

>FraEKlebsiella_sp._MS_92-3

LPHIVILATGGTIAGSAASNTQTTGYKAGALGVQTLINAVPEMSKIAHVEGEQVANIGSENMTSDIILQL
SKRVNALLARDDVDGVVITHGDTLDETPYFLNLTVKSINKPVVFTAAMRPATAISADGPMNLLAEVTVAA
DPDARGRGVMVVLNDRIGAARFVTKTNATSLDTFRAPEEYGLGVVVGKPKQFETRVDKIHTLRSVFDVRQ
LKVLPKVVIIIGYQDDPEYMYDAAIAHHDGIIYAGTGAGSVSVRSAAGIKKAQQAGIVVVRASRTGSGV
VPPDDSQPGLVADSLNPAKARILL

>FraEKlebsiella_pneumoniae_subsp._pneumoniae_WGLW1

LPHIVILATGGTIAGSAASNTQTTGYKAGAIGVQTLINAVPEMSKIAHVEGEQVANIGSENMTSDIILQL
SKRVNALLARDDVDGVVITHGDTLDETPYFLNLTVKSINKPVVFTAAMRPATAISADGPMNLLAEVTVAA
DPDARGRGVMVVLNDRIGAARFVTKTNATSLDTFRAPEEYGLGVVVGKPKQFETRVDKIHTLRSVFDVRQ
LKVLPKVVIIIGYQDDPEYMYDAAIAHHDGIIYAGTGAGSVSVRSAAGIKKAQQAGIVVVRASRTGSGV
VPPDDSQPGLVADSLNPAKARILL

>FraEKlebsiella_pneumoniae_subsp._pneumoniae_WGLW3

LPHIVILATGGTIAGSAASNTQTTGYKAGAIGVQTLINAVPEMSKIAHVEGEQVANIGSENMTSDIILQL
SKRVNALLARDDVDGVVITHGDTLDETPYFLNLTVKSINKPVVFTAAMRPATAISADGPMNLLAEVTVAA
DPDARGRGVMVVLNDRIGAARFVTKTNATSLDTFRAPEEYGLGVVVGKPKQFETRVDKIHTLRSVFDVRQ
LKVLPKVVIIIGYQDDPEYMYDAAIAHHDGIIYAGTGAGSVSVRSAAGIKKAQQAGIVVVRASRTGSGV
VPPDDSQPGLVADSLNPAKARILL

>FraEKlebsiella_pneumoniae_subsp._pneumoniae_WGLW5

LPHIVILATGGTIAGSAASNTQTTGYKAGALGVQTLINAVPEMSKIAHVEGEQVANIGSENMTSDIILQL
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DPDARGRGVMVVLNDRIGAARFVTKTNATSLDTFRAPEEYGLGVVVGKPKQFETRVDKIHTLRSVFDVRQ
LKVLPKVVIIIGYQDDPEYMYDAAIAHHDGIIYAGTGAGSVSVRSAAGIKKAQQAGIVVVRASRTGSGV
VPPDDSQPGLVADSLNPAKARILL

>FraEKlebsiella_oxytoca_10-5243

LPHIVILATGGTIAGSAASNTQTTGYKAGAIGVQTLINAVPEMSKVARVDGEQVANIGSENMTSDIILKL
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DPEAKGRGVMVVLNDRIGAARFVTKTNATSLDTFRAPEEYGLGVIVSGKPKQFETRVDKIHTVRSVFDVRN
LNALPKVVIIIGYQDDPEYMYDAAIAHHDGIIYAGTGAGSVSVRSAAGIEKAEKAGIVVVRASRTGSGV
VPVDGGQPGLVADSLNPAKARILL

>FraEKlebsiella_oxytoca_10-5250

LPHIVILATGGTIAGSAASNTQTTGYKAGAIGVQTLINAVPEMSKVARVDGEQVANIGSENMTSDIILKL
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DPQAKGRGVMVVLNDRIGAARFVTKTNATSLDTFKAPEEYGLGVIVSGRPQFETRVDKIHTVRSVFDVRQ
LSALPKVVIIIGYQDDPEYMYDAAIAHHDGIIYAGTGAGSVSVRSAAGIEKAEKAGIVVVRASRTGSGV
VPVDDGQPGLVSDSLNPAKARILL

>FraESalmonella_bongori_NCTC_12419

LPHIVILATGGTIAGTAANNTQTAGYKSGELGVQTLINAVPEMSNIARVDGEQVANIGSENMTSDIILKL
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DPNAKGRGVMVILNDRIGSARFVTKTNATSLDTFKAPEEYGLGVIVNGNPQFETRVEKIHTLRSVFDVRN
IKKLPNVVIIIGYQDDPEYMYDAAIAHHDGIIYAGTGAGSVSVRSAGIKKAEKAGIIVVRASRTGNGV
VPLDKGQPGLVSDSLNPAKARILL

>FraESalmonella_enterica_subsp._enterica_serovar_Paratyphi_C_str._RKS4
594

LPHIVILATGGTIAGTAANNTQTAGYKSGELGVQTLINAVPEMNNIARVDGEQVANIGSENMTSDIILKL
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DPNAKGRGVMVVLNDRIGSARFVTKTNATSLDTFKAPEEYGLGVIVNGQPQFETRVEKIHTLRSVFDVRN
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VPLDKGQPGLVSDSLNPAKARVLL

>FraESalmonella_enterica_subsp._enterica_serovar_Enteritidis_str._P125

109

LPHIVILATGGTIAGTAANNTQTAGYKSGELGVQTLINAVPEMNNIARVDGEQVANIGSENMTSDIILKL
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DPNAKGRGVMVVLNDRIGSARFVTKTNATTLDTFKAPEEYGLGVIVNGKPPQFETRVEKIHTLRSVFDVRN
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VPLDKGQPGLVSDSLNPAKARVLL

>FraESalmonella_LT2

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SQKVNALLARDDVDGVVITHGDTLDEYFLNLTVKSDKPVVFTAAMRPASAI SADGAMNLL EAVTVAA
DPNAKGRGVMVVLNDRIGSARFVTKTNATTLDTFKAPEEYGLGVIVNGKPPQFETRVEKIHTLRSVFDVRN
IKKLPNVVYIYGYQDDPEYMYDAAIAHHDGIIYAGTGAGSVSVRS DAGIKKAEKAGIIVRASRTGNGV
VPLDKGQPGLVSDSLNPAKARVLL

>FraESalmonella_enterica_subsp._enterica_serovar_Typhimurium_str._1402
8S

LPHIVILATGGTIAGTAANNTQTAGYKSGELGVQTLINAVPEMNNIARVDGEQVANIGSENMTSDIILKL
SQKVNALLARDDVDGVVITHGDTLDEYFLNLTVKSDKPVVFTAAMRPASAI SADGAMNLL EAVTVAA
DPNAKGRGVMVVLNDRIGSARFVTKTNATTLDTFKAPEEYGLGVIVNGKPPQFETRVEKIHTLRSVFDVRN
IKKLPNVVYIYGYQDDPEYMYDAAIAHHDGIIYAGTGAGSVSVRS DAGIKKAEKAGIIVRASRTGNGV
VPLDKGQPGLVSDSLNPAKARVLL

>FraESalmonella_enterica_enterica_sv._Typhimurium_LT2-4

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SQKVNALLARDDVDGVVITHGDTLDEYFLNLTVKSDKPVVFTAAMRPASAI SADGAMNLL EAVTVAA
DPNAKGRGVMVVLNDRIGSARFVTKTNATTLDTFKAPEEYGLGVIVNGKPPQFETRVEKIHTLRSVFDVRN
IKKLPNVVYIYGYQDDPEYMYDAAIAHHDGIIYAGTGAGSVSVRS DAGIKKAEKAGIIVRASRTGNGV
VPLDKGQPGLVSDSLNPAKARVLL

>FraECitrobacter_rodentium_ICC168

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SQQVNALLARDDVDGVVITHGDTLDEYFLNLTVKSDKPVVLTGAMRPATAMSADGAMNLL EAVTVAA
DPNARGRGVMVVLNDRIGSARFVTKTNATTLDTFKAPEEYGLGVMVNGKPPHFEMRVEKVHTLRSVFDVRN
LRKLPVAVIYGYQDDPEYLYDAAISHHVDGIIYAGTGAGSVSVRSEAGIRKAEKAGIIVRASRTGNGV
VPVDQGPGLVAGSLNPAKARILL

>FraECitrobacter_freundii_GTC_09629

QPHIVILATGGTIAGTAANTTQTSYKSGEIGVQTLINAVPEIKNIARVDGQQIANIGSENMTSDIILKL
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DPNARGRGVMVVLNDRIGSARFVTKTNATTLDTFKATEQGYLGIIVNGTPQFETRVEKVHTLRSVFDVRN
LRKLPVVVIYGYQDDPEYMYDAAISHHVDGIIYAGTGAGSVSVRSEAGIRKAEKAGIIVIRSSRTGNGV
VPVDKGPGLVADSLNPAKARILL

>FraEEscherichia_hermannii_NBRC_105704

LPHITILATGGTIAGGGASATQSAYKAGKSVENLVDAVPELKSIAQIKGEQVVSIGSQDMNDQVWLT
KINSECDSTDGVVITHGDTMEETAYFLDLTVKCDKPVVMVGAMRPSTAMSADGPFNL YNAVITAADPQ
SARRGVLVAMNDTVLDGRDVTKNTTVDVATFKGVNFGPLGYIHNGKVDYQRT PARKHTTQTPFNVNLT
LPKVGIVYSYANASDL PVKALVEGGYKGVISAGVGNLYKDVFDLATAAHNGVAVVRSSRVPTGSTTQ
DAEVDDAKYGFVASGTLNPQKARVLL

>FraEEscherichia_coli_str._K-12_substr._W3110

LPNITILATGGTIAGGGDSATKSNYTVGKGVENLVNAVPLKDIANVKGEQVNVIGSQDMNDNVWLT
KINTDCDKTDGFVITHGDTMEETAYFLDLTVKCDKPVVMVGAMRPSTSMSADGPFNL YNAVVTAA
SANRGVLVVMNDTVLDGRDVTKNTTVDVATFKSVNYGPLGYIHNGKIDYQRT PARKHTSDTPFDVSKLNE
LPKVGIVYNYANASDL PAKALVDAGYDGVISAGVGNLYKSVFDLATAAKTGTAVVRSSRVPTGATTQ
DAEVDDAKYGFVASGTLNPQKARVLL

>FraELactobacillus_vaginalis_ATCC_49540

TASALSFMLENLGKPVIVTGSQIPLAELRSDGQINLLNALYVAANYPINEVTLFFNNRLYRGNRTTKAHA
DGFDAFASPN

>FraESubdoligranulum_sp._4_3_54A2FAA

MKRVLMIGTGGTIASEMTGAGLVPELTTDQFLKYVPAVRELCDVTCRQVCNIDSTNMSPAYWLEIARAIR
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VQIVFGGAVILGTRARKTYSKSFAGFSSINYPVLGVVQDNCLVPYIRPQAQAEPVFDALNSRVALLKLI
PGASAGQLRFLLDENDAVILESFGVGGVPSGETGEFYEVIRKASAKGKTVVVTTQVQNEGSDLSIYNVGH
SLKNGLGVLEAFDMTTEAVVAKL

>FraEClostridium_acetobutylicum_ATCC_824

MKKVAVIFNGGTISMKFDSRVKAAVPALSGEEIMSMVTGIEKFAEIESFNFSEEPGPHMTPEKMMELSNF
IKDILKRDDIVGAVVTHGTDLSLEETAYFLDLTIKNEKPVVVTGSMRNSSELGYDGPANLSAAICTAISEE
SRNKGVLVCFSDENLASEVTKVHSMHLNAFESPDFGLGIVDTNKPIFYRDKVYNDYIETSSVESKVAL
IKTAVGMNSDFIDFAVEKGYKGIVIEAMGRGNVPPYMEVIERALKKNVPVVLVSRCYKGRVLDYGYHG
GGKELRNIGVIFGDNLPGQKARIKL

>FraEClostridium_symbiosum_WAL-14163

LKKISVLTGTTIAYTWKNGGPQIGDLTGFDLSLDEVKKEADITVKAFRQKSSSSMVISDIIGLAAEIQS
LLEGETEGVVVQGTDTIEETAFALEMLLDSEKPVAVTGAMRNPDMRGADGPANLLAAIRTVSCSRREL
GVMVVFNDAIYPALYVRKIHPQSTEFAAAECGPLGYLAEGKPSIRMKPLQRRIPGLAINKWNVDGKRPDQ
PVSUPIYAVPVGDDGKLLKCALDCKIDGLVLEAMGGGHTPSELVETLKQLADKMPVVLASRIGRGMMLTG
TYAGYPGSETSLLSKGLISSGFLDGRKARLLL

>FraEClostridium_symbiosum_WAL-14673

LKKISVLTGTTIAYTWKNGVQPQIGDLTGFDLSLDEVKKEADITVKAFRQKSSSSMVISDITGVAAEIQS
LLEGETEGVVVQGTDTIEETAFALEMLLDSEKPVAVTGAMRNPDMRGADGPANLLAAIRTVSCSRREL
GVMVVFNDAIYPALYVRKIHPQSTEFAAAECGPLGYLAEGKPSIRMKPLQRRIPGLAINRWNVDGKRPDQ
PVSUPIYAVPVGDDGKLLKCALDCKIDGLVLEAMGGGHTPSELVETLKQLADKMPVVLASRIGRGMMLTG
TYAGYPGSETSLLSKGLISSGFLDGRKARLLL

>FraEClostridium_sp._7_3_54FAA

MKNISVLTGTTIAYTWKNGVQPQIGDLTGFDLSLDEVKKEADITVKAFRQKSSSSMVISDITGLAAEIQS
LLEGETEGVVVQGTDTIEETAFALEMLLDSEKPVAVTGAMRNPDMRGADGPANLLAAIRTVSCSRREL
GVMVVFNDAIYPALYVRKIHPQSTEFAAAECGPLGYLAEGKPSIRMKPLQRRIPGLAINKWNVDGKRPDQ
PVSUPIYAVPVGDDGKLLKCALDCKIDGLVLEAMGGGHTPSELVETLKQLADKMPVVLASRIGRGMMLTG
TYAGYPGSETSLLSKGLISSGFLDGRKARLLL

>FraECollinsella_aerofaciens_ATCC_25986

MKRILLIATGGTIASTEDGNGLSPALTGEELAQSVPEISGLCKLDVVQPMNIDSTNMRPDWMRIRDVVV
KGYADHDGFVILHGTDTMSYTAALSYLIQDSPKPIVLTGSQKPMGNPFTDAKLNLYQSLLYALDENSHD
VSIVFGGVAIAGTRARKQRTMSFNAFISVNYPPIAYIRNDRIVRNLHGTHQGENPVRFYDSIDPRVFL
KLTPGVNPGILDALADSYDAVILETFGIGGIPEFGESGESFQEAIFRWVDSGRTVVMTTQVPEEGLDLGV
YEVGRAYADHPGILRGDDMTTETLVAKT

