

>ZB04031934(ZJ-8)-2-M13-

TGTAGTCATATGCTTGTCTCAAAGATTAAGCCATGCACGTCTAAGTACATGCCGACTTAAGGCGAAACCGCGAAT
GGCTCATTAAATCAGTTACGGTTCCTACTGATTCTAACTTCCTACTTGGATAACTGTGGTAATTCTAGAGCTAATAC
ATGCCTCGGGTTCTCAACTGCGTGCCAGGCAACTGGTTGCAGACGAGACGCACTTATTAGACCAAGACCAGCC
CCGTCAGCAATGGCGGGCAATCTGTTGGTGA CTCTGGATAATTATCGCATGACCGCATGGCCTCGTGCCGGCGG
CTAGTACATCAAGTGTCTGCCTTATCAACTGTCGATGGTGGGTTATACGCCACCATGGTTGCAACGGGTAACGG
GGAAT

Description	Max score	Total score	Query cover	E value	Ident	Accession
Uncultured eukaryote partial 18S rRNA gene, clone A2-14	553	553	99%	1e-153	93%	AM409623.1
Paal uncultured eukaryote partial 18S ribosomal RNA, clone RPZ4YC22	540	540	99%	8e-150	93%	FO181430.1
Uncultured eukaryote partial 18S rRNA gene, clone 01DPZ110600090	525	525	99%	2e-145	92%	FN394868.1
Uncultured eukaryote partial 18S rRNA gene, clone 01DPZ110600065	525	525	99%	2e-145	92%	FN394851.1
Derocheilocaris typicus 18S ribosomal RNA gene, complete sequence	316	316	99%	1e-82	82%	L81937.1
Nymphon gracile 18S ribosomal RNA gene, partial sequence	307	307	99%	8e-80	82%	AY446920.1
Nymphon chariotei 18S ribosomal RNA gene, partial sequence	305	305	99%	3e-79	82%	AY446931.1
Nymphon stroemi strain C28 18S ribosomal RNA gene, partial sequence	302	302	99%	4e-78	82%	EU420136.1
Austropallene cornigera 18S ribosomal RNA gene, partial sequence	289	289	99%	3e-74	81%	AY446918.1
Nymphon gracile voucher MNHN-JAA25 18S ribosomal RNA gene, partial sequence	285	285	96%	4e-73	81%	FJ862851.1

>ZB04031934(ZJ-8)-3-M13-

TGTAGTCATATGCTTGTCTCAAAGATTAAGCCATGCACGTCTAAGTACATGCCGACTTAAGGCGAAACCGCGAAT
GGCTCATTAAATCAGTTACGGTTCCTACTGATTCTAACTTCCTACTTGGATAACTGTGGTAATTCTAGAGCTAATAC
ATGCCTCGGGTTCTCAACTGCGCGCCAGGCAACTGGTTGCAGACGAGACGCACTTATTAGACCAAGACCAGCC
CCGTCAGCAATGGCGGGCAATCTGTTGGTGA CTCTGGATAATTATCGCATGACCGCATGGCCTCGTGCCGGCGG
CTAGTACATCAAGTGTCTGCCTTATCAACTGTCGATGGTGGGTTATACGCCACCATGGTTGCAACGGGTAACGG
GGAAT

Description	Max score	Total score	Query cover	E value	Ident	Accession
Uncultured eukaryote partial 18S rRNA gene, clone A2-14	547	547	99%	4e-152	93%	AM409623.1
Paal uncultured eukaryote partial 18S ribosomal RNA, clone RPZ4YC22	540	540	99%	8e-150	93%	FO181430.1
Uncultured eukaryote partial 18S rRNA gene, clone 01DPZ110600090	525	525	99%	2e-145	92%	FN394868.1
Uncultured eukaryote partial 18S rRNA gene, clone 01DPZ110600065	525	525	99%	2e-145	92%	FN394851.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
Derocheilocaris typicus 18S ribosomal RNA gene, complete sequence	316	316	99%	1e-82	82%	L81937.1
Nymphon gracile 18S ribosomal RNA gene, partial sequence	307	307	99%	8e-80	82%	AY446920.1
Nymphon charioti 18S ribosomal RNA gene, partial sequence	305	305	99%	3e-79	82%	AY446931.1
Nymphon stroemi strain C28 18S ribosomal RNA gene, partial sequence	302	302	99%	4e-78	82%	EU420136.1

>ZB04031935(ZJ-9)-1-M13-

TATCCCCGTTACCCGTTGGAGCCATGGTAGACACAGATTCTACCATCGACAGTTGATAAGTCAGGCATTTGAAA
GATAAGTCGTCGGTTCTGGGACCATACGATCTGATGTGTTATCTAGGTTTCATCAAGCATACGCCCAACAAGCCG
GGCGAATGGTTTTGATCTAATAAAAAGCGCCCTTCCGTGAAAAGTCAGGGCTTTGTTGCATGTATTAGCTCTAGAA
TTACCACAGTTGTCCAAAGACAGTCAAGTTTACTCAAGTGAATCAAACTGGTTTACTGAGCCTTTTGGCGTTT
CACTTTAATACAGTCTGTACTGAGACTTGCATGGCTTAAGCTTTGAGACAAGCATATGACTAC

