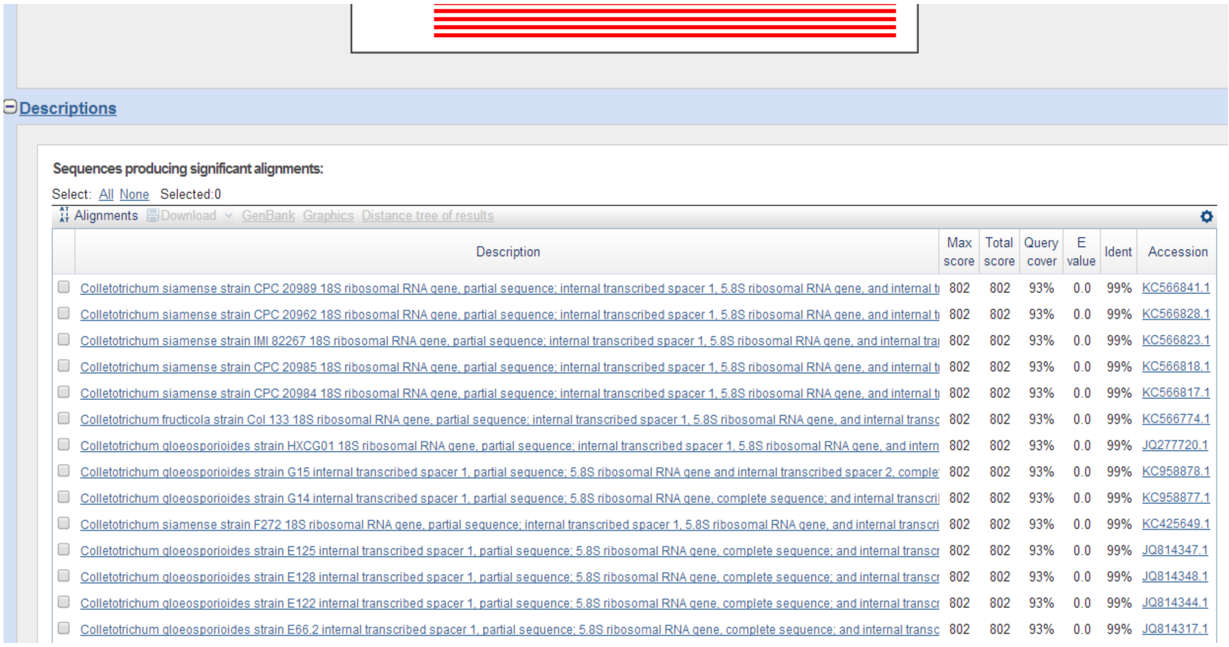
Sequence Similarity Blast Search

1. PBL2



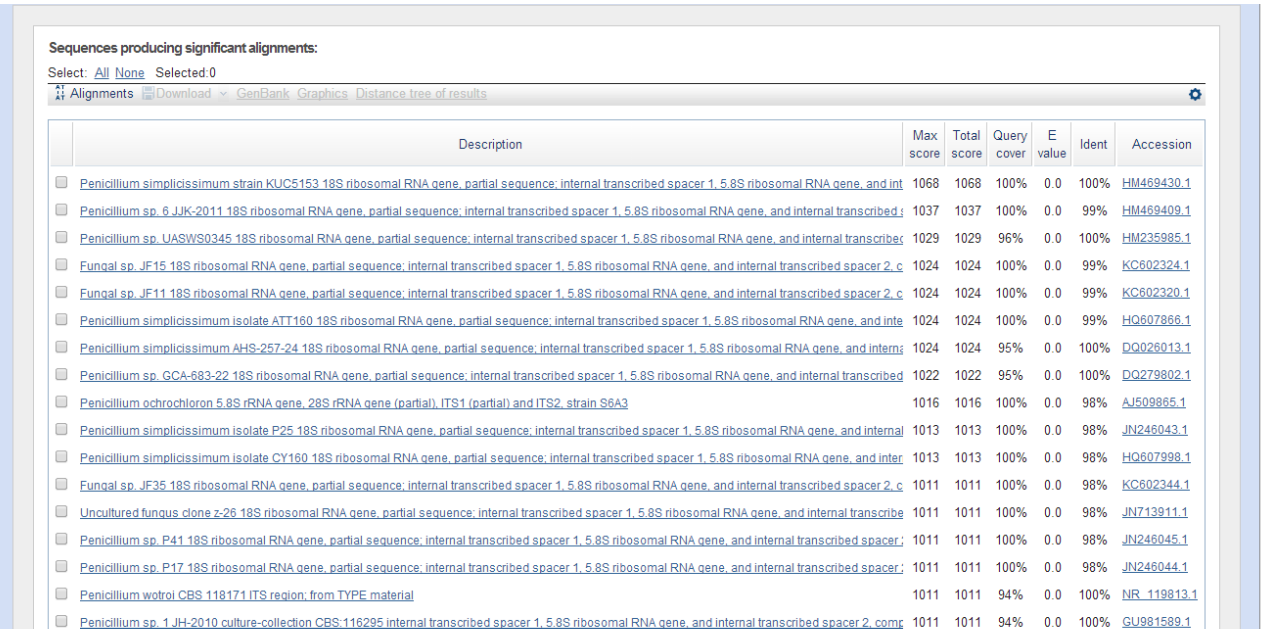
Descriptions

Sequences producing significant alignments:

Select: All None Selected:0

	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	Colletotrichum siamense strain CPC 20989 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal t	802	802	93%	0.0	99%	KC566841.1
☐	Colletotrichum siamense strain CPC 20962 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal t	802	802	93%	0.0	99%	KC566828.1
☐	Colletotrichum siamense strain IMI 82267 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal tra	802	802	93%	0.0	99%	KC566823.1
☐	Colletotrichum siamense strain CPC 20985 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal t	802	802	93%	0.0	99%	KC566818.1
☐	Colletotrichum siamense strain CPC 20984 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal t	802	802	93%	0.0	99%	KC566817.1
☐	Colletotrichum fructicola strain Col 133 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transc	802	802	93%	0.0	99%	KC566774.1
☐	Colletotrichum gloeosporioides strain HXCG01 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and intern	802	802	93%	0.0	99%	JQ277720.1
☐	Colletotrichum gloeosporioides strain G15 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene and internal transcribed spacer 2, comple	802	802	93%	0.0	99%	KC958878.1
☐	Colletotrichum gloeosporioides strain G14 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcri	802	802	93%	0.0	99%	KC958877.1
☐	Colletotrichum siamense strain F272 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcri	802	802	93%	0.0	99%	KC425649.1
☐	Colletotrichum gloeosporioides strain E125 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcr	802	802	93%	0.0	99%	JQ814347.1
☐	Colletotrichum gloeosporioides strain E128 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcr	802	802	93%	0.0	99%	JQ814348.1
☐	Colletotrichum gloeosporioides strain E122 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcr	802	802	93%	0.0	99%	JQ814344.1
☐	Colletotrichum gloeosporioides strain E66.2 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transc	802	802	93%	0.0	99%	JQ814317.1

2. PBL3

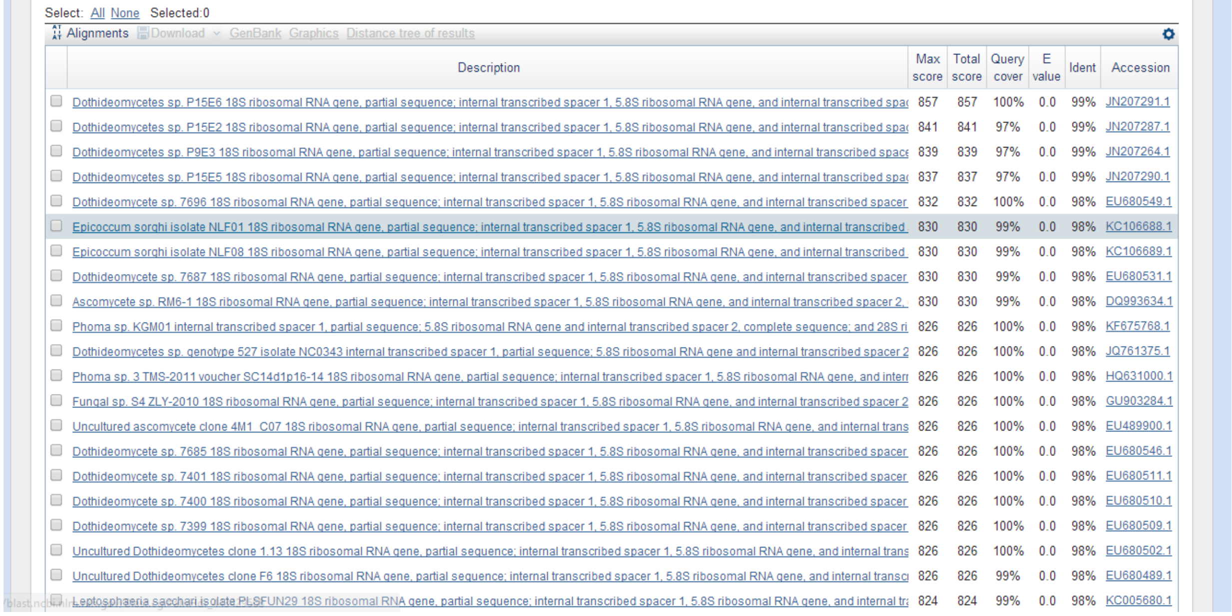


Sequences producing significant alignments:

Select: All None Selected:0

	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	Penicillium simplicissimum strain KUC5153 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and int	1068	1068	100%	0.0	100%	HM469430.1
☐	Penicillium sp. 6 JJK-2011 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed	1037	1037	100%	0.0	99%	HM469409.1
☐	Penicillium sp. UASWS0345 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribe	1029	1029	96%	0.0	100%	HM235985.1
☐	Fungal sp. JF15 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, c	1024	1024	100%	0.0	99%	KC602324.1
☐	Fungal sp. JF11 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, c	1024	1024	100%	0.0	99%	KC602320.1
☐	Penicillium simplicissimum isolate ATT160 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and inte	1024	1024	100%	0.0	99%	HQ607866.1
☐	Penicillium simplicissimum AHS-257-24 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and interna	1024	1024	95%	0.0	100%	DQ026013.1
☐	Penicillium sp. GCA-683-22 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed	1022	1022	95%	0.0	100%	DQ279802.1
☐	Penicillium ochrochloron 5.8S rRNA gene, 28S rRNA gene (partial), ITS1 (partial) and ITS2, strain S6A3	1016	1016	100%	0.0	98%	AJ509865.1
☐	Penicillium simplicissimum isolate P25 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal	1013	1013	100%	0.0	98%	JN246043.1
☐	Penicillium simplicissimum isolate CY160 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and inter	1013	1013	100%	0.0	98%	HQ607998.1
☐	Fungal sp. JF35 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, c	1011	1011	100%	0.0	98%	KC602344.1
☐	Uncultured fungus clone z-26 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribe	1011	1011	100%	0.0	98%	JN713911.1
☐	Penicillium sp. P41 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer	1011	1011	100%	0.0	98%	JN246045.1
☐	Penicillium sp. P17 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer	1011	1011	100%	0.0	98%	JN246044.1
☐	Penicillium wotroi CBS 118171 ITS region; from TYPE material	1011	1011	94%	0.0	100%	NR_119813.1
☐	Penicillium sp. 1 JH-2010 culture-collection CBS:116295 internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, comp	1011	1011	94%	0.0	100%	GU981589.1

