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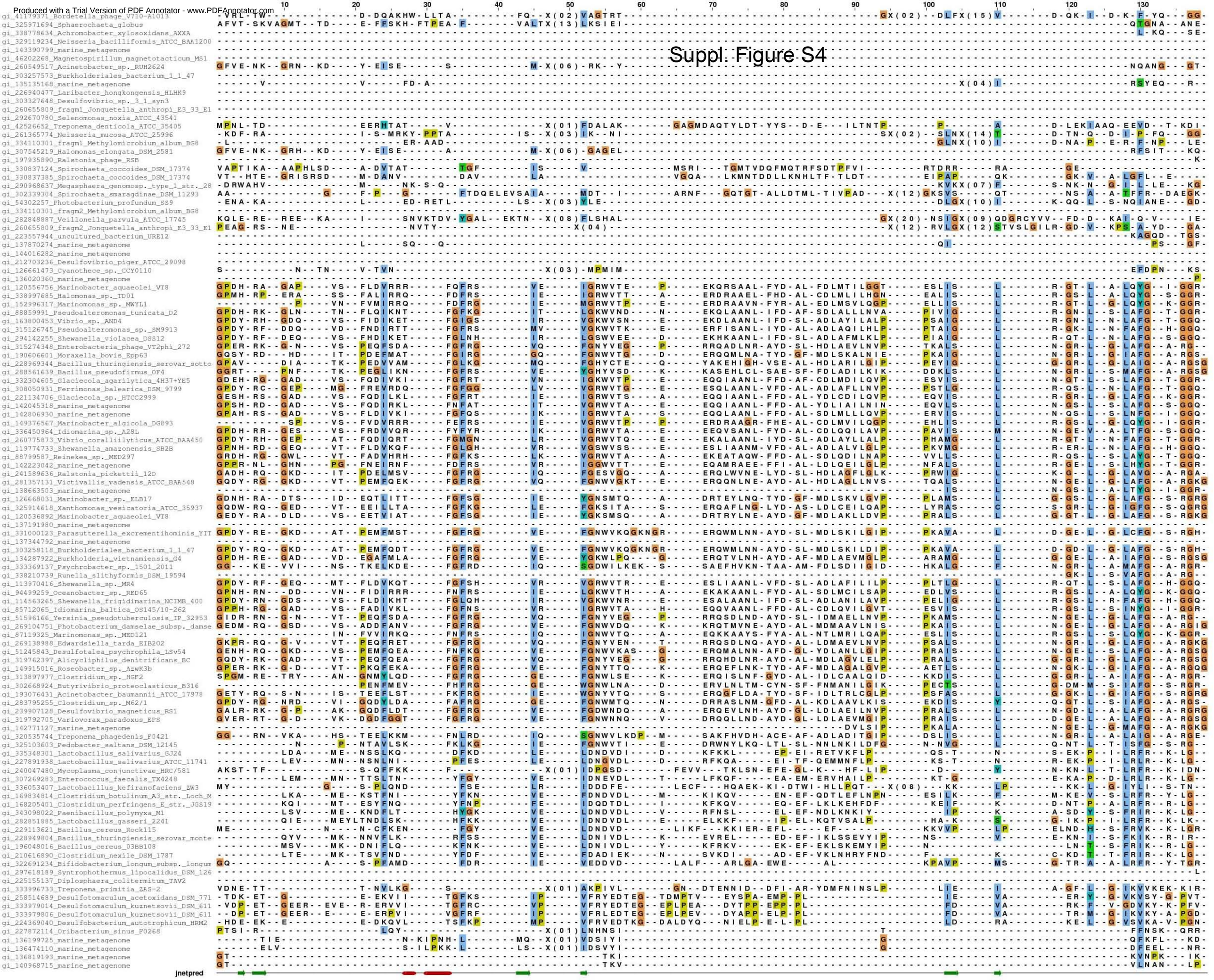
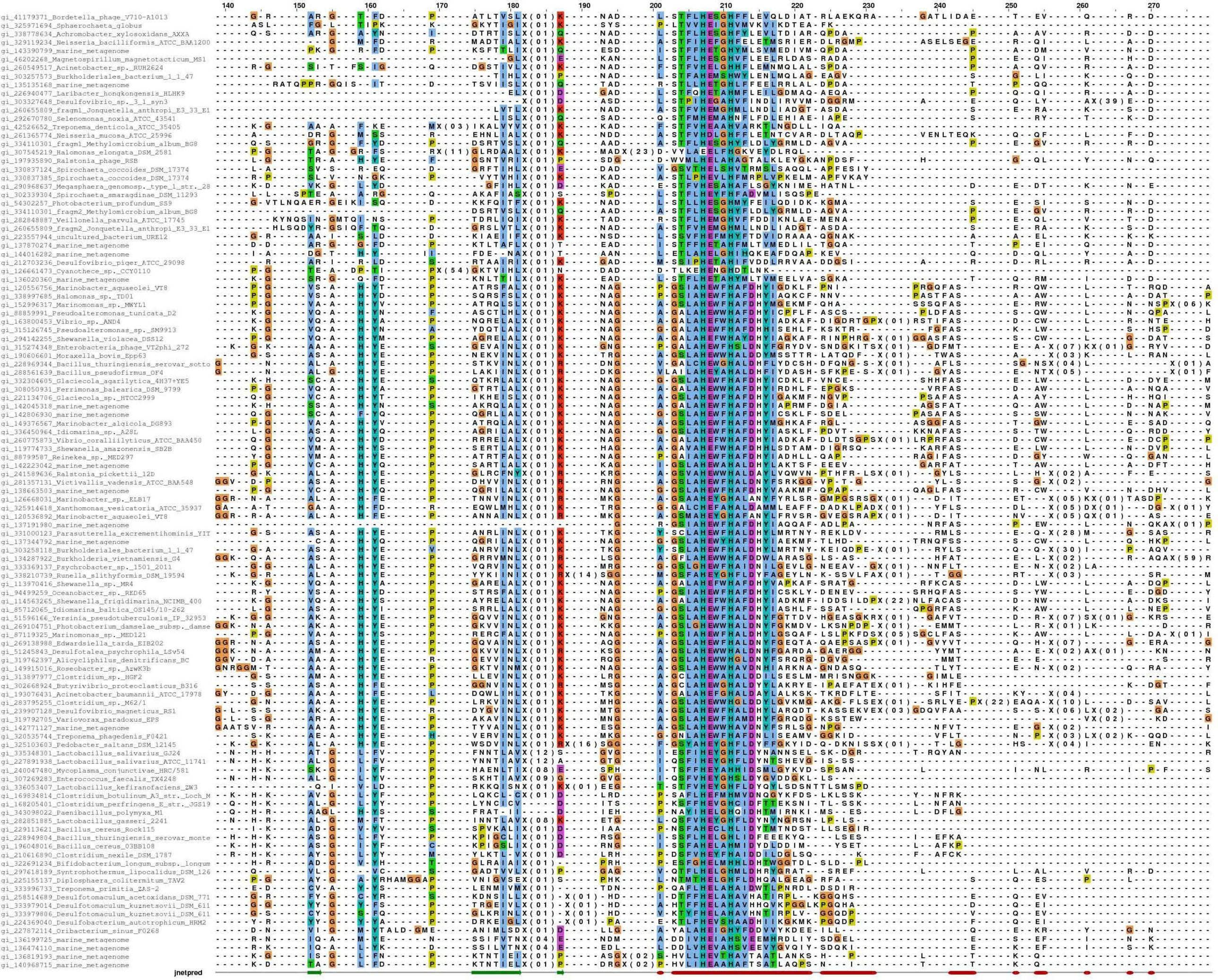
Suppl. Figure S4

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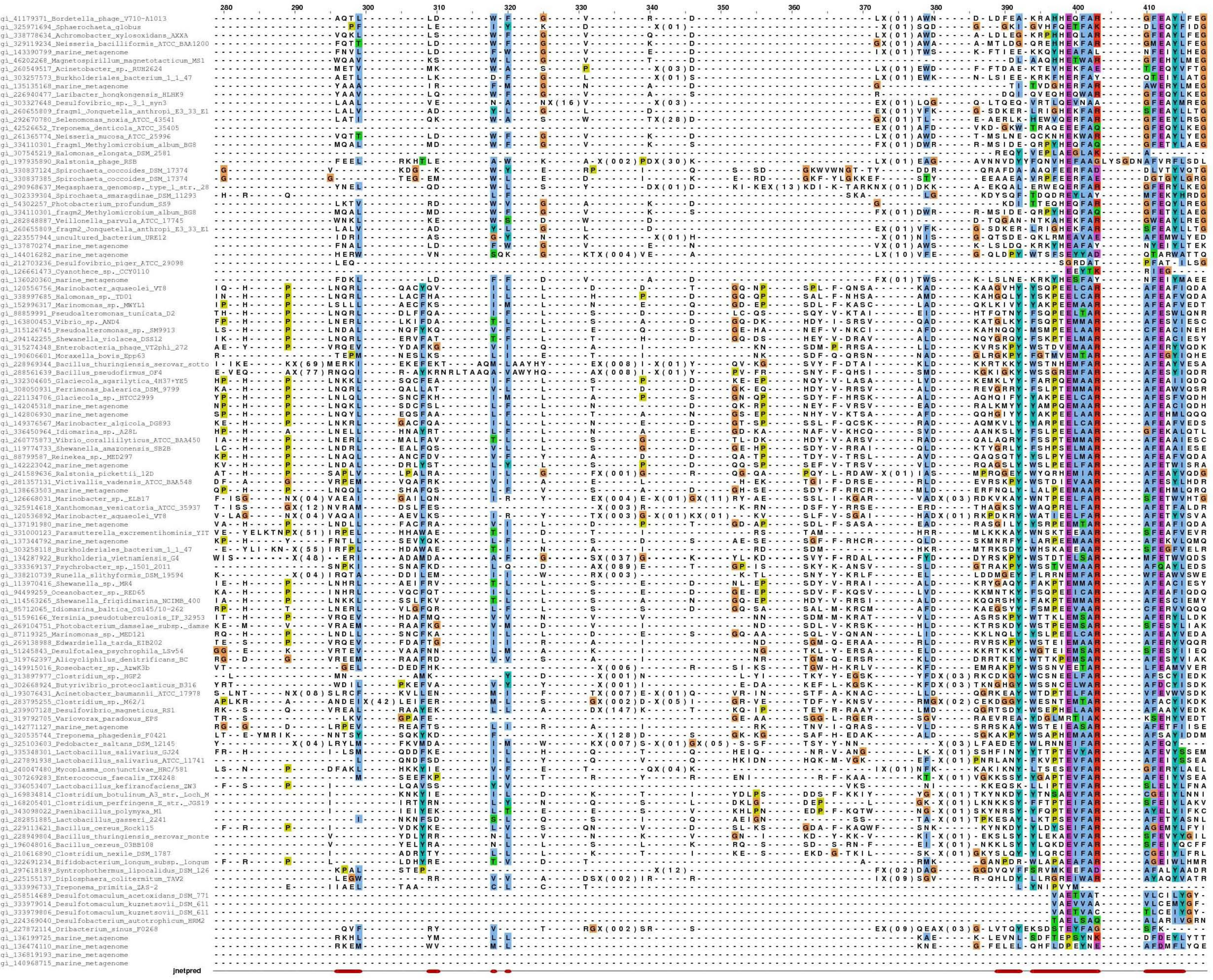
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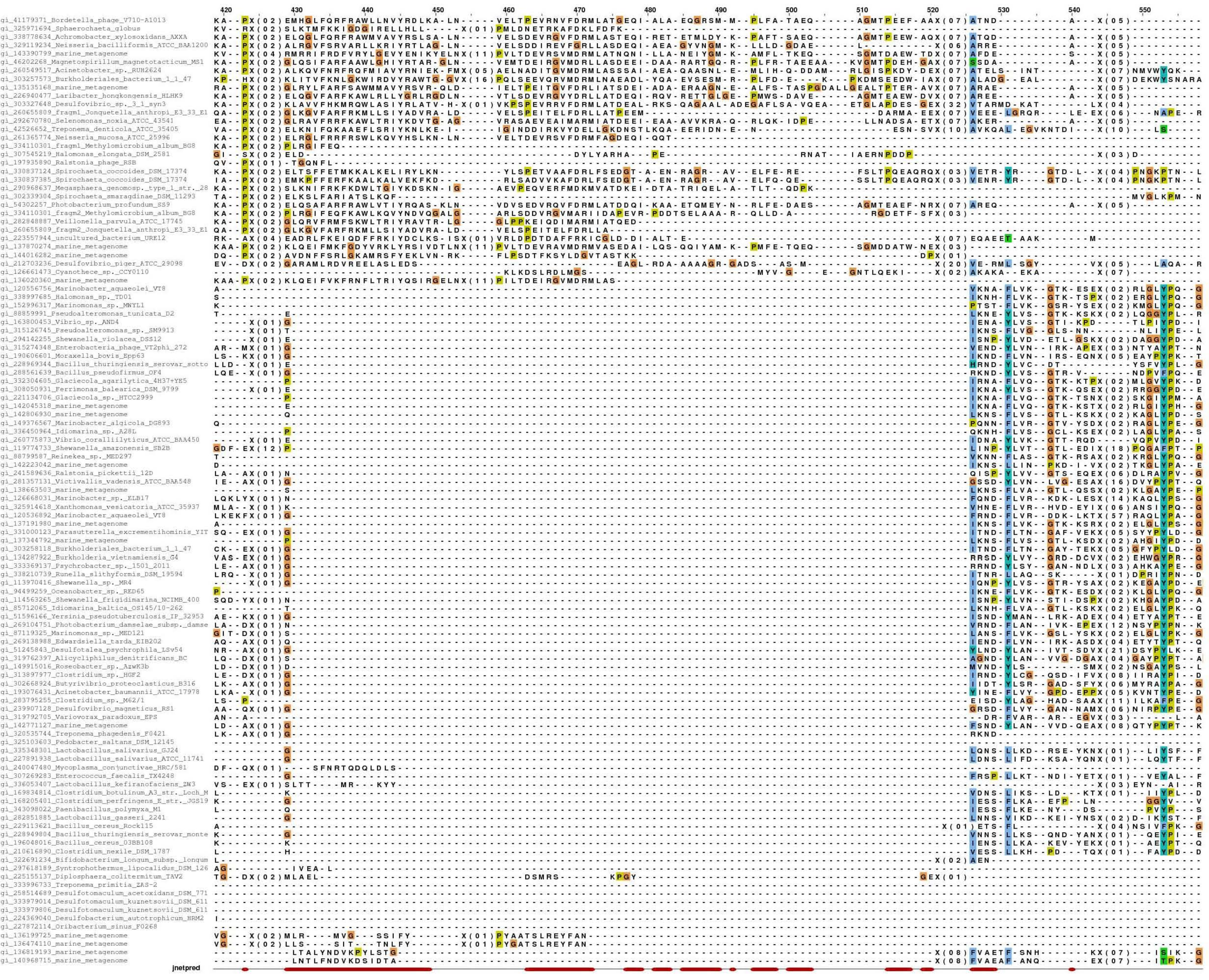
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gi_292670780_Selenomonas_noxia_ATCC_43541         ----X(07)------------X(06)AHME-EY-E------AQL-KAEMRE
gi_42526652_Treponema_denticola_ATCC_35405        ----X(10)----KAVEK-SEX(01)NGF--T--RK-----EHY-GAVAEI
gi_261365774_Neisseria_mucosa_ATCC_25996          ------------------------------QY-IN-----DMA-PLSDNK
gi_334110301_fragm1_Methylomicrobium_album_BG8    ------------------------------------------FK-AWLKQV
gi_307545219_Halomonas_elongata_DSM_2581          ----------------GGSGMTN-----A---------E-----AAE-VIERVA
gi_197935890_Ralstonia_phage_RSB                  ----X(01)----KAV-Q-IVX(01)-DL--LG-LT-----NLQ-TNALVR
gi_330837124_Spirochaeta_coccoides_DSM_17374      T-ERX(03)TVRTTAFKN-WF-----GDW--------------E-TVIPDA
gi_330837385_Spirochaeta_coccoides_DSM_17374      T-ERX(03)VTVRTTAFKN-W------GDW-E---AA----ENF-KWLMNA
gi_290968637_Megasphaera_genomosp._type_1_str._28 --------------------X(05)EDIR-AK-A------KET-VFADML
gi_302339304_Spirochaeta_smaragdinae_DSM_11293    E-D-------------LRK-AY----------------------D-ALYSLR
gi_54302257_Photobacterium_profundum_SS9          ----X(08)------------X(07)KDAE-ID-MR-----DQV-MAEMAE
