| Aved_18-Q3-R54-62_BAT3C.540 Proteobacteria Deltaproteobacteria Myxococcales P3OB-42 | Percent_identity 20 25 30 35 40 Function Export GT MOD Polymerization NA |
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| midas_g_6017 midas_s_601 Aved_18-Q3-R54-62_BATAC.192 Chloroflexi Anaerolineae Ardenticatenales | GT WeeterragA/Crist family and present an interest end pone in the compone in the |
| Ca_Promineofilaceae midas_g_461 midas_s_46 Aved_18-Q3-R54-62_BATAC.253 Proteobacteria Alphaproteobacteria | GT 12 GT 14 GT 91 O-Antigen gase Polysacchample piosynthesis GT 14 GT 91 O-Antigen gase Polys |
| Sphingomonadales Sphingomonadaceae midas_g_59 midas_s_35 | gumD |
| | gumb gumb gumb gumb gumb gumb gumb gumb |
| Aved_18-Q3-R54-62_BATAC.601 | 29% 28% 23% 25% QumD QumD |
| Aved_18-Q3-R54-62_MAXAC.392 Proteobacteria Alphaproteobacteria Micavibrionales Micavibrionaceae midas_g_2943 midas_s_294 | 21% 28% 21% 23% gumC gumD gumD VanZ ike family beta-barrel pojin 2 Chain length Geterminant protein Polysaccharide his succharide his succh |
| Bjer_18-Q3-R1-45_BAT3C.347 Proteobacteria Gammaproteobacteria Betaproteobacteriales B1-7BS midas_g_190 midas_s_48 | 26% 24% Qumb Qu |
| Bjer_18-Q3-R1-45_MAXAC.024 Bacteroidetes Bacteroidia Chitinophagales midas_f_536 midas_g_536 midas_s_53 | 10000 20000 30000 22% 22% 22% 21% guml Quml Quml Quml Quml Quml Quml Polysaccharide biosynthesis protein Polysaccharide biosyn |
| Bjer_18-Q3-R1-45_MAXAC.141 Proteobacteria Gammaproteobacteria Betaproteobacteriales Burkholderiaceae Candidatus Symbiobacter | 0 5000 10000 15000 20000 32% 21% 22% 20% 25% 21% 27% 20mb gumC gumJ gumL gumL gumL gumL gumL gumL gumL gumL |
| midas_s_30 Bjer_18-Q3-R1-45_MAXAC.222 Bacteroidetes Bacteroidia Chitinophagales | PBIG-128 PBI |
| Chitinophagaceae Niabella midas_s_71 Damh_18-Q3-R51-60_MAXAC.008 Chloroflexi Anaerolineae | GT g1 |
| Ardenticatenales Ca_Promineofilaceae midas_g_461 midas_s_46 Ega_18-Q3-R5-49_BATAC.118 Bacteroidetes | gumb |
| Ignavibacteria Kryptoniales BSV26 <i>midas_g_627</i> <i>midas_s_62</i> Ega_18-Q3-R5-49_BATAC.204 | gumC gumB gumD gumD gumD gumD gumD gumD gumD gumD |
| Proteobacteria Gammaproteobacteria Betaproteobacteriales B1-7BS midas_g_190 midas_s_48 | 24% Quml Q |
| Ega_18-Q3-R5-49_MAXAC.075 Bacteroidetes Bacteroidia Sphingobacteriales AKYH767 midas_g_283 midas_s_28 | 22% 20% 28% gumC gumC gumC gumC SprB [speat Bacterial sugar ransferase Oxidorectificate and polysaccharide best and polysacc |
| Ejby_18-Q3-R6-50_BAT3C.362 Proteobacteria Deltaproteobacteria Bdellovibrionales Bdellovibrionaceae OM27_clade midas_s_81 | 23% 24% 25% gumD gumC gumD gumC 0 5000 10000 15000 20000 |
| EsbE_18-Q3-R3-47_BAT3C.110 Proteobacteria Deltaproteobacteria Syntrophobacterales Syntrophaceae midas_g_134 midas_s_126 | 22% 21% 20% gumB gumC gumJ QumH |
| EsbE_18-Q3-R3-47_BATAC.463 Proteobacteria Alphaproteobacteria Sphingomonadales Sphingomonadaceae midas_g_59 midas_s_5 | 0 5000 10000 15000 34% 22% 25% gumb gumb gumb |
| EsbE_18-Q3-R3-47_MAXAC.131 Proteobacteria Gammaproteobacteria Betaproteobacteriales Rhodocyclaceae Propionivibrio | 5000 10000 38% 23% 30% 38% 38% gumC gumD gumD |
| EsbW_18-Q3-R4-48_BAT3C.113 Ca_Fermentibacteroia Ca_Fermentibacteria midas_o_753 midas_f_1938 | Adultransferase tamily O-Antigen Dase Weck TragAVC)sF family 212 CobQ/CobB/MinD/P Transcelebide binding domain Putative beta-battle Printing Aprailing transferase Putative Battle Printing Transferase Put |
| | 0 5000 10000 15000 20000 25000 25000 25000 21% 33% |
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| Nitrospirae Nitrospirae Nitrospirales Nitrospiraceae Nitrospiraceae Nitrospira defluvi | 21% 27% 21% 23% 37% guml guml guml guml guml guml guml guml |
| Fred_18-Q3-R57-64_BAT3C.529_sub Chloroflexi Anaerolineae Ardenticatenales Ca_Promineofilaceae midas_g_461 midas_s_46 | 21% 21% 23% 34% QumH QumI QumJ QumD GT 12 GT 14 GT g1 GT 14 GT g1 OAntigen gase Polysacchande biosynthesis protein Chain length determinant protein length determinant le |