Description	Max score	Total score	Query cover	E value	Ident	Accession
Nabis ferus 18S ribosomal RNA gene, partial sequence	593	593	93%	5e-166	98%	EF487300.1
Nabis brevis 18S ribosomal RNA gene, partial sequence	588	588	90%	3e-164	99%	DQ199630.1
Nabis punctatus mimoferus 18S ribosomal RNA gene, partial sequence	582	582	93%	1e-162	98%	EF487315.1
Nabis ferus 18S ribosomal RNA gene, partial sequence	582	582	90%	1e-162	99%	DQ199629.1
Nabis limbatus 18S ribosomal RNA gene, partial sequence	577	577	90%	5e-161	98%	DQ199631.1
Nabis stenoferus 18S ribosomal RNA gene, partial sequence	575	575	89%	2e-160	99%	GQ258426.1
Nabis flavomarginatus 18S ribosomal RNA gene, partial sequence	571	571	90%	3e-159	98%	DQ199628.1
Nabis biformis 18S ribosomal RNA gene, partial sequence	560	560	90%	6e-156	98%	DQ199633.1
Nabis flavomarginatus 18S ribosomal RNA gene, partial sequence	558	558	89%	2e-155	98%	GQ258424.1

>ZB04031936(ZJ-10)-1-M13-

TGTAGTCATATGCTTGTCTCAAAGATTAAGCCATGCATGTCTAAGTACGCACGGCCGGTACAGTGAAACTGCGA
ATGGCTCATAAATCAGTTATGGTTCCTTTGGTCGCTCGCTCCTCTCTACTTGGATAACTGTGGTAATTCTAGAG
CTAATACATGCCGACGGGCGCTGACCCCTTCGCGGGGGGATGCGTGCATTTATCAGATCAAAACCAACCCGG
TCAGCCTCCTCCCGCCCCGGCCGGGGGCGGGCGCCGGGCTTTGGTGACTCTAGATAACCTCGGGCCGAT
CGCACGCCCCCGTGGCGGCGACGACCCATTGAAACGTCTGCCCTATCAACTTTTCGATGGTAGTCGCTGTGCT
ACCATGGTGACAACGGGTAACGGGAAT

Description	Max score	Total score	Query cover	E value	Ident	Accession
Uncultured eukaryote isolate DGGE gel band 7 18S ribosomal RNA gene, partial sequence	726	726	100%	0.0	99%	KF650051.1
Uncultured eukaryote isolate DGGE gel band JLJ-11-80 18S ribosomal	717	717	99%	0.0	99%	JN846872.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
RNA gene, partial sequence						
Bubalus bubalis 18S ribosomal RNA gene, internal transcribed spacer 1, 5.8S ribosomal RNA gene, internal transcribed spacer 2, and 28S ribosomal RNA gene, complete sequence	717	717	99%	0.0	99%	JN412502.1
Odocoileus virginianus 18S ribosomal RNA gene, partial sequence	717	717	99%	0.0	99%	EU823286.1
Equus caballus 18S ribosomal RNA (RN18S), ribosomal RNA	715	715	98%	0.0	99%	NR_046271.1
PREDICTED: Bos taurus uncharacterized LOC104975904 (LOC104975904), ncRNA	712	712	99%	0.0	99%	XR_815498.1
Bos taurus 18S ribosomal RNA (RN18S1), ribosomal RNA	712	712	99%	0.0	99%	NR_036642.1
Bos taurus 45S ribosomal RNA (RN45S), ribosomal RNA	712	712	99%	0.0	99%	NR_046257.1
Ovis canadensis canadensis isolate 43U chromosome 24 sequence	708	708	99%	0.0	99%	CP011909.1
Budorcas taxicolor 18S ribosomal RNA gene, complete sequence	706	706	99%	0.0	99%	HQ658084.1
Dasypus novemcinctus partial 18S rRNA gene	704	704	98%	0.0	99%	AJ311674.1
Uncultured Chordata clone D0735 45 S small subunit ribosomal RNA gene, partial sequence	702	702	99%	0.0	98%	EU647001.1

>ZB04031937(ZJ-11)-1-M13-

TGTAGTCATATGCTTGTCTCAAAGATTAAGCCATGCATGTGCAAGTATGAACTAATTCGAACTGTGAACTGCGA
ATGGCTCATTAAATCAGTTATAGTTTGTGTTGATGGTACGTGCTACTCGGATAACCGTAGTAATTCTAGAGCTAATA
CGTGCAACAAACCCCGACTTCCGGGAGGGGCGCATTTATTAGATAAAAAGGCTGACGCGGGCTCTGCTCGCTGAT
CCGATGATTCATGATAACTTGACGGATCGCACGGCCCTCGTGCCGCGACACATCATCAAATTTCTGCCCTATC
AACTTTTCGATGGTAGGATAGGGCCTACCATGGTGGCAACGGGTAACGGGGAAT

