

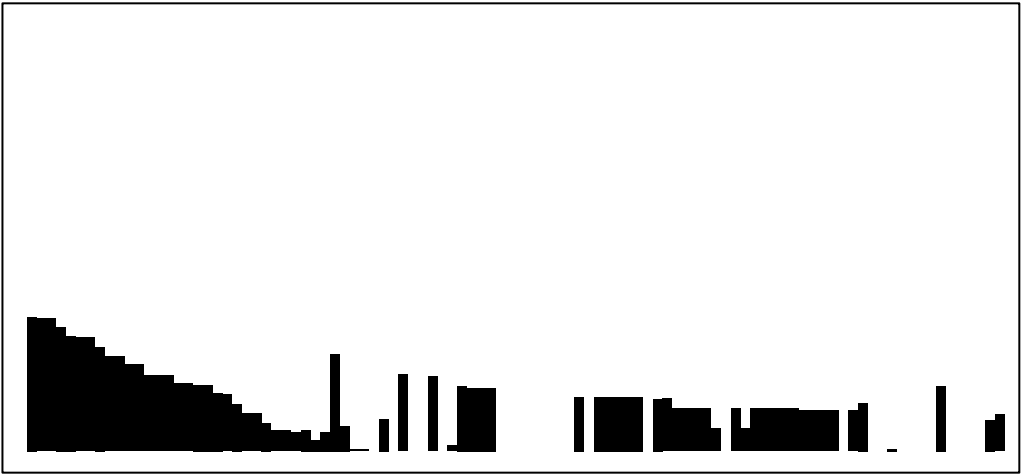
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Sphingomonas wittichii RW1

Sphingomonadaceae

Sphingomonadales

86.28



Sphingomonas wittichii RW1, complete genome	CP000699	86.28	100	4.27374e-68	Sphingomonadales	Sphingomonadaceae	Sphingomonas wittichii RW1
Sphingobium sp. YBL2, complete genome	CP010954	86.22	99.56	1.49168e-67	Sphingomonadales	Sphingomonadaceae	Sphingobium sp. YBL2
Sphingopyxis alaskensis RB2256, complete genome	CP000356	86.22	99.56	1.49168e-67	Sphingomonadales	Sphingomonadaceae	Sphingopyxis alaskensis RB2256
Sphingomonas sanxanigenens NX02, complete genome	CP006644	85.84	100	5.20648e-67	Sphingomonadales	Sphingomonadaceae	Sphingomonas sanxanigenens DSM 19645 = NX02
Sphingobium sp. EP60837 chromosome 1, complete seq	CP015986	85.4	100	2.21385e-65	Sphingomonadales	Sphingomonadaceae	Sphingobium sp. EP60837
Sphingobium sp. TKS chromosome 1, complete sequenc	CP005083	85.33	99.56	7.7271e-65	Sphingomonadales	Sphingomonadaceae	Sphingobium sp. TKS
PREDICTED: Pantholops hodgsonii cytochrome c oxida	XM_005971211	85.33	99.56	7.7271e-65		Bovidae	Pantholops hodgsonii
Sphingobium sp. MI1205 chromosome 1, complete sequ	CP005188	84.89	99.56	9.41354e-64	Sphingomonadales	Sphingomonadaceae	Sphingobium sp. MI1205
Sphingobium sp. SYK-6 DNA, complete genome	AP012222	84.44	99.56	4.00274e-62	Sphingomonadales	Sphingomonadaceae	Sphingobium sp. SYK-6
Sphingobium chlorophenolicum L-1 chromosome 1, com	CP002798	84.44	99.56	4.00274e-62	Sphingomonadales	Sphingomonadaceae	Sphingobium chlorophenolicum L-1
Sphingopyxis terrae NBRC 15098 strain 203-1, compl	CP013342	84.07	100	1.39709e-61	Sphingomonadales	Sphingomonadaceae	Sphingopyxis terrae NBRC 15098
Sphingobium japonicum UT26S DNA, chromosome 1, com	AP010803	84.07	100	1.39709e-61	Sphingomonadales	Sphingomonadaceae	Sphingobium japonicum UT26S
Sphingopyxis macrogoltabida strain 203N, complete	CP013344	83.56	99.56	2.07347e-59	Sphingomonadales	Sphingomonadaceae	Sphingopyxis macrogoltabida
Sphingobium baderi strain DE-13, complete genome	CP013264	83.56	99.56	2.07347e-59	Sphingomonadales	Sphingomonadaceae	Sphingobium baderi
Sphingopyxis macrogoltabida strain 203, complete g	CP009429	83.56	99.56	2.07347e-59	Sphingomonadales	Sphingomonadaceae	Sphingopyxis macrogoltabida
Sphingomonas taxi strain ATCC 55669, complete geno	CP009571	83.19	100	7.23712e-59	Sphingomonadales	Sphingomonadaceae	Sphingomonas taxi
Sphingomonas sp. MM-1, complete genome	CP004036	83.19	100	7.23712e-59	Sphingomonadales	Sphingomonadaceae	Sphingomonas sp. MM-1
Altererythrobacter epoxidivorans strain CGMCC 1.77	CP012669	83.11	99.56	2.526e-58	Sphingomonadales	Erythrobacteraceae	Altererythrobacter epoxidivorans
