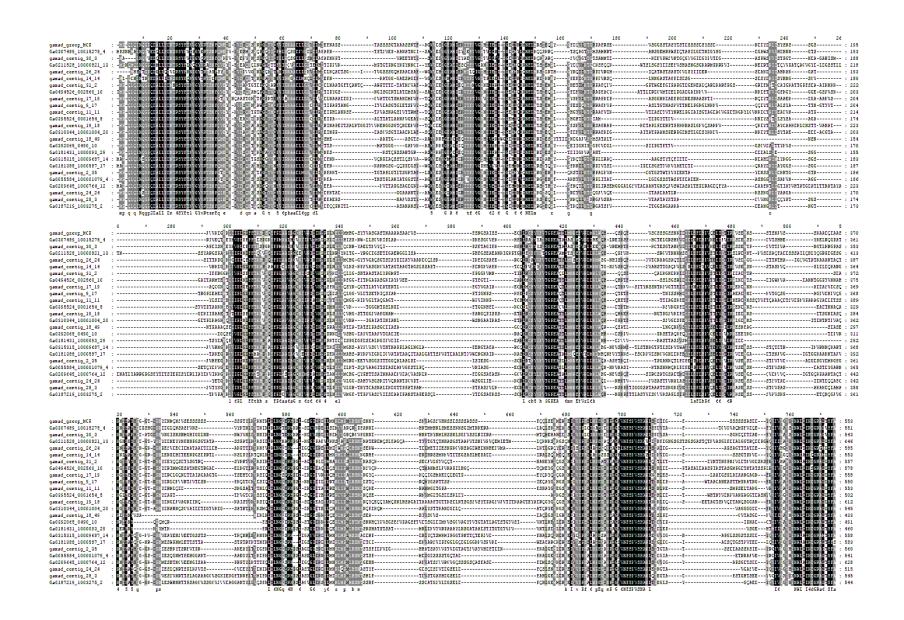
## **Supplementary figures**

- S1 Multiple sequence alignment (MSA) of Yaraviridae MCP proteins.
- S2 MSA of "Gamadviridae" MCP proteins.
- S3 Top hits of HHpred searches initiated with Yaraviridae and "Gamadviridae" MCP protein MSAs.
- S4 VLTF2 protein MSA.
- S5. Top hits of HHpred searches initiated with Mriyavirus VLTF2 protein MSA.
- S6. Top HHpred hits for "Gamadviridae" (right) and Yaraviridae (left) RuvC MSAs.
- S7. Phylogenetic tree of RuvC proteins.
- S8. MSA of selected SF3 hel1 proteins.
- S9. Phylogenetic tree of SF3 hel1 proteins.
- S10. SF3\_hel2 protein MSA.
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- S12. MSA of HUH and C-terminal domain of HUH\_long proteins.
- S12. MSA of mriyavirus PDDEXK nuclease.
- S13. Phylogenetic tree of PDDEXK nucleases.
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- S15. A, Phylogenetic tree of Mriya 48; B, predicted structures of two Mriya 48 proteins.
- S16. MSA of Yaravirus gene 50 and its homologs in mriyaviruses (Mriya\_50) and in NCBI Genbank (nr) database.
- S17. Predicted structure of Mriya\_50 (exemplified with Ple2@KY346835\_21). Leucine site chains highlighted in magenta.
- S18. MSA of conserved domain of Yaravirus gene 1 and its homologs in mriyaviruses (Mriya\_1).
- S19. Predicted structure of Mriya\_1, exemplified with Ple2@KY346835\_29.
- S20. A, MSA of Yaravirus gene 51 with mriyavirus and nr homologs. B, Predicted structure of Yaravirus gene 51.
- S21. A, Predicted structure of PEV\_22; B, same structure overlayed with 6g41\_A the structure of minor capsid protein of Cafeteria mavirus.
- S22. Predicted structure of PEV\_26 superimposed with gp2.5, a single strand DNA binding protein from bacteriophage T7 (pdb 1je5, green, z-score 13.3).
- S23. Predicted structure of Yaravirus minor capsid protein
- S24. MSA of Yaravirus minor capsid protein and related sequences.

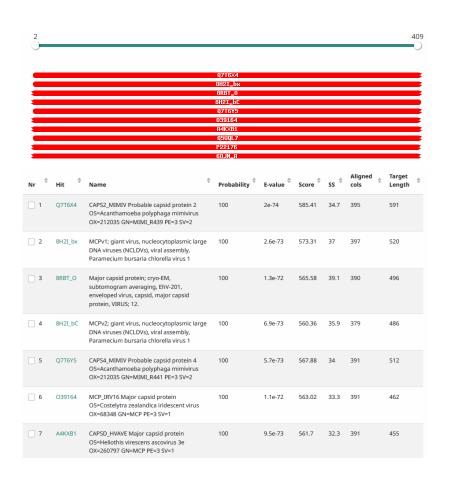
# *Yaraviridae* MCP

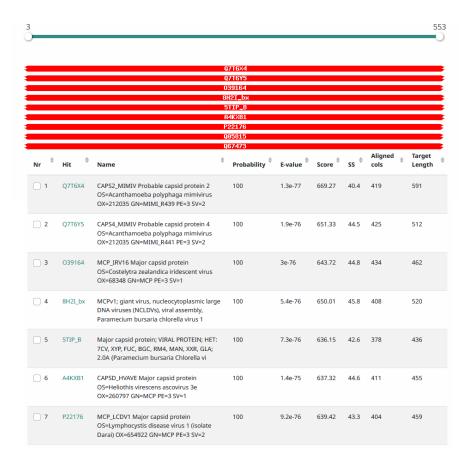
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## "Gamadviridae" MCP

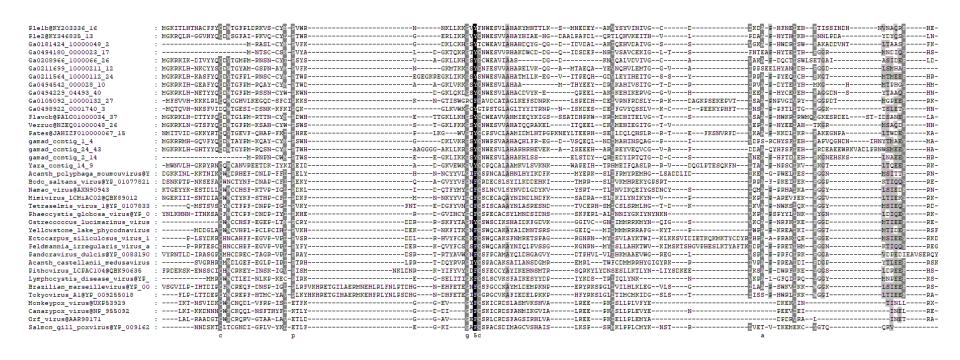


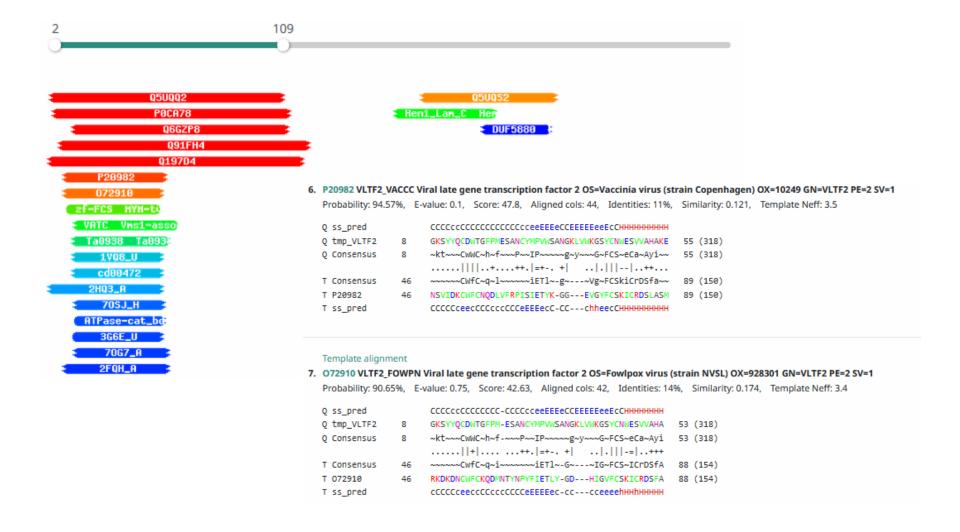
HHpred search initiated from both MCP alignments brings mimi-, irido-, asco-, and phycodnavirus MCP with high confidence.

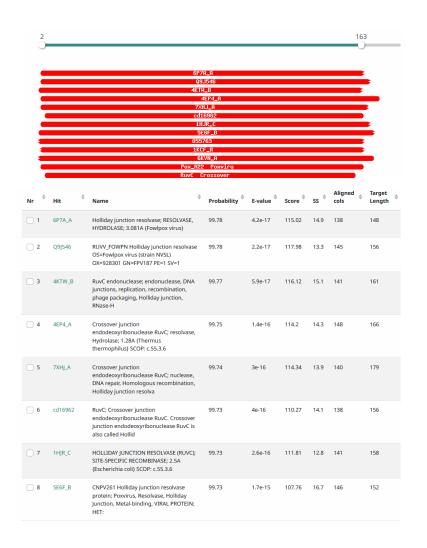


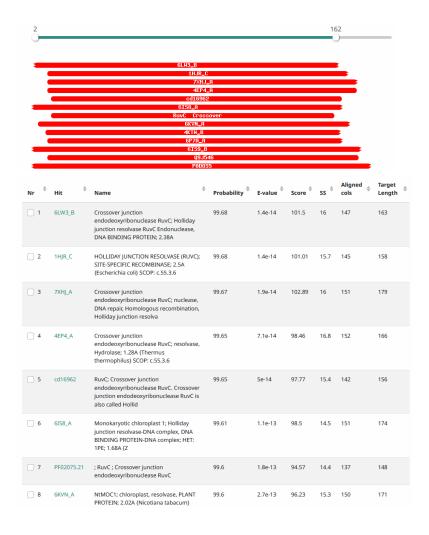


top HHpred hits for Yaraviridae (left) and "Gamadviridae" (right) MCP alignments

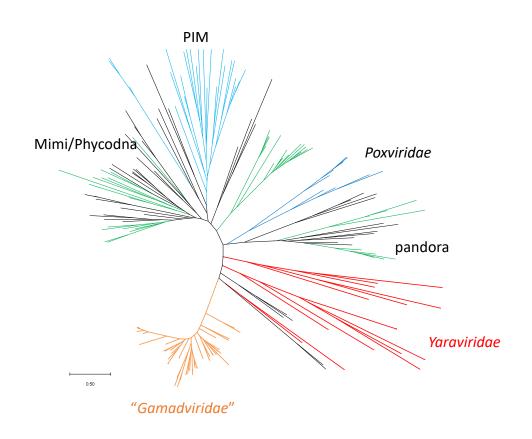




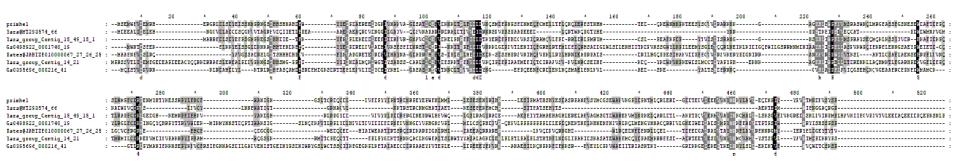




top HHpred hits for "Gamadviridae" (right) and Yaraviridae (left) RuvC alignments



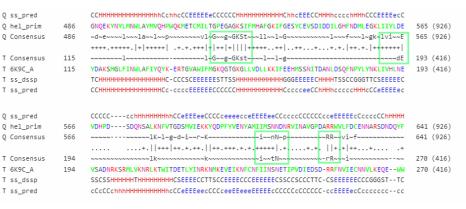
## SF3\_hel1 (most of Yaraviridae; Yaravirus gene 69)