Description	Max score	Total score	Query cover	E value	Ident	Accession
Sorghum bicolor hypothetical protein (SORBIDRAFT_1205s002020) mRNA, complete cds	630	630	99%	4e-177	99%	XM_002488912.1
Sorghum bicolor hypothetical protein (SORBIDRAFT_1236s002010) mRNA, complete cds	630	630	99%	4e-177	99%	XM_002488909.1
Sorghum bicolor hypothetical protein (SORBIDRAFT_1506s002010) mRNA, complete cds	630	630	99%	4e-177	99%	XM_002488893.1
Saccharum hybrid cultivar R570 clone BAC 039D18 complete sequence	625	8754	99%	2e-175	99%	KF184927.1
Uncultured eukaryote clone SA27 18S ribosomal RNA gene, partial sequence	614	614	99%	4e-172	98%	KC922256.1
Uncultured eukaryote clone SA23 18S ribosomal RNA gene, partial sequence	614	614	99%	4e-172	98%	KC922252.1
Uncultured eukaryote clone CA79 18S ribosomal RNA gene, partial sequence	614	614	99%	4e-172	98%	KC922228.1

>ZB04031938(ZJ-1)-1-M13-

TGTAGTCATATGCTTGTCTCAAAGATTAAGCCATGCATGTCTAAGTATAAAAAGTATTCTATACTTGAACTGCGAA

TAGCTCATTAATCAGTTATAGTTTATTTGATGGTGCCTTACTACATGGATACCCGTAGTAATTCTAGAGCTAATAC
ATGCCAAAAAACCCAACCGCAAGGGCGGGTTGTATTTATTAGATAAAAACCATTACTCGCAAGAGTTTTTGTG
GTGATTCATAATAACTGTTTGAATCGCATGCCGCAAGGGCGGCATAGATCATTCAAATTTCTGCCCTATCAGCTCT
CGACGGTAGTGTAGTGGACTACCGTGGCATCAACGGGTAACGGGGAAT

Description	Max score	Total score	Query cover	E value	Ident	Accession
Uncultured eukaryote clone P3S3-1 e11 isolation-source soil anoxic incubation T70h 18S ribosomal RNA gene, partial sequence	638	638	100%	2e-179	99%	KF356929.1
Uncultured Cercomonas clone EF C09 18S ribosomal RNA gene, partial sequence	636	636	99%	9e-179	99%	KP686487.1
Paracercomonas sp. HFCC 910 18S ribosomal RNA gene, partial sequence	636	636	99%	9e-179	99%	HM536155.1
Soil flagellate AND3 18S ribosomal RNA gene, partial sequence	636	636	99%	9e-179	99%	AY965859.1
Cercomonas sp. SmallSA 18S ribosomal RNA gene, partial sequence	636	636	99%	9e-179	99%	AF534712.1
Paracercomonas sp. CWPL small subunit ribosomal RNA gene, partial sequence	634	634	99%	3e-178	99%	KF589954.1
Uncultured Cercomonas clone EF F11 18S ribosomal RNA gene, partial sequence	630	630	99%	4e-177	99%	KP686498.1
Anoplodactylus pycnosoma 18S ribosomal RNA gene, partial sequence	625	625	99%	2e-175	99%	AY446925.1

>ZB04031939(ZJ-2)-1-M13-

TATCCCCGTTACCCGTTGTAACCATGGCAGGCCAAGACCCTGCCATCGAAAGTTGATAGGGCAGAAATTTGAA
TGAACCATCGCCGGCGCAAGGCCATGCGATTGAGAAGTTATTATGAATCACCAGAGAGCCCCGAAGGGCATT
GGTTTTTAATCTAATAAATACATCCCTTCGTGAGTCGGGATTTTTAGCATGTATTAGCTCTAGAATTACCACGATTA
TCCAAGTAGTAAGGTACTATCAAATAAACGATAACTGATTTAATGAGCCATTTCGCAGTTTCGCTGTATAATTGCTT
ATACTTAGACATGCATGGCTTAATCTTTGAGACAAGCATATGACTAC

Description	Max score	Total score	Query cover	E value	Ident	Accession
Amphisphaeriaceae sp. E00175 18S ribosomal RNA gene, partial sequence	614	614	98%	4e-172	99%	DQ872672.1
Seiridium sp. A9-1 18S ribosomal RNA gene, partial sequence	614	614	98%	4e-172	99%	AF346559.1
Xylariales sp. H15 18S ribosomal RNA gene, partial sequence	612	612	99%	1e-171	99%	DQ310771.1
Xylariales sp. H12 18S ribosomal RNA gene, partial sequence	612	612	99%	1e-171	99%	DQ310768.1
Balen uncultured eukaryote partial 18S ribosomal RNA, clone RBA2YD01	606	606	97%	7e-170	99%	FO181483.1
Pestalospaeria sp. NK101 18S ribosomal RNA gene, partial sequence	603	603	98%	9e-169	99%	HM130668.1
Pestalotiopsis sp. YN-6 18S ribosomal RNA gene, partial sequence	603	603	98%	9e-169	99%	EU375525.1
Muscodor sp. A10-1 18S ribosomal RNA gene, partial sequence	603	603	98%	9e-169	99%	AY049023.1

