-N-GKRC-YA-IFADT-GP-AN-KIGEGSVFLA  
ref\_bact\_OYW53258.1Roonan427227-365  
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ref\_bact\_WP\_194406846.1Roonan426227-365  
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KVL---RLGDVGVAYNKL-N-KGIC-FC-QFAET-GP-AD-KIGEGSIALA  
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ref\_bact\_PZR11156.1Roonan328137-269  
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ref\_bact\_WP\_018970930.1Roonan405206-344  
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ref\_bact\_AP40793.1Roonan21231-175  
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---EGI-VLGCARAT-Y-N-GQSV-DC-VVADV-SS-SK-KVGEISIAA  
ref\_bact\_KML46109.1Roonan21130-174  
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SY-IGV-VKRCARV-T-W-QKSV-DC-VVADV-GP-AN-RIGEASIAA  
ref\_bact\_TDR36594.1Roonan21130-174  
DAIDADG-A-NGQGGGPAAYRT-DD-DG-TEALANG-MKIV-GKV-VCAR-AWARSIVLDA-D-N-EP-KVFPVGI-A-SMTWYRH-PGV-P-ASD-PT-AYDSETPYVPLVPLV-Q-KT-  
---AGV-VKRCARV-F-N-GKTV-DC-VVADR-GP-AA-KIGESIAA  
ref\_bact\_TQK0128.1Roonan39423-257  
DAIDADG-A-NGQNGQAAYVRA-DD-DG-TEKLANG-MRID-GKV-ICEK-AWARDVILGA-D-N-EP-KVFRDGV-A-STTWYRH-PGK-A-PDD-PS-AYDAETIPYVPLVPLV-Q-  
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GGAIDADG-ANG-QKN-VKHFAYRR-D-D-HG-L-DLQNA-GY-PDGDWRGVL-GA-DRGD-G-EP-LDDGHNLVYSQTYAW-KGRPI-PKRYVDAATIPYVPLVPLV-RH-  
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GAIDADG-ANG-QKN-VKHFAYRR-D-D-HG-L-DLQNA-GY-PDGDWRGVL-GA-DRGD-G-EP-LDDGHNLVYSQTYAW-KGRPI-ATRYVDAATIPYVPLVPLV-RH-  
ref\_bact\_ROS27566.1Roonan35134-130  
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ref\_bact\_AEF46206.1Roonan4229-137  
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NASTDIDG-A-PN-APAL-DPT-G-QL-ETSLRR-SNG-WSG-EG-EYVNSLIPYVPLVPLVFNKVK-TGHPQC-LGDIKALTYK-  
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ref\_bact\_BA109338.1Roonan32243-142  
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ref\_bact\_EDY21054.1Roonan22962-158  
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ref\_bact\_AW10090.1Roonan22679-174  
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DKVV YA VVGDL GP KP IIGESYALA  
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E-DKVV YG VIGDK GP DS IIGESYAMA  
>ref\_bact\_WP\_165237426.1Ruonan391/92-187  
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G-NRVA YA VVGDS GP VN MIGESYKLA  
>ref\_bact\_SDM91431.1Ruonan228/82-177  
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>ref\_bact\_AHH99783.1Ruonan220/73-168  
DMDIDCDG QP S-THC SR S-T-DP DFQAEAFN DSH GK A-LRAETLPHYVVP GVSSWNY-RD SGI RGGTVAVVY-D  
NKLT YA VVGDV GP AK AIGESYATA  
>ref\_bact\_WP\_165234508.1Ruonan228/81-176  
DMDIDCDG QP T-ERC NK K-T-DP WFPQETAQ QSD GR H-LNSAALPFVVP LPSKWDY-RG AGI GGTIAVH-K  
GEVQ YA VVGDL GP KK IIGESYASA  
>ref\_bact\_WP\_161694136.1Ruonan225/78-173  
DLVDVDCDG RP S-QVC NK R-T-DP YFQPETAQ DSR GQ Q-LNSAALPFVVP GASKMWNH-RD AKV WGGGLAAVY  
R-KVQ YA VVGDT GP TD IIGESYATA  
>ref\_bact\_WP\_187813211.1Ruonan293/147-242  
DLVDVDCDG RP S-RVC NK R-T-DP FFLPTAFQ DSA GR H-LNSAALPFVVP GPSKVDH-RR WGV HGGVAVH-R  
KVE YA VVGDT GP TD IIGESYATA  
>ref\_bact\_SCK41613.1Ruonan228/81-176  
DMDIDCDG RJ T-KAC NS R-T-DP SFQQTAFQ TSA GK P-LDSARLPVVP GPGPLWDY-RK SGI RGGVAVH-D  
KVR YA VVGDT GP TG IIGESYAAA  
>ref\_bact\_PVC84861.1Ruonan259/112-207  
DMDIDCDG RK T-KAC NT R-T-DP YFQPETAQ TSR GK P-LDSARLPVVP GPGPVDY-RK SGI TGGTVAVH-K  
GEVR YA VIGDT GP AG IIGESYALA  
>ref\_bact\_EHM26394.1Ruonan293/147-242  
DMDIDCDG RR T-KVC NR K-T-DP YFLPETAQ SSR GE P-LDSAVLPHVVP GPGKVDY-RK SGI TGGSVAVVY  
R-DRV YA VVGDT GP TG IIGESYAMA  
>ref\_bact\_SCK60839.1Ruonan317/171-266  
DMDIDCDG RR T-KVC NK K-T-DP YFQPQTAFT SSR GK P-LNSAALPFVVP APSRTWDY-RK SGI TGGSVAVVY-E  
GRV YA VIGDT GP AG IIGESYAMA  
>ref\_bact\_TXS18782.1Ruonan225/78-173  
DMDIDCDG QV S-TVC NT R-T-DP SFQPQTAQ GSD GK Y-LDSSEVPHYVVP GPGPLWNY-TT SGI KGGVAVH-G  
DKVR YA VVGDT GP TG IIGESYALA  
>ref\_bact\_TRO60880.1Ruonan274/127-222  
DMDIDCDG QV T-AEC NK R-T-DP WFDQTAQH QSD GR P-LNSELPHYVVP GPSGWNY-AS SGI RGGVAVH-G  
DEIQ YA VVGDT GP TK IIGESYATA  
>ref\_bact\_PRY40270.1Ruonan238/91-186  
DLVDVDCDG KV T-AKC NG D-T-DP WFDQDTAFH DSK GA P-LQADKLPVVP SPSGTWDY-RN SGI RGGVAVVY-N  
NKVE YA VVGDT GP TA IIGESYATA  
>ref\_bact\_WP\_185001842.1Ruonan221/75-170  
DLVDVDCDG QJ T-PEC NK N-T-DP WFPDPTAFH QSD GK P-LISARLPVVP SPSGTFDY-RK HGI VGGVAVVY-N  
NKVQ YA VVGDT GP AS IIGESYAAA  
>ref\_bact\_POX46163.1Ruonan237/90-185  
DMDIDCDG RP T-AKC ST S-T-DP WFDQDTAFH QLD GR P-LRADRLPHYVVP GVSDIWDY-RA AGV KGGGLAVH  
D-PQVE YA VVGVDV GP KK IIGESYATA  
>ref\_bact\_AWT46396.1Ruonan244/97-192  
DLVDVDCDG QR T-ERC NE R-T-DP WYQDPTAFH DSA GP P-LRADRLPHYVVP GPSGVDH-RS AGV EGGSVAVR  
G-DRVH YA VVGDT GP KE IIGESHATA  
>ref\_bact\_WP\_108952784.1Ruonan248/102-197  
DLVDVDCDG LR T-RLC NE R-T-DP YFRPDTAFH QAD GM P-LRADRLPHYVVP EPGRAWDH-AT AGV DAGDPVLLH  
G-DRIA YA VVGDL GP AG IIGESYAAA  
>ref\_bact\_ANS69194.1Ruonan235/88-183  
DMDIDCDG QR T-ARC NE N-T-DP WFPDPTAFH QSD GR P-LRSDTLPVVP SISETWNY-PG AGI GGGVAVH-G  
GRVQ YA VVGDT GP KR IIGESYATA  
>ref\_bact\_KOG42964.1Ruonan231/84-179  
DMDIDCDG RR T-AKC NE R-T-DP WPHPTAFH QSD GR P-LRSDTLPVVP GASALWKP-AA SGI RGGVAVH-D  
KVR YA VVGDT GP SQ IIGESYAAA  
>ref\_bact\_GCB4466.1Ruonan265/118-213  
DMDIDCDG QR T-VRC NE D-T-DP WFGQDTAFR QSD GE P-LKSDTLPVVP SPSRWNY-RA AGI KGGVAVH-R  
DQVQ YA VVGDT GP RK IIGESYATA  
>ref\_bact\_SH24002.1Ruonan275/128-223  
DMDVDCDG QR T-AKC NE S-T-DP WYQDPTAFH QSD GK A-LRADSLPHYVVP SSSSLWNY-GS AGI KGGVAVVY  
Q-NKVE YA VVGDT GP TK IIGESYATA  
>ref\_bact\_WP\_161180469.1Ruonan231/82-177  
DMDVDCDG LR T-DKC NK D-R-DP WYQDPTAFH QSD GK P-LRADSLPHYVVP GSSALWDY-TK SGV KGGVAVVH  
G-NKVE YA VVGDT GP SR IIGESYAAA  
>ref\_bact\_WP\_109279675.1Ruonan232/85-180  
SMTIDCDG QR T-AQC SE A-T-DK HFRNDTAVH RSD HQ P-FDAAVPHYVVP WHSAWNY-TT AGI RPDGVAVVY-Q  
QOVE YA VVGDT GP EE KIGESYATA  
>ref\_bact\_GDY31502.1Ruonan250/103-198  
DMDIDCDG QR T-SQC NE N-T-DP CFQADTSFH QSD GR P-LNSAALPFVVP LPSGRWDY-QK AGI QGGDVAVVY  
N-GRVE YA VFGDE GP SG IIGESYATA  
>ref\_bact\_QUQ62609.1Ruonan238/91-186  
GMNIDCDG QT T-AQC NK N-T-DC CYQNDTSFH LAN T-AQC GK P-LSAAVPHYVVP LPSRFKY-GS NGI KGGDILAVVY-N  
NQVE YA VFGDE GP SD IIGESYATA  
>ref\_bact\_QUQ66075.1Ruonan388/241-336  
GMAVDCDG QR T-ATC NE N-T-DC CFYNDTSFH QSD GK P-FDAAQPHYVVP LPSRWNY-GD AGV EGGDILAVVY  
H-GHVE YA VFGDE GP DD IIGESYATA  
>ref\_bact\_VVJ24105.1Ruonan233/86-181  
DMDIDCDG QR S-SQC NE D-T-DC CYQDPTAFH QSD GK P-LNSAALPFVVP SSSSIWNY-SS SGL KGGGCAVY-N  
KVE YA VIGDT GP TQ IIGESYATA  
>ref\_bact\_TDP98023.1Ruonan229/81-176  
DMDIDCDG QR T-TQC NE D-T-DC CFPDPTAFH TSD DQ P-LNSAALPFVVP SPSGTWDY-GD YGL DGGSVAVVY-N  
GHVE YA VVGDT GP TG IIGESYAAA  
>ref\_bact\_TDP94022.1Ruonan362/86-181  
DMDIDCDG VR T-TQC NE N-T-DC CFPDPTAFH TST DQ P-LNSAALPFVVP QPSTWNY-RN YGI DGGSVAVVY-Q  
GRVE YA VVGDT GP TG IIGESYATA  
>ref\_bact\_WP\_084580438.1Ruonan356/78-173  
DMDVDCDG VR T-SQC NE Q-T-DC CFPDPTAFH TST DQ P-LNSAALPFVVP SPSGTWDY-RT AGI EGGAVVAVY-N  
NQVT YA VVGDT GP TG IIGESYATA  
>ref\_bact\_TDV54840.1Ruonan229/82-177  
DMDIDCDG VR T-TQC NE D-T-DC CFPDPTAFH TST DQ P-LNSAALPFVVP SPSSTWDY-RN YGI RGGVAVVY-G  
NKVE YA VVGDT GP TA IIGESYAAA  
>ref\_bact\_WP\_184833869.1Ruonan486/338-433  
DMDIDCDG IR T-AQC NE D-T-DC CFLPDTAFH ASN GS A-LNSAALPFVVP SSSSIWNY-AN FQI GCGTVAVY-N  
NQVL YA VVGDT GP TQ IIGESYATA  
>ref\_bact\_SNS42910.1Ruonan610/461-556  
DMDIDCDG IR T-TQC NE D-T-DC CFLPETACE TSG GA A-LNSAALPFVVP SSSGWNY-TT KGI GCGTVAVY-N  
GQIE YA VVGDT GP SE IIGESYRKA  
>ref\_bact\_WP\_157247302.1Ruonan577/428-523  
DMDIDCDG VR T-AQC NE D-T-DC CFQPQPTCT ASG GG Y-LNSAALPFVVP SPSGTWDY-RS RGI GCGTVAVY  
N-GRVE YA VVGDT GP AA IIGESYAAA  
>ref\_bact\_ETK32074.1Ruonan349/200-295



