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>WP_085441360_NuoL_Magnetofaba_australis
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VPRFFSYLSLFSFAMLSLVTAPNFLQLFFGWEGVGLASYLLIGFWFKKESACNAAIKAFLVNRVGDFGFALGVF
GVFMVFGTLDFLGDKGVFMALTNYQAT---
MMFLGHEFNTMTLICLLLFMGAMGKSAQFFLHTWLPDAMEGPTPVSALIHAATMVTAGVFLVCRASPLFEQSET
ALMVVTVIGAVTAIFAASVGLVQNDIKRVIAYSTCSQLGYMFFAAGVSAYAASMFHLMTHAFFKALLFLGAGAV
IHAMHHEQDMRKMGGLWKKIPLTYALMMIGTLALT--GFPY---------
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HEAPWFMRAPNLLLAVGALLAGYLGHGIIEAG--------WF--
KDAIFLAEGHDALAHAHHAPAHVKWLPFVMFLGGLFLALLMYIWV-----------------------------
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PTLPKKVSELCPRGYQFLLNAWYFDKLYDAIFIKPAKAIGKGLWQT-GDATIIDGYGVNGTA-
NLMVRMGAVLKRMQSGYVVYHYAFAMLAGVLVLITFYA-----------
>WP_011715163_NuoL_Magnetococcus_marinus
MST-----YKLIVLLPLLGSLIAGLLG----RTIGTRMSQMVTIGGIGLSLLLSIQAFWQIAV--NDGE-
VVREIFWSWVISGDFQVTLGVLVDRLTAVMLIVVTGVSTLVHIYSVDYMHEDPD-------
NPRFFSYLSLFSFAMLMLVTSPNFLQLFFGWEGVGLASYLLIGFWFKKESACNAAIKAFLVNRVGDFGFALGVL
AIFMVFGTLDY--SAVFGAARGEFNQT---
MHFLGYEFTTITLICLLLFLGAMGKSAQLFLHTWLPDAMEGPTPVSALIHAATMVTAGVFLVCRASPLFELSET
ALAVVTIIGALTAFFAATVGMVQNDIKRVVAYSTCSQLGYMFFAAGVSAYAASMFHLMTHAFFKALLFLGAGAV
IHAMHHEQDMRKMGGLVKKIPLTYGLMMIGTLALT--GFPG---------
LAGFFSKDAILESAYAAHSATGTFAFWLGIMAAGMTTFYSFRLVFMTFHGKPK---DHHAYDHA----------
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HEAPWFMRGPNIALAIGALFAGYLGVPLIEAG--------WF--
KEAIVLAAGHNALEHAHHVPAWVKWLPFVMFVLGLSVAVVLYVLA-----------------------------
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PTLPAKIAQMCPRGYNFLLNAWYFDKLYDKLFVKGAQCLGQGLWKT-ADETIVDGYGVNGWA-
RTLGRWGASLRRMQSGYVVYHYAFAMFVGVLALATFYS-----------
>WP_068489994_NuoL_Magnetospirillum_marisnigri
MI-------TATVFLPLLGAAVAGLLG----RFIGDRGAQILTCGLLLISAVLAGLIFQTVAL--GHQP-
QTVVIA-DWITSGTFNVAWTLKVDTLTAVMLIVVTWVSAAVHVYSVGYMSHDTS-------
IARFQSYLSLFTFAMLMLVTSDNLVQMFFGWEGVGVASYLLIGFWYEKPSASAAAIKAFVVNRVGDFGFALGIF
GVYFMFGTVGF--DAIFAAAPDKAAAT---
VTFFGVEWHAITICCLLLFVGAMGKSAQLGLHTWLPDAMEGPTPVSALIHAATMVTAGVFMVARMSPLFEFSDT
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IHAMSDEQDIRRMGGIWKHVKVTWVLMWIGSLALA--GIPV---------
FAGYYSKDTILEAAWASHSIAGQGAYWLGCTAAFLTAFYSWRLLLLTFHGRPR--ADEHVMAHV----------
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HESPAVMLIPLLFLALGAVFAGWLGYDLFVGH-HNAE---FW--
GKSILVTAAHPSLENAHHVPSWAALLPTVVAVSGIALAYLLYSFA-----------------------------
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PGIPGALAKAFQPIYLFLLNKWYFDELYDKIFVKPAFKLGKGLWQG-GDGALIDGVGPDGVA-
AGTLAVARKVGRMQSGYLYHYAYAMLIGVAVFVTWYVFNAR--------
>WP_014745483_NuoL_Tistrella_mobilis
MY-------VALILLPLAAAIVAGFFG----RVIGDRGSQLVTTGAVGLAALLSVVAFFDVAV--GGNA-
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KPRFMAYLSLFTFAMLTLVTADNLVQMFFGWEGVGLASYLLIGFWYKRPSANKAAMKAFVVNRVGDFGFSLGIF
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IDFLGMTLPTIEVIAVLLFIGAMGKSAQLGLHTWLPDAMEGPTPVSALIHAATMVTAGVFMVARLSPVFELTSF
TSDMITVIGASTAFFAATVGLTQTDIKRVIAYSTCSQLGYMFFAAGVGAYPAAIFHLMTHAFFKALLFLGAGSV
IHAMSDEQDMRKMGGIWKLIPVTYTFMWIGSLALA--GLPP---------
FAGFFSKDMILETAYAAHTGVGAYAFWLGIAAAFMTAFYSWRLLFMTFHGKPR--ADKHTMDHV----------
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HESPLVMTAPLFPLAVGAIVAGYIGLPMVDPE-LH-----FW--
NGAITMLGEHNILEEAHHVPGWVKLLPLVMSVGGIALAWFLYIRR-----------------------------
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PDLPGKIARDFSGLHKFLLNKWYFDELYDAIFVRPSLWIGRVLWQA-GDRKIIDGLGPDGIA-
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GVFLVTGSVTF--DAVFGELGNVAGTT---
IDFLGMSLPTIEVLGVLLFIGAMGKSAQLGLHTWLPDAMEGPTPVSALIHAATMVTAGVFMVARLSPLFELTVF
TSDMITVIGASTAFFAATIGLTQTDIKRVIAYSTCSQLGYMFFAAGVGAYPAAIFHLMTHAFFKALLFLGAGSV
IHAMSDEQDMRRMGGIWKLIPVTYMMMWIGSLALA--GIPP---------
FAGFFSKDMILETAYAAHSTVGAYAFWMGIAAAFMTAFYSWRLLFMTFHGKPR--ADKHTMEHV----------
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GLFALFGTIGL--DAIFAAP-AKAGAT---
LTVLGLKINAITVCCLLLFVGAMGKSAQLGLHTWLPDAMEGPTPVSALIHAATMVTAGVFLVARMSPLFELSDA
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IHAMSDEQDIRRMGGIWKHVKVTWALMWVGSLALA--GIPF---------
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VPRFMAYLSFFTFCMLMLVTADNLLQMFFGWEGVGVASYLLIGFWYDKPSANAAAIKAFLVNRVGDFGFALGIF
GTFLLFDTISL--DAIFAAVPGKADTM---
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ALMVVTYVGAFTAFFAATVGLVQNDIKRVIAYSTCSQLGYMFFACGVSAYSAGIFHLMTHASFKALLFLGAGSV
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FAGFFSKDMILESAWGAHSSVGNLAFWLGVAAAFMTAFYSMRLLMMTFHGKPR--ADETTMAHV----------
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HESPKVMILPLLVLAAGAIGAGYMGYEYFVGH-DAAA---FW--
GNAIYVAEHHQALENAHHAPGWVKLLPLVMGVSGLGLGFLFYGPM-----------------------------
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SSMPGWLVTNFRSVYDLLLNKWWFDELYDFLFVRPAFKLGRGFWKG-GDGAVIDGCGPDGIA-
SGVLRWVRRATSMQTGFVYHYAFSMLIGVAGLVTWYLFTLG--------
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KPRFMAYLSLFTFAMLMLVTADNLIQLFFGWEGVGLASYLLIGFWYSKPSASAAAIKAFVVNRVGDFGFALGIF
AVYVLFDSVQF--DVIFANAEEVAGTT---
LLFLGHEFSALEITCFLLFIGAMGKSAQLGLHTWLPDAMEGPTPVSALIHAATMVTAGVFMVARLSPIFEYAET
TLAIITVVGASTAFFAATIGCVQNDIKRVIAYSTCSQLGYMFFACGVSAYSAGVFHLMTHGFFKALLFLGAGSV
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HESPAVMTLPLLFLTIGAIFAGWFAKDWFGGG-DYEEMLAFW--
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AVYVLFGTVQF--DTIFANAEEISGST---
LVFLGHDFSALNIATFLLFIGAMGKSAQLGLHTWLPDAMEGPTPVSALIHAATMVTAGVFMVARLSPIFEYAET
TLAIVTVVGATTAFFAATIGCVQNDIKRVIAYSTCSQLGYMFFACGVSAYSAGVFHLMTHGFFKALLFLSAGSV
IHAMSDEQDMRKMGGIWKMVPLTFGVMIIGTLAIT--GVPG---------
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HESPAVMTVPLLILAVGAVFAGWFAVNWFGGN--YEEMLSFW--
NGAIFVAENHQALEHSHHVPEWVKMAPFVAMMLGLALAVLMYRLV-----------------------------
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QTISLL-NWIDTGPLSVDWAIRLDTLTAVMLIVVTGVSSMVHVYSIGYMSHDHS-------
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AAFFLFGTLQF--DQIFAAAPGAVGKT---
FHFLSWDVDALTCTSILLFIGAMGKSAQLGLHTWLPDAMEGPTPVSALIHAATMVTAGVFMVCRLSPLLEYSND
ALHFIAIIGAATAIFAASVGMAQNDIKRVIAYSTCSQLGYMVFAAGVSAYPAAMFHLATHASFKALLFLSAGSV
IHAMSGEQDMRKMGGLWKLIPVTYVMMWIGNLALA--GIPP---------
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RTHSLL-LWINSGTFVADWALKFDTLTAVMLIVVNTVSAMVHIYSIGYMSHDHS-------
KPRFFAYLSLFTFAMLMLVTADNLIQLFFGWEGVGLASYLLIGFWYEKESARAAAVKAFLVNRVGDFGFALGIF
AVYKIFGTVRY--EEIFAVP-HMVDAR---
INFLGMDLPALTTACLLLFVGAMGKSAQLGLHTWLPDAMEGPTPVSALIHAATMVTAGVFMLARMSPLFEYAPD
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IHAMGGEQDMRKMGGIWRLIPTTYALMWIGSLALAGIGIPGV------
FGFAGFYSKDMILEAAWAAHSGVGNLAYWLGVIAALMTAFYSGRLLFLTFHGKPR--ADHHTMEHA--------
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KPRFMSYLSLFTFMMLMLVTSDNLVQMFFGWEGVGVASYLLINFWFEKKSANDASMKAFLVNRVGDFGFALGIF
SIFIIFGSVEF--GTIFPAAAGKAHAT---
FNFLGWHVSALDCACLLLFVGAMGKSAQLGLHTWLPDAMEGPTPVSALIHAATMVTAGVFMLARMSPVFEYAPT
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TVFVIFGTVEF--KPIFAAA-SQAHAT---
FNFLGWNVSALDCACLLLFVGAMGKSAQLGLHTWLPDAMEGPTPVSALIHAATMVTAGVFMLARMSPVFEYAPT
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IHAMSGEQDMRKMGGIWKLIPFTYAVMWIGNLALAGVGIPGV------
YGFAGFYSKDIILEAAYGSGTAVGHFAYWLGIAAAFMTAFYSWRLLILTFHGKPR--ATKDVMDHV--------
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ATFAIFGTIQF--DAIFGAVPQAANQD---
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AIYMIFGTVEF--DGIFAQAASKADAT---
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AVFVIFGTVQF--DEIFAQAASKADAS---
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TIFMVFGTVQF--QGIFDQAAQHKDTM---
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HESPPVMIVPLVVLALGALFSGWLAYEAFVGH-DQKA---FW--
GASIFVASHHDPLEAAHHVPGWVKLLPIFVAVAGIALAWIAYIAR-----------------------------
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PDLPRLAAEALRPVHRFFFNKWYFDELYDRIFVRPSFYLGRGLWKT-GDGALIDGVGPDGVA-
AATQAMSIRASRLQTGYVYHYAFAMLIGVVVLVSWYLYVRI--------
>MBT5660202_NuoL_partial_Rhodospirillaceae_SI073_bin103_UBA11136
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------------------------------------VHVYSIGYMAKDDA-------
IPRFFAYLNLFTFFMLMLVTADNMVQLFFGWEGVGLASYLLIGFWYKRPAANAAAVKAFVVNRVGDFGFALGIF
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AIFLLFGSVNF--GEIFAAAPHHAEAT---
MSFLGFDFHAYTIICLLLFMGAMGKSAQIGLHIWLPDAMEGPTPVSALIHAATMVTAGVFMVVRLSPLFEYAPG
VLNVIAVVGGTTAFFAATIAITQNDIKKVIAYSTCSQLGYMFCAIGVSAYGAAIFHLMTHAFFKSLLFLCAGSV
IHAMSDEQDMRKMGGIWRKVPVTYTMMWIGSLALA--GVPF---------
FAGYYSKDMILEAAWGAHSLPGGYAFLMGTIAAFLTAFYIFRLIFLTFHGEPR--ADEKVMAHI----------
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HESPKSMTVPLVVLAVGAIFAGYLGYDSFVGE-GEKA---FW--
GTSILVLDSHTALIDGHHAPFGIKILPVILGALGILLAYITYFMF-----------------------------
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PGLASHAAERFPGLYAFLYNKWYFDELYDRLIVKPALVLGRGLWKS-GDGEVIDGVGPDGIA-
ASVIALGRRIAGIQSGYVYHYAFAMIIGIAGILTCFLYASVG-------
>MBL6935107_NuoL_Alphaproteobacteria_BS150m-G7_UBA11136
LY-------VATIFLPLIGAIAAGLFG----RWVGDRGAQLIACGMMVLSGLFSIIIFRDVAL--DGNE-
RVIELF-TWIRSGGFEASWALKFDTLSAVMVFVVSVVSALIHIYSIGYMAKDPS-------
IPRFFSYLSLFTFFMLMLVSADNLVQLFFGWEGVGLCSYLLIGFWYDRDSANAAAIKAFVLNRIGDFGFALGIF
AVFYLFGSVSF--ETIFAAAPAQAETS---
FEFLGLEVHALTLICLLLFIGAMGKSAQIGLHVWLPDAMEGPTPVSALIHAATMVTAGVFMVVRMSPLFELAPS
VLALVAVIGALTAFMAGTIALAQNDIKRVIAYSTCSQLGYMFFAIGVSAYGAAIFHLMTHAFFKSLLFLGSGSV
IHAMSDEQDMRKMGGIWRKIPLTYAVMWVGSLALV--GIPF---------
FAGYYSKDIIIESAWGAHSLVGNFAYVIGVVVAFLTAFYSCRLLFMTFHGEPR--ADEKVMAHV----------
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HESPKVMTVPLVLLAVGAIFSGSLGYDLFVGD-GGEG---FW--
RASILVLPGHDALAEAHHAPWYIKLTPLVLAVLGMALAFLVYFMF-----------------------------
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PGLAGHAAERFPRVHAFLYNKWYFDEIYDRLLVRPALILGRGLWKS-GDGELIDGIGPDGIA-
ASVMRMGRRAAALQSGYVYHYAFAMIIGVVGFISWYLYGLMG-------
>MAG23701_NuoL_Rhodospirillaceae_ARS27_o_UBA1136
LY-------VATIFLPLIGAVVAGLCG----RWTGDRGAQLVTCGLMVLSGLFSIVIFREVAL--DGNE-
RAIELF-TWIRSGGLEAAWALKFDTLTAVMVFVVSVVSALIHIYSIGYMAKDPS-------
IPRFFSYLSLFTFFMLMLVSADNLVQLFFGWEGVGLCSYLLIGFWYDRDSANAAAIKAFVLNRIGDFGFVLGIF
AVFYLFGSVNF--ETIFTAAPDQAETT---
FEFLGLEVHALTLICLLLFVGAMGKSAQLGLHVWLPDAMEGPTPVSALIHAATMVTAGVFMVVRMSPLFELAPL
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IHAMSDEQDMRKMGGLWRRIPLTYTVMWVGSLALA--GIPF---------
FAGYYSKDIIIESAWAAHGVVGNFTYILSVVVAFLTAFYSYRLLFMTFHGESR--ADERVMAHV----------
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HESPKVMTVPLVLLSVGAIFSGYLGYDLFVGD-GGEE---FW--
RASILVLPGHDALAEAHHVHWYIKIVPLVMAGLGILLAFVVYFMF-----------------------------
