

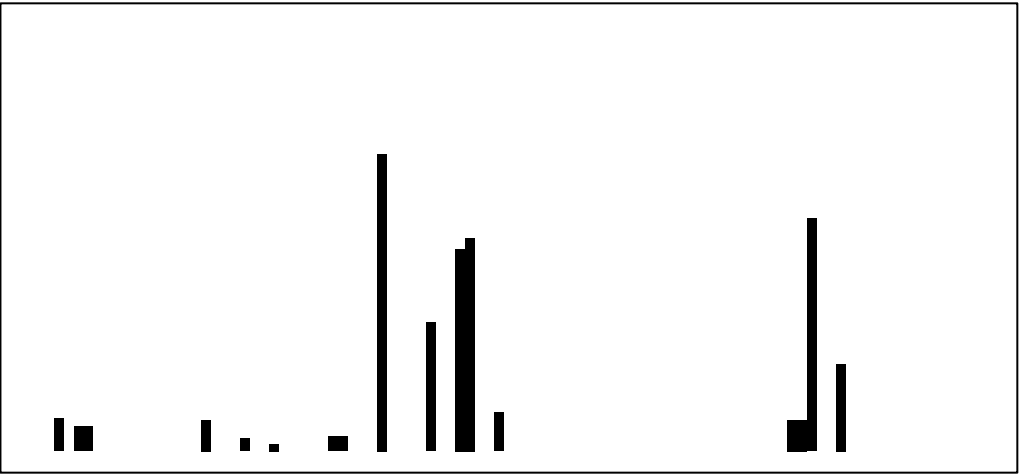
OTU_116.csv

Strongyloides stercoralis

Strongyloididae

Rhabditida

71.01



Strongyloides stercoralis genome assembly S_sterco	LL999055	71.01	87.59	1.62533e-06	Rhabditida	Strongyloididae	Strongyloides stercoralis
Cyprinus carpio genome assembly common carp genome	LN591245	73.61	93.1	1.98006e-05	Cypriniformes	Cyprinidae	Cyprinus carpio
Candidatus Zinderia insecticola CARI, complete gen	CP002161	71.67	82.07	6.9111e-05	Burkholderiales	Oxalobacteraceae	Candidatus Zinderia insecticola CARI
Strongyloides stercoralis genome assembly S_sterco	LL999054	81.54	43.45	0.000241221	Rhabditida	Strongyloididae	Strongyloides stercoralis
Vitis vinifera contig VV78X250204.3, whole genome	AM435003	70.86	96.55	0.000241221	Vitales	Vitaceae	Vitis vinifera
Cucumis melo genomic chromosome, chr_1	LN713255	81.16	44.83	0.000841944	Cucurbitales	Cucurbitaceae	Cucumis melo
Cucumis melo genomic scaffold, anchoredscaffold000	LN681792	81.16	44.83	0.000841944	Cucurbitales	Cucurbitaceae	Cucumis melo
Strongyloides ratti genome assembly S_ratti_ED321	LN609396	76.14	58.62	0.000841944	Rhabditida	Strongyloididae	Strongyloides ratti
Barnettozyma californica strain CBS 252 mitochondr	KC993183	71.43	96.55	0.000841944	Saccharomycetales	Phaffomycetaceae	Barnettozyma californica
Dracunculus medinensis genome assembly D_medinensi	LK978196	69.86	94.48	0.00293867	Spirurida	Dracunculidae	Dracunculus medinensis
Phytophthora alticola isolate P16053 SecY (secY) g	JF770686	79.1	46.21	0.00293867	Peronosporales		Phytophthora alticola
Phytophthora frigida isolate P16059 SecY (secY) ge	JF770489	79.1	46.21	0.00293867	Peronosporales		Phytophthora frigida
Zebrafish DNA sequence from clone CH73-348D8 in li	FQ311917	70.14	97.24	0.00293867	Cypriniformes	Cyprinidae	Danio rerio
Chrysozephyrus smaragdinus 16S ribosomal RNA gene,	GU372446	70.07	97.24	0.00293867	Lepidoptera	Lycaenidae	Chrysozephyrus smaragdinus
Zebrafish DNA sequence from clone CH73-151L10 in l	FP102802	70.14	97.24	0.00293867	Cypriniformes	Cyprinidae	Danio rerio
Candida castellii complete mitochondrial genome, s	FM995165	72.58	84.14	0.00293867	Saccharomycetales	Saccharomycetaceae	Candida castellii
Plasmodium falciparum 3D7 chromosome 6	AL844505	77.03	51.03	0.00293867	Haemosporida	Plasmodiidae	Plasmodium falciparum 3D7
Plasmodium falciparum strain 3D7, chromosome 1	AL844501	71.63	94.48	0.00293867	Haemosporida	Plasmodiidae	Plasmodium falciparum 3D7
Spiroplasma litorale strain TN-1, complete genome	CP012357	81.48	36.55	0.010257	Entomoplasmatales	Spiroplasmataceae	Spiroplasma litorale
Botrytis cinerea B05.10 chromosome 15, complete se	CP009819	74.68	53.79	0.010257	Helotiales	Sclerotiniaceae	Botrytis cinerea B05.10
Ichneumonidae sp. MT-2014 isolate CL118 mitochondr	KM244711	77.46	43.45	0.010257	Hymenoptera	Ichneumonidae	Ichneumonidae sp. MT-2014
Dracunculus medinensis genome assembly D_medinensi	LK978189	70.37	89.66	0.010257	Spirurida	Dracunculidae	Dracunculus medinensis
