

OTU\_137;size=5020;.csv

Protula pacifica

Serpulidae

Sabellida

82.95

|  |              |       |       |             |                      |                      |   |
|--|--------------|-------|-------|-------------|----------------------|----------------------|---|
| Protula pacifica voucher BIOUG<CAN>:BAMPOL0473 cyt | HM473658     | 82.95 | 83.41 | 1.28657e-42 | Sabellida            | Serpulidae           | Protula pacifica                                      |
| Serpulidae sp. BOLD:AAG0874 voucher BIOUG<CAN>:WS0 | HM417793     | 81.42 | 86.73 | 5.47063e-41 | Sabellida            | Serpulidae           | Serpulidae sp. BOLD:AAG0874                           |
| Spirorbis sp. CMC01 voucher BIOUG<CAN>:HUNTSPOL020 | HQ024244     | 83.23 | 76.3  | 2.83385e-38 | Sabellida            | Serpulidae           | Spirorbis sp. CMC01                                   |
| Spirorbis sp. CMC01 voucher BIOUG<CAN>:HUNTSPOL020 | HQ024243     | 83.23 | 76.3  | 2.83385e-38 | Sabellida            | Serpulidae           | Spirorbis sp. CMC01                                   |
| Polynucleobacter asymbioticus QLW-P1DMWA-1, comple | CP000655     | 80.23 | 83.89 | 4.20581e-36 | Burkholderiales      | Burkholderiaceae     | Polynucleobacter asymbioticus QLW-P1DMWA-1            |
| Nitrosomonas ureae strain Nm10, complete genome    | CP013341     | 76.78 | 100   | 1.46797e-35 | Nitrosomonadales     | Nitrosomonadaceae    | Nitrosomonas ureae                                    |
| Protolaeospira eximia voucher BIOUG<CAN>:BAMPOL046 | HM473657     | 79.19 | 81.99 | 7.60429e-33 | Sabellida            | Serpulidae           | Protolaeospira eximia                                 |
| Protolaeospira eximia voucher BIOUG<CAN>:BAMPOL046 | HM473656     | 79.19 | 81.99 | 7.60429e-33 | Sabellida            | Serpulidae           | Protolaeospira eximia                                 |
| Protolaeospira eximia voucher BIOUG<CAN>:BAMPOL046 | HM473655     | 79.19 | 81.99 | 7.60429e-33 | Sabellida            | Serpulidae           | Protolaeospira eximia                                 |
| Neanthes sp. RP2011-N cytochrome oxidase subunit I | JX866607     | 76.06 | 99.53 | 2.65416e-32 | Phyllodocida         | Nereididae           | Neanthes sp. RP2011-N                                 |
| Spongiibacter sp. IMCC21906, complete genome       | CP011477     | 81.21 | 70.62 | 1.12858e-30 | Cellvibrionales      | Spongiibacteraceae   | Spongiibacter sp. IMCC21906                           |
| Spirorbis sp. CMC02 voucher BIOUG<CAN>:HUNTSPOL020 | HQ024247     | 74.42 | 99.05 | 1.12858e-30 | Sabellida            | Serpulidae           | Spirorbis sp. CMC02                                   |
| Uncultured organism isolate Los Vilos_40 cytochrom | FJ541283     | 75.74 | 95.73 | 1.12858e-30 |                      |                      | uncultured organism                                   |
| Uncultured organism isolate Constitucion_16 cytoch | FJ541282     | 75.74 | 95.73 | 1.12858e-30 |                      |                      | uncultured organism                                   |
| Uncultured organism isolate Constitucion_12 cytoch | FJ541280     | 75.74 | 95.73 | 1.12858e-30 |                      |                      | uncultured organism                                   |
| Uncultured organism isolate Constitucion_24 cytoch | FJ541278     | 75.74 | 95.73 | 1.12858e-30 |                      |                      | uncultured organism                                   |
| Uncultured organism isolate Constitucion_21 cytoch | FJ541275     | 75.74 | 95.73 | 1.12858e-30 |                      |                      | uncultured organism                                   |
| Uncultured organism isolate Constitution_13 cytoch | FJ541274     | 75.74 | 95.73 | 1.12858e-30 |                      |                      | uncultured organism                                   |
| Uncultured organism isolate Chipana_1 cytochrome o | FJ541273     | 75.74 | 95.73 | 1.12858e-30 |                      |                      | uncultured organism                                   |