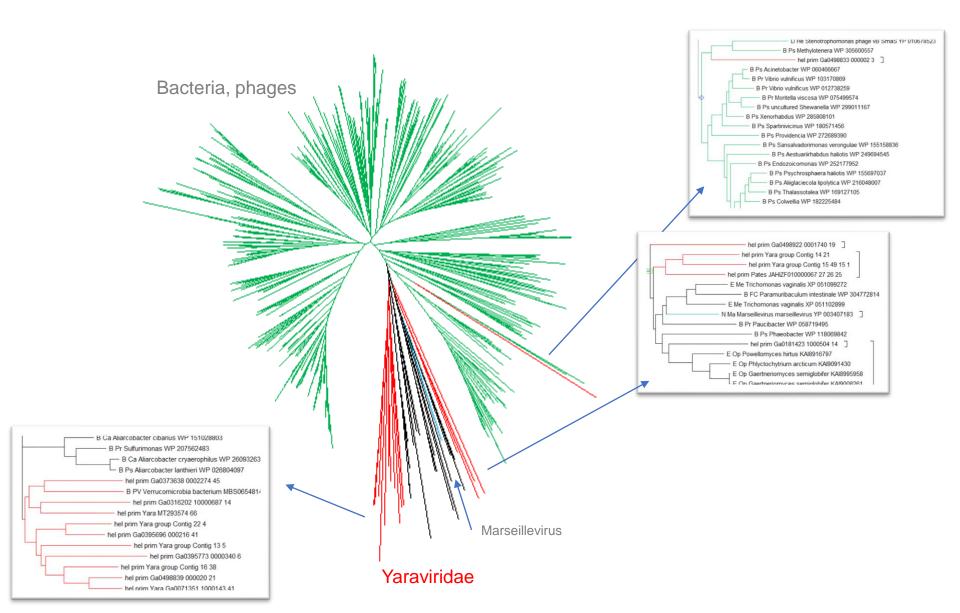
## primase domain

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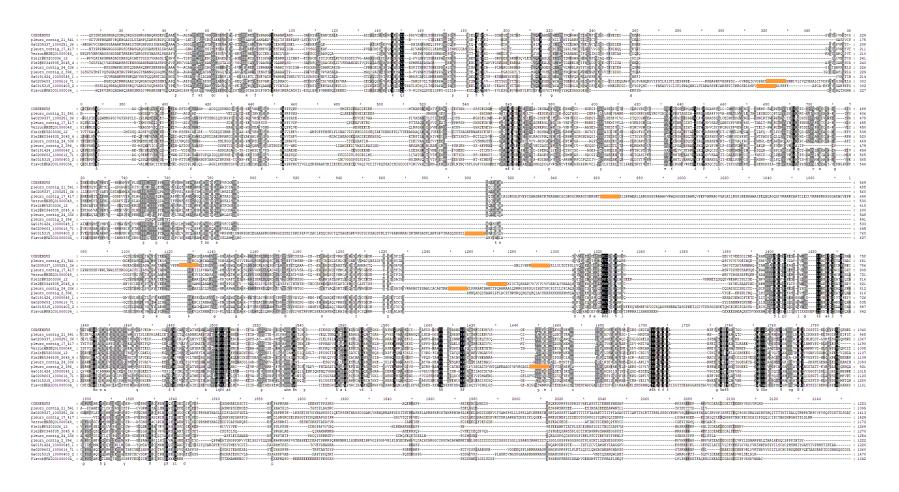
### helicase domain



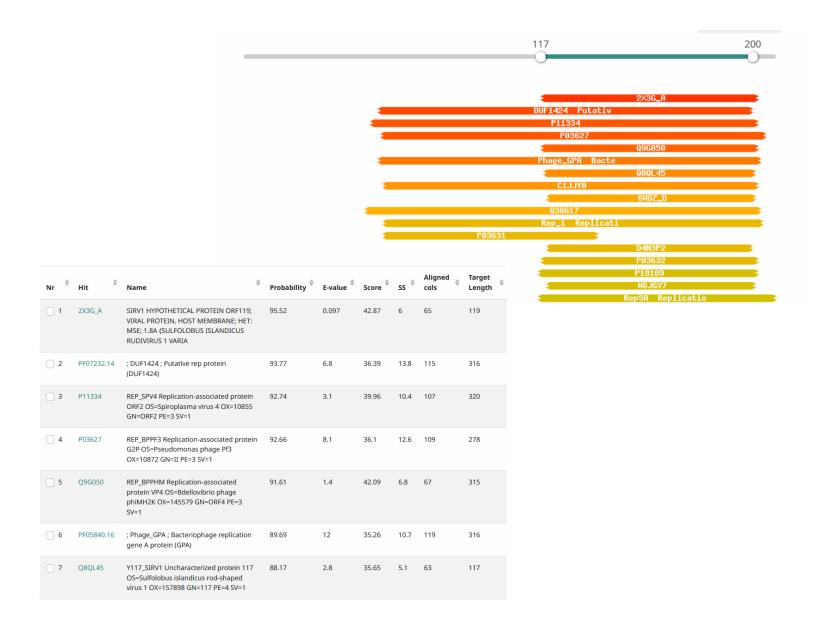
# SF3\_hel1 (Yaravirus gene 69)



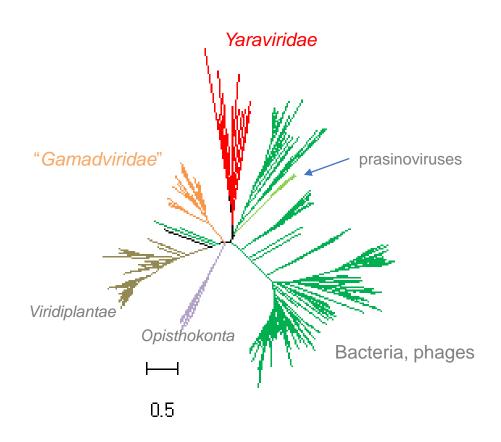
SF3\_hel2



some SF3\_hel2 proteins have frameshifts (marked in orange on the figure).



