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Your results are filtered to match records with query coverage between 90 and 100. **Filter Results** pdb|6KFS|A Job Title **RID** Download All ∨ **OBN3H81S016** Search expires on 01-20 01:33 am Organism only top 20 will appear exclude **Program** Citation ~ PSI-BLAST Iteration 8 Type common name, binomial, taxid or group name See details **∨ Database** refseq_protein + Add organism 6KFS A **Query ID Description** None **Percent Identity Query Coverage** E value Molecule type amino acid to to 90 to 100 **Query Length** 267 **PSI-BLAST incl. threshold** <u>Distance tree of results</u> <u>Multiple alignment</u> <u>MSA viewer</u> ? **Other reports** Filter Reset 1e-40 **Run PSI-Blast iteration 9** 500 **Number of sequences** Run **Descriptions Graphic Summary** Alignments Taxonomy 500 **Y** New Select columns Y Show **Download Sequences producing significant alignments** Multiple alignment Mew MSA Viewer sequences newly added this iteration ? Distance tree of results 165 sequences selected <u>GenPept</u> <u>Graphics</u> No new sequences were found above the 9.99995e-41 threshold Sequences with E-value BETTER than threshold select all 165 sequences selected **PSI-BLAST iteration 8** Select Used Acc. Max Total Query Per. Newly Scientific Name Description Accession Score | Score | Cover value Ident Len build added **PSSM** blast 248 <u>WP_073235363.1</u> hypothetical protein [Pedobacter caeni] Pedobacter caeni 407 407 31.10% **~** 247 WP 015332822.1 hypothetical_protein_[Fibrella_aestuarina] 406 94% 27.95% Fibrella aestuarina 406 3e-141 <u>hypothetical protein [Chryseobacterium shigense]</u> 93% 3e-140 27.09% 247 WP 184160290.1 <u>Chryseobacterium shige</u>... 403 403 245 WP 110366918.1 <u>hypothetical protein [Chryseobacterium sp. CBTAP 102]</u> Chryseobacterium sp. C... 403 92% 27.60% 403 3e-140 244 WP 084085857.1 hypothetical protein [Chryseobacterium sp. YR221] Chryseobacterium sp. Y... 403 403 93% 3e-140 27.49% hypothetical protein [Runella limosa] Runella limosa 403 403 93% 4e-140 29.08% 248 WP 028521775.1 <u>hypothetical protein [Chryseobacterium candidae]</u> Chryseobacterium candi... 402 402 92% 4e-140 27.60% 245 WP 136523142.1 hypothetical protein [Pedobacter steynii] Pedobacter stevnii 402 94% 32.28% 248 WP 069380885.1 402 5e-140 hypothetical protein [Runella sp. CRIBMP] Runella sp. CRIBMP 402 402 94% 5e-140 30.20% 248 WP 166559794.1 94% 29.92% 248 WP 074610199.1 hypothetical protein [Pedobacter steynii] Pedobacter steynii 402 402 5e-140 hypothetical protein [Runella defluvii] 248 <u>WP_183971264.1</u> Runella defluvii 402 402 93% 6e-140 29.08% hypothetical protein [Runella sp. HYN0085] Runella sp. HYN0085 29.80% 402 402 94% 6e-140 248 <u>WP_114067546.1</u> hypothetical_protein_[Flavobacterium_croceum] Flavobacterium croceum 402 402 94% 7e-140 27.17% 247 WP_103727191.1 **~** hypothetical protein [Chryseobacterium sp. OV705] Chryseobacterium sp. O... 402 93% 8e-140 27.89% WP 047493470.1 402 <u>hypothetical protein [Chryseobacterium sp. BLS98]</u> 402 402 93% 8e-140 27.49% 244 WP 048503838.1 <u>Chryseobacterium sp. BL...</u> hypothetical protein [Chryseobacterium rhizosphaerae] 93% 1e-139 28.29% 244 WP 115919248.1 <u>Chryseobacterium rhizos</u>... 