| Methylophilales bacterium MBRSG12 genome           | CP011003     | 78.92 | 78.67 | 3.93912e-30 | Methylophilales      |                      | Methylophilales bacterium MBRSG12                     |
| Methylophilales bacterium MBRSH7 genome            | CP011002     | 78.92 | 78.67 | 3.93912e-30 | Methylophilales      |                      | Methylophilales bacterium MBRSH7                      |
| Methylophilales bacterium MBRSF5 genome            | CP011001     | 78.92 | 78.67 | 3.93912e-30 | Methylophilales      |                      | Methylophilales bacterium MBRSF5                      |
| Spirorbis sp. CMC02 voucher BIOUG<CAN>:HUNTSPOL020 | HQ024246     | 74.42 | 99.05 | 3.93912e-30 | Sabellida            | Serpulidae           | Spirorbis sp. CMC02                                   |
| Spirorbis sp. CMC02 voucher BIOUG<CAN>:HUNTSPOL020 | HQ024245     | 74.42 | 99.05 | 3.93912e-30 | Sabellida            | Serpulidae           | Spirorbis sp. CMC02                                   |
| Nitrosomonas sp. AL212, complete genome            | CP002552     | 80.13 | 73.93 | 3.93912e-30 | Nitrosomonadales     | Nitrosomonadaceae    | Nitrosomonas sp. AL212                                |
| Collimonas arenae strain Ter282, complete genome   | CP013235     | 78.79 | 78.2  | 1.37489e-29 | Burkholderiales      | Oxalobacteraceae     | Collimonas arenae                                     |
| Collimonas arenae strain Ter10, complete genome    | CP013233     | 78.79 | 78.2  | 1.37489e-29 | Burkholderiales      | Oxalobacteraceae     | Collimonas arenae                                     |
| Beta proteobacterium CB, complete genome           | CP004348     | 77.4  | 83.89 | 1.37489e-29 |                      |                      | beta proteobacterium CB                               |
| Uncultured organism isolate Constitucion_8 cytochr | FJ541277     | 75.25 | 95.73 | 1.37489e-29 |                      |                      | uncultured organism                                   |
| Uncultured gamma proteobacterium clone SW002 cytoc | FJ868208     | 79.01 | 76.78 | 1.37489e-29 |                      |                      | uncultured gamma proteobacterium                      |
| Methylophilus sp. TWE2, complete genome            | CP012020     | 74.41 | 100   | 4.79883e-29 | Methylophilales      | Methylophilaceae     | Methylophilus sp. TWE2                                |
| Ciona intestinalis cytochrome oxidase subunit I mi | AY116597     | 79.35 | 73.46 | 4.79883e-29 | Enterogona           | Cionidae             | Ciona intestinalis                                    |
| Insecta sp. SHSY141205 cytochrome oxidase subunit  | KU720137     | 74.29 | 99.53 | 1.67496e-28 |                      |                      | Insecta sp. SHSY141205                                |
| Limnohabitans sp. 63ED37-2, complete genome        | CP011774     | 78.18 | 78.2  | 1.67496e-28 | Burkholderiales      | Comamonadaceae       | Limnohabitans sp. 63ED37-2                            |
| Gyнуella sunshinyii YC6258, complete genome        | CP007142     | 78.18 | 78.2  | 1.67496e-28 | Oceanospirillales    | Saccharospirillaceae | Gyнуella sunshinyii YC6258                            |
| Polynucleobacter necessarius subsp. necessarius ST | CP001010     | 78.18 | 78.2  | 1.67496e-28 | Burkholderiales      | Burkholderiaceae     | Polynucleobacter necessarius subsp. necessarius STIR1 |
| Saccharophagus degradans 2-40, complete genome     | CP000282     | 79.11 | 74.88 | 1.67496e-28 | Burkholderiales      | Burkholderiaceae     | Saccharophagus degradans 2-40                         |
| Betaproteobacteria bacterium UKL13-2, complete gen | CP012157     | 74.4  | 98.1  | 5.84617e-28 | Cellvibrionales      | Cellvibrionaceae     | Betaproteobacteria bacterium UKL13-2                  |
| Uncultured organism isolate Pumillahue_D_4 COI gen | FJ541269     | 77.84 | 79.15 | 5.84617e-28 |                      |                      | uncultured organism                                   |