>FraEClostridiales_butyrate-producing_bacterium_SS3/4

MKHLLLLGTGGTIAACKRGENGLTPLLTDGDELLSYVPDAKKFCEVETVQVLNIDSTNMHPKHWLKLAQVLE
ENYDDYDGFVICHGDTMAYTAAAMSYLVQHSSKPIVITGAQKPIDLDVTDARTNLLDSLRFASERAHG
VTIVFDGKVIAGTRGKRSAAARATTPSPASTSR

>FraEClostridium_sp._M62/1

MKKLLLLSTGGTIASVMTENGLAPAATPKELLSYIPEAGKFCEISVRQLFNLDSTNFQPEHWIRISEEIR
REYEVYDGFIVTHGDTMAYTAAALSYLIQNPEKPIILTGSQKPIVITDARKNLMDSLRFASRDGVRG
VYLVFDGKAILGTRARKIRSKSYSAFESINYPVAAFIDENRIIQYVDGESRTGETVFYDRLNPRVFLKL
IPGIEPEILQYIGERYDAIIIESYGVGGIPFYNKRNFSLGLEDLTEKGKIVVIATQVMLEGSDAEVYEVG
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>FraE0ribacterium_asaccharolyticum_ACB7

MKKLLLLIGTGGTIASTRETGDGLSPGLQAEIIVSFVPEVRNLCEIEVLQLCNIDSTNMNPKIWRVQLVQAIK

ENFDRYDGFVVLHGTDTMAYTSAVLSYMIQHSRKPIVVTGSQKPIDREGTDARVNLRDSILYAMDDYSEN
VVLIFDGNVIAGTRAKKMQARSFNAFQSVNFPVLARVQDGRIIRYLPYIPEREVPRFFTEISDSVCFKL
IPGTRPELLSYLFENYDCIVIESFGVGGIPDALLDTVYREMKNWKESGKVLVMATQVMNEGSNMEIYRVG
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>FraE0ribacterium_sp._oral_taxon_108_str._F0425

MKRIILLGTGGTIACKRTDKGLKPVITPDEILSYVPDSQSYCEIHSIQLMNIDSTNIQPCHWLAIEQAIE
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VVLIFDGNVIAGTRAKKMQARSFNAFQSVNFPVLARVQDGRIIRYLPYIPEREVPRFFTEISDSVCFKL
IPGTRPELLSYLFENYDCIVIESFGVGGIPDALLDTVYREMKNWKESGKVLVMATQVMNEGSNMEIYRVG
QKIKKDFQLIEAYDMTLEAVVTKL

>FraEClostridium_bolteae_90A9

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ENYARYDGFVITHGTDTMAYTAAALSYLIQHSPKPIIITGAQKPIDMENTDARTNLADSLFASCPGAHD
VNIVFDGKVIAGTRGKKEWTKSYHAFSSINFPYVAIIQDGQIIFYLDDKDRDKKPVCFYRQMDGDVGLMK
LIPSMASLLDYMAEHYDAVIESFGVGGLPYQGDYHGAIARWTGLGKTVMITTTQVTNEGSMSVYEV
GRSIKQEFGLLEAYDMTLEAVVTKI

>FraEClostridium_bolteae_90B3

MKRILLGTGGTIACKRTDKGLKPVITPDEILSYVPDSQSYCEIHSIQLMNIDSTNIQPCHWLAIEQAIE
ENYARYDGFVITHGTDTMAYTAAALSYLIQHSPKPIIITGAQKPIDMENTDARTNLADSLFASCPGAHD
VNIVFDGKVIAGTRGKKEWTKSYHAFSSINFPYVAIIQDGQIIFYLDDKDRDKKPVCFYRQMDGDVGLMK
LIPSMASLLDYMAEHYDAVIESFGVGGLPYQGDYHGAIARWTGLGKTVMITTTQVTNEGSMSVYEV
GRSIKQEFGLLEAYDMTLEAVVTKI

>FraEClostridium_clostridioforme_90A7

MKRILLGTGGTIACKRTDKGLKPVITPDEILSYVPDSQSYCEIHSIQLMNIDSTNIQPCHWLAIEQAIE
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VNIVFDGKVIAGTRGKKEWTKSYHAFSSINFPYVAIIQDGQIIFYLDDKDRDKKPVCFYRQMDGDVGLMK
LIPSMASLLDYMAEHYDAVIESFGVGGLPYQGDYHGAIARWTGLGKTVMITTTQVTNEGSMSVYEV
GRSIKQEFGLLEAYDMTLEAVVTKI

>FraEClostridium_bolteae_ATCC_BAA-613

MKRILLGTGGTIACKRTDKGLKPVITSDEILSYVPDSQSYCEIHSIQLMNIDSTNIQPCHWLAVEKAIE
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VNIVFDGKVIAGTRGKKEWTKSYHAFSSINFPYVAIIQDGQIIFYLDDKDRDKEPVCFYRQMDGDVGLMK
LIPSMASLLDYMAEHYDAVIESFGVGGLPYQGDYHGAIARWTGLGKTVMITTTQVTNEGSMSVYEV
GRSIKQEFGLLEAYDMTLEAVVTKI

>FraEClostridium_bolteae_90A5

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VNIVFDGKVIAGTRGKKEWTKSYHAFSSINFPYVAIIQDGQIIFYLDDKDRDKEPVCFYRQMDGDVGLMK
LIPSMASLLDYMAEHYDAVIESFGVGGLPYQGDYHGAIARWTGLGKTVMITTTQVTNEGSMSVYEV
GRSIKQEFGLLEAYDMTLEAVVTKI

>FraEClostridium_bolteae_90B7

MKRILLGTGGTIACKRTDKGLKPVITSDEILSYVPDSQSYCEIHSIQLMNIDSTNIQPCHWLAVEKAIE
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VNIVFDGKVIAGTRGKKEWTKSYHAFSSINFPYVAIIQDGQIIFYLDDKDRDKEPVCFYRQMDGDVGLMK
LIPSMASLLDYMAEHYDAVIESFGVGGLPYQGDYHGAIARWTGLGKTVMITTTQVTNEGSMSVYEV
GRSIKQEFGLLEAYDMTLEAVVTKI

>FraEClostridium_bolteae_90B8

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VNIVFDGKVIAGTRGKKEWTKSYHAFSSINFPYVAIIQDGQIIFYLDDKDRDKDPVCFYRQMDGDVGLMK

LIPSMASLLDYMAEHYDAVIIIESFGVGGLPSYQGDYHGAIARWTGLGKTVMITTTQVTNEGSDMSVYEV
GRSIKQEFGLLEAYDMTLEAVVTKI

>FraEClostridium_clostridioforme_2_1_49FAA

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VNLVFDGKVIAGTRGKKEWTKSYHAFSSINFPYVAIIQDGQIIFYLDDKDRDKKPVCFYRQMDGDVGLMK
LIPSMASLLDYMAEHYDAVIIIESFGVGGLPSYQGDYHGAIARWTGLGKTVMITTTQVTNEGSDMSVYEV
GRSIKQEFGLLEAYDMTLEAVVTKI

>FraEClostridium_clostridioforme_90A8

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ENYGQYDGFVITHGDTMAYTAAALSYLIQHSPKPIITGAQKPIDMENTDARTNLADSLFASCPGAHD
VNLVFDGKVIAGTRGKKEWTKSYHAFSSINFPYVAIIQDGQIIFYLDDKDRDKKPVCFYRQMDGDVGLMK
LIPSMASLLDYMAEHYDAVIIIESFGVGGLPSYQGDYHGAIARWTGLGKTVMITTTQVTNEGSDMSVYEV
GRSIKQEFGLLEAYDMTLEAVVTKI

>FraEClostridium_clostridioforme_90A1

MKRILLLGTGGTIACKRTDKGLKPVITSDEILSYVPDSRSYCEIHSIQLMNIDSTNIQPCHWLAVEKAIE
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VNLVFDGKVIAGTRGKKEWTKSYHAFSSINFPYVAIIQDGQIIFYLDDKDRDKKPVCFYRQMDGDVGLMK
LIPSMASLLDYMAGHYDAVIIIESFGVGGLPSYQGDYHGAIARWTGLGKTVMITTTQVTNEGSDMSVYEV
GRSIKQEFGLLEAYDMTLEAVVTKI

>FraEClostridium_clostridioforme_90A3

MKRILLLGTGGTIACKRTDKGLKPVITSDEILSYVPDSRSYCEIHSIQLMNIDSTNIQPCHWLAVEKAIE
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VNLVFDGKVIAGTRGKKEWTKSYHAFSSINFPYVAIIQDGQIIFYLDDKDRDKKPVCFYRQMDGDVGLMK
LIPSMASLLDYMAGHYDAVIIIESFGVGGLPSYQGDYHGAIARWTGLGKTVMITTTQVTNEGSDMSVYEV
GRSIKQEFGLLEAYDMTLEAVVTKI

>FraEClostridium_clostridioforme_90A4

MKRILLLGTGGTIACKRTDKGLKPVITSDEILSYVPDSRSYCEIHSIQLMNIDSTNIQPCHWLAVEKAIE
ENYGQYDGFVITHGDTMAYTAAALSYLIQHSPKPIITGAQKPIDMENTDARTNLADSLFASCPGAHD
VNLVFDGKVIAGTRGKKEWTKSYHAFSSINFPYVAIIQDGQIIFYLDDKDRDKKPVCFYRQMDGDVGLMK
LIPSMASLLDYMAGHYDAVIIIESFGVGGLPSYQGDYHGAIARWTGLGKTVMITTTQVTNEGSDMSVYEV
GRSIKQEFGLLEAYDMTLEAVVTKI

>FraEClostridium_clostridioforme_90A6

MKRILLLGTGGTIACKRTDKGLKPVITSDEILSYVPDSRSYCEIHSIQLMNIDSTNIQPCHWLAVEKAIE
ENYGQYDGFVITHGDTMAYTAAALSYLIQHSPKPIITGAQKPIDMENTDARTNLADSLFASCPGAHD
VNLVFDGKVIAGTRGKKEWTKSYHAFSSINFPYVAIIQDGQIIFYLDDKDRDKKPVCFYRQMDGDVGLMK
LIPSMASLLDYMAGHYDAVIIIESFGVGGLPSYQGDYHGAIARWTGLGKTVMITTTQVTNEGSDMSVYEV
GRSIKQEFGLLEAYDMTLEAVVTKI

>FraEClostridium_clostridioforme_90B1

MKRILLLGTGGTIACKRTDKGLKPVITSDEILSYVPDSRSYCEIHSIQLMNIDSTNIQPCHWLAVEKAIE
ENYGQYDGFVITHGDTMAYTAAALSYLIQHSPKPIITGAQKPIDMENTDARTNLADSLFASCPGAHD
VNLVFDGKVIAGTRGKKEWTKSYHAFSSINFPYVAIIQDGQIIFYLDDKDRDKKPVCFYRQMDGDVGLMK
LIPSMASLLDYMAGHYDAVIIIESFGVGGLPSYQGDYHGAIARWTGLGKTVMITTTQVTNEGSDMSVYEV
GRSIKQEFGLLEAYDMTLEAVVTKI

>FraEClostridiales_bacterium_1_7_47FAA

MKRILMLGTGGTIACKRTERGLKPVITSEEILSYVPDSRSTYQCIDTIQILNIDSTNIQPShwLTIASAIE
AHYDQYDGFVITHGDTMAYTAAALSYLIQHSHKPIVITGSQKPIDMENTDARTNLADSLRFASDPRAHD
VNIVFDGKAIAGTRGKKERTKSYNAFSSINFPNVAIIQEDHIIIFYLDDKDRSTEPVRFHEDSNVGLMK
LIPSTDTSLDYMAGHFDALIIIESFGVGGLPSYEKGDYRAIGHWTGRGKTVMITTTQVTNEGSNMSVYEV
GRNIKQEFGLLEAYDMTLEAVVTKT

>FraEClostridium_asparagiforme_DSM_15981
MKHILMLGTGGTIAACKRSDAGLKPVITSEEILSYVPDSKRYCDIDSLQVFNIDSTNMQPSHWLAVARAIE
EHYDRYDGFVICHGDTMAYTAAALSYLVQDSPKPIVITGAQKPIDMENTDARTNLADSLFFASNDRAHG
VNIVFDGKVIAGTRGKKERTKSYNAFSSINFPYIAAIQEDHILFYLDKPEHAQVKFYHEMSSGVVLLKL
IPSMASLLDYMAEHYDAVIVESFGVGGGPSYDSGDYYRAVGRWTALGKTVVMTTQVTNEGSNMSVYEVG
KNIKQEFGLLESYDMTLEATVTKI

>FraEClostridium_hylemonae_DSM_15053
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MVAFFDDKIINGCRATKVRTLGFNAFESISANYLGEVYADGVHLYDNYKVVHTEEKPFCLKENLCPNVFLL
KLIPGTNPDIFECLLMGYRGIVIEAFGAGGTHFERRNLIPKLLKLDHGVSIVARSQCLYEKSDFSLYE
VGRKLLDCGVIPGRDMTTEAIVTKL

>FraEClostridium_hathewayi_WAL-18680
MKRILMIATGGTIAASKRDVNLKPLITSEEILSYVPDTREFCQTDTLQLFNIDSTNIQPMHWLAMANAIE
ERYMEYDGFVICHGDTMAYTAAALSYLIQNSRKPIVITGAQKPIDMEITDAKTNLSDSLLFASHDSAYG
VSIVFDGKVIAGTRGKKERTKSYNAFSSINFPYIASVQDSRVIFYLDDKNQLDEPVTFYHKLNSNVALLK
LIPSMDATVLDYMAGHYDAVIESFGVGGGPSYETGAYHPVVEKWVSLGKTVVMTTQVTNEGSNMSVYEV
GHSIKQEFGLLEAYDMTLEATVTKL

>FraELachnospiraceae_bacterium_oral_taxon_082_str._F0431
MKKILVIGTGGTIAASKQMGEGSPALSAPEILTYVPEVEKLCEIDVLQICNIDSTNITPKIWDIAGTIK
KIYDFYDGFVILHGTDTMAYTSAALSYMIQNSRKPIVITGAQKPINIDGTDKVNLRDSILYACDDYSQN
IVLVFDGNVIAGTRAKMMARSFNAFHSVNFPIIARIQEKHIIRYIPYIPMRERVRFFLDLNDSDVCLKV
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>FraEClostridium_hathewayi_12489931
MKKILMLGTGGTIAACKRGESGLKPLISSEELLSYVPDAKQFCQADSLQILNIDSTNMQPKHWLTMAEAEIE
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VTIVFDGKAIAGTRGKKERTKSYNAFSSINFPYIAMIQDGHVIFYLDEKEHLTDHVQFYRTLNPVALLK
LIPSMGADVLDYMAGHYDAVIESFGVGGGPSYDSGDFYKAIEKWISLGKTVVMTTQVTNEGSNMSVYEV
GRSIKKEFGLLEAYDMTLEATVTKL