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PGLAGHAAERFPRLHTFLYNKWYFDEVYDRLLVRPALAFGRALWKT-GDGELIDGIGPDGIA-
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>MDP7045168_NuoL_Alphaproteobacteria_Arabian9_MAG_19
LY-------VATIFLPLIGAVVAGLCG----RWTGDRGAQLVTCGLMVLSGLFSIVIFREVAL--DGNE-
RAIELF-TWIRSGGLEAAWALKFDTLTAVMVFVVSVVSALIHIYSIGYMAKDPS-------
IPRFFSYLSLFTFFMLMLVSADNLVQLFFGWEGVGLCSYLLIGFWYDRDSANAAAIKAFVLNRIGDFGFVLGIF
AVFYLFGSVNF--ETIFTAAPDQAETT---
FEFLGLEVHALTLICLLLFVGAMGKSAQLGLHVWLPDAMEGPTPVSALIHAATMVTAGVFMVVRMSPLFELAPL
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IHAMSDEQDMRKMGGLWRRIPLTYTVMWVGSLALA--GIPF---------
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HEAPKVMTVPLVLLSVGAIFSGYLGYDLFVGD-GGEE---FW--
RASILVLPGHDALAEAHHVPRYIKIVPLVMAGLGILLAFVVYFMF-----------------------------
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LY-------VATIFLPLIGAVVAGLCG----RWTGDRGAQLITCGLMVLSGLFSIVIFREVAL--DGNE-
RVIELF-TWIRSGGLEAAWALKFDTLTAVMVFVVSVVSALIHIYSIGYMAKDPS-------
IPRFFSYLSLFTFFMLMLVSADNLVQLFFGWEGVGLCSYLLIGFWHDRDSANAAAIKAFVLNRIGDFGFVLGIF
AVFYLFGSVNF--ETIFTAAPDQAETT---
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IHAMSDEQDMRKMGGLWRRIPLTYTVMWVGSLALA--GIPF---------
FAGYYSKDIIIESAWAAHGVVGNFTYILGVVVAFLTAFYSCRLLFMTFHGESR--ADERVMAHV----------
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HESPKVMTVPLVLLSVGAIFSGYLGYDLFVGD-GGEE---FW--
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HESPKVMTVPLVLLSVGAIFSGYLGYDLFVGD-GGEE---FW--
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IHAMSDEQDMRKMGGLWRRIPLTYTVMWVGSLALA--GIPF---------
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AVFYLFGSVNF--ETIFTAAPDQAETT---
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IHAMSGERDMRQMGGIWRRIPLTYVAMCVGSLSLI--GIPF---------
FAGYYSKDIILESAWEAHGFAGNFAYILGVVVAFLTAFYSYRMLFMTFHGDSR--AGEKVMAHV----------
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HESPKVMTVPLIILSVGAIFSGYLGYDLFVGD-GGEG---FW--
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VKVEVA-SWIVSGTFDVSWSLRIDQLTAVMLVVVNGVSALVHVYSVGYMSHDPH-------
KPRFMAYLSLFTFAMLMLITSDNFLQMFFGWEGVGLASYLLIGFWYHKPAANAAAIKAFLVNRIGDFGFGLGIM
ATFMVFGSVDF--DTVFAASPDQVGKT---
FHFLSWEWDVMTTICILLFIGAMGKSAQVPLHTWLPDAMEGPTPVSALIHAATMVTAGVFLVARCSPMFEFSPT
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HESPWSMLVPLYFLAAGSILSGILFVHYFVGD-GAGA---FW--
GNSIFMLPDNNILEAMHHVPTWVKVAPIVAGLFGILVAWQFYIRR-----------------------------
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KERFFAYLSLFTFAMLALVTSDDLVQLFFGWEGVGLASYLLIGFWYKKPSANAAAIKAFVVNRVGDFGFLLGIF
TIFYVFGAVQY--DTIFAAAPDQVGKT---
ITFLSWEVPALELMCFLLFMGAMGKSAQFLLHTWLPDAMEGPTPVSALIHAATMVTAGVFMVARMSPLFDLAPY
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IHTLADNQDMRRMGGLRKIIPFTWVMMLIGSLALT--AFPL---------
TSGFVSKDFIIETTWFDHTAVGQYTYWMVLIAAFLTSLYTWRLMFMTFEGNFR--GPKDVKAHA----------
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HEPPWTMGVPLMVLAAGALFAGLGFRHLFIGA-DQAS---FW---NRDSIVLPH---
GGHHDVPFWLVLSPTIAMTLGFLIAWYCYMWR------------------------------------------
-----------------PLVPFGLLKRFPATNQFFFHAWYFDALYDRIFVRPAKWLGNFLWKV-
GDGKIIDGLGPNGVA-ARVLDITRGVVKLQTGYIYHYAFIMLIGVALLITYFIVTGGAKP-----
>PJK29752_NuoL_Minwuia_thermotolerans
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GIFLVFEDVTF--AGVFAATPEVAGQT---
FQFLGYEVDILTTICLLLFMGAMGKSAQLPLHTWLPDAMEGPTPVSALIHAATMVTAGVFLVVRCSHMFEYSPD
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IHAVADEQDMRKMGGLARHIKKTYIMMWIGSLALAGIGIPG------
FAYVFGFYSKDLIVESAFGAGSGVGQFAYIMGVGAAIMTAFYSWRLLFMTFHGKPR--APRETMAHI-------
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HDSPPVMMIPLYILAVGAVFSGLLFIGPLTGH-HWHD---FW--
GDSILILPQHGAMEAAHEVPLWVKLSPLVASLVGILIAWVMYVRK-----------------------------
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GIYVLFGSISF--DTIFANASAMQEQT---
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IHAVSDEQDMRRMGGLRKHIKLTYLMMLVGTFALTGVGIPGT-----
ILGFAGFNSKDAIIESAFAAQNGMANYAFAMTVIAALFTSFYSWRLIFLTFHGRER--MSADVKAHI-------
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IHAMSDEQDMRKMGGIWKKIPLTYAMMWIGTLALIGFGIPGIG------
GFAGFYSKDAILEAAYASNGSFHLYAFWMGVLAAVLTAFYSGRLIFLSFHGEPR--ADHHTMEHV---------
----------------------------------------------------
HESPPIMTVPLMVLGVGAVIAGFVAFGMVEPE-GN-----WW--
GGAIFTGPENHVLHAMHEVPLWVSLAPFFAMAFGLGLSWVFYIAM-----------------------------
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PGTAPKIAAAVRPLDNFLRNKWYFDELYDRIFVRPALALGRGLWHG-GDQGIIDRFGPDGVA-
GTTWGTALRIARLQTGYVYHYAFVMLIGVAVFVSWYLFLQR--------
>TVQ34661_NuoL_Geminicoccaceae_bacterium
MY-------TAIVFLPLLGAIVAGLFG----RIIGDRAAQIVTCSLLCISALLSGIALLTVPF--GEP--
FKVPLA-TWIVSGSFEVDWALRIDALTVVMLVVVTWVSALVHIYSIGYMSHDAS-------
IARFMSYLSLFTFAMLMLVTADNFLQLFFGWEGVGVASYLLIGFWYEKASANNAAMKAFIVNRVGDFALILGIA
AIFLVFDSVDF--DTVFAAAPAFAEHQ---
IALFGVTWSTLDLICILLFIGAMGKSAQLGLHTWLPDAMEGPTPVSALIHAATMVTAGVFLIARVSPIIEYAPV
ALAVIVLIGATTAFFAATVALTQNDIKRVIAYSTCSQLGYMFFALGVGAYAAAIFHLFTHAFFKALLFLAAGSV
IHGMSNEQDMRRMGGIWRHMKFTYAMMWIGSLALV--GVPF---------FAGFYSKDLILEAAFAA-
GGVGFYAFALGIAAAVMTAFYSGRLLFMTFHGKPR--ASEEVMHHV----------------------------
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---------------------------------HESPLVMTIPLGLLAVGAVFAGYLGLPMVADD-HA-----
FW--GGSIYLEMERNIIYLAHYVPTWVVIAPIVAGFVGLGLAYVIYIQR-------------------------
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TELADRLAERFRPLYQFSLNKWYFDELYDALFVRPARQAGTFLWRR-VDAGIIDDYGPNGVA-
ATALEGTKRVVKLQTGYIYHYAFVMLIGVAALVSWFLFVARG-------
>WP_138380149_NuoL_Luteithermobacter_gelatinilyticus
MY-------QAIVFLPLLGAIIAGFFG----KQIGDRGAQIVTCSFLVISALLSWIAFGQVAL--GHQE-
AYVTVL-NWISSGDLQLDWAFRIDTLTAVMLVVVTTVSALVHIYSVGYMSHDPH-------
IPRFMSYLSLFTFAMLMLVTADNFLQLFFGWEGVGLASYLLIGFWYKKPSANAAAIKAFVVNRVGDFGFALGIV
AIFMAFGSLDF--TTVFSSVPDYTDNV---
IYFLGMELDLITTISILLFIGAMGKSAQLGLHTWLPDAMEGPTPVSALIHAATMVTAGVFMVARCSPIFEYSPD
ALAFVTFIGASTAIFAATIGVAQNDIKRVIAYSTCSQLGYMFFALGVSAYGAAIFHLFTHAFFKALLFLGSGSV
IHAMSDEQDMRKMGGLWKKIPITFAMMTIGTLALT--GFPF---------
FAGYYSKDMIIESAFASSASMSDYAFAMGVLAALFTSFYSWRLVFMTFFGESR--ASKKVQDHV----------
---------------------------------------------------
HESPQVMLIPLYLLAVGAIASGFVFSEYFTGH-HYED---FW--GTSLKV-
LGDNVMEAAHHVPAWVVWSPFIAMVTGFAVAFYSYILA------------------------------------
-----------------------PETPAAAARTFKYLYNLFLNKWYVDEIYDFLFVRPAKRLGAFLWKK-
GDLGTIDRYGPDGVS-ATVVALARKFREMQTGYLYHYAFAMLIGVAAFTTWFIV--GGN------
>WP_139938140_NuoL_Emcibacter_nanhaiensis
MY-------QTIVFLPLVMSFIAGMFG----NRIGDRGAQIITCGGLIVSAILSWVAFFDIAL--GHNV-
AHVEVL-SWIVSGDFNLSWAFKVDTLTSVMLVVVTTVSCVVHIYSVGYMSHDPD-------
IPRFVSYLSLFTFAMLMLVTADNFLQMFFGWEGVGLASYLLIGFWYKKPSACAAAIKAFVVNRVGDFGFALGIF
AIFMTFGTLDF--ATVFASVPDVAGQK---
IHFLNWELDLITTICILLFIGAMGKSAQLGLHTWLPDAMEGPTPVSALIHAATMVTAGVFMVARCSPIFEYSPD
ALAVVCVIGASTAIFAATIGVAQNDIKRVIAYSTCSQLGYMFFAIGVSAYGAAIFHLFTHAFFKALLFLGSGSV
IHAMSDEQDMRKMGGLWKKIPVTFGLMTIGTLALT--GFPF---------
FAGYYSKDMIIESAFASHSPVGPYAFAMGVVAALFTSFYSWRLVFMTFFGESR--ASKKVQDHV----------
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HESPQVMLVPLYILAVGAVFAGWVFHEYFTGH-HYEE---FW--GHALKL-
VGDNVMHEAHHVPGWVVWSPFVAMVTGFAVAWISYIYA------------------------------------
-----------------------PWIPGAAASTFKYLYNLFLNKWYVDEIYDFLFVRPAKRLGVFLWKR-
GDEQTIDRYGPDGVS-ASVAALARKFKEMQTGYLYHYAFVMLIGVAAITTWFIV--GGN------
>WP_099472212_NuoL_Paremcibacter_congregatus
MY-------QIIVFGPLLAAIIAGLFG----RKLGDKGAQAITCGALILSAILSWVAFFQIGL--GHTV-
EHVTVM-NWVTSGDLSFNWAFKVDTLTAVMLVVVNTVSCLVHIYSVGYMSHDPH-------
KPRFMAYLSLFTFAMLMLVTADNFVQMFFGWEGVGLASYLLIGFWYKKPSACAAAIKAFLVNRVGDFGFALGIL
LVFMATGSVDF--ETVFAKIPELQGQQ---
IHFLWMELDLITTMCILLFIGAMGKSAQLGLHTWLPDAMEGPTPVSALIHAATMVTAGVFMVARCSPIFEFSPD
ALAFVTLVGASTAIFAATIGTTQNDIKRVIAYSTCSQLGYMFFALGVSAYGAAIFHLFTHAFFKALLFLGSGSV
IHAMSDEQDMRKMGGLWNKIPITFAMMTIGTLALT--GFPF---------
LAGFYSKDMIIESAFAANNPWSDYAFFMGVFAALLTSFYSWRLVFMTFFGKSR--ASQSVQDHV----------
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HESTNWMLVPLYVLAAGALAAGFVFKENFVGH-HYED---FW--
GQALFLDAAANVMEAAHHVPGWVVAAPFVVMVLGFLGAIYAYIWK-----------------------------
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PETPAAFAGSFRYLYNLFYNKWYIDEIYDFLFVEPAKKIGVFLWKK-GDENVIDRFGPDGAA-
ASVMTLARRFKALQSGYVYHYAFAMLMGVAAFVTWFI---GGAS-----
```

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>WP_085883634_NuoL_Oceanibacterium_hippocampi
MY-------VLIVFLPLAAALIAGFFG----RQLGDRGAQVVTSGAVLTSALLSWVALFQVAF--GHAP-
VTITLF-DWVVSGDFAASWAIRVDALTAVMLVVVNTVSSLVHVYSIGYMSHDKA-------
KGRFMAYLSLFTFAMLMLVTADNLLQLYFGWEGVGLASYLLIGFWYHKASANAAAIKAFVVNRVGDFGFALGVV
GIFYIFGSIEF--DQIFAAAPEQVGKS---
FVFMGMEVDVLTTLCLLLFLGAMGKSAQLFLHTWLPDAMEGPTPVSALIHAATMVTAGVFMVARLSPLFEYAPD
ALTVVTVVGGSTAFFAATVGLVQNDIKRVIAYSTCSQLGYMFFAAGVSAYPVAIFHLFTHAFFKALLFLCAGSV
IHAVSDEQDMRRMGGLWKHIKATYVLMWIGSLALA--GIWP---------
FAGYFSKDMVLEAAYAAGTTVGSYAFWLGIAAAIMTAFYSWRLLFMTFHGAPR--ASKEVMDHV----------
---------------------------------------------------
HESPKVMLIPLYVLALGSICAGFIFAPYMVGH-HYQE---FW--
GNSILVLEEHVAMAEAHDVAAWVKFLPLVAGVVGILIAFQLYIRR-----------------------------
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PEMPAELARTHQALYQFLLNKWYFDELYDWIFVRPATWLGRVLWKG-GDGRIIDGLGPDGIA-
MTVVRVAARAKQIQTGYIYHYAFAILIGIAAFVTLFFY--GVD------
>MBT5765548_NuoL_Kordiimonadaceae_SI072_bin64
MY-------QTIVFLPLLASIIAGLFG----NRIGVRGAQGVTCGALIVSAVLSWVAFFQVAMAPGDHA-
THVQVL-SWIVSGDFNVNWAFQIDTLTAVMLVVVNTVSCLVHIYSVGYMSHDPH-------
IQRFMSYLSLFTFAMLMLITSDNFVQMFFGWEGVGLASYLLIGFWYKKPSACAAAIKAFVVNRVGDFGFALGIF
AIFMTFGSADF--AVVFASVGDHVDKT---
IHFLGMELDLLTTICLLLFIGAMGKSAQLGLHTWLPDAMEGPTPVSALIHAATMVTAGVFMVARCSPLFEYSPD
ALAVVAVIGASTAFFAATVGMSQFDIKRVIAYSTCSQLGYMFFALGVSAYGAAVFHLFTHAFFKALLFLGSGSV
IHASSDEQDMRNMGGLRKQIPVTFWMMTIGTLALT--GFPF---------
LAGYYSKDMIIESAFAAHSGVGTYAFGLGVAAALMTSFYSWRLVFMTFFGESR--ASKEVQDHV----------
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HESPQVMLIPLYVLALGALLSGFVFKEYFVGH-NYEE---FW--AGALFL-
IGDNVMEAAHHVPTWVIASPFIAMVVGFATAWYFYVKE------------------------------------
-----------------------PSMPGKFTSTFRFAHALSFNKWYFDELYDIIFVKPAMKLGMIFWKR-
GDENIIDRYGPDGVS-AAVVRVAQKFKQFQTGYLYHYAFVMLIGLSALVTFFV--MGGL------
>MBT6031505_NuoL_Kordiimonadaceae_SI072_bin126
MY-------QTIVFLPLLASLIAGLFG----NRIGDRGAQIVTCGAMIVSAVLSWVAFYQVALTPGDNS-
LHVQVL-SWIVSGDFNVNWAFQIDSLTAVMLVVVNTVSCLVHIYSVGYMSHDPH-------
IPRFMSYLSLFTFAMLMLITSDNFVQMFFGWEGVGLASYLLIGFWYKKPSACAAAIKAFVVNRVGDFGFALGIF
AIFMTFGSADF--AVVFADVGSYTDKS---
IHFLGMELDLLTTICILLFIGAMGKSAQLGLHTWLPDAMEGPTPVSALIHAATMVTAGVFMVARCSPLFEYAPA
ALEVVCIVGASTAFFAATVGMSQFDIKRVIAYSTCSQLGYMFFALGVGAYGAAIFHLFTHAFFKALLFLGSGSV
IHASSDEQDMRNMGGLRKKIPLTFWMMTIGTLALT--GFPF---------
LAGYYSKDMIIESAFAAHSSVGSYAFAMGVAAALMTSFYSWRLVFMTFFGESR--ASKEVQDHV----------