401 401 hypothetical protein [Sphingobacterium sp. DR205] Sphingobacterium sp. D... 402 402 93% 1e-139 27.09% 246 WP 165307541.1 244 WP_106011341.1 hypothetical_protein_[Elizabethkingia_anophelis] Elizabethkingia anophelis 401 401 93% 1e-139 27.49% 401 93% 28.69% 245 <u>WP 142686817.1</u> hypothetical protein [Chitinophaga polysaccharea] Chitinophaga polysaccha. 401 2e-139 hypothetical protein [Runella sp. YX9] Runella sp. YX9 401 401 94% 2e-139 29.80% 248 WP 114460255.1 2e-139 27.89% hypothetical_protein_[Sphingobacterium_sp._DR205] 93% 244 <u>WP 165308671.1</u> Sphingobacterium sp. D... 401 401 hypothetical protein [Sphingobacterium composti Ten et al. 2007 non Yoo et al. 2... 245 <u>WP 159635845.1</u> <u>Sphingobacterium comp</u>... 401 401 93% 3e-139 27.89% WP 184628527.1 hypothetical protein [Pedobacter cryoconitis] Pedobacter cryoconitis 94% 400 400 5e-139 30.71% 248 248 <u>WP 184184064.1</u> hypothetical protein [Chryseobacterium defluvii] 400 93% 26.69% <u>Chryseobacterium defluvii</u> 400 7e-139 hypothetical protein [Chryseobacterium echinoideorum] 399 399 92% 7e-139 27.20% 246 WP 144282205.1 Chryseobacterium echin... 245 WP 123983592.1 hypothetical_protein_[Chryseobacterium_sp._G0201] 399 399 93% 8e-139 28.57% Chryseobacterium sp. G... hypothetical protein [Runella sp. SP2] Runella sp. SP2 399 93% 28.69% 248 <u>WP 122929104.1</u> 399 1e-138 hypothetical protein [Cellulophaga sp. BC115SP] 247 WP 166549273.1 Cellulophaga sp. BC115SP 398 398 94% 4e-138 29.02% hypothetical_protein_[Pedobacter_sp._KBW06] Pedobacter sp. KBW06 397 397 94% 5e-138 30.31% 248 WP 124576869.1 hypothetical protein [Chryseobacterium caeni] 244 WP 027384690.1 397 397 7e-138 26.69% Chryseobacterium caeni <u>hypothetical protein [Chryseobacterium elymi</u> <u>Chryseobacterium elymi</u> hypothetical protein [Chryseobacterium geocarposphaerae] 245 WP 100375240.1 396 396 94% 2e-137 25.69% Chryseobacterium geoca... 396 396 93% 2e-137 26.69% 244 WP 089871418.1 <u>hypothetical protein [Chryseobacterium hungaricum]</u> Chryseobacterium hunga... 396 396 94% 2e-137 29.02% 248 WP_055131730.1 **~** hypothetical_protein_[Pedobacter_sp._Hv1] Pedobacter sp. Hv1 Chryseobacterium phosp... 247 <u>WP_103248721.1</u> hypothetical protein [Chryseobacterium phosphatilyticum] 396 396 93% 3e-137 26.29% 30.16% hypothetical protein [Spirosoma sp. 209] Spirosoma sp. 209 396 396 93% 3e-137 255 <u>WP 077921918.1</u> 94% 30.20% 247 <u>WP 109673212.1</u> hypothetical protein [Dyadobacter jejuensis] Dyadobacter jejuensis 395 395 4e-137 hypothetical protein [Chitinophaga ginsengisegetis] 27.27% WP 079467908.1 Chitinophaga ginsengise... 395 395 94% 4e-137 248 WP 160376098.1 hypothetical protein [Flavobacterium sp. GA093] Flavobacterium sp. GA093 395 395 94% 4e-137 29.80% hypothetical protein [Chryseobacterium sp. FH2] 394 394 93% 27.09% WP 048510624.1 <u>Chryseobacterium sp. FH2</u> 8e-137 hypothetical protein [Chryseobacterium sp. 16F] 28.29% 245 <u>WP 173779818.1</u> 394 394 93% 1e-136 <u>Chryseobacterium sp. 16F</u> hypothetical_protein_[Spirosoma_sordidisoli] Spirosoma sordidisoli 394 394 93% 1e-136 30.56% 255 WP_129601184.1 hypothetical protein [Haliscomenobacter hydrossis] 94% 31.62% 249 WP 044234271.1 Haliscomenobacter hydr... 393 393 2e-136 MULTISPECIES: hypothetical protein [Elizabethkingia] 