Strongyloides ratti genome assembly S_ratti_ED321	LN609530	80.6	46.21	0.010257	Rhabditida	Strongyloididae	Strongyloides ratti
Cyprinus carpio genome assembly common carp genome	LN593469	78.79	45.52	0.010257	Cypriniformes	Cyprinidae	Cyprinus carpio
Brassica rapa subsp. pekinensis clone KBrB022F09,	AC240998	76.39	48.28	0.010257	Brassicales	Brassicaceae	Brassica rapa subsp. pekinensis
Candidatus Sulcia muelleri DMIN, complete genome	CP001981	80.36	38.62	0.010257	Flavobacteriales		Candidatus Sulcia muelleri DMIN
Brassica rapa subsp. pekinensis clone KBrH006C14,	AC189554	76.39	48.28	0.010257	Brassicales	Brassicaceae	Brassica rapa subsp. pekinensis
Zebrafish DNA sequence from clone CH211-206N3 in l	CT009597	69.92	88.28	0.010257	Cypriniformes	Cyprinidae	Danio rerio
Zebrafish DNA sequence from clone DKEY-19718 in li	CR388181	68.09	97.24	0.010257	Cypriniformes	Cyprinidae	Danio rerio
F.caudatus 16S rRNA gene, partial	Z93695	70.47	93.1	0.010257	Hymenoptera	Braconidae	Epopus caudatus
Epipremnum aureum chloroplast, complete genome	KR872391	72.39	88.28	0.0358004	Alismatales	Araceae	Epipremnum aureum
Cucumis melo genomic chromosome, chr_6	LN713260	80.7	37.24	0.0358004	Cucurbitales	Cucurbitaceae	Cucumis melo
Cucumis melo genomic scaffold, anchoredscaffold000	LN681851	80.7	37.24	0.0358004	Cucurbitales	Cucurbitaceae	Cucumis melo
Fusarium graminearum chromosome 1, complete genome	HG970332	73.08	70.34	0.0358004	Nectriaceae	Nectriaceae	Fusarium graminearum
Fusarium graminearum chromosome 2, complete genome	HG970333	69.23	96.55	0.0358004	Hypocreales	Nectriaceae	Fusarium graminearum
Protopolystoma xenopodis genome assembly P_xenopod	LM884722	76.62	50.34	0.0358004	Polypisthocotylea	Polystomatidae	Protopolystoma xenopodis
Schistosoma curassoni genome assembly S_curassoni_	LM070743	93.94	22.07	0.0358004	Strigeidida	Schistosomatidae	Schistosoma curassoni
Heligmosomoides polygyrus genome assembly H_bakeri	LL216568	69.5	92.41	0.0358004	Rhabditida	Heligmosomatidae	Heligmosomoides polygyrus
Dracunculus medinensis genome assembly D_medinensi	LK978218	69.06	91.72	0.0358004	Spirurida	Dracunculidae	Dracunculus medinensis
Strongyloides ratti genome assembly S_ratti_ED321	LN609529	70.54	83.45	0.0358004	Rhabditida	Strongyloididae	Strongyloides ratti
Cameraria ohridella mitochondrion, partial genome	KJ508042	75.71	46.9	0.0358004	Lepidoptera	Gracillariidae	Cameraria ohridella
Solanum lycopersicum chromosome ch03, complete gen	HG975515	86.05	29.66	0.0358004	Solanales	Solanaceae	Solanum lycopersicum
Solanum pennellii chromosome ch09, complete genome	HG975448	72.18	86.21	0.0358004	Solanales	Solanaceae	Solanum pennellii
Candidatus Sulcia muelleri PSPU DNA, complete geno	AP013293	73.56	57.93	0.0358004	Flavobacteriales		Candidatus Sulcia muelleri PSPU
Emticicia oligotrophica DSM 17448, complete genome	CP002961	89.47	26.21	0.0358004	Cytophagales	Cytophagaceae	Emticicia oligotrophica DSM 17448
Flavobacterium branchiophilum FL-15, complete geno	FQ859183	90	27.59	0.0358004	Flavobacteriales	Flavobacteriaceae	Flavobacterium branchiophilum FL-15