DMDDICDG --VR-- T-TQC--NE-- N-T-DC-- CFQADTACH-- TSG-- DS-- P-LNAAGLPYVVP-- STSSIWKY-TS-- VGI-- GCGSVVAIVY--N-  
GKIE--YA-- VVGDY-- IGEASYKTA  
>ref\_bact\_TMI28961.1Ruonan363/214-309  
DMDDICDG --KT-- T-TQC--NK-- N-T-DC-- CYQNDTFCH-- DSH-- DA-- P-LDSAHLPLYVVP-- SESGIWNY-TK-- FGI-- RCGQVGVVY--N-  
GKLT--YA-- VMGDT-- IGEASYNLA  
>ref\_bact\_SDX78569.1Ruonan356/209-304  
DMDDICDG --QR-- VVGDY-- T-TQC--NE-- N-T-DC-- CFQPDFAFH-- QSD-- T-GK-- P-LNAATLPYVVP-- SSSSTWDY-TK-- FGI-- QGGGVVAIVY--N-  
NQVL--YA-- VVGDY-- IGEASYATA  
>ref\_bact\_KAA2261911.1Ruonan233/86-181  
DMDDICDG --QR-- T-AQC--NE-- K-T-DC-- CFQPDFAFH-- QSD-- T-GK-- P-LNAAKLPYVMP-- SPSAIWDY-RK-- SGI-- QGGSVVAIVY--N-  
NKVI--YA-- VVGDY-- IGEASYATA  
>ref\_bact\_AXB2115.1Ruonan217/70-165  
DMDDICDG --QV-- T-DLC--NA-- D-T-DP-- AFQNDTAFH-- QSN-- GD-- P-LIADQLPYVVP-- GRSKIWNF-AR-- SGI-- RGGGVVAIVY--  
N-DTVQ--YA-- VVGDY-- IGEASYATA  
>ref\_bact\_CEL21509.1Ruonan224/77-172  
DMDDICDG --QR-- T-ARC--NE-- Q-T-DP-- WFPETAFAE-- RSD-- T-GK-- P-LIADQTHFVLP-- SESSTWRF-SS-- SGL-- AGASACAVIY--N-  
NKVL--YA-- SVGDT-- IGEASYATA  
>ref\_bact\_WP\_037308310.1Ruonan228/82-177  
DMDDICDG --QP-- T-ARC--NK-- N-T-DP-- WFPDTAFAE-- RSD-- T-GK-- P-LIADQTHFVLP-- SISSTWRF-EK-- AGL-- KGGGSCAVIY--N-  
NKVL--YA-- VVGDY-- IGEASYATA  
>ref\_bact\_RZS36610.1Ruonan232/82-177  
DMDDICDG --QR-- T-DKC--NE-- N-T-DP-- SFYPDFAFH-- QSD-- T-GK-- P-LVADTLPYVLP-- GKSIDIWDY-AA-- SGI-- KGGGSCVIVY--G-  
DKVL--YG-- VVGDY-- IGEASYAAA  
>ref\_bact\_GIL30293.1Ruonan229/82-177  
DMDDICDG --QT-- T-DAC--NS-- D-T-DP-- WYQDDTAFH-- QSD-- T-GQ-- P-LDAAGLPYVVP-- QNNDIFRY-SD-- HDI-- DGGVAIVY--G-  
DQVE--YA-- VVGDY-- IGEASYATA  
>ref\_bact\_OKJ75028.1Ruonan275/124-219  
DLDDICDG --RA-- T-AAC--NA-- A-T-DP-- SFHGDFAFH-- ASD-- T-GR-- P-LNAEALPYVVP-- APSGTWDY-AK-- SGI-- RGGGVVAIVY--  
G-GKVE--YA-- VVGDY-- IGEASYATA  
>ref\_bact\_WP\_169133653.1Ruonan247/100-195  
DMDDICDG --VE-- T-EQC--NK-- D-A-DP-- AYQDDTAFH-- TSD-- T-DQ-- P-LNAEKMPYVVP-- SKSDIWNF-AD-- SGI-- KGGGIVAVIS--G-  
DKVT--YA-- AVGDT-- IGEASYATA  
>ref\_bact\_ROQ60187.1Ruonan279/132-227  
DMDDICDG --QV-- T-TAC--NE-- D-T-DP-- WYQDDTAFH-- TSG-- T-DQ-- P-LNAEKLPLYVVP-- SSSSIWNY-GS-- AGI-- KGGGVVAIVY--  
N-GKVE--YA-- VVGDY-- IGEASYATA  
>ref\_bact\_THA79300.1Ruonan267/120-215  
DMDDICDG --RV-- T-KEC--NA-- D-T-DP-- GFQGDFAFH-- TSD-- T-DR-- P-LDARNLAYVVP-- SRSLTWFDF-GS-- AGI-- KGGGVVAIVY--  
A-GRVE--YA-- VVGDY-- IGEASYATA  
>ref\_bact\_TXS39132.1Ruonan293/146-241  
DLDDICDG --QV-- T-KAC--NV-- D-T-DP-- WYQDDTAFH-- TSG-- T-DR-- P-LNAEALPYVVP-- SRSLTWFDF-SD-- SGI-- KGGGVVAIVY--  
A-GKVE--YA-- VVGDY-- IGEASYATA  
>ref\_bact\_PIN02699.1Ruonan239/92-187  
DLDDICDG --RA-- T-AAC--NK-- A-T-DP-- WYQDDTAFH-- QSN-- T-DK-- P-LDAEKVSYVVP-- NASPLWNY-SA-- SGI-- KGGGVAIVYVY--  
G-NRVE--YA-- VVGDY-- IGEASYATA  
>ref\_bact\_WP\_030019196.1Ruonan239/92-187  
DMDDICDG --QV-- T-AKC--NK-- N-T-DP-- WYQDDTAFH-- QSD-- T-GK-- P-LNAEKLPLYVVP-- SVSGIWNF-ES-- AGI-- KGGGIVAVIS--K-  
NKVE--YA-- VVGDY-- IGEASYAAA  
>ref\_bact\_THI20732.1Ruonan289/142-237  
DLDDICDG --QV-- T-ARC--NK-- R-T-DP-- WYQDDTAFH-- QSN-- T-GE-- P-LNAEKLPLYVVP-- APSKIWDY-RA-- AGV-- RGGGVVAIVY--  
K-GRVE--YA-- VVGDY-- IGEASYAAA  
>ref\_bact\_KIF66552.1Ruonan252/105-200  
DMDDICDG --QV-- T-AHC--NS-- A-T-DP-- WYQDDTAFH-- QSD-- T-GK-- P-LNSEKLPYVVP-- APGGTWDY-TA-- SGI-- NGGGIAIVY--D-  
GRVQ--YA-- VVGDY-- IGEASYATA  
>ref\_bact\_QIQ06330.1Ruonan253/102-197  
DMDDICDG --QV-- T-AHC--NT-- T-T-DP-- WYQDDTAFH-- QSD-- T-GK-- P-LNSEKLPYVVP-- APSERWTY-TA-- SGI-- RGGGVVAIVY--  
G-GRVQ--YA-- VVGDY-- IGEASYAAA  
>ref\_bact\_WP\_078849624.1Ruonan172/24-119  
DMDDICDG --KV-- T-RRC--NE-- D-T-DG-- SFQDMTAFH-- RSD-- T-GA-- P-LDAAKLPYVVP-- DPGDTWDY-RS-- SGI-- RGGGLAAVYVY--  
R-GRVE--YA-- VVGDY-- IGEASYATA  
>ref\_bact\_WP\_107069048.1Ruonan202/55-150  
DLDDICDG --QA-- T-ARC--NP-- T-T-DD-- SFQDMTAFH-- QSD-- T-GK-- P-LNAEKLPLYVVP-- GAGENWDY-RS-- SNI-- KGGGVAIVY--G-  
DSVQ--YA-- VVGDY-- IGEASYATA  
>ref\_bact\_TQK51019.1Ruonan249/102-197  
DMDDICDG --QR-- T-SAC--NT-- R-T-DP-- WYQDDTAFH-- QSD-- T-GL-- P-LDAERLPYVVP-- TPGSIWDY-RT-- SDI-- GGTVAIVY--G-  
DRVQ--YA-- VVGDY-- IGEASYATA  
>ref\_bact\_SCF99708.1Ruonan272/125-220  
DMDDICDG --QV-- T-DRC--NT-- R-T-DP-- YFQSMTAYT-- ESS-- T-GR-- A-LNAEKLPLYVVP-- TPSAIWNY-RS-- SGI-- SGGVAAIVY--G-  
DRVQ--YA-- VVGDY-- IGEASLATA  
>ref\_bact\_WP\_046496713.1Ruonan292/145-240  
DMDDICDG --QV-- T-DRC--NK-- R-T-DP-- YFQSMTAYT-- ESS-- T-GR-- A-LNAEKLPLYVVP-- TPRSRIWNY-RN-- SGI-- SGGVAAIVY--G-  