>ZB04031940(ZJ-3)-1-M13-

TGTAGTCATATGCTTGTCTCAAAGATTAAGCCATGCATGTCTAAGTACTTGCCGAAATAAGGTGAAACCGCGAAT
GGCTCATTAAATCAGTTACGGTTCTATAGATATTGACTATCTACATGGATAACTGTGGTAATTCTAGAGCTAATACA
TGCACAAAAGCCCTAACCTTGC GGGAGGGGCGCATTATTAGAACAAAGACCAATGGGGCTCCTTGTGGGTCCTT
ACGTTGGTGACTCTGGATAACTTCAGCTGATCGCACGGCCTCCGAGCCGGCGACGAATCTTTCAAGTGTCTGCC
TTATCAACTGTTCGATGGTAGGTTATGCGCCTACCATGGTTGCAACGGGTAACGGGGAAT

Description	Max score	Total score	Query cover	E value	Ident	Accession
Alicorhagia environmental sample isolate DGGE gel band 5 18S ribosomal RNA gene, partial sequence	662	662	99%	0.0	100%	KF650049.1
Limulidae environmental sample clone Amb 18S 691 18S ribosomal RNA gene, partial sequence	662	662	99%	0.0	100%	EF023363.1
Uncultured fungus isolate DGGE gel band 10 18S ribosomal RNA gene, partial sequence	658	658	100%	0.0	99%	KF650054.1
Uncultured eukaryote clone 31 isolation-source soil oxic incubation T0h 18S ribosomal RNA gene, partial sequence	658	658	100%	0.0	99%	KF357066.1
Uncultured fungus clone FN4 18S ribosomal RNA gene, partial sequence	658	658	100%	0.0	99%	HQ190186.1
Uncultured eukaryote clone 41 isolation-source soil oxic incubation T0h 18S ribosomal RNA gene, partial sequence	656	656	99%	0.0	99%	KF357077.1
Uncultured fungus clone YSL-F-144 18S ribosomal RNA gene, partial sequence	656	656	99%	0.0	99%	JX003498.1
Uncultured fungus isolate DGGE gel band F36 18S ribosomal RNA gene, partial sequence	656	656	99%	0.0	99%	HM004651.1

>ZB04031941(ZJ-4)-2-M13-

TGTAGTCATATGCTTGTCTCCAGTTGCTAACCTCAAATTTCTCAAACAGTTTCCATATAACACAAGTTTCATAAA
ATGTTTTGCAACCAAAGGTTCTATGGTAAAGTAAGTCTCAGAAACACTCTATACACAATGAAATGCAATTACTT
TTGGAGACATTCTTTGTAATAATTGGCTTATCCCAATGTTTTCAAACATTTGATTTTCAGCACTAATATATGTATC
TATGTGCATATGTATAAATATACTTAAGTGTGTGTATCAGGCGTAGTTCTCCAGAGAAATAGAACCAACGGGTAA
CGGGGAAT

Description	Max score	Total score	Query cover	E value	Ident	Accession
Ovis canadensis canadensis isolate 43U chromosome 15 sequence	436	436	89%	8e-119	95%	CP011900.1

>ZB04031941(ZJ-4)-3-M13-

TGTAGTCATATGCTTGTCTCAAAGATTAAGCCATGCATGTGCAAGTATGAACTAATTCGAACTGTGAAACTGCGA
ATGGCTCATTAAATCAGTTATAGTTTGTGATGGTATGTGCTACTCGGATAACCGTAGTAATTCTAGAGCTAATA
CGTGCATCAAACCCGACTTCCGGGAGGGGCGCATTATTAGATAAAAAGGCTGACGCGGGCTCTGCTCGCTGAT
CCGATGATTCATGATAACTTGACGGATCGCACGGCCCTCGTGCCGCGACGCATCATTCAAATTTCTGCCCTATC
AACTTTGATGGTAGGATAGGGCCTACCATGGTGGCAACGGGTAACGGGGAAT

Description	Max score	Total score	Query cover	E value	Ident	Accession

Description	Max score	Total score	Query cover	E value	Ident	Accession
Saccharum hybrid cultivar R570 clone BAC 039D18 complete sequence	619	8676	99%	9e-174	98%	KF184927.1
Sorghum bicolor hypothetical protein (SORBIDRAFT_1205s002020) mRNA, complete cds	614	614	99%	4e-172	98%	XM_002488912.1
Sorghum bicolor hypothetical protein (SORBIDRAFT_1236s002010) mRNA, complete cds	614	614	99%	4e-172	98%	XM_002488909.1
Sorghum bicolor hypothetical protein (SORBIDRAFT_1506s002010) mRNA, complete cds	614	614	99%	4e-172	98%	XM_002488893.1
Uncultured eukaryote clone SA27 18S ribosomal RNA gene, partial sequence	608	608	99%	2e-170	98%	KC922256.1
Uncultured eukaryote clone SA23 18S ribosomal RNA gene, partial sequence	608	608	99%	2e-170	98%	KC922252.1
Uncultured eukaryote clone CA79 18S ribosomal RNA gene, partial sequence	608	608	99%	2e-170	98%	KC922228.1