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HESPQVMLVPLYVLAFGALFSGFIFHEYFVGA-HYED---FW--AGALFL-
VGDNVMEAAHHVPMWVVEAPFVAMTVGLATAYYFYIRR------------------------------------
-----------------------PEMPGKFVETFRFLHAISFNKWYFDELYDILFVRPAMKLGYILWKR-
GDENIIDRYGPDGVS-AAVVRVAEKFRSLQTGYLYHYAFAMLIGLSAFVTWFV--MGGQ------
>MBT3790209_NuoL_Alphaproteobacteria_SI054_bin61
MY-------TALVFLPLLGAVLAGLFG----RILGDRGSQAVTLIGITTSALLSVYVFFDVT---
GNNNPVVVDLF-TWIESDSFEVSWALRVDQLTAVMLMVVCVVSAVVHWYSVGYMSHDKA-------
IPRFMSYLSLFTFAMLMLVTADNFLQMFFGWEGVGLCSYLLIGFWYDRPSANAAAIKAFLVNRVGDFGFALGIM
AIFFTFNSVEF--DVVFAAAPEMAGKT---
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FMFLGQEWDILTTITMLLFVGAMGKSAQLGLHTWLPDAMEGPTPVSALIHAATMVTAGVFMLARCSYLFEYAPF
TLEVVTVIGATTAFVAATIGLVQNDIKRVIAYSTMSQLGYMFFAIGVSAYPAAIFHLLTHAFFKALLFLGAGSV
IHAMSDEQDMRNMGGIYKLIPGTYLMMWIGSLALA--GVPL---------FAGYYSKDMIIEVAFAG-
SGVGTYAFTMGILAALMTAFYSWRLLFMTFHGPAR--ADEKVMAHV----------------------------
---------------------------------HESPKVMMLPLLVLALGAIFAGWFWAGDMIGD-GRVA---
FW-GGESIFIQPANHIFENAHHVSAWVKYSPTALGAIGILLAWWFYIKN-------------------------
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PNIPKAIATMHREAHLFLLNKWYFDELYDLIFVNPAKRLGHFLWKF-GDGKIIDGLGPDGIS-
RLVLNITRRAQTLQSGYVYHYAFAMMLGVAGFVSWFVFGLGG-------
>MBT4017013_NuoL_Alphaproteobacteria_SI053_bin31
MY-------TALVFLPLLGAVIAGLFG----RVLGDRGSQAVTLIGITTSALLSLYVFFDVT---
GNNNPVVIELF-TWMESDSFEVSWALRIDQLTAVMLMVVTVVSAVVHWYSVGYMSHDKA-------
IPRFMAYLSLFTFAMLMLVTADNFMQMFFGWEGVGLCSYLLIGFWYDRPSANAAAIKAFLVNRVGDFGFALGIM
AIFFTFNSVEF--DVVFAAAPDVAGKT---
FVFLGQEWDILTTITMLLFVGAMGKSAQLGLHTWLPDAMEGPTPVSALIHAATMVTAGVFMLARCSPIFEFAPF
TLEVVTIIGATTAFVAATIGLVQNDIKRVIAYSTMSQLGYMFFAIGVSAYPAAIFHLMTHAFFKALLFLGAGSV
IHAMSDEQDMRKMGGIYKLIPGTYLMMWIGSLALA--GVPL---------
FAGYYSKDMIIEVAFASNSGVGMYAFTMGILAALMTAFYSWRLIFMTFHGPAR--ADEKVMAHV----------
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HESPKVMMLPLLVLAFGAIFAGWFWFDDMVGD-GRAA---FW--
GQSIFIQPANQIFENAHHVSAWVKYSPTALGAFGILLAWWFYIKN-----------------------------
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PGIPKTIATAHREVHSFLLNKWYFDELYDLIFVRPAKRIGYFLWKI-GDGKIIDGFGPDGIS-
RLVLNITRRAQALQTGYVYHYAFAMMLGVAGFVSWFVFGLGG-------
>MBT7747133_NuoL_Alphaproteobacteria_SI037_bin135
MY-------TALVFLPLLGAVLAGLFG----RILGDRGSQAVTLIGITTSALLSVYVFFDVT---
GNNNPVVVDLF-TWIESDSFEVSWALRVDQLTAVMLMVVCVVSAVVHWYSVGYMSHDKA-------
IPRFMSYLSLFTFAMLMLVTADNFLQMFFGWEGVGLCSYLLIGFWYDRPSANAAAIKAFLVNRVGDFGFALGIM
AIFFTFNSVEF--DVVFAAAPEMAGKT---
FMFLGQEWDILTTITMLLFVGAMGKSAQLGLHTWLPDAMEGPTPVSALIHAATMVTAGVFMLARCSYLFEYAPF
TLEVVTVIGATTAFVAATIGLVQNDIKRVIAYSTMSQLGYMFFAIGVSAYPAAIFHLLTHAFFKALLFLGAGSV
IHAMSDEQDMRNMGGIYKLIPGTYLMMWIGSLALA--GVPL---------
FAGYYSKDMIIEVAFASGSGVGTYAFTMGILAALMTAFYSWRLLFMTFHGPAR--ADEKVMAHV----------
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HESPKVMMLPLLVLALGAIFAGWFWAGDMIGD-GRVA---FW--
GESIFIQPANHIFENAHHVSAWVKYSPTALGAIGILLAWWFYIKN-----------------------------
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PNIPKAIATMHREAHLFLLNKWYFDELYDLIFVNPAKRLGHFLWKF-GDGKIIDGLGPDGIS-
RLVLNITRRAQTLQSGYVYHYAFAMMLGVAGFVSWFVFGLGG-------
>MBT5047508_NuoL_Rhodospirillaceae_SI074_bin93_MPNO01
MLY------VLCIFLPLIGAAIAGLLG----PWIKARGAMIVTCGALLISALISPFILIEVGL--EGKT-
TTIQIF-NWISSGAFEVDWALRFDTLTAVMLVVVTVVSCAVHFYSIGYMSHDPS-------
IPRFFSYLSLFTFFMLMLVTADNFLQLFFGWEGVGLASYLLIGFWYEKPSANAAAIKAFLVNRVGDFGFALGIM
GVFLLYGTVSF--DAVFDATPGKAAAT---
IEFLGGQYHALTVICLLLFVGAMGKSAQLGLHTWLPDAMEGPTPVSALIHAATMVTAGVFMVARLSPMFEYSPS
ALAVVTVVGASTAIFAATVGVCQNDIKRVIAYSTCSQLGYMFFACGVSAYAAGIFHLFTHAFFKALLFLGAGSV
IHAMSDEQDMRKMGGIWRMIPVTYAVMWIGSLALA--GIPP---------
FAGFYSKDIVLEAAYASNTGIGEYAFWMGIAAAFLTAFYSWRLLLMTFHGEAR--ADERVMAHV----------
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HESPKVMLIPLILLAVGAIFAGYIGVSYFVGE-GAVE---FW--
GNAILVLPSHPALEAAHHVPFWVKALPLVVGVSGIALAYILYVLA-----------------------------
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PGLPAAIAGRFRFIHQFLLNKWYFDELYDFLFVRPAFILGRGFWKS-GDGALIDGIGPDGIA-
AATLNLARRAAALQSGYLYHYAFAMLTGVVVLVTWYLFHQVG-------
>MBT4689853_NuoL_Rhodospirillaceae_SI039_bin92
MY-------HAIVFLPLIAFLIVGPFG----RVLGDKPSQWITCGAVITSAVLSIVAFWQIAL--
GGGDTVKVEIA-SWIVSGTFDVSWALRIDALTAVMLVVVNGVSALVHVYSVGYMSHDPH-------
KPRFMAYLSLFTFAMLMLITSDNFLQMFFGWEGVGLASYLLIGFWYHKPSANAAAIKAFLVNRVGDFGFGLGIM
AIFMVFGSLDF--DTVFAAVPGQVGNT---
FHFLNWEFDIITTICILLFIGAMGKSAQVPLHTWLPDAMEGPTPVSALIHAATMVTAGVFLVARCSPMFEFSPT
ALVVVTIVGGFTAFFAATVGLVQNDIKRVIAYSTCSQLGYMFFALGVGAYPVAIFHLFTHAFFKALLFLGSGSV
IHAMSDEQDMRRMGGIFKYVPQTAIMMWIGSLALA--GLPI---------
FAGFYSKDAILESAFAAHTGAGMFAFYAGMAAAVMTAFYSWRLLFMTFNGDPR--ASQEVMSHV----------
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HESPPSMLIPLYFLAAGSILSGMLFVHYFVGD-GHQA---FW--
GDAIFMGPENHILEAMHHVPTWVKIGPIAAGIIGIFVAWLFYIKR-----------------------------
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KDIPVNLAKVHHEVYLFLLNKWYFDELYDLIFVRPAKWLGRILWRG-GDGRIIDGYGPDGIA-
AMVMHLARRASALQSGYLYHYAFAMLIGVAVLVTWYY-TTGGGH-----
>MBV40747_NuoL_Rhodospirillaceae_NP113_oxycline
MY-------HAIVFLPLLAFLIVGTFG----RVFGDKPSQWITCGAVIASAILSLVAFWQVAL--GGNP-
VKVEIA-SWIVSGTLDVSWALRIDALTAVMLVVVNGVSALVHVYSIGYMSHDPH-------
KPRFMAYLSLFTFAMLMLITSDNFLQMFFGWEGVGLASYLLIGFWYHKPSANAAAIKAFLVNRVGDFGFGLGIM
ATFMVFGSIDF--NTVFAAAPDQVGKT---
FHFLSWEWDVMTTICILLFIGAMGKSAQVPLHTWLPDAMEGPTPVSALIHAATMVTAGVFLVARCSPMFEFSPT
ALVVVTVVGGSTAFFAATVGLVQNDIKRVIAYSTCSQLGYMFFALGVGAYPVAIFHLFTHAFFKALLFLGSGSV
IHAMSEEQDMRRMGGIFKYVPQTAILMWVGSLALA--GLPI---------
FAGFYSKDAILESAFAAHTGAGDYAFYLGLAAAVMTAFYSWRLLFMTFHGIPR--ASQAVMSHV----------
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HESPLVMLMPLYFLAAGSILSGILFVHYFVGD-GHQA---FW-
RGQAIFMAEGNDILESFHHVPIWVKVAPIAAGVFGIFVAWLFYIRN----------------------------
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QDLPAKLAKLHYPLYLFLLNKWYFDELYDLILVNPAKWLGRLLWKG-GDGKIIDGFGPDGIA-
ATVMNLARRASALQSGYLYHYAFAMLIGAVVLVTWYYTSTGGGH-----
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MY-------HAIVFLPLLAFLIVGTFG----RVLGDRPSQWITCGAVITSAILSLVAFWQVAL--GGQP-
VKVEIA-SWIVSGTFDVSWALRIDALTAVMLVVVNGVSALVHVYSVGYMSHDPH-------
KPRFMAYLSLFTFAMLMLITSDNFLQMFFGWEGVGLASYLLIGFWYHKPSANAAAIKAFLVNRVGDFGFGLGIM
ATFMVFGSLDF--DTVFAASPDQVGKT---
FLFLSWEWDVMTTICILLFIGAMGKSAQVPLHTWLPDAMEGPTPVSALIHAATMVTAGVFLVARCSPMFEFSPT
ALVVVTIVGGTTAFFAATVGLVQTDIKRVIAYSTCSQLGYMFFALGVGAYPVAIFHLFTHAFFKALLFLGSGSV
IHAMSDEQDMRRMGGIFKYVPQTAILMWIGSLALA--GLPI---------
FAGFYSKDAILESAFAAHTGAGDYAFYLGLAAAVMTAFYSWRLLFMTFNGTPR--ASQEVMSHV----------
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HESPLVMLIPLYFLAAGSILSGILFVHYFVGD-GAEA---FW--
GQAIFMAEGNNILEAMHHVPMWVKIAPIAAGVIGILLAWQFYIRR-----------------------------
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TDIPVKLAKMHHELYLFLLNKWYFDELYDLIFVNPAKWLGRVLWKG-GDGRIIDGFGPDGIA-
ATVMRVARRASALQSGYLYHYAFAMLIGVAVLVSWYYLSSGGGH-----
>MBL6951394_NuoL_Alphaproteobacteria_BS150m-G9_BlackSea
MY-------HAIVFLPLLAFLIVGSLG----RVLGDRPSQWITCGAVIISALLSLLAFWQVAL--GGQA-
VRVDIG-SWIVSGTFDVSWALRIDQLTAVMLVVVNGVSALVHVYSVGYMSHDPH-------
KPRFMAYLSLFTFAMLMLVTADNFLQLFFGWEGVGLASYLLIGFWYHRPTANAAAIKAFLVNRVGDFGLALGIM
AIFTVFGSLDF--DTVFAATPGQVGKS---
FNFLSWEWDVMTTICILLFIGAMGKSAQVPLHTWLPDAMEGPTPVSALIHAATMVTAGVFLVARCSPMFEFSPT
ALVVVTIVGGTTAFFAATVGLVQNDIKRVIAYSTCSQLGYMFFALGVGAYPMAIFHLFTHAFFKALLFLGSGSV
IHAMSDEQDMRRMGGIYKYVPQTTGLMWVGSLALA--GFWP---------
LAGYYSKDAILESAFAVHTGAGEYAFWLGMAAAVMTAFYSWRLLFMTFAGEPR--ASQEVMRHV----------
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HESPLSMLIPLYFLAAGSILSGVLFVHYFVGE-GHVE---FW--
GQAIFMAPGNDVMEAVHHVPTWVKVAPLVAGIVGILVAWQFYIRR-----------------------------
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RDIPAGLAKINHEVYEFLLNKWYFDELFELIFVRPAKWLGRLLWKT-GDGRIIDGFGPDGIA-
ASVLNLARRASALQSGYLYHYAFAMLIGVAALVSWYYISSGGGH-----
>MDP6874949_NuoL_Alphaproteobacteria_Arabian9_MAG_8_ODZ
MY-------HAIVFLPLLAFLIVGALG----RILGDKPSQWITCGAVITSAILSLVSFWQVAL--GGQP-
VKVEIA-SWIVSGTFDVSWALRIDALTAVMLVVVNGVSALVHVYSVGYMSHDPH-------
KPRFMAYLSLFTFAMLMLITSDNFLQMFFGWEGVGLASYLLIGFWYHKPSANAAAIKAFLVNRIGDFGFGLCIM
ATFMVFGSVDF--DTVFAAAPDQVGKT---
LHFLNWEWDVMTTICILLFIGAMGKSAQVPLHTWLPDAMEGPTPVSALIHAATMVTAGVFLVARCSPMFEYSPV
ALTVVTIVGASTAFFAATVGLVQNDIKRVIAYSTCSQLGYMFFALGVGAYPVAIFHLFTHAFFKALLFLGSGSV
IHAMSDEQDMRRMGGIFKYVPQTAIMMWIGSLALA--GLPI---------
FAGFYSKDAILESAFAAHTGAGDYAFYLGLAAAVMTAFYSWRLLFMTFNGTPR--ASQEVMSHV----------
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HESPPSMLIPLYFLAAGSILSGILFSHYFIGE-GHEA---FW--
GQGIFMLPDNDILEALHHVPMWVKIAPIAAGIIGILVAWQFYIRR-----------------------------
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TDLPAKLAKVHHEAYLFLLNKWYFDELYDLIFVNPAKWLGRLLWKG-GDGRIIDGFGPDGIA-
ATVMRVARRASALQSGYLYHYAFAMLIGVGVLVTWFYTSSGGGH-----
>MBM3510012_NuoL_Alphaproteobacteria_K_Offshore_80m_m2_115
MFY------AAIVFLPLVGAIAAGLFG----RLLGVRASQLVTCLALTLSGVLATWGLYETAV-IGPDK-
QQIVLF-TWIVSGDFDVSWTLRIDTLTAVMLFTVSVISSIIHWYSIGYMAHDPH-------
IPRFFAYLSLFTFAMLVLVTADNFLQLYFGWEGVGLCSYFLIGFWYDRPSANAAAIKAFVVNRVGDFGFALGIM
AMFFTFNSVNF--DTVFAGAPAVAGKT---
FEFLGAEYDILTVTTLLLFIGAMGKSAQVPLHTWLPDAMEGPTPVSALIHAATMVTAGVFLVARCSPLFEYAPT
TLAIVTVIGAFTAFFAATVGLVQNDIKRVIAYSTCSQLGYMFFACGVGAYAVAIFHLFTHAFFKALLFLGSGSV
IHGFSDEQDMRRMGGVWRKMPVTYAVMWVGSLALA--GIPF---------
FAGYYSKDLIIESAFAASTEVGYLAFYLGVGAALLTAFYSWRLLFMTFHGPTR--ANPEVYEHV----------
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HESPKIMTVPLLALAVGALFAGVAGYDAFVGD-GRAA---FW--
REAIFLLPGHDVIEAAHHVPLWVKLLPIAIASAGIALAWQFYIRR-----------------------------
------------------------------
TELPGALAKTHADLYQFLLNKWYFDELYDAIFVRPAKFLGRALWHG-GDGRIIDGFGPNGIA-
QVVIQLARRASLLQTGYLYHYAFAMLIGVAALVTWFTRTGGGAP-----
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>MBM3570281_NuoL_Alphaproteobacteria_M_DeepCast_65m_m2_129
MLY------GLIVFLPLIAAIVAGFGG----RALGDRGAQVVTCGALIVSALLSGVAFYQVAW--KGQP-
VTVELL-TWIDSGAFDVMWSLRIDQLTAVMLVVVTWVSAVVHVYSVGYMAHDPH-------
IPRFMAYLSLFTFAMLMLVTSDNFVQLYFGWEGVGLASYLLIGFWYHKPSANAAAIKAFVVNRIGDFGFGLGIC
GVFLVFGTVEF--DPVFQTAPGFAGKT---
FEFLGMKLDMLTVICLLLFMGAMGKSAQVPLHTWLPDAMEGPTPVSALIHAATMVTAGVFLVARCSPLFEYAPD
ALAVVACIGAFTAFFAATVGLCQNDIKRVIAYSTCSQLGYMFFAAGLSAYAAAIFHLFTHAFFKALLFLGSGSV
IHGMSGEQDMRRMGGLLAPLKITYVLMWIGSLALA--GVPL---------
FAGYYSKDAIVETAFMAGGKLGSFAFVMGVAAAFMTAFYSWRLLFMTFHGQNR--HPDRVIEHAH---------
---------------------------------------------------
HESPAVMLVPLYVLAAGSIFAGALFAQAFIGE-GSPI---FG--ASILVL-
PGHDALAQAHHAPLWVKLAPVAVGLAGIALAWWMYVRR------------------------------------
-----------------------PDLPGKLAAMHGDAHRFLLNKWYFDELYDALFVRPAKWLGHALWKR-
GDGKVIDGLGPDGIA-ALTLDIAKRATRLQTGYVYHYAFAMLIGVALLVSWYLY-RGGM------
>OUR77105_NuoL_Alphaproteobacteria_46_93_T64_Sneathiellales