>FraECoprococcus_comes_ATCC_27758
MKKILMLGTGGTIASRQTKDGLAPGLTPEDILSYIPAVKNVCEVQTKQVCNLDSTNVTPHVKMMVKAVE
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VNLVFDGKVIIVGTRAKKEHAKSYNAFSSINFPYLAVIQDGLVRYIPEIPCRHAVKFYYDMKDSVYVLLK
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KLSRISI

>FraEEnterococcus_faecium_R497
MKKILVLHTGGTIAMKENMLTGGVSPDVANPLLDAAEITIPKHVELLVEDIFNLSPHIMP SHMLVLKERI
LSAYASGISGVVITHGDTLEETAFFLDTTIGNKLPVLTGAMRSSNELGSDGLYNFESAIRVASCEEAL
DKGVLVVMNDEIHSARYVTKHTTNVATFRTPTLGPVGLVTKNRILFLQELLETKRLDISAVDGTIPIVK
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KELEKMGIIFCNSINSQKARLKL

>FraBLM_ORIG_scaffold_17
MNRPEELIKKIYEEQGRINDVFLTACGGSLVDLYPGYYFLNAESETMHAHWLTAKELVVSPSKFLKKGAL
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LLKMQEESYSKYDAVLDGLEKADGIVRAAVKVKVNRWTWVFAEKYFEFPFLYIMGSGASYSQAYGFSICSL
QEMQWMDCCYLHSGEYFHGPFECTDEDHLYILLMGTGAARTMDERALVFLKKYAKKYEVIDAVELGIDAI
DASVNEYFCPMVYAMSVAYRTGLQDKRRHPLDMRRYMGVVEY*

>FraBLM_ORIG_scaffold_39

MIKGMQEVIDVMARVKSDDLKNGGLKQVVFVACGGSFASSYPARFLLNQESALRVQGYNSSEFVYATPKN
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QGTALKIAFWLLREYDRYAAYDMAMEGFLEAIYAGAYQSVKADAARFGMTYKDDQVWVMSSGAWEV
SYSDAFCFFQEMQTVHCVPIHSGEYFHGAFETCEKDLAILLFSIGRTRPVDERAERFLNQFGGHHWIMD
ARDFGLDGLDERVAEYFNSLLFHPLSKQFITAMADVRMHPMGYRRYMWKFDY*

>FraBLM_ORIG_scaffold_211

MNKTVKEIIAEIKEKTDARGGLKHVYFVACGGSKAAIFPGLYLLQSEARTFSATTYTSNEFVHATPKELD
GRCVAVICSLKATAETVEAVKTANQAGALTIAMTGSMETGMAQVQYVVVTSNGDDQVYSDSNQANSLRI
GFELLHQIEGWEHYDKAMEAYSHIDQIVAEKGESCLPAARAWAEKVKDEPVFVYVLASGPNYGVAYSMMM
HFMEMQWKHAVCLHTGEYFHGPFETTDKALPMVLLMSEGRTRALDERCLKFLNTYGENFIIIDFQELNKG
RIHPSVVEFFNPVMIPIERYYSQMAELRGHSMDERRYMWKVEY*

>FraBLM_ORIG_scaffold_458

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GPDSVVITCSHSGNTPETVKATEIAREKGATTIALSNLVDSPWKAAYPIHYDWGKEADASDLNKAVLY
SLIFGILNTVAPCDKYEKGIASVENINEVIEKAKAQYADTVKGGWKKYKREKLIYTMGSGACYGETYSFA
ICLLMEMQWIHSSCIHSGEYFHGPFVETDFDVPFIIIVKGLGATRPLDERAHNFCQKYSNIMLVDCEFTD
MTGIDEEVREYFAPLVAGAVLRSLADAFAYERGHDLGVRRYMWKMEY*

>FraBLM_ORIG_scaffold_551

MEIRDLMEKIIKDMAAGGIKNVWVAAGGSHDGHYAAQYFMDRESTAVRSQMITSSSEFVYAPPKNVKGK
TIVVLTSMRGTKETIEAAKVAKELGAVTVSQQYVDESGLTEVCDYNVQYISIWEDDRDQSRNAGNALRMA
MAIVDIVEGYADYADAMDAFAKVQPAYIKAREYCAPLAVKWAAQAKDEKCITVLASGPAYGSGHIFSTCN
ILEMLQIHSPTFNSCDFHGPFEITDKNQSFLLIADGRTRKADERAITFVKKYAGDKVYILDAKELGLD
NLKDSVSEYFNHLLFTPVLNNVYMKELSKATGIDYTTTRYMWKVEY*

>FraBLM_ORIG_scaffold_593

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SRCLAVICSLKATPETVEAVRTANAAGAVTIAMTGSMETGMAKVQYVVVTSNGDEQVYSDSNQSNALRI
GFELLHQIEGWKDYEKAMAAYAQIDAIVAEGKERCLAERSWAKEYQDEPIFYVLASGPNYGVAYSMMM
HFMEMQWKHAVCLHTGEYFHGPFETTDALPMVLLMSEGRTRPLDERCLRFLEQYAENYITIDFQELNAG
RIDPEVAEFFNPVLIPIERFYVAQMAELRGHSMDERRYMWKVPY*

>FraBLM_ORIG_scaffold_634

MEPKQIIIEAIKKEVPAAKSVYFVCGGASKAELYPGKYFLEANARNIRVGHYTANEFYATPVAVDETAIV
VTCSLGGTTPETVAASKKAMD LGAKVAVTHVDGSP LAKNAHYVVLHGFEKNYAAKLEKMTKVL SLAVEI
LHQYEGYDRYDDMQTAFGKIYDLIEKAVSFVVPAAKNFAEDYKDAPVVYVMSSGATQEVAYAFSICLLME
MQWVNSGSFHDGEFFHGPFEIVEKDVPFILLMNEGRTRALDSRALDFLNRFAQKTTVLDGKDFGLASEVP
ASVAEYFNPMVLSAVLRVYAEQLAIKRNHPLTQRRYMWKLEY*

>FraBLM_ORIG_scaffold_1033

MNAKAVIEGILKEKGTQVQYVWVACGGSLIDLPAHFMLNAESATVESGWYTSKEFVLSTPKKLGKDSMV
VVC SHGNTQEA VDAAILAKEAGAAVITLTDGKGSKCDDERFIAWYYPWGEVPTAEVPSGITLLLAAEL
LKAQEGFDKYDALCDGIQKMDGIVAAAKVKVNAEMGEAFKACQENSFFYILGSGATFSQTYGFAICSLM
EMQWQNCAYIHSGEYFHGPFVETENGVFYFLQMGSGACRPMDERALFLKTHTDRLMVLDA LDHGMDAVD
AGVRDYLDVLFYAMNVELRAARGRVFDHSPDIRRYMGIETY*

>FraBLM_ORIG_scaffold_1182

MKYEAKAWKETQGPLRNFDQKQIDS VNGALALRPQIESIIDRIWEDGFDGIYFAGIGGTYASGMQAEV
YMRGRSSLPVFVENAAEFLTTGNKRFTKSVVIYSSVSGNTSEMVLVERVREIGARIFAFIDTPGSVLT
QPDKQDYLVVYPMNEQLKFYMVANYLMYKNGEFAEYERYNKEMEAHLAQAQAQVEKDADAWAYEYAKNKV
AFLNGHRDLPHYFIGSGNQYGATYSYAMCYWEEQMWIRTKSISCQEFFHGMQEIIVADTPVTLFMGEDEQ
RPLAERVAKFLPRVNANYTIIDTKEHELKGISPEFRGTISHLVMHG VNNRVDAYMELFLRHPLSIRRYR
QFEY*

>FraBLM_ORIG_scaffold_2447

MIKGMQEVIQVMEQAKAALEANGGLNQVVFVACGGSLASSYPARYLLNQESSLRVQGYNSSEFVNATPKS

VDKHTLVIATSTKATPETVEAIKAANAKGAVTIGLSGYADSLTAQSANYYYITYYHADEWYQDPTLVHCNS
QGTALKIAFWLLKEYDNYASYDKALEAFEKMPQLYQAYQSVKADAAKFAMAYKDDAVWNVMSGAAWEV
AYSDAFCFFQEMQTVHCVPIHSGEYFHGAFETCDKDLAILLFKSVGRTRPLDDRAEHFLEKFGGHHWIID
AKELGLDQLDESVAEYFNAMMMHPISKQFISAMGDVRMHPMSYRRYMWKFEY*

>FraBLM_ORIG_scaffold_2639

MTIQEIVATIKAKQPEIKTVYFVCGGASMSDLFPAKYFLENNAKLRTSIYTANNFNYSTPAAVDNTSIV
ITCSLSGNTPETVAATKLAVEKGAHVISITINAESGLAKNSQYQIIHGFYESYGAKMEKPARALELACEI
LNEYEGYEHYDDLHDGLNKIFDLINTSAPLFRSTARKFAEENYNAPILYVMSSGATQYTAYGFSMFLMME
MQWLESSTFHTGEFFHGPFEADENAHYVLMNDGPTPLDARALTFIQRMNAKYTLIDAKDFGLSSH
STVVEYFNPLMIGGLTRLLGEEIAIKREHPLTMRRYMWKLEY*

>FraBLM_ORIG_scaffold_3412

MSYTGSDMKSIIGEILEKKAADGGVKSIFYVCGGSLGALYPAKSFMERESADIKCALISSNEFVHSTPK
DFGKNSVICLACHKGNTPETIAAARLGKEKGAAVIILTWEQSEIVAYGDYVVCYAFDASPDLAGDIDY
GQEKTVCALLVAVELLEQTSGYENYDKFMAGREMLTSVIRNARAHVAKRALAFAEEYKDDSVIYTMGSGA
GYGAAYMESICIFMEMQWLDSSSIHTGEYFHGPFEITDENRPFMIQVSEGSTRPLDERCLNFLRNYAKRI
EVLDAKELGLSVIDPAVVDFNHSLFNNVYPIYNHALAEARKHPLPTRRYMWKVEY*

>FraBLM_ORIG_scaffold_4469

MFYTSANMRDIIGEILAAKKEQGGVKSIFYVCGGSLGALYPAKTFMEREKAGIKSALISSNEFVHSTPR
DFGKNSIICLACHKGNTPETIAAARLGREKGAAVIVLTWEQSEIVEHSDYTVLYSFDASPDLAGDIDY
AGEKTMCALLVAVELLQQTAGYENYEKFLAGREMLTAVIRKARAQVAKRALAFAQEYKDDSVIYTMGSGA
GYGAAYMESICIFMEMQWLDSSSIHTGEYFHGPFEITDVNRPFMIQVSEGSTRPLDERCLKFLRTYKRI
EVLDAKELGLSVIDPAVVDFNHSLFNNVYPIYNHALAEARKHPLPTRRYMWKVEY*

>FraBLM_ORIG_scaffold_4493

MNAKTVIEEILKEKGSIKQVYVWACGGSLIDLYPAHFMAESATIESGWYTSKEFILSTPKKLGNLSLV
VMCSHSGNTQESVDAAVLAKEAGASVIALTDGKGSKSDPRFIAWVYPWGDGVPTSEVPSGITLLAAEL
IKAQEGFDKYDALCDGIKKMDGIVAAAKTKVNAELGDAFAKACQDNKFFYILGSGANFSQTYGFAICSLM
EMQWQNCYSIHSGEYFHGPFEVTENGVFYFLQMGSGKCRPMDERALAFLKTHDRLMVLDTLEYGMDAVD
LSVRDYLDSVLLYAMNVELRAARGKVFHDSPDIRRYMGIEKY*

>FraBLM_ORIG_scaffold_6500

MNQTVKEIIAEIKQALEAKGGLKHVYFVACGGSKAAIFPGLYLLQSEAKTFGATTYTSNEFVHATPKELD
ERCIavicSLKATPETVEAVKTANAAGAVSIAMTGSMTGMAKVGQYVVTYSNGDDQVYSDSNQSNLSRI
GFELLHQFEGWANYDKAMDAYAQLDAMIDEAKQELLPAAQAWAAKVKDEPVFVVLASGSNYGVAYSMTCC
HFMEMQWKHAVCLHTGEYFHGPFEETDKQLPMLILLMGEGRTRALDERCLKFLQTYAENFITIDFAKINKG
RIDPSVVEFFNPVVMIPVERYYSQMAELRGHSMDEIRRYMWKVEY*

>FraBLM_ORIG_scaffold_6921

MVTFDENKILSNGEYIYKQRAEIERIADCVCCKGFENLLFTSSGGLAMMQPFDYMISAMSGMEVCSQVA
GDLLLGTGNRLTEKTLVFMASKSGDTKETVEAARYVKERGAIVSVLGVEDSPLGELSTYSVVFKNRPO
ELVLLLLIGRILYRKGFDDYMQFADELGNLPAALVSVGKASDLKAREYALKYKDAPYQIWIWISGNLWGP
VYSFAMCVLEESLWMRTKSVSSPEFFHGTIELMEKGVCVLALAMTEGPTPLDERVKKFILKYGEQVTVFD
TADYQLPGISDRFRWMLSPVVINAVLSRISKNEEMKAHSLEIRRYRRVDY*

>FraBLM_ORIG_scaffold_6947

MKQEHIDQINVAVKAVAEEKKNINHFYFVACGGSQAFMMPAQYMFDRDIATPASIYTSNEFVHRAPKALGP
DSVVITCSHSGNTPETVKATEVARAKGATTIALSHLVDSPLWKAAYPIHYDWGKEADASDLNKAVLYSL
IFRILNAVAPCEKYEKGIASVENINDVIEKAKTQFADTVKAWGKYYKRELIYTMGSGACYGEAYSFAIC
LLMEMQWIHSNCIHSGEYFHGPFEVTFDFVPFIIVKGLGATRPLDERAYNFCQKYSDSIMLVDCETFDMT
GIDQEVREYFAPLVAGAVLRSLADAFAYERGHDLGVRRYMWKMEY*

>FraBLM_ORIG_scaffold_8780

MFNFDEAKIRQEHQNGVDIIHQVEKHVDQVCKDGYSGIFYIGIGGTVLYANQMMHIAKQLGSKLPLYIEN
AADFNLVGNPFDEKSVVIESISGDTREVVEAVDKAHAAGARVIGYVEKEGTPLYEKSDYLVTTVGGGY
YFWYTVTLRFLKNAGQFEKYDQFFKEIVHMPDNVQIYKDADEDARAYAKEYCDEPITYLVGSGNLEDWA