DRVQ--YA-- VVGDY-- IGEASFAA  
>ref\_bact\_WP\_129767759.1Ruonan309/162-257  
DMDDICDG --QT-- T-AHC--NS-- A-A-DP-- YFQDDTAYL-- QSD-- T-GR-- A-LNPEELPLYVVP-- LSSSIWNF-RS-- SGI-- RGGVAAIVY--R-  
DKVE--YA-- VVGDY-- IGEASYATA  
>ref\_bact\_ATW51487.1Ruonan249/92-187  
DMDDICDG --RR-- T-ERC--NR-- D-T-DP-- SYLPITSTFT-- ESD-- T-GE-- Y-LNAEKLPLYVVP-- VPSRIWDY-RS-- SGI-- RGGSVVAMVY--D-  
CKVV--YG-- VVGDY-- IGEASYAAA  
>ref\_bact\_AXG76441.1Ruonan259/112-207  
DMDDICDG --QI-- T-ERC--NL-- D-T-DP-- YFQNSTAYT-- ESD-- T-GR-- T-LNAETLPYVVP-- MPSEIWNY-RA-- SGI-- RGGVAAIVY--A-  
NKVV--YA-- VVGDY-- IGEASYAAA  
>ref\_bact\_KAA093086.1Ruonan230/83-178  
DLDDICDG --QV-- T-ARC--NR-- R-S-DP-- WYQAGTAFH-- QSD-- T-GR-- P-LNSEKLPYVVP-- SPGRWLRY-AD-- SGV-- RGGVAAIVYVY--  
E-GRIR--YA-- VVGDY-- IGEASYATA  
>ref\_bact\_WP\_119295503.1Ruonan315/168-263  
DMDDICDG --QV-- G-RQC--NK-- K-K-DP-- LFQAATAFQ-- QSD-- T-GK-- P-LDSARLPYVVP-- GASKIKWH-ED-- SGI-- KGGVAAIVY--  
D-GHIT--YA-- VVGDY-- IGEASYATA  
>ref\_bact\_WP\_079185200.1Ruonan262/114-209  
DMDDICDG --RP-- G-RYC--NK-- E-T-DP-- SFTAMTAFQ-- QSD-- T-GR-- Y-LSAEALPLYVVP-- ARGSRWKH-SD-- HGV-- HGGSVVAIVY--E-  
DKVL--YA-- VVGDY-- IGEASYAAA  
>ref\_bact\_OON72185.1Ruonan340/193-288  
DLDDICDG --RP-- G-RHC--DR-- R-T-DP-- YFQNTTAYA-- QSD-- T-GR-- S-LSADELPLYVVP-- GAGSRWNP-SA-- SGV-- RGGVAAIVY--Q-  
GRVV--YA-- VVGDY-- IGEASWATA  
>ref\_bact\_WP\_106432938.1Ruonan299/152-247  
DLDDICDG --RP-- G-RHC--NR-- R-T-DP-- LFLNATAHQ-- QSD-- T-GR-- H-LSAEKLPLYVVP-- GRSRIWNP-AR-- SGI-- RGGTVAIVY--R-  
GRVL--YA-- VVGDY-- IGEASYAAA  
>ref\_bact\_WP\_161301096.1Ruonan269/119-214  
DLDDICDG --RP-- G-RRC--NA-- E-T-DP-- MFADTAFQ-- QSD-- T-GR-- Q-LSAEQLPLYVVP-- GSSDIWSP-AR-- SGI-- RAGTVAIVY--R-  
DRVV--YA-- VVGDY-- IGEASYAAA  
>ref\_bact\_WP\_07849082.1Ruonan271/122-217  
DLDDICDG --RP-- G-PVC--NA-- A-S-GP-- YFQGTAWN-- GSD-- T-GR-- P-LSADEPLYVVP-- GPSARWRP-AA-- SGV-- TGGTLAVLVY--  
G-GRVR--YA-- VVGDY-- IGEASYAAA  
>ref\_bact\_QES40097.1Ruonan260/113-208  
DMDDICDG --RP-- G-KAC--NR-- R-T-DP-- LFPATAFQ-- QSD-- T-GR-- H-LDAENLPYVVP-- GPSRRWNH-TE-- HGV-- TGGTVAIVY--  
R-DKWH--YA-- VVGDY-- IGEASYATA  
>ref\_bact\_TGB03022.1Ruonan250/103-198  
DMDDICDG --RP-- G-KAC--NR-- R-T-DP-- LFLHGTAFQ-- QSD-- T-GR-- Q-LDAERLPYVVP-- GASRRWNH-AA-- HGV-- DGGVAAIVY--  
R-GKVL--YA-- VVGDY-- IGEASYAAA  
>ref\_bact\_WP\_098240884.1Ruonan327/180-275  
DMDDICDG --RP-- T-KAC--NR-- R-T-DP-- LFFHATAFQ-- QSD-- T-GR-- Q-LDAEHLPLYVVP-- GASRRWKH-AA-- HGI-- TGGTVAIVY--  
R-DKVQ--YA-- VVGDY-- IGEASYATA  
>ref\_bact\_TXS57519.1Ruonan237/83-178  
DLDDICDG --VP-- T-THC--NS-- R-T-DR-- YFQPTAFQ-- QSD-- T-GR-- H-LNAEALPLYVVP-- GVSQVWNY-RS-- SGV-- RGGVAAIVY--R-  
GRVV--YA-- VVGDY-- IGEASYAAA  
>ref\_bact\_ARP73549.1Ruonan251/86-181  
DLDDICDG --RP-- T-VRC--NR-- R-T-DP-- LFTAATAFQ-- QSD-- T-GR-- Q-LNAEALPLYVVP-- APSRIWDH-RA-- AGV-- RGGVAAIVYVY--R-  
GRVQ--YA-- VVGDY-- IGEASYATA  
>ref\_bact\_WP\_079147025.1Ruonan240/93-188  
DLDDICDG --RP-- T-ARC--NP-- R-T-DP-- SFTAATAFQ-- QPD-- T-DR-- H-LSAEFPYVVP-- APSGIWDH-RA-- HGI-- GGGVAAIVY--R-  
GRVQ--FA-- VVGDY-- IGEASYATA  
>ref\_bact\_WP\_106432297.1Ruonan246/98-193  
DLDDICDG --RP-- T-AHC--NH-- R-T-DP-- TFAATTAFAE-- QSD-- T-GR-- M-LNAEKLPLYVVP-- PAGPRWSH-RA-- HGI-- KGGVAAIVY--R-  
DRVV--YA-- VVGDY-- IGEASYATA  
>ref\_bact\_SED85472.1Ruonan228/81-176  
DLDDICDG --QR-- T-AHC--NR-- A-A-DP-- AFTAATAFQ-- QSN-- T-GR-- Q-LNAEKLPLYVVP-- GPSRRWNH-RK-- SGV-- RGGVAAIVYVY--  
K-GRVQ--YA-- VVGDY-- IGEASYATA  
>ref\_bact\_WP\_161333774.1Ruonan296/95-190  
DLDDICDG --RP-- T-AHC--NR-- R-T-DP-- MFAATAFQ-- QSD-- T-GR-- H-LNAEKLPLYVVP-- APSRRWNP-WR-- HGV-- RGGVAAIVYVY--  
R-DRVR--YA-- VVGDY-- IGEASYATA  
>ref\_bact\_WP\_15345822.1Ruonan266/119-214  
DLDDICDG --RS-- T-ARC--NR-- R-T-DP-- QFAGMTAYQ-- QSD-- T-GR-- H-LNAETLPYVVP-- APSRIWNP-RK-- HGV-- RGGVAAIVYVY--R-  
GRVQ--YA-- VVGDY-- IGEASYATG  
>ref\_bact\_WP\_079071240.1Ruonan344/197-292  
DLDDICDG --RP-- G-ARC--NP-- R-T-DP-- QFAATAFQ-- QSD-- T-GR-- Y-LNAETLPYVVP-- APSPLWDP-GE-- LGV-- RGGVAAIVYVY--R-  
GRVQ--YA-- VVGDY-- IGEASYATA  
>ref\_bact\_QIS69545.1Ruonan298/151-246  
DLDDICDG --RP-- T-ARC--NR-- R-T-DP-- VFAPATAFV-- GSD-- T-GR-- R-LNAETLPYVVP-- APSRRWDH-RA-- SGV-- RGGVAAIVYVY--G-  
DRVR--YA-- VVGDY-- IGEASYATA  
>ref\_bact\_WP\_171158894.1Ruonan269/122-217  
DLDDICDG --RP-- T-THC--NS-- A-T-DP-- VFAPATAFQ-- QSD-- T-GL-- D-LNAETLPYVVP-- APSRWWDY-RA-- HGI-- RGGVAAIVYVY--G-  
DRVQ--YA-- VVGDY-- IGEASYATA