MY-------VLIVFLPLLAALIAGFGA----RQLGDRGSQIVTSGAVSASAILSWVALFQVAF--GSAP-
TTIELF-TWINSGTFDVSWSLRVDSLTAVMLVVVNTVSALVHIYSIGYMSHDPH-------
KPRFMSYLSLFTFAMLMLVTSDNFLQMYFGWEGVGLASYLLIGFWFNKPSANAASIKAFVVNRVGDFGFALGIM
AIYLVFDSISF--DTVFAAVPEKVGET---
FNFLGYEVDVITTIALLLFLGAMGKSAQLGLHTWLPDAMEGPTPVSALIHAATMVTAGVFMVARCSPIFEFSPT
ALAVVTVVGASTAFFAATVGLVQNDIKRVIAYSTCSQLGYMFFAIGVGAYPVAIFHLFTHAFFKALLFLGSGAV
IHAVSDEQDMRKMGGLGKHIKITYAMMFIGTVALT--GVPF---------
FAGFYSKDAIIESAFMAGTDVGNYAFWCGIGAALMTAFYSWRLMFMTFHGKPR--ASKEVMSHV----------
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HESPNVMLIPLYVLAAGAIGAGFVFYEPMVGH-GYKE---FW--
GNAILLRESNTIMTDFHNIPSWVFWAPMIAMIAGFLLAFNMYIRR-----------------------------
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TDIPVQLAKTHSALYQFLLNKWYFDELYDVVFVRPARWIGSKLWTI-GDGKIIDGLGPDGIA-
ARVLDLAKRASMLQSGYLYHYAFAMMIGVAAFVSFFFL-AGGGH-----
>WP_144258814_NuoL_Ferrovibrio_terrae
MY-------HLIVFLPLLAAIIAGLFG----RRIGDVASMAVTCVAVIISAVLSWVAFYLVIS--KGMV-
VTVKVL-DWIDSGTFSVDWALKIDQLTAVMLVVVNTVSAVVHVYSVGYMSHDPH-------
RSRFFSYLSLFTFAMLMLITADNFVQLYMGWEGVGLASYLLIGFWFHKPSANAASIKAFVVNRVGDFGFALGIM
ALFFATGSVTF--EAVFAAAPDLAGKT---
FHFLWKDWDILTVATFLLFLGAMGKSAQLGLHTWLPDAMEGPTPVSALIHAATMVTAGVFMVARCSPLFEYAPD
TLAFVTVIGASTAFFAATVGLAQNDIKRVIAYSTCSQLGYMFFALGVSAYPAAIFHLFTHAFFKALLFLGAGSV
IHAVDGEQDMRRMGGLWKHIKITYAMMWIGSLALA--GFPI---------FAGYYSKDMILEVAYAA-
GGVGQYAYIMGMAAAILTAFYSWRLLFMTFHGKPR--ADHHVMEHV----------------------------
---------------------------------HESPMVMLIPLFVLATGAVLAGIVFYDGFVGH-HWKE---
FW--GSSILILENHKAMDEAHHVPFLVKVGPIIVGVIGIFIAWIAYIRD-------------------------
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TSLPGRTAAQHHMLYSFLLNKWYFDELYDRVFVRPTFWLGNLLWKG-GDGKIIDGLGPDGLA-
ATVVRLARRASILQSGYVVHYAFAMLIGVAVLVTYFFSAMGH-------
>WP_206376079_NuoL_Sneathiella_chungangensis
MMY------VLIVFLPLLAALIAGLFG----RSLGDRGSQLITCGAVIISAILSWVALYQIAF--QQTT-
EAVELL-TWINSGDFDVNWALRIDSLTAVMLVVVNTVSAVVHVYSIGYMSHDPH-------
KPRFMAYLSLFTFAMLMLVTSDNFVQLYFGWEGVGLASYLLIGFWYKKPAANAAAIKAFVVNRVGDFGFALGIM
GIYFVFNSVSF--DEVFAAAPSQAGQT---
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FEFLGYQVDILTTLCLLLFVGAMGKSAQIGLHTWLPDAMEGPTPVSALIHAATMVTAGVFMVARCSPIFEYSPE
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IHAVSDEQDMRKMGGLWKHIKVTYAMMWIGSLALA--GIPL---------
FAGYYSKDLIIESAFAAHTGVGDYAFWAGVAAALLTAFYSGRLIFMTFHGEPR--ASKEVMAHV----------
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HESPMVMLIPLGVLAAGAIFAGMLFAGPMTGE-DFRE---FW--
GASILMLENSTAMLDAHHVPLWVKLLPLVLGVFGIALTYQMYIRR-----------------------------
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TDIPVQLAKTHSALYQFLLNKWYFDELYDFLFVRPAKAIGRFFWTF-GDGKVIDGLGPDGIA-
GRVLVLARRASQLQSGYMYHYAFAMLLGVAAFVSYFFFAGGH-------
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MSQF-----HIIVFGPLLGFLIAGLFA----KQIGDRGAMAVTTGLVTLSAILSAFVLKDVAF--DHNQ-
YRILVL-EWVRSGSLSFDWTLYIDSLTAVMLVVVNTVSALVHWYSIGYMSHDPH-------
RARFFAYLSLFTFAMLMLVTSDNLVQMFFGWEGVGLASYLLIGFWFKKPSANAAAIKAFVVNRVGDFGFSLGIF
ALFLLTGSVIF--EDIFQSLEGFADAR---
FVFLGMDVHALTTIAVLLFVGAMGKSAQLFLHTWLPDAMEGPTPVSALIHAATMVTAGVFLMARMSPLLELAPG
ALTLIMIIGGATAFFAASVGLVQNDIKRVIAYSTCSQLGYMFVAIGASAYGAAIFHLFTHAFFKALLFLGAGSV
IHAMSDEQDMRKMGGLSKMVPLTYLMMMVGTLALT--GFPY---------
TAGFFSKDMIIESAFATHNPAASFGFLMTVIAAFMTSFYSWRLVFMTFHGTPR--ADEKTLSHV----------
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HESPAVMWVPLAILAVGAVIAGVVFSDAFIGE-GRLA---FW--AGSLVA-
GEGDVMDEAHHIASWIKWLPTGMMALGFALSFLFYIAK------------------------------------
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GDQKTIDGLGPDGIA-AQVMAAARRVRVLQSGYVYHYAFAMLIGIALVITYFVLTGGGF------
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RSRFFAYLSLFTFAMLMLVTSDNLVQMFFGWEGVGLASYLLIGFWFKKPSANAAAIKAFVVNRVGDFGFSLGIF
ALFMLTGSVVF--ADIFASLDGVADAR---
FIFLGYEVHALTTIAVLLFIGAMGKSAQLFLHTWLPDAMEGPTPVSALIHAATMVTAGVFLMARMSPILELAPG
AMTLIMVIGGATAFFAASVGLVQNDIKRVIAYSTCSQLGYMFVAIGASAYGAAIFHLFTHAFFKALLFLGAGSV
IHAMSDEQDMRKMGGLSKMIPLTYVMMMVGTLALT--GFPY---------
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HESPAVMWVPLAILAVGAIAAGFVFSDYFIGH-DRFD---FW--AGALVT-
SHGDVMDEAHHIPGWIKWLPTGMMALGFLLSVLFYVVK------------------------------------
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GDQKTIDGFGPDGIA-ATVLAAAKRIRVLQSGYVYHYAFAMLIGIAIVISYFVLTGGGF------
>RMF12532_NuoL_Alphaproteobacteria_J084
MNQ-----FHVIVFGPLVGFLIAGLFG----RRIGDRASMLLTSLLVSLSAVLSIPVFIDTAF--SGGQ-
FSVPVL-EWVQVGMLHFTWSLHVDTLTAVMLVVVTVVSSLVHWYSIGYMDEDPD-------
KPRFFAYLSLFTFAMLMLVSADNLVQTFFGWEGVGLASYLLIGFWFKKPSANAAAIKAFVVNRVGDFGFSLGIF
ALFMVTGSVGF--EKIFAKVPSLAQAD---
FIFLGHQAHALTVIGVLLFIGAMGKSAQILLHTWLPDAMEGPTPVSALIHAATMVTAGVFLVARMSPLYEHAPA
AADLVTFIGATTAFFAATVGLVQNDIKRVIAYSTCSQLGYMFVAAGVSAYGAAIFHLFTHAFFKALLFLGAGSV
IHAMHHEQDMRRMGGLRPMIPLTYLMMIVGTLALT--GFPL---------
TAGYFSKDSIIEAAFAHGGSIGEYAFVMTVVAAALTSFYSWRLIFLTFHGRPR--ASEEVLAHV----------
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HESPAVMTIPLMVLAAGALFAGWGFHEFFVGE-ARGE---FW--NGALAA-
GGGRVLDHIHHLPWTITYLPTVMMVLGFVIAFWFYLAN------------------------------------
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GDGRIIDGLGPDGVA-RAVMAGAARIRRIQTGCIYTYAFAMLIGVVLLVATVMLAERGF------
>NVJ99269_NuoL_Alphaproteobacteria_HF-Din21
MES------KFIVFLPLVGFLIAGMFG----RNIGDRASQVLTSSLVTIGAALSWYVFADVAF--VHNV-
YPVHVL-DWVKSGTLEFAWAFKIDTLTAVMLVVVNTVSALVHWYSMGYMEEDPD-------
KPRFFAYLSLFTFAMLMLVTSDNLVQMFFGWEGVGLASYLLIGFWFKKPSANAAAIKAFVVNRVGDFGFALGIY
AVFLMTGSVEF--DVIFANIGDYQTAT---
MTFLGHEYHAITVICLLLFVGAMGKSAQLGLHTWLPDAMEGPTPVSALIHAATMVTAGVFLVARFSPVFEYSEY
ALQVVTIVGASTAFFAASVGLVQNDIKRVIAYSTCSQLGYMFFALGVGAYGGAVFHLFTHAFFKALLFLGAGSV
IHALHHEQDMRNMGGLFKKIPFTGTVMIIGTLAIT--GVPF---------
LSGFYSKDLIIEAAYASDAGASQFAFVMGVAAAFMTSFYSWRLIFLTFFGETR--AKQKYFDHA----------
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HEGPIFIKVPLAILALGALGAGFIFKEFFIGH-ERVA---FW--NGALVT-
AMDDVMEAAHHVPGAVIAAPFVVMLLGFLLAFAFYGRK------------------------------------
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GDEQTIDGFGPNGVS-AAVAAVAAKARKLQTGYVYHYAFAMIIGLAVVVTWFMAQSGAH------
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MLY------KLIVFLPLIGFLVAGLFG----RRIGDRGSQLLTSGLVTISAILSWTAFVDVAL--LHNK-
YSIHVL-DWVTSGSLEFNWAFKIDTLTAVMLVVVNSVSALVHWYSMGYMHEDPD-------
KPRFFAYLSLFTFAMLMLVTADNLVQMFFGWEGVGLASYLLIGFWYTKPSANAAAIKAFVVNRIGDFGFSLGIF
AVFVLFNTVQF--DGIFTQVETYKDAT---
MVFLGQEYHALTVISLLLFVGAMGKSAQLGLHTWLPDAMEGPTPVSALIHAATMVTAGVFLVARFSPVFDLAPD
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IHAMHHEQDMRKMGGVRQYAPLTYGMMIIGTLALT--GFPF---------
TAGYYSKDMIIEAAYASHSAGAQFAFVMGVAAALMTSFYSWRLIFMTFTGECR--ADEHTRLHA----------
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HESPWIMLIPLVLLSLGALFAGFGFHEMFIGH-DRIA---FW--NGSLVT-
AAGDVIDEAHHVPFGVKLAPMVAMALGFLMAWIMYIRS------------------------------------
-----------------------TDIPGRLAKTWDGLYAFLLNKWYVDELYNLIFVRPAFWIGRQFWKR-
GDQQTIDGLGPNGVS-GAVAAIAARARKLQSGYLYHYAFAMIVGLALVVTWFMVRAGG-------
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MMY------KLIVFLPLIGFLFAGLFG----SKFSDRISQLVTAGLVTVSAVLSWMAFADVAL--GGNQ-
YTVLVL-EWVSSGALSFDWAFKIDTLTVVMLVVVNSVSALVHWYSFGYMEDDPS-------
KPRFFGYLSLFTFAMLMLVTSDNLVQMFFGWEGVGLASYLLIGYYYKKPSANAAAIKAFVVNRVGDFGFSLGIF
GAFALFGSVMF--DDIFASADQYADYY---
INFLGTDFHAITVICILLFVGAMGKSAQLGLHTWLPDAMEGPTPVSALIHAATMVTAGVFLVARFSPVFEMSPT
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IHAMHHEQDMRNYGGLAKKIPFTFAMMTIGTIALT--GFPG---------
TAGFYSKDMILEAAYASHAFGAQYAFVLGIAAAFMTSFYSWRLAHLTFFGECR--ADEHTASHA----------
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HEAPWIMRLPLVILAVGALFAGVVFADMFVGE-GRFA---FW--NGALVT-
SVGDVLDEAHHVPFAVKAAPFVVMLLGFIFATVMYYKV------------------------------------
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GDEATIDGFGPNGVS-HAIAFVAARARKLQTGYVYHYAFAMIIGLSLAITWFMVTGSSH------
>WP_068306026_NuoL_Kordiimonas_lacus
MET----AAKFIVFLPLVGFLIAGMFG----RTIGDRVSQVLTSSLVTIGAILSWLVFVDVAL--AGNK-
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FVVTLL-DWVKSGDLEFAWALQVDTLTAVMLVVVNTVSALVHWYSMGYMEEDPD-------
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AVFLLTGSVQF--DVIFSTIGNYETAT---
LSFLGHEYHAITVVCLLLFVGAMGKSAQLGLHTWLPDAMEGPTPVSALIHAATMVTAGVFLVARFSPVFEYSAY
ALEVVAIVGATTAFFAASVGLVQNDIKRVIAYSTCSQLGYMFFALGVGAYGGAIFHLFTHAFFKALLFLGAGSV
IHALHHEQDMRKMGGLFKKIPITATVMTIGTLAIT--GFPL---------
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HEGPITIMGPLLILATGAVFAGAVFSSYFVGD-DRVA---FW--NGALVT-
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GDEQTIDGFGPNGVS-STVALVAAKARKLQTGYVYHYAFAMIIGLAVVVTWFMAQSGAH------
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AVFLLTGSVQF--DVIFGSIGNYQEAT---
LSFLGHDYHAITVVCLLLFVGAMGKSAQLGLHTWLPDAMEGPTPVSALIHAATMVTAGVFLVARFSPVFEYSEY
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IHALHHEQDMRNMGGLFKKIPMTGTVMLIGTLAIT--GFPL---------
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HEGPIFIKAPLVILALGAVFAGAVFKEYFVGH-ERVA---FW--NGSLVT-
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GDEQTIDGFGPNGVS-ATVALVAAKARKLQTGYVYHYAFAMIIGLALVVTWFMAQSGAH------
>MBO6503706_NuoL_Kordiimonadaceae_HXMU1429-5
MLF------KLIVFLPLVGFLIAGMFG----RQIGDRASMILTSGLVSIAGILSWFAFFDVTA--GGNQ-
YSVHVL-SWVTSGTLTFDWAFHIDTLTAVMLIVVNTVSALVHWYSMGYMEEDPH-------
KPRFFAYLSLFTFAMLMLVTSDNLVQMFFGWEGVGLASYLLIGFWYKKPSANAAAIKAFVVNRVGDFGFALGIY
AVFLLVGSVEF--STIFARIGEFETAT---
VSFLGTEYHAITVAALLLFVGAMGKSAQLGLHTWLPDAMEGPTPVSALIHAATMVTAGVFLVARFSPLFDLSPV
ALSVVTYIGAATALFAASVGLVQNDIKRVIAYSTCSQLGYMFVALGVTAYGGAIFHLFTHAFFKALLFLGAGSV
IHAMHHEQDMRKMGGIYKKIPLTYIVMLIGTLAIT--GVPF---------
LSGYYSKDLIIEAAYAADAPGAQFAFVMTVVAALMTSFYSWRLIFLTFHGQTR--ADNHTFDHA----------
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HEGPAVMTIPLIMLAVGALAAGGYFASSFIGD-GRFA---FW--NGALVT-
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KPRFFAYLSLFTFAMLMLVTSDNLVQMFFGWEGVGLASYLLIGFWYKKPSANAAAIKAFVVNRVGDFGFALGIY
AVFVLFGSVEF--ETIFANAGNYQDAT---
LNFLGHDYHALTVICLLLFVGAMGKSAQLGLHTWLPDAMEGPTPVSALIHAATMVTAGVFLVARFSPVFQYSPD
ALAVVTVVGAMTAFFAASVGLVQNDIKRVIAYSTCSQLGYMFFALGVGAYGGAIFHLFTHAFFKALLFLGAGSV
IHAMHHEQDMRNMGGLYKKIPFTFGVMLVGTLAIT--GFPF---------
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LSGYFSKDMIIEAAYASHSAGSEFAFVMGVTAALMTSFYSWRLIYMTFFGKTR--ADHHTFDHA----------
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HEGPWVMRIPLFLLAVGAVFAGGVFAGEFIGH-DKVE---FW--NNALVV-
AAGDVMDEAHHVPAAVKFAPFVAMVLGFVLATFFYLRK------------------------------------
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GDEQTIDGFGPNGVS-HAVAVIATKVRKLQTGYVYHYAFAMIVGLAAVVTWFMVNTGGSH-----
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MI-------ELIVFLPLAGFLAAGLAG----QSLGDRGSMLLTSSFVTVSALLSVALFFEVS---