| Uncultured organism isolate Tumbes_D_1 cytochrome  | FJ541268     | 77.84 | 79.15 | 5.84617e-28 |                      |                      | uncultured organism                                   |
| Uncultured organism isolate Tumbes_D_7 cytochrome  | FJ541267     | 77.84 | 79.15 | 5.84617e-28 |                      |                      | uncultured organism                                   |
| Uncultured organism isolate Loncoyen_D_9 cytochrom | FJ541266     | 77.84 | 79.15 | 5.84617e-28 |                      |                      | uncultured organism                                   |
| Nitrosomonas europaea ATCC 19718, complete genome  | AL954747     | 79.87 | 70.62 | 5.84617e-28 | Nitrosomonadales     | Nitrosomonadaceae    | Nitrosomonas europaea ATCC 19718                      |
| Polychaeta sp. EBS61o-Po36 cytochrome oxidase subu | KJ736175     | 78.85 | 73.93 | 2.04051e-27 |                      |                      | Polychaeta sp. EBS61o-Po36                            |
| Uncultured organism isolate Algarrobo_3 cytochrome | FJ541272     | 74.04 | 98.58 | 2.04051e-27 |                      |                      | uncultured organism                                   |
| Uncultured organism isolate Algarrobo_2 cytochrome | FJ541271     | 74.04 | 98.58 | 2.04051e-27 |                      |                      | uncultured organism                                   |
| Uncultured organism isolate Algarrobo_1 cytochrome | FJ541270     | 74.04 | 98.58 | 2.04051e-27 |                      |                      | uncultured organism                                   |
| Limnohabitans sp. 103DPR2, complete genome         | CP011834     | 77.58 | 78.2  | 7.1221e-27  | Burkholderiales      | Comamonadaceae       | Limnohabitans sp. 103DPR2                             |
| Polynucleobacter duraquae strain MWH-MoK4, complet | CP007501     | 77.58 | 78.2  | 7.1221e-27  | Burkholderiales      | Burkholderiaceae     | Polynucleobacter duraquae                             |
| Methylotenera versatilis 301, complete genome      | CP002056     | 74.87 | 92.42 | 7.1221e-27  | Methylophilales      | Methylophilaceae     | Methylotenera versatilis 301                          |
| Collimonas arenae strain Cal35, complete genome    | CP009962     | 77.64 | 76.3  | 2.48586e-26 | Burkholderiales      | Oxalobacteraceae     | Collimonas arenae                                     |
| Nitrosomonas eutropha C91, complete genome         | CP000450     | 74.53 | 99.53 | 2.48586e-26 | Nitrosomonadales     | Nitrosomonadaceae    | Nitrosomonas eutropha C91                             |
| Cnemidocarpa verrucosa mitochondrial partial COI g | AJ830012     | 79.19 | 70.62 | 2.48586e-26 | Stolidobranchia      | Styelidae            | Cnemidocarpa verrucosa                                |
| Marinobacter sp. LQ44, complete genome             | CP014754     | 77.3  | 77.25 | 8.67649e-26 | Alteromonadales      | Alteromonadaceae     | Marinobacter sp. LQ44                                 |
| Methylomonas denitrificans strain FJG1, complete g | CP014476     | 79.05 | 70.14 | 8.67649e-26 | Methylococcales      | Methylococcaceae     | Methylomonas denitrificans                            |
| Nitrosospira briensis C-128, complete genome       | CP012371     | 76.22 | 86.73 | 3.02839e-25 | Nitrosomonadales     | Nitrosomonadaceae    | Nitrosospira briensis C-128                           |
| Uncultured gamma proteobacterium clone SW004 cytoc | FJ868209     | 77.16 | 76.78 | 3.02839e-25 |                      |                      | uncultured gamma proteobacterium                      |
| Collimonas fungivorans strain Ter6, complete genom | CP013232     | 78.62 | 68.72 | 3.68934e-24 | Burkholderiales      | Oxalobacteraceae     | Collimonas fungivorans                                |
| Paucibacter sp. KCTC 42545, complete genome        | CP013692     | 78.62 | 68.72 | 3.68934e-24 | Burkholderiales      | Oxalobacteraceae     | Paucibacter sp. KCTC 42545                            |