Plasmodium falciparum 3D7 chromosome 9	AL844508	75.34	48.28	0.0358004	Haemosporida	Plasmodiidae	Plasmodium falciparum 3D7
Plasmodium falciparum 3D7 chromosome 5	AL844504	77.63	51.72	0.0358004	Haemosporida	Plasmodiidae	Plasmodium falciparum 3D7
M.truncatula DNA sequence from clone MTH2-67A13 on	CT962508	81.82	36.55	0.0358004	Fabales	Fabaceae	Medicago truncatula
Homo sapiens 3 BAC RP11-392H18 (Roswell Park Cance	AC009520	79.41	46.21	0.0358004	Primates	Hominidae	Homo sapiens
Zebrafish DNA sequence from clone DKEY-34F16 in li	BX248390	77.27	45.52	0.0358004	Cypriniformes	Cyprinidae	Danio rerio
Cloning vector pDXA-GST	AJ510166	70.08	83.45	0.0358004			Cloning vector pDXA-GST
Cloning vector pDXA-3FLAG	AJ510165	70.08	83.45	0.0358004			Cloning vector pDXA-3FLAG
Cloning vector pDXA-3strep	AJ510164	70.08	83.45	0.0358004			Cloning vector pDXA-3strep
Cloning vector pDXA-MCS-YFP	AJ510163	70.08	83.45	0.0358004			Cloning vector pDXA-MCS-YFP
Cloning vector pDXA-YFP-NotI	AJ510162	70.08	83.45	0.0358004			Cloning vector pDXA-YFP-NotI
Cloning vector pDXA-YFP-MCS	AJ510161	70.08	83.45	0.0358004			Cloning vector pDXA-YFP-MCS
Cloning vector pDXA-CFP-MCS	AJ510160	70.08	83.45	0.0358004			Cloning vector pDXA-CFP-MCS
Cloning vector pDXA-yFP	AJ510159	70.08	83.45	0.0358004			Cloning vector pDXA-yFP
Cloning vector pDXA-CFP	AJ510158	70.08	83.45	0.0358004			Cloning vector pDXA-CFP
Cloning vector pDXA-GFP2, complete sequence	AF269235	70.08	83.45	0.0358004			Cloning vector pDXA-GFP2
Homo sapiens, clone RP11-99A1, complete sequence	AC007673	78.38	48.28	0.0358004	Primates	Hominidae	Homo sapiens
Cloning vector pDXA-FLAG, complete sequence	AF269236	70.08	83.45	0.0358004			Cloning vector pDXA-FLAG
Dictyostelium discoideum actin A-6 gene, 5' flank	M29116	70.08	83.45	0.0358004	Dictyosteliida		Dictyostelium discoideum
Artificial sequences cloning vector DNA pDXD-3H	X85120	70.08	83.45	0.0358004			synthetic construct
Artificial sequences cloning vector DNA pDXD-3C	X85121	70.08	83.45	0.0358004			synthetic construct
Artificial sequences cloning vector DNA pDXA-HY	X85122	70.08	83.45	0.0358004			synthetic construct
Artificial sequences cloning vector DNA pDXA-HC	X85123	70.08	83.45	0.0358004			synthetic construct
Artificial sequences cloning vector DNA pDXA-3H	X85119	70.08	83.45	0.0358004			synthetic construct
Artificial sequences cloning vector DNA pDXA-3C	X85118	70.08	83.45	0.0358004			synthetic construct
Ovis canadensis canadensis isolate 43U chromosome	CP011893	75	49.66	0.124956		Bovidae	Ovis canadensis canadensis
Strongyloides venezuelensis genome assembly S_vene	LM524998	70.77	87.59	0.124956	Rhabditida	Strongyloididae	Strongyloides venezuelensis
Francisella guangzhouensis strain 08HL01032, compl	CP010427	76.67	41.38	0.124956	Thiotrichales	Francisellaceae	Francisella guangzhouensis
Sigalphus bicolor mitochondrion, partial genome	KF385878	75.68	50.34	0.124956	Hymenoptera	Braconidae	Sigalphus bicolor
Pambolus sp. QL-2013 mitochondrion, partial genome	KF385875	69.3	75.86	0.124956	Hymenoptera	Braconidae	Pambolus sp. QL-2013