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KPRFFAYLSLFTFAMLMLVTADNLVQMFFGWEGVGLASYLLIGFWYQKPSANAASIKAFVVNRIGDFGYSLGIF
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LDFVGYDVPALTLVALLLFVGAMGKSAQLILHTWLPDAMEGPTPVSALIHAATMVTAGVFLIARMSPLFEAAPD
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LIGFSGFYSKDIVIEAAYAGEVGGSLFAFVMGIAAVFMTSFYSWRLMFMTFENKPR--ASKDVMGHI-------
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HESPMVMLVPLFVLAGGAVFAGLAFQDWFVGD-GRLA---FW--AGSIVQ-
GEHDVIEQAHHVSKWVKWLPTAMMALGLGAAWLFYIRS------------------------------------
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HESPMVMLVPLFVLAGGAVFAGFAFQDWFVGD-GRLA---FW--AGSIVQ-
GEHDVVDKAHHVSKWVEWLPTAMMALGLGAAWLFYIRS------------------------------------
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KSRFFSYLSLFTFAMLMLVTSNNFLQLFFGWEGVGLCSYLLIGFWFKKQSANAAAIKAFIVNRVGDLGLILGIC
IIYKLTGSLDF--DKVFEKTSLFLESS---
ILFFNFSIPYIELACFLLFIGAMGKSAQIGLHTWLADAMEGPTPVSALIHAATMVTAGVFLVARCSPLFEYAPV
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IHALSDEQDIRKMGGLAKVLPYTCAAMWIGSLALA--GLPP---------
FAGFFSKDIILEAAWGHHSIFGYIAFYLGLIAAFLTAFYSWKILFMVFHGKPR-----TDISKA----------
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HESPLYILIPLLILSIGAIISGWLGYSM-VDT-HHD----FW--
LESILILDNHQALVNAHHVPLLVKLSPIIVAILGIYFAWIFYIKK-----------------------------
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VDLPKKNADKFPKLYNISKNKFWFDEIYDLILTRQLKNIGNILWTK-GDIRIIDRFGPNGIA-
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FNILGYNISAIEISCMLLFIGCMGKSAQLGLHIWLPDAMEGPTPVSALIHAATMVTAGVFLLVRCSWLFQYAPI
VLYIITVIGALTCIFAATIALTQNDIKKIIAYSTCSQLGYMFFACGVSAYNVALFHLATHAFFKALLFLGAGSV
IHAMSGEQDINKMGGIWRKIPFTYLMMWIGSLALA--GIYP---------
FAGYYSKDMIIEAAYLSPSESGRFAYWIGISAAFCTAFYSWRLLIKVFHGKFK--NEPTVWKRV----------
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HESPLFMTIPLFILSLGAIFSGIIGEKLHIVD-NTNK---FW--HGAIEIFHSHS-----
HHIPVLYKFMPMGVGILGIVIAVIYYVVF---------------------------------------------
--------------KVLPDITKSTISPLYNLSYYKYYWDEIYEYIVIKPIRCLSVVLWKK-
IDNVIIDGLGPNGVV-KIINLLSTKVTKMQTGYLYHYAYIMLGAVMVLTSWYIFNIIN-------
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IIRFLSFLSLFTFFMLMLVSSDNFLQLFFGWEGVGVCSYLLIGFWYSKESANKAAIKAFIINRASDFAFILGVI
TIIVYCGSANY--KDVLSSAELLSNIK----IFL--
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GSFMFIFGIAAAILTAIYSMKIIMLVFHGKTK--LEKDVFEHA-------------------------------
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HASLFNLHIYKLL--ISHPPLYIKLLPMAVGIVGIVTGIYLYKSSTV---------------------------
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MSFPQKILRSSRGMTPLVLNKYYFDEIYNCLIVKPINCLASLFYL--GDQQIIDRFGPNGFS-
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MNMYLHNLSLSVVFLPLLASIPVGLNT----NKVKPVIAQIITISFVSIAAIFSWIIFYYTCF--DGQI-
IHLKLI-NWLNLGELKADWSIYIDPLTAIMFLVVNTVSTLVHIYSVSYMSHDPN-------
QPRFFSYLSLFTFFMLVLVSADNFAQLFVGWEGVGLSSYLLIGFWFHKKSAYSAAMKAFLVNRVGDIGLAIGIF
LIAMKFGSVEY--ATVFSKTKYLSEET---
INFLSVDTRLLTVICIALFIGCMGKSAQLGLHTWLPDAMEGPTPVSALIHAATMVTAGVFLLARCSYLFEYSEI
ALDLVTIVGAATCLFAATIATAQNDIKKIIAYSTCSQLGYMFFACGVSAYSAGIFHLLTHAFFKALLFLGAGSI
IHALADEQNIKKMGGIWKKLPYTHALMWIGSIALA--GIPP---------
LSGFFSKDLILEAAYASDSRFGHLAYWLGVAAATLTAFYSCRLLFLVFYAPTN--ADKKIFTEI----------
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PIVSSWSYKNFRNINSFLEKKWYFDEVYEFILIKPVKLLGTSLWRF-VDVGFIDGI-PNYSA-
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QPRFFAYLSLFTFAMLMLVTADNLVQMFFGWEGVGLASYLLIGFWFRKPSASAAAIKAFVVNRVGDFGFMLGIF
GTYLVFQTVSI--PEILAAAPGMAGST---
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FGFAGFYSKDAILEAAFARGTNLGNLAFWMGTIAALLTSFYSWRLVFLTFYGKPRWIESEHIQHSVHKTPEQAG
EDT------------------------------TGGYHP--------------
HESPLPMLVPLLALSVGAVFAGFVFAPAFVESAE------FW--QGSVFF-NEGL-
MHAMHGIPAWAKWSATVAMLIGLAIAFQGYIRD-----------------------------------------
------------------KELPARIAGQLGPVYRFVYNKWYFDELYHFLFVKPAFWLGNKFWKW-
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GTYLVFQTVSI--PEILAAAPGMAGST---
IGFLGHRVDTMDLLCILLFIGAMGKSAQLGLHTWLPDAMEGPTPVSALIHAATMVTAGVFMVCRLSPMFEAAPA
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IHAMHHEQDMRYYGGLRKHIPITFWAMLAGTLAIT--GVGLAGV----
FGFAGFYSKDAILEAAFARGTNLGNLAFWMGTIAALLTSFYSWRLVFLTFYGKPRWIESEHIQHSVHKTAEQAG
EDT------------------------------TGGYHP--------------
HESPLPMLVPLLALSVGAVFAGFVFAPAFVESAE------FW--QGSVFF-NEDL-
MHAMHGIPAWAKWSATVAMLIGLAIAFQGYIRD-----------------------------------------
------------------KELPARIAGQLGPVYRFVYNKWYFDELYHFLFVKPAFWLGNKFWKW-
GDIGIIDRFGPNGAA-WLVTQGTAAAKKVQSGYLYSYALVMLIGVVVAISWVMVR----------
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IGFLGYRMQTMDILCILLFIGAMGKSAQLGLHTWLPDAMEGPTPVSALIHAATMVTAGVFMVCRLSPMFETAPV
ALGFVTFIGAATCLFAATVGTTQWDIKRVIAYSTCSQLGYMFFAAGVGAYGAAMFHLFTHAFFKALLFLGAGSV
IHSMHHEQDMRYYGGLRKKIPLTFFAMLAGTLAIT--GVGIYWLH---
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EDT------------------------------TGGYHP--------------
HESPLSMLVPLGILSIGAVFAGFVFNPQFLDSAE------FW--AGSIYY--ENL-
IHAMHAVPLWVKLSATIVMLLGVLIAWMAYIRD-----------------------------------------
------------------TSIPGKFVEQFRNLHNFVYNKWYFDELYNLVFVRPAFWLGRKFWKI-
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IHAMHHEQDMRYYGELRKHIPLTFWAMMAGTLAIT--GVGIYHLG---
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ADT------------------------------TGGYHP--------------
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IHAMHNVPYLVKYAALIVMVIGLVVAWYAYIKD-----------------------------------------
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------------------TSIPAKTAEQLGPIYRFLYNKWYFDELYHYLFVVPAFWLGRQFWKI-
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TFVTLIGGLTCLFAATIGTTQWDIKRVIAYSTCSQLGYMFFAAGVGAYGVAMFHLFTHAFFKALLFLGAGSVIH
SMHHEQDMRYYGALRKQIPVTFWAMMAGTLAIT--GVGVYWLH---
AGFAGYHSKDAILEAAFASGTEMGRTAFWLGAIAALLTSFYSWRLMFLTFWGKPRWSQSEHIQHAVHHGHDEPE
EANPARQED-------SGHDVSHHVPSPEEDDGTAGYHP--------------
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MHEMHGIPTWVKLSASIAMLIGLAVAWFAYIKD-----------------------------------------
------------------TSIPGKFVNQFRQVHAFLYNKWYFDELYNLIFVRPAFWLGKVFWKQ-
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VGFLGSRVMVMDVLCILLFIGAMGKSAQLGLHTWLPDAMEGPTPVSALIHAATMVTAGVFMVCRLSPMFETAPV
ALAFVTFIGAATCLFAATVGTVQWDIKRVIAYSTCSQLGYMFFAAGVGAYGAAMFHLFTHAFFKALLFLGAGSV
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EANPARQEN-------AGHVAMHDVPSPEQAEGTAGYHP--------------
HESPVSMLIPLAVLSLGAIFAGWLFSEAFLDSAE------FW--NGSIYY-NDGL-
IHAMHATPLWVKLTATIVMLAGLLIAWFAYIRD-----------------------------------------
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GDEGGIDRFGPDGAA-WLVAQGSAGARRFQSGYLYSYALIMLLGVVAAITWVLM-----------
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EHNPAIQED-------AGHDVTHTVPSPNYSAGTGGYHP--------------
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MHAMHEVPWWVKWSATIVMITGFLIALWAYVLD-----------------------------------------
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HESPLVMLIPLIILAFGAVFAGSIFYDAFVGH-YAKE---FW--
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TIFWMYGTIEF--AELFPLVATKAGTT---
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SHAQLETHSE------------PVSDAHAHDDHAHDDHGHHGPLQP--------
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VQTDHDKTTAAASAHADGDHA------------HSHDD--GHGHGHGHHTP--------------
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ALVVDVTNRVVKLQSGYVYHYAFAMLIGLAALVTWMMLGGAL-------
>WP_075697151_NuoL_Pseudovibrio_brasiliensis
MF-------SAIVFLPLLGFLIVGLFG----NRLGVKASEYITSGFMIVAALLSWVVFFQYGL--
GSESTQLITIF-RWITSGDLSVNWTIRVDTLTAVMLVVVNSVSCLVHIYSIGYMHHDPH-------
RPRFFAYLSLFTFAMLTLVTADDLLQMFFGWEGVGLASYLLIGFWYQKPSANAAAMKAFIVNRVGDFGFALGIF
GVFYLYGSIDF--
TSIFASGPSLLENKLNFLGYELMAEPALTVVCLLLFMGAMGKSAQFLLHTWLPDAMEGPTPVSALIHAATMVTA
GVFMVARLAPIFELAPTAMTVVTFFGATTAFFAATIGCVQNDIKRVIAYSTCSQLGYMFVALGVGAFGVGIFHL
FTHAFFKALLFLCAGSVIHAVSDEQDMRKMGGLRKHIPWTYWTMMIGTLALTGFGIPG-LAG-----
TAGFVSKDAIIEAAYVGHNAFASYAYWATVLAALLTSFYSWRLVFMTFHGKPR--ASVDVMKHI----------
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HESPWVMLVPLILLSIGALFAGMAFKEAFMGH-DYAH---FW-
KDVFGGTNSELAVIEEMHHVHWLVAWSPTFAMITGFIIAYVFYIAK----------------------------
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PDMPKALAERHQPLYKFLLNKWYFDELYDFLFVKPAMALGRFLWKR-GDGTVIDGLGPDGIA-
SRVQQVTGWVVRLQSGYIYHYAFAMLIGVAFFVTLAMFSGGGVH-----
>WP_046478826_NuoL_Ca._Filomicrobium_marinum
MI-------LAIVFLPIVGALIAGLFG----RFIGARASEFITTGLLIIAAVLSWVAFVRVGF--
DAETARVPVM--RWITSGELDIAWSLRIDTLTAVMLVVVTTVSALVHVYSIGYMHEDPS-------
RSRFFAYLSLFTFAMLMLVTSDNLLQMFFGWEGVGLASYLLIGFWYTKPEANAAAIKAFVVNRVGDFGFMLGMF
GLFFVFNTLNF--DPLFEATAQAAGKS---
FNFLGYEVDILTTLCLLLFMGAMGKSAQFLLHTWLPDAMEGPTPVSALIHAATMVTAGVFMVARLSPIFEYAPT
ALEVVTLVGTVTAFFAATVGLVQNDIKRVIAYSTCSQLGYMFAALGVGAYSVGIFHLFTHAFFKALLFLGAGSV
IHAMHHEQDMRNMGGLAGKIPITWAMMLIGTLALTGVGIPH-VAG-----
FAGFHSKDAIIEATFAAHTPGNFVFWVLV-FTAFLTAFYSWRLVFMTFHGKTR--AAPDVFKHA----------
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HESPWVMLVPLFVLAFGAVVAGFVFAPYFIGE-SYAE---FW--
GKALFTAPSNHILHDMHHVEEWVYWAPFLAMASGFALSWIFYVQA-----------------------------
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PWLPEATARTFRPIYLFLLNKWYFDELYNWLFVRSAKGLGRFLWKA-GDGAVIDGTI-NGTA-
DSVQWTTGRVVKLQSGYIYHYAFAMLIGVALILTYFLRGLVMTGGAGQ-
>WP_111433419_NuoL_Rhodobium_orientis
MY-------SAIVFLPLLGFLIAGLFG----RIIGDKASEYITSGLLVVSCLLSWIAFFSVGY--
GDGPVEQVPIA-TWITSGALSIDWSLRIDTLTVVMLVVVTTISALVHIYSIGYMHHDPS-------
RARFFAYLSLFTFAMLMLVTADNLLQMFFGWEGVGLASYLLIGFWYHKPSANAAAMKAFIVNRVGDFGFSLGIF
ALFALTGSIGL--DAVFAAAGDLQETT---
FLFLSWDVNALTVICLLLFMGAMGKSAQFLLHTWLPDAMEGPTPVSALIHAATMVTAGVFMVARLSPLFELSHT
ALTVVVIIGATTAFFAATVGLVQNDIKRVIAYSTCSQLGYMFVALGVGAYGAGIFHLFTHAFFKALLFLSAGSV
IHAVSDEQDMRKMGGLRNHIPVTFWMMIIGTLALTG--FPL---------
TAGFFSKDAIIESSFVGHGAAAEYAFWMVVIAALFTSFYSWRLIFMTFFGKPR--ASAEVMGHV----------
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HESPRVMTVPLMILALGALAAGVLFAGSFIGE-GYGE---FW--
KTALFVSEENHILHEMHNVPLWVKFAPFVMMVAGFVIAFYFYIMS-----------------------------
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PETPKKLAKQHDGLYQFLLNKWYFDELYDVLFVRSAKWLGRFLWKQ-GDGRVIDGYGPDGVS-
ARVLQATGWVVRLQTGYLYHYAFAILIGVAALITWAMFTGGGAN-----
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MY-------AAIVFLPLIGFLVAGIFG----RLIGARASEIVTTSLLFVSAILSWVAFIHVGF--
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ALFMLVGSVDL--DTIFGHGEELSTTT---
FSFLGYQVNAVETICFLLFIGAMGKSAQLGLHTWLPDAMEGPTPVSALIHAATMVTAGVFMVARMSPLFEYAPA
ALTFVTFIGATTAFFAATIGCTQNDIKRVIAYSTCSQLGYMFAALGVGAYSAGIFHLMTHGFFKALLFLCAGSV