>ZB04031942(ZJ-5)-2-M13-

TATCCCCGTTACCCGTTGCAACCATGGTAGGGCGCATAACCGACCATCGACAGTTGATAAGGCAGACACTTGAA
AGATTCATCGCCGGCTCTTAGGCCATGCGATTAGCAAGTTATTCAGAGTCACCACCGTAAGGAGTTCGGTGAA
GAACCCATTGGTCTTGGTCTAATAAATGCGCTTCTTCCATTACGGTCAAGCTTTTGTGCATGTATTAGCTCTAG
AATTACCACAGTTATCCATGTAGATAGTCAACATCTAAGGAACCGTAAGTATTAATGAGCCATTCGCGGTTTC
GCCTTAATACGGCATGTACTTAGACATGCATGGCTTAATCTTTGAGACAAGCATATGACTAC

Description	Max score	Total score	Query cover	E value	Ident	Accession
Xenillus tegeocranus 18S ribosomal RNA gene, partial sequence	593	593	99%	5e-166	96%	AF022042.1
Euzetes globulosus 18S ribosomal RNA gene, partial sequence	582	582	99%	1e-162	96%	AF022030.1
Parhypochothonius aphidinus 18S ribosomal RNA gene, partial sequence	577	577	99%	5e-161	96%	EU432215.1
Eupelops plicatus 18S ribosomal RNA gene, partial sequence	573	573	100%	7e-160	95%	EF091419.2
Eupelops hirtus isolate 07EH 18S small subunit ribosomal RNA gene, partial sequence	573	573	100%	7e-160	95%	EF093783.1
Eupelops hirtus isolate 08EH 18S small subunit ribosomal RNA gene, partial sequence	573	573	100%	7e-160	95%	EF093782.1
Platynothrus peltifer 18S ribosomal RNA gene, partial sequence	571	571	99%	3e-159	95%	EF091422.2
Achipterina coleoprata 18S ribosomal RNA gene, partial sequence	571	571	99%	3e-159	95%	EF091418.2
Allonothrus russeolus 18S ribosomal RNA gene, partial sequence	564	564	99%	4e-157	95%	AF022025.1

>ZB04031942(ZJ-5)-3-M13-

TATCCCCGTTACCCGTTGCAACCATGGTAGGGCGCATAACCGACCATCGACAGTTGATAAGGCAGACACTTGAA
AGATTCATCGCCGGCTCTTAGGCCATGCGATTAGCAAAGTTATTCAGAGTCACCACCGTAAGGAGTTCGGTGAA

GAACCCATTGGTCTTGGTCTAATAAATGCGCTTCTCCATACGGTTCGAAGCTTTTGTGCATGTATTAGCTCTAG
AATTACCACAGTTATCCATGTAGATAGTCAACATCTAAGGAACCGTAACTGATTTAATGAGCCATTCGCGGTTTC
GCCTTAATACGGCATGTACTTAGACATGCATGGCTTAATCTTTGAGACAAGCATATGACTAC

Description	Max score	Total score	Query cover	E value	Ident	Accession
Xenillus tegeocranus 18S ribosomal RNA gene, partial sequence	599	599	99%	1e-167	97%	AF022042.1
Euzetes globulosus 18S ribosomal RNA gene, partial sequence	588	588	99%	3e-164	96%	AF022030.1
Parhypothonius aphidinus 18S ribosomal RNA gene, partial sequence	582	582	99%	1e-162	96%	EU432215.1
Eupelops plicatus 18S ribosomal RNA gene, partial sequence	579	579	100%	2e-161	96%	EF091419.2
Eupelops hirtus isolate 07EH 18S small subunit ribosomal RNA gene, partial sequence	579	579	100%	2e-161	96%	EF093783.1
Eupelops hirtus isolate 08EH 18S small subunit ribosomal RNA gene, partial sequence	579	579	100%	2e-161	96%	EF093782.1
Platynothrus peltifer 18S ribosomal RNA gene, partial sequence	577	577	99%	5e-161	96%	EF091422.2
Achipteria coleoprata 18S ribosomal RNA gene, partial sequence	577	577	99%	5e-161	96%	EF091418.2
Allonothrus russeolus 18S ribosomal RNA gene, partial sequence	569	569	99%	9e-159	95%	AF022025.1

>ZB04031943(ZJ-6)-1-M13-

TGTAGTCATATGCTTGTCTCAAAGATTAAGCCATGCATGTGCAAGTATGAACCAATTTGAACTGTGAAACTGCGA
ATGGCTCATTAAATCAGTTATAGTTTGTGGATGGTACGTGCTACTCGGATAACCGTAGTAATTCTAGAGCTAATA
CGTGCAACAAACCCCGACTTCTGGGAGGGGCGCATTTATTAGATAAAAGGCTGACGCGGGCTCTGCCCGCTGAT
CCGATGATTCATGATAACTCGACGGATCGCACGGCCCTCGTGCCGCGACGCATCATTCAAATTTCTGCCCTATC
AACTTTTCGATGGTAGGATAGGGCCTACCATGGTGGCAACGGGTAACGGGGAAT