gi_334110301_fragm2_Methylomicrobium_album_BG8    ----X(05)---SGTLRQ-LLX(02)--VD-QD-AA-----DLK-NIDAAT
gi_282848887_Veillonella_parvula_ATCC_17745       ----------------------------ID-AY-TK-----EQA-LEQFES
gi_260655809_fragm2_Jonquetella_anthropi_E3_33_E1 ------------------------------------------T-PEEMDA
gi_223557944_uncultured_bacterium_URE12           ----X(03)-----------S-----EN-G-TK-LY-----QAP-YNETGS
gi_137870274_marine_metagenome                    --------------------AI---------Q--E-T------QDA-AIDSLT
gi_144016282_marine_metagenome                    ----X(04)----DEQSS-AAX(03)AGTQ--Q--K-----PKK-SDYRDR
gi_212703236_Desulfovibrio_piger_ATCC_29098       R-DMX(03)----RRFAG-MA-----ED-G-GL-TA-----EQW-REVQEY
gi_126661473_Cyanothece_sp._CCY0110               ----X(06)----TMQMD-TL-----G---------K-----KYD-KLTDHG
gi_136020360_marine_metagenome                    ------------------------------------------EQE-IIQSQK
gi_120556756_Marinobacter_aquaeolei_VT8           E-QR-----DRINAAFRT-YF-----HSL-G----R-----ALQQKNGVKH
gi_338997685_Halomonas_sp._TD01                   E-QR-----ERINALFSA-YF-----ASL-G----K-----AL----SKES
gi_152996317_Marinomonas_sp._MWYL1                E-QR-----HRVNKAFHN-YF-----SLL-G------------------HALK
gi_88859991_Pseudoalteromonas_tunicata_D2         V-HQ-----LKYGACLYD-YF-----SLL-G----E------L----LESK
gi_163800453_Vibrio_sp._AND4                      A-HR-----HAIHQAMQA-YF-----RPL-G----D-----------ALSCK
gi_315126745_Pseudoalteromonas_sp._SM9913         N-HT-----LHANEALNH-YF-----QLL-G----Y-----------ALHQ