TCYGMCIMEEMQWMRTRPISAAFFHGTLEVIERDIPVILIKGEDMTRPQMERVEKFVNTISAKVTVFDT
KNFKLKGISDEFRGLAPIVMRSFQRVNVHLEHCRRHPLAIRRYRRLDY*

>FraBLO_ORIG_scaffold_34

MIKGMQEVIDVMARVKSDDLKNGGLKQVVFVACGGSFASSYPARFLLNQESALRVQGYNSSEFVYATPKN
IDKNTLVIGTSTKATAETVEALKKAKEKGAVTVGLSGYADSLTAQTADYYITYYHADEWYQDPTLIHYN
QGTALKIAFWLLREYDRYAAYDMAMEGFEKLEAIYAGAYQSVKADAARFGMTYKDDQVWVMSSGAWEV
SYSDAFCFFQEMQTVHCVPVHSGEYFHGAFETCEKDLAILLFKSIGRTRPVDERAERFLNQFGGHHWIMD
ARDFGLDGLDERVAEYFNLLFHPLSKQFITAMADVMMHPMGYRRYMWKFDY*

>FraBLO_ORIG_scaffold_315

MNRPEELIKKIYEEQGRINDVFLTACGGSLVDLYPGYYFLNAESETMHAHWLTAKELVVSPSKFLKKGAL
VILCSHGNTGETVEAARLAKEHGAAIITMTHNPESICAREEMNPVVYSWEDDTNEKDRPQGIVMRVLNE
LLKMQEESYSKYDAVL DGLEKADGIVRAAVKVKVNRWVFAEKYFEEPFLYIMGSGASYSQAYGFSICSL
QEMQWMDCCYLHSGEYFHGPFECTDEDHLYILLMGTGAARTMDERL VFLKKYAKKYEVIDAVELGIDAI
DASVNEYFCPMVYAMSVAYRTGLQDKRRHPLDMRRYMGVVEY*

>FraBLO_ORIG_scaffold_504

MIMKQEHMDQIGVAVKAVAACKDINHFFVACGGSQAFMMPAQYMFDRREIAIPASIYSSNEFVHRLPKAL
GPDSVVITCSHSGNTPETVKATEIAREKGATTIALSNL VDSPLWKAAYPIHYDWGKEADASDLNKAVLY
SLIFGILNTVAPCDKYEKGIASVENINEVIEKAKAQYADTVKGWGKKYKREKLIYTMGSGACYGETYSFA
ICLLMEMQWIHSSCIHSGEYFHGPFVDFDFVPIIVKGLGATRPLDERAHNFCQKYSNIMLVDCETFD
MTGIDEEVREYFAPLVAGAVLRSLADAFAYERGHDLGVRRYMWMKMEY*

>FraBLO_ORIG_scaffold_585

MTMTVKEIVGEIKEKLERAGGLKHVYFVACGGSKAAIFPGLYLLQSEARTFGATTYTSNEFVHAAPKELD
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GFELLHQIEGWDKYEKAMAAYAQIDAIVAEGKERCLAEARSWAEKYQDEPIFYVLASGPNYGVAYSMCCC
HFMEMQWKHAVCLHTGEYFHGPFETDRALPMVLLMSEGRTRPLDERCLRFLEQYAENYITIDFQELNAG
RIDPEVAEFFNPVLIPIERFYVAQMAELRGHSM DERRYMWKVPY*

>FraBLO_ORIG_scaffold_688

MEPKQIIEAIKKEVPAAKSVYFVCGGASKAELYPGKYFLEANARNIRVGHYTANEFYATPVAVDETAIV
VTCSLGGTTPETVAASKKAMD LGAKVVAVTHVDGSPLAKNAHYVVLHGF EKNYAAKLEKMTKVL SLAVEI
LHQYEGYDRYDDMTAFGKIYDLIEKAVSFVPAKNFAEDYKDAPVVYVMSSGATQEVAYAFSICLLME
MQWVNSGSFHDGEFFHGPFEIVEKDVPFILLMNEGRTRALDSRALDFLNRFAQKTTVLDGKDFGLASEVP
ASVAEYFNPMVLSAVLRVYAEQLAIKRNHPLTQRRYMWKLEY*

>FraBLO_ORIG_scaffold_1461

MKYEAKAWKETQGPLRNFDQKQIDS VNGALALRPQIESIIDRIWEDGFDGIYFAGIGGTYASGMQAEV
YMRGRSSLPVFVENAAEFLTTGNKRFTKSVVIYSSVSGNTSEM VQLVERVREIGARIFAFIDTPGSVLT
QPDKQDYLVVYPMNEQLKFYMVANYLMYKNGEFAEYERYNKEMEAHLAQAQAQVEKDADAWAYEYAKNKV
AFLNGHRDLPHYFIGSGNQYGATYSYAMCYWEEQMWIRTKSISCOEFFHGMQEIIVADTPVTLFMGEDEQ
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QFEY*

>FraBLO_ORIG_scaffold_1593

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LNEYEGYEHYDDLHDGLNKIFDLINTSAPLFRSTARKFAEENYNAPILYVMSSGATQYTAYGFSMFLMME
MQWLESSTFHTGEFFHGPFE MADENAHYVLMNDGPTRPLDARALTFIQRMNAYTLIDAKDFGLSSH
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>FraBLO_ORIG_scaffold_2136

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QGTALKIAFWLLKEYDNYASYDKALEAFEKMPQLYGQAYQSVKADAARFAMAYKDDAVWVMSSGAWEV
AYSDAFCFFQEMQTVHCVPVHSGEYFHGAFETCDKDLAILLFKSVGRTRPLDDRAEHFLEKFGGHHWIID

AKELGLDQLDESVAEYFNAMMMHPISKQFISAMGDVRMHPMSYRRYMWKFEY*
>FraBLO_ORIG_scaffold_2583
MFYTSANMRDIIGEILAAKKEQGGVKSlyFVGCSSLGALYPAKTFMEREKAGIKSALISSNEFVHSTPR
DFGKNSIICLACHKGNTPETIAAARLGREKGAIVLWLEQSEIVEHSDYTVLYSFDASPDHLAGDIDY
AGEKTMCALLVAVELLQQTAGYENYEKFLAGREMLTAVIRKARAQVAKRALAFAQEYKDDSVIYTMGSGA
GYGAAYMESICIFMEMQWLDSSSIHTGEYFHGPFEITDVRNPFMIQVSEGSTRPLDERCLKFLRTYGKRI
EVLDKELGLSVIDPAVVDFNHSLFNNVYPIYNHALAEARKHPLPTRRYMWKVEY*
>FraBLO_ORIG_scaffold_2686
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VMCSHSGNTQESVDAAVLAKEAGASVIALTDGKGSKSDPRFIAWVYPWGDGVPTSEVPSGITLLAAEL
IKAQEGFDKYDALCDGIKKMDGIVAAAKTKVNAELGDFAKACQDNKFFYILGSGANFSQTYGFAICSLM
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LSVRDYLDVLLYAMNVELRAARGKVFHDSPDIRRYMGIEKY*
>FraBLO_ORIG_scaffold_4979
MSFEAKAWKETEGPFLKDFNEKEAIDSVNGALALRPQIEKVIDQIWDNGFDGIYFIGIGGTYASSMQVEV
YMRGRSKLPVFNAAEFLTTGNKRFTDKSVVIYSSVSGNTKEMVQLVDRVHEIGAKVFAFIDTPGTTLT
APDKQDYLYMYPKNEQLKfYmVANYLMYKNGEFPQYEAYNKEMEAHLAQLVDVEKEADAWAYEYAKNKV
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QFDY*
>FraBLO_ORIG_scaffold_6866
MNFNDEAKIRQEHQNGVDIIHQVEKHVDQVCKDGYSIGFYIGIGGTVLYANQMMHIAKQLGSKLPLYIEN
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YFWYTVTLRFLKNAGQFEKYDQFFKEIVHMPDNVVQIYKDADEDARAYAKEYCDEPITYLVGSGNLEDWA
TCYGMCIEMEEMQWMRTRPISAAFFHGTLEVIERDIPVILIKGEDMTRPQMERVEKFVNTISAKVTVFDT
KNFKLKGISDEFRGLAPIVMRSARQVNVHLEHCRRHPLAIRRYRRLDY*
>FraBLO_ORIG_scaffold_12091
MNKTVKEIIAEIKEKTDARGGLKHVYFVACGGSKAAIFPGLYLLQSEARTFSATTYTSNEFVHATPKELD
GRCVAVICSLKATAETVEAVKTANQAGALTIAMTGSMETGMAQVGGYVVYTSNGDDQVYSDSNQANSLRI
GFELLHQIEGWEHYDKAMEAYSHIDQIVAEGKESCLPAARAWAEKVKDEPVFVVLASGPNYGVAYSMMMCC
HFMEMQWKHAVCLHTGEYFHGPFEETDKALPMVLLMSEGRTRALDERCLKFLNTYGENFIIIDFQELNKG
RIHPSVVEFFNPVVMPIPIERYYSQMAELRGHSMDERRYMWKVEY*
>FraBLP_ORIG_scaffold_34
MIKGMQEVIDVMARVKSDDLKNGGLKQVVFVACGGSFASSYPARFLLNQESALRVQGYNSSEFVYATPKN
IDKNTLVIGTSTKATAETVEALKKAKEKGAFTVGLSGYADSLTAQTADYYITYYHADEWYQDPTLIHNS
QGTALKIAFWLLREYDRYAAYDMAMEGFEKLEAIYAGAYQSVKADAARFGMTYKDDQVWVMSSGAWEV
SYSDAFCFFQEMQTVHCVPIHSGEYFHGFETCEKDLAILLFSIGRTRPVDERAERFLNQFGGHHWIMD
ARDFGLDGLDERVAEYFNLSLLFHPLSKQFITAMADVRMHPMGYRRYMWKFDY*
>FraBLP_ORIG_scaffold_242
MNRPEELIKKIYEEQGRINDVFLTACGGSLVDLYPGYYFLNAESETMHAHWLTAKELVVSFSPKFLKKGAL
VILCSHGNTGETVEAARLAKEHGAIIITMTHNPESICAREEMNPVVYSWEDDTNEKDRPQGIVMRVLNE
LLKMQEESYSKYDAVLDGLEKADGIVRAAVKKVKNRTWVFAEKYFEFPFLYIMGSGASYSQAYGFSICSL
QEMQWMDCCYLHSGEYFHGPFECTDEDHLYILLMGTGAARTMDERLALVFLKKYAKKYEVIDAVELGIDAI
DASVNEYFCPMVYAMSVAAYRTGLQDKRRHPLDMRRYMGVVEY*
>FraBLP_ORIG_scaffold_427
MNKTVKEIIAEIKEKTDARGGLKHVYFVACGGSKAAIFPGLYLLQSEARTFSATTYTSNEFVHATPKELD
GRCVAVICSLKATAETVEAVKTANQAGALTIAMTGSMETGMAQVGGYVVYTSNGDDQVYSDSNQANSLRI
GFELLHQIEGWEHYDKAMEAYSHIDQIVAEGKESCLPAARAWAEKVKDEPVFVVLASGPNYGVAYSMMMCC
HFMEMQWKHAVCLHTGEYFHGPFEETDKALPMVLLMSEGRTRALDERCLKFLNTYGENFIIIDFQELNKG
RIHPSVVEFFNPVVMPIPIERYYSQMAELRGHSMDERRYMWKVEY*

>FraBLP_ORIG_scaffold_519

MIMKQEHMDQIGVAVKAVAAKDDINHFYFVACGGSQAFMMPAQYMFDRDREIAIPASIYSSNEFVHRLPKAL
GPDSVVITCSHSGNTPETVKATEIAREKGATTIALSNLVDSPWKAAYPIHYDWGKEADASDLNKAVLY
SLIFGILNTVAPCDKYEKGIASVENINEVIEKAKAQYADTVKGWGKKYKREKLIYTMGSGACYGETYSFA
ICLLMEMQWIHSSCIHSGEYFHGPFVETDFDVPFIIVKGLGATRPLDERAHNFCQKYSNIMLVDCETFD
MTGIDEEVREYFAPLVAGAVLRSLADAFAYERGHDLGVERRYMWKMEY*

>FraBLP_ORIG_scaffold_665

MTMTVKEIVGEIKEKLERAGGLKHVYFVACGGSKAAIFPGLYLLQSEARTFGATTYTSNEFVHAAPKELD
SRCLAVICSLKATPETVEAVRTANAAGAVTIAMTGSMTGMAKVGGYVVTYSNGDEQVYSDSNQSNALRI
GFELLHQIEGWDKYEKAMAAYAQIDAIVAEGKERCLAERSWAKEYQDEPIFYVLASGPNYGVAYSMMCCC
HFMEMQWKHAVCLHTGEYFHGSFETTDRLPMVLLMSEGRTRPLDERCLRFLEQYAENYITIDFQELNAG
RIDPEVAEFFNPVLIPIERFYVAQMAELRGHSMDERRYMWKVPY*

>FraBLP_ORIG_scaffold_731

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VTCSLGGTTPETVAASKKAMD LGAKVVAVTHVDGSP LAKNAHYVVLHGFEKNYAAKLEKMTKVL SLAVEI
LHQYEGYDRYDDMQTAFGKIYDLIEKAVSFVVPAAKNFAEDYKDAPVVYVMSSGATQEVAYAFSICLLME
MQWVNSGSFHDGEFFHGPFEIVEKDVPFILLMNEGRTRALDSRALDFLNRFAQKTTVLDGKDFGLASEVP
ASVAEYFNPMVLSAVLRVYAEQLAIKRNHPLTQRRYMWKLEY*

>FraBLP_ORIG_scaffold_1333

MFNFDQEKIRREHQNGIDIIPQVEKFVDQVCSNGYSNIFYIGIGGTVLYANQMMHIAKQLGSKLPLFIEN
AADFNLVGNPFFDERSIVVIESISGDTKEVVEAVDKAHAMGAKVIGYVEKEGTPLYEKSDYLVTTVGGGY
YFWYTVTLRFMKNAGQFDKYDQFFQEI VHMPPDNV VQIYKDADADAKAYAEQYCDEPLTYLVGAGNLEDWA
VCYGMCIMEEMQWMRTRPISAAFFHGTLEVIERDIPVILIKGEDMARPQMERVEKFVNTISAKVIVFDT
KNFKLEGISQEFRGMLSPIVMRSFQRINVHLEHCRRHPLPIRRYYRRLDY*