Description	Max score	Total score	Query cover	E value	Ident	Accession
Balen uncultured eukaryote partial 18S ribosomal RNA, clone RBA1YC19	630	630	99%	4e-177	99%	FO181533.1
Restionaceae environmental sample clone Elev 18S 537 18S ribosomal RNA gene, partial sequence	630	630	99%	4e-177	99%	EF024189.1
Uncultured soil eukaryote clone L 18S ribosomal RNA gene, partial sequence	625	625	99%	2e-175	99%	JX014283.1
Uncultured marine streptophyte partial 18S rRNA gene, clone BS12_C1	625	625	99%	2e-175	99%	FN598332.1
Uncultured streptophyte clone D0810 21 M small subunit ribosomal RNA gene, partial sequence	625	625	99%	2e-175	99%	EU647131.1
Restionaceae environmental sample clone Elev 18S 1302 18S ribosomal RNA gene, partial sequence	625	625	99%	2e-175	99%	EF024795.1
Uncultured eukaryote clone Amb 18S 6891 18S ribosomal RNA gene, partial sequence	625	625	99%	2e-175	99%	EF024091.1
Restionaceae environmental sample clone Elev 18S 715 18S ribosomal RNA gene, partial sequence	625	625	99%	2e-175	99%	EF024309.1
Uncultured eukaryote gene for 18S rRNA, partial sequence, clone:	623	623	99%	7e-175	99%	AB222295.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
d0-Band L-TrP+B-Lower						
Lolium multiflorum 18S ribosomal RNA gene, partial sequence	623	623	99%	7e-175	99%	AY846367.1

>ZB04031944(ZJ-7)-1-M13

TATCCCCCGTTACCCGTTGCCACCATGGTAAGCATATCACTTACCATCGACAGTTGATAGGGCACACACTTGAAA
GATACGTCGCCGGCACCAGGCCATGCGATCAGCTCGAAGTTATCCAGAGTCACCAAACGTACGGACCCGCGAA
GGCCCGATTGGTTTTGATCTAATAAACGCGCTCTTTCCAAATCCGGCCGCCACCCGAGAGCAACGACCCGCCG
GGTCGGAGCTTGCTTGCATGTATTAGCTCTAGAATTACCACAGTTATCCAAGTAGGATTGTACAATCTAATAAATC
ATGGGTGGCCTAATGAGCCATTCGCAGCTTCACCGTGTAAGGTCTGTGCTTAGACATGCATGGCTTAATCTTTG
AGACAAGCATATGACTACA

Description	Max score	Total score	Query cover	E value	Ident	Accession
Uncultured fungus isolate DGGE gel band f19 18S ribosomal RNA gene, partial sequence	704	704	99%	0.0	99%	KJ425571.1
Uncultured fungus isolate DGGE gel band 12 18S ribosomal RNA gene, partial sequence	699	699	99%	0.0	99%	KF650056.1
Uncultured fungus isolate DGGE gel band 1-1 18S ribosomal RNA gene, partial sequence	654	654	95%	0.0	98%	KP059035.1
Uncultured fungus isolate DGGE gel band 16D 18S ribosomal RNA gene, partial sequence	636	636	90%	1e-178	99%	JN583491.1
Uncultured fungus isolate DGGE gel band 49D 18S ribosomal RNA gene, partial sequence	625	625	89%	2e-175	99%	JN583521.1
Uncultured fungus isolate DGGE gel band 5 18S ribosomal RNA gene, partial sequence	562	562	99%	2e-156	93%	FJ608623.1
Enchytraeus environmental sample isolate DGGE gel band S2-10 18S ribosomal RNA gene, partial sequence	551	551	99%	4e-153	92%	GQ995691.1
Enchytraeus albidus 18S ribosomal RNA gene, partial sequence	534	534	99%	4e-148	92%	GU453340.1
Enchytraeus sp. 'Aguinaldo, 1997' 18S ribosomal RNA gene, complete sequence	529	529	99%	2e-146	92%	U95948.1
Enchytraeus crypticus isolate CE2183 18S ribosomal RNA gene, partial sequence	527	527	99%	6e-146	92%	GU901874.1

>ZB04031945(ZJ-12)-2-M13-

TATCCCCCGTTACCCGTTGTACCATGGTAGGCACAGCGACTACCATCGAAAAGTTGATAGGGCAGACGTTTCGAA
TGGGTCTCGCCGCCACGGGGGGCGTGCGATCGGCCCGAGGTTATCTAGAGTCACCAAAGCCGCCGGCGCCCCG
CCCCCGGCCGGGGCCGGGAGGAGGCTGACCGGGTTGGTTTTGATCTGATAAATGCACGCATCCCCCGCGGA
AGGGGGTCAGCGCCCGTCGGCATGTATTAGCTCTAGAATTACCACAGTTATCCAAGTAGGAGAGGAGCGAGCG
ACCAAAGGAACCATAACTGATTAATGAGCCATTCGCAGTTTCACTGTACCGGCCGTGCGTACTTAGACATGCAT
GGCTTAATCTTTGAGACAAGCATATGACTAC