| Pseudohongiella spirulinae strain KCTC 32221, comp | CP013189     | 76.36 | 78.2  | 3.68934e-24 |                      |                      | Pseudohongiella spirulinae                            |
| Burkholderia rhizoxinica HKI 454, complete genome  | FR687359     | 76.36 | 78.2  | 3.68934e-24 | Burkholderiales      | Burkholderiaceae     | Paraburkholderia rhizoxinica HKI 454                  |
| Teredinibacter turnerae T7901, complete genome     | CP001614     | 76.33 | 79.15 | 3.68934e-24 | Cellvibrionales      | Cellvibrionaceae     | Teredinibacter turnerae T7901                         |
| Herminiimonas arsenicoxydans chromosome, complete  | CU207211     | 76.36 | 78.2  | 3.68934e-24 | Burkholderiales      | Oxalobacteraceae     | Herminiimonas arsenicoxydans                          |
| Polynucleobacter sp. QLW-P1FAT50C-4 genome         | CP015922     | 78.72 | 66.82 | 1.28771e-23 | Burkholderiales      | Burkholderiaceae     | Polynucleobacter sp. QLW-P1FAT50C-4                   |
| Zhongshania aliphaticivorans strain SM2, complete  | CP014544     | 76.79 | 79.15 | 1.28771e-23 | Cellvibrionales      | Spongiibacteraceae   | Zhongshania aliphaticivorans                          |
| Collimonas pratensis strain Ter91, complete genome | CP013234     | 76.4  | 76.3  | 1.28771e-23 | Burkholderiales      | Oxalobacteraceae     | Collimonas pratensis                                  |
| Uncultured Pseudomonas sp. clone GP0154 cytochrome | KJ885299     | 75.74 | 80.09 | 1.28771e-23 | Pseudomonadales      | Pseudomonadaceae     | uncultured Pseudomonas sp.                            |
| Uncultured Pseudomonas sp. clone GP0151 cytochrome | KJ885296     | 75.74 | 80.09 | 1.28771e-23 | Pseudomonadales      | Pseudomonadaceae     | uncultured Pseudomonas sp.                            |
| Uncultured Pseudomonas sp. clone GP0150 cytochrome | KJ885295     | 75.74 | 80.09 | 1.28771e-23 | Pseudomonadales      | Pseudomonadaceae     | uncultured Pseudomonas sp.                            |
| Uncultured Pseudomonas sp. clone GP0149 cytochrome | KJ885294     | 75.74 | 80.09 | 1.28771e-23 | Pseudomonadales      | Pseudomonadaceae     | uncultured Pseudomonas sp.                            |
| Uncultured Pseudomonas sp. clone GP0148 cytochrome | KJ885293     | 75.74 | 80.09 | 1.28771e-23 | Pseudomonadales      | Pseudomonadaceae     | uncultured Pseudomonas sp.                            |
| Didemnum candidum isolate GAPB2 cytochrome c oxida | KJ725168     | 75.9  | 78.67 | 1.28771e-23 | Enterogona           | Didemnidae           | Didemnum candidum                                     |
| Cycloclasticus zancles 78-ME, complete genome      | CP005996     | 76.22 | 77.73 | 1.28771e-23 | Thiotrichales        | Piscirickettsiaceae  | Cycloclasticus zancles 78-ME                          |
| Glaciecola psychrophila 170, complete genome       | CP003837     | 75.74 | 80.09 | 1.28771e-23 | Alteromonadales      | Alteromonadaceae     | Paraglaciecola psychrophila 170                       |
| Cycloclasticus sp. P1, complete genome             | CP003230     | 76.22 | 77.73 | 1.28771e-23 | Thiotrichales        | Piscirickettsiaceae  | Cycloclasticus sp. P1                                 |
| Janthinobacterium sp. Marseille, complete genome   | CP000269     | 76.4  | 76.3  | 1.28771e-23 | Burkholderiales      | Oxalobacteraceae     | Janthinobacterium sp. Marseille                       |
| Didemnum candidum cytochrome oxidase subunit I gen | AY116602     | 75.9  | 78.67 | 1.28771e-23 | Enterogona           | Didemnidae           | Didemnum candidum                                     |
| Marinobacter psychrophilus strain 20041, complete  | CP011494     | 76.83 | 77.25 | 4.49453e-23 | Alteromonadales      | Alteromonadaceae     | Marinobacter psychrophilus                            |
| Alteromonas australica strain DE170, complete geno | CP010912     | 75.76 | 78.2  | 4.49453e-23 | Alteromonadales      | Alteromonadaceae     | Alteromonas australica                                |
| Alteromonas australica strain H 17, complete genom | CP008849     | 75.76 | 78.2  | 4.49453e-23 | Alteromonadales      | Alteromonadaceae     | Alteromonas australica                                |