>ref\_bact\_WP\_093892974.1Ruonan301/154-249  
 DLDDCDG---QA---T-VHC---NG---Q-A-DP---LYSPSTAYV---QSD---GQ---P-LNAETLPYIVVP---AASSRWSW-GA---SGV---RGGVSAVVY---Q  
 DRVQ---YA---VVGDT---GP---SD---LIGASYATA  
 >ref\_bact\_WP\_051866101.1Ruonan245/89-184  
 DLDDCDG---RP---G-AHC---NR---R-T-DP---WFSRATAYQ---QSD---GR---P-LSAETLPYIVVP---APSSRWK-RE---HGV---RGGVSAVVH---G  
 DRVQ---YA---VVGDA---GP---AD---LIGASYATA  
 >ref\_bact\_AWE48754.1Ruonan231/84-179  
 DMDDCDG---RP---T-ARC---SR---R-T-DP---HFSATAFT---QSD---GR---Y-LSAEKLPIYIVVP---TPSTIWDY-RD---HGI---RGGSLAAVIH---Q  
 GRVY---YA---VVGDV---GP---YD---LIGASYAAA  
 >ref\_bact\_SEB78192.1Ruonan330/183-278  
 DMDDCDG---QS---T-GHC---NS---A-T-DP---YFSGTAFQ---QSD---GR---Y-LSAEHLPIYIVVP---TPSGIWDY-RA---DSI---RGGVSAVVY---G  
 GRVQ---YA---VVGDV---GP---RD---LIGASYATA  
 >ref\_bact\_KU05092.1Ruonan255/88-183  
 DMDDCDG---RP---S-DHC---NR---R-T-DP---YFSPVYATQ---QSD---GR---H-LNAERLPYIVVP---TPSGIWDH-EA---DGV---HGGVAAVVY---  
 R-GRVY---YA---VVGDV---GP---RD---LIGASYATA  
 >ref\_bact\_PIM96866.1Ruonan301/128-223  
 DMDDCDG---RP---T-ARC---NR---S-T-DP---QFSPTAAEY---QSN---GH---R-LDAERLPYIVVP---APSRWDH-RA---HGV---GGGSAVVY---  
 G-DRVQ---YA---VVGDI---GP---RE---VIGASYATA  
 >ref\_bact\_WP\_112468756.1Ruonan286/92-187  
 DMDDCDG---RP---T-ARC---NH---R-T-DP---HFSGAAAYT---QSN---GH---R-LNAERLPYIVLP---AASRIWDH-RA---HGV---GGGSAVVY---  
 R-GRVQ---YA---VVGDI---GP---RG---LIGASYATA  
 >ref\_bact\_WP\_15272654.1Ruonan267/76-171  
 DMDDCDG---RP---G-PRC---NR---A-T-DP---WFWPATAYK---QSD---GR---Y-LNAETLPYIVLP---APSDIWDH-RA---HGV---RGGVSAVVY---R  
 DRVQ---YA---VVGDI---GP---RQ---LIGASYATA  
 >ref\_bact\_WP\_152861548.1Ruonan258/111-206  
 DIDDDCDG---RP---G-SRC---NH---T-T-DP---WFWPSTAYK---QSD---GR---Y-LNAETLPYIVVP---APSGIWDH-RA---HGV---GAGVSAVIH---E  
 GRIQ---YA---VVGDI---GP---HH---LIGASYATA  
 >ref\_bact\_PTM93123.1Ruonan231/84-179  
 DMDDCDG---RP---G-PRC---NR---R-T-DP---LFSAAATAYQ---QSD---GR---A-LSAERLPYIVVP---AADSWSN-VA---YGV---RGGTVAVVY---  
 R-DRVQ---YA---VVGDI---GP---RG---LIGASYATA  
 >ref\_bact\_WP\_107104455.1Ruonan360/87-182  
 DMDDCDG---RP---G-PEC---NS---R-T-DP---LFSGATAYQ---QSD---GR---Y-LSAETLPYIVVP---GVSIDLWDH-RD---HGV---RGGVSAVVY---  
 R-DRVQ---YA---VVGDT---GP---SG---LIGASYATA  
 >ref\_bact\_WP\_079142171.1Ruonan331/87-182  
 DMDDCDG---SP---S-LRC---NS---S-T-DP---LFSGATAYQ---QSD---GR---Y-LSAETLPYIVVP---GVSALWDY-RA---HGV---GGGSAVVY---G  
 DRVE---YA---VVGDI---GP---RE---LIGASYATA  
 >ref\_bact\_AVV46401.1Ruonan330/87-182  
 DMDDCDG---RP---G-PHC---NS---G-T-DP---LFSGTAFQ---QSD---GR---Y-LSADSLPIYIVVP---GASDVWDH-RD---HGV---RGGVSAVVY---  
 R-DRVA---YA---VVGDT---GP---RE---LIGASYAAA  
 >ref\_bact\_SMF44955.1Ruonan316/87-182  
 DMDDCDG---RP---G-THC---NS---T-T-DP---LFSDATAFT---QSD---GR---Y-LSAETLPYIVVP---GASDIWNY-RD---HGV---RGGVSAVVY---K  
 DRVQ---YA---VVGDT---GP---SD---LIGASYATA  
 >ref\_bact\_WP\_107122262.1Ruonan316/87-182  
 DMDDCDG---RP---G-AHC---NS---G-T-DP---LFSDTTAYT---QSD---GR---Y-LSAETLPYIVVP---QASDRWNP-RD---HGV---RGGVAAVVY---  
 R-DRVQ---YA---VVGDV---GP---PD---LIGASYATA  
 >ref\_bact\_SHI7347.1Ruonan338/87-182  
 DMDDCDG---RP---G-TQC---NS---G-T-DP---LFSDTTAYQ---QSD---GR---Y-LSAETLPYIVVP---GVSIDWNH-RD---HGV---RGGVSAVVY---R  
 DRVQ---YA---VVGDT---GP---RE---LIGASYATA  
 >ref\_bact\_PKT17840.1Ruonan236/89-184  
 DMDDCDG---RA---G-PLC---NS---R-T-DP---LFSGTAFQ---QSD---GR---Y-LSAETLPYIVVP---APSDIWNH-RD---HGI---GPGVSAVIY---Q  
 DRVQ---YA---VVGDV---GP---QD---LIGASYATA  
 >ref\_bact\_TQJ86073.1Ruonan291/144-239  
 DLDDCDG---RA---G-RRC---NR---R-T-DP---QFSSLTAYQ---QSD---GR---H-LSAERLPYIVVP---AVSRLWNH-RD---HGV---RGGVSAVVY---  
 R-DRVQ---YA---VVGDI---GP---RD---LIGASYATA  
 >ref\_bact\_WP\_107122566.1Ruonan321/174-269  
 DMDDCDG---RP---S-RRC---NR---R-T-DP---SFSAAATAFQ---QSD---GR---P-LDAGHLPYIVVP---APSRISNY-RD---HGV---RGGVSAVVY---R  
 DRVQ---YA---VVGDV---GP---RD---LIGASYATA  
 >ref\_bact\_GAP49853.1Ruonan334/184-279  
 DMDDCDG---RP---G-PRC---NR---R-T-DP---YFSDSTAYA---QSD---GR---P-LSAERLPYIVVP---APSRWDY-RE---HGV---GGGSAVVH---R  
 DRVQ---YA---VVGDT---GP---QD---LIGASYATA  
 >ref\_bact\_PWJ6406.1Ruonan257/109-204  
 DMDDCDG---QP---G-VRC---NT---R-T-DP---HFSATTAFQ---QSD---GR---P-LKSETLPYIVVP---APSTLWDY-RA---HGV---RGGVSAVVY---R  
 DRVQ---YA---VVGDT---GP---AG---LIGASYATA  
 >ref\_bact\_WP\_167990378.1Ruonan226/79-174  
 DMDDCDG---RP---G-TYC---NA---R-T-DP---HFSASTAFA---QSD---GR---P-LSEQLPPIVVP---APSTLWDY-RA---SGV---RGGVSAVIH---G  
 DRVQ---YA---VVGDT---GP---AG---LIGASYATA  
 >ref\_bact\_WP\_121740414.1Ruonan340/192-287  
 DMDDCDG---RP---G-RHC---NA---A-T-DP---HFSSTAFA---QSD---GR---A-LSEKLPYIVVP---APSSLWDY-RE---HGV---RGGVSAVVY---R  
 DRVY---YA---VVGDT---GP---AD---LIGASHAAA  
 >ref\_bact\_QER88154.1Ruonan383/235-330  