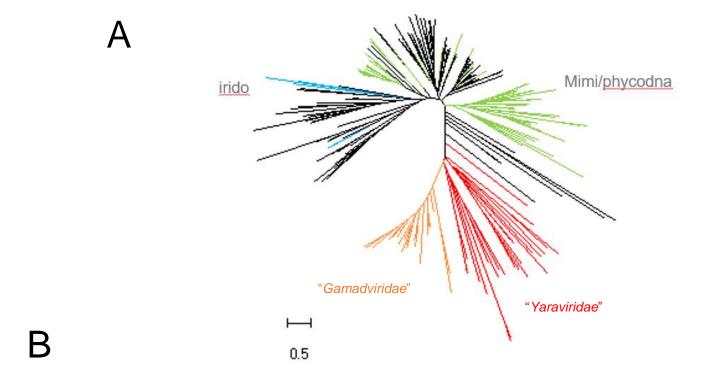
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| Yara@MT293574_2  | :MEGRGEENCETUNGELEINATEH-CAMPAGNIANY   | UVEGYSBAKAYBEALG   |  |  | ING-BREEETGISV   |  | EIRASVEA-BEGSERE-I : 133                             |
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| Yara_contig_15_40  | :mgal  | CLINYTERRELLETER   | FIGUEREBGIV  | IESYMHWGICMECTALAFVIEFFEH  | TIGREFCCBIENIVHGCNHB   | WCGTFTGITBEIGMEIE  | EVECEAHESFELCHE : 110                                |
| Yara_contig_16_7   | : MITHGIEBNITHNIHFAHIEGGGVIHGBIBSMER GS EEGEA  | (VSFVISBBÇIHEBRH   | GNWAFSEVA  | TRMMAH SHA BEAFFICKSWEHT   | TIGBEFCCBIENIVH  | IMIYCCIFICIOWEGGIIVAT  | EIFCEEGI-TVYCIII : 156                               |
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| gamad_contig_24_27   | :MSGICCBTFARHIA BGHEVASNIGAA   | GCVSIVSBAAAYBBAM   | EÇEÇ   | GNIAIHYGNINDANGIVAYCI  | ITG-) V CSTGIFVHFHHIW  | IAGSEIGEVGIEGMI  |  |
| gamad_contig_26_20   | :MASANIÇORTEA HAN BGHI ACNIGSA   | CICENTERÇÇAYNBANGIER   | YALKBBERNIGGWHBBERN VEBALBEI   | GNIATRETHNGANGILAYSA   | HTG-) V E ETGLF VH   | LAGSETCELTGTEGLT<br>LAGSETCEVGTEGLT  | EVBGENWI-BBIGSBI : 147                               |
| gamad_contig_2_32  | :MAHICORSEA YIA BGH W CONIGAL  | C(VSIVSBNEATERCIG  | IEGBEAL-BABE   | IGHE VEHENERCTOR VINSENGIVAYMC   |  | AGSISTIC FOR A SECOND FOR A SEC | FVFGFFYB-BBIGSSB-I : 134<br>FVFGFFYA-BBIGSSB-V : 121 |
| Ga055584_100001079_8<br>Ga0181288_1000587_20   | NAME OF THE PARTY  | CC VSTISBECATERAL  |  | GRNATQRFTIN FRGISATRE  |  | AGSERGEGEEGE   | EVECENTB-BBIGSSB-V : 121                             |
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| G#0335016 0001472 5  | :MISSICCGIFE HEARIG NO ACTUGAN   | CICLWISE VAENBAN   | GIIVEE   | GNIATBY SNN INAILAYSA  | HTG-NI ENTGLEVHEHTEW   | AGSETGIVGTEGN  | PAR GENWH-BG V : 117                                 |
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| Ga0378408_0034991_8  | :NAFIIFSL  | GEGNESBETMIASHRE   | EYVEREKEREV  | GRMCIEGNIC FLAAATIYKIYFI   | HMWBEGSIGYYIESCN   | BGQF LITMELSGBFVE  | EIFTBCWFVEILEENFVE : 114                             |
| G=0485836_0001023_3  | : SILSITA VYEYALYISHIEÇNTLE MSISHB-FHIRASALFAA   | CULIYRTEAKLYBELKI  | ENIVE) VTEYA   | UÇMMDYGRBNDFVAYEVVEKEVKE   |  |  | EIFCFASG-) VYEGI : 149                               |
|  |  |  |  |  |  |  | EVF GENYE-BI : 116                                   |
| Ga0498833_000002_28  | :MGIGYLTBIHYLIEL NG-HE HSCECALS  | ELEÇAÇEHGBKEEKLAC  | ILEE   | ITIRMHSENFIGEVENÇITYIT   |  | GAME CIYIF-ETKCIAI   | INTERPOLE : 120                                      |
| Ga0498922_0001740_24   | :MNCBCGEE INCHYN-AM GEIVANI  | CVIETISEVELEISEC   | BEILELANANTMI  | BIIINNCIBYDIVANEDEINWER  | HRGYIVEYT  | ECG 1:0 YIAEINNEKIV  | PHETHE YEGINEAREYYS : 130                            |
| Estes@JAHIZE010000067_10<br>Ele2@NY346835_28   | :MRREKSCRITEGAYETEMHKI WINGS ETGE V  | CITEACIBBHILEARA   | ECREVILLESSIE  | TIFFIBICIA PERMITVARRATTI  |  | CG 10:11   | ENTENDED FOR THE STREET                              |
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| Vibrio_phage_vE_VnaS_13@UTG75845   | ·PEGRSHE FGA HNFUNG VIGAT  | CLSEENKERTUNESNU   | BAHHGAE-SEEC   | GNIATNYCIVE EMATRICEEI   |  | GASENGE G TTA VI   | FIR SENGH-BNGGE : 120                                |
| u_un_Erck_dsINA_virus@GIF53747   | :MKCRSFE FEA IN-FU ASNUGAD   | CINEYMTBINAMBANU   | BESIGAEBEG   | GN VATENGINN FGAMILYBI   | ETI-HE EEVGEIEHEIW   | ACUSTERCESGENGG  | EIRGENGI-BRAEAIV-E : 121                             |
| unc Caudovirales phage@CAE4157722  | : MECRITE FAR BGB A SUGAI  | GRAFYATBIIVMBBN V  | BEVVGAETEEE  | GNIATEVGIBNDAGALTEVCM  | ETG-NF GFVGFVTBEDW   | AGOSFICESSINYGI  | EIR SEEGI-BRIEVEA : 120                              |
| u.w. Esch_dalRA_virus[CIS2347<br>uc_Candevirale_phage(EA94197022<br>E_Fr_Alphagrot_hacteriumgERC82419702<br>E_Fr_Ender_hioglobusgEII20748<br>E_Fr_EpitacteriumgERC8297741<br>E_Fr_EnderhiomgETA0877741<br>E_Fr_EnderhiomgETA0877741<br>E_Fr_EnderhiomgETA0877741<br>E_Fr_EnderhiomgETA0877741<br>E_Fr_EnderhiomgETA0877741<br>E_Fr_EnderhiomgETA0877741<br>E_Fr_EnderhiomgETA0877741<br>E_Fr_EnderhiomgETA0877741<br>E_Fr_EnderhiomgETA0877741<br>E_Fr_EnderhiomgETA0877741<br>E_Fr_EnderhiomgETA0877741<br>E_Fr_EnderhiomgETA0877741<br>E_Fr_EnderhiomgETA0877741<br>E_Fr_EnderhiomgETA0877741<br>E_Fr_EnderhiomgETA087741<br>E_Fr_EnderhiomgETA087741<br>E_Fr_EnderhiomgETA087741<br>E_Fr_EnderhiomgETA087741<br>E_Fr_EnderhiomgETA087741<br>E_Fr_EnderhiomgETA087741<br>E_Fr_EnderhiomgETA087741<br>E_Fr_EnderhiomgETA087741<br>E_Fr_EnderhiomgETA087741<br>E_Fr_EnderhiomgETA087741<br>E_Fr_EnderhiomgETA087741<br>E_Fr_EnderhiomgETA087741<br>E_Fr_EnderhiomgETA087741<br>E_Fr_EnderhiomgETA087741<br>E_Fr_EnderhiomgETA087741<br>E_Fr_EnderhiomgETA087741<br>E_Fr_EnderhiomgETA087741<br>E_Fr_EnderhiomgETA087741<br>E_Fr_EnderhiomgETA087741<br>E_Fr_EnderhiomgETA087741<br>E_Fr_EnderhiomgETA087741<br>E_Fr_EnderhiomgETA087741<br>E_Fr_EnderhiomgETA087741<br>E_Fr_EnderhiomgETA087741<br>E_Fr_EnderhiomgETA087741<br>E_Fr_EnderhiomgETA087741<br>E_Fr_EnderhiomgETA087741<br>E_Fr_EnderhiomgETA087741<br>E_Fr_EnderhiomgETA087741<br>E_Fr_EnderhiomgETA087741<br>E_Fr_EnderhiomgETA087741<br>E_Fr_EnderhiomgETA087741<br>E_Fr_EnderhiomgETA087741<br>E_Fr_EnderhiomgETA087741<br>E_Fr_EnderhiomgETA087741<br>E_Fr_EnderhiomgETA087741<br>E_Fr_EnderhiomgETA087741<br>E_Fr_EnderhiomgETA087741<br>E_Fr_EnderhiomgETA087741<br>E_Fr_EnderhiomgETA087741<br>E_Fr_EnderhiomgETA087741<br>E_Fr_EnderhiomgETA087741<br>E_Fr_EnderhiomgETA087741<br>E_Fr_EnderhiomgETA087741<br>E_Fr_EnderhiomgETA087741<br>E_Fr_EnderhiomgETA087741<br>E_Fr_EnderhiomgETA087741<br>E_Fr_EnderhiomgETA087741<br>E_Fr_EnderhiomgETA087741<br>E_Fr_EnderhiomgETA087741<br>E_Fr_EnderhiomgETA087741<br>E_Fr_EnderhiomgETA087741<br>E_Fr_EnderhiomgETA087741<br>E_Fr_EnderhiomgETA087741<br>E_Fr_EnderhiomgETA087741<br>E_Fr_EnderhiomgETA087741<br>E_Fr_EnderhiomgETA087741<br>E_Fr_EnderhiomgETA08774 | :MTENINGBSSE HAA EN-BU A NEATA   | @INCYMSBACIMBECI   |  | GNEATQHEVINDATAIELYEG  | VIG-HQ VEIGIHIHBEEEC   | GCSERGIIGSIGG  | EVE GENYHMC : 118                                    |
| E_Fr_Cand_Thioglobus@HII20745  | :G.BCGAT   | GINEYSKEKI VIBEMI  | BEHE) VEBEFA   | GNEATEXCNTH-GSAINAYES  |  | EYSERCSTASEAL  | ECF GSESB-BI : 121                                   |
| E_Fr_Epibacterium@MCJ8334600   | :  | CISEHISÇKAAWBSIV   | BEVHGGEDIME  | INFAMAKCBMHDIGABGEYIW  | ETG-NA-T(VGEVEV  | AGASEIGIVGEIGII  | PHFCHESI-BCEGE: 118                                  |
| E_Fr_Halothiobacillus@MEA3877741   | :AECRIFE EEA BGBW A AUGAI  | CPAFTASBILIMBBN V  | BESCGAESEES  | GNIATEWGINNDAGAIVEWCM  | EIG-II IFVGFVIBEIG   | AGCSENGINGIIGGN  | ENE  |
| E_Er_Froteob_bacterium@MIA0664245  | :MHNTTELBGGTAE LLA BNL GENESAA   | CUNBURSBAALWREYK   | NIVESET  | GNAATRECCENT FIVIAGYEH   | APG-CS VPTGIHIHSSIIW   | EGCSFICT   | EIFCEFNHFEF : 120                                    |
| E_Fs_Microbulbifer_thermotolerans@WF_266066192   | :MSNIEGCNAD HKQ: AGRIM G: FUGAD  | CRSEEARGEIVIBERU   | BIYHGAE-BEFE   | GIVATENGNEHDNTAIAAIEG  | ETG-E1:ISTGEFVH  | GASERGIIGIIGIV   | EIRCENGI-BNSISEE : 125                               |
| E_Te_Cyanobium@MAE41647  | :MGBTAEFEGN:BNN-A-FVGAA  | CC VALUEBRANTERAL  | G-IISFE  | GRIATEWIAHDEEALAN  | YEB-CT GETGIHGH  | AGSFICIGIIGI   | FVFGENEG-IYBGF: 114<br>BINGENEGH-BHIGNII-I: 126      |
| I_me_ididmarinaceae_pnage_Eniim2_2grE_009104296  | :  | CISESTELL VERENU   | BEINGAL-BEEK   | CALLED CONTRACTOR OF THE CALLED  | EIG-NI EEREI\VEIG-FI   | GGS IFGFIGNG   | W GSAG-GI : 121                                      |
| T He uncultured Caudovirales phagegone 153635  |  | CIGE-MESQUIMESMS   |  | GNEAT GREEN VIEW TOUGHT AND VIEW TOUGHT AN     | WINCOMF CUGFUD   | GASE FTS G. TPG  | EIFI: 121  |
| E Ha Chrusochronulina tobinii8ECC22991   | ·MTTALCGGTER HAN NG NO AS NUGAR  | CICINTSREVAENBAN   | GTTTEE   | GNTATBICSNN-ENATIAYSA  |  | AGSTRICTS GTEGN  | A  |
| E Vi Carica papaya@XE 021899674  | :IIHSSGICHWENN CEC BHB A TEGGA   | FWE-RREVCIALENI  | GAIEFES  | GNIATC SNIM-EEALERY  | ITG-NT LFENECIYGENHFEDIW   | AASISIGUSIHIVYGISSEGIN   | ETFGEFEN-GIMSNAS-E : 135                             |
