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Arachnida sp. BOLD:ACL9059

75.5

Arachnida sp. BOLD:ACL9059 voucher BIOUG10983–E03	KR100193	75.5	92.17	1.42334e–29			Arachnida sp. BOLD:ACL9059
Dinobryon pediforme strain LO2_26_KS cytochrome ox	KJ579421	75.25	91.24	1.73398e–28	Chromulinales	Dinobryaceae	Dinobryon pediforme
Dinobryon pediforme strain LO2_36_3 cytochrome oxi	KJ579420	75.25	91.24	1.73398e–28	Chromulinales	Dinobryaceae	Dinobryon pediforme
Dinobryon pediforme strain LO2_36_2 cytochrome oxi	KJ579419	75.25	91.24	1.73398e–28	Chromulinales	Dinobryaceae	Dinobryon pediforme
Candidatus Caedibacter acanthamoebae, complete gen	CP008936	74	92.17	8.98223e–26	Rickettsiales		Candidatus Caedibacter acanthamoebae
Picea glauca clone GQ03405_M22 mRNA sequence	BT113356	76.07	75.12	4.65291e–23	Pinales	Pinaceae	Picea glauca
Alisma plantago–aquatica cytochrome oxidase subuni	DQ630730	75.46	75.12	1.62403e–22	Alismatales	Alismataceae	Alisma plantago–aquatica
Splachnidium rugosum mitochondrial cox1 gene for c	AB776661	75.88	76.96	5.66841e–22	Scytothamnales		Splachnidium rugosum
Copepoda sp. RR–2014 cytochrome oxidase subunit I	KJ433980	75.78	74.19	5.66841e–22			Copepoda sp. RR–2014
Pseudotsuga macrocarpa isolate mach05015 cytochrom	GU457455	75.46	75.12	5.66841e–22		Pinaceae	Pseudotsuga macrocarpa
Pseudotsuga brevifolia isolate bre051001 cytochrom	GU457449	75.46	75.12	5.66841e–22		Pinaceae	Pseudotsuga brevifolia
Dacrycarpus imbricatus cytochrome c oxidase (coxI)	EU161430	75.78	74.19	5.66841e–22	Araucariales	Podocarpaceae	Dacrycarpus imbricatus
Araucaria brasiliensis cytochrome oxidase subunit	EU165027	75.6	76.96	5.66841e–22	Araucariales	Araucariaceae	Araucaria angustifolia
Araucaria bidwillii cytochrome oxidase subunit 1 (EU165026	75.6	76.96	5.66841e–22	Araucariales	Araucariaceae	Araucaria bidwillii
Dacrydium pierrei cytochrome c oxidase subunit I (DQ478772	75.78	74.19	5.66841e–22	Araucariales	Podocarpaceae	Dacrydium elatum
Dacrycarpus imbricatus cytochrome c oxidase subuni	DQ478771	75.78	74.19	5.66841e–22	Araucariales	Podocarpaceae	Dacrycarpus imbricatus
Hyphomicrobium sp. MC1 chromosome, complete genome	FQ859181	72.86	91.24	1.97847e–21	Rhizobiales	Hyphomicrobiaceae	Hyphomicrobium sp. MC1
Saccharina bongardiana voucher Lbong3 cytochrome o	GU097729	81.2	53.92	1.97847e–21	Laminariales	Laminariaceae	Saccharina bongardiana
Saccharina bongardiana voucher Lbong5 cytochrome o	GU097727	81.2	53.92	1.97847e–21	Laminariales	Laminariaceae	Saccharina bongardiana
Microstrobos fitzgeraldii cytochrome c oxidase (co	EU161440	75.15	76.04	1.97847e–21	Araucariales	Podocarpaceae	Pherosphaera fitzgeraldii
Lepidothamnus laxifolius cytochrome c oxidase (cox	EU161434	75.15	76.04	1.97847e–21	Araucariales	Podocarpaceae	Lepidothamnus laxifolius
Methyloceanibacter caenitepidi DNA, complete genom	AP014648	77.3	64.98	6.90553e–21	Rhizobiales		Methyloceanibacter caenitepidi
Araucaria araucana cytochrome oxidase subunit I (c	FJ179546	75	76.96	6.90553e–21	Araucariales	Araucariaceae	Araucaria araucana
Wollemia nobilis cytochrome oxidase subunit 1 (cox	EU165029	77.3	64.98	6.90553e–21	Araucariales	Araucariaceae	Wollemia nobilis
Agathis robusta cytochrome oxidase subunit 1 (coxI	EU165025	77.3	64.98	6.90553e–21	Araucariales	Araucariaceae	Agathis robusta
Agathis alba cytochrome oxidase subunit 1 (coxI) g	EU165023	77.3	64.98	6.90553e–21	Araucariales	Araucariaceae	Agathis alba
Elodea sp. Duvall s.n. cytochrome oxidase subunit	DQ630731	74.85	75.12	6.90553e–21	Alismatales	Hydrocharitaceae	Elodea sp. Duvall s.n.