| Fred_18-Q3-R57-64_BAT3C.6 Gemmatimonadetes Gemmatimonadales Gemmatimonadales Gemmatimonadaceae midas_g_395 midas_s_39 | 21% 22% 29% 23% 22% 21% gumb |
| Fred_18-Q3-R57-64_BAT3C.705 Acidobacteria Blastocatellia (Subgroup 4) Blastocatellales Blastocatellaceae Stenotrophobacter midas_s_118 | 29% 28% 24% 25% Qumb gumb gumb gumb gumb gumb gumb gumb harder transferase of Weck transferase (GNAT) domain named to the polysaccharide bipsynchride bipsynchride bipsynchride to the polysaccharide bipsynchride bip |
| Fred_18-Q3-R57-64_BATAC.274 Bacteroidetes Bacteroidia Sphingobacteriales AKYH767 midas_g_283 midas_s_28 | Polysaccharide Control |
| Fred_18-Q3-R57-64_BATAC.422 Proteobacteria Gammaproteobacteriales Betaproteobacteriales Nitrosomonadaceae | 0 5000 10000 15000 20000 34% 32% 21% 21% gumD gumD gumD gumD gumD gumD gumD gumD |
| Nitrosomonadaceae oc32 midas_s_288 Fred_18-Q3-R57-64_BATAC.601 Proteobacteria Alphaproteobacteria Rhizobiales | PPRISE domain transferase COA be Polysaccharide by transferase CT 14 GT 91 Cellulase (GH5) 1 5000 1 5000 1 5000 21% 21% 26% 20% 26% 30mB 30m |
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| Alphaproteobacteria Dongiales Dongiaceae Dongia midas_s_405 | gumD gumD gumD gumH gumJ polysaccharide pyruvylltransferase Polysaccharide biosynthesis protein Polysaccharide biosynthes |
| Proteobacteria Deltaproteobacteria Myxococcales Sandaracinaceae midas_g_4101 midas_s_410 | 29% 21% 20% 38% gumb gumb gumb gumb gumb gumb gumb gumb |
| Fred_18-Q3-R57-64_MAXAC.330_cln Planctomycetes Phycisphaerae Phycisphaerales Phycisphaeraceae SM1A02 midas_s_491 | 28% 20% 21% Qumb |
| Hade_18-Q3-R52-61_BATAC.316 Proteobacteria Gammaproteobacteria Betaproteobacteriales B1-7BS midas_g_190 midas_s_51 | 30% 20% 21% 23% 34% 37% Sum June 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 |
| Hade_18-Q3-R52-61_MAXAC.056 Proteobacteria Alphaproteobacteria Sphingomonadales Sphingomonadaceae Sphingorhabdus midas_s_10 | 21% 26% 31% 34% gumD GT 14 GT 91 GT 14 GT 91 Bacterial Sugar transferase GT 4- (like ob Patr 91) G-tich 690 818 Millian Market and biodyces in Artigen lighase Polysaccharide biodyces in Artigen lighase |
| Hade_18-Q3-R52-61_MAXAC.304 Proteobacteria Gammaproteobacteria Betaproteobacteriales Rhodocyclaceae Propionivibrio | 5000 10000 38% 30% 23% 37% qumD qumB qumC |
| midas_s_42 Hirt_18-Q3-R61-65_BATAC.102 Bacteroidetes Bacteroidia Flavobacteriales | yrial transferase rekapep to the control of the con |
| NS9_marine_group midas_g_385 midas_s_455 Hirt_18-Q3-R61-65_MAXAC.142 Chloroflexi Anaerolineae | AANVCGAR AND COMPANIE TO TOO TEN TO TOO TOO TOO TOO TOO TOO TOO TOO TOO |
| Ardenticatenales Ca_Promineofilaceae midas_g_1951 midas_s_195 Hirt_18-Q3-R61-65_MAXAC.229 Proteobacteria | Helix-ture la function and the state of the |
| Deltaproteobacteria Myxococcales | 20% 36% Qum Qum |
| Proteobacteria Gammaproteobacteria Betaproteobacteriales B1-7BS | 21% 23% 24% 22% Quint Q |
| Hjor_18-Q3-R7-51_BAT3C.155_A Proteobacteria Alphaproteobacteria Rhizobiales Beijerinckiaceae <i>midas_g_534</i> <i>midas_s_529</i> | 31% 20% 27% 21% GumD gumD gumC GT g1 GT g1 GT g1 GT g1 GT g1 GT g1 O 5000 10000 15000 |
| Hjor_18-Q3-R7-51_BAT3C.155_B Proteobacteria Alphaproteobacteria Rhizobiales Beijerinckiaceae <i>midas_g_534</i> <i>midas_s_529</i> | 33% 20% 32% 22% gumD gumB gumB GT 14 GT 91 Polysaccharide bid sand learn length determinant protein G-rich domain on putative tyrosine kinase Acetyltransferase (GNAT) domain Polysaccharide deacetylase |
| Hjor_18-Q3-R7-51_BAT3C.262_A Proteobacteria Alphaproteobacteria Rhizobiales Hyphomicrobiaceae Hyphomicrobium midas_s_59 | 2500 5000 7500 10000 33% 21% 31% 20% gumD gumH gumB gumC Coabinding domain Becterial sugar transferase GT 14 GT g1 Polysaccharide bid sants 1888 MRRPrt protein |
| | |
| Hjor_18-Q3-R7-51_BAT3C.262_B Proteobacteria Alphaproteobacteria Rhizobiales Hyphomicrobiaceae Hyphomicrobium midas_s_59 | 0 2500 5000 7500 30% 20% 21% 31% 31% gumE gumH gumC gumD gumD |
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