| E_Vi_Manihot_esculenta@XE_021633438  | :CITHECVICESEE FAL BIB A TESTA   | CEWEGNBBLELWNERU   | BAFELNITE  | ASKRIVEXCVINGARIVISYKI   | ITS-HE NHIGEAIHFACEEIW   | UGASERGIIII  | EVE GENNEGHESALE : 129                               |
| E_Vi_Spirodela_intermedia@CAA2628851   | :  | CEWEGNERSELWHOLV   | ESFIAITIS  | SIGBAAMEK VINGAAAIEBYBS  | ITG-DE GTIGEAMHFIASEAW   | GASERGUIGEGFEGGII  | EVEGEENKGREEIGIE : 134                               |
| Yara@MT293574_2<br>Yara_contig_13_10   | A 260 A 280 : IFV FBIIF IIQ CLIGBRECL AB- NGBNAIG  | * 300<br>MICEYEAT-IMGLIENTIES  | ^ 320 ^ 340 VCHHINIBEFFHN-MTMGSEGWIAB  | CCLELEMICYNCHEVRALEFIEFEHREFH  | * 400 * 420  | * 440 *<br>:: 242  |  |
|  | : HIHEFIHYLLOWMIQEHITEVIGENEVS-ETFSYIN   | EBBERLLE-AWHYDDELDID   | ITTYINGSNN#FETIGHNIHH VTILLEN  | VERETYBESIWEIE-INNSCHSHELYNGIGWBEIGTGE   |  | : 322  |  |
| Yara contio 15 40  | <ul> <li>YETHILLIFI-NYEARHICTYHELLNAFHGYIVC-HTMENGMSH</li> </ul>   | ENABBLICMEEBINIELIIS   | KVVGDISENTRGE  | BNYHARMIAENTEVERII   |  | : 202  |  |
| Yara_contig_15_40<br>Yara_contig_16_7  | : YET ILIEL-NYEA GIY ELINAFHGYIVC-TMENGMS<br>: SIT ILNELHYICOSO LATGCKGGY AC-TELHTL  | EVERBRICHEERIVIELIES<br>IV:FASSECENKEVETEUCE   | VGIISEFVINGEWISHIEG  | EFVYCIGWSGC-CWFBRYNTNENHILNYICECCI   | NTFFVLIATISAGTVSSNIIIGGCTCTSLA   | GECTELBH: 202  |  |
| Yara_contig_15_40<br>Yara_contig_16_7<br>Yara_contio 1 89  | : YETGILIFI-KYEAG #GTY ELINAFHGYIVC-KTMEMGMS<br>: SIT IIKEIHYICKGSQ IATGCKGGY#AC-#TFIKTL<br>: BFY#KNSHYICKGME-MATSTIVGF#YU-KTFEESD   | FUTHERICMEERIVIELIES<br>IY: FASSECEMENTELIUGE<br>ARTHRAREM-ECRIVICKAED   | YCGSSIC FSEWISHIEG<br>YCGSSIC FSEWISHIEG<br>FILEFURENLEFNE-FURGINICWIYFUND   | EF VYCIGWSGC-CWERRYRTNERRMINYICECGI<br>SCISCICEIW VIA-RGIEGYTEFIEWS VSRIYENAGU   | NTEF VLIATISAGI VSSKI LIGGCICISLA  | : 202<br>:GEÇTELBK:: 304<br>:: 290   |  |
| Yara_contig_15_40<br>Yara_contig_16_7<br>Yara_contig_1_95<br>gamad_contig_24_27  | : YETGILIFI-KYEAG #GTY ELINAFHGYIVC-KTMEMGMS<br>: SIT IIKEIHYICKGSQ IATGCKGGY#AC-#TFIKTL<br>: BFY#KNSHYICKGME-MATSTIVGF#YU-KTFEESD   | FUTHERICMEERIVIELIES<br>IY: FASSECEMENTELIUGE<br>ARTHRAREM-ECRIVICKAED   | YCGSSIC FSEWISHIEG<br>YCGSSIC FSEWISHIEG<br>FILEFURENLEFNE-FURGINICWIYFUND   | EF VYCIGWSGC-CWERRYRTNERRMINYICECGI<br>SCISCICEIW VIA-RGIEGYTEFIEWS VSRIYENAGU   | NTEF VLIATISAGI VSSKI LIGGCICISLA  | : 202<br>:GEÇTELBK:: 304<br>:: 290   |  |
| Yara_contig_16_10 Yara_contig_16_7 Yara_contig_16_7 Gamad_contig_24_27 Gamad_contig_24_27  | : YE: LIIEL-NYE. CIT EILMEHCYIVC- THE-MGMS: SIT IIHE-HY! CSC LAIGCHGEVAC- IFINYI BEY N-N-SHYI CME NATSIIVGE NV- IEEESI : HSI IEHY! NAL EZIGERACI VC- ZEEGSV HS TEHY! NAL EZIGERACI VC- ZEEGSV  | EV HRNICMEERIVIEIIIS IY: FASSECEMES UTIFUÇE AN UNAAEM-EÇALUIÇKAEI YE UBIAÇ-VELELITYYEÇ YE TRIKE-LHEALMEÇYIN  | VGILSEFUTKEEWISHIEG<br>YCGSSIC#SFWISHIEG<br>IIIFUBERIF#RB-FURGIRIUWTFUKE<br>  TAAMCAGASN#EF-INBIERIKIEYEIGE<br>  TAAMCMMACAFULITEIRRFIERIUWE   |  |  | : 202<br>GEGTELBN : 304<br>:   |  |
| Yara_contig_16,7 Yara_contig_16,7 Yara_contig_1,86 gamad_contig_26,27 gamad_contig_26,20 gamad_contig_26,20  | : YEN ITTEL-MERA CTW DIMARBETTUC- THE-MGMS; SETT HIME-THELOUGO TANGERROFT AC-TETHIL SETY BW-SRIT COME MAISTINGEN TO TEZEST HEN FEHYM WALL BINGEOUS VC-A CGN THE FEHYM WALL STREET TE CGN THE FAHYM WALL STREET THE THE THE   | EVHABNICHEBRUIELLIS IY EASSECEMBUETHUGE AF WAAEN-EGALVICHAE YE UNDAG-VEIELITYGG YE INDINE-HEALMGGYIN EE HOTILTETYLISYNA  | VVG-TISETTINGE   |  | NIEPVLIATISAGIVSSBILIGGCICTSLA   | . 202 GECTIERN   |  |
| Yara_contig_1E, 40 Yara_contig_1E, 7 Yara_contig_1E, 85 gamad_contig_2E, 27 gamad_contig_2E, 20 gamad_contig_2E, 20 gamad_contig_2E, 20 Gamad_contig_2E, 20  | THE STATE OF THE S | EV HBBICKEEBIUSELIIS<br>IY BASSECEMBUSTUCKABI<br>YB UMBAGM-EGAIUICKABI<br>YB UMBAG-UETELIYYEG<br>YB IBINE-IHBAIMGCYIN<br>EBUHBITI-IEIYIISYYAJ<br>YB UMBE-IEIYIICHYIA   | VVCLISEFUTNCE  | -BUYCLORSCC. CHERRICARY LURITELVYCLORSCC. CHERRY LURITRERMITHINICCCL:SCLESICETUVIA-ROCHEVITETERK VURSTURAKYAIDSVUCTERKESUCCHELESSIETEREUSUCCHULTERKE VVIALDEFRETEVILMMSBURGSAMIRKULTIFURAE HINTERRETES   | WIFVULATISACIVASHILGGGCCISIA TREMNANFULIERINI ERICATIFFANNOHLEVAGEE BGGASGERE SELVASEASHANIANELEGGE BELVASEASHGGGIVCITIAGYCHWCTAKISII IIFAANGGIZESETTEGGSHIVETENGNIVCIEN   |  |  |
| Yara_contig_1E, 40 Yara_contig_1E, 7 Yara_contig_1E, 85 gamad_contig_2E, 27 gamad_contig_2E, 20 gamad_contig_2E, 20 gamad_contig_2E, 20 Gamad_contig_2E, 20  | THE STATE OF THE S | EV HBBICKEEBIUSELIIS<br>IY BASSECEMBUSTUCKABI<br>YB UMBAGM-EGAIUICKABI<br>YB UMBAG-UETELIYYEG<br>YB IBINE-IHBAIMGCYIN<br>EBUHBITI-IEIYIISYYAJ<br>YB UMBE-IEIYIICHYIA   | VVCLISEFUTNCE  | -BUYCLORSCC. CHERRICARY LURITELVYCLORSCC. CHERRY LURITRERMITHINICCCL:SCLESICETUVIA-ROCHEVITETERK VURSTURAKYAIDSVUCTERKESUCCHELESSIETEREUSUCCHULTERKE VVIALDEFRETEVILMMSBURGSAMIRKULTIFURAE HINTERRETES   | WIFVULATISACIVASHILGGGCCISIA TREMNANFULIERINI ERICATIFFANNOHLEVAGEE BGGASGERE SELVASEASHANIANELEGGE BELVASEASHGGGIVCITIAGYCHWCTAKISII IIFAANGGIZESETTEGGSHIVETENGNIVCIEN   |  |  |
| Yara_contig_1E, 40 Yara_contig_1E, 7 Yara_contig_1E, 85 gamad_contig_2E, 27 gamad_contig_2E, 20 gamad_contig_2E, 20 gamad_contig_2E, 20 Gamad_contig_2E, 20  | THE STATE OF THE S | EV HBBICKEEBIUSELIIS<br>IY BASSECEMBUSTUCKABI<br>YB UMBAGM-EGAIUICKABI<br>YB UMBAG-UETELIYYEG<br>YB IBINE-IHBAIMGCYIN<br>EBUHBITI-IEIYIISYYAJ<br>YB UMBE-IEIYIICHYIA   | VVCLISEFUTNCE  | -BUYCLORSCC. CHERRICARY LURITELVYCLORSCC. CHERRY LURITRERMITHINICCCL:SCLESICETUVIA-ROCHEVITETERK VURSTURAKYAIDSVUCTERKESUCCHELESSIETEREUSUCCHULTERKE VVIALDEFRETEVILMMSBURGSAMIRKULTIFURAE HINTERRETES   | WIFVULATISACIVESELIGGCICISLA TREMNANFLITENTI ELECATIF SANDRUK VANCEL BGGASCERE SELVETATI SANDRUK VANCEL BGGASCERE BELVETAS SANDRUK VANCEL SANDRUK VANCEL SANDRUK VANCEL SANDRUK VANCEL SANDRUK VANCEL S  |  |  |
| Yara_contig_1E, 40 Yara_contig_1E, 7 Yara_contig_1E, 85 gamad_contig_2E, 27 gamad_contig_2E, 20 gamad_contig_2E, 20 gamad_contig_2E, 20 Gamad_contig_2E, 20  | THE STATE OF THE S | EV HBBICKEEBIUSELIIS<br>IY BASSECEMBUSTUCKABI<br>YB UMBAGM-EGAIUICKABI<br>YB UMBAG-UETELIYYEG<br>YB IBINE-IHBAIMGCYIN<br>EBUHBITI-IEIYIISYYAJ<br>YB UMBE-IEIYIICHYIA   | VVCLISEFUTNCE  | -BUYCLORSCC. CHERRICARY LURITELVYCLORSCC. CHERRY LURITRERMITHINICCCL:SCLESICETUVIA-ROCHEVITETERK VURSTURAKYAIDSVUCTERKESUCCHELESSIETEREUSUCCHULTERKE VVIALDEFRETEVILMMSBURGSAMIRKULTIFURAE HINTERRETES   | WIFVULATISACIVESELIGGCICISLA TREMNANFLITENTI ELECATIF SANDRUK VANCEL BGGASCERE SELVETATI SANDRUK VANCEL BGGASCERE BELVETAS SANDRUK VANCEL SANDRUK VANCEL SANDRUK VANCEL SANDRUK VANCEL SANDRUK VANCEL S  |  |  |
| Yara_contig_18, 40 Yara_contig_18, 7 Yara_contig_18, 7 Yara_contig_18, 95 gamad_contig_26, 27 gamad_contig_26, 20 gamad_contig_26, 20 Gamad_contig_19, 20 Gamad_contig   | 121   111    | I'V HANICHERSIUETITS TY FASSEGERMY FITUGE AN NAARN-EGATUGEAET YE UBIAG-UETEITYYGG YE THEE-HERAIMGYUM EF HHII-TETYILSYMA YE YELE-TETYILGYMA YE THEE-HERAIMGYUM YE THEE-HERYILISYUG BB HEUR-LWEGHERHG-   | VNG-LISSVINGE KISHIEG IIIIUSENIESS J-JACISITSTI VBS IIIIUSENIESS J-JACISITSTI VBS IIIIUSENIESS J-JACISITSTI VBS IIIIUSENIESS J-JACISITSTI VBS IIIIUSENIESS J-LISSI INSTITUTIONI INSIITATI INSTITUTIONI INSTITUTIONI INSTITUTIONI INSIITATI I              |  | NIEPVIINIERGUSSELIIGGCICISIA TREMNANTILIERNI DEURANTILIERNI DEURANTILIERNI DEURANTIA IRANGEL BGGASCIERE SERIVSEESSEGGE VOLTITAKTON VOLTASIII TIERANGGRIERESTEGESETITTEGIGNI VOLTA TESCHIERGEREARA DEURANGGRIERESTEGESTEGENEESSEGE      | 202  |  |
| Yara_contig_18, 40 Yara_contig_18, 7 Yara_contig_18, 7 Yara_contig_18, 95 gamad_contig_26, 27 gamad_contig_26, 20 gamad_contig_26, 20 Gamad_contig_19, 20 Gamad_contig   | 121   111    | I'V HANICHERSIUETITS TY FASSEGERMY FITUGE AN NAARN-EGATUGEAET YE UBIAG-UETEITYYGG YE THEE-HERAIMGYUM EF HHII-TETYILSYMA YE YELE-TETYILGYMA YE THEE-HERAIMGYUM YE THEE-HERYILISYUG BB HEUR-LWEGHERHG-   | VNG-LISSVINGE KISHIEG IIIIUSENIESS J-JACISITSTI VBS IIIIUSENIESS J-JACISITSTI VBS IIIIUSENIESS J-JACISITSTI VBS IIIIUSENIESS J-JACISITSTI VBS IIIIUSENIESS J-LISSI INSTITUTIONI INSIITATI INSTITUTIONI INSTITUTIONI INSTITUTIONI INSIITATI I              |  | NIEPVIINIERGUSSELIIGGCICISIA TREMNANTILIERNI DEURANTILIERNI DEURANTILIERNI DEURANTIA IRANGEL BGGASCIERE SERIVSEESSEGGE VOLTITAKTON VOLTASIII TIERANGGRIERESTEGESETITTEGIGNI VOLTA TESCHIERGEREARA DEURANGGRIERESTEGESTEGENEESSEGE      | 202  |  |
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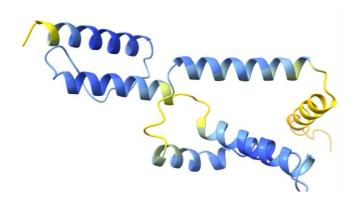