>FraBLP_ORIG_scaffold_1817

MTIQEIVATIKAKQPEIKTVYFVCGGASMSDLFPAKYFLENNAKLRTSIYTANNFNYSTPAAVDNTSIV
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LNEYEGYEHYDDLHDGLNKIFDLINTSAPLFRSTARKFAEENYNAPILYVMSSGATQYTAYGFSMFLMME
MQWLESSTFHTGEFFHGPFEADENAHYVLMNDGPTPLDARALTFIQRMNAKYTLIDAKDFGLSSH
STVVEYFNPLMIGGLTRLLGEEIAIKREHPLTMRRYMWKLEY*

>FraBLP_ORIG_scaffold_1968

MKQEHIDQINVAVKAVAEKKNINHFYFVACGGSQAFMMPAQYMFDRDREIATPASIYTSNEFVHRAPKALGP
DSVVITCSHSGNTPETVKATEVARAKGATTIALSHLVDSPWKAAYPIHYDWGKEADASDLNKAVLYSL
IFRILNAVAPCEKYEKGIASVENINDVIEKAKTQFADTVKAWGKKYKREELIYTMGSGACYGEAYSFAIC
LLMEMQWIHNSCIHSGEYFHGPFVETDFDVPFIIVKGLGATRPLDERAYNFCQKYSDSIMLVDCETFD
MTGIDEEVREYFAPLVAGAVLRSLADAFAYERGHDLGVERRYMWKMEY*

>FraBLP_ORIG_scaffold_1969

MKYEAKAWKETQGPSLRNFDEQKQIDSVNGALALRPQIESIIDRIWEDGFDGIYFAGIGGTYASGMQAEV
YMRGRSSLPVFVENAAEFLTTGNKRFTKSVVIYSSVSGNTSEMVQLVERVREIGARIFAFIDTPGSVLT
QPKQDYLVVYPMNEQLKFYMVANYLMYKNGEFAEYERYNKEMEAHLAQAQAQVEKDADAWAYEYAKNKV
AFLNGHRDLPHYFIGSGNQYGATYSYAMCYWEEQMWIRTKSISCQEFFHGMQEIIIVADTPVTLFMGEDEQ
RPLAERVAKFLPRVNANYTIIDTKEHELKGISPEFRGTISHLVMHGVMNRVDAYMELFLRHPLSIRRYR
QFEY*

>FraBLP_ORIG_scaffold_2458

MIKGMQEVIVMEQAKAALEANGGLNQQVVFVACGGSLASSYPARYLLNQESSLRVQGYNSSEFVNATPKS
VDKHTLVIAATSTKATPETVEAIKANAAGAVTIGLSGYADSLTAQSANYIITYYHADEWYQDPTLVHCNS
QGTALKIAFWLLKEYDNYASYDKALEAFEKMPQLYQYQSVKADAAKFAMAYKDDAVNVMSSGAWEV
AYSDAFCFFQEMQTVHCVPIHSGEYFHGAFETCDKDLAILLFKSVGRTRPLDDRAEHFLEKFGGHHWIID
AKELGLDQLDESVAEYFNAMMMHPISKQFISAMGDVRMHPMSYRRYMWKFEY*

>FraBLP_ORIG_scaffold_3016

MFYTSANMRDIIGEILAAKKEQGGVKS LYFVGC GSSLGALYPAKTFMERE CAGIKSALISSNEFVHSTPR
DFGKNSIICLACHKGNTPETIAAARLGREKGA AVIVLTWLEQSEIVEHSDYTVLYSFDASPDHLAGDIDY
AGEKTMCALLVAVELLQQTAGYENYEKFLAGREMLTAVIRKARAQVAKRALAFAQEYKDDSVIYTMGSGA
GYGAAYMESICIFMEMQWLDSSSIHTGEYFHGPFEITD VNRPFMIQVSEGSTRPLDERCLKFLRTYGKRI
EVLDAKELGLSVIDPAVVDFNHSLFNNVYPIYNHALAEARKHPLPTRRYMWKVEY*

>FraBLP_ORIG_scaffold_3029

MNAKTVIEEILKEKGSIKQVYVWACGSSLIDLYPAHFMLNAESATIESGWYTSKEFILSTPKKLGKNSLV
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IKAQEGFDKYDALCDGIKKMDGIVAAAKTKVNAELGDAFAKACQDNKFFYILGSGANFSQTYGFAICSLM
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LSVRDYLDVLLYAMNVELRAARGKVFHDSPDIRRYMGIEKY*

>FraBLP_ORIG_scaffold_3339

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DFGKNSVICLACHKGNTPETIAAARLGKEKGA AVIILT WLEQSEIVAYGDYVVCYAFDASPDHLAGDIDY
GQEKTVCALLVAVELLEQTSGYENYDKFMAGREMLTSVIRNARAHVAKRALAFAEEYKDDSVIYTMGSGA
GYGAAYMESICIFMEMQWLDSSSIHTGEYFHGPFEITDENRPFMIQVSEGSTRPLDERCLNFLRNYAKRI
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>FraBLP_ORIG_scaffold_3360

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MAIVDIVEGYADYADAMDAFAKVQPAYIKAREYCAPLAVKWAAQAKDEKCITVLASGPAYGSGHIFSTCN
ILEMLQIHSPTFNSCDFHFGPFEITDKNQSFLLIADGRTRKADERAITFVKKYAGDKVYILD AKELGLD
NLKDSVSEYFNHLLFTPVLNNVYMKELSKATGIDYTTTRRYMWKVEY*

>FraBLP_ORIG_scaffold_6191

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KFYMTANRLMYNNGEFPEYDRYNKEMEEHLAEALVNVEKKADAWAAEYAKEVYAYVKANPDMPHYFVGS
NQWGATYSYAMCYWEEQLWIRTKSITCAEFFHGMLLEVVEAETPVTLFMGEDSQRPLAERVAGFLPKVCKN
YVVIDSKDYELEGISTEFRGSLSHLVMHAVNNRVD AHLLEDEFRHPMVIRRYRQFEY*

>FraBLP_ORIG_scaffold_7856

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AADFNLVGNPFFDEKSVVIESISGDTREVVEAVDKAHAAGARVIGYVEKEGTPLYEKSDYLVTTVGGGY
YFWYTVTLRFLKNAGQFEKYDQFFKEIVHMPDNV VQIYKDADEDARAYAKEYCDEPITYLVGSGNLEDWA
TCYGMCIMEEMQWMRTRPISAAANFFHGTLEVI ERDIPVILIKGEDMTRPQMERVEKFVNTISAKVTVFDT
KNFKLKGISDEFRGLAPIVMRS AFQRVNVHLEHCRRHPLAIRRYRRLDY*

>FraB*Escherichia coli*_str._K-12_substr._w3110

VEKVLSHDVPLVHAIIVEEMVKRDIDRIYFVACGSPLNAAQTAKHLADRFSDLQVY AISGWFCDNTPYRL
DDRCAVIGVSDYGKTEEVIKALELGRACGALTA AFTKRADSPITSAAEFSIDYQADCWEIHL LLYCYSVV
LEMITRLAPNAEIGKIKNDLKQLPNALGHLV RTWEEKGRQLGELASQWPMIYTVAAAGPLRPLGYKEGIVT
LMEFTWTHGCVIESGEFRHGPLEIVEPGVPFL FLLGNDESRTTERAINFVKQRTDNVIVIDYAEISQGL
HPWLAPFLMFVPMEWLCYYLSIYKDHNPDERRYYGGLVEY

>FraB*Clostridiales bacterium*_1_7_47FAA

AIALRPQIEKAVDEIC SQYTNIFFIGCGGT YAHS LPMKYWLDTTSQIDTYSVIAAEFMAAGHRKFTKDS
VCVFSTRSGNTKEIVAAAKYCKEAGARTVVVYV SNDNTPVCEFADYKLF SFAEDDCLCEAIYTYMIALLAR
FKKNAGEFDKYEEFMDQYAGIVPYLIKAKEQYEDRCAKMAQE HKD TDYH MVIGAGMMWGEAYDYAMCILE
EMQWIKTKSIAAEYFHGTLELVEEDTSLILFYGEDETRPLMDRVMDFSKKVTKVINVFD TKEIELPFTE
AEYRKIVSPMVMYAMTERLSCHLEKERNHPLTTRRYRQMEY

>FraB*Coprococcus comes*_ATCC_27758

MIGFIDVATAELAKLVYVITYPANEQLKFYMVADR FMYNAGEFPEYEDLYKELDQYLATALVEVEKEAD
AFGEEFANRHKDDKIHYFVGAGNQYGATYSYAMCYWEEQH WIRTKSIHSAEFFHGMLEIIDKDTPVTVFI

GEDSQRSLSERVANFLPRICGKYNIIDTKKFELKGISPEYRGYISHLVMHAVTQRIDVHMEKVNCHPMEI
RRYYRCLDY

>FraBSubdoligranulum_sp._4_3_54A2FAA

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>FraBClostridium_hathewayi_12489931

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MQWIHSHAIHSGEYFHGPF E V T D F D V P F I I E G I G A T R P L D E R A Y N F C Q K Y S D K I M L V D A E T F D M T G I D E
EVREYFAPLLAGAVLRSLADAFAYERGHDSLVRRYMWRMEY

>FraBCollinsella_aerofaciens_ATCC_25986

VKD V V S Q V L A D K A D K G G I K R V V W I G A G G S N G G N Y P A Q Y F M E H E A T Q V V S S S Y T S N E F V H A T P A Y V N E N T L
AVVSMRGTKETIVAAQVAKDHGASTIAIYVDESGLTEVCDYKIQYDSLAVDESCMGR TNSAVVTMIAME
LTQQTEGYAEYETAMAAFDLVDPIYRKAVEYTRPLAAKWAEQNADKPCINVMAQGPLFGAAYVFSICNVQ
EMLQIDSCTINTCDFHFGPF E I L D K R T S L F Q L I S V G R S R C N D E R G I R F V N Q Y G G E R V Y Q L D A K E L G L N D I
KDSVSEYFNHLIFAPILNNVYMRALS AVTHKDYMTRRYMWKLDY

>FraBClostridium_hylemonae_DSM_15053

IRKIIETIVKDREACGGIKNVVWLAAGGSNGGNYP AQYFMDREAKGIRSQMFTSNEFVYAPPKFVGENTI
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IVDVTEGYEHYKDAMAAYDILDKVYNDAKAYCMLAEKWAEQNKEEHTISVMASGPAYAAGYIFSICNIM
EMLQIQSPTINCCEFFHFGPF E V L D K N E S F F L L V S E G R T R K A D E R A V K F L R E Y G G D K I Y I L D A K E L G I N R F
KDSVAEYFNHMLFSPILNNTYMKKLSAATKIDYLRRYMWKVQY

>FraBClostridiales_butyrate-producing_bacterium_SS3/4

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AVICSLKATPETVKAVETANAAGAITIAMTGMQTGMKAVGQYVVVTYSNGDHQDYSDSNQANALRIGFEV
LHQFENWDKYDKAMDAYQYIDEIVSEGKKNCLPAAQAWAEKVEHEPVFYVLASGPNYGVAYSMCCCHFME
MQWRHAVCLHTGEYFHGPF E T T D K K L P M I L L M S E G R T R A L D E R C L K F L N T Y A E N F I I I D F E K L N G G K I D P
SVAEFFNPVVMPIPIERYVVSQLA EKTGHSM D E R R Y M W K V E Y

>FraBClostridium_sp._M62/1

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LKQFENYENYDKAMAAYTEIDQIVAEGKEKALPIAQKWADTYKDEPIFYVLASGPNYGVAYSMCCCHFME
MQWKHAVCLHTGEYFHGPF E T T D K Q L P I V L L M S E G R T R A L D E R C L K F L R Q Y A E N Y I T I D F K E L N Q G R I A P
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>FraBClostridium_sp._7_3_54FAA

VKEIVAEIKAKMDQAGGLKHVYFVACGGSKAAIYPGLYLLQSEAKTFGATTYTSNEFVHATPKELDSRCV
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LKQIENYENYDKAMEAYQYIDEIVEAGKKNVLYAATEWAQKYKDEPVFYVLASGPNYGVAYSMCCCHFME
MQWKHAVCLHTGEYFHGPF E T T D K E L P M V L L M S E G R T R F L D E R C L K F L E K Y A K N Y I V I D F K E L N A G K I D P
AVAEFFNPVVMPIPIERYVVSQMAEVRGHSM D E R R Y M W K V E Y

>FraBClostridium_symbiosum_WAL-14163

VKEIVAEIKTKMDQAGGLKHVYFVACGGSKAAIYPGLYLLQSEAKTFGATTYTSNEFVHATPKELDSRCV
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LKQIENYENYDKAMEAYQYIDEIVEAGKKNVLYAATEWAQKYKDEPVFYVLASGPNYGVAYSMCCCHFME
MQWKHAVCLHTGEYFHGPF E T T D K E L P M V L L M S E G R T R F L D E R C L K F L E K Y A K N Y I V I D F K E L N A G K I D P
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>FraBClostridium_symbiosum_WAL-14673
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MQWKHAVCLHTGEYFHGPFETTDKELPMVLLMSEGRTRFLDERCLKFLEKYAKNYIVIDFKELNAGKVDP
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>FraBClostridium_acetobutylicum_ATCC_824
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ALLVAVELLAQT EGYENYNKFYEGTKMISNIIKNARNHVAERAVKFAEKYKDDSVIYTMGSGASYGAAYM
ESICIFMEMQWLNSSSIHTGEYFHGPF EITDANRPFMIQISEGSTRDLDERALKFLNTYAKRIEVLDAKE
LGLSTIDASVVDYFNHSLFNNVYPIYNHELATKREHPLPTRRYMWKVEY

>FraBClostridium_bolteae_90A9
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ALLVAVELTAQT EGYENYDKFQEGLMISNIIKNARAHVAERALEFAETYKNDPVIYTMGSGAAYGAAYM
ESICIFMEMQWLDSSSIHTGEYFHGPF EITDANRPFMIQISEGSTRPLDERALKFLRTYAKRIEVLDAKE
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>FraBClostridium_bolteae_90B3
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ESICIFMEMQWLDSSSIHTGEYFHGPF EITDANRPFMIQISEGSTRPLDERALKFLRTYAKRIEVLDAKE
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>FraBClostridium_clostridioforme_90A7
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ALLVAVELTAQT EGYENYDKFQEGLMISNIIKNARAHVAERALEFAETYKNDPVIYTMGSGAAYGAAYM
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>FraBClostridium_bolteae_90A5
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ALLVAVELTAQT EGYENYDKFQEGLMISNIIKNARAHVAERALEFAETYKNDPVIYTMGSGAAYGAAYM
ESICIFMEMQWLDSSSIHTGEYFHGPF EITDANRPFMLQISEGSTRPLDERALKFLRTYAKRIEVLDAKE
LGLSTIDASVVDYFNHSLFNNVYPIYNHALAEKREHPLVTRRYMWKVEY