393 393 93% 3e-136 27.09% 245 <u>WP 078674445.1</u> <u>Elizabethkingia</u> Elavobacterium_johnsoniae 393 94% 3e-136 27.45% 247 <u>WP 012026570.1</u> hypothetical_protein_[Flavobacterium_johnsoniae] 393 hypothetical protein [Chryseobacterium sp. YR460] 392 WP_047400736.1 Chryseobacterium sp. Y... 392 93% 4e-136 26.69% 244 <u>hypothetical protein [Flavobacterium johnsoniae]</u> Flavobacterium johnsoniae 392 392 94% 4e-136 27.45% 247 <u>WP 073408386.1</u> 392 392 245 <u>WP_106635994.1</u> **~** <u>hypothetical protein [Siphonobacter sp. BAB-5404]</u> <u>Siphonobacter sp. BAB-5..</u> 93% 5e-136 27.38% hypothetical protein [Emticicia aquatilis] 392 392 94% 6e-136 28.35% WP 188764399.1 Emticicia aquatilis hypothetical_protein_[Dyadobacter_jiangsuensis] Dyadobacter_jiangsuensis 392 392 94% 9e-136 25.59% 249 <u>WP 106599283.1</u> 26.40% 392 392 92% 244 WP 068484510.1 <u>hypothetical protein [Maribacter sp. T28]</u> Maribacter sp. T28 9e-136 Flavobacterium chilense <u>hypothetical protein [Flavobacterium chilense]</u> 392 392 93% 9e-136 29.08% 250 <u>WP_068842713.1</u> **✓** 243 <u>WP 182804567.1</u> **~** hypothetical_protein_[Lacibacter_sp. S13-6-6] Lacibacter sp. S13-6-6 391 391 93% 1e-135 29.08% hypothetical protein [Flavobacterium sp. ASV13] 392 392 93% 1e-135 29.08% 250 WP 198999553.1 <u>Flavobacterium sp. ASV13</u> hypothetical protein [Terrimonas sp. NS-102] 391 391 94% 2e-135 26.67% 248 <u>WP_116873322.1</u> Terrimonas sp. NS-102 247 WP 071505270.1 <u>hypothetical protein [Arsenicibacter rosenii]</u> <u>Arsenicibacter rosenii</u> 391 94% 3e-135 27.56% 391 hypothetical protein [Emticicia sp. CRIBPO] 92% 30.40% 249 <u>WP 166563382.1</u> Emticicia sp. CRIBPO 391 391 3e-135 **~** hypothetical_protein_[Flavobacterium_johnsoniae] Elavobacterium johnsoniae 390 390 94% 3e-135 27.45% 247 WP_121360601.1 WP_041518387.1 390 5e-135 29.30% 250 <u>hypothetical protein [Flavobacterium hibernum]</u> Flavobacterium hibernum 390 95% hypothetical protein [Chitinophaga sp. SYP-B3965] 389 389 95% 7e-135 28.12% 248 <u>WP 153657706.1</u> Chitinophaga sp. SYP-B... 249 WP 133527124.1 hypothetical protein [Flavobacterium_sp._245] Flavobacterium sp. 245 389 389 93% 8e-135 28.69% 389 94% 1e-134 28.06% 248 <u>WP 163490139.1</u> hypothetical protein [Fluviicola sp. SGL-29] 389 <u>Fluviicola sp. SGL-29</u> hypothetical protein [Pedobacter sp. LMG 31462] Pedobacter sp. LMG 31462 389 389 1e-134 27.84% 248 WP 182959330.1 hypothetical protein [Pedobacter sp. RP-1-13] Pedobacter sp. RP-1-13 389 389 29.13% 248 <u>WP 131554884.1</u> 2e-134 252 <u>WP_108686810.1</u> ✓ 93% 27.38% hypothetical protein [Chitinophaga parva] 389 389 2e-134 Chitinophaga parva hypothetical_protein_[Flavobacterium_sp._JRR_20_7] Flavobacterium sp. JRR ... 388 388 93% 28.29% 248 WP 121319619.1 4e-134 hypothetical protein [Flavobacterium johnsoniae] 387 387 93% 6e-134 28.69% 247 WP 121360438.1 Flavobacterium johnsoniae hypothetical protein [Flavobacterium sp. KBS0721] 386 386 93% 1e-133 27.89% 247 WP 078005321.1 Flavobacterium sp. KBS0... 28.69% hypothetical_protein_[Flavobacterium_johnsoniae] Flavobacterium johnsoniae 386 386 93% 1e-133 WP 073408637.1 93% 249 <u>WP_071634644.1</u> <u>hypothetical protein [Flavobacterium johnsoniae]</u> Flavobacterium johnsoniae 386 386 1e-133 27.49% hypothetical protein [Flavobacterium piscis] 386 386 93% 2e-133 27.89% 255 WP 065450348.1 ***** Flavobacterium piscis 28.24% hypothetical protein [Pedobacter sp. PACM 27299] 386 94% 254 WP 062549423.1 Pedobacter sp. PACM 27. 