gi_294142255_Shewanella_violacea_DSS12            Q-HR-----QQIFSALIA-YF-----EPL------------------GDAL
gi_315274348_Enterobacteria_phage_VT2phi_272      A-ELX(01)GGIREAFDH-LF-----RTL-K----TX(07)-AF-YSRKGV
gi_190606601_Moraxella_bovis_Epp63                D-EL-----EQFSKAYTA-V--------------------------FDTL
gi_228969344_Bacillus_thuringiensis_serovar_sotto E-QR-----EHLNR-----SI--------------------------KSL
gi_288561639_Bacillus_pseudofirmus_OF4            L-ER-----KQINEAMDV-YI--------------------------KLL
gi_332304605_Glaciecola_agarilytica_4H37+YE5      T-HR-----RTVQDHFLR-YF-----VHL-G----Q-----AL----ESKS
gi_308050931_Ferrimonas_balearica_DSM_9799        A-HL-----KRIDLAIRG-YF-----APL-G----Q-----------ALSR
gi_221134706_Glaciecola_sp._HTCC2999              S-HR-----KCVNEQFAA-YF-----SQL-G----H-----------AMGH
gi_142045318_marine_metagenome                    N-LR-----TSLNQALML-YF-----YQL-G----V------A----ISHK
gi_142806930_marine_metagenome                    A-LS-----SVLAQHWLG-YF-----SLL-G------------------RVLR
gi_149376567_Marinobacter_algicola_DG893          H-QR-----QRINDAFEC-YF-----VAL-G----G-----ALY--REHAE
gi_336450964_Idiomarina_sp._A28L                  A-LN-----LQLQKAWLD-YF-----GAL-G----N-----AL----DRQS
gi_260775873_Vibrio_coralliilyticus_ATCC_BAA450   A-HR-----QAIYRALHA-YF-----GPL-G----Q-----------ALS
gi_119774733_Shewanella_amazonensis_SB2B          I-HR-----QAIMKAMAG-YF-----RPL-G----R-----------ALAK
gi_88799587_Reinekea_sp._MED297                   T-HR-----QTINRAFAQ-YF-----GSL-G----A-----VL----RRQH