 DMDDCDG---RP---G-RRC---NA---R-T-DP---SFSSTAFA---QSD---GR---A-LSEKLPYIVVP---APSDLWDY-RD---DGV---RGGVSAVVY---R  
 DKVS---YA---VVGDT---GP---TD---LIGASHAAA  
 >ref\_bact\_PNV35918.1Ruonan344/196-291  
 DMDDCDG---RP---S-RRC---NA---R-T-DP---YFSSSTAFA---QSD---GR---A-LSEKLPYIVVP---APSGIWDH-RD---HGV---RGGVSAVVY---R  
 DRVS---YA---VVGDT---GP---TD---LIGASYAAA  
 >ref\_bact\_WP\_189558782.1Ruonan353/205-300  
 DMDDCDG---RP---G-RRC---NA---R-T-DP---HFSASTAFA---QSD---GR---P-LSAEKLPIYIVVP---APSAVWNH-RS---DGV---RGGVSAVVY---  
 R-DRVR---YA---VVGDT---GP---AG---LIGASHAAA  
 >ref\_bact\_GGP62105.1Ruonan274/126-221  
 DMDDCDG---RP---G-RRC---NA---R-T-DP---YFSASTAFQ---QSD---GR---P-LSEELPYIVVP---APSTVWNY-RA---HGV---RGGVSAVIH---R  
 DRVR---YA---VVGDV---GP---AD---LIGASYAAA  
 >ref\_bact\_TQL18735.1Ruonan286/138-233  
 DMDDCDG---RP---G-PRC---NS---G-T-DP---YFSASTAYA---QSD---GR---P-LSEETPYIVVP---APSDVWDH-RS---HGV---RGGVSAVVY---R  
 DRVR---YA---VVGDT---GP---AD---LIGASHATA  
 >ref\_bact\_WP\_078914010.1Ruonan307/159-254  
 DMDDCDG---RP---G-PRC---NA---R-T-DP---YFSSSTAFV---QSD---GR---P-LSSEETPYIVVP---APSTVWNH-RS---HGV---RGGVSAVVY---R  
 DRVR---YG---VVGDT---GP---AD---VIGASYAMA  
 >ref\_bact\_PWJ08435.1Ruonan313/166-261  
 DMDDCDG---RP---G-RHC---NV---L-N-DP---YFSAATAFA---QSD---GR---P-LSEDLPIVVP---APSAVWDY-RA---HGV---RGGVSAVVY---  
 Q-DRVQ---YQ---VVGDT---GP---AD---VIGASYAMA  
 >ref\_bact\_WP\_155059586.1Ruonan319/172-267  
 DLDDCDG---RP---G-PHC---NA---R-A-DP---HFSDTTAYQ---QSD---GS---Q-LDAERLPYIVVP---VPGSIWDH-RA---HGV---AGGVAVVH---  
 G-DRVQ---YA---VVGDT---GP---HD---LIGASYATA  
 >ref\_bact\_IKT09716.1Ruonan299/88-183  
 DLDDCDG---RP---G-RHC---NA---R-T-DP---LFPAGTAFQ---QSD---GR---D-LSAETLPYIVVP---APSDIWDH-RR---DGV---HGGVSAVVY---G  
 DRVQ---YA---VVGDV---GP---DD---LIGASYATA  
 >ref\_bact\_KAA0942012.1Ruonan269/122-217  
 DMDDCDG---RP---G-RHC---NA---R-T-DP---LFSENTAYQ---QSD---GR---Q-LSAERLPYIVVP---APSRRWNH-RK---HDV---RRGTVAVVH---  
 G-DRVG---YA---VVGDT---GP---DD---LIGASYALA  
 >ref\_bact\_WP\_190854307.1Ruonan306/159-254  
 DLDDCDG---RP---G-PHC---NE---R-T-DP---LFSDTTAYQ---QSD---GR---Q-LSAERLPYIVVP---APSHRWNH-QE---HDV---RRGTVAVVH---R  
 DRVR---YA---VVGDV---GP---DD---LIGASYALA  
 >ref\_bact\_BAC68998.1Ruonan257/110-205  
 DMDDCDG---RP---G-LLC---NE---S-T-DP---SFSDATAFQ---QSD---GR---Q-LNAETLPYIVVP---TAGDIWDH-RE---HGV---RGGVSAVIY---Q  
 DRVQ---YT---VVGDT---GP---HD---LIGASYATA  
 >ref\_bact\_WP\_055612472.1Ruonan253/94-189  
 DLDDCDG---RR---G-PYC---NE---S-T-DP---LFSATAFQ---QSD---GN---Q-LDAATLPYIVVP---AASHIWDH-EE---HGV---RSGTVAVIH---G  
 DRVQ---YA---VVGDL---GP---EG---LIGASYATA  
 >ref\_bact\_ELP70556.1Ruonan250/81-176  
 DMDDCDG---QA---G-PRC---NA---R-T-DP---YFADITAYQ---QSD---GR---Y-LDPERLPYIVVP---VASGIWNY-RD---HGI---RGGVSAVIY---K  
 DRVQ---YA---VVGDT---GP---QD---LIGASYAAA  
 >ref\_bact\_GAQ65826.1Ruonan314/153-248  
 DMDDCDG---RP---S-PHC---NS---D-T-DP---WFOPTISL---QSD---GR---Y-LRSELPYIVVP---VASRIWDH-RV---HGI---RGGVSAVVY---K  
 DRVQ---YA---VVGDT---GP---QN---LIGASYATA  
 >ref\_bact\_SBT89661.1Ruonan231/84-179  
 DLDDCDG---QP---G-HRC---NS---E-T-DP---YFHDATAFQ---QSD---GR---Y-LDAERLPYIVVP---APSRWDY-RD---HGI---RGGVSAVVH---  
 E-DRVR---YA---VVGDV---GP---QD---LIGASYAAA  
 >ref\_bact\_KOV53892.1Ruonan253/106-201  
 DMDDCDG---RP---G-DRC---NS---S-T-DP---YFSAGTAFQ---QSD---GR---H-LDAETLPYIVVP---VPSAVWDH-RD---HGV---RGGVSAVVH---  
 G-DRVQ---YA---VVGDT---GP---HD---LIGASYATA  
 >ref\_bact\_WP\_104532217.1Ruonan340/193-288  
 DMDDCDG---QP---G-ARC---NH---R-T-DP---SFTAATAYQ---RSD---GR---P-LDAERLPYIVVP---GAGRIWDH-RA---HGV---QGGVSAVIH---  
 G-DRVR---YA---VVGDT---GP---RG---LIGASYAAA  
 >ref\_bact\_WP\_130335819.1Ruonan260/112-207  
 DMDDCDG---RP---G-TRC---NR---R-T-DP---DFSPATAFQ---QSD---GR---P-LDAERLPYIVVP---PAGPLWDH-RA---HGV---RGGVSAVLY---G  
 DRVR---YA---VVGDT---GP---RD---LIGASYATA  
 >ref\_bact\_WP\_100086067.1Ruonan301/136-231  
 DMDDCDG---RP---G-RHC---NR---R-T-DP---HFASTAFQ---GAD---GH---R-LDAERLPYIVVP---EPSRIWNH-RA---DGI---RGGVSAVIH---G  
 DRLE---YA---VVGDT---GP---RD---LIGASYAAA  
 >ref\_bact\_AIR96662.1Ruonan349/134-229  
 DMDDCDG---RP---G-RRC---NR---R-T-DP---SFSAVTAFQ---GSD---GR---R-PDAERLPYIVVP---APSRVWDH-RA---HGV---RGGVSAVIY---R  
 DRVR---YA---VVGDV---GP---GH---LIGASYAAA  
 >ref\_bact\_WP\_053913342.1Ruonan283/136-231  
 DLDDCDG---RP---G-ARC---NL---G-T-DP---HFSPATAYS---ASG---GG---P-LDAERLPYIVVP---EPGIWDH-RE---HGV---HGGVSAVVH---G  
 DRVR---YA---VVGDV---GP---RD---VIGASYATA  
 >ref\_bact\_WP\_161228481.1Ruonan352/205-300  
 DLDDCDG---RP---G-EHC---NA---D-T-DP---HFDTATAYT---GPD---GR---P-LDAERLPYIVVP---EPSEIWDH-RE---HGI---GGGSAVVY---E  
 DRVQ---YA---VVGDV---GP---RD---LIGASYAAA  
 >ref\_bact\_CAC01568.1Ruonan388/241-336