>FraBClostridium_bolteae_90B7
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ALLVAVELTAQT EGYENYDKFQEGLMISNIIKNARAHVAERALEFAETYKNDPVIYTMGSGAAYGAAYM
ESICIFMEMQWLDSSSIHTGEYFHGPF EITDANRPFMLQISEGSTRPLDERALKFLRTYAKRIEVLDAKE
LGLSTIDASVVDYFNHSLFNNVYPIYNHALAEKREHPLVTRRYMWKVEY

>FraBClostridium_bolteae_90B8
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ALLVAVELTAQT EGYENYDKFQEGLMISNIIKNARAHVAERALEFAETYKNDPVIYTMGSGAAYGAAYM
ESICIFMEMQWLDSSSIHTGEYFHGPF EITDANRPFMLQISEGSTRPLDERALKFLRTYAKRIEVLDAKE
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>FraBClostridium_bolteae_ATCC_BAA-613
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ALLVAVELTAQTEGYENYDKFQEGLGMISNIIKNARAHVAERALEFAETYKNDPVIYTMGSGAAYGAAYM
ESICIFMEMQWLDSSSIHTGEYFHGPF EITDANRPFMLQISEGSTRPLDERALKFLR TYAKRIEVLDAKE
LGLSTIDASVVDYFNHSLFNNVYPIYNHALAEKREHPLVTRRYMVKVEY

>FraB*Escherichia_hermannii*_NBRC_105704

IKEIVSGIVESKADKGGITHVYYYVACGGSYAAFYPAKAFLEKEATKVTVGLYNSGEFINNPPVALGKNAV
VVVASHKGNTPETIKAAELAQSRGVPVIGL TWVTDSP LVAHCDYVETYSFGDGKDIAEEKTLKGLITAVE
ILNQTEGYAHYEDFQDGLSKINRIVYRAWDLQNRAQAF AQEYKDDKVIYTMASGAGYGAAYLQSICIFM
EMQWIHSACIHSGEFFHGPFEITDANTPFFFQFSEGSTRAVDERALNFLK KYGRRIEVVDAKELGLSTIK
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>FraB*Salmonella_enterica_subsp._enterica_serovar_Enteritidis_str._P125*
109

MKETVSNIVTSQAEKGGIKHVYYYVACGGSYAAFYPAKAFLEKEAKALTVGLYNSGEFINNPPVALGENAV
VVVASHKGNTPETIKAAE IARQH GAPVIGL TWVMDSP LVAHCDYVET YTFGDGKD IAGEKTMKGLLSAVE
LLQQTEGYAHYDDFQDGVSKINRIVWRACEQVAERAQAF AQEYKDDKVIYTVASGAGYGAAYLQSICIFM
EMQWIHSACIHSGEFFHGPFEITDANTPFLFQFSEGNTRAVDERALNFLK KYGRRIEVVDAKELGLSTIK
TTVIDYFNHSLFNNVYPVYNRALAEARQHPLTTRRYMVKVEY

>FraB*Salmonella_bongori*_NCTC_12419

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LLQQTEGYAHYDDFQDGVSKINRIVWRACEQVAERAQAF AQEYKDDKVIYTVASGAGYGAAYLQSICIFM
EMQWIHSACIHSGEFFHGPFEITDANTPFFFQFSEGNTRAVDERAL TFLK KYGRRIEVVDAKELGLSTIK
TTVIDYFNHSLFNNVYPVYNRALAEARQHPLTTRRYMVKVEY

>FraB*Salmonella_enterica_subsp._enterica_serovar_Paratyphi_C_str._RKS4*
594

MKETVSNIVTSQAEKGGVKYVYYYVACGGSYAAFYPAKAFLEKEAKALTVGLYNSGEFINNPPVALGENAV
VVVASHKGNTPETIKAAE IARQH GAPVIGL TWIMDSPLVAHCDYVET YTFGDGKD IAGEKTMKGLLSAVE
LLQQTEGYAHYDDFQDGVSKINRIVWRACEQVAERAQAF AQEYKDDKVIYTVASGAGYGAAYLQSICIFM
EMQWIHSACIHSGEFFHGPFEITDANTPFFFQFSEGNTRAVDERALNFLK KYGRRIEVVDAKELGLSTIK
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>FraB*Salmonella_enterica_enterica_sv._Typhimurium_LT2-4*

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LLQQTEGYAHYDDFQDGVSKINRIVWRACEQVAERAQAF AQEYKDDKVIYTVASGAGYGAAYLQSICIFM
EMQWIHSACIHSGEFFHGPFEITDANTPFFFQFSEGNTRAVDERALNFLK KYGRRIEVVDAKELGLSTIK
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>FraB*Salmonella_LT2*

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LLQQTEGYAHYDDFQDGVSKINRIVWRACEQVAERAQAF AQEYKDDKVIYTVASGAGYGAAYLQSICIFM
EMQWIHSACIHSGEFFHGPFEITDANTPFFFQFSEGNTRAVDERALNFLK KYGRRIEVVDAKELGLSTIK
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>FraB*Salmonella_enterica_subsp._enterica_serovar_Typhimurium_str._1402*
85

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LLQQTEGYAHYDDFQDGVSKINRIVWRACEQVAERAQAF AQEYKDDKVIYTVASGAGYGAAYLQSICIFM
EMQWIHSACIHSGEFFHGPFEITDANTPFFFQFSEGNTRAVDERALNFLK KYGRRIEVVDAKELGLSTIK
TTVIDYFNHSLFNNVYPVYNRALAEARQHPLTTRRYMVKVEY

>FraB*Citrobacter_freundii_GTC_09629*

MKEIVSEILVSQEDKGGVKYVYVACGGSYAAFYPAKAFLEKEAKGLTVGLYNSGEFINNLPSALGENAV
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FLQQTEGYIHYDDFLDGVSKINRIVRACEHVAERAVSFAQEYKDDNVIYTVASGAGYGAAYLQSIICIFM
EMQWIHSACIHSGEFFHGPFEITDANTPFFFQFSEGSARPVDERALNFKKYGRRIVVDAKELGLSTIN
TTVIDYFNHSLFNNVYPVYNRALARARQHPLTTRRYMwKVEY

>FraBCitrobacter_rodentium_ICC168

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FLQQTEGYAHYADFQDGLSKINRIVRACEHVAERAAFAQNYKDDRVIYTMASGAGYGAAYLQSIICIFM
EMQWIHSACIHSGEFFHGPFEITDANTPFFFQFSEGSTRPVDERALNFKKYGRRIEVVDAKELGLSTIK
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>FraBLactobacillus_vaginalis_ATCC_49540

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LGESNNYNEMVQGLSVVDEVANDAAASVDNDAQKFAERYKDEDKVFTLSSGSNRGVGYSTANFIFMEMQW
ITGVNLDSEAEFHGPFELAVKEAPFLLFMSDGRTRHLDRALEFLQRFGTKYTVIDAKDYWLNSKMDASV
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>FraBClostridium_asparagiforme_DSM_15981

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CSLGGTTPETVASKMAREKGSPIVCLTAPESPLAQNADYPIIHGFHESYSAKMQLTKCLQLAAEILE
QYEGYEDYEDMMKGVEKIYGVIDAAPYAKPLAEKFARENKDERVIYVMGSGPSQQVAYTFSSFILMEMQ
WVDSASFSAGEFFHGPFEIVDKDVPFLLLMNDGNTRPMDVRALEFLNRFDAKTTVVDAKDYGLGNEIPAS
VKDYFNPIILLDGLRVYGEAIAEARKHPLTQRRYMwKLENY

>FraBClostridium_clostridioforme_2_1_49FAA

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QYEGYEHYQDMMTGFGKIFDLIEDAVSFVVPsAKKFAENYKDAPVIYVMSSGATHMVAYSFSICLLMEMQ
WINSGSFHDGFEFFHGPFEIVDKDVPFLLLMNDGSTRALDSRALDFLNRFAQKTTLIDAKDFGLGsvIPAT
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>FraBClostridium_clostridioforme_90A1

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QYEGYEHYQDMMTGFGKIFDLIEDAVSFVVPsAKKFAENYKDAPVIYVMSSGATHMVAYSFSICLLMEMQ
WINSGSFHDGFEFFHGPFEIVDKDVPFLLLMNDGSTRALDSRALDFLNRFAQKTTLIDAKDFGLGsvIPAT
VKDYFNPLITAVLRVYAEQLAILRNHPLTQRRYMwKLEY

>FraBClostridium_clostridioforme_90A3

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QYEGYEHYQDMMTGFGKIFDLIEDAVSFVVPsAKKFAENYKDAPVIYVMSSGATHMVAYSFSICLLMEMQ
WINSGSFHDGFEFFHGPFEIVDKDVPFLLLMNDGSTRALDSRALDFLNRFAQKTTLIDAKDFGLGsvIPAT
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>FraBClostridium_clostridioforme_90A4

LKKIIEEIKAEERPEITSVIFVCGGASQAELYPAKYFLEGNACKLRTSLYTANEFVHATPACVGKESIIIT
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QYEGYEHYQDMMTGFGKIFDLIEDAVSFVVPsAKKFAENYKDAPVIYVMSSGATHMVAYSFSICLLMEMQ
WINSGSFHDGFEFFHGPFEIVDKDVPFLLLMNDGSTRALDSRALDFLNRFAQKTTLIDAKDFGLGsvIPAT
VKDYFNPLITAVLRVYAEQLAILRNHPLTQRRYMwKLEY

>FraBClostridium_clostridioforme_90A6

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QYEGYEHYQDMMTGFGKIFDLIEDAVSFVVPsAKKFAENYKDAPVIYVMSSGATHMVAYSFSICLLMEMQ
WINSGSFHDGEFFHGPFEIVDKDVPFLLLNMNDGSTRALDSRALDFLNRFAQKTTLIDAKDFGLGSVIPAT
VKDYFNPMLITAVLRVYAEQLAILRNHPLTQRRYMWKLEY

>FraBClostridium_clostridioforme_90A8

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QYEGYEHYQDMMTGFGKIFDLIEDAVSFVVPsAKKFAENYKDAPVIYVMSSGATHMVAYSFSICLLMEMQ
WINSGSFHDGEFFHGPFEIVDKDVPFLLLNMNDGSTRALDSRALDFLNRFAQKTTLIDAKDFGLGSVIPAT
VKDYFNPMLITAVLRVYAEQLAILRNHPLTQRRYMWKLEY

>FraBClostridium_clostridioforme_90B1

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QYEGYEHYQDMMTGFGKIFDLIEDAVSFVVPsAKKFAENYKDAPVIYVMSSGATHMVAYSFSICLLMEMQ
WINSGSFHDGEFFHGPFEIVDKDVPFLLLNMNDGSTRALDSRALDFLNRFAQKTTLIDAKDFGLGSVIPAT
VKDYFNPMLITAVLRVYAEQLAILRNHPLTQRRYMWKLEY

>FraBLachnospiraceae_bacterium_oral_taxon_082_str._F0431

AEELIRDVLKTKNIKDVFFVACGGSLVDLYPGFYFLNSESGTIHAHWMTAKEMSVAPSKFLNENALVLAC
SHGGNTKEVINAVKVALKNGASVITMTHNPESICAREFNTVLYDWDDKTENERPQGIVLRILNELLKEK
EPDYKKYDSILDGLENIDSIVRTATSKVKNRtWLFaEKYHNEKFLYIMGSGASYSQAYGFAICSLQEMQW
MDCCYLHSGEYFHGPFECTDKDHLyILLMGTGNAREMDERCLDFLKkYGNKYEVIDAKDLGIDEIDESVN
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>FraB0ribacterium_asaccharolyticum_ACB7

MKELVTQILNGREKIEDVYFVACGGSLVDLYPGYYFVRtESRTMHADWITSKEFVVTPPAHLGKtSLVFI
CSHGGNTKETVEAAHLAKDLGAaVAMTHTPGSACDSSLNPIVYsWEDDTNEKDKPQGIVLNILNELMK
AQEPDYKLYDAVADGLEKADGIVRAAVKSVKNRtWLFaEKYAKEPFLYIMGSGAAyAAVYGFAICSLQEM
QWIDCCYLNSAEYFHGPFEVtDEDHLyILLKSRGRNRVMDEraEVFLNKYAKKYEVIDANDLGLDAIDDS
CVEYFNAMVFYAMSVAYRNALQDKRCHPTDMRRYMGVVEY

>FraB0ribacterium_sp._oral_taxon_108_str._F0425

MKELVTQILNGREKIEDVYFVACGGSLVDLYPGYYFVRtESRTMHADWITSKEFVVTPPAHLGKtSLVFI
CSHGGNTKETVEAAHLAKDLGAaVAMTHTPGSACDSSLNPIVYsWEDDTNEKDKPQGIVLNILNELMK
AQEPDYKLYDAVADGLEKADGIVRAAVKSVKNRtWLFaEKYAKEPFLYIMGSGAAyAAVYGFAICSLQEM
QWIDCCYLNSAEYFHGPFEVtDEDHLyILLKSRGRNRVMDEraEVFLNKYAKKYEVIDANDLGLDAIDDS
CVEYFNAMVFYAMSVAYRNALQDKRCHPTDMRRYMGVVEY

>FraBClostridium_hathewayi_WAL-18680

MKELVAKILEGREKIEDVYFVACGGSLVDLYPGYYFVRtESKTMHADWITSKEFVVTPPthLgKtSLVFI
CSHGGNTKETVEAAHLSREKGAaVtMTHNPDSACNDNTMFPIVYDwADTVNEKDKPQGIVLNILNELMK
VQEPDYPLYDAIVAGLEKADGIVRAAVKkVQNKtWLFaEKYAKEPFLYVMGSGASyASAYGFAICSLQEM
QWIDCCYLNSAEYFHGPFEVtDEDHLyILLKGRGRNRVMDErVETFLQYgKkYEIIDANELGLEAIDDS
CVEYFNPMVFYAMSVAYRNALQDKRCHPTDLRRYMGVVEY

>FraBEnterococcus_faecium_R497

VAKTVNAIVEKNDGEISGIYLVACGGSLVDMYVSDYFLKAEASKCITGLYTANEFNHVTPKQLDDKSVVI
LCSHGGNTAETVKAGEVAQARGAVTVGLTHNKtADLLKvSDHSFLYEWGDDAKIVNNPMAIILDltVSLV
NVTETFEHYGKFREGMKVIDTviENGIKQVQDRIKVFADKYKDETMFYILGSGPSYGHAYGFSICSLMEM
QWLDSTSVHSGEFFHGPFEVtDKDtnFILLMSIGRTRALDERAKRFLDKYAERVEIVDAKELGLDMISDE
VSEFFNPILFYSILSEYRSALADVRNHDLVRRYMGKVEY