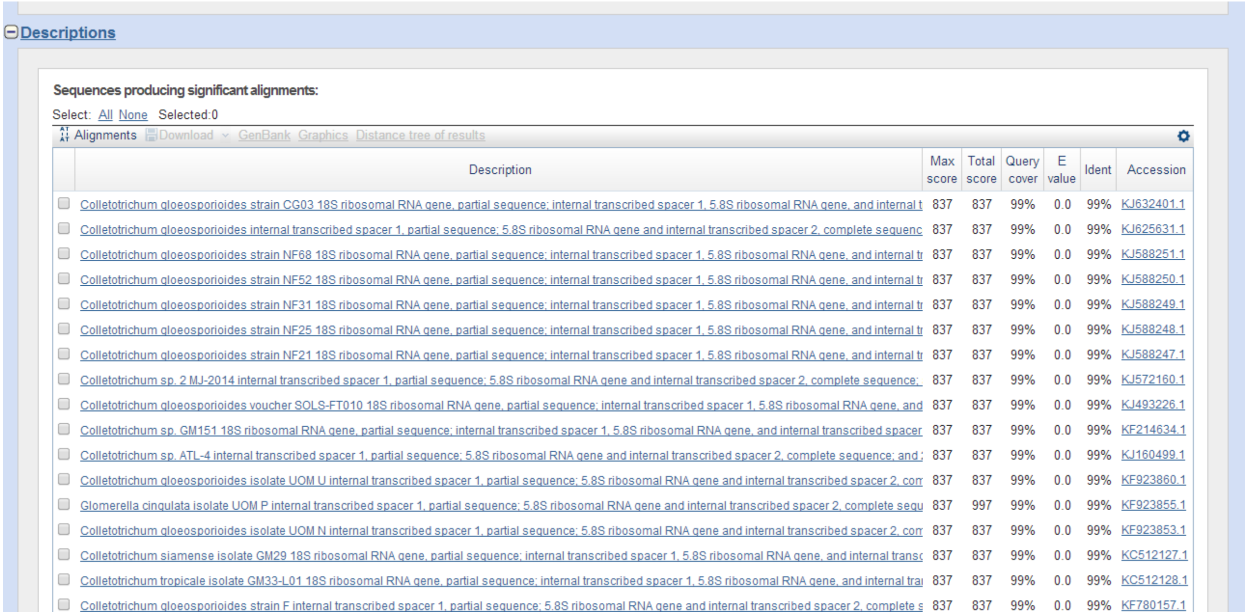
3. PBS1



Select: All None Selected:0

	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	Dothideomycetes sp. P15E6 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spa	857	857	100%	0.0	99%	JN207291.1
☐	Dothideomycetes sp. P15E2 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spa	841	841	97%	0.0	99%	JN207287.1
☐	Dothideomycetes sp. P9E3 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed space	839	839	97%	0.0	99%	JN207264.1
☐	Dothideomycetes sp. P15E5 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spa	837	837	97%	0.0	99%	JN207290.1
☐	Dothideomycete sp. 7696 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer	832	832	100%	0.0	98%	EU680549.1
☐	Epicoccum sorghi isolate NLF01 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed	830	830	99%	0.0	98%	KC106688.1
☐	Epicoccum sorghi isolate NLF08 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed	830	830	99%	0.0	98%	KC106689.1
☐	Dothideomycete sp. 7687 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer	830	830	99%	0.0	98%	EU680531.1
☐	Ascomycete sp. RM6-1 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2,	830	830	99%	0.0	98%	DQ993634.1
☐	Phoma sp. KGM01 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene and internal transcribed spacer 2, complete sequence; and 28S ri	826	826	100%	0.0	98%	KF675768.1
☐	Dothideomycetes sp. genotype 527 isolate NC0343 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene and internal transcribed spacer 2	826	826	100%	0.0	98%	JQ761375.1
☐	Phoma sp. 3 TMS-2011 voucher SC14d1p16-14 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and interr	826	826	100%	0.0	98%	HQ631000.1
☐	Fungal sp. S4 ZLY-2010 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2	826	826	100%	0.0	98%	GU903284.1
☐	Uncultured ascomycete clone 4M1_C07 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal trans	826	826	100%	0.0	98%	EU489900.1
☐	Dothideomycete sp. 7685 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer	826	826	100%	0.0	98%	EU680546.1
☐	Dothideomycete sp. 7401 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer	826	826	100%	0.0	98%	EU680511.1
☐	Dothideomycete sp. 7400 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer	826	826	100%	0.0	98%	EU680510.1
☐	Dothideomycete sp. 7399 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer	826	826	100%	0.0	98%	EU680509.1
☐	Uncultured Dothideomycetes clone 1.13 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal trans	826	826	100%	0.0	98%	EU680502.1
☐	Uncultured Dothideomycetes clone F6 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transci	826	826	99%	0.0	98%	EU680489.1
☐	Leptosphaeria sacchari isolate PLSFUN29 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal tra	824	824	99%	0.0	98%	KC005680.1

4. PBL4



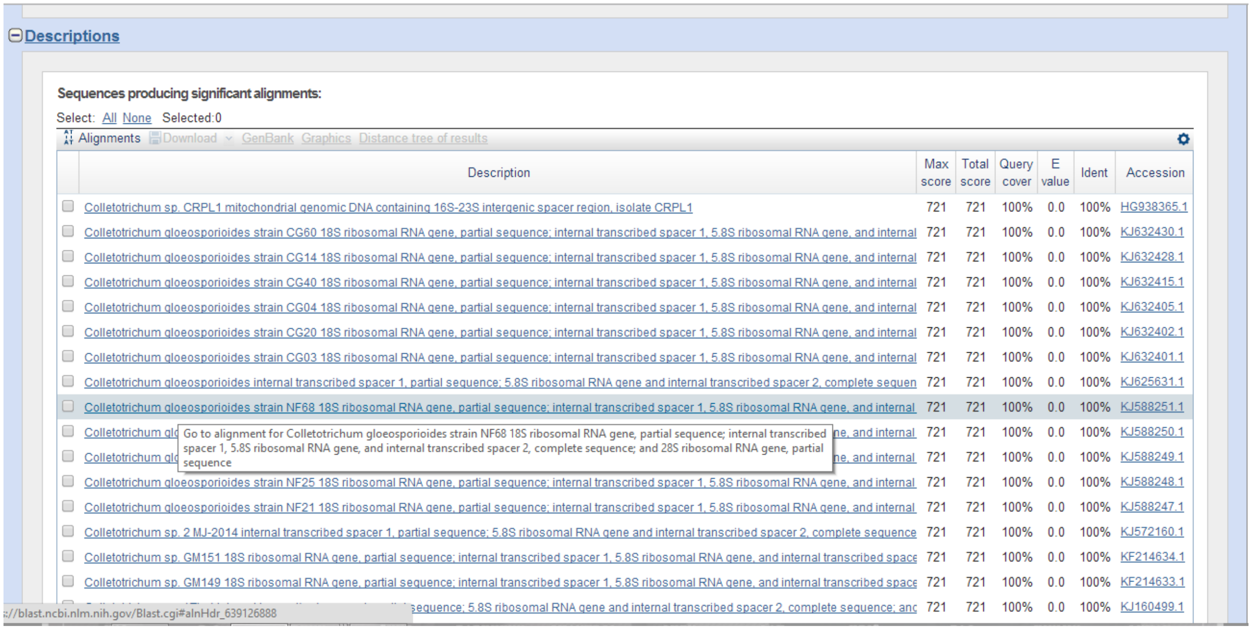
Descriptions

Sequences producing significant alignments:

Select: All None Selected:0

	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	Colletotrichum gloeosporioides strain CG03 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal t	837	837	99%	0.0	99%	KJ632401.1
☐	Colletotrichum gloeosporioides internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene and internal transcribed spacer 2, complete sequenc	837	837	99%	0.0	99%	KJ625631.1
☐	Colletotrichum gloeosporioides strain NF68 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal tr	837	837	99%	0.0	99%	KJ588251.1
☐	Colletotrichum gloeosporioides strain NF52 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal tr	837	837	99%	0.0	99%	KJ588250.1
☐	Colletotrichum gloeosporioides strain NF31 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal tr	837	837	99%	0.0	99%	KJ588249.1
☐	Colletotrichum gloeosporioides strain NF25 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal tr	837	837	99%	0.0	99%	KJ588248.1
☐	Colletotrichum gloeosporioides strain NF21 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal tr	837	837	99%	0.0	99%	KJ588247.1
☐	Colletotrichum sp. 2 MJ-2014 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene and internal transcribed spacer 2, complete sequence;	837	837	99%	0.0	99%	KJ572160.1
☐	Colletotrichum gloeosporioides voucher SOLS-FT010 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and	837	837	99%	0.0	99%	KJ493226.1
☐	Colletotrichum sp. GM151 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer	837	837	99%	0.0	99%	KF214634.1
☐	Colletotrichum sp. ATL-4 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene and internal transcribed spacer 2, complete sequence; and :	837	837	99%	0.0	99%	KJ160499.1
☐	Colletotrichum gloeosporioides isolate UOM U internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene and internal transcribed spacer 2, con	837	837	99%	0.0	99%	KF923860.1
☐	Glomerella cingulata isolate UOM P internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene and internal transcribed spacer 2, complete sequ	837	997	99%	0.0	99%	KF923855.1
☐	Colletotrichum gloeosporioides isolate UOM N internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene and internal transcribed spacer 2, con	837	837	99%	0.0	99%	KF923853.1
☐	Colletotrichum siamense isolate GM29 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transc	837	837	99%	0.0	99%	KC512127.1
☐	Colletotrichum tropicale isolate GM33-L01 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal tra	837	837	99%	0.0	99%	KC512128.1
☐	Colletotrichum gloeosporioides strain F internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene and internal transcribed spacer 2, complete s	837	837	99%	0.0	99%	KF780157.1