Croceicoccus naphthovorans strain PQ-2, complete g	CP011770	83.11	99.56	2.526e-58	Sphingomonadales	Erythrobacteraceae	Croceicoccus naphthovorans
Sphingopyxis macrogoltabida strain EY-1, complete	CP012700	82.74	100	3.0773e-57	Sphingomonadales	Sphingomonadaceae	Sphingopyxis macrogoltabida
Citromicrobium sp. JL477, complete genome	CP011344	82.67	99.56	1.07408e-56	Sphingomonadales	Sphingomonadaceae	Citromicrobium sp. JL477
Sphingomonas sp. WHSC-8, complete genome	CP010836	82.22	99.56	1.3085e-55	Sphingomonadales	Sphingomonadaceae	Sphingomonas hengshuiensis
Sphingopyxis fribergensis strain Kp5.2, complete g	CP009122	81.78	99.56	5.56389e-54	Sphingomonadales	Sphingomonadaceae	Sphingopyxis fribergensis
Erythrobacter litoralis HTCC2594, complete genome	CP000157	81.78	99.56	5.56389e-54	Sphingomonadales	Erythrobacteraceae	Erythrobacter litoralis HTCC2594
Porphyrobacter neustonensis strain DSM 9434, compl	CP016033	81.33	99.56	6.77821e-53	Sphingomonadales	Erythrobacteraceae	Porphyrobacter neustonensis
Sphingomonas sp. NIC1, complete genome	CP015521	80.97	100	8.25755e-52	Sphingomonadales	Sphingomonadaceae	Sphingomonas sp. NIC1
Polymorphum gilvum SL003B-26A1, complete genome	CP002568	80.97	100	8.25755e-52		Polymorphum gilvum SL003B-26A1	
Sphingorhabdus sp. M41, complete genome	CP014545	80.89	99.56	2.88217e-51	Sphingomonadales	Sphingomonadaceae	Sphingorhabdus sp. M41
Sphingopyxis granuli strain TFA, complete genome	CP012199	81	97.79	1.00598e-50	Sphingomonadales	Sphingomonadaceae	Sphingopyxis granuli
Sphingomonas sp. NX-3 cytochrome c oxidase subunit	KF999931	80.53	100	1.00598e-50	Sphingomonadales	Sphingomonadaceae	Sphingomonas sp. NX-3
Sphingopyxis sp. 113P3, complete genome	CP009452	80.91	97.35	3.5112e-50	Sphingomonadales	Sphingomonadaceae	Sphingopyxis sp. 113P3
Azospirillum brasilense strain Az39, complete geno	CP007793	84.57	83.19	3.5112e-50	Rhodospirillales	Rhodospirillaceae	Azospirillum brasilense
Rhodopseudomonas palustris DX-1, complete genome	CP002418	81.19	96.46	3.5112e-50	Rhizobiales	Bradyrhizobiaceae	Rhodopseudomonas palustris DX-1
Novosphingobium pentaromativorans US6-1, complete	CP009291	80.09	100	4.27752e-49	Sphingomonadales	Sphingomonadaceae	Novosphingobium pentaromativorans US6-1
Uncultured zooplankton clone 22_277 cytochrome c o	KC732316	80.09	100	4.27752e-49		zooplankton environmental sample	
Methylocystis sp. SC2 complete genome	HE956757	79.91	100	4.27752e-49	Rhizobiales	Methylocystaceae	Methylocystis sp. SC2
Brevundimonas subvibrioides ATCC 15264, complete g	CP002102	81.52	93.36	4.27752e-49	Caulobacterales	Caulobacteraceae	Brevundimonas subvibrioides ATCC 15264
Altererythrobacter marensis strain KCTC 22370, com	CP011805	80	99.56	1.493e-48	Sphingomonadales	Erythrobacteraceae	Altererythrobacter marensis