386 2e-133 hypothetical protein [Flavobacterium sp. CSZ] 386 386 93% 2e-133 27.89% 248 <u>WP 194618990.1</u> Flavobacterium sp. CSZ hypothetical_protein_[Leadbetterella_byssophila] 386 386 94% 3e-133 27.67% 245 WP 013407705.1 Leadbetterella byssophila 386 92% 29.20% 249 <u>WP 156309406.1</u> <u>hypothetical protein [Sphingobacterium endophyticum]</u> <u>Sphingobacterium endop</u>... 386 3e-133 hypothetical protein [Flavobacterium johnsoniae] 93% ***** 385 385 3e-133 28.69% 247 WP 012026804.1 <u>Flavobacterium johnsoniae</u> hypothetical_protein_[Pseudoflavitalea_rhizosphaerae] 385 385 93% 6e-133 25.79% 247 <u>WP 127125117.1</u> Pseudoflavitalea rhizosp... 248 <u>WP 173970031.1</u> hypothetical protein [Flavobacterium bizetiae] Flavobacterium bizetiae 384 384 93% 7e-133 28.69% hypothetical protein [Sphingobacterium endophyticum] 384 384 92% 8e-133 29.20% 250 <u>WP_197091696.1</u> <u>Sphingobacterium endop</u>.. hypothetical protein [Flavobacterium caeni] Flavobacterium caeni 384 384 94% 1e-132 26.09% WP_091140989.1 <u>hypothetical protein [Chryseobacterium sp. 1_F178]</u> 384 92% 2e-132 29.08% 248 <u>WP_115970805.1</u> Chryseobacterium sp. 1_... 384 hypothetical protein [Siphonobacter aquaeclarae] Siphonobacter_aquaeclarae 382 382 93% 4e-132 28.29% <u>WP 093196548.1</u> 7e-132 26.19% 245 <u>WP_165308567.1</u> <u>hypothetical protein [Sphingobacterium sp. DR205]</u> Sphingobacterium sp. D.... 382 382 93% WP 183916567.1 381 29.08% hypothetical protein [Sphingobacterium sp. JUb56] Sphingobacterium sp. JU... 381 92% 3e-131 hypothetical protein [Flavobacterium sp. YO64] Flavobacterium sp. YO64 381 381 93% 3e-131 26.69% 249 WP 129052752.1 93% hypothetical protein [Flavobacterium sp. 2] 380 380 4e-131 27.09% Flavobacterium sp. 2 ***** <u>hypothetical protein [Spirosoma sp. HMF4905]</u> Spirosoma sp. HMF4905 380 380 93% 6e-131 28.29% 249 WP 157588272.1 hypothetical protein [Flavobacterium oncorhynchi] Flavobacterium oncorhyn... 379 379 93% 8e-131 26.69% WP 089053068.1 249 WP 089058649.1 hypothetical protein [Flavobacterium plurextorum] 379 379 93% 9e-131 26.69% Flavobacterium plurextor... hypothetical protein [Pedobacter sp. LMG 31464] Pedobacter sp. LMG 31464 379 95% 28.12% 249 <u>WP 182921498.1</u> 379 1e-130 255 WP 152124200.1 hypothetical protein [Rudanella paleaurantiibacter] Rudanella paleaurantiiba... 378 378 94% 3e-130 29.41% <u>hypothetical protein [Sphingobacterium puteale]</u> Sphingobacterium puteale 377 93% 26.69% 245 <u>WP 121122592.1</u> 377 6e-130 hypothetical_protein_[Sphingobacterium_athyrii] 8e-130 26.69% 245 WP 108635588.1 377 Sphingobacterium_athyrii 8e-130 26.88% hypothetical protein [Pedobacter sp. LMG 31463] Pedobacter sp. LMG 31463 248 WP_173087507.1 Flavobacterium sp. YO12 376 1e-129 26.29% 249 WP 129022758.1 <u>hypothetical protein [Flavobacterium sp. YO12]</u> 376 <u>hypothetical protein [Nonlabens dokdonensis]</u> Nonlabens dokdonensis 362 362 94% 5e-124 27.95% 248 <u>WP_015361113.1</u> hypothetical protein [Pedobacter nyackensis] 93% 6e-122 25.00% 245 <u>WP 084289446.1</u> <u>Pedobacter