Description	Max score	Total score	Query cover	E value	Ident	Accession
Uncultured eukaryote isolate DGGE gel band 7 18S ribosomal RNA gene, partial sequence	725	725	99%	0.0	99%	KF650051.1
Uncultured eukaryote isolate DGGE gel band JLJ-11-80 18S ribosomal RNA gene, partial sequence	717	717	99%	0.0	99%	JN846872.1
Bubalus bubalis 18S ribosomal RNA gene, internal transcribed spacer 1, 5.8S ribosomal RNA gene, internal transcribed spacer 2, and 28S ribosomal RNA gene, complete sequence	717	717	99%	0.0	99%	JN412502.1
Odocoileus virginianus 18S ribosomal RNA gene, partial sequence	717	717	99%	0.0	99%	EU823286.1
Equus caballus 18S ribosomal RNA (RN18S), ribosomal RNA	715	715	98%	0.0	99%	NR_046271.1
PREDICTED: Bos taurus uncharacterized LOC104975904 (LOC104975904), ncRNA	712	712	99%	0.0	99%	XR_815498.1
Bos taurus 18S ribosomal RNA (RN18S1), ribosomal RNA	712	712	99%	0.0	99%	NR_036642.1
Bos taurus 45S ribosomal RNA (RN45S), ribosomal RNA	712	712	99%	0.0	99%	NR_046257.1

>ZB04031945(ZJ-12)-3-M13-

TATCCCCGTTACCCGTTGCCACCATGGTAGGCCACTATCCTACCATCGAAAGTTGATAGGGCAGAAATTTGAAT
GAACCATCGCCGCGCAAGGCCATGCTATTCGAGAAGTTATTATGAATCACCAAGAAGCCCCGAAGGGCATTGG
TTTTTTATCTAATAAATACACCCCTTCCGAAGTCGAGGTTTTTAGCATGTATTAGCTCTAGAATTACCACAGGTAT
CCATGTAGTAAGGTACTATCAAATAAGCGATAACTGATTTAATGAGCCATTCGCAGTTTCACCGTATAGATTGCTT
ATACTCAGACATGCATGGCTTAATCTTTGAGACAAGCATATGACTAC

Description	Max score	Total score	Query cover	E value	Ident	Accession
Malbranchea cinnamomea strain CBS 343.55 small subunit ribosomal RNA gene, partial sequence	614	614	99%	4e-172	99%	JQ067912.1
Malbranchea cinnamomea strain Zhei20 18S ribosomal RNA gene, partial sequence	608	608	99%	2e-170	98%	JX268593.1
Uncultured fungus clone SIP Fungi M2 05 18S ribosomal RNA gene, partial sequence	603	603	99%	9e-169	98%	HM475189.1
Neocarpenteles acanthosporus gene for 18S rRNA, partial sequence, strain:IFO9490	603	603	99%	9e-169	98%	AB002075.1
Blastomyces dermatitidis 18S ribosomal RNA	603	603	99%	9e-169	98%	M63096.1
Blastomyces dermatitidis small subunit ribosomal RNA gene sequence	603	603	99%	9e-169	98%	M55624.1
Aphanoascus terreus strain NBRC 32655 18S ribosomal RNA (SSU) gene, partial sequence	599	599	99%	1e-167	98%	JN941596.1

>ZB04031946(ZJ-13)-1-M13-

TGTAGTCATATGCTTGTCTCAAAGATTAAGCCATGCATGTCTAAGTACGCACGGCCGGTACAGTGAACTGCGA
ATGGCTCATTAAATCAGTTATGGTTCCTTTGGTCGCTCGCTCCTCTCCTACTTGGATAACTGTGGTAATTCTAGAG
CTAATACATGCCGACGGGCGCTGACCCCTTCGCGGGGGGATGCGTGCATTTATCAGATCAAACCAACCCGG
TCAGCTCCTCCCGCCCCGGCCGGGGGGCGGGCGCCGGCGGCTTTGGTACTCTAGATAACCTCGGGCCGAT

CGCACGCCCCCGTGGCGGCGACGCCATTTCGAACGTCTGCCCTATCAACTTTTCGATGGTAGTCGCTGTGCCT
ACCATGGTAACAACGGGTAACGGGGAAT

Description	Max score	Total score	Query cover	E value	Ident	Accession
Uncultured eukaryote isolate DGGE gel band 7 18S ribosomal RNA gene, partial sequence	721	721	100%	0.0	99%	KF650051.1
Uncultured eukaryote isolate DGGE gel band JLJ-11-80 18S ribosomal RNA gene, partial sequence	712	712	99%	0.0	99%	JN846872.1
Bubalus bubalis 18S ribosomal RNA gene, internal transcribed spacer 1, 5.8S ribosomal RNA gene, internal transcribed spacer 2, and 28S ribosomal RNA gene, complete sequence	712	712	99%	0.0	99%	JN412502.1
Odocoileus virginianus 18S ribosomal RNA gene, partial sequence	712	712	99%	0.0	99%	EU823286.1
Equus caballus 18S ribosomal RNA (RN18S), ribosomal RNA	710	710	98%	0.0	99%	NR_046271.1
PREDICTED: Bos taurus uncharacterized LOC104975904 (LOC104975904), ncRNA	706	706	99%	0.0	99%	XR_815498.1
Bos taurus 18S ribosomal RNA (RN18S1), ribosomal RNA	706	706	99%	0.0	99%	NR_036642.1
Bos taurus 45S ribosomal RNA (RN45S), ribosomal RNA	706	706	99%	0.0	99%	NR_046257.1