| Alteromonas macleodii str. 'Balearic Sea AD45', co | CP003873     | 77.93 | 68.72 | 4.49453e-23 | Alteromonadales      | Alteromonadaceae     | Alteromonas macleodii str. 'Balearic Sea AD45'        |
| Alteromonas macleodii str. 'English Channel 673',  | CP003844     | 77.93 | 68.72 | 4.49453e-23 | Alteromonadales      | Alteromonadaceae     | Alteromonas macleodii str. 'English Channel 673'      |
| Marinobacter sp. BSs20148, complete genome         | CP003735     | 76.83 | 77.25 | 4.49453e-23 | Alteromonadales      | Alteromonadaceae     | Marinobacter sp. BSs20148                             |
| Collimonas fungivorans Ter331, complete genome     | CP002745     | 77.93 | 68.72 | 4.49453e-23 | Burkholderiales      | Oxalobacteraceae     | Collimonas fungivorans Ter331                         |
| Tetranchyroderma sp.3 TK-2011 voucher MT30 cytochr | JF432035     | 75.76 | 78.2  | 4.49453e-23 | Macrodasysida        | Thaumastodermatidae  | Tetranchyroderma sp.3 TK-2011                         |
| Nitrosomonas sp. Is79A3, complete genome           | CP002876     | 73.43 | 97.63 | 4.49453e-23 | Nitrosomonadales     | Nitrosomonadaceae    | Nitrosomonas sp. Is79A3                               |
| Curvibacter putative symbiont of Hydra magnipapill | FN543104     | 75.76 | 78.2  | 4.49453e-23 | Burkholderiales      | Comamonadaceae       | Curvibacter putative symbiont of Hydra magnipapillata |
| PREDICTED: Priapulus caudatus probable cytochrome  | XM_014825104 | 77.18 | 70.62 | 1.56875e-22 |                      | Priapulidae          | Priapulus caudatus                                    |
| Nitrosomonas communis strain Nm2, complete genome  | CP011451     | 72.99 | 99.53 | 1.56875e-22 | Nitrosomonadales     | Nitrosomonadaceae    | Nitrosomonas communis                                 |
| Coelomactra antiquata strain GY cytochrome oxidase | FJ653656     | 75.15 | 80.09 | 1.56875e-22 | Veneroida            | Macrtridae           | Coelomactra antiquata                                 |
| Coelomactra antiquata strain LYG-116 cytochrome ox | GQ406236     | 75.15 | 80.09 | 1.56875e-22 | Veneroida            | Macrtridae           | Coelomactra antiquata                                 |
| Collimonas pratensis strain Ter291, complete genom | CP013236     | 75.78 | 76.3  | 5.47546e-22 | Burkholderiales      | Oxalobacteraceae     | Collimonas pratensis                                  |
| Roseateles depolymerans strain KCTC 42856, complet | CP013729     | 75.78 | 76.3  | 5.47546e-22 | Burkholderiales      | Oxalobacteraceae     | Roseateles depolymerans                               |
| Didemnum candidum isolate GAAAC13 cytochrome c oxi | KJ725164     | 75.3  | 78.67 | 5.47546e-22 | Enterogona           | Didemnidae           | Didemnum candidum                                     |
| Marinobacter hydrocarbonoclasticus str. ATCC 49840 | F0203363     | 75.78 | 76.3  | 5.47546e-22 | Alteromonadales      | Alteromonadaceae     | Marinobacter hydrocarbonoclasticus ATCC 49840         |
| Alteromonas sp. SN2, complete genome               | CP002339     | 75    | 79.62 | 5.47546e-22 | Alteromonadales      | Alteromonadaceae     | Alteromonas naphthalenivorans                         |
| Legionella longbeachae NSW150, complete genome     | FN650140     | 76.28 | 73.93 | 5.47546e-22 | Legionellales        | Legionellaceae       | Legionella longbeachae NSW150                         |
| Kangiella korensis DSM 16069, complete genome      | CP001707     | 77.4  | 69.19 | 5.47546e-22 | Oceanospirillales    | Alcanivoracaceae     | Kangiella korensis DSM 16069                          |
| Phascolosoma esculenta cytochrome c oxidase subuni | EF521190     | 76.82 | 71.56 | 5.47546e-22 | Phascolosomatiformes | Phascolosomatidae    | Phascolosoma esculenta                                |
| Marinobacter aquaeolei VT8, complete genome        | CP000514     | 75.78 | 76.3  | 5.47546e-22 | Alteromonadales      | Alteromonadaceae     | Marinobacter hydrocarbonoclasticus VT8                |