DLDDVDCG-RP-G-DRC-NS-G-T-DP-HFSPATAYT-GSD-GR-P-LDAERLPYVVP-GPSDTWDH-RE-DGV-RGGSLAALVH-  
 G-DRVR-YA-VVGDV-LIGEASAAA  
 -ref\_bact\_CA8907.1Roonan400253-348  
 DLDDVDCG-RP-G-DRC-NT-R-T-DP-HFPTATAYT-RSD-GT-P-LDAERLPYVVP-QPSRIWDH-RA-DGV-HGGSVAALVH-  
 G-DRVR-YA-VVGDV-LIGEASAAA  
 -ref\_bact\_WP\_107482063.1Roonan295148-243  
 DLDDVDCG-RS-VVGDV-LIGEASAAA-HFTAATAYT-RSG-GG-P-LDAERLPYVVP-RPSGWNH-RA-DGV-HGGSVAALVH-  
 G-DRVR-YA-VVGDV-LIGEASAAA  
 >exp.virus\_3300009181\_Ga0114969\_1000130\_9020-159  
 GMMIDGDA-RN-IY-AP-RGFSPLDFIANA-GE-PGNWVGIVT-DN-GKAS-G-KP-VIQKGD-PPFGYYSATSIEF-PGF-S-RGD-PY-RYVDSATVPYVLPVSHWR-A-EA-EA-  
 HGV-VLCKAQIEDTH-T-GNVI-DS-VVADF-GP-RG-KLGEASIAAA  
 >exp.virus\_3300027754\_Ga0209596\_1000127\_1820-159  
 GMMIDGDA-RN-IY-AP-RGFSPLDFIANA-GE-PGNWVGIVT-DN-GKAS-G-KP-VIQKGD-PPFGYYSATSIEF-PGF-S-RGD-PY-RYVDSATVPYVLPVSHWR-A-EA-EA-  
 HGV-VLCKAQIEDTH-T-GNVI-DS-VVADF-GP-RG-KLGEASIAAA  
 >exp.virus\_3300009159\_Ga0114978\_10000954\_1818-159  
 GMAIDADG-ANGHDGSGRA-GP-KG-INPLDYLANA-GK-EGNWWGIVT-KN-G-IP-VIQKRD-PAEGYYSITSYQR-KPF-C-DTD-PD-RYLDATENFVPSVHWR-S-EI-  
 KGV-VLCKAEVKNTK-T-GKVV-VG-IVGDF-GP-KT-KLGEASMAIA  
 >exp.virus\_3300027782\_Ga0209500\_10002238\_1018-159  
 GMAIDADG-ANGHDGSGRA-AY-GP-KG-INPLDYLANA-GK-EGNWWGIVT-KN-G-IP-VIQKRD-PAEGYYSITSYQR-KPF-C-DTD-PD-RYLDATENFVPSVHWR-S-EI-  
 KGV-VLCKAEVKNTK-T-GKVV-VG-IVGDF-GP-KT-KLGEASMAIA  
 >exp.virus\_3300027754\_Ga0209596\_1000555\_4823-167  
 GMRIDADG-ANGHDGSGRA-AYAD-GK-NG-TQPLDYLANA-GG-AGNWWGIVT-D-KQ-G-NP-IKQTADD-PAPGYYSITSYTH-PGK-L-ATD-PA-RYLDAAVDRFVLPVSHWR-A-  
 EA-RGV-VLGCCHVYDLR-T-KTSC-DA-VVGDV-GP-KD-KLGEASIALA  
 >exp.virus\_3300000730\_fDRAFT\_1008667\_2650-184  
 ARGLHVEG-QER-VL-VAYR-ND-EGPRRLWNHTEPK-GLD-APENMT-GPK-VVQTSQ-PGACAYLSETALVD-GRY-P-EGD-PR-RYDSSAVPGWVPRGAF-  
 PGM-DVALGDLAETH-N-GVSV-WA-MAYDV-GP-ASS-KLLEMSVKIC  
 >exp.virus\_3300032954\_Ga033083\_10000404\_3948-195  
 GAIBADG-A-PN-AYAL-PS-SG-LHGLDNIL-NALDDPGHVYVDS-HGDP-IGPWAGVIVG-P-N-G-KP-IHQTSQPW-AG-FCLSPALSD-HNF-P-ETD-YR-RFVDATRIAYISVPPQLR-Q-M-  
 -GV-CLGDLVADADK-T-GLS-DA-QA-LVADI-GP-RM-HLGEVSAPCA  
 >exp.virus\_3300032893\_Ga033069\_10000845\_5721-152  
 GYEVADAG-C-PR-AYHP-GG-GG-LDALGNAR-AD-DGAWVGIVT-N-AM-G-SP-LVQGPDD-PAPGYYSITLQD-RSR-A-FDD-PA-RYVDSMVPYISPEPE-L-ER-RGV-  
 -KLDELVMVAYKE-RAV-AA-IVADV-GP-HR-KLGEASIALA  
 >exp.virus\_3300027655\_Ga0209388\_1000050\_427-160  
 GYTNADG-A-PN-AYAP-DA-SG-LTALDYLANA-G-CPGNWVGIAC-D-SS-G-TP-VYVQSD-PAAPGFVYSTALCN-SKY-P-DHH-PS-RYVDSERYCFVLPJG-G-  
 TSYA-QLGDVGLAYNQA-T-GDMN-YF-AVGDV-GP-SD-QIQUESMLG  
 >exp.virus\_3300021478\_Ga0210402\_10000601\_2124-156  
 GATVNDG-S-PH-CYHP-ND-GE-GLDYLANA-G-SPGNWVGIVT-D-SS-D-RP-VVQSIY-PAPGYYSITLALVN-PAY-P-ENH-PD-AYIDSEKVPVCPVPMF-G-QGW-  
 -QLGDVGLVNEK-T-GDNC-YC-ATCDI-GP-QN-HIGEVSMILA  
 >exp.virus\_3300026324\_Ga0209470\_1001151\_2228-160  
 SEAVNADG-S-PH-AYGP-ND-SG-LDYTDNA-G-KPGNWWGIVT-D-GK-G-LP-ILQAAIYH-PAPYYSITLALVD-PNY-P-ENH-PA-RYVDSERYGFVVPJG-G-ESFC-  
 -RLGDVGLALNTK-T-GDMN-YF-AMADI-GP-KD-QIQUESMLA  
 >exp.virus\_3300021479\_Ga0210389\_10001107\_1436-168  
 GAMVNADG-S-PN-CYGP-DA-SG-IDYTAG-G-TPGNWVGIVT-D-SK-G-MP-VIQKIYE-PSPGMYVGTALIN-PTF-P-ESS-QY-RYVNSEIPEFVPMGTH-Y-TGA-  
 -KPGDGLVNLNLA-T-GDNC-FA-VFGDV-GP-KD-KIGEISIRLA  
 >exp.virus\_3300020582\_Ga0210395\_10003499\_936-168  
 GAMVNADG-S-PN-CYGP-DA-SG-IDYTAG-G-TPGNWVGIVT-D-SK-G-MP-VIQKIYE-PSPGMYVGTALIN-PTF-P-ESS-QY-RYVNSEIPEFVPMGTH-Y-TGA-  
 -KPGDGLVNLNLA-T-GDNC-FA-VFGDV-GP-KD-KIGEISIRLA  
 >exp.virus\_3300021479\_Ga0210410\_10001803\_3044-176  
 GAMVNADG-S-PN-CYGP-DA-SG-IDYTAG-G-TPGNWVGIVT-D-SK-G-MP-VIQKIYE-PSPGMYVGTALIN-PTF-P-ESS-QY-RYVNSEIPEFVPMGTH-Y-TGA-  
 -KPGDGLVNLNLA-T-GDNC-FA-VFGDV-GP-KD-KIGEISIRLA  
 >exp.virus\_3300021405\_Ga0210387\_10000245\_2544-176  
 GAMVNADG-S-PN-CYGP-DA-SG-IDYTAG-G-TPGNWVGIVT-D-SK-G-MP-VIQKIYE-PSPGMYVGTALIN-PTF-P-ESS-QY-RYVNSEIPEFVPMGTH-Y-TGA-  
 -KPGDGLVNLNLA-T-GDNC-FA-VFGDV-GP-KD-KIGEISIRLA  
 >exp.virus\_3300021405\_Ga0210387\_10000062\_10836-168  
 GAMVNADG-S-PN-CYGP-DA-SG-IDYTAG-G-TPGNWVGIVT-D-SK-G-MP-VIQKIYE-PSPGMYVGTALIN-PTF-P-ESS-QY-RYVNSEIPEFVPMGTH-Y-TGA-  
 -KPGDGLVNLNLA-T-GDNC-FA-VFGDV-GP-KD-KIGEISIRLA  
 >exp.virus\_3300026285\_Ga0209438\_1001046\_4331-164  
 GMAIDADG-S-PN-AYGP-DA-SG-LDYTAG-G-DGNGWVGIVT-D-SN-G-KP-VIQKIYE-PSPGMYVGTALIN-PTF-P-ESS-QY-RYVNSEIPEFVPMGTH-Y-TGA-  
 -KPGDGLVNLNLA-T-GDNC-FA-VFGDV-GP-KD-KIGEISIRLA  
 >exp.virus\_3300026285\_Ga0209438\_1000629\_331-164  
 GMAIDADG-S-PN-AYGP-DA-SG-LDYTAG-G-DGNGWVGIVT-D-SN-G-KP-VIQKIYE-PSPGMYVGTALIN-PTF-P-ESS-QY-RYVNSEIPEFVPMGTH-Y-TGA-  
 -KPGDGLVNLNLA-T-GDNC-FA-VFGDV-GP-KD-KIGEISIRLA  
 >exp.virus\_3300026304\_Ga0209240\_1000230\_331-164  
 GMAIDADG-S-PN-AYGP-DA-SG-LDYTAG-G-DGNGWVGIVT-D-SN-G-KP-VIQKIYE-PSPGMYVGTALIN-PTF-P-ESS-QY-RYVNSEIPEFVPMGTH-Y-TGA-  
 -KPGDGLVNLNLA-T-GDNC-FA-VFGDV-GP-KD-KIGEISIRLA  
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 -KLDGLAMCFNTQ-N-GKKS-WA-IVADV-GP-KN-G-KP-VIQKTD-PAAPGFVYSTALVD-SAF-K-ENH-PA-KYVDSGLPFIPLVSKP-T-FS-PEQ-  
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>exp\_virus\_330000439\_TBL\_comb48\_EPIDRAFT\_1003500\_8/26-115-----VVADI-----GP-RR-----KIGELSPAAA-----