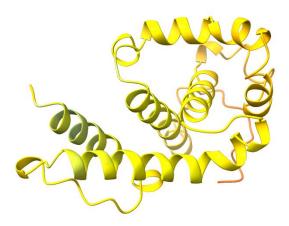
## gene48 with nr hits

|  | . 20   |              | 40                      |  |                                | 80 .                                   | 100                          | . 120                        |                   | 140       | 160                          | . 100                                 | * 300                       | . 22  |  | . 250                                  |
|--|--|--------------|-------------------------|--|--------------------------------|--|------------------------------|------------------------------|-------------------|-----------|------------------------------|---------------------------------------|-----------------------------|---|--|--|
| gene48_with_nr_consensus   | :SSEEKPSPQMSYE-                                |              | -EE SEL N               | ERL-EKKGFPV<br>RAVLVKMFPSAT                          | NKRYNME-SSEE                   | RODYER KEELDKE                         | -NSIKEQRE                    | RMIMACTE                     | FLNNRF            |           | O DEWSESVOEN                 |                                       | MKSKAKMAS<br>NCVVE-EEKSSV   |   | MFKSAMPNMDDVMKQNFDL                            | MKQMASAAQNSMG                          |
| ORF056L NF 612278<br>B PV Verrucomicrobia bacterium@MBS0654651                                       | :AMESLNKKMQTET-                                |              |                         | YAYRRHFPKLD  | YSSMPDT-ASFE                   | AWSAFLED VNCNAEE                       | -GSVQTLKH                    |                              | WEVILGEL          | N         | D REFAHQQIQG<br>N RTLPAVAKTA | IHEKNFLEKEFOR                         | ENCVVEEEKSSVE<br>LHPEWCRPGE |   | TGAVYTAPED                                     | WEMFLPKEG                              |
| Verruc@JAFEGS010000061_7<br>Ga0456371 00004425 32  | :CTET-   |              | -GDVARIOSC              | YAYRRHEPKLC  | YSSMPDT-ASFE                   | AWSAFLED VNCNAEE                       | GSVCTLKE                     | HVYCILLEVG RE                | NMFLG<br>FSCTTLVF | I-G       | N RTLPAVAKTA                 |                                       | LHPENCRPG                   | FARICIATLGLIREVHNAE   | TGAVYTAPED<br>CEAMCLDF                         | SKTVSSRATNKYS                          |
| Yara contig 13 23  | :  | EIV          | -RESVLOFY               | FWPEYE   | PRSPPRDDAP E                   | VWER LTR WSTKINT-                      | -DAFPMMKG                    | LFNAM GE                     | FFGALY            | (FPS)     | Q RELTLELSSBLPE              | VKAL-NIEDDIKEET                       | GHLLKVCV                    | LSU GKIVYAIHMM  |  | HVMAAEVSPNKMD                          |
| B_Te_Mycoplasmataceae_bacterium@MBR2022471<br>E_Vi_Tetradesmus_obliquus@WIA10847                     | :DPPVNNLEILHA-<br>: CDAAAIDCEOCOPGPOPGGEYV-    |              | NTORELDY:<br>DELADLTF:  | QQL-QNKLYDVEI  | -NPKTYTTA-DS S<br>RRFAGCSIAD R | E GS FDR TIIKNGK-<br>D RA FNR KTETEFD- |                              | KILFGVTKE<br>KALCGVTSV       | MEMENGKA          | G F-D     | M DEWSTEIASN                 | ADEFDE FD NT                          | GGTFGVEKKIA                 |   | LTSSYNNRPEFSEIINKDFVL<br>MFKCAMLSGGGANFDF      | RERFLKTATEIQL                          |
| B_FC_Flavobacteriaceae_bacterium@MBT7243665  | :PAPAPAPRLTEA-<br>: SSTSSTVDKKKOKRVTKENKSE-    |              | -AE FKY RY<br>-KE SEL Y | ESL-EKKGIPV  | SRKYDMK-SP D                   | E KARYEL KGECEKK                       |                              | KMLMAA Te                    | Maylnskf          | III F-D   | O NewGESVEEN                 | KEEYSD FASHH                          | KTKASIA                     | IND FLOAGSATMVHMT   | MFCPCLFGMEDLVCHNFEL                            | ANRIAGAAADGLV                          |
| Bun_bacterium@NBU33705<br>Bun_bacterium@NDC95014   | :SSIVDKKKGKRVEKENKND-                          | DIR          | -KE SEL 1               | FNKMNVKGKWS  | SLKLDMN-SS D                   | E RN YER RNEIGTE                       | -RSVGFFKF                    | RMLLLG Q c                   | MINTER            | M-G       | DED:WSESMGYS                 | MENG-EYBE LASHY                       | KGRGCMS                     | L HE FM USSGVMFSISK   |  | LKNFMGASQSQQP                          |
| B_un_bacterium@NDD83477<br>B_un_bacterium@NDG30840   | :SSIVDKKKGKRVEKENKND-<br>:SSIVDKKKGKRVEKENKND- | DIR          | -KO SEF Y               | FNKMNVRGKWS  | SLKLDMN-SS D                   | E RN YER RNEIGTE                       |                              | RMLLLG CC<br>RMLLLG CC       | MEMLNTKF          | BEM-G     | DEDEWSESMGYS                 | MENG-EYDEULASHYI<br>MENG-EYDEULASHYI  | KGRGCMS                     | LNOV FM ISSGVMFSISK   | ITKMDAASL                                      | LKNFMGASQSQQP                          |
| B un bacterium@NBX51244  | :AESSVVESDYPRRMSNE-                            | EII          | -CANCEL YO              | FDRL-EKKGMRL   | PRKFTMC-SS E                   | D KAPYAR KROREID                       | -NSIKEGRP                    | KVMMAV Se                    | WELLNNKF          | DFF-N     | ON NEWSDSVHDN                | I                                     | SGKAKIA                     | I DO MM GGSAF   |  |  |
| V_Ba_Yellowstone_lake_phycodnavirus_3@YP_009174394<br>B un bacterium@NBX49648                        | : GEGGSSQCMPSEGYK-                             |              | -DE ADL N               | MARL-VKKGIAS   | SQRLTIY-SD E<br>SNRLTSY-SD E   |  |                              | RMLIACTT                     | MEFLNDKF          | 0 F-D     | ENCWSCNAMEN                  | VEDYDG FE WY                          | KTKVCVA                     |   | MFKAAVPNVNGVMGGNPEL<br>MFKSAMPNMNGVLKGNPDL     | MRNMVAAVERTNN<br>VKNMVDAVQRTQN         |
| V_Ba_Dishui_lake_phycodnavirus_1@YP_009465773  | : RSAPQQAQPSS-G-YS-                            | TID          | -DE CDL S               | QRLGCKKGVVV  | NKRLNVY-TPEE                   | D RASYKR TYGIEIE-                      | -QSVKFSRF                    | RALVACLTE                    | WINKRY            | II L-S    | ENNEWSESVMES                 | LDDYDP LEST A                         | KNSMCMAS                    | V 30 MM AGSGFAFHLS  | MFKALPNMTDVLKQNFEL                             | VGCMFSAVCKTCA                          |
| B_FC_Flavobacteriaceae_bacterium@MDA9846582<br>B Pr Betaproteobacteria bacterium@MBT6185503          | : GGGGGDEPSR-G-YH-<br>: APEEEAEGPSP-G-YK-      |              | -DE ADL N               | ARL-EKKGFNV  | NKRLNAY-SS S<br>NKRMNVY-SN E   | E RT YKR TYSIEVD<br>D RT VKR TYSIDVD   |                              | RMLVACTS                     | MOFWNKRY          |           | Y ESWSESVVEN                 | LDDYDG FED Y                          | KTKMNVA                     | IN MM GGSAMMFHLT  | MFKSAIPNMNCVLKKNPCL<br>MFKCVMPNMNCVMKCNPCL     | VKSMVEAVQNNGQ<br>VCNMMSAVCTTMA         |
| B_un_bacterium@MDB4346067<br>B_Te_Dehalococcoidia_bacterium@MAT63669                                 | : MEPPEDTPSP-G-YK-<br>:FDYGCMEPCEECPSPGYK-     |              | -EE SDL N               | GRL-EKRGENV  | NKRLNAY-SP D<br>NKRLNAY-SP D   | E RT VKR TYSIEVD                       |                              | RMLIACTE                     | #FLNKRY           | WF-D      | CHECWSENVMET                 | CDDYDE FERRE                          | RTKMNIA                     |   | MFKCVMPNMNDVMKCNPDL<br>MFKSVMPNVNDVMKCNPDL     | VNNMMSAVQNTMA                          |
| V Ba Bathycoccus sp RCC716 virus@CCR60318  | : GGYMMEEEEKPSP-G-FK-                          | TVD          | -EE ADL N               | GRL-EKKGFTV  | NKRLNAY-SP D                   | E RN VKR TYSIDVD                       | -KSIKESRE                    | RMLIACTT:                    | FMNKKY            |           | Q DEWSENVMEN                 | VEDYDEN FERRY                         | AN RSKMHVA                  | I WO MM GGSAMMFHLT  | MFKSVMPNMNDVIKQNFGL                            | VQNMVSAVQNTVP                          |
| N Ph Bathycoccus sp RCC1105 virus@ADQ91226<br>V Ba Prasinovirus@BCV07047                             | : GGYMMEEEEEKPSP-G-FK-<br>: VPDGGMEEDKPSPGFK-  |              | -EE ADL N               | GRL-EKKGFTV  | NKRLNAY-SP D                   | E RNOVKR TYSIDVD                       |                              | RMLIACTT                     | DEFLNKKY          |           | O DOWSENVMEN                 | VDDYDE FERRY<br>VDDYDE FERRY          | A RTKMHVA                   |   | MFKSVMPNMNDVIKCNPGL<br>MFKSVMPNMNDVIKCNPEL     | VCNMMSAVCNTVP                          |
| V Ba Bathycoccus sp RCC716 virus@QCR60636  | : GGIGGMSGGPYMEEEQPSPGYK-                      | TID          | -EE ADL N               | GRL-EKKGFTV  | NKRLNAY-SP D                   | E RT VKR TYSIDVD                       | -KSIKESRE                    | RMLIACTT                     | FMNKKY            | F-E       | Q DOWSENVMEN                 | VEDYDEV FEEL Y                        | RSKMHVA                     | INDUMNIGGSAMMFHLT   | MFKSVMPNMNDVIKQNPEL                            | VQNMMSAVQNTVP                          |
| B FC Flavobacteriales bacterium@MDB4676333<br>V Ba Dishui Lake phycodnavirus 3@QIG59670              | : MQPEEERPSP-G-YK-<br>: GYEQEERPSN-G-FT-       |              | -EE ADI N               | GRL-EKKGFTV  | NKRLNVY-SN D<br>NKRLTAY-SS E   |  |                              | RMLIACTT                     | FINKRY            |           | CHECWSENVMEN                 | VDDYDEV FERRY<br>CDDYDN FERRY         | ASSETKVNVASS                |   | MFKSVMPNMNDILKQNPAL<br>MMKAALPNMNDVLKQNPDL     | VQNMVDAVKNTTP                          |
| B un bacterium@MDB4588379  | : GGYEAEGPSP-G-FN-                             |              | -DE ADL N               | TRL-EKKGFSV  | NKRLNAY-SS C                   | E-RT-YKR-TYSIEVD-                      |                              | RMLVAC                       | ##FLNKRY          | F-E       | AHDEWSESVMEN                 | MDDYDG FE Y                           | ES KTKMHVA                  |   | MFKAAIPNMNCVVKCNFCL                            | VKSMMSAVQNTTR                          |
| N_Ph_Micromonas_pusilla_virus_12T@YP_007676125<br>B_FC_Bacteroidetes_bacterium@NBV31910              | : GGYTEEQPSK-G-YA-                             |              |                         | ARL-EKKGVNT  | NKRLNAY-SH                     | E RT VKR TYGIEVD<br>E RT VKR TYSIEVE   | -QSVKESRE                    | RMLVAC T<br>RMLIAC T         | MEFLNKRY          |           | OLESWSENVMES                 | VEDYDTV FESSIY<br>VDYDGV FESSIH.      | A W KNKWKWA:                | INDUMNIGGSAMMFHLT   | MFKAALPNMGDVLKQNFGL                            | VQNMMSAVQN-TQ                          |
| B_un_bacterium@MBE29209<br>N Ph Micromonas pusilla virus SP1@YP 009665108                            | : PGMQEEKPSS-G-YT-<br>: ISQEEQPSK-G-YT-        |              | -EE SDL N               | ARL-EKKGFAV<br>TRL-EKKGFAV                           | NKRLTAY-SN D<br>NKRLNAY-SN E   |  |                              | RMXVAC Te                    | #FLNKRY           |           | QXECWSESVMEN                 | VDDYDSVFEEHY<br>VDDYDTVFEEHY          | AWRSKVSVA                   | V: MM GGSAMMFHLT  | MFKTAIPNMNDVIKQNPDL<br>MFKSVMPNMNDVIKQNPDL     | VKNMMQAVQNTTR                          |
| B Te Chloroflexi bacterium@MAX12437  | : PGEGGEGPSK-G-YT-                             | SID          | -EE SDL N               | ARL-EKKGFAV  | NKRLNAY-SN D                   | E RSPVKR TYSIDVE                       | -CSIRFSRF                    | RMLIAC Te                    | FLNKRY            |           | OFECWSESVMEN                 | VDDYDG FEED Y                         | AWRSKVSVA                   | VELLIMM GGSAMMFHLT  | MFKSVMPNMNDVIKQNPDL                            | VKNMMAAVQNTTR                          |
| V Ba Micromonas pusilla virus PL10AET43745<br>B FV Akkermansiaceae bacterium0MDB4675786              | : PSGEGPSK-G-YT-<br>:AGEEGPSKGYT-              |              | -EE SDL N               | TRL-EKKGESV  | NKRLNAY-SN E<br>NKRLNAY-SN E   |  |                              | RMLVACTT                     | MOFINKRY          |           | CHECWSESIMEN                 | VDDYDGE FERRY<br>VDDYDGE FERRY        | AWRSKVSVA                   |   | MFKSVMPNMNDVMKCNPDL<br>MFKSVMPNMNDVMKCNPDL     | VKNMMNAVCNTTR                          |
| B Te Dehalococcoidia bacterium@MAT63500  | : FQEETPSK-G-YT-<br>: FGMCEERPSK-G-YS-         | SID          | -EE SEL N               | ARL-EKKGFAI  | NKRLNAY-SN E                   |  | -CSIRESRE                    | RMLVAC TE                    | FLNKRY            | F-E       | QUESWSESVMEN                 | VDDYDG FEED Y                         | RSKVSVA                     | V:00 MM GGSAMMFHLT  | MFK-SVMPNM-NEVMKQNFEL<br>MFK-SALPNM-NEVLKCNFEL | VKNMMAAVQNTTR                          |
| V Ba Ostreococcus lucimarinus virus 10YF 004061703<br>V Ba Ostreococcus tauri virus RT 20110AFC34977 | : FGMGEERPSK-G-YS-<br>: GAGSEEAPSK-G-YS-       |              | -EE SDL N               | ARL-EKKGFTV  | NKRLTAY-SN D<br>NKRLNAY-SN E   | RT VKR TYSIDVE                         | -CSIRESRE                    | RMLVACTTG<br>RMLVACTTG       | #FLNKRY           |           | CHECWSESVMEN                 | VDDYDG FEED Y<br>VDDYDG FEED Y        | ASSKVNVA                    |   | MFKSALPNMNDVLKCNPEL<br>MFKSALPNMNDVLKCNPDL     | IKNMMSAVQNTTR<br>VKNMMSAVQNTTR         |
| B PV Verrucomicrobiales bacterium@MAB60941   | : MSMGGEGPSK-G-YS-                             |              | -EE SDL N               | GRL-EKKGFAV<br>RRL-QSKGIE                            | NKRLNAY-SSE<br>GVKMNMT-NSE     | D RT VKR TYSIDVE<br>E KA YSR SDSAGLE   | -CSIRFSRF                    | RMLVACVT:                    | Maringer          | F-E       | CHECWSESVMEN                 | VDDYDGVFE WY                          | RSKVNVA                     | V:00 MM GGSAMMFHLT:   | MFKSALPNMNDVLKQNFDL<br>FFR-SSKMPGMDEVLKRNFDL   | VKNMMSAVQNTTR                          |
| B Te Actinobacteria bacterium@NBU23896<br>B FC Bacteroidetes bacterium@NBF65703                      | :SISLTPAPPRDFE-                                |              | -CE IEY N               | QRL-ETKGYPV  | SKRFTMD-NTNE                   |  |                              | MLMGA Te                     | WMNDKF            | DE F-D    | KHQCWSESVHTN                 | VEDEDENFERNY                          | KDRGKMP                     |   | FFR-QKMPSMDDVLKSNEML                           | AKQMAQAAATQAG                          |
| B FC Flavobacteriia bacterium@NBC60610<br>B Te Actinobacteria bacterium@NBC09652                     | :VAFSPAGGGRDPE-<br>: ITLATAGREPE-              |              | -KD IEY N               | QRL-EQKGFPV  | ARRETMD-NS D                   |  |                              | DALMGV Te                    | MOWINGRE          | DE F-D    | N Dewsesvhen                 | AEDEDE FERRY                          | KDRGKMP                     |   | FMKQRMPSAADVLKNNPEL<br>FFRSKMPTMDDVLKRNPEL     | ARQFAAAAANQAG                          |
| B_PV_Spartobacteria_bacterium@NBS53630   | :PD-   | AEK          | -KE VEL N               | GRL-EAKGEPV  | TRHFTMD-NS E                   | E KÇEYLR VDARNLE                       | TSLREGRG                     | MTMGLETE                     | WMNNKE            | IF-D      | K E WSESVHEN                 | VEDFDE FESTY                          | KDRGKVA                     | V: FIMA AGSGFMCHMS  | FFRCKMPSMDDILKKNPEL                            | AKCMAAAAAAQAG                          |
| B_Te_Actinobacteria_bacterium@NBC09709<br>B_un_bacterium@NBV77836                                    | :FSLASASAPRMDPV-                               |              | -KE SEL N               | QRL-ESKGLQV  | AKRFTMD-NT D<br>SKRYTMD-NT E   | E KO YLR VDSRNLE-<br>E NO FNROVDARNLE- |                              | CALMSVETE                    | MOWANGRE          | F-D       | KUDEWSEAVHEN<br>KUDEWSEAVHEN | VEDEDEN FERN Y                        | KERGKMP                     | A THE MAIL AGSGEMENTS   | FLKSRMASVSTDDILKNNFDL<br>FLKSRMSNVSADDILKNNFDL | ARGFATAAAGGAG                          |
| B un bacterium@NBC72558  | :FSLSAAPTPRMDPE-                               | KER          | -KE NEV N               | QRL-ECKGFPV  | SKRYTMD-NS E                   | ENGINE VEARNLE                         | -ASLREGRG                    | DALMSV Te                    | MOWANSRF          | DEF-D     | K D WSEAVHEN                 | VEDEDE FERRY                          | OKOKERGKMPS                 |   | FLKSRMSNVSADDILKNN                             |  |
| B_FC_Bacteroidetes_bacterium@NBF66665<br>B_Fr_Rhodobacteraceae_bacterium@GIS52555                    | :SSTFTPVPNRVTI-                                |              | -VE CEM F               | KRL-EGRGIPL  | SKHYSAS-SSE                    | E KE YSR KNORDVE                       |                              | KTMLAFAS                     | WEFLNSKE          | F-D       | KID WSESLHEN                 | LSDYDD FE                             | KAKTNIA                     | I NO MM GGSAVMFHMT  | LFKNSMPQMDDILKNNFDL                            | ARGFASAAVSSST                          |