5. PBL5



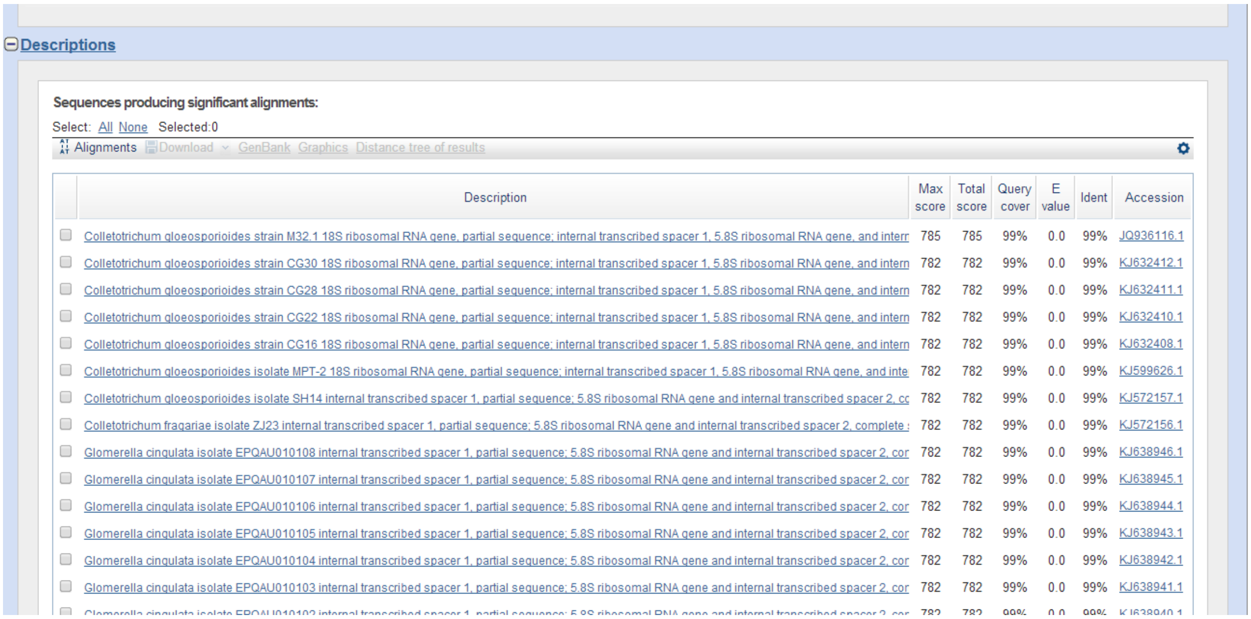
Sequences producing significant alignments:

	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	Colletotrichum sp. CRPL1 mitochondrial genomic DNA containing 16S-23S intergenic spacer region, isolate CRPL1	721	721	100%	0.0	100%	HG938365.1
☐	Colletotrichum gloeosporioides strain CG60 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal	721	721	100%	0.0	100%	KJ632430.1
☐	Colletotrichum gloeosporioides strain CG14 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal	721	721	100%	0.0	100%	KJ632428.1
☐	Colletotrichum gloeosporioides strain CG40 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal	721	721	100%	0.0	100%	KJ632415.1
☐	Colletotrichum gloeosporioides strain CG04 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal	721	721	100%	0.0	100%	KJ632405.1
☐	Colletotrichum gloeosporioides strain CG20 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal	721	721	100%	0.0	100%	KJ632402.1
☐	Colletotrichum gloeosporioides strain CG03 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal	721	721	100%	0.0	100%	KJ632401.1
☐	Colletotrichum gloeosporioides internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene and internal transcribed spacer 2, complete sequen	721	721	100%	0.0	100%	KJ625631.1
☐	Colletotrichum gloeosporioides strain NF68 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal	721	721	100%	0.0	100%	KJ588251.1
☐	Colletotrichum glo … ne, and internal	721	721	100%	0.0	100%	KJ588250.1
☐	Colletotrichum glo … ne, and internal	721	721	100%	0.0	100%	KJ588249.1
☐	Colletotrichum gloeosporioides strain NF25 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal	721	721	100%	0.0	100%	KJ588248.1
☐	Colletotrichum gloeosporioides strain NF21 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal	721	721	100%	0.0	100%	KJ588247.1
☐	Colletotrichum sp. 2 MJ-2014 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene and internal transcribed spacer 2, complete sequence	721	721	100%	0.0	100%	KJ572160.1
☐	Colletotrichum sp. GM151 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed space	721	721	100%	0.0	100%	KF214634.1
☐	Colletotrichum sp. GM149 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed space	721	721	100%	0.0	100%	KF214633.1
☐	sequence; 5.8S ribosomal RNA gene and internal transcribed spacer 2, complete sequence; anc	721	721	100%	0.0	100%	KJ160499.1

Go to alignment for Colletotrichum gloeosporioides strain NF68 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence

://blast.ncbi.nlm.nih.gov/Blast.cgi#alnHdr_639126888

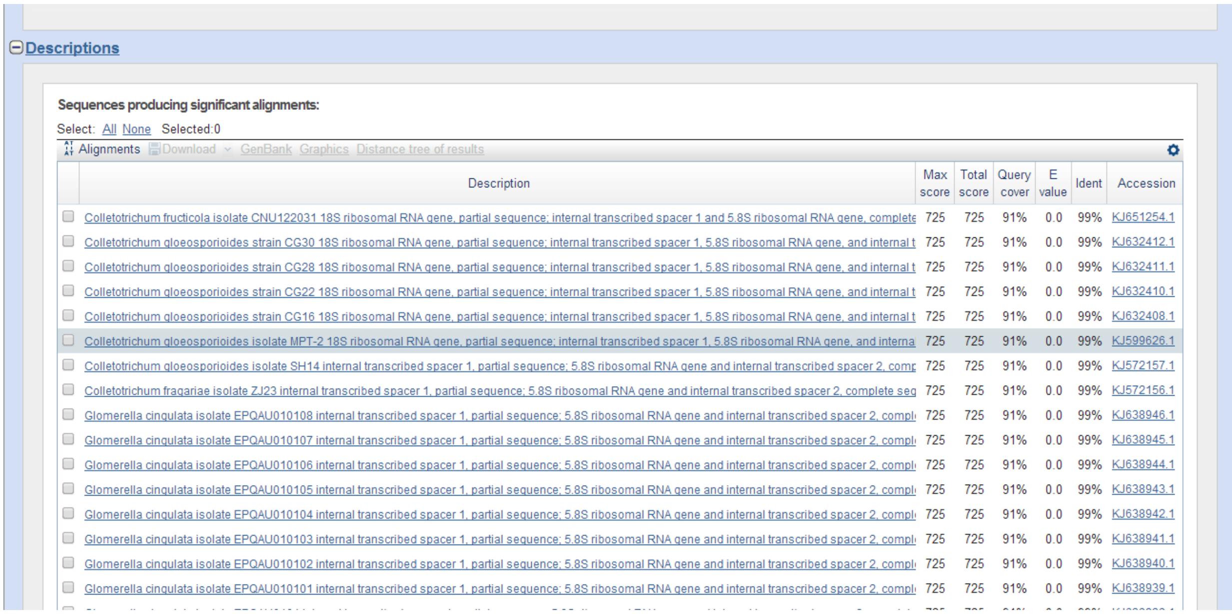
6. PBL6



Sequences producing significant alignments:

	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	Colletotrichum gloeosporioides strain M32.1 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and intern	785	785	99%	0.0	99%	JQ936116.1
☐	Colletotrichum gloeosporioides strain CG30 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and intern	782	782	99%	0.0	99%	KJ632412.1
☐	Colletotrichum gloeosporioides strain CG28 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and intern	782	782	99%	0.0	99%	KJ632411.1
☐	Colletotrichum gloeosporioides strain CG22 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and intern	782	782	99%	0.0	99%	KJ632410.1
☐	Colletotrichum gloeosporioides strain CG16 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and intern	782	782	99%	0.0	99%	KJ632408.1
☐	Colletotrichum gloeosporioides isolate MPT-2 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and inte	782	782	99%	0.0	99%	KJ599626.1
☐	Colletotrichum gloeosporioides isolate SH14 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene and internal transcribed spacer 2, cc	782	782	99%	0.0	99%	KJ572157.1
☐	Colletotrichum fragariae isolate ZJ23 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene and internal transcribed spacer 2, complete	782	782	99%	0.0	99%	KJ572156.1
☐	Glomerella cingulata isolate EPQAU010108 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene and internal transcribed spacer 2, cor	782	782	99%	0.0	99%	KJ638946.1
☐	Glomerella cingulata isolate EPQAU010107 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene and internal transcribed spacer 2, cor	782	782	99%	0.0	99%	KJ638945.1
☐	Glomerella cingulata isolate EPQAU010106 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene and internal transcribed spacer 2, cor	782	782	99%	0.0	99%	KJ638944.1
☐	Glomerella cingulata isolate EPQAU010105 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene and internal transcribed spacer 2, cor	782	782	99%	0.0	99%	KJ638943.1
☐	Glomerella cingulata isolate EPQAU010104 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene and internal transcribed spacer 2, cor	782	782	99%	0.0	99%	KJ638942.1
☐	Glomerella cingulata isolate EPQAU010103 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene and internal transcribed spacer 2, cor	782	782	99%	0.0	99%	KJ638941.1
☐	Glomerella cingulata isolate EPQAU010102 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene and internal transcribed spacer 2, cor	782	782	99%	0.0	99%	KJ638940.1