IHAMHDEQDMRKMGGLVKKIPLTYAGMVIGTLAITG--FPY---------
TSGYFSKDAIIEATFAAHNPFSAYAFWLTTLAALLTAFYSWRLIFMTFHGKTR--ASADVFKHA----------
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HESPPVMLIPLAVLSCGALFAGFILHGYFIGH-EYEH---FW--
RGSLYLGAENHILHDMHHLPAWVPLAPTVMMITGVAWAYWWYMLS-----------------------------
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PKTPAAVAREHPALYQFLLNKWYFDELYDFLFVRPTKRIGHFLWKK-GDGWLIDGFGPDGVS-
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RPRFFAYLSLFTFAMLMLVTADNLLQMFFGWEGVGLASYLLIGFWYEKPSANAAAMKAFVVNRIGDFGFILGIF
GVFVMTGAVNF--ETVFAQAPGLAGKT---
IAFLGHHWDAPTVIAVLLFIGAMGKSAQFLLHTWLPDAMEGPTPVSALIHAATMVTAGVFMVARMSPIFELSPS
ALDLVMIVGATTSMFAATIALVQTDIKKVIAYSTCSQLGYMFVAMGAGAYSIGMFHLLTHACFKALLFLSAGSV
INAMHHEQDMRNMGGLYKKIPFTYAMMLVGTLAITG--FPF---------
LAGYYSKDAIIESAWGSTNSFALYGWVMTVGAAALTSFYSWRLVFLTFHGQPHD-HHHYEAA------------
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HESPLVMTIPLGVLGFGSVVSGMILYPEFVGH-DVGE---FF--
RQSIFMGAENHVLHAMHDIPFWAKWMPTLMMALGLLVAYWFYVVD-----------------------------
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RTLPVRLAHSQDALYKFLLNKWYFDEIYDFLFVRPALFIGRVLWKQ-GDVRIIDGMGPDGVS-
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MY-------QAIVFLPLLGFLIAGLFG----KKIGDRASEVVTTSFLFVACLLAWIAFFAVGF--
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RPRFFAYLSLFTFAMLMLVTADNLLQLFFGWEGVGLASYLLIGFWYEKPSANAAAMKAFVVNRVGDFGFMLGIF
AIFVMTGSIAF--EEVFAAAPGLAGKT---
ISFLGHNWDAPTVIALLLFVGACGKSAQFLLHTWLPDAMEGPTPVSALIHAATMVTAGVFMVARMSPIFELSQT
ALNVVMLVGATTAFFAATVGLVQNDIKKVIAYSTCSQLGYMFVAMGAGAYSIGMFHLLTHAFFKALLFLGAGSV
IHAMHHEQDMRHMGGLRKKIPFTYWTMVIGTLAITG--FPF---------
LAGYYSKDAIIEAAYASHNYFHVYGYWMTVIAAALTAFYSWRLIFLTFWGHPHD-HHHYEAA------------
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HESPLVMTIPLGVLSLGALFAGIAFKNIFVGE-GVEH---FF--
RHSIFMGAENHILHAMHDIPGWAAFAPTVMMVVGSLFAIWFYIVN-----------------------------
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PKVPAQLAKSQDALYQFLLNKWYFDEIYNFLFVRPTLWLGRTLWKR-GDGTIIDGLGPDGVS-
ARVLDITRGVVRLQTGYLYHYAFVMLIGVAALITWFMFAGV--------
>WP_213363409_NuoL_Ancylobacter_defluvii
MY-------QAIVFLPLAGFLIAGLFG----RAIGARASELITTGLLFISALFAWIVFFQTAF--
GDGGGTVEIF--TWIASGALDVKWALRVDTLTAVMLVLVTTVSSLVHLYSMGYMHEDPS-------
RPRFFAYLSLFTFAMLMLVTSDNLVQLFFGWEGVGLASYLLIGFWYDKPSACAAAMKAFIVNRVGDFGFALGIF
AVFMMTGSVGF--EQVFAAAPSLMDKT---
IHFIGIDWHAPTIICLLLFIGAMGKSAQLGLHTWLPDAMEGPTPVSALIHAATMVTAGVFMVARLSPLFELSPV
ALNVVMFVGASTAMFAATVGCVQNDIKRVIAYSTCSQLGYMFTALGAGAYSVGVFHLFTHGFFKALLFLAAGSV
IHAMHHEQDMRHMGGLWRKIPFTYATMLIGGLALTG--FPF---------
TAGYFSKDAIIETAFMSHSPFSTYAFVMTVAAAALTSFYTWRQMFMTFHGHPHD-HHHYEHA------------
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HESPLTMLIPLGVLSLGALFAGMILYPYFVGH-DVEH---FF--
REAIFMGPDNKILEEIHHIPAWAKWSPTVMMVLGFVVAYWMYVAN-----------------------------
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PAVPKALARRNDVLYRFLLNKWYFDELYDFLFVRPTMWLGRFLWKQ-GDGRVIDGWGPNGIS-
ARVIDVTNRVVRLQTGYLYHYAFVMLVGVAALITWFMFGGAH-------
>WP_086090017_NuoL_Pseudorhodoplanes_sinuspersici
MY-------QAIVFLPLIGCLIAGLFG----RIIGARPAELVTTLLLFASAALSWYAFARVGF--
GHIDERIVLF--PWIQSGDFKVDWVIRVDTLTAVMLVVVTTVSSLVHLYSIGYMHEDPH-------
RQRFFAYLSLFTFAMLALVTADNLAQLFFGWEGVGLASYLLIGFWYQKPEANAAAIKAFVVNRVGDFGFALGIF
ALFMMTGAIDF--DTIFAQAPALTGKT---
IDFFGWHADALTLICLMLFMGAMGKSAQFLLHTWLPDAMEGPTPVSALIHAATMVTAGVFMVARLSPLFELAPV
ALMVVTLIGATTAMFAATVGLVQNDIKRIIAYSTCSQLGYMFVAMGVGAWSVGMYHLFTHAFFKALLFLGSGSV
IHAMHHEQDIRHMGGLKNKIPLTYWLMIIGTLALTG--FPF---------
TAGYFSKDAIIEAAYAGKNPFAVYGFACTVLAAALTSFYSWRLIFKTFHGEPHD-RHHYEEA------------
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HESPMVMLVPLMVLAAGSILAGYPFYEYFAGH-HVEE---FF--
RNSLAFSKTNTILEDMHHVPALVVWTPTVMMVLGFAIAYLFYIRD-----------------------------
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PRIPVEMARNHQLLYRFLLNKWYFDELYDLIFVRPAKWLGTTLWKR-GDGWLIDGFGPDGVS-
ARVLDVTRNVVRLQTGYLYHYAFAMLIGAAALITWFMFAGAH-------
>WP_109919883_NuoL_Zavarzinia_compransoris
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IPRFHAYLSLFTFAMLMLVTADNFLQVFFGWEGVGLASYLLIGFWYKKPSANAAAIKAFVVNRVGDFGFALGIF
AIFLVFNSVSF--DTVFAAAAGKAGQT---
FNFLGYDVDIMTTICLLLFVGCMGKSAQLGLHTWLPDAMEGPTPVSALIHAATMVTAGVFLVARASPLFEFAPS
ALAVVTVVGATTAFFAATVGLVQNDIKRVIAYSTCSQLGYMFFAAGVGAYEAAVFHLFTHAFFKALLFLGAGSV
IHAMHHEQDMRNMGGTWKYIKFTYAMMWIGNLALA--GVPF---------
FAGFYSKDMVLEVAYAAHSGVGTYAFWLGIIAASFTAFYSWRLLFLTFHGEKRW-GGHGH-GHGHDDHGHG---
--------------------HGHAHTP------------------------
HESPLAMTIPLALLAVGAVFSGFWFYDSFVGE-HREA---FW--
GGAIFVAEANKVIEHAHHVPGWVKLLPLIVTAGGIFVAWVFYILK-----------------------------
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PKWPDQLAKTHREAYAFLLNKWYFDELYDLLFVKGARLFGRVFWKQ-GDGAVIDGLGPNGIS-
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>WP_119778097_NuoL_Oleomonas_sp._K1W22B-8
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IPRFQAYLSLFTFAMLMLVTADNFVQVFFGWEGVGLASYLLIGFWYKKPSANAAAIKAFVVNRVGDFGFALGIF
AIFFVFNSVSF--DTVFAAAAGETGKT---
FNFLGYDVDILTTICLLLFVGCMGKSAQLGLHTWLPDAMEGPTPVSALIHAATMVTAGVFLVARCSPLFEHAPV
ALEVVTIVGASTAFFAATVGLVQNDIKRVIAYSTCSQLGYMFFAAGVGAYEASIFHLFTHAFFKALLFLGAGSV
IHAMHHEQDMRNMGGLWRHIKLTYALMWIGNLALA--GIPL---------
FAGYYSKDTILEVAFAAHTGVGTYAYILGTLAAMMTAFYSWRLLFMTFHGEARW--GHGH-GHG-DHGHGD---
--------------------HGHAHTP------------------------
HESPLVMTIPLIVLALGAAAAGIIFFDDFVGH-HREA---FW--
GGAIFVAETNKVLEEAHHIPEWAALLPLVLSVFGIFLAWVFYIAR-----------------------------
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PKWPAALAQTHKELYAFLLNKWYFDELYDLLFVRPAKAIGRLLWKG-GDGRIIDGLGPDGIS-
ARVLDIARRAVKLQSGFVYHYAFAMLIGVAALVSWYVYRIGVTP-----
>WP_091859036_NuoL_Bosea_robiniae
MY-------HAIVFLPLIGFLIAGLFG----RLIGARGSEIVTTSLLMVSAALSWVALTQVGF--
GSGTTRVQVA--SWISSGELQVDWAFRVDTLTAVMLVVVNTVSSLVHLYSIGYMHEDEH-------
RSRFFAYLSLFTFAMLMLVTADNLVQMFFGWEGVGLASYLLIGFWYQKPSANAAAMKAFIVNRVGDFGFLLGIF
LIFVLFGAVTF--DAIFPRAGEMVSQS---
FRFLGYDWNALTLTCLLLFMGAMGKSAQFLLHTWLPDAMEGPTPVSALIHAATMVTAGVFMVARLSPVFEYAPV
ALTVVVVIGATTAFFAATVGLVQNDIKRVIAYSTCSQLGYMFVALGVGNYGAGIFHLFTHAFFKALLFLGAGSV
IHAMHHEQDMRHMGGLRKHIPLTAAAMTIGTLALTG--FPG---------
FAGYFSKDAVIESAYASVAHGGLASSYAFVLAAGMTSFYSWRLYFMTFEGAPRWGHGHDAHGHGHDDHAHAAD-
--------------GHDDHGHGHDHTP------------------------
HESPWTMLVPLAVLSLGAIVAGYAFKEAFIGH-DFEH---FW--
KSALFMGKDNHILHAMHEVPKWVVWSPFVAMVIGFALAWYMYVRR-----------------------------
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PEIPGKLAAANPALYQFLLNKWYFDELYDFLFVRPAKWLGRFLWKK-GDGLVIDGFGPDGVS-
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GSGTTRIQVA--NWISSGQLQADWAFRIDTLTAVMLVVVNTVSSLVHLYSIGYMHEDPH-------
RPRFFAYLSLFTFAMLMLVTADNLVQMFFGWEGVGLASYLLIGFWYQKPSANAAAIKAFVVNRVGDFGFLLGIF
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LIFVLFGAVTF--DAIFPRAGEFVNTS---
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IHAMHHEQDMRHMGGLRKHIPLTAAAMTIGTLALTGVGIPGTI-----
FGFAGFFSKDAIIESAYASVATGGFASSVLLVVAACMTSFYSWRLYFMTFEGTPRWGHGHAHQGHDDHAHAAHA
H--DDH------------GHDDHGHDHTP------------------------
HESPWTMLLPLVLLSIGAIAAGFAFKEAFIGH-DFEH---FW--
KSALFMGKDNHILHAMHEVPKWVILSPFVAMVIGFLLAYWMYVRR-----------------------------
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PDIPGRLAAANPALYRFLLNKWYFDELYDFLFVRPAKWLGRFLWKK-GDGLIIDGFGPDGVS-
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LVFVLFGSVGF--DAIFPRVADLTNAT---
FHFLGRDWHALTLASLLLFMGAMGKSAQFLLHTWLPDAMEGPTPVSALIHAATMVTAGVFMVARLSPIFEYAPA
ALTVVIVIGATTAFFAATVGLVQNDIKRVIAYSTCSQLGYMFVALGVGAYSAGIFHLFTHAFFKALLFLGAGSV
IHAMHHEQDMRNMGGLRKHIPLTAAAMTIGTLALTG--FPL---------
FAGYFSKDAIIESAYASVAHTGFPASYAFVVAACMTSFYSWRLYFMTFEGKPRWGADA-
HAGHGHDAHDDHAHAAHAHDDNA-------HGDHGHGHAHTP------------------------
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KAALFTGKDNHILHEMHEVPGWVVASPFIAMVIGFLLSLYMYVLR-----------------------------
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PDVPGKLAAANPALYKFLLNKWYFDEIYDFLFVKPAMWLGKFLWKK-GDGFVIDGMGPDGIS-
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LVFVLFGTVGF--ESIFPRVGELTTQT---
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ALTVVVVVGATTAFFAATVGLVQNDIKRVIAYSTCSQLGYMFVALGVGAYAPAIFHLFTHAFFKALLFLGAGSV
IHAMHHEQDMRHMGGLRKHIPLTAAAMTIGTLALTG--FPF---------
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GHGHEAHGHDDHAHAAHGHDDH---------------GHGHAHTP------------------------
HESPLSMLIPLALLSLGAVAAGFAFKEAFIGH-DYEH---FW--
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PDIPGKLAAANPVLYRFLLNKWYFDEIYDFLFVKPSMWLGRFLWKK-GDGLVIDGMGPDGIS-
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FRFVGYEWNALTLTCLLLFMGAMGKSAQFLLHTWLPDAMEGPTPVSALIHAATMVTAGVFMVARLSPIFEYAPV
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GQGHDAHGHDAHGHDDHAAHGH------------DDHGHGHDHTP------------------------
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KAALFTGKDNHILHAMHEVPGWVVWSPFVAMVLGFLVALYMYVLR-----------------------------
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PDVPGKLAAANPALYQFLLNKWYFDEIYDFLFVKPAMWLGKFLWKK-GDGFVIDGMGPDGIS-
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HHDHHAHAPHSHEGVEHDDHNRDVEP---ASHAQHEHGHHGAHTP------------------------
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KGALFTRPENHILEEMHHLPGWVPLLPTIMMVLGFGLAWYMYIID-----------------------------
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NKQPAKLAADHPILYRFLLNKWYFDELYDAIFVRPAMAIGRFFWRT-GDQRIIDGLGPDGIS-
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TIFVLFNGVTF--DAIFPRVGEFANAR---
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ALTVVTVIGGITAFFAATVGLVQNDIKRVIAYSTCSQLGYMFVALGVGAYSAGMFHLFTHAFFKALLFLGAGSV
IHAMHHEQDMRNMGNLRRYIPLTTAMMAIGTLALTG--FPF---------
TAGYYSKDAIIEAAYASHSAAGSFAFLATVIAAFMTSFYSWRLFFMTFEGNARWGASHHHAPSDHEGVEHDERG
HDVEPAGH----ADHEHGHHGHGAHTP------------------------
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HESPLVMVLPLIVLAIGAVVAGIVFHDAFLGE-GHQE---FW--
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AKQPARLAADHPILYRFLLNKWYFDELYDAIFVRPAMAIGRFFWRT-GDQKIIDGLGPDGIS-
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TVFVLFNGVTF--DAIFPRVAELANAN---
FTFLGIEWHALTIACLLLFMGAMGKSAQFLLHTWLPDAMEGPTPVSALIHAATMVTAGVFMVARLSPIFEYAPA
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IHAMHHEQDMRHMGALRRYIPLTTAMMAIGTLALTG--FPF---------
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KGALFTRPENHILEEMHHLPAWVPLLPTVMMALGFVLAYYMYIVD-----------------------------
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TVFVLFNGVTF--DAIFPRVSEFANAR---
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IHAMHHEQDIRHMGALRRYIPLTTAMMAIGTLALTG--FPF---------
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HHDHHAHAPHSHEGVEHDDHNRDVEPAS---HAQHDHGHHGDHTP------------------------