| B Te Dehalococcoidaceae bacterium@MBR74524<br>B FC Flavobacteriaceae bacterium@MAH20629              | :NNCPSGYVPIHMMSQS-                             |              | -NE IDL Y               | FKKL-ENGGIDT   | TMNYNMN-SG D                   | E RNEYIKEKKORELE-<br>BEGEYEVHLAERERA-  |                              | KMLMAI TA                    | FLNGRE            | F-D       | KUNGWSESVNEN                 | IYDYDE FEWH                           | GGGTEMA                     |   | MLKSAMPSMDKLFEQNPDM<br>MFKSAMPGMDDIMRCNPEL     | MNKFANAAKGNFN                          |
| B Pr Rhodobacteraceae bacterium@MAR51406   | :PNMNIQQKTMKKE-                                | DEL          | -RE LKT R               | EAL-EKKGFRL  | TKKYGME-SS D                   | E TG YEM KNOVEKK                       | NSCKEQGF                     | KMLMAA Se                    | FLNSKF            | DFF-D     | K DEWAEAVNEN                 | LEEYDD FGELH                          | SSKAKMA                     | IN FM GGSAVMLHMT  | MFKSAMPGMDDIMKCNPDL                            | MCGFTNAAVNSMS                          |
| N Ph_Chrysochromulina_ericina_virus@YP_009173584<br>B_Te_Chloroflexi_bacterium@MAS50978              | : ININKTWDGYGKVNPIPVVSDE-<br>:PTAPPPEKKMSAE-   | AAMTREEL     | VRE FKF R               | EDL-ERKGANL  | TKKYTMD-SP-C                   | E CG YEM IAEREKT                       |                              | KMLMACTT                     | MOFINNER          |           | KIDSWGECVNEN                 | IDYDE FOR H                           | KSKAKLA                     |   | MFKSALPGMDDIMKCNPEL<br>MFKSAMPGMDDIMRCNPEL     | MCGFTGAAVNSMG                          |
| N eM Organic Lake phycodnavirus 1@ADX05922   | :EKEIKHVEHKTKE-                                | ETL          | -KE FNY R               | EQI-ESKGVQL  | SKRYSMD-SSED                   |  |                              | KVLTTLETE                    | FLNNKI            | D:F-D     | N Dewsequsen                 | LEDYDDIFSSIHI                         | KSKAKMA                     |   | MFKSAMPGMDDIMRQNPDL<br>MFKSSIPGMDDIMRCNPEL     | MNSFTKAAVNSME                          |
| V_Ba_Megaviridae_environmental_sample@QFG75018<br>B_Pr_Candidatus_Pelagibacter@MAV56252              | :VSTAPRLSPE-                                   | EVL          | -KE FSV R               | EGL-EAKGLKL  | TERYSME-SN H                   | E: KG: YEM: VAEKEKL                    | -NSVKEQGF                    | KMLMAA Te                    | FLNNRF            | DFF-D     | K DEWGECVNEN                 | INDYDD FGELH                          | KSKACMA                     | L FO AGSAIMVHMT   | MFKSSMPGMDDIMRCNFEL                            | MCGFTGAAVNSMG                          |
| B_Te_Actinobacteria_bacterium@NBC55737<br>A Ca_Candidatus_Poseidonia@NDA7464095                      | :VDAGPGMTKE-<br>:INKIKVEPGMSRE-                |              | -RE FKY R               | EDL-ECKGITL  | TKKYSME-SS A<br>TKKYDME-SN L   | E KG YETHLEERERR<br>E KG YESHISEKEKK   |                              | KMLMSVETE                    | HEYLNNKF          | II F-D    | K DOWSECVNEN                 | IDDYDE FSWH                           | KSKAKMA                     |   | MFKSAMPGMDDIMRCNPEL<br>MFKSAMPGMDDIMRCNPDL     | MCGFTAAAVNSMS                          |
| B FC Flavobacteriaceae bacterium@MAD12632  | :IMKEKPMSKEELL-                                |              | -RE FKY R               | EAL-EKKGVEL  | SKKYTME-SP Q                   | EN CONTENT MERKERS                     | -NSIKEQGN                    | MLMAC NE                     | FLNGKF            | F-D       | K DEWSECINEN                 | LNDYDE FG H                           | KSKATMA                     | Last FC GGSAMMVHMT  | MFKSAMPSMDDVLRQNPDL                            | MRSFQSAAVNTMG                          |
| B_un_bacterium@MDA9072678<br>B_FC_Candidatus_Marinimicrobia@MCJ7802941                               | :ANVPLEPKLS-NA-                                |              | -REFRYER                | EAL-EKKGVEL  | SKKYSME-SN-Q<br>SKKYTMD-SS-L   | E LG YET MDEKSKO<br>E CG YET MDEKTKO   |                              | NILMSCING                    | HEFLNGKF          |           | KUDEWSEGLSEN<br>KUDEWSEGLGEN | ITDYDD FSERY<br>ITDYDD FGERH          | KTKASMS                     |   | MFKSAMPGMDDIFRQNPDL<br>MFKSAMPGMDDIERQNPDL     | MRSFQSAAVNSMS                          |
| B_Ba_Candidatus_Elulimicrobium@NBP58644  | :DRNAPLEPRMSKE-                                |              | -RESEKY R               | EAL-EKKGVEL  | SKKYTMD-SS C<br>TKKYNMD-SN L   | EN CGRYET MEEKSKO<br>EN CGRYEM MEEKSRO |                              | MLMAVING                     | IDFLNGKF          | 0 F-D     | K Dewsecicen<br>K Dewgecinen | ITDYDD#FSE#H                          | KSKASMA                     |   | MFKSAMPGMDDILRCNPDL                            | MRSFCNAAVNSMA                          |
| B_FC_Crocinitomicaceae_bacterium@MCX8482046<br>B_Fr_Alphaproteobacteria_bacterium@NDA90557           | :DKPMSSGPGMSKE-                                |              | -REFKYR                 | EAL-ENKGVNL  | TKKYNMU-SN L<br>TKKYSMD-SP A   |  |                              | MMLMAC NE                    | EFLNNRF           | F-D       | K DEWSEGINEN                 | MTDYDD FG WY                          | KIKASMAN<br>KSKASMAN        |   | MFKSAMPGMDDILKCNPDL<br>MFKSAMPGMDDILRCNPDL     | MRQFQSAAVNSMA                          |
| Yara@MT293574_47<br>Ga0495673 0003879 12   | :MD-   | EA           | -MCDAKI E               | YHAREPEI   | LGRFQPI-NLAR<br>LGNYSPL-PPAR   |  |                              | MLAKSGEVEMAS<br>MLVMTGFTEFAA | F-WAWMTYCFNH:     |           |                              | WRSCEIMAP LID WI                      | 430 PSVFE                   | PLW RT HGIYLICKEV-  | GRFSH<br>GRFST                                 | ADQAPAG<br>ASQAPAG                     |
| E Ha Pavlovales@KAJ1639471   | :AAPPPPPPPPLPAPKA                              | RVETAAEREATE |                         | GKYRERFPKLKKR  | NGALSIK-SSEI                   | MD VHY VACLGRE                         | DTGPAG-SLKPANI               | LAFLGTEYE                    | WINGLCIY          |           | O K LGOTTCAS                 | LKTEEPCPEPAP                          | VIGVGAGAAI                  | VS PVIALHSWVRLENGT  | DALETLLEEYRVAAAEEEAAK                          | AAEECEAAKAAED                          |
| E_Ha_Pavlovales@KAJ1620103<br>Ga0335398 10007490 20  | : FGCVATIGEPEGPKAESAADRE-                      | LLEF         | EE GSL D<br>DQ SAL D    | GKYRERFFKLKKR  | NGTLSIK-SSEM<br>NGSLSAK-SADP   |  | -DSGPAG-SLKPGNI<br>AASDSNVGI | LAFIAADYE<br>INI FGAADNS     | MISTCLE           | W:L-N     | O RELECTIVOS                 | LKTFEP LN FM                          | HNMDVSASV                   | A: LG GALVMTVHAA  | GLEGAPREDPESSENVLAEVGSALE                      | IVCLLHMAWSTHCLEAAAAEE<br>LDRMNLAPDVSSA |
| Ga0055584_100001079_17<br>B_FV_Verrucomicrobiales_bacterium@MAH41486                                 | :SAPSKL  |              | -ADPOCL D               | GAYKDREPDLRTR  | NPKLSAK-SSE<br>RNKVSAK-STSD    | ENEDULHE ELQLGSS-                      | -KDTSLGSP                    | MLFVGSEVE                    | USTITCRY          | NEM-N     | R E LGKIAKON                 | INEFTP IDEUM                          | SAGLYVS                     | ARIALAVASLVMTVHSAR<br>MRIVMATATLMYTVHSAR                        | GDFRLAE  | ALKRVSEPVKKPVG                         |
| gamad contig 17 30   | :PLPPPP  |              | -KD SLM D               | EMYRCRESHLKS   | RNKLSGK-STAE                   | E ED THA ECCT CCK                      | DGHMGNF                      | HVFLLA ST                    | MENTTKH           | YN:L-G    | N ACLSCVAREN                 | CDCFGP LD V                           | ATNMYVG                     | M: AMATATLVYTVHAA   | GNPAV  | AGAMASMARFVAA                          |
| gamad_contig_12_32<br>Ple28KY346835_19   | :  | TVDSS        | -ED TKL D               | SAYKERFPH  | LETRNKTIKTAE<br>RNNVSAK-ST⊞E   |  |                              | TLLYGSLCE<br>MALHSA MA       | MOYSTAIW          | NEL-N     | NETELGEVIKON                 | MADEEP VDSHM<br>MSEFOP LDSHM          | GGAAYMP                     | YRU LA GAMVLIVHMAN<br>MRUALA SALIMIVHAAN                        | GDPAL  | AÇAVSKANATLKK                          |
| E Ha Chrysochromulina tobinii@RCC47056   | :APAAPPEPLPPSP-                                | 1,200        | -ECLRIM D               | SAYREREAH  | LESRNEKLSTPE                   | E ED LHY ELQLGSS                       | -QGVNEGAS                    | SGLCMALTC                    | RSTDYW            |           | N TELGNVTCON                 | MHEFGPUIDEM                           | NTGMYTP                     | W: ALA GATVVTVHAA   | KATE   | ARVMASSLVEYDT                          |
| gamad_contig_25_30<br>Ga0181424_10000048_35  | :  |              | -EELRVM D               | GAYKERFPHLKS   | RNKVGPR-SLPE<br>RNKVGPK-SSPE   |  |                              | VALCTAVAF<br>TALYCSVE        | HERSTDYF          |           | DERELGAVIKON<br>DETELGRVACSN | MHEFQP ID N L<br>MSDFQP LD N M        | NTGLYAP<br>CCGAYTS          | LEN MA GATVITVHAA   | hpevaka  | VRAMHKTVNKPAG<br>LSAMANAVKVPVG         |
| B PV Planctomycetaceae bacterium@MAT73277  | :TTPSNPTPPGV                                   |              | -EE SIM D               | YAYREREPHVKK   | RNSVTAK-STED                   | E GD LHY EVOLGSA                       | KCKMNEGAV                    | VVLVASUH:                    | DETITEDF          | Yel-L-N   | N TELGNVTCON                 | MAEFEPUIDSUM<br>MSEFGPULDSUM          | GASYYTS                     | weralargatvytynaar<br>weralargatvitynaar                        |  | MKNMHEKATPPKN                          |
| Ga0211617_10001448_4<br>B_FV_Planctomycetaceae_bacterium@MAT69666                                    |  |              | MIND                    | GAYREREPFLKK   | RNNVTAK-ST E                   | E AD LHYCELQLGSQ                       | NTSHQLSST                    | VLYGTVA:                     | TLTRDY            | WREL-G    | N N LGMVTQQN                 | MDQFQPildeim                          | HNAGTYTS                    | W: ALA GATVLTVNAA   | NPEMAQA  | VKAMNQAVTPPPG                          |
| B_FC_Flavobacteriales_bacterium@MAZ01246<br>B_Ba_Patescibacteria_group@MBU0706662                    | :AAPPEAPPPAPPPG-                               | ICD          | -CD SVL D               | GAYRERFFFLKK   |                                |  |                              |                              | TITEDY            | WEL-G     | N N LGMVTCON                 | MDCFCP LD M<br>MFNS-MLDP AND A        | HNAGMYTS                    | W: ALA GATVLTVNAA:  |  | VKAMNQAVTPPPG                          |
| Pates@JAHIZF010000067 35   | :AK-   | IQD          | -RD GREET               | HKYITNPHEAFLSEL-                                     | -HLRPLSQR-PTYE                 | E CFMYDA REAIDSR-                      | -NGCENIKNLAAGAA              | ASLVEQFWs                    | DGSKMTIL-P        | EEL-RE    | RNSATYMRSG                   | MFNS-MLDP ANEVA                       | E PILASAGLI                 | LRETAAAFLQMFAIVHKME   | EPNFKEAMSR                                     | LASMQAMSEAEMQ                          |
| Ga0376279_0003301_12<br>Yara_contig_14_26  | :  |              | -AIARGLAY<br>-KE RILEM  | KQYLERFPDLSPY<br>TKRYEAFPWLKEK                       | LPPLSRS-PGEG                   | ECETILGI RDRIQSK<br>E RETDELÇKLELDIS   | SEERFEKYLIGGE                | ALLEA WEDGS                  | FPRVPKPL          | RF        | D SCLGTFYNRG                 | LFTEFDF LASED                         | E PCFGCCNLE                 | FT A SAFAÇALFIVHKA :  | DPAT   | LSAMSMQTKEPVE                          |
| B_Te_Chloroflexi_bacterium@RPI88544  | :VKDE-   |              | -EL IKR LE              | RIMKRFEAFFWLCK                                       | TIPTPCTRSS G                   | KEIDISCKVELDLC                         | SAKGRIA-FGVKCGA              | ASLVED WEDGKI                | TWLPKSM           | R         | N TELSCIVEAN                 | FDRSIAP VESTA                         | ENPTLGMMSL                  | TV:W-NT_MTTLWMVHLN:<br>M:W-WTFATLVWAVHHN:<br>M:W-WTFATLVWAVHHN: | AGEKLAAMAAKPPMEAPTF                            | SFATVMECKSK                            |
| Yara_contig_15_32<br>Ga0498922_0001740_11  | :RD-   | LED          | -AREKDWAY               | NLYCEREPSVSAR  | LPKMKPT-ASEQ                   | ECEEVLCIAREIVSSC-                      | -NSVNNVIGTENMGN              | TIFEAYWE                     | DGSKMAKI          | HEMLG     | N TELSCIVDAN<br>N TEMSKLEREG | KFP-ELDP ICE D                        | E PWIGRRSLI                 | LI FAST GEMMMKVHLM  | NPAARKILEM                                     | ASSEPKIIDDTGL                          |
| Ga0172381 10005398 11<br>E Am Acytostelium subglobosum@XP 012747664                                  | :  |              | -VERRE H                | KMYIHHFPGCVE   |                                | EYECYSO KEERNAS<br>EYEE NIR EEALSCO    |                              |                              | TSLPPGL           | RE        |                              | WKFP-ELNDUMLSUD                       | IE PNLGSSSLN                | M.T.HA.TQVIVKVHMA:<br>I:: AATLRGFQQVHLY:                        | RARGANDPYAFGPPPT                               | MEQPAADISDLEK                          |
| Ga0316202 10000687 15  | :AD-   | EEA          | -AMEARIRL               | EAYTRRWPRKFEGH-                                      | DMRLKES-DS A                   | KHCAVDKE ECLVGCG-                      | -NSFELCKI                    | LMFCSGASE                    | AVSARFPGCV        | GGLHAG-NC | COL IGAAFANS                 | LCPDPHSGEASPMAEALE FS                 | CHYFSQSA                    | AS AVLFTCLAYSVECH   | KAKQANDFIAFQPFFI                               | CDASEKAAAHADL                          |
| Ga0364575 11239 34<br>Ga0395773 0000340 41   | :PE-   | EIN          | -DATAKIER<br>-RYYSEFSHE |  |                                | E KIHLAD EHELGKS:<br>D ED∍KKE KRSLADP: |                              |                              | RREYGTEH          |           | N CHYGKIAEGSLGI              | RVMPDGKISEAPMIPELKEFA<br>PDYVRPELROWA | DDWFSTRV                    | N DE INTCKAAGECHMEN   | BATMC  | CRMATATACPAC                           |
| B Ba Candidatus Dependentiae@MCA9770739  | : GALKKOVKWAMETLTGARRELS-                      |              | -KETVOLANE              | MNRYYESEPDLLGPNI                                     | HKGKKDVSK-VP⊞N                 | EFIDFKANFKCILACP-                      | -CSLSLVEI                    | DIYWSAMEV                    | A SLYMERFF        | GTEHDFLN  |                              | IDYVRPELTERA                          | E SQLLSLG 1                 | INTERMASDONIL   | SAKTNINDINNKYKNL                               | AASFAGLEKLENN                          |
| Ga0395696_000216_29<br>Yara_contig_22_16   | :  |              | AARSKIEHO               | DLYYGYFPFLMDLNG<br>DLYYRYFPELAEFG                    | K-KKIFTGK-TSE<br>K-KKIFTGK-TSE | E CG IERCKISLSSR                       | -ESLGNVKI                    | LAHCALFKE<br>FFDLLLFRE       | SLGVHI            |           | P WELSONCLDT                 |                                       |                             |   |  | SEAYVPSKQTMDN                          |
| Yara contig 20 9<br>Yara contig 16 26  | :  |              | -TE LKV K               | DLYYRYFPELAEFQC<br>DLSYKYYPQLLEGG<br>EMYYRYFPELEKSCI | R-KKPWDLN-CS K                 | GE EKR EFEKNTE                         | SALEILKP                     | KLDILVHF                     |                   |           |                              | GAEALETLGS S<br>GVLIEKELKS NA         | GHHLVLS                     | STY IR ICNAATVICM   | IGMTSQKRAEYDSDHVGSSPFG<br>GEVLQRNDAL-          | TKMDAKVLEELMK                          |
| Yara_contig_16_26<br>Ga0498839_000020_14   |  |              | -TA NSL K               | GMYYHHYPQLRETNI                                      | R-RGKWSAK-TSFK                 | D QD VNRCDSQLSLD                       | RS                           | SYLTMCS                      | DLFNNYL-AEI       | VLRQGF-G  | PAHCLAAEAKKS                 | QMVVEDELKERS                          | HDNLETGE                    | V:Y:IKFANRVSRVIER   | HGAPL  | EPAEEDVNFQNK                           |
|  |  |              |                         |  |                                | e                                      |                              | g                            | e                 | P         | g                            | e                                     | P                           | n   |  |  |