gi_142223042_marine_metagenome                    T-EA-----QAIDAAFED-YF-----GLL-G----Y-----------ALNR
gi_241589636_Ralstonia_pickettii_12D              E-ER-----KTINGHFDT-LF--------------------------AGL
gi_281357131_Victivallis_vadensis_ATCC_BAA548     K-ES-----AAVRKIFDE-FV--------------------------GTL
gi_138663503_marine_metagenome                    A-LS-----DRLSELWLG-YF-----STL-G----Q-----------ALQR
gi_126668031_Marinobacter_sp._ELB17               D-QL-----KNLDQAFKG-LF--------------------------KTV
gi_325914618_Xanthomonas_vesicatoria_ATCC_35937   Y-QR-----QELEKLFSE-LL--------------------------KHV
gi_120536892_Marinobacter_aquaeolei_VT8           S-EL-----DRIKDAFNK-LF--------------------------KTL
gi_137191980_marine_metagenome                    P-QR-----QRINQAFAC-YF-----SAL-G----Q-----ALS-PRSDQK
gi_331000123_Parasutterella_excrementihominis_YIT V-DV-----RRVSEKFKA-----------------------------LFE
gi_137344792_marine_metagenome                    A-LT-----DTLAAIWLQ-YF-----SLL-G----H-----GL----TNKN
gi_303258118_Burkholderiales_bacterium_1_1_47     K-DV-----EKVTNGFKR-IF-----KVI-K----TX(07)ALF-SKANQE
gi_134287922_Burkholderia_vietnamiensis_G4        I-ER-----RVIGAAIDR-Y--------------------------FET
gi_333369137_Psychrobacter_sp._1501_2011          E-ER-----MRINAAFDK-L--------------------------FK
gi_338210739_Runella_slithyformis_DSM_19594       A-EL-----EKIAP-----LF--------------------------RRF
gi_113970416_Shewanella_sp._MR4                   P-HR-----QRIFNALIA-YF-----EPL-G-----------MALGK