Rhodopseudomonas palustris BisB5, complete genome	CP000283	83.6	83.63	5.21108e-48	Rhizobiales	Bradyrhizobiaceae	Rhodopseudomonas palustris BisB5
Altererythrobacter ishigakiensis strain NBRC 10769	CP015963	79.56	99.56	1.81885e-47	Sphingomonadales	Erythrobacteraceae	Altererythrobacter ishigakiensis
Hoeflea sp. IMCC20628, complete genome	CP011479	79.56	99.56	1.81885e-47	Rhizobiales	Phyllobacteriaceae	Hoeflea sp. IMCC20628
Azospirillum brasilense Sp245 main chromosome comp	HE577327	83.51	83.19	1.81885e-47	Rhodospirillales	Rhodospirillaceae	Azospirillum brasilense Sp245
Novosphingobium aromaticivorans DSM 12444, complet	CP000248	79.56	99.56	1.81885e-47	Sphingomonadales	Sphingomonadaceae	Novosphingobium aromaticivorans DSM 12444
Rhodopseudomonas palustris CGA009 complete genome;	BX572595	80.28	96.46	1.81885e-47	Rhizobiales	Bradyrhizobiaceae	Rhodopseudomonas palustris CGA009
Bradyrhizobium oligotrophicum S58 DNA, complete ge	AP012603	83.07	83.63	6.3484e-47	Rhizobiales	Bradyrhizobiaceae	Bradyrhizobium oligotrophicum S58
Azospirillum humicireducens strain SgZ-5, complete	CP015285	82.98	83.19	2.21581e-46	Rhodospirillales	Rhodospirillaceae	Azospirillum humicireducens
Pannonibacter phragmitetus strain 31801, complete	CP013068	82.98	83.19	2.21581e-46	Rhodobacteriales	Rhodobacteraceae	Pannonibacter phragmitetus
Azospirillum brasilense strain Sp7, complete seque	CP012914	82.98	83.19	2.21581e-46	Rhodospirillales	Rhodospirillaceae	Azospirillum brasilense
Novosphingobium sp. PP1Y main chromosome, complete	FR856862	79.2	100	2.21581e-46	Sphingomonadales	Sphingomonadaceae	Novosphingobium sp. PP1Y
Parvibaculum lavamentivorans DS-1, complete genome	CP000774	79.64	97.79	2.21581e-46	Rhizobiales	Rhodobiaceae	Parvibaculum lavamentivorans DS-1
Brevundimonas naejangsanensis strain B17, complete	CP015614	79.11	99.56	7.73393e-46	Caulobacterales	Caulobacteraceae	Brevundimonas naejangsanensis
Aminobacter aminovorans strain KCTC 2477, complete	CP015005	79.55	97.35	7.73393e-46	Rhizobiales	Phyllobacteriaceae	Aminobacter aminovorans
Labrenzia sp. CP4, complete genome	CP011927	79.11	99.56	7.73393e-46	Rhodobacteriales	Rhodobacteraceae	Labrenzia sp. CP4
Erythrobacter atlanticus strain s21-N3, complete g	CP011310	79.11	99.56	7.73393e-46	Sphingomonadales	Erythrobacteraceae	Erythrobacter atlanticus
PREDICTED: Pantholops hodgsonii cytochrome c oxida	XM_005963570	79.11	99.56	7.73393e-46		Bovidae	Pantholops hodgsonii
Azospirillum lipoferum 4B main chromosome, complet	FQ311868	79.39	99.56	7.73393e-46	Rhodospirillales	Rhodospirillaceae	Azospirillum lipoferum 4B
Bradyrhizobium sp. BF49 genome assembly, chromosom	LN901633	82.54	83.63	2.69941e-45	Rhizobiales	Bradyrhizobiaceae	Bradyrhizobium sp.