HESPLVMLIPLIVLATGAVIAGIVFHGAFIGE-GYQE---FW--
KGALYTRPDNHILEEMHHLPGWVPLLPTIMMVLGFVLAWYMYIID-----------------------------
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-----------------HGHGHGDHTP------------------------
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PRMPAALAAQQPLLYRFLLNKWYFDELYDFLFVRPAMWLGRVFWKK-GDGWLIDGFGPDGVS-
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-----------------HHGHGHDHTP------------------------
HESPWVMLIPLAVLSLGAVAAGFVFKDAFIGH-DYEH---FW--
KAALFTGKDNHILHAMHEVPGWVVASPFVAMLIGLALAYYMYVRR-----------------------------
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PDVPGKLAAANPALYKFLLNKWYFDELYDFLFVKPAMWLGKFLWKK-GDGFVIDGMGPDGIS-
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IHAMHHEQDIRHMGALRRYIPFTTAMMAIGTLALTG--FPF---------
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DVEPASHAQHEHGHDDHAHGHHGSHMP------------------------
LESPLVMLLPLLVLAIGAVVAGFMFHGAFIGE-GYQE---FW--
KGALFTRPENKILETMHHLPGWVPLLPTIMMILGFLVAVYMYIID-----------------------------
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NKQPAKLAADHPILYRFLLNKWYFDELYDAIFVRPAMAIGRFFWRT-GDQRIIDGLGPDGIS-
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HGDHAHAHAPHDHEGVEHDAHGRDVEAASH-AQHEHGHHGGHTP------------------------
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LIFVLFKTVNF--DQIFPRVAEFEKAQ---
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IHAMHHEQDIRAMGGLRKYIPFTTGMMAIGTLALTG--FPF---------
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GEAHTHEGAEHNASGHDVSHAHAD-------HSHDDHGHGAHKP------------------------
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TKKPAQIAADHPILYRFLLNKWYFDELYDAIFVRPAMALGRFLWRT-GDGKIIDGLGPDGIS-
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IHAMHHEQDMRNMGALRRYIPVTTAMMAIGTLALTG--FPF---------
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NADHHAHGHHEGVEHDGHSH--DVEPAT---HAQHEHGHHGDHTP------------------------
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KGALFTRPENHILEEMHHLPGWVPLLPTVMMILGFVLAVYMYMID-----------------------------
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TPHGHDLAVSHHVESEDDSHGS-------HAHAGDHGHGHHEP------------------------
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LVFYITNSVAF--DPIFAAAPGLAHKT---
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INAMHHEQDMRKMGGLAKKIPFTFWMMVIGTLALTG--FPL---------
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LVFVLFGTTTY--SEIFAKIGEVKDAH---
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------------PYLPGELAASQPIAYRFLLNKWYFDELYDFLFVRPAKRLGYFLWKR-GDGTVIDGMGPDGIS
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LVFMLTGSISF--DVIFAAAPDLASKS---
VHAFGLDWNAMTLACLLLFMGAMGKSAQFLLHTWLPDAMEGPTPVSALIHAATMVTAGVFMVARLSPLFEQSAT
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>WP_183750461_NuoL_Pseudochelatococcus_contaminans
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GTETFYVPIA--RWITSGTLIVDWALRIDTLTVVMLVVVNSVSALVHLYSIGYMHEDPD-------
RPRFFAYLSLFTFAMLTLVTADNLVQMFFGWEGVGLASYLLIGFWYEKPSACAAAMKAFIVNRVGDFGFMLGLL
LTFIVFGSVSF--GDIFSRTAEFQDAT---
FNFIGFEWHTLTLISLLLFIGAMGKSAQFILHTWLPDAMEGPTPVSALIHAATMVTAGVFMVTRMSPVFEYAPS
ASTVIIVIGAVTAFFAATIGLVQNDIKRVIAYSTCSQLGYMFVALGVGAYSAGVFHLFTHAFFKALLFLGAGSV
IHAMHHEQDMRKMGGLRKYIPFTALAMTIGTLALTG--FPF---------
TSGFYSKDAIIESAFASHSSVAGFAFTSTIVAALMTSFYSWRLYFMTFEGKPRWE-
HHDDHAHGHDHAHDDGHDHKP------------------------------------------------
HESPLVMLLPLVVLSIGALFAGAVFYNAFIGS-GYDA---FW--
KGAIFTNPDNHILHDMHEVPLWVKLAPVVTMVIGFLLALWFYVLD-----------------------------
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TSKPRQLAAAFPGVYRFLLNKWYIDELYNFLFVRPAKELGRFFWKQ-GDGWLIDGHGPDGIS-
ARVLDVTGRVVKLQTGYVYHYAFAMLIGVAAFVTWYIFGGAV-------
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>WP_015821652_NuoL_Methylorubrum-extorquens
MY-------HAIVFFPLIGALIAGLFG----RFIGARMSELVTTGCLAFAALLSWGAFFLVTG--
DGRAETVPVA--QWFTAGDLVVDWAFKVDTLTAVMLVVVTSVSTLVHLYSIGYMHEDPH-------
RPRFFAYLSLFTFAMLMLVTADNLVQMFFGWEGVGLASYLLIGFWYEKPSANAAAMKAFIVNRVGDFGFSLGIF
LVFVLTGSVGF--DAIFAKAPELKDAT---
FHFLGHDWHALTLACLLLFMGAMGKSAQFLLHTWLPDAMEGPTPVSALIHAATMVTAGVFMVARLSPLFELAPT
ALTVVTVIGGITAFFAATVGLVQNDIKRVIAYSTCSQLGYMFVGLGVGAYATGVFHLFTHAFFKALLFLGAGSV
IHAMHHEQDMRNMGGLRRYIPFTTAMMTIGTIALIG--FPF---------
TSGYYSKDAIIEAAYMSDRPGHVLAFLATVIAALMTSFYSWRLFFLTFEGPQRWVAH-
GAHGHDDHAHAEHDHVHAASAHEADGAPGHHEGVAHDDHGHDVEPASHSAV--EHHDHAPLTP----
HESPLVMTIPLAILAFGALFAGLIFKERFIGH-DMDK---FW--
GNALPHGSGNDIMHKIHDAPGWVAASPFVMLVLGFLLAFWMYLRR-----------------------------
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PDLPHRLAESQPILYRFLLNKWYFDEIYDRIFVRPAKNFGLFLWKE-GDGRVIDGLGPDGIS-
ARVVDITRGVVRLQTGYVYHYAFVMLVGVAGLITWYLVSGVP--GGTH-
>KIU34726_NuoL_Methylobacterium_radiotolerans
MY-------HAIVFFPLIGFLIAGLFG----RYIGARACEYITTAFLAFTALIAWGVFLDG----GHAE-
RVQVA--SWFSAGDLQVDWAFKVDTLTRVMLVVVTTVSTLVHLYSVGYMEEDPH-------
RPRFFAYLSLFTFAMLMLVTADNLVQMFFGWEGVGLASYLLIGFWYEKPSANAAAMKAFIVNRVGDFGFSLGIF
LTFVLTGSVAF--DAIFGKVDAIKTLT---
FHFLGYDWNALTLACLLLFMGAMGKSAQFLLHTWLPDAMEGPTPVSALIHAATMVTAGVFMVARLSPLFEEAPN
ALIVVTVIGGVTAFFAATIGLVQNDIKRVIAYSTCSQLGYMFVALGVGAYSAGVFHLFTHAFFKALLFLGAGSV
IHAMHHEQDMRNMGGLRRYIPYTSAMMAIGSLALIG--FPY---------
TAGYYSKDAIIEAAYASTRPGHTLAFLCVVVAAFFTSFYSWRLFFMTFEGPARWGAHA-
AHSHHDAPAVAHSTMAHEADGAPGHTEGVAHDDKGHDVEPAHRSDLVADDHHGHGHHGDHTP----
HESPLVMTIPLAILAFGALFAGIIFHNRFIGE-GMDA---FW--
GHALAHGPNNHIMHEIHEVPALVSYSPLVMLILGFVLAYWMYIRR-----------------------------
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PELPGQLAAQQPSLYRFLLNKWYFDEIYDRIFVRPAKDFGLFLWKE-GDGRIIDGLGPNGIA-
ARVVDVTRGVVRLQTGYLYHYAFVMLIGVAGLISWYLMSGLP--KGAH-
>WP_18891554_NuoL_Salinarimonas_ramus
MY-------QAIVFLPLLGFLVAGIFG----RFIGARPSEIVTTALLVVSAALSWVAFFDVAL--
GEGPEVFRVQVATWMVSGGLSVDWAFRIDTLTVVMLVVVNTVSALVHLYSIGYMHEDPS-------
RPRFFAYLSLFTFAMLMLVTSDNLVQMFFGWEGVGLASYLLIGFWYQKPSANAAAMKAFVVNRVGDFGFALGIF
AVFFLFGSVQF--EEIFAAIPAYAETGGP-
VLLGLSSEGAITLAALLLFMGAMGKSAQFLLHTWLPDAMEGPTPVSALIHAATMVTAGVFLVARMSPLFEFAPT
ALTVVTYVGALTAFFAATVGLVQNDIKRVIAYSTCSQLGYMFVALGIGAYGAGIFHLFTHAFFKALLFLGAGSV
IHALHHEQDLRNMGGLRRHIPFTAAMMAIGTLALTG--FPF---------
TAGYYSKDAIIEAAYASPTTAGDVAFVATVIAALFTSFYSWRLFFLAFEGAPRWA-
GHGDATHAAHGHDDHEGVAHGAHDQDLEPAHAAAHEHA-DHGHG----------HGHGHGHGHAP----
HESPLVMTIPLGVLAVGALLAGMLFKESFVGH-DWHH---FW--
EGAIYTREGNTIMEDFHHVPAWVVWSPFVMMVLGFLGAFWMYIRD-----------------------------
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KAAPARLAGRHPVIYRFLLNKWYIDELYDMLFVQPSKRLGRFLWRT-GDGRVIDGLGPDGVS-
ARVLDATSWVVRLQTGYVYHYAFVMMIGVAALVTWYLVTGAR-------
>SEC00671_NuoL_Rhizobiales_GAS188
MY-------SAIVFLPLFGFIIAGGFG----RIIGARGAEVVTTGFLLLGMVLSWIAFFQVGL--
GHQSFHVDIA--PWIISGGLRTDWALRIDTLTAVMLVVVNTVSGLVHLYSIGYMAEDTS-------
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RPRFFAFLSLFTFAMLMLVTADNLVQMFFGWEGVGLASYLLIGFWYDRPSANAAAIKAFIVNRVGDFGFALGIF
LVFTLFGTVSL--SDIFARAPEMAKGS---
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AQTVVLAIGGMTAFFAATVGLVQNDIKRVVAYSTCSQLGYMFVGLGAGAYSVGIFHLFTHAFFKALLFLGAGSV
ITAMHHEQDMRKMGGLWKSIPFTGWMMVIGTLALTG--FPL---------
TAGFYSKDAIIEAAYATDRPGHVFAFLCTTIAALMTSFYSWRLIFMTFFGTPHWAAADGHGAADAHAHADAHGD
DDAHEHHGPIVP---------------------------------------
HESPLVMLVPLAVLALGSLFAGLAFKGVFFGG-AAEH---FW--NNSLIFDED--
IVKKIEEVPFWVEHSALVMMLIGGGVAYWFYVAN----------------------------------------
-------------------PSLPVRLAARNPILYQFLLNKWYFDEIYEVIFVRPAKAIGRFLWKQ-
GDGRMIDGLGPDGVS-ARVIDVARGAVRLQSGYLYHYAFAMLIGVAAFITYFMIAGAR-------
>WP_106748567_NuoL_Phreatobacter_cathodiphilus
MY-------QAIVFLPLVGFLIAGLFG----RAIGARASEIVTTSLLGIAALLSWVAFYQVGY-
AGQGTTVELMR---WISAGSLNVSWSLRIDTLTAVMLVVVNSVSFLVHLYSIGYMHEDPD-------
RPRFFAYLSFFTFAMLMLVTANDLLQMFFGWEGVGVASYLLIGFWYKKPSANAAAMKAFIVNRVGDFGFLLGIF
GLYTLTGSIGF--EAVFSAAQGLSGQK---
MAFLGYQLDALTVVCLLLFMGAMGKSAQFLLHTWLPDAMEGPTPVSALIHAATMVTAGVFMVARLSPVFEYAPG
ALQVVMFFGATTAFFAATVGLVQNDIKRVIAYSTCSQLGYMFVALGAGAYSVGIFHLFTHAFFKALLFLGAGSV
IHAMHHEQDIRRMGGLAPHIKFTYAMMVIGTLALTGFGIPFLH-----
IGFAGYHSKDAIIEVAYAAHGAMGPYAFFMTVIAALMTSFYSWRLIFMTFHGQPRW-AGAH-
GHHDDHAHADAAAHGHADPHAHAHGAK-DDHHHDDHGHGHAHQP---------------------
HESPLVMLIPLGALAVGAVFSGVVFMKKFTDE-AGIKG--FF--
RDSIFMRPENHIIHEFHSVPGWVPWTPFVMMAIGFALAWYMYIKR-----------------------------
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PDVPVQLAREHQGLYQFLLNKWYFDELYDRIFVRPARWLGRFFWKKGGDGWLIDGFGPDGIA-R-
VVDITRGVVRLQTGYVYHYAFAMLIGVAALATWFMFSGGVG------
>WP_136964045_NuoL_Phreatobacter_stygius
MY-------QAIVFLPLVGFLIAGLFG----RAIGARGSEIVTTSLLGISALLSWVAFVQVGF-
GGQTASIELFP---WISAGALEVSWTLRIDTLTAVMLVVVNSVSFLVHLYSIGYMNEDPH-------
RPRFFAYLSLFTFAMLMLVTADDLLQMFFGWEGVGLASYLLIGFWYQKPSANAAAMKAFIVNRVGDFGFALGIF
GLYKLTGSIEL--DTIFGAAQGLVGKK---
MEFLGYQLDALTVVCLLLFMGAMGKSAQFLLHTWLPDAMEGPTPVSALIHAATMVTAGVFMVARLSPVFEYSPT
ALSVVMFFGATTAFFAATVGLVQNDIKRVIAYSTCSQLGYMFVALGAGAYSVGIFHLFTHAFFKALLFLGAGSV
IHAMHHEQDMRNMGGLAPHIKVTYAMMLIGTLALTGFGIPFLH-----
VGFAGFHSKDAIIEVAYASHNVMGPYAFALTVVAAAMTSFYSWRLIFMTFHGKPRW-ANGH-
GAHGHDAHDEEEHGIGH-----------------EPGNGHDHQP---------------------
HESPAVMLIPLVLLAIGAVFAGVVFAYQFADH-HGVEK--FF--
RESLFFRPDNHIMDEFHHVPGWVPWTPFVMMAFGFVLAWYMYIRH-----------------------------
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PEMPGQLARRHPALYQFLLHKWYFDELYDRIFVRPARALGRFFWKQGGDGWLIDGFGPDGVA-R-
VVDVTRGVVRIQTGYVYHYAFAMLIGVAALATWFMFSGGLH------
>KKB10330_NuoL_Devosia_chinhatensis
MI-------QAIVFLPLIGALIAGLLG----
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TVSALVHVYSIGYMNEDPH-------
RSRFFAYLSLFTFAMLMLVTADNFLQMFFGWEGVGLASYLLIGFWYTRPSATAAAMKAFVVNRVGDFGFALGIF
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GVFMVARLSPLFETSPVALTVVIVVGAITAFFAATVGLVQNDIKRVIAYSTCSQLGYMFVALGVGAYSAGVFHL
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SHDEPIDDSNADDHGHHGHHHGSAYDNA-------------------------
HESPNVMLVPLYVLSVGAVLAGVVFYGMFFHD-VEHIHE-FF--AGSIFVDHQ--
IIEDAHHVPTWVKWSATIAMIAGFVAAWFMYIRR----------------------------------------
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TVSSLVHVYSIGYMAEDPH-------
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GSFMLLGTVDF--DTAFSNLPAVSNFT---
MRFLGWDVHALTVICLLLFMGAMGKSAQFLLHTWLPDAMEGPTPVSALIHAATMVTAGVFMVARLSPMFETSPT
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IHAMHHEQDMRNMGGLGKKIPITYAMMLIGTLALTGVGIPGTF-----
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HTAHPDVAHAAAETHHEPIDDSNAHDHGHHDHAHHGSAHDNA------------------------
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IIEGAHHVPLWVKWSATIAMIIGFVTAWFMYIKE----------------------------------------
-------------------PAVPGRIAAQNPGLYRFLLNKWYFDELYDRIFVRPAVWVGRAFWRG-
FDDWLINDKLTEGLG-RRVQNVTSWVVRLQSGYLYHYAFAMLIGIAALLTWAIAAGGLI------