gi_94499259_Oceanobacter_sp._RED65                Q-HR-----VRINYAFKD-YF-----QSL-G----Q-----AL----YRES
gi_114563265_Shewanella_frigidimarina_NCIMB_400   Q-HC-----REIYQAMME-YF-----EPL-G----L-----AFD-KQNGQK
gi_85712065_Idiomarina_baltica_OS145/10-262       D-EA-----NAVAECWLD-YF-----QSL-G------------------QALK
gi_51596166_Yersinia_pseudotuberculosis_IP_32953  A-ELX(01)GGVRQAFEH-LF--------------------------NTL
gi_269104751_Photobacterium_damselae_subsp._damse A-ES-----KNIRSSFDH-LF--------------------------NTI
gi_87119325_Marinomonas_sp._MED121                E-QR-----QNINLAFNE-YF-----KML-G-----------AYLNS
gi_269138988_Edwardsiella_tarda_EIB202            Q-ELX(01)GGIGAAFDT-LF--------------------------STL
gi_51245843_Desulfotalea_psychrophila_LSv54       D-EL-----KTVGPAFTD-LF-----KTL-K----SX(07)-LL-YSRSSV
gi_319762397_Alicycliphilus_denitrificans_BC      G-EL-----PQIREAFDA-FF--------------------------QTV
gi_149915016_Roseobacter_sp._AzwK3b               K-DM-----GELRSA-------------------------------FNN
gi_313897977_Clostridium_sp._HGF2                 E-ER-----KKINICFDK-LM-----EYL-K-----------EQGLLH
gi_302668924_Butyrivibrio_proteoclasticus_B316    E-ER-----NRINKAFDD-LI-----K--------------------HLF
gi_193076431_Acinetobacter_baumannii_ATCC_17978   Q-ER-----IRIVHYLDR-WL--------------------------SEL
gi_283795255_Clostridium_sp._M62/1                E-ER-----KAINAVFDE-VF-----SDL-K-----------R-QHFLTH
gi_239907128_Desulfovibrio_magneticus_RS1         A-ER-----KAINAAFDH-FF--------------------------ATV
gi_319792705_Variovorax_paradoxus_EPS             D-IR-----AGLAQALDA--R--------------------------YFK