>FraBKlebsiella_pneumoniae_subsp._pneumoniae_WGLW1

TKEIINAVAKEIEDKGGIRQVFLVACGGSLVDMYPaKYFLDSEATKLHVGMYTANEFVYATPKTLGENSL
VIVCSHGGNTPESVAAAKLAQQHQAHTITLTHNAQAQLIEYASHNILYAWGNDTNVVDNPMaIILNLCVD
TLQQVEGFNNYADFQQGMtQINGVIAHGRQqVADRCQRFAQKYQDEKLFYILSSGASyGHAYGFAICSLM
EMQWLHAAPiHSGEYFHGPFEVtNKETPFILLMNEGRTRAMDERALaFLTKYAekVEVDAKELGIGVLP

PSVVEFFNPVLFYSIMCEYRSALADIRQHPLDTRRYMGLVEY
>FraBKlebsiella_pneumoniae_subsp._pneumoniae_WGLW3
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VIVCSHGNTPEVSAAAKLAQQHQAHTITLTHNAQAQLIEYASHNILYAWGNDTNVVDNPMIILNLCVD
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>FraBKlebsiella_pneumoniae_subsp._pneumoniae_WGLW5
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>FraBKlebsiella_sp._MS_92-3
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VIVCSHGNTPEVSAAAKLAQQHQAHTITLTHNAQAQLIEYASHNILYAWGNDTNVVDNPMIILNLCVD
TLQQVEGFNNYADFQQGMTQINGVIAHGRQQVADRCQRFAQKYQDEKLFYILSSGASYGHAYGFAICSLM
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PSVVEFFNPVLFYSIMCEYRSALADIRQHPLDTRRYMGLVEY

>FraBKlebsiella_oxytoca_10-5250
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>FraBKlebsiella_oxytoca_10-5243
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TLQQVEGFDNYADFQQGMAQINGVIAHGRQQVADRCQRFAQKYQDEKLFYILSSGASYGHAYGFAICSLM
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>FraDEscherichia_coli_str._K-12_substr._W3110
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AFDFSDKWD SPLWQTLVPHLDFAFASAPQEDELRLKMKAI VARGAGTVIVTLGENGSI AWDGAQFWRQA
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>FraDCoprococcus_comes_ATCC_27758
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QVLDGKTAVTHVDIVDGRVFGKYEEGVLADFKLREQDISFIKKHDLAVTGIWGMIEDELPLISKEIPVA
FDFANKFANPIVEKAIPYVTYAFFSFDEESRNEFRQKYHSMGLKEKENCTEQLKEFMKAMQQKGPVIA
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>FraDClostridium_hylemonae_DSM_15053
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HHEKGS SGYALVDLKDGRVFLDWNKKGVTDLYPFTFTEEEITYIKTYDIACISWG ARVDKSRMKKLAGA
GVPICYDFYDNFTAEDIDSISP YIKFAFFSCSHMSEETKNILAACVRLGVRIAVGTRGGEP AIACDGSR
FYTQEVFRVKAKDTMGAGDSYISAF LTNYSAEADESFTAEDKITASL KKAEEFAAAVVKDGS LG

>FraDLactobacillus_vaginalis_ATCC_49540
MKVLAIGDNVMDIYLD SKRIFPGGNAVNF SVMATRIPKITSGYLGNFGNDNLAELMKSTLKT FNVNIDHC
RNLKGESGYSLVKVVNGDRKFLASNRGGVLNQG IKSDDKDYINAMDLIHLSVNGKGKEIINYINKPKIV

YDYSDFSNEDEITLTINNVDLACFSVGNISKDKVVERARQLQSMGNYHTILLFTMGKQGAMVFTGNRCYY
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>FraDSubdoligranulum_sp._4_3_54A2FAA

MKLLGIGDNVLDYRWRQELYPGGNSVNPVVLARRYDGSAAAYIGVLADDGAGLHFASALREEGVDIRV
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RVPLSLDFSGEYDRVNIAQLCPLLRFAFFSFGAASEEEVRALARTALDAGARTVVVTMGVRSYLLEQGR
EHRQECMRADVVDALGAGDAFIAAFLAEYHAGGGDLADAAQKASVFAAQCCGHYGAFG

>FraDClostridiales_butyrate-producing_bacterium_SS3/4

MIKIVIGIGDNVCDQYYPAKIMYPGGQAMNFSVYAKMLGAQSAYLGVFGKDRVAEHIISVLDEIGIDHSRC
RQYAGENGYAKVRENGDRQFIMSNRGGIVNEHPLDLKPEDISYIREFSLVHTSNNGHFDSQLKKVRETG
IPVSYDFSGHWNEEYLLKEIAPVVDYAFFSCGEIDEETAKAACKRFVSEGCKIAVATMGKRGSLAFDGKK
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>FraDClostridium_sp._M62/1

MRVIGIGDNVCDKYIYLNTMFPGGQALNFAVYTKMLGADSSYMGTFGRDEVAEHILATLDELGVKHERCR
QYDGENGYARVTLVDGDRVFLGSNKGKIAKEHPVVLDSDDMEYVKQFSHIHTSNNSYFDSQLPKLAEAGL
SVSYDFSGQWTDPEKVARVAPYIRYAFSLSCGSIPEVEAEKICRAIHEAGCPMVITTRGSYGSMLYDGNRF
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>FraDClostridium_sp._7_3_54FAA

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IPISYDFSGQWIDDGRVCRVAPYASYVFLSCGSVTEEEGREICHRMHARGCRFIVATRGSKGALVYDGH
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AFG

>FraDClostridium_symbiosum_WAL-14673

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IPISYDFSGQWIDDGRVCRVAPYASYVFLSCGSVTEEEGREICHRMHARGCRFIVATRGSKGALVYDGH
FYSQPPHLVEAIDTLGAGDSFATAFLLSLTQSRKEYRERMDSRKLRYRQLKEAMEKGASFAAATCLVQ
AFG

>FraDClostridium_symbiosum_WAL-14163

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IPISYDFSGQWIDDGRVCRVAPYASYVFLSCGSVTEEEGREICHRMHARGCRFIVATRGSKGALVYDGH
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AFG

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>FraDClostridium_acetobutylicum_ATCC_824

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>FraDClostridium_bolteae_90B3

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>FraDClostridium_clostridioforme_90A7

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>FraDLachnospiraceae_bacterium_oral_taxon_082_str._F0431

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>FraDCollinsella_aerofaciens_ATCC_25986

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>FraDOribacterium_asaccharolyticum_ACB7

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>FraDOribacterium_sp._oral_taxon_108_str._F0425

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>FraDClostridium_hathewayi_WAL-18680

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>FraDClostridium_asparagiforme_DSM_15981

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>FraDKlebsiella_pneumoniae_subsp._pneumoniae_WGLW3

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>FraDKlebsiella_pneumoniae_subsp._pneumoniae_WGLW5

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>FraDClostridium_clostridioforme_90B1

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>FraDClostridium_clostridioforme_90A8

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>FraDClostridium_bolteae_90B8

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DVNPDRLSEIINL*

>FraDLM_ORIG_scaffold_593

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QYEGENGFASVTLVEGDRVFLGNSNRGGAAREHLELTEEDLAYIRGFVSHVHTSNNSYFNSQLAKVKSTGV
SLSYDFSGRWRDEAFVAQAAPYADYAFLSCGSAPLEEAQEVCRRLCAAGCGRVIATRGSAGALYYDGADF
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FGHGKAFLPE*

>FraDLM_ORIG_scaffold_634

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RMEEGENGCARVRLVNGDRVFLGNHGGIARTKPPVLTKLDESYIAGFDLVHTSIYSYMEPELPLKRRAG
KFVSMDFSNHYDEAYLKQCCPYLDCAEISCGDMDEEEMHQTMEIISLGCKHMVIATRGSKGACVLVNGK
FYEQSSQLVQARDTMGAGDSFITSFLIHYLDGIRDAVDFSEESGERGIVSAAEYQDILIRLCLYRAAVFA
SGQCQRDGSFSGFKEVELTDQDVEVMEGNKALKF*

>FraDLM_ORIG_scaffold_1033

MARYDVSVLFGDNVVDKYEHIKTMYPGGNAVNFVFAKQLGAARSAYMGI FGSQDQEAHVSISSLTEEGI
ELIECRQVIGENGAARVTVEAGTGDRIFLGSNEGGIRGDMLFALDRFTMEYVRGFDLVHSGNYCFTEREL
PKIKAAGVPISFDFSDSTDEYFERIAPLVDFAFMSCGDMTLEETKAKLQKVSQLGPRFVCASRGSEGS
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WGHGKEYE*

>FraDLM_ORIG_scaffold_1182

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LQVKEGRTAVSQVTLTDGERVFGDYDEGMADYVLSEEDMDFICAHDVVCDLWGKVEGQFKDLKERGMT
TAFDCATRPEDPESQTAMPYTDYLLFSCDDGDTPELRAQMCRYHEKGPRLVVCMMGSDGSLCWDGREFHR
FGIVPCENLVDSMGAGDSYIAGFLLGITEGLPIEEAMEKGAANATVTLGYFGGW*

>FraDLM_ORIG_scaffold_2447

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RSYPGENGFARVTLVEGDRVFMGSNRGGVLQEHPIYLDQADLDYIAGFDLVHTTNGFVDSLLPQLSQLP
PFVSYDFSRYWNEEDRVERVCPYIDFAFLSCSLDDVQTQDLCRRLHEKGCVVATRGSKGATVFDGSR
FYEQSPHLVEPVDTMGAGDSFATAMLTSLQLALEREGRNAWSWESFRSNALPQALDKAAAFSARNCLVHG
AFGCGVPVPEELRPRMYEGIQ*

>FraDLM_ORIG_scaffold_2639

MNMAAIGFCCIDVYENIGKRYATGNGVDCIVHLARRGVETALVSVIGSDEYGKEMLELCREYKIDTAHLQ
VREGKTSVYRMALKNGVDRVHVENIPGVMADYTPTQSDLEFVKGFYVHTDLTGRVLHLLPELYEAGCKI
IFDFSMNKEEENLKQILPYVHCAFFSCEKKQPEIKDFLKKAKALGAKYVVATFGEEGSMCYDGEKFCEQG
IYKVPVNTVGAGDSFIAGFSWGLMCGKDVVEECLEEGARLSSWVQGFNPY*

>FraDLM_ORIG_scaffold_3412

MATEPRHIRIIAIGDNVCDKYL SRGKMYPGGQCVNTCAYVRMNGLEAAYLGKFGDDEVAACNRETLAKLD
IDTSHCRSFPGENGFALVTLQGS DRVFLG SNKGGIAKEHPFAFTQEDLRYISGFSLIYTNLNSYIEEDLP
LLAKTGVPIAYDFSLRWTDEYLARVAPYVTVAILSCAHLTPEEREREMKKAQAHGISIVLGTIGEEGSWV
LYRDNFYVTMAVRAEDVIDTMGAGDSYFAAFLCSLLSDSASGALIEDEEEMAARLKRAMNKGAAFAAKV
CAMEGAFGYGVPITGRTQL*

>FraDLM_ORIG_scaffold_4469

MKEVRILAIGDNVCDKYL SRGKMYPGGQCVNTCAYARMNQTEAAYLGKFGSDEVAAYNQEILARLGIDAS
RCRRFPGENGFALVTLRGNDRVFLG SNKGGVAKEHPFSFTPEDLDYIRGFSLIYTNLNSYIEEDLPLKE
TGVPIAYDFSLRWND EYLAKVAPYVTVAILSCAHLTPEEREREMKKAQSHGIAIVLGTIGEEGSWVLYGD
RFYYPAPVAHAEDVIDTMGAGDSYFAAFLCSLLRDSATGALIEGDEAEMAARLQRAMNRGAAFAAQVCAME
GAFGYGTPIILGRTEV*

>FraDLM_ORIG_scaffold_4493

MGSYQVSVLGF GDNVVDKYEHIKTMYPGGNAVNF AVFAKQLGAQRSAYMGI FGSDQEAHV IASLQEEGV
ELAKCQQVVGPNGAARVTVEEGTGDRIFLGSNEGGIRGDMFLVLD RFTLEYVKGF DLVHSGNYCF TEREL
PKIKAAGVPISFDFSDSTDEY YERIAPLVDYAFMSCGDMTPEETRKRLEKVAALGPKFVCASRGSEGC I
AYDGKEFYEQGIRPVEHLVD TMAAGD SLLTAFLVEYVDM EKQKGKGPDAIRACLYDAAGLASHTCGLAGS
WGHGKVYD*

>FraDLM_ORIG_scaffold_6500

MRVIGIGDNVCDKYEHQKTMYPGGQALNFSIYARMLGVESAYIGVFGTDEVAQHVM AALDKYQVDRSRCR
QYEGENG CARVTLVDGDRVFLG SNKGGVLRDHP IELGDVDLNYIKQFALCHTSNNSYMSQLPRLKQAGI
SVSYDFSGQWDAER VERVAPCIDYAF LSCGGAAPQETAADICRMINGKGTGMVIATR GSEGAMLYDGTD
FYTQPPKLV EAVDTLGAGDSFAAFL LLAWLKRKDRAEQDPSIRPAVLREALEQAAEFSSKTCLVYGAFGE
GTA FEPMGKGEA*

>FraDLM_ORIG_scaffold_6921

MKIAGIGDNVIDRYINRGVIFPGGNAVNVAAHA AKLGAGAAVYVGSIGADREGRIVKEALKTLEVDLSQCI
FEQGT TTKRCDVNVYD GERSYIGTDTGNNWAHMKEIRD RDLEYL KDFQVIHTSCNAKLHQDIYRLKDLKG
MVTDFDFSEKEKYSKEFLAVVCPYLEL GQF SCTGM EEEQIGRLLAVHEL GCKNAVATMGSSQIFYNGE
VFVRGQACYVKPLDTMGAGDSFLAALLV TLLKSGWEK GARLSPDVINTALKEAARYSAENCMAEGGF GFK
HRI*

>FraDLM_ORIG_scaffold_6947

MTDCYVDEGVYFPGGNAVNVAVNCKKNGAEKVNYIGVFGD DERADYIKECLAKEGV EFKRSR KVC AHTAQ
PRVYLKDGDRVFGPGPRDSCQHLFSIKIVAEDMEVIRDFD ICHTSCFSNLEYELPAISEICQVSDFSER
REEDYLKRTCPYLTF AFFSGSEMEERECEELLKKVHGLG TKVVGITRGSKGAI FYDGEKIYRQGIKPV E
VDTMGAGDSFIAGFLTAYGDGKT MEEALDYGAERS SRTCMVRGGFGYPHKA*