Rhodopseudomonas palustris BisA53, complete genome	CP000463	78.95	60.83	6.90553e–21	Rhizobiales	Bradyrhizobiaceae	Rhodopseudomonas palustris BisA53
Podocarpus macrophyllus cytochrome c oxidase (coxI	AF020575	75.16	74.19	6.90553e–21	Araucariales	Podocarpaceae	Podocarpus macrophyllus
Agathis australis cytochrome c oxidase (coxI) gene	AF020557	77.3	64.98	6.90553e–21	Araucariales	Araucariaceae	Agathis australis
Cannabis sativa cultivar Sievers Infinity mitochon	KU363807	74.85	75.12	2.41027e–20	Rosales	Cannabaceae	Cannabis sativa
Cannabis sativa mitochondrion, complete genome	KU310670	74.85	75.12	2.41027e–20	Rosales	Cannabaceae	Cannabis sativa
Cannabis sativa voucher Ahrendsen_22 cytochrome c	KT458835	74.85	75.12	2.41027e–20	Rosales	Cannabaceae	Cannabis sativa
Cannabis sativa cultivar Carmagnola mitochondrion,	KR059940	74.85	75.12	2.41027e–20	Rosales	Cannabaceae	Cannabis sativa
Agrobacterium tumefaciens strain Ach5 chromosome c	CP011246	76.35	68.2	2.41027e–20	Rhizobiales	Rhizobiaceae	Agrobacterium tumefaciens
Ochrobactrum anthropi strain OAB chromosome 1, com	CP008820	75.48	71.43	2.41027e–20	Rhizobiales	Brucellaceae	Ochrobactrum anthropi
Agrobacterium tumefaciens LBA4213 (Ach5) circular	CP007225	76.35	68.2	2.41027e–20	Rhizobiales	Rhizobiaceae	Agrobacterium tumefaciens LBA4213 (Ach5)
Asclepias syriaca mitochondrion, complete genome	KF541337	74.85	75.12	2.41027e–20	Gentianales	Apocynaceae	Asclepias syriaca
Gossypium hirsutum isolate D8CMS8518 cytochrome c	KC149545	74.85	75.12	2.41027e–20	Malvales	Malvaceae	Gossypium hirsutum
Gossypium hirsutum isolate 8518 cytochrome c oxida	KC149544	74.85	75.12	2.41027e–20	Malvales	Malvaceae	Gossypium hirsutum
Agrobacterium sp. H13–3 circular chromosome, compl	CP002248	76.35	68.2	2.41027e–20	Rhizobiales	Rhizobiaceae	Agrobacterium sp. H13–3
Larix griffithiana isolate Lar9801 cytochrome oxid	GU457457	74.85	75.12	2.41027e–20	Pinales	Pinaceae	Larix griffithii
Microcachrys tetragona cytochrome c oxidase (coxI)	EU161439	77.14	64.52	2.41027e–20	Araucariales	Podocarpaceae	Microcachrys tetragona
Larix gmelinii var. principis–rupprechtii isolate	EF053147	74.85	75.12	2.41027e–20	Pinales	Pinaceae	Larix gmelinii var. principis–rupprechtii
Asclepias tuberosa cytochrome oxidase subunit I (c	EU281054	74.85	75.12	2.41027e–20	Gentianales	Apocynaceae	Asclepias tuberosa
Humulus lupulus cytochrome oxidase subunit I (coxI	EU281047	74.85	75.12	2.41027e–20	Rosales	Cannabaceae	Humulus lupulus
Ochrobactrum anthropi ATCC 49188 chromosome 1, com	CP000758	75.48	71.43	2.41027e–20	Rhizobiales	Brucellaceae	Ochrobactrum anthropi ATCC 49188
Asparagus officinalis cytochrome oxidase subunit 1	DQ508957	74.85	75.12	2.41027e–20	Asparagales	Asparagaceae	Asparagus officinalis
Goodenia ovata cytochrome oxidase subunit I gene,	AY053575	74.85	75.12	2.41027e–20	Asterales	Goodeniaceae	Goodenia ovata
Hoya sikkimensis cox1 gene (partial), exons 1–2	AJ247588	74.85	75.12	2.41027e–20	Gentianales	Apocynaceae	Hoya lanceolata
Allium sativum cytochrome c oxidase subunit I gene	AF356823	78.2	61.29	2.41027e–20	Asparagales	Amaryllidaceae	Allium sativum