Rhodoplanes sp. Z2-YC6860, complete genome	CP007440	78.76	100	2.69941e-45	Rhizobiales	Hyphomicrobiaceae	Rhodoplanes sp. Z2-YC6860
Bradyrhizobium sp. CCGE-LA001, complete genome	CP013949	82.54	83.63	2.69941e-45	Rhizobiales	Bradyrhizobiaceae	Bradyrhizobium sp. CCGE-LA001
Bradyrhizobium japonicum strain E109, complete gen	CP010313	82.54	83.63	2.69941e-45	Rhizobiales	Bradyrhizobiaceae	Bradyrhizobium japonicum
Bradyrhizobium japonicum USDA 6 DNA, complete geno	AP012206	82.54	83.63	2.69941e-45	Rhizobiales	Bradyrhizobiaceae	Bradyrhizobium japonicum USDA 6
Bradyrhizobium sp. BTAi1, complete genome	CP000494	82.54	83.63	2.69941e-45	Rhizobiales	Bradyrhizobiaceae	Bradyrhizobium sp. BTAi1
Rhodopseudomonas palustris HaA2, complete genome	CP000250	82.54	83.63	2.69941e-45	Rhizobiales	Bradyrhizobiaceae	Rhodopseudomonas palustris HaA2
Altererythrobacter atlanticus strain 26DY36, compl	CP011452	78.67	99.56	9.42185e-45	Sphingomonadales	Erythrobacteraceae	Altererythrobacter atlanticus
Hyphomicrobium sp. MC1 chromosome, complete genome	FQ859181	82.45	83.19	9.42185e-45	Rhizobiales	Hyphomicrobiaceae	Hyphomicrobium sp. MC1
Sordaria macrospora k-hell hypothetical protein (S	XM_003343148	82.47	85.4	9.42185e-45	Sordariales	Sordariaceae	Sordaria macrospora k-hell
Bradyrhizobium sp. G22 genome assembly, chromosome	LN907826	82.01	83.63	3.28855e-44	Rhizobiales	Bradyrhizobiaceae	Bradyrhizobium sp.
Bradyrhizobium diazoefficiens USDA 110, complete g	CP011360	82.01	83.63	3.28855e-44	Rhizobiales	Bradyrhizobiaceae	Bradyrhizobium diazoefficiens USDA 110
Bradyrhizobium japonicum SEMIA 5079 genome	CP007569	82.01	83.63	3.28855e-44	Rhizobiales	Bradyrhizobiaceae	Bradyrhizobium japonicum SEMIA 5079
Bradyrhizobium sp. S23321 DNA, complete genome	AP012279	82.01	83.63	3.28855e-44	Rhizobiales	Bradyrhizobiaceae	Bradyrhizobium sp. S23321
Caulobacter crescentus NA1000, complete genome	CP001340	81.07	90.71	3.28855e-44	Caulobacterales	Caulobacteraceae	Caulobacter crescentus NA1000
Agrobacterium tumefaciens str. C58 circular chromo	AE007869	78.83	98.23	3.28855e-44	Rhizobiales	Rhizobiaceae	Agrobacterium tumefaciens str. C58
Bradyrhizobium sp. ORS278,complete sequence	CU234118	82.01	83.63	3.28855e-44	Rhizobiales	Bradyrhizobiaceae	Bradyrhizobium sp. ORS 278
Caulobacter crescentus CB15, complete genome	AE005673	81.07	90.71	3.28855e-44	Caulobacterales	Caulobacteraceae	Caulobacter crescentus CB15
Bradyrhizobium japonicum USDA 110 DNA, complete ge	BA000040	82.01	83.63	3.28855e-44	Rhizobiales	Bradyrhizobiaceae	Bradyrhizobium diazoefficiens USDA 110
Bradyrhizobium japonicum putative epoxide hydrolas	U33883	82.01	83.63	3.28855e-44	Rhizobiales	Bradyrhizobiaceae	Bradyrhizobium japonicum
Bradyrhizobium japonicum coxB, coxA, coxE, coxF, c	AJ242592	82.01	83.63	3.28855e-44	Rhizobiales	Bradyrhizobiaceae	Bradyrhizobium japonicum
B.japonicum coxA gene for cytochrome aa(3) subunit	X54318	82.01	83.63	3.28855e-44	Rhizobiales	Bradyrhizobiaceae	Bradyrhizobium japonicum