nyackensis</u> 357 357 hypothetical_protein_[Vaginella_massiliensis] Vaginella_massiliensis 355 355 93% 2e-121 27.09% 247 WP 068598662.1 93% <u>hypothetical protein [Tamlana crocina]</u> <u>Tamlana crocina</u> 346 346 2e-117 29.64% 254 WP 092853592.1 <u>hypothetical protein [Algibacter pectinivorans]</u> 345 345 93% 4e-117 30.83% <u>Algibacter pectinivorans</u> hypothetical_protein_[Flavobacterium_cheongpyeongense] 344 344 93% 1e-116 29.13% 251 WP_110305092.1 <u>Flavobacterium cheongp</u>... 30.43% 254 WP 194527250.1 <u> MULTISPECIES: hypothetical protein [unclassified Zobellia]</u> unclassified Zobellia 343 343 93% 1e-116 255 WP 106567585.1 <u>hypothetical protein [Cecembia rubra]</u> 340 94% 30.86% Cecembia rubra 340 4e-115 hypothetical protein [Maribacter forsetii] Maribacter forsetii 339 339 94% 30.08% 5e-115 hypothetical protein [Sediminitomix flava] Sediminitomix flava 5e-115 31.69% 237 <u>WP_109617172.1</u> 339 339 90% 6e-115 32.10% 237 WP_100926505.1 hypothetical_protein_[Tenacibaculum_sp._SZ-18] Tenacibaculum sp. SZ-18 339 339 90% 237 WP 073315401.1 <u>hypothetical protein [Aquimarina spongiae]</u> 338 338 90% 9e-115 31.28% Aquimarina spongiae 237 WP 062621620.1 hypothetical protein [Flammeovirga sp. SJP92] 337 90% 32.92% <u>Flammeovirga sp. SJP92</u> 337 2e-114 hypothetical protein [Tenacibaculum_agarivorans] 337 337 90% 2e-114 31.69% 237 WP_075343881.1 **~** Tenacibaculum_agarivorans <u>hypothetical protein [Arcticibacter eurypsychrophilus]</u> <u> Arcticibacter eurypsychro</u>... 337 337 94% 29.07% 254 WP 069659777.1 <u>hypothetical protein [Flavobacterium sp. T13(2019)]</u> Flavobacterium sp. T13(... 336 336 93% 8e-114 31.50% 251 WP 180907624.1 336 336 93% 1e-113 28.85% 254 <u>WP 076455290.1</u> <u>hypothetical protein [Zobellia uliginosa]</u> Zobellia uliginosa hypothetical protein [Cecembia calidifontis] 93% 255 WP 130277659.1 Cecembia calidifontis 336 336 1e-113 31.10% MULTISPECIES: hypothetical_protein_[unclassified_Flavobacterium] unclassified Flavobacteri... 336 336 93% 1e-113 31.10% 251 WP_154784978.1 **✓** 254 WP 095164579.1 < hypothetical protein [Flectobacillus sp. BAB-3569] Flectobacillus sp. BAB-3... 335 335 93% 3e-113 28.85% <u>hypothetical protein [Aureitalea marina]</u> 334 334 90% 32.10% 237 <u>WP_104813660.1</u> <u>Aureitalea marina</u> 4e-113 hypothetical_protein_[Emticicia_sp._ODNR4P] 93% 7e-113 28.85% 254 WP_166579201.1 Emticicia sp. QDNR4P 334 334 hypothetical protein [Cellulophaga sp. BC115SP] Cellulophaga sp. BC115SP 334 334 93% 9e-113 28.85% 254 <u>WP_166551039.1</u> WP 157361546.1 93% 1e-112 30.43% <u>hypothetical protein [Winogradskyella endarachnes]</u> Winogradskyella endarac... 334 334 hypothetical protein [Flavobacterium daejeonense] 333 93% 1e-112 30.71% 251 <u>WP_035141483.1</u> Flavobacterium daejeone... 333 WP 044208460.1 1e-112 32.51% hypothetical protein [Flammeovirga sp. OC4] Flammeovirga sp. OC4 333 333 90% 237 hypothetical_protein_[Flammeovirga_yaeyamensis] 332 332 90% 2e-112 34.02% 238 WP_169662917.1 Flammeovirga yaeyamen. hypothetical protein [Arcticibacter pallidicorallinus] Arcticibacter pallidicoralli... 