>FraDLM_ORIG_scaffold_8780

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AEAAYLGTFGDDEIGRHVYSVIRELGIDISHCRMEEGENG CARVQLVDGERVFLPGNQGGIAGAKPPVLS
KLDEAYISGFDLIHTSIFSHMEPEL PKIRRVGK FVSMDFSDRYDEDYLRCCPYIDCGEISCGDMDEKEI
RQIMDQIMKFGCKHMVIATRGSKGAYVLADG SFYEQSPCLVKAKDTMGAGDSFIASFLVNYLDGISM AVD

FPEKSGRGLVTAEGYKDALIRVSLYRAAVFSSCQCQRDGSFGHGKPVQRWAEGDAMEE*

>FraDL0_ORIG_scaffold_34

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RCEGENAFARVTLVDGDRVFRGNSRGGVLLQHPHLYLDEADLAYADAFDLIHTTNGFIDGLL
PALRELRPLISYDFSYRWNEEDRVDRVCPYIDFGFLSCSDLGDEETEALCRRLCDKGC
GVVATRGSKGATVYDGSQFYSQLPDYVTPIDTMGAGDSFATAMLVTLQSM
EKQGRTDWENSILRAYLLPGALKAAAAFSARTCLVNGAFGGAAVPE
SLRARLYGES*

>FraDL0_ORIG_scaffold_315

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GENGWSKCTLVGDRIFGDYNEGGVGRKNPYILDRFDLE
YMKQFDFVHTGNICYTESQLKTMKEAGIKVSFDFSD
SSREYYEKYAPFVTYAFCSFNGDDEAAKEHLRFVH
SLGPELVSLTRGSKGCLMYDGEFYVQPATMIEHV
VDTMGAGDSFLTSFMDCYIDQVKRGTDKPEAIRIS
LAEASKFAAHVCTLDGAFGYGKPYEDK*

>FraDL0_ORIG_scaffold_504

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VYLKDGDRVFGPGPRDSCQHLFAIKLVTEDMDLIRE
FDICHTSCYSNLEYELPALSRICQVSFDFSDKR
DDAYLERVCPYLTFAFFSGSDLEKDRCAALLRKARE
LGVKIAGITRGAKGAIIFYDGENFYHQGIKETE
VDTMGAGDSFIAGFLTAYGDKKPIKEALDYAACRS
ALTCTVRGGFGHPHKA*

>FraDL0_ORIG_scaffold_585

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GADASYMGVFGRDEVADHVLTLLDQLQVEHGRCR
QYEGENGFASVTLVEGDRVFLGNSRGGAREHPLE
LTEEDLAYIRGFVHTSNNSYFNSQLAKVKSTGV
SLSYDFSGRWRDEAFVAQAAPYADYAFSLCSGSA
PLEEAQEVCRRLCAAGCGRVIATRGSAGALYDGA
DFEQPPDPVEPVDTLGGAGDSFATAFLLSFLES
LERAGERMAADRPLYEEEVRAALRRGAFAAKTCL
VQGAFGHGKAFLPE*

>FraDL0_ORIG_scaffold_688

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HCRMEEGENGCARVRLVNGDRVFLGNHGGIARTK
PPVLTKLDESUYIAGFDLVHTSIYSYMEPELPL
KRRAGKFVSMDFSNHYDEAYLKQCCPYLDCAEIS
CGMDDEEEMHQTMEEIISLGCKHMVIATRGS
KGACVLVNGKFYEQSSQLVQARDTMGAGDSFITS
FLIHYLDGIRDAVDFSEESGERGIVSAAEYQD
ILIRLCLYRAAVFASGQCQRDGSFGFGKEVEL
TDQDVEVMEGNKALKF*

>FraDL0_ORIG_scaffold_1461

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DISRLQVKEGRTAVSQVTLTDGERVFGDYDEG
VMADYVLSEEDMDFICAHDVVCDLWGKVEGQ
FKDLKERGMTAFDCASTRPEDPESQTAMPYTD
YLFSCDDGDTPELRAQMCRYHEKGPRLVVC
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VTLYYFGGW*

>FraDL0_ORIG_scaffold_1593

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TAHLQVREGKTSVYRMALKNVDRVHVENIPG
VMADYTPQTSDLEFVKGFYVHTDLTGRV
LHLLPELYEAGCKIIFDFSMNKEEENLKQIL
PYVHCAFFSCEKKQPEIKDFLKKAKALGAKY
VVATFGEESMICYDGEKFCEQGIYKVPV
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EGARLSSWVVQGFNPY*

>FraDL0_ORIG_scaffold_2136

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SNRGGVLLQEHPIYLDQADLDYIAGFDLVHT
TNGFVDSLLPQLSQLPFFVSYDFSYRWNE
EDRVDRVCPYIDFAFLSCSLDDVQTQDL
CRRLHEKGCVVATRGSKGATVFDGSRFYE
QSPHLVEPVDTMGAGDSFATAMLSLLQAL
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SARNCLVHGAFGCGVPVPEELRPRMYEGIQ*

>FraDL0_ORIG_scaffold_2583

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FLGNSKGGVAKEHPFSFTPEDLDYIRGFSL
IYTNLNSYIEEDLPLLKETGVPIAYDFSL
RWNDEYLAKVAPYVTVAILSCAHLTPEER
EREMKKAQSHGIAIVLGTIGEEGSWVLYGD

RFYYAPAVHAEDVIDTMGAGDSYFAAFLCSLLRDSATGALIEGDEAEMAARLQRAMNRGAFAAAQVCAME
GAFGYGTPIILGRTEV*

>FraDLO_ORIG_scaffold_2686

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PKIKAAGVPISFDFSDSTDEYYERIAPLVDYAFM SCGDMTLEETRKRLEKVAALGPKFVCASRGSEGC I
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WGHGKVYD*

>FraDLO_ORIG_scaffold_4979

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TAFDCADRPEDEASQVAMPHSDYLFFSSEAGDTAALRDQMKGYSRGPKLVIAM LGEHGS LCYDGKEFHK
FGIVPCDKVVDTMGAGDSYIAGFLLGITDGLTIDQAMEKGAANATETLKYFGAW*

>FraDLO_ORIG_scaffold_6866

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AEAAYLGTFGDDEIGRHVYSVIRELGIDISHCRMEEGENGCARVQLVDGERVFLPGNQGGIAGAKPPVLS
KLDEAYISGFDLIHTSIFSHMEPELPIKIRRVGK FVSMDFSDRYDEDYLRCCPYIDCGEISCGDMDEKEI
RQIMDQIMKFGCKHMVIATRSGKAYVLADGSFYEQSPCLVKAKDTMGAGDSFIASFLVNYLDGISM AVD
FPEKSGRGLVTAEGYKDALIRVSLYRAAVFSSCQCQRDGSFGHGKPMQRWAEGDAMEE*

>FraDLO_ORIG_scaffold_12091

CHTTNNSYMDEQLPRLREAGVPVSYDFSGQWTD EARVERVAPHVDY AFLSCGSVSLEQAQD ICRRMQGAG
AGMVIATR GSEGAVLFDGQDFYLRPPQLVEAVDTLGAGDSFATAFLLSWRAGQLEHGEDMDSALRARLLE
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>FraDLP_ORIG_scaffold_34

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RCYEGENAFARVTLVDGDRVFRGSRGGV LQQHPIYLDEADL AYADAFDLIHTTNGFIDGLL PALREL R
PLISYDFSYRWNEEDRVDRVCPYIDFGFLSCSDLGDEETEALCRRLCDKGC GVVTATRGSKGATVYDGSQ
FYSQLPDYVTPIDTMGAGDSFATAMLVTL LQSM EKQGR TDWENSILRAYLLPGALKAAA AFSARTCLVNG
AFGGGAAPESLRARLYGES*

>FraDLP_ORIG_scaffold_242

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ETVKCRQLVGENGWSKCTLVGDRIFGDYNEGGVRGKNPYILDRFDLEYMKQFDFVHTGN YCYTESQLKT
MKEAGIKVSFDFSDSSREYYEKYAPFVTYAFCSFN GDDEAAKEHLRFVHSLGPELVSLTRGSKGCLMYD
GEEFYVQPATMIEHVVDTMGAGDSFLTSFMDCYIDQVKRGTDKPEAIRISLAEASKFAAHVCTLDGAFGY
GKPYEDK*

>FraDLP_ORIG_scaffold_427

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QYEGENGCARVSLVNGDRVFLGSRGGV LREHPLELDGEDLAYIGGFDLCHTTNNSYMDEQLPRLREAGV
PVSYDFSGQWTD EARVERVAPHVDY AFLSCGSVSLEQAQD ICRRMQGAGAGMVIATR GSEGAVLFDGQDF
YLRPPQLVEAVDTLGAGDSFATAFLLSWRAGQLEHGEDMDSALRARLLEGALERAAGFSAQTCLVCGAFG
EGKAYDPEQDG*

>FraDLP_ORIG_scaffold_519

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PRVYLKDGDRVFGPGPRDSCQHLFAIKLVTEMDLIREFDICHTSCYSNLEYELPALS RICQVSFDFSDK
RDDAYLERVCPYLTFAFFSGSDLEKDR CQALLRKARELGVKIAGITRGAKGAI FYDGENFYHQGIKETE V
VDTMGAGDSFIAGFLTAYGDKPIKEALDYAACRSALTCTVRGGFGHPHKA*

>FraDLP_ORIG_scaffold_665

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QYEGENGFASVTLVEGDRVFLGSRGGAAREHPLEL TEEDLAYIRGF SHVHTSNNSYFNSQLAKVKSTGV
SLSYDFSGRWRDEAFVAQAAPYADY AFLSCGSAPLEEAQEVCRRLCAAGCGRVIATRGSAGALYYDGADF

FQPPDPVEPVDTLGAGDSFATAFLLSFLESLEAGERMAADRPLYEEEEVRAALRRGAFAAKTCLVQGA
FGHGKAFLPE*

>FraDLP_ORIG_scaffold_731

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KFVSMDFSNHYDEAYLKQCCPYLDCAEISCGDMDEEEMHQTMEEIISLGCKHMVIATRSGKACVLVNGK
FYEQSSQLVQARDTMGAGDSFITSFLIHLYLDGIRDAVDFSEESGERGIVSAAEQDILIRLCLYRAAVFA
SGQCQRDGSFSGFKEVELTDQDVEVMEGNKALKF*

>FraDLP_ORIG_scaffold_1333

MIRVLGIGDNVCDKYLHRTIYPPGGNALNIAVFGKMLGAEAYLGTFGDDEVGRHVYSVVRNMGIDISHC
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KFVSMDFSDSYEEELKCCPYLDCAVISCAGMAEIRKVMKDITEFGCKHMVIATRSGKACVMADGD
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SRQCQRDGSFSGHKAVELSDQDQVMNG*

>FraDLP_ORIG_scaffold_1817

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IFDFSMNKEEENLKQILPYVHCAFFSCEKKQPEIKDFLKKAKALGAKYVVATFGEESMICYDGEKFCEQG
IYKVPVNTVGAGDSFIAGFSWGLMCGKDVEECLEEGARLSSWVVQGFNPY*

>FraDLP_ORIG_scaffold_1968

MTDCYVDEGVYFPGGNAVNAVNCCKNGAEKVNIGVFGDDERADYIKECLAKEGVEFKRSRKCVAHTAQ
PRVYLKGDVRFVGPGRDSCQHLFSIKIVAEDMEVIRDFDICTSCFSNLEYELPAISEICQVSDFSER
REEDYLKRTCPYLTFAFFSGSEMEERECEELLKVVHGLGTVVGITRSGKAIIFYDGEKIYRQGIKPV
VDTMGAGDSFIAGFLTAYGDGKTMEEALDYGAERSSRTCMVRGGFGYPHKA*

>FraDLP_ORIG_scaffold_1969

MKLAAVGNSCIDYYENMEGGKAYPPGGPVNMAVYTVRLGGEASYIGPVGTDLYGGIMREAIRNKGVDISR
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TAFDCATRPEDPESQTAMPYTDYLFSCDDGDTPELRAQMCRYHEKGPRLVVCMMGSDGSLCWDGREFHR
FGIVPCENLVDSMGAGDSYIAGFLLGITEGLPIEEAMEKGAANATVTLGYFGGW*

>FraDLP_ORIG_scaffold_2458

MVKVLGLGDNVCDVYLHTGMTYPGGQAVNFAVYAGQLGAQADFMGVFGGDAVARHVQSTLDEKGVGRSHC
RSYPGENGFARVTLVEGDRVFMGSNRGGVLQEHPIYLDQADLDYIAGFDLVHTTNGFVDSLLPQLSQLP
PFVSYDFSRYWNEEDRVERVCPYIDFAFLSCSLDDVQTDLCRRLHEKGCVVATRSGKATVFDGSR
FYEQSPHLVEPVDTMGAGDSFATAMLSLLQALEREGRNAWSWESFRSNALPQALDKAAAFSARNCLVHG
AFGCGVPVPEELRPRMYEGIQ*

>FraDLP_ORIG_scaffold_3016

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TGVPIAYDFSLRWNDEYLAKVAPYVTVAILSCAHLTPPEEREREMKKAQSHGIAIVLGTIGEEGSWVLYGD
RFYYAPAVHAEDVIDTMGAGDSYFAAFLCSLLRDSATGALIEGDEAEMAARLQRAMNRGAFAAQVCAME
GAFGYGTPILGRTEV*

>FraDLP_ORIG_scaffold_3029

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PKIKAAGVPISFDFSDSTDEYYERIAPLVDYAFMSCGDMTLEETRKRLEKVAALGPKFVCASRGSEGC
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WGHGKVYD*

>FraDLP_ORIG_scaffold_3339

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LLAKTGVPIAYDFSLRWTDEYLARVAPYVTVAILSCAHLTPEEREREMKKAQAHGISIVLGTIGEEGSWV
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CAMEGAFGYGVPITGRTQL*

>FraDLP_ORIG_scaffold_3360

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AAGVTVCYDFYDNFTDEDIMGISPYIQYGFSCSHISEEEAKAVLKKCIESGCKIAVATRGHEATVAYDG
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DVNPDRLSEIINL*

>FraDLP_ORIG_scaffold_6191

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FDAATRPDDEAARIAIPSDYLFFAADDGDTPELRAQMKEIFDRGPKLVITTLGEKGSIVYDGKTYTTFG
IIPCHVVDTMGAGDSYIAGFLKGILEEKSVEECMKAGASNSSVTLEYNGAW*

>FraDLP_ORIG_scaffold_7856

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KLDEAYISGFDLIHTSIFSHMEPELPIKIRRVGKVFVSMDFSDRYDEDYLRCCPYIDCGEISCGDMDEKEI
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