**S15** 



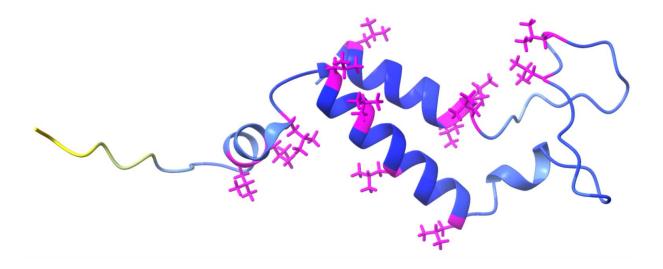




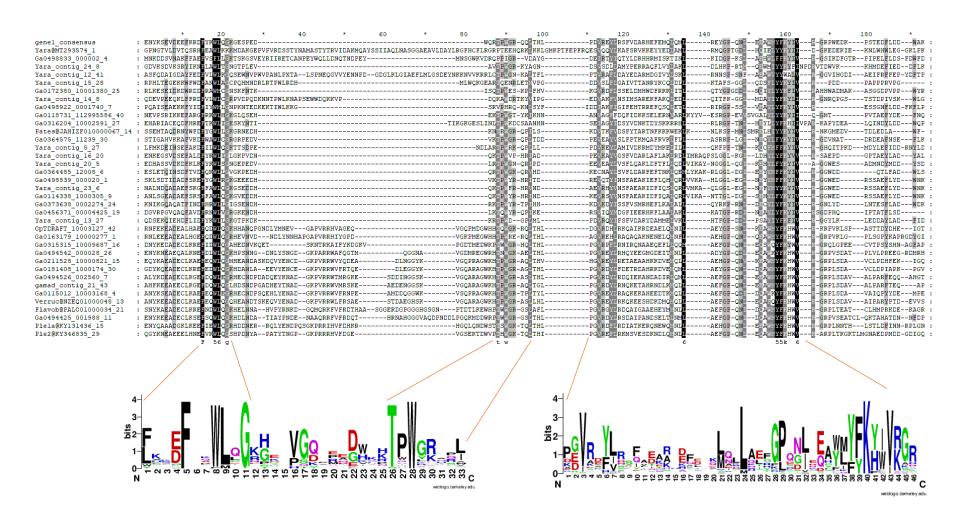
gene48 (Ple2@KY346835\_19)

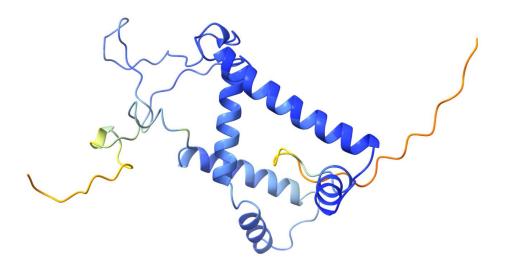
(Yaravirus)

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: ------MMMFM-RNNPLMMAIIIYLIIFAIIYYLK-ESFMENE-DCSTREEGIGHK-----NKTIIFFWUVATILAUISYLFV-:
 gene50 nr consensus
 B Ba Patescibacteria group@MBU0706664
                               : ------GLD-NVSPVFRGAITAGVITLAVSTIK-FSFM1DD-E-SPLFMSITAGKEE----ESALIPWW1PGVFGFVVGGLLI- :
                               N Ph Pyramimonas orientalis virus@QCI90441
 N eM Catovirus CTV1@ARF09377
 u_Ya_Yasminevirus_sp_GU_2018@VBB18307
                               : ------MSTIFD-PYREAYNTIIVYVIIIIIFLITK-:GFM:DSVNKKF:Q:GCDKG------Q:LLPFF-LC:TCG:IVMILF-:
 N eM Edafosvirus@AYV78907
                               : ------CUFFAFFEVVEASVELFYFFFF :
 N eM Indivirus ILV1@ARF09426
                              V Ba Fadolivirus algeromassiliense@YP 010803412
 B Pr Magnetococcales bacterium@MBA42803
 N eM Homavirus@AYV82364
 B PV Verrucomicrobiales bacterium@MAH34298
 u Vi Virus NICZ UU159@QPI16780
                               V_Ba_Tetraselmis_virus_1@YP_010783191
                              V Ba Mimiviridae sp ChoanoV1@QDY51765
 B Pr Alphaproteobacteria bacterium@NDB84211
 B Pr Alphaproteobacteria bacterium@NDB81941
 B FC Crocinitomicaceae bacterium@NBR14461
 B un bacterium@NDG30571
                              B FC Flammeovirgaceae bacterium@MAE87058
B Te Acidimicrobiaceae bacterium@MBG01367
 N eM Organic Lake phycodnavirus 1@ADX05840
 B un bacterium@MBI96883
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Mriya\_50 (Ple2@KY346835\_21)





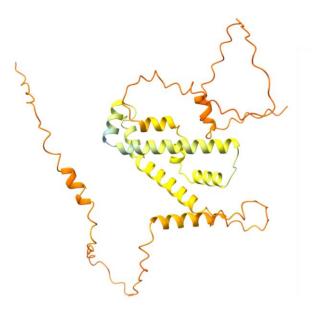
Mriya\_1, exemplified with Ple2@KY346835\_29