7. PBL8

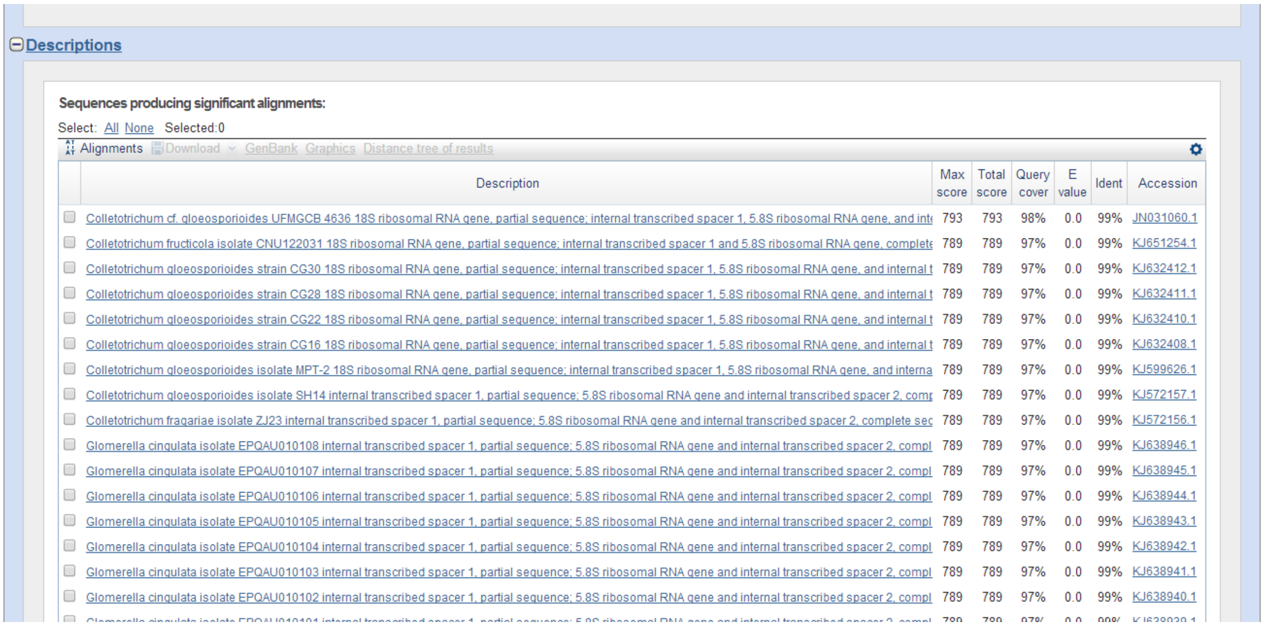


Sequences producing significant alignments:

Select: All None Selected:0

	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	Colletotrichum fructicola isolate CNU122031 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1 and 5.8S ribosomal RNA gene, complete	725	725	91%	0.0	99%	KJ651254.1
☐	Colletotrichum gloeosporioides strain CG30 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal t	725	725	91%	0.0	99%	KJ632412.1
☐	Colletotrichum gloeosporioides strain CG28 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal t	725	725	91%	0.0	99%	KJ632411.1
☐	Colletotrichum gloeosporioides strain CG22 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal t	725	725	91%	0.0	99%	KJ632410.1
☐	Colletotrichum gloeosporioides strain CG16 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal t	725	725	91%	0.0	99%	KJ632408.1
☐	Colletotrichum gloeosporioides isolate MPT-2 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and interna	725	725	91%	0.0	99%	KJ599626.1
☐	Colletotrichum gloeosporioides isolate SH14 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene and internal transcribed spacer 2, comp	725	725	91%	0.0	99%	KJ572157.1
☐	Colletotrichum fragariae isolate ZJ23 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene and internal transcribed spacer 2, complete seq	725	725	91%	0.0	99%	KJ572156.1
☐	Glomerella cingulata isolate EPQAU010108 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene and internal transcribed spacer 2, compl	725	725	91%	0.0	99%	KJ638946.1
☐	Glomerella cingulata isolate EPQAU010107 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene and internal transcribed spacer 2, compl	725	725	91%	0.0	99%	KJ638945.1
☐	Glomerella cingulata isolate EPQAU010106 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene and internal transcribed spacer 2, compl	725	725	91%	0.0	99%	KJ638944.1
☐	Glomerella cingulata isolate EPQAU010105 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene and internal transcribed spacer 2, compl	725	725	91%	0.0	99%	KJ638943.1
☐	Glomerella cingulata isolate EPQAU010104 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene and internal transcribed spacer 2, compl	725	725	91%	0.0	99%	KJ638942.1
☐	Glomerella cingulata isolate EPQAU010103 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene and internal transcribed spacer 2, compl	725	725	91%	0.0	99%	KJ638941.1
☐	Glomerella cingulata isolate EPQAU010102 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene and internal transcribed spacer 2, compl	725	725	91%	0.0	99%	KJ638940.1
☐	Glomerella cingulata isolate EPQAU010101 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene and internal transcribed spacer 2, compl	725	725	91%	0.0	99%	KJ638939.1

8. PBS2

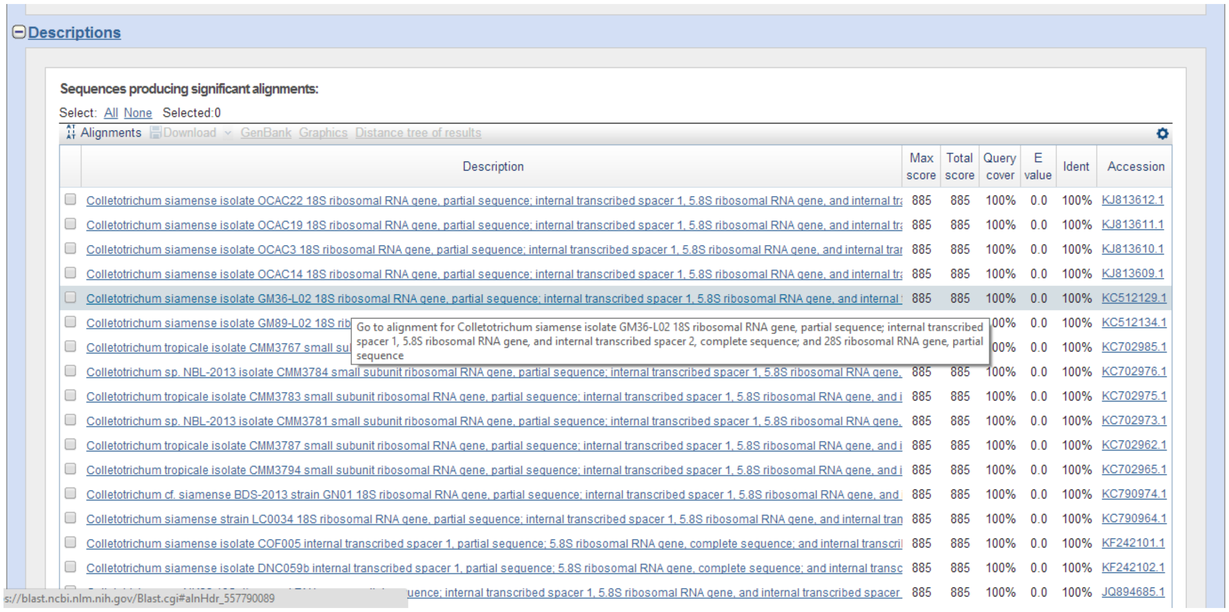


Sequences producing significant alignments:

Select: All None Selected:0

	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	Colletotrichum cf. gloeosporioides UFMGCB 4636 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and inte	793	793	98%	0.0	99%	JN031060.1
☐	Colletotrichum fructicola isolate CNU122031 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1 and 5.8S ribosomal RNA gene, complete	789	789	97%	0.0	99%	KJ651254.1
☐	Colletotrichum gloeosporioides strain CG30 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal t	789	789	97%	0.0	99%	KJ632412.1
☐	Colletotrichum gloeosporioides strain CG28 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal t	789	789	97%	0.0	99%	KJ632411.1
☐	Colletotrichum gloeosporioides strain CG22 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal t	789	789	97%	0.0	99%	KJ632410.1
☐	Colletotrichum gloeosporioides strain CG16 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal t	789	789	97%	0.0	99%	KJ632408.1
☐	Colletotrichum gloeosporioides isolate MPT-2 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and interna	789	789	97%	0.0	99%	KJ599626.1
☐	Colletotrichum gloeosporioides isolate SH14 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene and internal transcribed spacer 2, comp	789	789	97%	0.0	99%	KJ572157.1
☐	Colletotrichum fragariae isolate ZJ23 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene and internal transcribed spacer 2, complete sec	789	789	97%	0.0	99%	KJ572156.1
☐	Glomerella cingulata isolate EPQAU010108 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene and internal transcribed spacer 2, compl	789	789	97%	0.0	99%	KJ638946.1
☐	Glomerella cingulata isolate EPQAU010107 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene and internal transcribed spacer 2, compl	789	789	97%	0.0	99%	KJ638945.1
☐	Glomerella cingulata isolate EPQAU010106 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene and internal transcribed spacer 2, compl	789	789	97%	0.0	99%	KJ638944.1
☐	Glomerella cingulata isolate EPQAU010105 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene and internal transcribed spacer 2, compl	789	789	97%	0.0	99%	KJ638943.1
☐	Glomerella cingulata isolate EPQAU010104 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene and internal transcribed spacer 2, compl	789	789	97%	0.0	99%	KJ638942.1
☐	Glomerella cingulata isolate EPQAU010103 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene and internal transcribed spacer 2, compl	789	789	97%	0.0	99%	KJ638941.1
☐	Glomerella cingulata isolate EPQAU010102 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene and internal transcribed spacer 2, compl	789	789	97%	0.0	99%	KJ638940.1

9. PBL9



Sequences producing significant alignments:

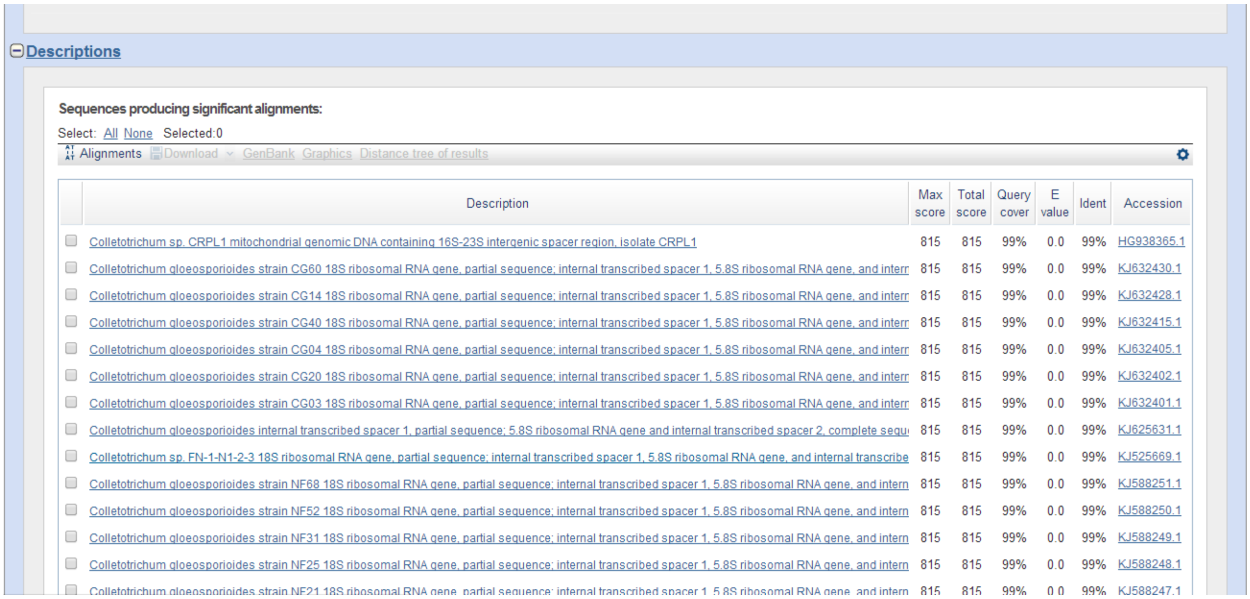
Select: All None Selected:0

	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	Colletotrichum siamense isolate OCAC22 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal tr	885	885	100%	0.0	100%	KJ813612.1
☐	Colletotrichum siamense isolate OCAC19 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal tr	885	885	100%	0.0	100%	KJ813611.1
☐	Colletotrichum siamense isolate OCAC3 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal tra	885	885	100%	0.0	100%	KJ813610.1
☐	Colletotrichum siamense isolate OCAC14 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal tr	885	885	100%	0.0	100%	KJ813609.1
☐	Colletotrichum siamense isolate GM36-L02 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal	885	885	100%	0.0	100%	KC512129.1
☐	Colletotrichum siamense isolate GM89-L02 18S rib			00%	0.0	100%	KC512134.1
☐	Colletotrichum tropicale isolate CMM3767 small su			00%	0.0	100%	KC702985.1
☐	Colletotrichum sp. NBL-2013 isolate CMM3784 small subunit ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene,	885	885	100%	0.0	100%	KC702976.1
☐	Colletotrichum tropicale isolate CMM3783 small subunit ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and i	885	885	100%	0.0	100%	KC702975.1
☐	Colletotrichum sp. NBL-2013 isolate CMM3781 small subunit ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene,	885	885	100%	0.0	100%	KC702973.1
☐	Colletotrichum tropicale isolate CMM3787 small subunit ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and i	885	885	100%	0.0	100%	KC702962.1
☐	Colletotrichum tropicale isolate CMM3794 small subunit ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and i	885	885	100%	0.0	100%	KC702965.1
☐	Colletotrichum cf. siamense BDS-2013 strain GN01 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and	885	885	100%	0.0	100%	KC790974.1
☐	Colletotrichum siamense strain LC0034 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal tran	885	885	100%	0.0	100%	KC790964.1
☐	Colletotrichum siamense isolate COF005 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcri	885	885	100%	0.0	100%	KF242101.1
☐	Colletotrichum siamense isolate DNC059b internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transc	885	885	100%	0.0	100%	KF242102.1
☐	uence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer	885	885	100%	0.0	100%	JQ894685.1

Go to alignment for Colletotrichum siamense isolate GM36-L02 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence

s://blast.ncbi.nlm.nih.gov/Blast.cgi#alnHdr_557790089

10. PBL10

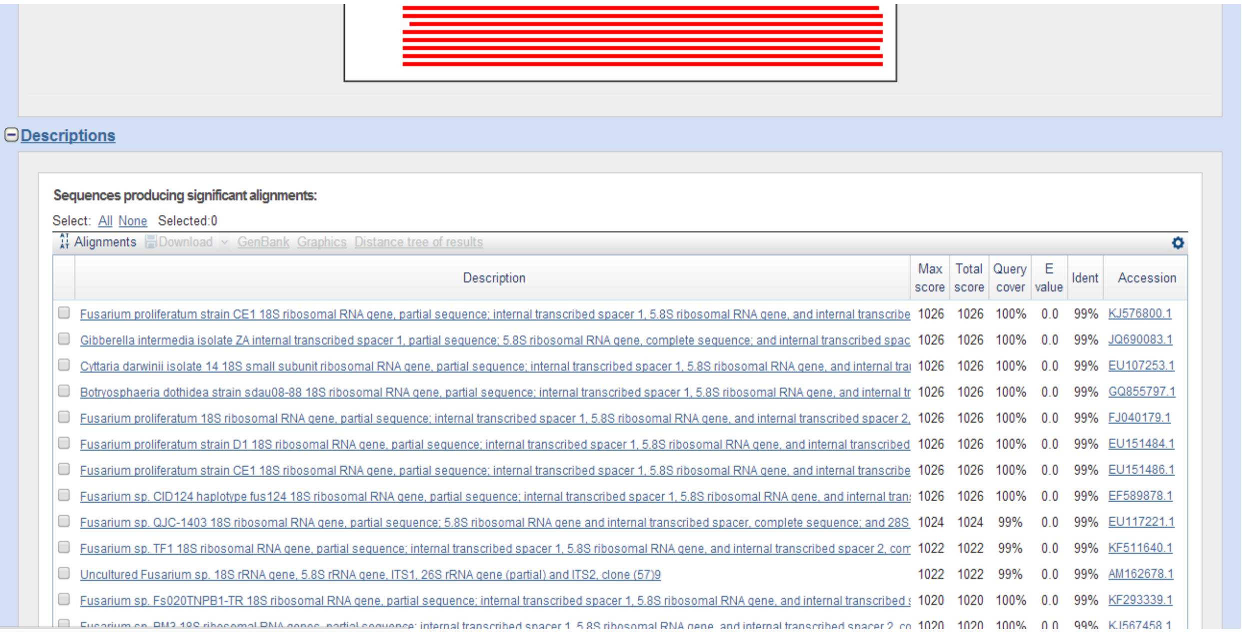


Sequences producing significant alignments:

Select: All None Selected:0

	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	Colletotrichum sp. CRPL1 mitochondrial genomic DNA containing 16S-23S intergenic spacer region, isolate CRPL1	815	815	99%	0.0	99%	HG938365.1
☐	Colletotrichum gloeosporioides strain CG60 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and interr	815	815	99%	0.0	99%	KJ632430.1
☐	Colletotrichum gloeosporioides strain CG14 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and interr	815	815	99%	0.0	99%	KJ632428.1
☐	Colletotrichum gloeosporioides strain CG40 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and interr	815	815	99%	0.0	99%	KJ632415.1
☐	Colletotrichum gloeosporioides strain CG04 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and interr	815	815	99%	0.0	99%	KJ632405.1
☐	Colletotrichum gloeosporioides strain CG20 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and interr	815	815	99%	0.0	99%	KJ632402.1
☐	Colletotrichum gloeosporioides strain CG03 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and interr	815	815	99%	0.0	99%	KJ632401.1
☐	Colletotrichum gloeosporioides internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene and internal transcribed spacer 2, complete sequ	815	815	99%	0.0	99%	KJ625631.1
☐	Colletotrichum sp. FN-1-N1-2-3 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribe	815	815	99%	0.0	99%	KJ525669.1
☐	Colletotrichum gloeosporioides strain NF68 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and intern	815	815	99%	0.0	99%	KJ588251.1
☐	Colletotrichum gloeosporioides strain NF52 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and intern	815	815	99%	0.0	99%	KJ588250.1
☐	Colletotrichum gloeosporioides strain NF31 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and intern	815	815	99%	0.0	99%	KJ588249.1
☐	Colletotrichum gloeosporioides strain NF25 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and intern	815	815	99%	0.0	99%	KJ588248.1
☐	Colletotrichum gloeosporioides strain NF21 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and intern	815	815	99%	0.0	99%	KJ588247.1

11. PBL11

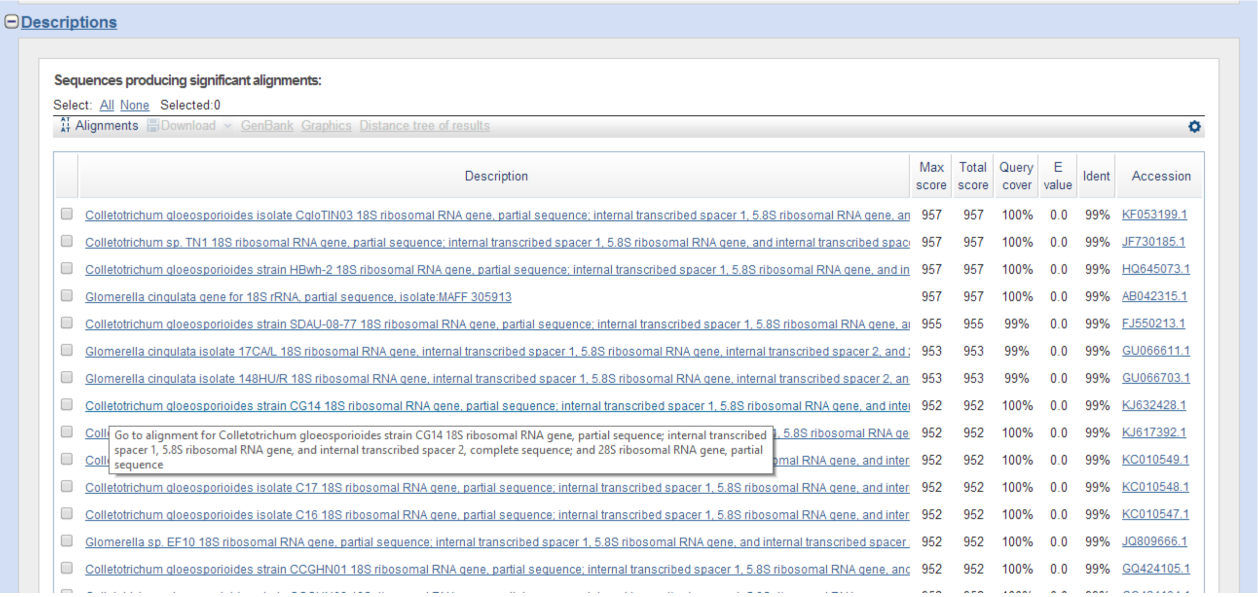


Sequences producing significant alignments:

Select: All None Selected:0

	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	Fusarium proliferatum strain CE1 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribe	1026	1026	100%	0.0	99%	KJ576800.1
☐	Gibberella intermedia isolate ZA internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spac	1026	1026	100%	0.0	99%	JQ690083.1
☐	Cyttaria darwinii isolate 14 18S small subunit ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal tra	1026	1026	100%	0.0	99%	EU107253.1
☐	Botryosphaeria dothidea strain sdau08-88 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal tr	1026	1026	100%	0.0	99%	GQ855797.1
☐	Fusarium proliferatum 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2,	1026	1026	100%	0.0	99%	FJ040179.1
☐	Fusarium proliferatum strain D1 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed	1026	1026	100%	0.0	99%	EU151484.1
☐	Fusarium proliferatum strain CE1 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribe	1026	1026	100%	0.0	99%	EU151486.1
☐	Fusarium sp. CID124 haplotype fus124 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal tran:	1026	1026	100%	0.0	99%	EF589878.1
☐	Fusarium sp. QJC-1403 18S ribosomal RNA gene, partial sequence; 5.8S ribosomal RNA gene and internal transcribed spacer, complete sequence; and 28S	1024	1024	99%	0.0	99%	EU117221.1
☐	Fusarium sp. TF1 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, com	1022	1022	99%	0.0	99%	KF511640.1
☐	Uncultured Fusarium sp. 18S rRNA gene, 5.8S rRNA gene, ITS1, 26S rRNA gene (partial) and ITS2, clone (57)9	1022	1022	99%	0.0	99%	AM162678.1
☐	Fusarium sp. Fs020TNPB1-TR 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed s	1020	1020	100%	0.0	99%	KF293339.1

12. PBL12



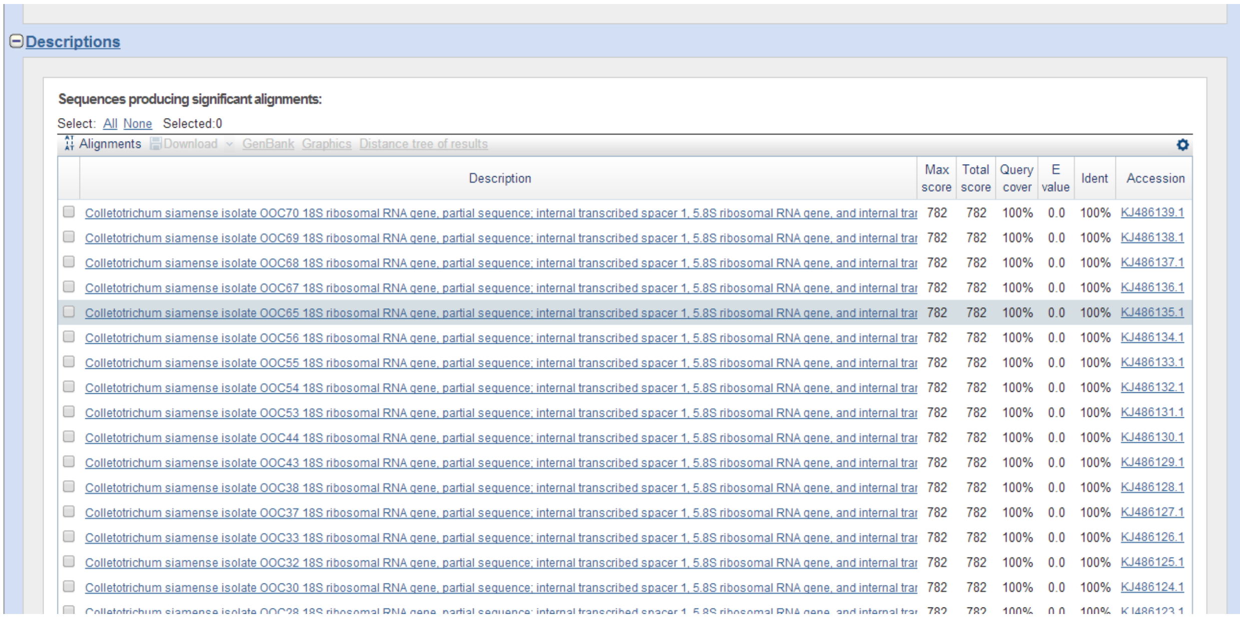
Sequences producing significant alignments:

Select: All None Selected:0

	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	Colletotrichum gloeosporioides isolate CgloTIN03 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, an	957	957	100%	0.0	99%	KF053199.1
☐	Colletotrichum sp. TN1 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spac	957	957	100%	0.0	99%	JF730185.1
☐	Colletotrichum gloeosporioides strain HBwh-2 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and in	957	957	100%	0.0	99%	HQ645073.1
☐	Glomerella cingulata gene for 18S rRNA, partial sequence, isolate:MAFF 305913	957	957	100%	0.0	99%	AB042315.1
☐	Colletotrichum gloeosporioides strain SDAU-08-77 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, ai	955	955	99%	0.0	99%	FJ550213.1
☐	Glomerella cingulata isolate 17CA/L 18S ribosomal RNA gene, internal transcribed spacer 1, 5.8S ribosomal RNA gene, internal transcribed spacer 2, and :	953	953	99%	0.0	99%	GU066611.1
☐	Glomerella cingulata isolate 148HU/R 18S ribosomal RNA gene, internal transcribed spacer 1, 5.8S ribosomal RNA gene, internal transcribed spacer 2, an	953	953	99%	0.0	99%	GU066703.1
☐	Colletotrichum gloeosporioides strain CG14 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and inte	952	952	100%	0.0	99%	KJ632428.1
☐	Coll [illegible] , 5.8S ribosomal RNA ge	952	952	100%	0.0	99%	KJ617392.1
☐	Coll [illegible] omal RNA gene, and inter	952	952	100%	0.0	99%	KC010549.1
☐	Colletotrichum gloeosporioides isolate C17 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and inter	952	952	100%	0.0	99%	KC010548.1
☐	Colletotrichum gloeosporioides isolate C16 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and inter	952	952	100%	0.0	99%	KC010547.1
☐	Glomerella sp. EF10 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer :	952	952	100%	0.0	99%	JQ809666.1
☐	Colletotrichum gloeosporioides strain CCGHN01 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, anc	952	952	100%	0.0	99%	GQ424105.1

Go to alignment for Colletotrichum gloeosporioides strain CG14 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence

13. PBS3



⊟ Descriptions

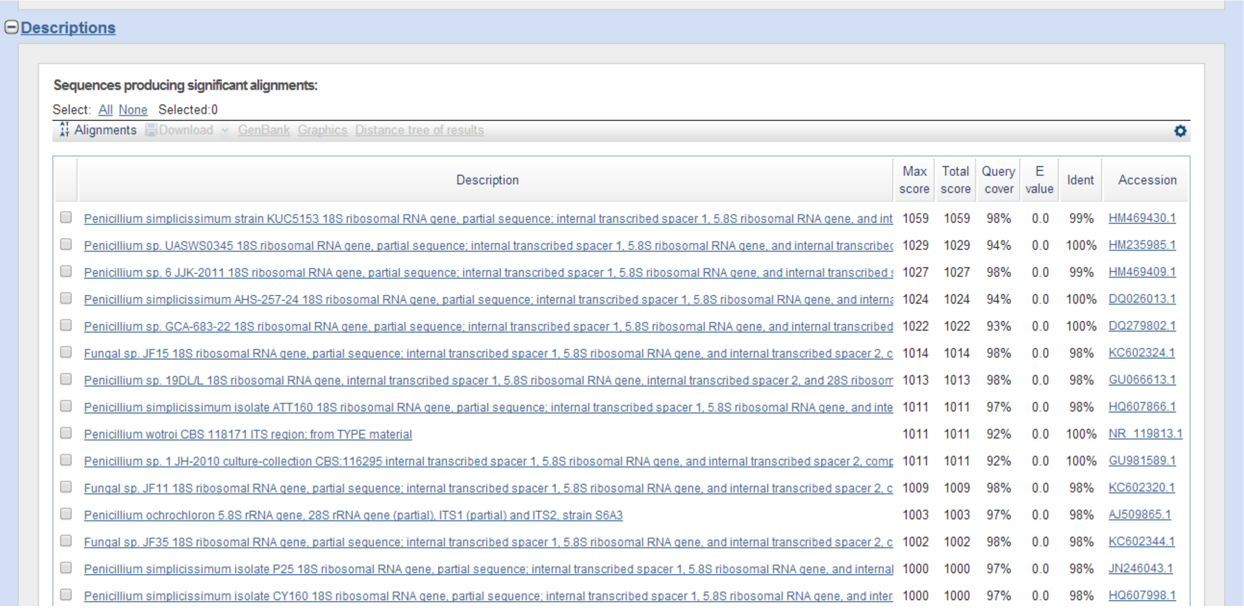
Sequences producing significant alignments:

Select: All None Selected:0

Alignments Download GenBank Graphics Distance tree of results

	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	Colletotrichum siamense isolate OOC70 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal tra	782	782	100%	0.0	100%	KJ486139.1
☐	Colletotrichum siamense isolate OOC69 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal tra	782	782	100%	0.0	100%	KJ486138.1
☐	Colletotrichum siamense isolate OOC68 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal tra	782	782	100%	0.0	100%	KJ486137.1
☐	Colletotrichum siamense isolate OOC67 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal tra	782	782	100%	0.0	100%	KJ486136.1
☐	Colletotrichum siamense isolate OOC65 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal tra	782	782	100%	0.0	100%	KJ486135.1
☐	Colletotrichum siamense isolate OOC56 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal tra	782	782	100%	0.0	100%	KJ486134.1
☐	Colletotrichum siamense isolate OOC55 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal tra	782	782	100%	0.0	100%	KJ486133.1
☐	Colletotrichum siamense isolate OOC54 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal tra	782	782	100%	0.0	100%	KJ486132.1
☐	Colletotrichum siamense isolate OOC53 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal tra	782	782	100%	0.0	100%	KJ486131.1
☐	Colletotrichum siamense isolate OOC44 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal tra	782	782	100%	0.0	100%	KJ486130.1
☐	Colletotrichum siamense isolate OOC43 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal tra	782	782	100%	0.0	100%	KJ486129.1
☐	Colletotrichum siamense isolate OOC38 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal tra	782	782	100%	0.0	100%	KJ486128.1
☐	Colletotrichum siamense isolate OOC37 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal tra	782	782	100%	0.0	100%	KJ486127.1
☐	Colletotrichum siamense isolate OOC33 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal tra	782	782	100%	0.0	100%	KJ486126.1
☐	Colletotrichum siamense isolate OOC32 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal tra	782	782	100%	0.0	100%	KJ486125.1
☐	Colletotrichum siamense isolate OOC30 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal tra	782	782	100%	0.0	100%	KJ486124.1
☐	Colletotrichum siamense isolate OOC28 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal tra	782	782	100%	0.0	100%	KJ486123.1