Diospyros virginiana mitochondrial coxI gene, mito	AJ223417	74.85	75.12	2.41027e–20	Ericales	Ebenaceae	Diospyros virginiana
Saccharina japonica isolate C10 NADH dehydrogenase	KT963124	80.34	53.92	8.41266e–20	Laminariales	Laminariaceae	Saccharina japonica
Laminaria sinclairii voucher GWS022049 cytochrome	KJ960264	80.34	53.92	8.41266e–20	Laminariales	Laminariaceae	Laminaria sinclairii
Laminaria sinclairii voucher GWS022027 cytochrome	KJ960246	80.34	53.92	8.41266e–20	Laminariales	Laminariaceae	Laminaria sinclairii
Chordariopsis capensis voucher SAFR–2001 cytochrom	JF796537	79.83	54.84	8.41266e–20	Ectocarpales	Chordariaceae	Chordariopsis capensis
Gagea cossoniana cox1 gene, partial sequence; mito	GQ337045	74.39	75.58	8.41266e–20	Liliales	Liliaceae	Gagea cossoniana
Carpoglossum confluens isolate B327 cytochrome oxi	GU289311	79.83	54.84	8.41266e–20	Fucales	Sargassaceae	Carpoglossum confluens
Carpoglossum confluens isolate B162 cytochrome oxi	GU289290	79.83	54.84	8.41266e–20	Fucales	Sargassaceae	Carpoglossum confluens
Saccharina bongardiana voucher Lbong4 cytochrome o	GU097728	80.34	53.92	8.41266e–20	Laminariales	Laminariaceae	Saccharina bongardiana
Riedelia sp. MVSP–2007 cytochrome oxidase subunit	EU069568	76.76	65.44	8.41266e–20	Zingiberales	Zingiberaceae	Riedelia sp. MVSP–2007
Oryza minuta voucher W1340 mitochondrion, complete	KU176938	74.23	75.12	2.93631e–19	Poales	Poaceae	Oryza minuta
Salix purpurea mitochondrion, complete genome	KU198635	74.23	75.12	2.93631e–19	Malpighiales	Salicaceae	Salix purpurea
Bosea sp. PAMC 26642, complete genome	CP014301	76.22	65.9	2.93631e–19	Rhizobiales	Bradyrhizobiaceae	Bosea sp. PAMC 26642
Salix suchowensis mitochondrion, complete genome	KU056812	74.23	75.12	2.93631e–19	Malpighiales	Salicaceae	Salix suchowensis
Salix interior voucher Ahrendsen_11 cytochrome c o	KT458866	74.23	75.12	2.93631e–19	Malpighiales	Salicaceae	Salix interior
Populus tremula x Populus alba mitochondrion, comp	KT429213	74.23	75.12	2.93631e–19	Malpighiales	Salicaceae	Populus tremula x Populus alba
Oryza sativa Japonica Group DNA, chromosome 12, cu	AP014968	74.23	75.12	2.93631e–19	Poales	Poaceae	Oryza sativa Japonica Group
Oryza sativa Japonica Group DNA, chromosome 9, cul	AP014965	74.23	75.12	2.93631e–19	Poales	Poaceae	Oryza sativa Japonica Group
Populus tremula mitochondrion, complete genome	KT337313	74.23	75.12	2.93631e–19	Malpighiales	Salicaceae	Populus tremula
Ginkgo biloba mitochondrion, complete genome	KM672373	74.23	75.12	2.93631e–19	Ginkgoales	Ginkgoaceae	Ginkgo biloba
Beckmannia syzigachne cytochrome c oxidase subunit	KP852121	74.23	75.12	2.93631e–19	Poales	Poaceae	Beckmannia syzigachne
Salix glauca voucher SALIX389_08_47_UBC_60831 cyto	KM001944	74.23	75.12	2.93631e–19	Malpighiales	Salicaceae	Salix glauca
Salix glauca x Salix brachycarpa voucher SALIX387_	KM001943	74.23	75.12	2.93631e–19	Malpighiales	Salicaceae	Salix glauca x Salix brachycarpa
Salix glauca x Salix brachycarpa voucher SALIX386_	KM001942	74.23	75.12	2.93631e–19	Malpighiales	Salicaceae	Salix glauca x Salix brachycarpa