Mriya\_51 **S20** 

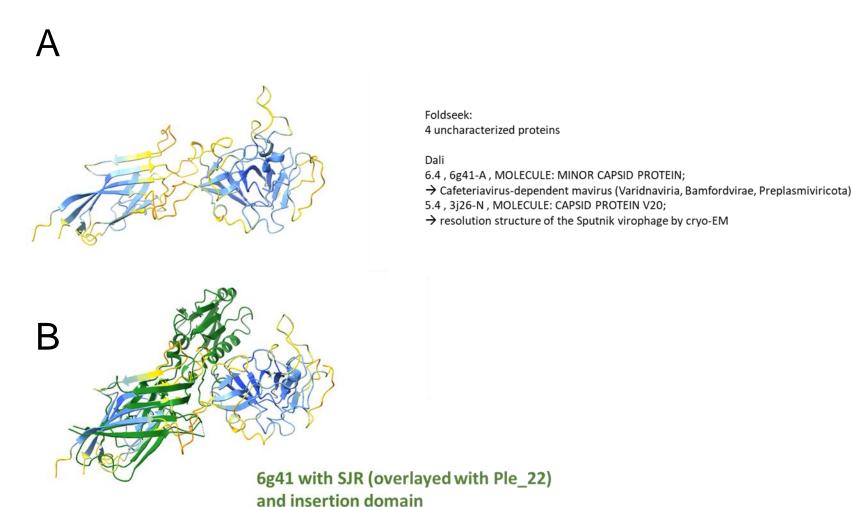
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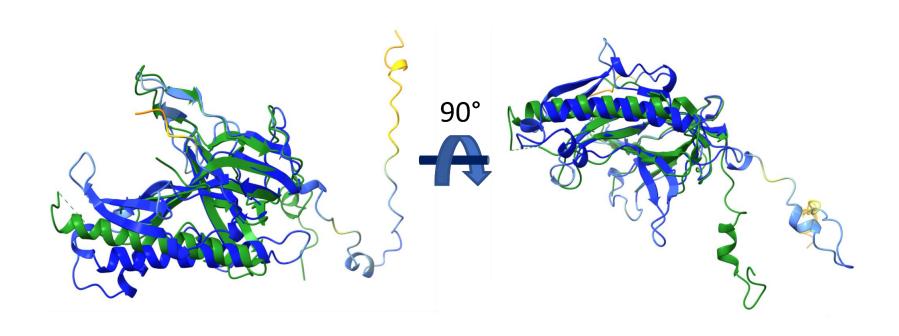
|  | * 20   | * 40               | * 60               | * 80         |               | 100 *                 | 120          | *            | 140 *         | 160 *             | 180          | *          | 200          | * 22        |                     | 40 *      | 260 *         | 280 *            |             |
|--|--|--------------------|--------------------|--------------|---------------|-----------------------|--------------|--------------|---------------|-------------------|--------------|------------|--------------|-------------|---------------------|-----------|---------------|------------------|-------------|
| gene51 with nr consensus                                 | : PAKNCADSCAKEEMRERYDVMEAVAA                                     | PSGGNAVORTAN TDE   | E-FIDYMCENCIMAELAK | DOMINSTF-DER | NEGNMEWECKEY  | EYFER MECVCEEYEFCL    | RVAMEKMWEVN- | -TDEBH-HEMM  | MUBOGCMEYMT-  | MP                | CTALADPASS   | SNORR      | LESPFRF-     | WOS         | -DDKNRSAMGLPFPSCS   | FGPNAATGD | MSRAARGS      | PMGSSGNTL        | AEFAROM- :  |
| B Pr Bradyrhizobium japonicum@                           |  | TGVPGKTKWMPSTAEV   | K-SACDDRMAEKARKER  | ENGGLNNV-DAD | ERERMKD-CG I  | PPRES PTI.DELKAKYGPI  | NWETG-       | -GDVEPVKTLO  | BUBTKARY      | TA                | HPAIGDILR    | AMARTLEDGE | SWIMPELVGI - | NRA         | -SSCPDOVSPHEGRAPARI | TDPAMAALE |               | PIVIDGVTL        | DOGADE :    |
| E Am Acytostelium subglobosum@                           | PTREDSROYKYERKIOIAK  | DIRPAGUNTEGENUPE   | SEYCYGLEARRAHERAC  | DRUTLGSL-DEN | -NEACTOR ESYR | FI.VNEPRRYFEERI.RVI.O | RIENERLTERO- | -SREDY-FEME  |               | CYCLLVOWKPPGTKVNP | SNGITTVDH    | TRIBHGAGI  | FMAPODT-     | CRY         | -DWSGGLTLKSMLNGR1   | MDGETPAVG |               | SRVTKPLSVI       | PONTABLE :  |
|  | : HARACPALYYKKGEAELLNEICPLLAKTY                                  |                    |                    |              |               |                       |              |              |               |                   |              |            |              |             |                     |           |               |                  |             |
|  | : PVEVAPYNESEANIREKVDILKGFAGD                                    |                    |                    |              |               |                       |              |              |               |                   |              |            |              |             |                     |           |               |                  |             |
|  | : AGE GLVRPFKTERLEEPSILEKTGAARI                                  |                    |                    |              |               |                       |              |              |               |                   |              |            | LESUMIDT     |             |                     |           | HWFSSRKNGKAAN |                  |             |
|  | : AGE-GLVRPFKTERLEEPSILEKTQAARI                                  |                    |                    |              |               |                       |              |              |               |                   |              |            | LESCHLET     | WROTVNLTYDH | -ENRNRAADGYEVSAVSOS | PGPVAATDP | HWFSSRKNGKAAN | NVWNCNAALGRERALE | AETRAEF- :  |
|  | PI   |                    |                    |              |               |                       |              |              |               |                   |              |            | PLSVFGL-     | AES         | -DDKSRINNAVNI.PROJ  | FRPAGEGHS | KIYRGG        | DGTAASMOLS       | SOYGRSA- :  |
| E Ha Pavlovales@KAJ1620872                               | : FGAMCRDSHAAEQERDFYDTVDAVSLRT-                                  |                    |                    |              |               |                       |              |              |               |                   |              |            |              |             |                     |           | MSRINRGG      |                  |             |
|  | : FGANCROSHAAEELROFYDTVDAVAARAA                                  |                    |                    |              |               |                       |              |              |               | мр                |              |            |              |             |                     |           | MTKILRGTDN    |                  |             |
| E Ha Pavlovales@KAJ1632903                               | : FGANGCDSGAAEELRDFYDTVDAVALRP-                                  |                    |                    |              |               |                       |              |              |               | мр                |              |            |              |             |                     |           |               |                  |             |
| E Ha Pavlovales@KAJ1637090                               | : FGAN SCAAEELRDFYDTVDAVACRPV                                    |                    |                    |              |               |                       |              |              |               | мР                |              |            |              |             |                     |           | MSRILLGTTN    |                  |             |
| E Ha Pavlovales@KAJ1625672                               | : FGANGRESCAREELREFYETVEAVONREI                                  |                    |                    |              |               |                       |              |              |               | MP                |              |            |              |             |                     |           | MSKILRGTSDNVI |                  |             |
| E Ha Pavlovales@KAJ1636204                               | : FGANGRESCARECEREFYETVEAVSSRA-                                  |                    |                    |              |               |                       |              |              |               | MP                |              |            |              |             |                     |           | YAVRAC-       |                  |             |
| E Ha Pavlovales@KAJ1629339                               | : FGANGRESCAAECLREFYETVEAVASRAI                                  |                    |                    |              |               |                       |              |              |               |                   |              |            |              |             |                     |           | ASRINRTG      |                  |             |
| E Ha Pavlovales@KAJ1631354                               | : FGANCTDSHAACNMENFYDTMDAVAVENO                                  |                    |                    |              |               | VLVCR MDAICELSCESL    |              |              |               | MP                |              |            |              |             |                     |           | ADMINITO      |                  |             |
| E Ha Pavlovales@KAJ1630371                               | : FGSVCRDSHAACDMRNFYDTMDAVAARPI                                  |                    |                    |              |               | VLVCROMDAICELSCESL    |              |              |               | MP                |              |            |              |             |                     |           | ANDNLRNI      |                  |             |
| E Ha Pavlovales@KAJ1629638                               | : FGANCRDSHAACDMRNFYDTMDAVANREI                                  |                    |                    |              |               | VLVCR IDAICEVSCEAL    |              |              |               | MP                |              |            |              |             |                     |           | ATIS          |                  |             |
| E Ha Pavlovales@KAJ1616912                               | : FGANCRDSHAACEMENFYDTMDAVANRSE                                  |                    |                    |              |               |                       |              |              |               |                   |              |            |              |             |                     |           | ARIDRGSGP     |                  |             |
|  | : FGA CHDSHAACEMENFYDTMDAVANESE                                  |                    |                    |              |               |                       |              |              |               |                   |              |            |              |             |                     |           |               |                  |             |
|  | : PVPODAASACKEHIRLKODVYEARKRAC                                   |                    |                    |              |               |                       |              |              |               |                   |              |            |              |             |                     |           |               |                  |             |
| E Ha Chrysochromulina tobinii@                           |  |                    |                    |              |               |                       |              |              |               |                   |              |            |              |             |                     |           |               |                  |             |
| B PV Planctomycetaceae bacteri                           |  |                    |                    |              |               |                       |              |              |               |                   |              |            |              |             |                     |           | DRSDANR       |                  |             |
|  | : PAKODMPSSAKERMMAKQALRESV                                       |                    |                    |              |               |                       |              |              |               |                   |              |            |              |             |                     |           | WICTGGGC      |                  |             |
| B PV Verrucomicrobiales bacter                           |  |                    |                    |              |               |                       |              |              |               |                   |              |            |              |             |                     |           | BWTCSDAGC     |                  |             |
|  | : PAK SVPNEMKERMVARAAIRNAAA                                      |                    |                    |              |               |                       |              |              |               |                   |              |            |              |             |                     |           |               |                  |             |
|  | : AVP AAPSOCKENMVLRAAVREAANECIE                                  |                    |                    |              |               |                       |              |              |               |                   |              |            |              |             |                     |           |               |                  |             |
|  | : PVPWSAPSAGKENMIIRSAVRDAANAEIN                                  |                    |                    |              |               |                       |              |              |               |                   |              |            |              |             |                     |           |               |                  |             |
|  | : PVPSAPSAGKENMIIKSAVKUAANAEIN<br>: PVPSAPSAGKENMILKSAVKUAANAEIN |                    |                    |              |               |                       |              |              |               |                   |              |            |              |             |                     |           |               |                  |             |
| Flavob@PALC01000034_28<br>Pleurochrysis sp endemic virus |  |                    |                    |              |               |                       |              |              |               |                   |              |            |              |             |                     |           |               |                  |             |
|  |  |                    |                    |              |               |                       |              | -TPUB -HPKM  |               |                   |              |            |              |             |                     |           | PEYWSIEDTG    |                  |             |
| Pleurochrysis_sp_endemic_virus                           |  |                    |                    |              |               |                       |              | -Trubb -HFKO |               | GP1               |              |            |              |             |                     |           | EWEMTDERN     |                  |             |
| Yaravirus brasiliensis@YP_0108                           |  |                    |                    |              |               |                       |              |              |               |                   |              |            |              |             |                     |           |               |                  |             |
|  | : PAV GVDMAERKRQAILRDITYKGQTSST<br>: PAG RADRVFTATEKAEFSK        |                    |                    |              |               |                       |              |              |               |                   |              |            |              |             |                     |           |               |                  |             |
|  | : PASSIVNVSPEDSKIDALTOH  |                    |                    |              |               |                       |              |              |               |                   |              |            |              |             |                     |           |               |                  |             |
|  |  |                    |                    |              |               |                       |              |              |               |                   |              |            |              |             |                     |           |               |                  |             |
|  | : PAR YKKOKLODEFYIRGKLVE<br>: PAR LARSEPPIREKSRVIRALNTAY         |                    |                    |              |               |                       |              |              |               |                   |              |            |              |             |                     |           |               |                  |             |
|  |  |                    |                    |              |               |                       |              |              |               |                   |              |            |              |             |                     |           |               |                  |             |
|  | : PIAPPHTRDPPMIDKMNFGK   |                    |                    |              |               |                       |              |              |               |                   |              |            |              |             |                     |           |               |                  |             |
| B_Te_Chloroflexi_bacterium@RPI                           | : FADESLPGRLPYAEKRAFA  |                    |                    |              |               |                       |              |              |               |                   |              |            |              |             |                     |           |               |                  |             |
|  | : FAD SLPGRLPYAEKRAFA  |                    |                    |              |               |                       |              |              |               |                   |              |            |              |             |                     |           |               |                  |             |
|  | : PACEFORNNSARKIAVACKYAKOLVCKFF                                  |                    |                    |              |               |                       |              |              |               |                   |              |            |              |             |                     |           |               |                  |             |
| B_Ba_Patescibacteria_group@MBU                           | : PTSEAHTTDPPLLEKREYAGESL  |                    |                    |              |               |                       |              |              |               |                   |              |            |              |             |                     |           |               |                  |             |
|  | : PTSSAHTTDPPLLEKREYAGESL  |                    |                    |              |               |                       |              |              |               |                   |              |            |              |             |                     |           |               |                  |             |
| Ga0373638_0002274_12                                     | : PAKE-VGSDPDEDTKQIAKIEYLK                                       | RFSADDVPILKTTDE    | D-WKMTWDKETCELEAT  | ENOFGELF-BLE | DINKERTAGE Y  | EYFKM:ESEIMKQAELQKI   | RLAIDKLYEPR- | TLED -QFL    | VYLQGESGIRNVP | LH                | RLDKRDGDPA-E | ROWR       | VFSPSRF-     | FRL         | -ETISHKPQGFS        | LRTLVDNVD |               | PTAVNKLNR        | RKILQQNR- : |
| B_FV_Verrucomicrobia_bacterium                           | : PAQEFPDQQEEDERIQMKM  | RLLQGRDRPLGDAM@TDQ | D-MAYFMKKEETKCHIL  | DEMFSRLF-ETK | DINKRRLAGE≣Y  | EYYON EEEIDRQAAIQK    | KIAMUKLEEIK- | DLDDM-KFVE   | AMCSGDTVLRK-  | YPLYN             | LDAPQEDSSA   | BERK       | LFNPARK-     | SKA         | -DDGYTGPIS          | LGRNMFTAE | GIP           | DIGALAPVP        | PAGFADAV- : |
|  |  |                    |                    |              | p 1           | P                     | g            |              |               |                   |              | 9          |              |             |                     |           |               |                  |             |

B

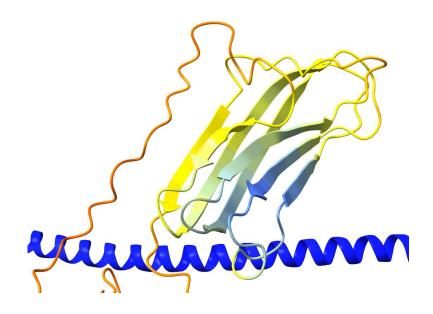


(Yara@MT293574\_50, aka YP\_010800671)

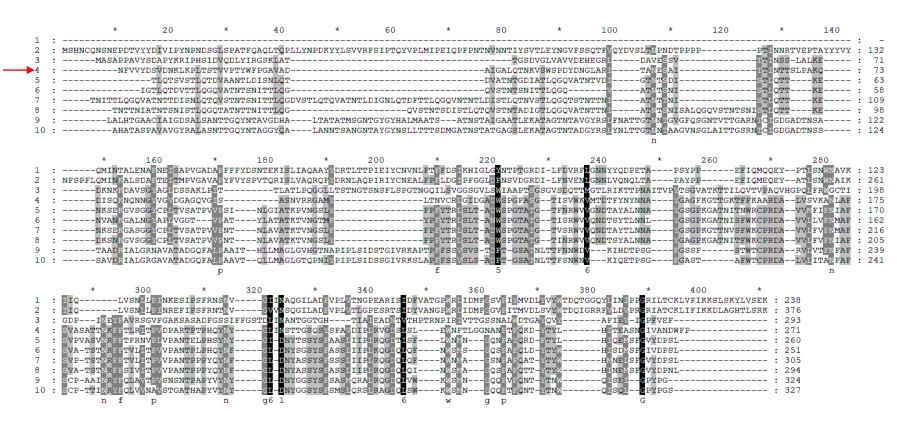




Yaravirus minor capsid protein (YP\_010800666.1)



## Yaravirus minor capsid protein (C-terminal of YP 010800666.1)



1 Sputnik\_UMZ08530 .1 minor virion protein [Mimivirus-dependent virus Sputnik]
2 Zamilon\_YP\_008859634 .1 minor virion protein [Zamilon virus]
3 YP\_010800667.1 hypothetical protein QKS73\_gp57 [Yaravirus brasiliensis]
4 YP\_010800666.1:200-470 tail needle DNA stabilization protein [Yaravirus brasiliensis]
5 YP\_009507121.1:265-524 chromosome segregation protein (SMC) [Tunisvirus fontaine2]

6 YP\_009094634.1:305-555 hypothetical protein MEL\_133 [Melbournevirus]
7 YP\_009345180.1:241-545 hypothetical protein B1750\_gp035 [Noumeavirus]
8 YP\_009238991.1:321-614 hypothetical protein A3303\_gp486 [Brazilian marseillevirus]
9 YP\_010804828.1:961-1284 hypothetical protein QKU73\_gp304 [Acanthamoeba castellanii medusavirus]
10 YP\_010802084.1:451-777 hypothetical protein QKT49\_gp315 [Acanthamoeba castellanii medusavirus]