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LVFALTQSVGL--DQIFAAAPALAHKS---
IHVFGSDLDALTVACLLLFMGAMGKSAQFLLHTWLPDAMEGPTPVSALIHAATMVTAGVFMVARLSPLFEQAPA
ALSFVIFIGATTAFFAATVGLVQNDIKKVIAYSTCSQLGYMFVGLGVGGYSLGIFHLFTHAFFKALLFLGAGSV
IIALHHEQDMRMMGGLWRKIPFTFAMMVIGTLALTG--FPF---------
TAGYYSKDAIIEAAFESGRVGAFYGFILTTLAAGLTSFYSWRLVFLTFFGAPRWAALA-
ELPKSGLAHEQSANAGTGQAHEDHAFD-HP------------------------------------
HESALTMLIPLAVLAAGALFAGIIFSSDFIG-HGATG--FW--KALILASTN--
EVTEGHTLPSYVSIGPTALMVIGFVVALAFYILW----------------------------------------
--------------------PTIPSLLAKSLRPLYEFLLNKWYFDELYDKIFVRPAFALGRLFWK-
GGDGAIIDRFGPDGVAARVIEITGRVVKLQSGYIYHYAFAMLVGLAAVITWYTAWGIR--------
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RARFFAYLSLFTFAMLMLVTADNFLQMFFGWEGVGLASYLLIGFWYKKPSANAAAMKAFVVNRVGDFGFALGIF
GTFYLVGSLGF--EDTFAALPGLADAT---
IPILGGEYHALTVVCLLLFMGAMGKSAQFLLHTWLPDAMEGPTPVSALIHAATMVTAGVFLVARLSPMFEMSET
ATLVIIYVGAITAFFAATVGLVQNDIKRVIAYSTCSQLGYMFVALGVGAYSAGVYHLFTHAFFKALLFLGAGSV
IHAMHHEQDMRNMGGIARKIPITYAMMIIGTLALTGVGIPGTM-----
FGFAGFFSKDAIIEAAYAFGGPAGQLAFWMLVIAALFTSFYSWRLIHLTFHGKTRADQHT--FDHA--------
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HESPRIMLVPLYILAAGAVLAGVVFYDVFFGH-AEHVEH-FF--HGAVVVDAE--
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IIDAAHYVPFWVKASAAMAMLAGFVLAWYFYIRR----------------------------------------
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RARFFAYLSLFTFAMLMLVTADNFLQMFFGWEGVGLASYLLIGFWYKKPSANAAAMKAFVVNRVGDFGFALGIF
GTFFLFGTLGF--DETFAVLSGAEGMT---
IPFLGAEFDAMTVICLLLFMGAMGKSAQFLLHTWLPDAMEGPTPVSALIHAATMVTAGVFMVARLSPMFEMSET
ATLVVIYIGAITAFFAATVGLVQNDIKRVIAYSTCSQLGYMFVALGVGAYSAGIFHLFTHAFFKALLFLGAGSV
IHAMHHEQDMRNMGGIAKKVPLTYWMMIIGTLALTGVGIPGTM-----
FGFAGFFSKDAIIEAAYAFGGPAGTLSFWLLVVAALFTSFYSWRLIHLTFHGKTRADHHT--FDHA--------
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HESPNVMLIPLYVLAVGAVLSGVIFYDVFFGH-AEHVEH-FF--HGSIVVDAA--
IIDAAHYVPTWVKWSATVAMLAGFVGAWYFYIRS----------------------------------------
-------------------PETPKQLAAEHPHLYKFFLNKWYFDELYHHIFVRPARWLGNALWKG-
FDDWFIDQTVVEGLG-RRVKQVTAQVVKLQSGYLYHYAFAMLIGVAALITWAIAAGGLLG-----
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GAFFLLGTLDF--DATFAALPGFADAT---
ISFLWWEAHAMTVICLLLFMGAMGKSAQFLLHTWLPDAMEGPTPVSALIHAATMVTAGVFMVARLSPMFELSEA
ATLFIIYIGAITAFCAATIGLVQNDIKRVIAYSTMSQLGYMFVALGVGAYSAGVFHLFTHAFFKALLFLGAGSV
IHAMHHEQDMRNMGGIRKKVPLTYAMMLIGTLALTGVGIPGTS-----
FGFAGFFSKDAIVEAAYAFGGTAGSFSFWMLVTAALFTSFYSWRLIHLTFHGPTRADHHT--FDHA--------
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-------------------PSAPKQLAEEHRGLYQFLLNKWYFDELYDRIFVRPARWVGTALWKG-
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AIWFIFRDVNF--DTIFAAAKEHQATT---
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ALLVVTCVGAITAFFAATVGLAQNDIKRVIAYSTCSQLGYMFVALGLSAYGAAVFHLFTHAFFKALLFLGAGSV
IHALHGEQDLRKMGGMRKAIPFTFGMMVIGTLSLTG--FPF---------
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HESPPVMTGPLLILAAGALFAGLIFAPYFVGA-DYAQ---FW--RSSLLFLHG---
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------------------PGIPAWTVKTFKPIHAFLYNKWYFDELYDWIFVRPTRWIARVLWKY-
GDGAIIDGLGPDGVA-ASVIATTKRVVRIQTGFVYTYAFVMLIGVTVLITWFAYLYRGALFTL--
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DGETARVTLF--EWIVSGDMVAEWSLRIDTLTAVMLVVVTTVSSLVHIYSIGYMEHDEG-------
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QPRFFAYLSLFTFAMLALVTADNLLQLFFGWEGVGLASYLLIGFWYHKPSANAAAIKAFVVNRVGDFGFLLGIF
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IHALHEEQDLRKMGGIARKIPLTWAMMLIGTLALTG--FPL---------
TAGYYSKDAVVEAAYAGANPVAMYAFWATVIAAFLTSAYSWRLMFMAFHGQPRMGDEA--LGKV----------
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GVFMVARLSPLFEHAPDALIVVTVVGAITAFFAATVGLVQNDIKRVIAYSTCSQLGYMFVALGLGAYSVAIFHL
FTHAFFKALLFLGAGSVIHAVSDEQDMRRMGGLRRVIPVTYAMMLVGTLALTG--FPF---------
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HESASVMLIPLYVLAAGALLAGIAFSGLFIGE-AQEG---FW--
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PDTPRRIGEQHEGLYRFLLNKWYFDELYDFLFVRPVMALGRFLWKR-GDGWLIDGFGPDGVS-
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GLFVLFGSISF--
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FTHAFFKALLFLGAGSVIHAVSDEQDMRKMGGLWRKIPLTYALMLVGTLALTG--FPM---------
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HESPQVMLMPLYILAAGALFGGLLFAAAFIDP-ERSVE--FW--
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PETPKALAQRMGSLYRFLLNKWYFDELFDAMFVRPAFALGRFLWRR-GDEGTIDRLGPDGIS-
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GIYLFFHTISF--DAIFANAHSLEGAS---
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IHAMSDEQDMRRMGGLRKLIPFTYWMMIIGTLALTG--FPL---------
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AVFLVYGSVNF--EVIFANAADAEGMT---
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IMAMHHEQDIRNMGGLRKKIPFTYWMMVIGTLALTG--FPF---------
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INF--DDIFAATPMLAETQ---
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IHAMHHEQDMMNYGGLRKKIPYTFWAMMIGTLAITGVGIPLTH-----IGFAGFLSKDAIIESAYA---
GGSMYGFWMLVIAAAMTSFYSWRLIFLTFYGKPR--GDKHTHDHA-----------------------------
--------------------------------HESPMVMLVPLGVLALGAVFSGMVWYNSFFGHTDTVGK--
FYGIPYAEAAEADNTLLDDAHAVNKWVKVSPFIAMVLGLSLAIWFYIVN-------------------------
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TSDNLLQMFFGWEGVGVASYLLIGFYYRKPSANAAAMKAFIVNRVGDFGFLLGIFATYMLVDSIRF--
DDIFAAAPALAEES---
FHFLSWEVPAVETIAVLLFIGAMGKSAQLFLHTWLPDAMEGPTPVSALIHAATMVTAGVFLVCRMSPVMEYAPG
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IHAMHHEQDMRNYGGLRSKIPYTFWAMMLGTLAITGVGIPLTH-----
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HESPMVMVVPLGILALGAIFAGMIWYEDFFGHHAKE----FFGA--
SVFMHPDNHVMHDAHEVSKLVKVSPFLAMLVGLALAYWFYIVN-------------------------------
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TDIFAAAPELAETQ---
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IGFAGFASKDAVIESAFAGTNAAHMYAFWMLVIAALMTSFYSWRLMFMTFYGTPR--GDKHTHEHA--------
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HESPPVMLVPLYVLGAGALLAGILFEHFFIGE-GYGE---FW--
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QSLPARTAATNPGLYRFLLNKWYFDELYDVVFVRSAKALGRFFWKTGGDQKVIDGLGPDGIS-
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IHAMSDEQDMRKMGGLFPHLKKTWAMMLVGTLALTG--FPL---------
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IHAMSDEQDMRKMGGLFRMIPATWLMMIIGTLALTG--FPF---------
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GCYMVFQSIEF--ETIFACAPLYANQT---
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ALSVIAFFGASTAFFAATTGLLQNDLKKVIAYSTCSQLGYMCFAVGLSKYSVSFFHLANHAFFKALLFLSAGCV
IHAMQDEQEMRRMGGLLSSLPFTYSTMTLGSLALMG--TPF---------
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HDAPGIVLVALCPLAVGSIWSGYFGADMFLGV-GTP----FW--
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HSLFNEQDIRRIGSLLRILPIAYLMIMIGSLSLIG--IPF---------
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VIFLKFHSVDY--LTVFNLVPNVFFES---
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IHAFLNEQDIRFIGGLKNLLPFTYAIMIVGSFSLLG--FPF---------
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NDCSFYIKTSLTFLAIGSIFLGYLTKEMLVGM-GTD----FW--
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HYSSSWMIVPLVILIIGSIYFGFILKDIIIGL-GTD----FW--
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IHSFQDEQDMRKMGGLGLILPYSYSMILIGSLSLMG--FPF---------
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LIFCGFEVDSLTLICILLFVGAVGKSAQLGLHTWLPDAMEGPTPVSALIHAATMVTAGVFMIARCSPLFEFAPT
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IHAMSDEQDMRRMGGLAQIIPFTYVMMVIGSLSLMG--FPF---------
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HESSFVMLLPLILLSFGSIFVGYLTKDMIIGL-GTS----FWGNSIFTLP-TNITMVDAEF-
LPYYIKLIPVILSLSGAVISLLVYHFMSQ---------------------------------------------
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-NVVSRVSSLTSALHTGYIYHYAFVMFVGVVFILRI------------IF
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IIFVEYKAVDY--ATVFALTPIFTNKV---
FHFLNFDFDLISLICFFLFIGAVGKSAQLGLHTWLPDAMEGPTPVSALIHAATMVTAGVFLIARTSPLFEYTSS
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IHAVADEQDMRKMGGLKKLVPFTYSMMVIGSLALIG--FPF---------
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SEGGKAIGFVLGLLAIPSIFVGYFSRDLFIGL-GTH----FWGSSLFCLP-SNLSLIDAEF-
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GIFYTFQSVDF--SVLLAL-SASEHSS--------
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ALVGAMTAFFAATTGAAQNDLKRVIAYSTCSQLGYMVFASGLSHYDLSVFHLMNHAFFKALLFLGAGSVIHALS
DEQDLRRMGGLVQLLPFTYTMMLIGSLSLVG--IPF---------
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GRFTIFQTVDF--STLFACVSAFSEPYHY-
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FIFALKTSTLGNRLYCFLNKRWFFDKVFNDFIVRSFLRFGYEVSFKVLDKGAIEILGPYGIS-
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FVYDFKTSSLGRRFYTFLNKRWLFDKVLNEFLAQSVLRFGYSISFVTLDKGVIELLGPYGIA-
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FIYVLKTSTLGTKCYCFLNKRWLFDKVFNDFIAKSFLRFGYEVSLKTLDKGAISILGPYGIS-
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MY-------LLIVFLPLLGSSVAGFFG----RFLGSEGTAIMTTTCVSFSSILSLIAFYEVALG-ASA--
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LVFLVFKSVDF--SVIFTIAPFITEYT---
INLLGYEVNAITLIGSFIVIGVVGKSAQLGLHMWLPDAMEGPTPVSALLHAATMVTAGVFLVLRTSPLLSYSIT
ILNILTIIGALTTLFATTIGIVQNDIKRVIAYSTCSQLGYMIFACGLLNYNASIYHLTTHAFFKALLFLSAGSV
IHGLNDEQDMRKMGGLVNLMPLTYQCMLIGTLALTG--FPF---------
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HEASTNMVIPLVILALCSIFIGYVTKDFFVGL-GTP----VWNNSFFAYP-YNNLILESEV-
LQRELKLLPLFAFIYGVITPVLFYFNIKEID-------------------------------------------
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AAFIVFKTTNF--SVIFSLVPYYVNHE---
IFFFTYKCNAITLIGLLLFIGSVGKSAQLGLHTWLPDAMEGPTPVSALIHAATMVTAGVFLIIRCSPLYEYSES
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ALLVVTIIGGTTAFFAATTGLVQNDLKRVIAYSTCSQLGYMIFACGLSGYSIGMFHLMNHAFFKALLFLSAGSV
IHALADEQDMRKMGGMLNIVPLTYTMMLIGSMSLMG--FPF---------
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>YP_007890522_NAD5_Andalucia_godoyi
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IPTPIKLLPVILSIVGASLAIILNNFYAT---------------------------------------------
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GDEQDMRKMGGLIRLLPFTYVMILIGSLSLMG--FPF---------
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LPFFIKLIPVIFSLFGAFLGYTLYSSNI----------------------------------------------
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FLFCNLELDQLTVICLLLFVGAVGKSAQLGLHTWLPDAMEGPTPVSALIHAATMVTAGVFMICRCSPLFEYAPD
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