333 2e-112 28.68% 254 <u>WP 106290784.1</u> 333 94% hypothetical protein [Roseivirga misakiensis] Roseivirga misakiensis 332 332 90% 3e-112 31.69% 237 WP 069836112.1 hypothetical_protein_[Flammeovirga_sp._MY04] Flammeovirga sp. MY04 332 332 90% 3e-112 33.61% 238 <u>WP 066212370.1</u> hypothetical protein [Seonamhaeicola marinus] 332 WP 148544644.1 332 4e-112 31.97% <u>Seonamhaeicola marinus</u> <u>hypothetical protein [Dyadobacter arcticus]</u> <u>Dyadobacter arcticus</u> 331 331 92% 7e-112 27.02% 246 <u>WP_167271559.1</u> <u>hypothetical protein [Arcticibacter svalbardensis]</u> Arcticibacter svalbardensis 331 331 95% 28.96% 254 <u>WP 016196613.1</u> 1e-111 <u>hypothetical protein [Cyclobacterium xiamenense]</u> Cyclobacterium xiamene... 330 330 90% 2e-111 30.86% 237 WP_154858054.1 Reichenbachiella versicolor 329 329 90% 3e-111 31.28% 237 WP_109830319.1 **~** hypothetical_protein_[Reichenbachiella_versicolor] WP_092168055.1 <u>hypothetical protein [Cyclobacterium xiamenense]</u> <u>Cyclobacterium xiamene</u>... 329 329 90% 5e-111 30.86% 237 328 90% 30.86% <u>WP 162418506.1</u> <u>hypothetical protein [Cyclobacterium sp. SYSU L10180]</u> Cyclobacterium sp. SYS... 328 1e-110 237 Hyunsoonleella pacifica 30.86% 90% hypothetical_protein_[Hyunsoonleella_pacifica] 327 327 2e-110 237 WP_130936555.1 326 93% 2e-109 32.28% 266 <u>WP_080053967.1</u> <u>hypothetical protein [Spirosoma aerolatum]</u> 326 <u>Spirosoma aerolatum</u> 324 324 90% 3e-109 32.10% 239 <u>WP_147168135.1</u> <u>hypothetical protein [Phaeodactylibacter luteus]</u> Phaeodactylibacter luteus 254 <u>WP 013632480.1</u> 324 <u>hypothetical protein [Pseudopedobacter saltans]</u> Pseudopedobacter saltans 324 95% 7e-109 25.58% hypothetical protein [Muricauda pacifica] 323 323 90% 8e-109 32.51% 237 WP 106144355.1 Muricauda pacifica hypothetical protein [Siphonobacter sp. BAB-5404] 318 318 92% 2e-106 31.33% 255 WP_106638196.1 <u>Siphonobacter sp. BAB-5</u>. 91% 26.32% 239 WP 194120019.1 hypothetical protein [Dyadobacter sp. UP-52] 315 315 9e-106 <u>Dyadobacter sp. UP-52</u> <u>hypothetical protein [Algoriphagus resistens]</u> <u>Algoriphagus resistens</u> 314 314 92% 3e-105 26.21% 248 <u>WP_057937867.1</u> WP_159471428.1 91% 2e-104 26.72% 239 hypothetical_protein_[Dyadobacter_sp._3J3] Dyadobacter sp. 3J3 312 312 26.32% WP_137339906.1 hypothetical protein [Dyadobacter frigoris] **Dyadobacter frigoris** 311 311 91% 4e-104 239 93% 30.86% 257 <u>WP 190890830.1</u> hypothetical protein [Spirosoma sp. BT702] Spirosoma sp. BT702 311 311 7e-104 253 <u>WP_036305061.1</u> 95% <u>hypothetical protein [Methylobacter tundripaludum]</u> 309 309 5e-103 24.61% Methylobacter tundripalu... 9e-103 24.61% 253 WP 104428652.1 <u>hypothetical protein [Methylobacter tundripaludum]</u> 308 308 95% Methylobacter tundripalu... hypothetical_protein_[Methylobacter_tundripaludum] 308 308 95% 1e-102 24.61% 253 WP 036244726.1 Methylobacter tundripalu... 2e-102 24.61% 253 <u>WP_006893469.1</u> ✓ <u>hypothetical protein [Methylobacter tundripaludum]</u> 307 307 95% Methylobacter tundripalu... <u>hypothetical protein [Methylobacter tundripaludum]</u> 306 306 95% 6e-102 25.10% 253 <u>WP 104422403.1</u> **~** Methylobacter tundripalu... hypothetical protein [Pedobacter antarcticus] 304 304 94% 5e-101 27.17% 254 WP 074591362.1 **~** Pedobacter antarcticus 27.17% hypothetical protein [Pedobacter antarcticus] 304 304 94% 5e-101 254 WP 037437692.1 Pedobacter antarcticus