>ZB04031947(ZJ-14)-1-M13-

TGTAGTCATATGCTTGTCTCAAAGATTAAGCCATGCATGTCTAAGTGCGCACGGCCGGTACAGTGAAACTGCGA
ATGGCTCATTAAATCAGTTATGGTTCCCTTGGTCGCTCGCTCCTCTCCTACTTGGATAACTGTGGTAATTCTAGAG
CTAATACATGCCGACGGGCGCTGACCCCTTCGCGGGGGGATGCGTGCATTTATCAGATCAAACCAACCCGG
TCAGCCTCCTCCCGGCCCGGCCGGGGGGCGGGCGCCGGCGGCTTTGGTGACTCTAGATAACCTCGGGCCGAT
CGCACGCCCCCGTGGCGGCGACGCCATTTCGAACGTCTGCCCTATCAACTTTTCGATGGTAGTCGCTGTGCCT
ACCATGGTGACAACGGGTAACGGGGAAT

Description	Max score	Total score	Query cover	E value	Ident	Accession
Uncultured eukaryote isolate DGGE gel band 7 18S ribosomal RNA gene, partial sequence	721	721	100%	0.0	99%	KF650051.1
Uncultured eukaryote isolate DGGE gel band JLJ-11-80 18S ribosomal RNA gene, partial sequence	712	712	99%	0.0	99%	JN846872.1
Bubalus bubalis 18S ribosomal RNA gene, internal transcribed spacer 1, 5.8S ribosomal RNA gene, internal transcribed spacer 2, and 28S ribosomal RNA gene, complete sequence	712	712	99%	0.0	99%	JN412502.1
Odocoileus virginianus 18S ribosomal RNA gene, partial sequence	712	712	99%	0.0	99%	EU823286.1
Equus caballus 18S ribosomal RNA (RN18S), ribosomal RNA	710	710	98%	0.0	99%	NR_046271.1
PREDICTED: Bos taurus uncharacterized LOC104975904 (LOC104975904), ncRNA	706	706	99%	0.0	99%	XR_815498.1
Bos taurus 18S ribosomal RNA (RN18S1), ribosomal RNA	706	706	99%	0.0	99%	NR_036642.1
Bos taurus 45S ribosomal RNA (RN45S), ribosomal RNA	706	706	99%	0.0	99%	NR_046257.1

>ZB04031948(ZJ-15)-1-M13-

TATTCCCCGTTACCCGTTGTCACCATGGTAGGCACAGCGACTACCATCGAAAGTTGATAGGGCGGACGTTTCGAA

TGGGTCGTCGCCACGGGGGGCGTGCGATCGCCCCGAGGTTATCTAGAGTCACCAAAGCCGCGGCCCGCC
CCCCCGGCCGGGGCCGGGAGGAGGCTGACCGGGTTGGTTTTGATCTGATAAATGCACGCATCCCCCGCGA
AGGGGGTCAGCGCCCCGTCGGCATGTATTAGCTCTAGAATTACCACAGTTATCCAAGTAGGAGAGGAGCGAGCG
ACCAAAGGAACCATAACTGATTTAATGAGCCATTTCGAGTTTCACTGTACCGGCCGTGCGTACTTACACATGCAT
GGCTTAATCTTTGAGACAAGCATATGACTAC

Description	Max score	Total score	Query cover	E value	Ident	Accession
Uncultured eukaryote isolate DGGE gel band 7 18S ribosomal RNA gene, partial sequence	713	713	99%	0.0	99%	KF650051.1
Uncultured eukaryote isolate DGGE gel band JLJ-11-80 18S ribosomal RNA gene, partial sequence	706	706	99%	0.0	99%	JN846872.1
Bubalus bubalis 18S ribosomal RNA gene, internal transcribed spacer 1, 5.8S ribosomal RNA gene, internal transcribed spacer 2, and 28S ribosomal RNA gene, complete sequence	706	706	99%	0.0	99%	JN412502.1
Odocoileus virginianus 18S ribosomal RNA gene, partial sequence	706	706	99%	0.0	99%	EU823286.1
Equus caballus 18S ribosomal RNA (RN18S), ribosomal RNA	704	704	98%	0.0	99%	NR_046271.1
PREDICTED: Bos taurus uncharacterized LOC104975904 (LOC104975904), ncRNA	701	701	99%	0.0	98%	XR_815498.1
Bos taurus 18S ribosomal RNA (RN18S1), ribosomal RNA	701	701	99%	0.0	98%	NR_036642.1
Bos taurus 45S ribosomal RNA (RN45S), ribosomal RNA	701	701	99%	0.0	98%	NR_046257.1
Ovis canadensis canadensis isolate 43U chromosome 24 sequence	697	697	99%	0.0	98%	CP011909.1
Budorcas taxicolor 18S ribosomal RNA gene, complete sequence	695	695	99%	0.0	98%	HQ658084.1