WFRVVDG-D-----P-----TNH--YHDP-CWQAEITSLGP-----D-G-KP-I-----DAMQVPYIVANPIA-Q-----MV-PGV-----VLGCGIQTATYR---

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WFRVVDG-D-----P-----TNH--YHDP-CWQAEITSLGP-----D-G-KP-I-----DAMQVPYIVANPIA-Q-----MV-PGV-----VLGCGIQTATYR---

>exp\_virus\_3300021139\_Ga0214166\_1000301\_5/27-116-----VIGDV-----GP-RR-----KIGEGSIALA-----

WFRVVDG-D-----P-----TNH--YHDP-CWQAEITSLGP-----D-G-KP-I-----DAMQVPYIVANPIA-Q-----MV-PGV-----VLGCGIQTATYR---

>exp\_virus\_3300031524\_Ga0302320\_10005537\_8/30-119-----VIGDV-----GP-RR-----KIGEGSIALA-----

KAIDSDG-S-----GSS-HGDP-DQEQTSLH-T-----N-G-KP-L-----NADVDRYIVPPQVI-Q-----GT-KGI-----VLGCRAVVTNQL-T-GIQV-

>exp\_virus\_3300031788\_Ga0302319\_10002010\_6/30-119-----VVGDI-----GP-RR-----KIGEGSIALA-----

KAIDSDG-S-----GSS-HGDP-DQEQTSLH-T-----N-G-KP-L-----NADVDRYIVPPQVI-Q-----GT-KGI-----VLGCRAVVTNQL-T-GIQV-

>exp\_virus\_3300029922\_Ga0311363\_10000523\_93/27-113-----VVGDI-----GP-RR-----KIGEGSIALA-----

EAMISDGT-----DA-----VIGDQ-----GP-SL-----KIGEMSIATA-----Y-L-----NADLDRYIVLPPQF-A-----GV-KPM-----VLGCKVEVNLN-T-GLYT-

>exp\_virus\_3300010362\_Ga0126377\_10000413\_12/29-115-----VVGDI-----GP-RR-----KIGEGSIALA-----

NLDVCTDG-T-----GPA-HGDT-SHLNKTAY-----T-PS-L-----KAGETAIVMA-----NADVDFYIVLHPKMR-T-----GV-RPV-----VLGCMGRVTNLR-T-

>exp\_virus\_3300010362\_Ga0126377\_10000082\_45/30-120-----VVGEV-----GP-SN-----KAGETAIVMA-----

DLDCNDG-S-----GPP-HGDP-SYQSETAYY-N-----G-G-KY-L-----NADKDRYIVPPQVR-K-----MV-PPV-----VMGQGRVVTNLR-

KPAQSS-----WG-----VVGDI-----GP-RR-----KIGEGSIALA-----

>exp\_virus\_3300003911\_JGI2540532794\_10000041\_18/28-117-----VVGDI-----GP-RR-----KIGEGSIALA-----

NLDICNDG-S-----GPS-HGDP-SYQSETAYY-N-----G-G-KY-L-----NADVDRYIVPPQVR-T-----MV-PPV-----VMGQARMTNML-T-

AKWH-----AA-----VTGEI-----GP-SN-----KTGEAAICLA-----

>exp\_virus\_3300005937\_Ga0081455\_10000183\_26/28-117-----VTGEI-----GP-SN-----KTGEAAICLA-----

NLDICNDG-S-----GPS-HGDP-SYQSETAYY-N-----G-G-KY-L-----NADVDRYIVPPQVR-T-----MV-PPV-----VMGQARMTNML-T-

AKWH-----AA-----VTGEI-----GP-SN-----KTGEAAICLA-----

>exp\_virus\_3300010376\_Ga0126381\_100000306\_58/39-128-----VVGDI-----GP-RR-----KIGEGSIALA-----

DLDCNDG-S-----GPS-HGDP-SYQSETAYY-N-----G-G-KF-L-----NADKDFYIVPPQVR-S-----GV-DPV-----VMGQAKLTRL-D-T-

MESS-----PA-----VTGEI-----GP-RR-----KIGEGSIALA-----

>exp\_virus\_3300012971\_Ga0126369\_100004632\_5/39-128-----VVGDI-----GP-RR-----KIGEGSIALA-----

NLDVCTDG-T-----GPH-HGDT-SPOQDETAYY-N-----G-G-KF-L-----NADVDRYIVPPQVR-S-----MV-APV-----VMGQAKMTRL-D-S-

MATIS-----PA-----VTGEI-----GP-RR-----KIGEGSIALA-----

>exp\_virus\_3300012971\_Ga0126369\_10000399\_5/44-130-----VVGDI-----GP-RR-----KIGEGSIALA-----

NLDVCTDG-T-----GDH-HGDN-SPLDQATY-----N-PY-L-----KTGEAAICLA-----NADKDRYIVPPQVR-M-----MP-EPV-----VLGCGKLTRL-D-S-

MKSS-----PG-----VIGEL-----GP-RR-----KIGEGSIALA-----

>exp\_virus\_3300040633\_Ga0066395\_10000709\_14/42-131-----VIGEL-----GP-RR-----KIGEGSIALA-----

DLDCNDG-S-----GNH-HGDN-TPQDETAYY-N-----G-G-KF-L-----NADVDRYIVPPQVR-S-----MV-PPV-----VMGQARLTQLD-T-

QOAS-----PA-----VTGEI-----GP-RR-----KIGEGSIALA-----

>exp\_virus\_3300005764\_Ga0066903\_100000166\_28/44-133-----VVGDI-----GP-RR-----KIGEGSIALA-----

DLDCNDG-S-----GPS-HGDP-SYQSETAYY-N-----G-G-KF-L-----NADVDRYIVPPQVR-S-----MV-APV-----VMGQAKLTRL-D-S-

ALQH-----AA-----VVGEI-----GP-RR-----KIGEGSIALA-----

>exp\_virus\_3300010361\_Ga0126378\_10000419\_32/39-128-----VVGEI-----GP-RR-----KIGEGSIALA-----

DLDCNDG-S-----GDD-HGDP-SYQSETAYY-N-----N-G-KF-L-----NADKDRYIVPPQVR-S-----MV-PPV-----VMGQAKLTRL-D-S-

MAHS-----AA-----VVGEI-----GP-RR-----KIGEGSIALA-----

>exp\_virus\_3300010366\_Ga0126379\_10000390\_18/26-115-----VVGEI-----GP-RR-----KIGEGSIALA-----

DLDCNDG-S-----GPS-HGDD-DYQSETAYY-N-----G-G-KY-L-----NADVDRYIVPPQVR-S-----MV-PPV-----VMGSRARLTNLL-T-

METS-----AA-----VTGEI-----GP-RR-----KIGEGSIALA-----

>exp\_virus\_3300005526\_Ga0073909\_10000172\_25/59-148-----VVGDI-----GP-RR-----KIGEGSIALA-----