PREDICTED: Camelina sativa ATP-dependent DNA helic	XM_010481052	78.12	43.45	0.124956	Brassicales	Brassicaceae	Camelina sativa
Strongyloides stercoralis genome assembly S_sterco	LL999073	78.46	44.14	0.124956	Rhabditida	Strongyloididae	Strongyloides stercoralis
Strongyloides stercoralis genome assembly S_sterco	LL999051	70.83	80	0.124956	Rhabditida	Strongyloididae	Strongyloides stercoralis
Brugia pahangi genome assembly B_pahangi_Glasgow ,	LK964287	81.48	37.24	0.124956	Spirurida	Onchocercidae	Brugia pahangi
Brugia timori genome assembly B_timori_Indonesia_v	LK919421	81.48	37.24	0.124956	Spirurida	Onchocercidae	Brugia timori
Strongyloides ratti genome assembly S_ratti_ED321	LN609528	90.91	22.76	0.124956	Rhabditida	Strongyloididae	Strongyloides ratti
Strongyloides ratti genome assembly S_ratti_ED321	LN609402	72.09	86.21	0.124956	Rhabditida	Strongyloididae	Strongyloides ratti
Cyprinus carpio genome assembly common carp genome	LN594801	75.68	50.34	0.124956	Cypriniformes	Cyprinidae	Cyprinus carpio
Cyprinus carpio genome assembly common carp genome	LN591896	84.09	28.97	0.124956	Cypriniformes	Cyprinidae	Cyprinus carpio
Cyprinus carpio genome assembly common carp genome	LN590692	68.84	91.72	0.124956	Cypriniformes	Cyprinidae	Cyprinus carpio
Solanum lycopersicum chromosome ch12, complete gen	HG975524	76.47	45.52	0.124956	Solanales	Solanaceae	Solanum lycopersicum
Solanum pennellii chromosome ch12, complete genome	HG975451	76.47	44.83	0.124956	Solanales	Solanaceae	Solanum pennellii
Solanum pennellii chromosome ch08, complete genome	HG975447	70.87	82.76	0.124956	Solanales	Solanaceae	Solanum pennellii
Homo sapiens glutamate receptor, ionotropic, delta	NG_034113	75	51.03	0.124956	Primates	Hominidae	Homo sapiens
Rapisma zayuanum mitochondrion, complete genome	KF626447	75.34	50.34	0.124956	Neuroptera	Rapismatidae	Rapisma zayuanum
Rapisma xizangense mitochondrion, complete genome	KF626446	75.34	50.34	0.124956	Neuroptera	Rapismatidae	Rapisma xizangense
Fusarium fujikuroi IMI 58289 draft genome, chromos	HF679032	77.78	48.28	0.124956	Hypocreales	Nectriaceae	Fusarium fujikuroi IMI 58289
Phytophthora plurivora isolate P1805 SecY (secY) g	JQ439396	70.29	90.34	0.124956	Peronosporales		Phytophthora plurivora
Phytophthora plurivora isolate P10627 SecY (secY)	JQ439395	70.29	90.34	0.124956	Peronosporales		Phytophthora plurivora
Phytophthora aff. citricola 1 FM-2012 isolate P107	JQ439304	70.29	90.34	0.124956	Peronosporales		Phytophthora aff. citricola 1 FM-2012
Phytophthora aff. citricola 1 FM-2012 isolate P107	JQ439303	70.29	90.34	0.124956	Peronosporales		Phytophthora aff. citricola 1 FM-2012
Phytophthora aff. citricola 1 FM-2012 isolate P107	JQ439302	70.29	90.34	0.124956	Peronosporales		Phytophthora aff. citricola 1 FM-2012
Vitis vinifera contig VV78X177641.5, whole genome	AM440566	70	69.66	0.124956	Vitales	Vitaceae	Vitis vinifera
Ovis canadensis canadensis isolate 43U chromosome	CP011895	76.19	42.07	1.52227		Bovidae	Ovis canadensis canadensis