B.japonicum coxA gene for subunit I of cytochrome	X54800	82.01	83.63	3.28855e-44	Rhizobiales	Bradyrhizobiaceae	Bradyrhizobium japonicum
Azospirillum thiophilum strain BV-S chromosome 1,	CP012401	81.91	83.19	1.14782e-43	Rhodospirillales	Rhodospirillaceae	Azospirillum thiophilum
Bradyrhizobium diazoefficiens DNA, complete genome	AP014685	81.91	83.19	1.14782e-43	Rhizobiales	Bradyrhizobiaceae	Bradyrhizobium diazoefficiens
Rhodospirillum centenum SW, complete genome	CP000613	81.91	83.19	1.14782e-43	Rhodospirillales	Rhodospirillaceae	Rhodospirillum centenum SW
Azospirillum sp. B510 DNA, complete genome	AP010946	81.91	83.19	1.14782e-43	Rhodospirillales	Rhodospirillaceae	Azospirillum sp. B510
Rhodopseudomonas palustris TIE-1, complete genome	CP001096	78.9	96.46	1.14782e-43	Rhizobiales	Bradyrhizobiaceae	Rhodopseudomonas palustris TIE-1
Nitrobacter hamburgensis X14, complete genome	CP000319	81.91	83.19	1.14782e-43	Rhizobiales	Bradyrhizobiaceae	Nitrobacter hamburgensis X14
Rhodopseudomonas palustris BisB18, complete genome	CP000301	82.26	82.3	1.14782e-43	Rhizobiales	Bradyrhizobiaceae	Rhodopseudomonas palustris BisB18
Nitrobacter winogradskyi Nb-255, complete genome	CP000115	78.9	96.46	1.14782e-43	Rhizobiales	Bradyrhizobiaceae	Nitrobacter winogradskyi Nb-255
Mesorhizobium loti NZP2037, complete genome	CP016079	78.64	97.35	4.00627e-43	Rhizobiales	Phyllobacteriaceae	Mesorhizobium loti NZP2037
Caulobacter henricii strain CB4, complete genome	CP013002	80.09	92.92	4.00627e-43	Caulobacterales	Caulobacteraceae	Caulobacter henricii
Agrobacterium tumefaciens strain Ach5 chromosome c	CP011246	78.22	99.56	4.00627e-43	Rhizobiales	Rhizobiaceae	Agrobacterium tumefaciens
Mesorhizobium huakuii 7653R genome	CP006581	78.64	97.35	4.00627e-43	Rhizobiales	Phyllobacteriaceae	Mesorhizobium huakuii 7653R
Agrobacterium tumefaciens LBA4213 (Ach5) circular	CP007225	78.22	99.56	4.00627e-43	Rhizobiales	Rhizobiaceae	Agrobacterium tumefaciens LBA4213 (Ach5)
PREDICTED: Pantholops hodgsonii cytochrome c oxida	XM_005964101	78.64	97.35	4.00627e-43		Bovidae	Pantholops hodgsonii
Micavibrio aeruginosavorus EPB, complete genome	CP003538	83.06	80.09	4.00627e-43	Rhizobiales	Micavibrio aeruginosavorus EPB	
Agrobacterium sp. H13-3 circular chromosome, compl	CP002248	78.22	99.56	4.00627e-43	Rhizobiales	Rhizobiaceae	Agrobacterium sp. H13-3
Agrobacterium sp. ATCC 31749 cytochrome c oxidase	GQ428131	78.22	99.56	4.00627e-43	Rhizobiales	Rhizobiaceae	Agrobacterium sp. ATCC 31749
Uncultured marine organism clone IOBCBE001_14-G04-	GQ234900	78.48	97.35	4.00627e-43		uncultured marine organism	
Mesorhizobium loti MAFF303099 DNA, complete genome	BA000012	78.64	97.35	4.00627e-43	Rhizobiales	Phyllobacteriaceae	Mesorhizobium loti MAFF303099
Devosia sp. A16, complete genome	CP012945	81.48	83.63	1.39833e-42	Rhizobiales	Hyphomicrobiaceae	Devosia sp. A16
Mesorhizobium australicum WSM2073, complete genome	CP003358	81.72	82.3	1.39833e-42	Rhizobiales	Phyllobacteriaceae	Mesorhizobium australicum WSM2073