gi_142771127_marine_metagenome                    D-EL-----GVINPAFRA-LF--------------------------DTL
gi_320535744_Treponema_phagedenis_F0421           ------------------------------------------------YL
gi_325103603_Pedobacter_saltans_DSM_12145         -------------------------------------------------I
gi_335348301_Lactobacillus_salivarius_GJ24        TDNTX(01)KKIVNYFDN-K-----------F-----------------PDYR
gi_227891938_Lactobacillus_salivarius_ATCC_11741  TDDIX(01)AKITEYFD-------------------------------NKF
gi_240047480_Mycoplasma_conjunctivae_HRC/581      ----X(09)----KDTKD-DFX(01)KMY--ED-IF-----EVK-KKMEFV
gi_307269283_Enterococcus_faecalis_TX4248         DKDMX(01)EELTTYFDQ-R--------------------------FPA
gi_336053407_Lactobacillus_kefiranofaciens_ZW3    E-A------------AMSQ-VV-----------------------I-YFDKLF
gi_169834814_Clostridium_botulinum_A3_str._Loch_M E-QLX(01)LLIKEYYSS-L-----------F---------------DIRDKI
gi_168205401_Clostridium_perfringens_E_str._JGS19 SDKYX(01)KELTEYFND-L-----------I---------------NKLDLN
gi_343098022_Paenibacillus_polymyxa_M1            EKTFX(01)NLIQSYFNN-L-----------F---------------FKFVSG
gi_282851885_Lactobacillus_gasseri_2241           TPDIX(01)KKISSYFDK-Q--------------------------FPT
gi_229113621_Bacillus_cereus_Rock115              E-EF--------MNMITD-YF-----NWL---------------L-RKLKAN
gi_228949804_Bacillus_thuringiensis_serovar_monte DEEYX(01)NMVRSYFEK-V-----------L---------------KNKPIN
gi_196048016_Bacillus_cereus_03BB108              DEEYX(01)RAVKLYFDK-F-----------F---------------LDKDI