DLDCNDG-S-----GPS-HDDS-SYQSETAYY-N-----G-G-KF-L-----NADVDRYIVPPQVR-S-----MT-AGV-----VMGQAKLTNLD-T-

GVEI-----PA-----VVGDI-----GP-RR-----KIGEGSIALA-----

>exp\_virus\_3300027821\_Ga0209811\_10000270\_8/59-148-----VVGDI-----GP-RR-----KIGEGSIALA-----

DLDCNDG-S-----GPS-HDDS-SYQSETAYY-N-----G-G-KF-L-----NADVDRYIVPPQVR-S-----MT-AGV-----VMGQAKLTNLD-T-

GVEI-----PA-----VVGDI-----GP-RR-----KIGEGSIALA-----

>exp\_virus\_3300010366\_Ga0126379\_10000347\_19/40-129-----VVGDI-----GP-RR-----KIGEGSIALA-----

DLDCNDG-T-----GPR-HGDK-HYQPTAYY-N-----K-G-KF-L-----NADVDPYIVPMCLR-K-----LL-KKK-----SMGCKAQLSQVE-S-

GAI-----PA-----VCGEL-----GP-RR-----KIGEGSIALA-----

>exp\_virus\_3300010376\_Ga0126381\_100000274\_36/29-118-----VVGDI-----GP-RR-----KIGEGSIALA-----

DLDCNDG-T-----GPR-HGDK-HYQPTAYY-N-----K-G-KF-L-----NADVDPYIVPMCLR-K-----LL-KKK-----SMGCKAQLSQVE-S-

GAI-----PA-----VCGEL-----GP-RR-----KIGEGSIALA-----

>exp\_virus\_3300010376\_Ga0126381\_100000470\_39/28-117-----VVGDI-----GP-RR-----KIGEGSIALA-----

DLDCNDG-S-----GPS-HGDP-SYQSETAYY-N-----G-G-KY-L-----NADVDRYIVPPQVR-R-----MI-VPV-----VMGQARLTNML-T-

ALWY-----PA-----MTGDI-----GP-RR-----KIGEGSIALA-----

>exp\_virus\_3300010048\_Ga0126373\_10000021\_42/30-117-----MTGDI-----GP-RR-----KIGEGSIALA-----

NLDIDNDG-T-----GPS-HGDP-SYQSETAYY-N-----S-PY-L-----KCGEAAICLA-----NADVDRYIVPPQVR-K-----GV-APV-----VIGQARVTLNH-

KPDQW-----WG-----VTGDI-----GP-RR-----KIGEGSIALA-----

>exp\_virus\_3300006854\_Ga0075425\_100000201\_58/34-121-----VVGDI-----GP-RR-----KIGEGSIALA-----

DLDCNDG-T-----GNS-YGDP-SYQPTTLH-Y-----N-G-RA-L-----NSDVFYIVLPPLI-K-----AV-AGK-----VLGCKAKVF-Y-R-

GKSC-----DA-----VVGDI-----GP-RR-----KIGEGSIALA-----

>exp\_virus\_3300007076\_Ga0075435\_100000075\_12/34-121-----VVGDI-----GP-RR-----KIGEGSIALA-----

DLDCNDG-T-----GNS-YGDP-SYQPTTLH-Y-----N-G-RA-L-----NSDVFYIVLPPLI-K-----AV-AGK-----VLGCKAKVF-Y-R-

GKSC-----DA-----VVGDI-----GP-RR-----KIGEGSIALA-----

>exp\_virus\_3300010233\_Ga0136235\_1000189\_28/33-122-----VVGDI-----GP-RR-----KIGEGSIALA-----

DMDIDVDG-S-----GNS-HGDP-SYQPTTLH-Y-----Q-G-KA-L-----KIGEGSIALA-----DSDVDFYIVLPPLI-Q-----RV-KGI-----VLGQARVVTNLR-N-

GKFC-----DA-----VVGDI-----GP-RR-----KIGEGSIALA-----

>exp\_virus\_3300010233\_Ga0136235\_1000188\_39/34-124-----VVGDI-----GP-RR-----KIGEGSIALA-----

DADICCDG-S-----GG-----NP-----D-N-DP-----YFQPTAYHY-----QG-QALNAYKVPFVPPQSI-----NA-VKI-----VLGCKARMTYR---

TKMT-----VEC-----IVGDI-----GP-RR-----KIGEGSIALA-----

>exp\_virus\_3300010233\_Ga0136235\_1000369\_4/26-125-----IVGDI-----GP-RR-----KIGEGSIALA-----

ALQIDG-D-----LNL-----E-G-DPD-----FQDITSLHYG-----DTPD-----YSDKT-----KALNSRKVPFVPPQSI-----RA-VPQV-----VLG-S-G-

GTAI-----NTNAS-----SPLVVDV-----GP-RR-----KIGEGSIALA-----

>exp\_virus\_3300029953\_Ga0311343\_10000042\_75/28-119-----SPLVVDV-----GP-RR-----KIGEGSIALA-----

GMDIDG-D-----G-----G-----E-N-DPD-----FQPTSLR-----NPD-----GS-----SLNSRAECGVLPGKLM-----RA-FQEI-----ALGCRAYVRS-G-

LTGL-----FTDA-----VVADI-----GP-RR-----KIGEGSIALA-----

>exp\_virus\_3300009154\_Ga0114963\_10000394\_11/43-133-----VVADI-----GP-RR-----KIGEGSIALA-----

DLDLTDG-ADDVTV-----GP-RR-----KIGEGSIALA-----

DREP-----VYA-----VFADY-----GP-RR-----KIGEGSIALA-----

>exp\_virus\_3300022745\_Ga0228698\_1000621\_24/49-136-----VFADY-----GP-RR-----KIGEGSIALA-----

DLDLTDG-G-----HA-----IVADI-----GP-RR-----KIGEGSIALA-----

NKVY-----AA-----IVADI-----GP-RR-----KIGEGSIALA-----

>exp\_virus\_3300021478\_Ga0210402\_10000026\_183/40-186-----IVADI-----GP-RR-----KIGEGSIALA-----

EMTIDG-D-----PH-----TYNP-----ED-----TG-LDFLANG-----G-----YPDDGCGYMTDPE-----DS-E-DPADCILQEMHY-----PAPGFVFSATSLN-----EIF-P-SS-----PD-----HYNSNEPIIFVPGHDDPD-----PVGW-----DA-

FGV-----SLGDFVFWNTA-----T-DPDC-----FA-----LVADV-----GP-RR-----KIGEGSIALA-----

>exp\_virus\_3300002408\_B57012932\_109959582\_20/408-498-----B57012932\_109959582\_20/408-498-----Y-N-DP-----DWQPETSL-----RLN-----GT-----P-VDAKVPYVVV-----SPDA-Q-KA-----HGI-----KTGDWALVTN-Q-

KLRVDTDG-----AP-----RVADV-----GP-RR-----KIGEGSIALA-----

>exp\_virus\_3300002835\_B57040625\_100000081\_20/408-498-----RVADV-----GP-RR-----KIGEGSIALA-----

KLRVDTDG-----AP-----RVADV-----GP-RR-----KIGEGSIALA-----

>exp\_virus\_3300020550\_Ga0208600\_1000021\_2/408-498-----RVADV-----GP-RR-----KIGEGSIALA-----

KLRVDTDG-----AP-----RVADV-----GP-RR-----KIGEGSIALA-----

>exp\_virus\_3300009185\_Ga0114971\_10000002\_127/162-246-----RVADV-----GP-RR-----KIGEGSIALA-----

TLNIDTDG-----IG-----SP-----TN-DS-----TRQNQTSVQG-----LNANTQSFVLPNKPE-----YK-Y-----K-----KAIYAKN-----N-----TTGKSI-----

MG-----IVGDI-----GP-RR-----KIGEGSIALA-----

>exp\_virus\_3300027746\_Ga0209597\_1000003\_90/162-246-----IVGDI-----GP-RR-----KIGEGSIALA-----

TLNIDTDG-----IG-----SP-----TN-DS-----TRQNQTSVQG-----LNANTQSFVLPNKPE-----YK-Y-----K-----KAIYAKN-----N-----TTGKSI-----

MG-----IVGDI-----GP-RR-----KIGEGSIALA-----

>exp\_virus\_3300027911\_Ga0209698\_10001340\_22/62-158-----IVGDI-----GP-RR-----KIGEGSIALA-----

KMAHDADGVAAG-----GTQ-----L-DPS-----DGQNDTSFH-----FPD-----GSP-----LSERHPFVLP-----LGVFRA-----ATGL-----SVGLAVVIY-R-

DLT-----AA-----ICGDI-----GP-RR-----KIGEGSIALA-----

**Supplementary dataset 1. Multiple alignment of bacterial, fungal and viral chitosanase protein sequences.** Sequences with headers containing 'ref\_bact', 'ref\_fungi' and 'exp\_virus' are bacterial, fungal and viral chitosanase sequences, respectively. The chitosanase sequences were aligned with a phage lysozyme (YP\_006987285, 'OutGroup') as an outgroup sequence for the phylogenetic tree construction. '-' represents the gap within the alignments.