<u>predicted protein [Phaeodactylum tricornutum CCAP 1055/1]</u>

predicted_protein_[Thalassiosira_pseudonana_CCMP1335]

<u>predicted protein [Phaeodactylum tricornutum CCAP 1055/1]</u>

predicted_protein_[Phaeodactylum_tricornutum_CCAP_1055/1]

predicted_protein_[Phaeodactylum_tricornutum_CCAP_1055/1]

hypothetical protein EMIHUDRAFT_457739 [Emiliania huxleyi CCMP1516]

hypothetical_protein_EMIHUDRAFT_249864 [Emiliania_huxleyi_CCMP1516]

predicted protein [Thalassiosira pseudonana CCMP1335]

hypothetical protein [Paludisphaera sp. JC665]

<u>hypothetical protein [Tautonia plasticadhaerens]</u>

hypothetical protein [Chryseolinea serpens]

hypothetical protein [Chryseolinea soli]

hypothetical protein [Pedobacter quisquiliarum]

hypothetical protein [Planctomyces sp. SH-PL62]

<u>hypothetical protein [Paludisphaera soli]</u>

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Run PSI-BLAST Iteration 9 with max number of sequences Run

500

Phaeodactylum tricornut...

Pedobacter quisquiliarum

Planctomyces sp. SH-PL62

Thalassiosira pseudonan...

<u>Phaeodactylum tricornut</u>...

Phaeodactylum tricornut...

Thalassiosira pseudonan...

Paludisphaera sp. JC665

Phaeodactylum tricornut...

Tautonia plasticadhaerens

Emiliania huxleyi CCMP1...

Emiliania huxleyi CCMP1...

<u>Chryseolinea serpens</u>

Chryseolinea soli

<u>Paludisphaera soli</u>

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93%

5e-98

1e-94

6e-92

7e-91

3e-89

2e-88

9e-87

2e-84

8e-84

2e-83

2e-81

9e-81

2e-77

28.46%

27.86%

43.60%

27.10%

59.27%

59.27%

43.32%

24.80%

25.00%

23.81%

48.83%

26.92%

27.34%

27.45%

Resources Literature Health Genomes Genes **Proteins**

Chemicals

Actions Submit Download Learn Develop Analyze

Research

Support Center

100.00% 517 <u>XP 002177507.1</u>

249 <u>WP 188626824.1</u> <

✓

273 <u>WP_068420066.1</u>

297 XP_002297283.1

273 <u>WP 165253308.1</u>

568 XP 002177506.1

545 XP_002177505.1

310 XP 002297285.1

273 <u>WP_165068168.1</u> ✓

289 WP 073135631.1

269 <u>WP 145270246.1</u>

267 XP_002177508.1

475 <u>XP_005776873.1</u>

304 XP 005758903.1

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