Salix alaxensis voucher SALIX385_08_78_UBC_162474	KM001941	74.23	75.12	2.93631e–19	Malpighiales	Salicaceae	Salix alaxensis
Salix lucida voucher SALIX326_08_07_GWA_14352 cyto	KM001937	74.23	75.12	2.93631e–19	Malpighiales	Salicaceae	Salix lucida
Salix pseudomonticola voucher SALIX316_08_07_GWA_1	KM001935	74.23	75.12	2.93631e–19	Malpighiales	Salicaceae	Salix pseudomonticola
Salix candida voucher SALIX312_08_07_GWA_14337 cyt	KM001933	74.23	75.12	2.93631e–19	Malpighiales	Salicaceae	Salix candida
Salix sp. C DMP–2014 cytochrome oxidase subunit 1	KM001926	74.23	75.12	2.93631e–19	Malpighiales	Salicaceae	Salix sp. C DMP–2014
Salix nakamurana voucher SALIX196_08_07_UBCBG_2635	KM001925	74.23	75.12	2.93631e–19	Malpighiales	Salicaceae	Salix nakamurana
Salix nivalis voucher SALIX157_08_07_DPQC_0041 cyt	KM001920	74.23	75.12	2.93631e–19	Malpighiales	Salicaceae	Salix nivalis
Salix bebbiana voucher SALIX121_08_07_EM_0628 cyto	KM001918	74.23	75.12	2.93631e–19	Malpighiales	Salicaceae	Salix bebbiana
Amborella trichopoda cytochrome c oxidase subunit	KF798329	74.53	74.19	2.93631e–19	Amborellales	Amborellaceae	Amborella trichopoda
Oryza rufipogon mitochondrial DNA, complete genome	AP012528	74.23	75.12	2.93631e–19	Poales	Poaceae	Oryza rufipogon
Oryza rufipogon mitochondrial DNA, complete genome	AP012527	74.23	75.12	2.93631e–19	Poales	Poaceae	Oryza rufipogon
Lolium perenne mitochondrion, complete genome	JX999996	74.23	75.12	2.93631e–19	Poales	Poaceae	Lolium perenne
Oryza sativa Indica Group mitochondrion, complete	JN861112	74.23	75.12	2.93631e–19	Poales	Poaceae	Oryza sativa Indica Group
Oryza sativa Indica Group cultivar Hassawi mitocho	JN861111	74.23	75.12	2.93631e–19	Poales	Poaceae	Oryza sativa Indica Group
Oryza sativa Indica Group strain WA–CMS mitochondr	JF281154	74.23	75.12	2.93631e–19	Poales	Poaceae	Oryza sativa Indica Group
Oryza sativa Indica Group mitochondrion, complete	JF281153	74.23	75.12	2.93631e–19	Poales	Poaceae	Oryza sativa Indica Group
Streptopus lanceolatus cytochrome oxidase subunit	GQ337051	74.23	75.12	2.93631e–19	Asparagales	Asparagaceae	Streptopus lanceolatus
Scoliopus bigelovii cytochrome oxidase subunit I (GQ337050	74.23	75.12	2.93631e–19	Liliales	Melanthiaceae	Scoliopus bigelovii
Prosartes hookeri cytochrome oxidase subunit I (co	GQ337049	74.23	75.12	2.93631e–19	Liliales	Colchicaceae	Prosartes hookeri
Medeola virginiana cytochrome oxidase subunit I (c	GQ337047	74.23	75.12	2.93631e–19	Liliales	Liliaceae	Medeola virginiana
Lloydia serotina cox1 gene, partial sequence; mito	GQ337046	74.23	75.12	2.93631e–19	Liliales	Liliaceae	Gagea serotina
Calochortus macrocarpus cytochrome oxidase subunit	GQ337041	74.23	75.12	2.93631e–19	Liliales	Liliaceae	Calochortus macrocarpus
Oryza sativa Indica Group mitochondrial DNA, compl	AP011077	74.23	75.12	2.93631e–19	Poales	Poaceae	Oryza sativa Indica Group
Oryza rufipogon mitochondrial DNA, complete genome	AP011076	74.23	75.12	2.93631e–19	Poales	Poaceae	Oryza rufipogon
Salix sitchensis voucher SALIX210_08_07_DPQC_Whist	KM001928	73.01	75.12	4.35787e–17	Malpighiales	Salicaceae	Salix sitchensis