gi_210616890_Clostridium_nexile_DSM_1787          D-ELX(01)ALIY---------------------------------DYYS
gi_322691234_Bifidobacterium_longum_subsp._longum ------------------------------------------------SLLSD
gi_297618189_Syntrophothermus_lipocalidus_DSM_126 ----X(01)----STW-E-EVX(01)AKY--AA-RF------EY-FDSLFS
gi_225155137_Diplosphaera_colitermitum_TAV2       ----X(04)----AEEF---------APIA--E--E-----IDD-VFRQKG
gi_333996733_Treponema_primitia_ZAS-2             ---------------------------F--HS--R-----LYI-RYYAKG
gi_258514689_Desulfotomaculum_acetoxidans_DSM_771 ----------------EG-YV-----YHGY-KY--I-----KHY-ADEHSA
gi_333979014_Desulfotomaculum_kuznetsovii_DSM_611 ----------------SG-YI-----WHGW-E-----------YI-RHYAGQ
gi_333979806_Desulfotomaculum_kuznetsovii_DSM_611 ----------------TG-YA-----WHGW-Q-----------YI-KACAGG
gi_224369040_Desulfobacterium_autotrophicum_HRM2  ----------------ED-TT-----GNSY-RY-------------IKGYAE
gi_227872114_Oribacterium_sinus_F0268             ------------------------------------------AYVDTP
gi_136199725_marine_metagenome                    ----------------------------------GF-----EAF-YYFDDY
gi_136474110_marine_metagenome                    ----------------------------------GF-----EA---FFLRE
gi_136819193_marine_metagenome                    Q-PV----------RALQR-FF-----N---------------SVV-NFLRRM
gi_140968715_marine_metagenome                    K-PL----------SALRR-FG-----N---------------IIA-NMLRRL
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