14. PBL13



⊟ Descriptions

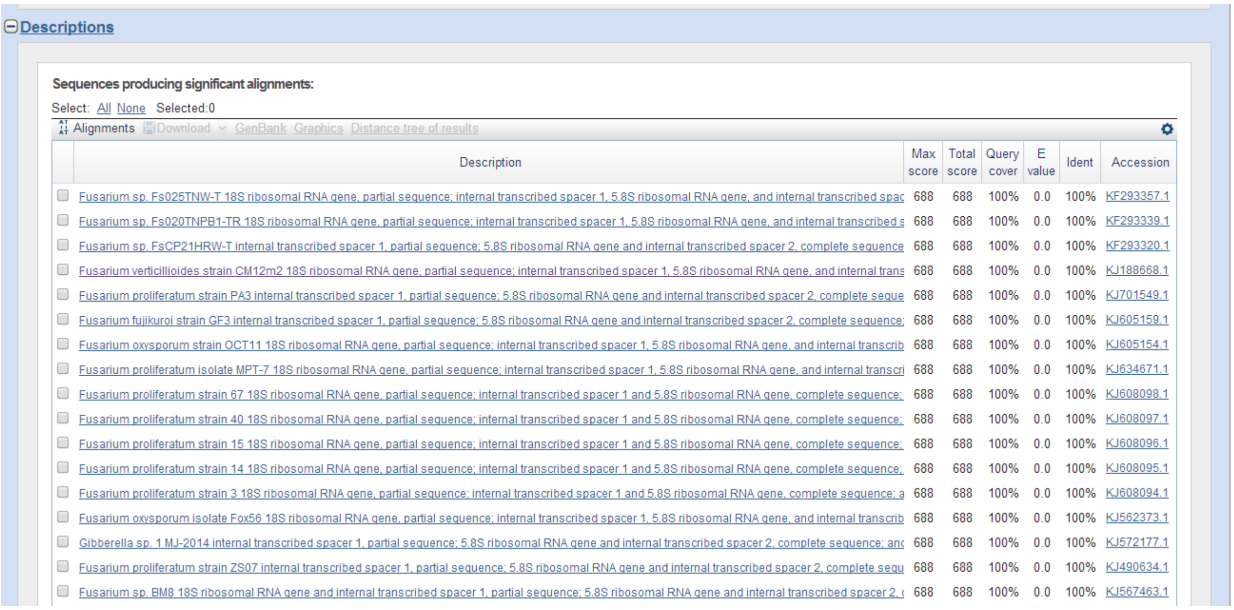
Sequences producing significant alignments:

Select: All None Selected:0

Alignments Download GenBank Graphics Distance tree of results

	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	Penicillium simplicissimum strain KUC5153 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and int	1059	1059	98%	0.0	99%	HM469430.1
☐	Penicillium sp. UASWS0345 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribe	1029	1029	94%	0.0	100%	HM235985.1
☐	Penicillium sp. 6 JJK-2011 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed	1027	1027	98%	0.0	99%	HM469409.1
☐	Penicillium simplicissimum AHS-257-24 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and intern	1024	1024	94%	0.0	100%	DQ026013.1
☐	Penicillium sp. GCA-683-22 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed	1022	1022	93%	0.0	100%	DQ279802.1
☐	Fungal sp. JF15 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, c	1014	1014	98%	0.0	98%	KC602324.1
☐	Penicillium sp. 19DL/L 18S ribosomal RNA gene, internal transcribed spacer 1, 5.8S ribosomal RNA gene, internal transcribed spacer 2, and 28S ribosom	1013	1013	98%	0.0	98%	GU066613.1
☐	Penicillium simplicissimum isolate ATT160 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and inte	1011	1011	97%	0.0	98%	HQ607866.1
☐	Penicillium wotroi CBS 118171 ITS region; from TYPE material	1011	1011	92%	0.0	100%	NR_119813.1
☐	Penicillium sp. 1 JH-2010 culture-collection CBS:116295 internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, com	1011	1011	92%	0.0	100%	GU981589.1
☐	Fungal sp. JF11 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, c	1009	1009	98%	0.0	98%	KC602320.1
☐	Penicillium ochrochloron 5.8S rRNA gene, 28S rRNA gene (partial), ITS1 (partial) and ITS2, strain S6A3	1003	1003	97%	0.0	98%	AJ509865.1
☐	Fungal sp. JF35 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, c	1002	1002	98%	0.0	98%	KC602344.1
☐	Penicillium simplicissimum isolate P25 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal	1000	1000	97%	0.0	98%	JN246043.1
☐	Penicillium simplicissimum isolate CY160 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and inter	1000	1000	97%	0.0	98%	HQ607998.1

15. ODL1

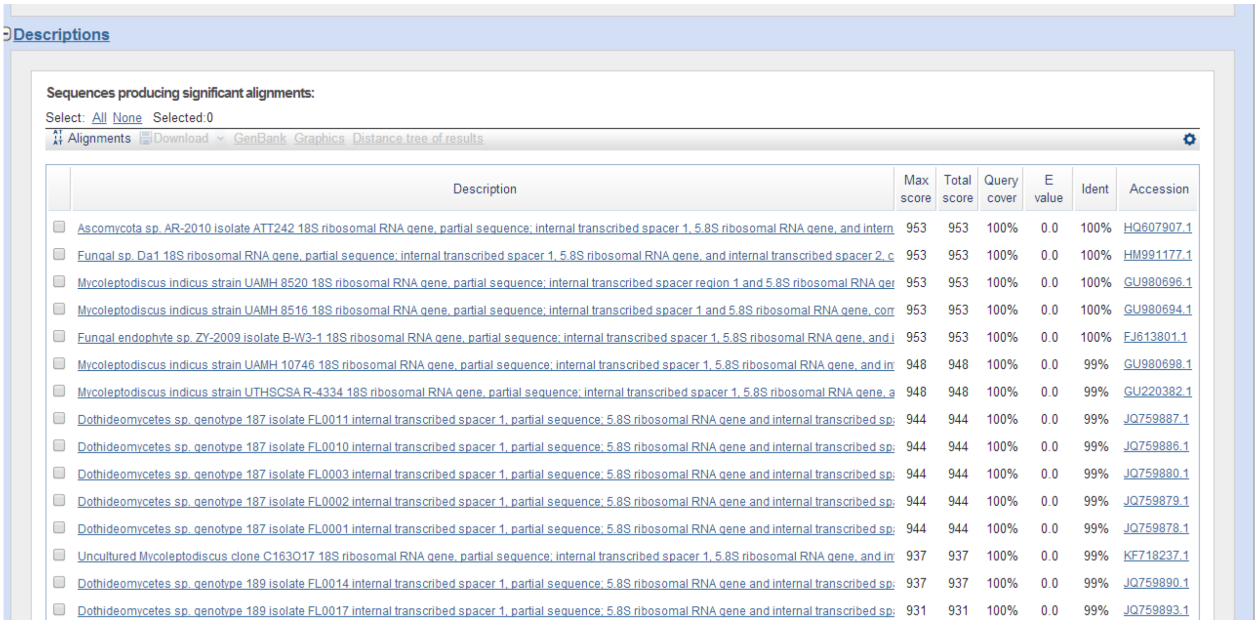


Sequences producing significant alignments:

Select: All None Selected:0

	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	Fusarium sp. Fs025TNW-T 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spac	688	688	100%	0.0	100%	KF293357.1
☐	Fusarium sp. Fs020TNPB1-TR 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed s	688	688	100%	0.0	100%	KF293339.1
☐	Fusarium sp. FsCP21HRW-T internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene and internal transcribed spacer 2, complete sequence	688	688	100%	0.0	100%	KF293320.1
☐	Fusarium verticillioides strain CM12m2 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal trans	688	688	100%	0.0	100%	KJ188668.1
☐	Fusarium proliferatum strain PA3 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene and internal transcribed spacer 2, complete seque	688	688	100%	0.0	100%	KJ701549.1
☐	Fusarium fujikuroi strain GF3 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene and internal transcribed spacer 2, complete sequence;	688	688	100%	0.0	100%	KJ605159.1
☐	Fusarium oxysporum strain OCT11 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcrib	688	688	100%	0.0	100%	KJ605154.1
☐	Fusarium proliferatum isolate MPT-7 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcri	688	688	100%	0.0	100%	KJ634671.1
☐	Fusarium proliferatum strain 67 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1 and 5.8S ribosomal RNA gene, complete sequence;	688	688	100%	0.0	100%	KJ608098.1
☐	Fusarium proliferatum strain 40 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1 and 5.8S ribosomal RNA gene, complete sequence;	688	688	100%	0.0	100%	KJ608097.1
☐	Fusarium proliferatum strain 15 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1 and 5.8S ribosomal RNA gene, complete sequence;	688	688	100%	0.0	100%	KJ608096.1
☐	Fusarium proliferatum strain 14 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1 and 5.8S ribosomal RNA gene, complete sequence;	688	688	100%	0.0	100%	KJ608095.1
☐	Fusarium proliferatum strain 3 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1 and 5.8S ribosomal RNA gene, complete sequence; a	688	688	100%	0.0	100%	KJ608094.1
☐	Fusarium oxysporum isolate Fox56 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcrib	688	688	100%	0.0	100%	KJ562373.1
☐	Gibberella sp. 1 MJ-2014 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene and internal transcribed spacer 2, complete sequence; anc	688	688	100%	0.0	100%	KJ572177.1
☐	Fusarium proliferatum strain ZS07 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene and internal transcribed spacer 2, complete sequ	688	688	100%	0.0	100%	KJ490634.1
☐	Fusarium sp. BM8 18S ribosomal RNA gene and internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene and internal transcribed spacer 2, (	688	688	100%	0.0	100%	KJ567463.1

16. ODL2

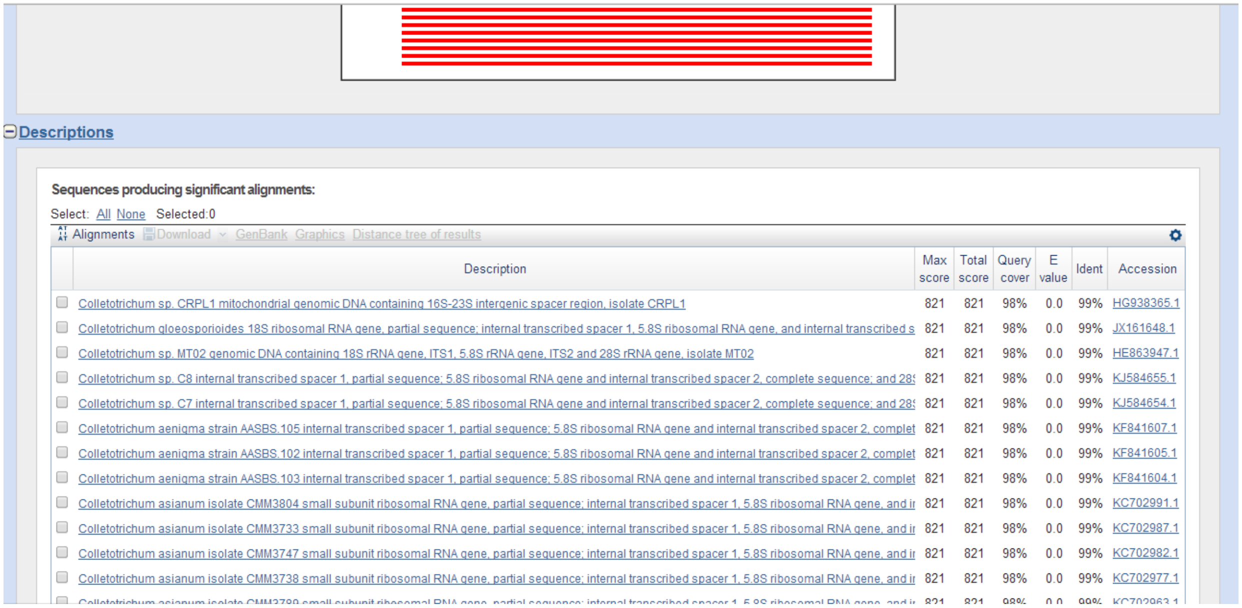


Sequences producing significant alignments:

Select: All None Selected:0

	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	Ascomycota sp. AR-2010 isolate ATT242 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and intern	953	953	100%	0.0	100%	HQ607907.1
☐	Fungal sp. Da1 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, c	953	953	100%	0.0	100%	HM991177.1
☐	Mycoleptodiscus indicus strain UAMH 8520 18S ribosomal RNA gene, partial sequence; internal transcribed spacer region 1 and 5.8S ribosomal RNA ger	953	953	100%	0.0	100%	GU980696.1
☐	Mycoleptodiscus indicus strain UAMH 8516 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1 and 5.8S ribosomal RNA gene, com	953	953	100%	0.0	100%	GU980694.1
☐	Fungal endophyte sp. ZY-2009 isolate B-W3-1 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and i	953	953	100%	0.0	100%	FJ613801.1
☐	Mycoleptodiscus indicus strain UAMH 10746 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and in	948	948	100%	0.0	99%	GU980698.1
☐	Mycoleptodiscus indicus strain UTHSCSA R-4334 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, a	948	948	100%	0.0	99%	GU220382.1
☐	Dothideomycetes sp. genotype 187 isolate FL0011 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene and internal transcribed sp;	944	944	100%	0.0	99%	JQ759887.1
☐	Dothideomycetes sp. genotype 187 isolate FL0010 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene and internal transcribed sp;	944	944	100%	0.0	99%	JQ759886.1
☐	Dothideomycetes sp. genotype 187 isolate FL0003 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene and internal transcribed sp;	944	944	100%	0.0	99%	JQ759880.1
☐	Dothideomycetes sp. genotype 187 isolate FL0002 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene and internal transcribed sp;	944	944	100%	0.0	99%	JQ759879.1
☐	Dothideomycetes sp. genotype 187 isolate FL0001 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene and internal transcribed sp;	944	944	100%	0.0	99%	JQ759878.1
☐	Uncultured Mycoleptodiscus clone C163O17 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and in	937	937	100%	0.0	99%	KF718237.1
☐	Dothideomycetes sp. genotype 189 isolate FL0014 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene and internal transcribed sp;	937	937	100%	0.0	99%	JQ759890.1
☐	Dothideomycetes sp. genotype 189 isolate FL0017 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene and internal transcribed sp;	931	931	100%	0.0	99%	JQ759893.1

17. ODL3



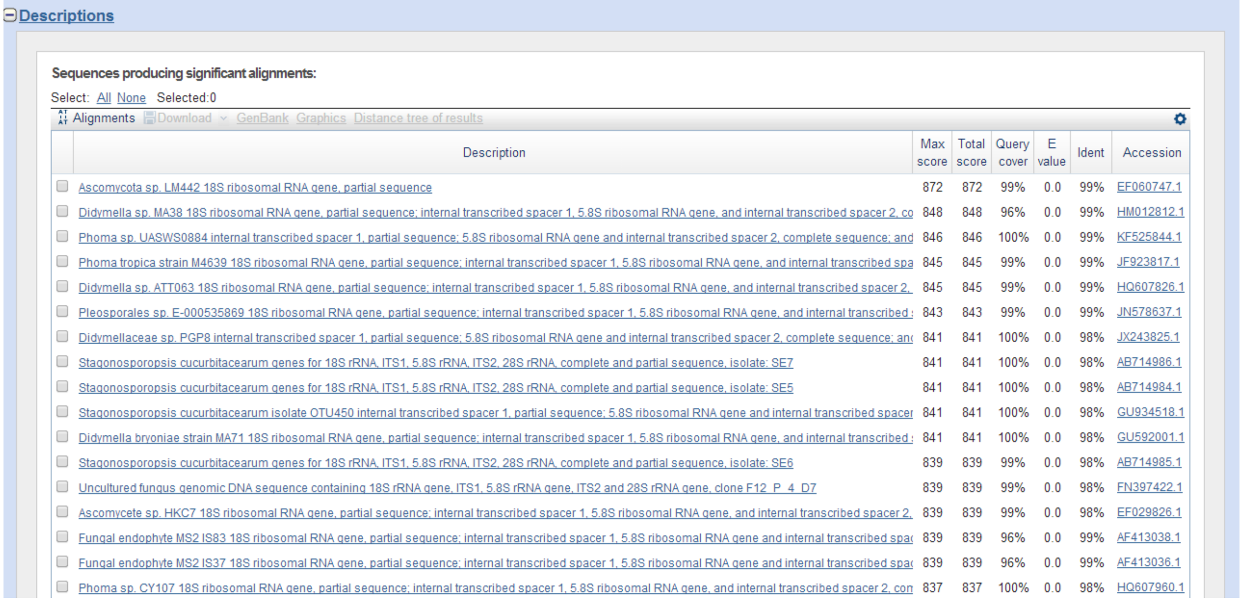
Descriptions

Sequences producing significant alignments:

Select: All None Selected:0

	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	Colletotrichum sp. CRPL1 mitochondrial genomic DNA containing 16S-23S intergenic spacer region, isolate CRPL1	821	821	98%	0.0	99%	HG938365.1
☐	Colletotrichum gloeosporioides 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed s	821	821	98%	0.0	99%	JX161648.1
☐	Colletotrichum sp. MT02 genomic DNA containing 18S rRNA gene, ITS1, 5.8S rRNA gene, ITS2 and 28S rRNA gene, isolate MT02	821	821	98%	0.0	99%	HE863947.1
☐	Colletotrichum sp. C8 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene and internal transcribed spacer 2, complete sequence; and 28	821	821	98%	0.0	99%	KJ584655.1
☐	Colletotrichum sp. C7 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene and internal transcribed spacer 2, complete sequence; and 28	821	821	98%	0.0	99%	KJ584654.1
☐	Colletotrichum aenigma strain AASBS.105 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene and internal transcribed spacer 2, complet	821	821	98%	0.0	99%	KF841607.1
☐	Colletotrichum aenigma strain AASBS.102 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene and internal transcribed spacer 2, complet	821	821	98%	0.0	99%	KF841605.1
☐	Colletotrichum aenigma strain AASBS.103 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene and internal transcribed spacer 2, complet	821	821	98%	0.0	99%	KF841604.1
☐	Colletotrichum asianum isolate CMM3804 small subunit ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and ir	821	821	98%	0.0	99%	KC702991.1
☐	Colletotrichum asianum isolate CMM3733 small subunit ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and ir	821	821	98%	0.0	99%	KC702987.1
☐	Colletotrichum asianum isolate CMM3747 small subunit ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and ir	821	821	98%	0.0	99%	KC702982.1
☐	Colletotrichum asianum isolate CMM3738 small subunit ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and ir	821	821	98%	0.0	99%	KC702977.1

18. ODL4



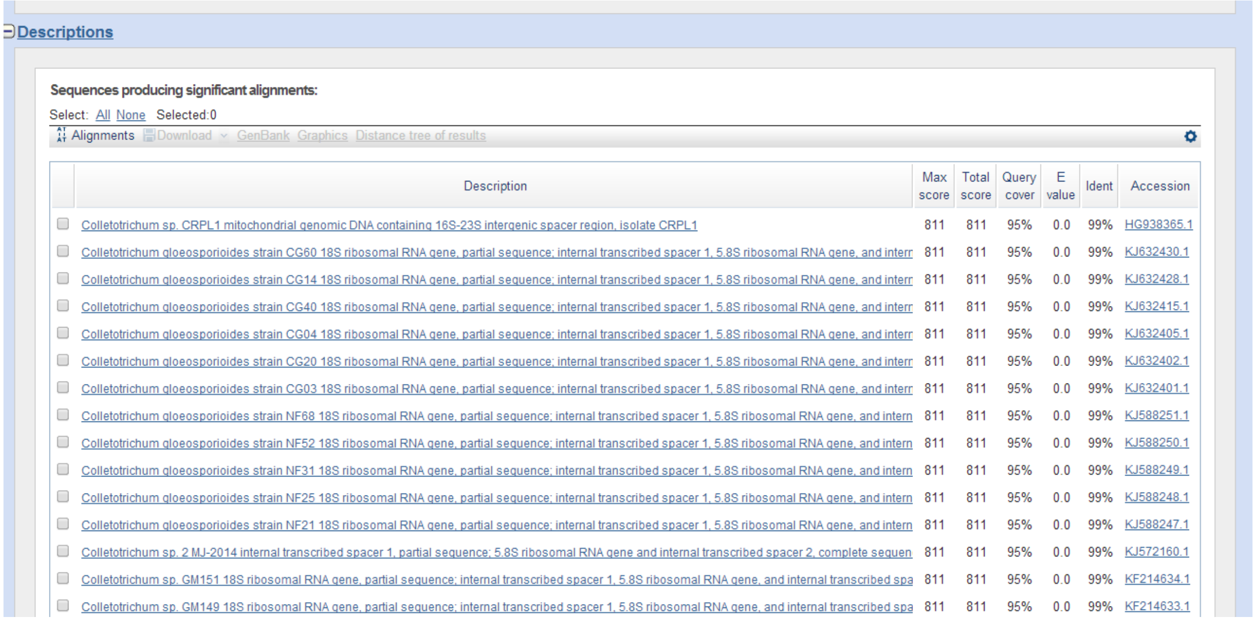
Descriptions

Sequences producing significant alignments:

Select: All None Selected:0

	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	Ascomycota sp. LM442 18S ribosomal RNA gene, partial sequence	872	872	99%	0.0	99%	EF060747.1
☐	Didymella sp. MA38 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, co	848	848	96%	0.0	99%	HM012812.1
☐	Phoma sp. UASWS0884 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene and internal transcribed spacer 2, complete sequence; and	846	846	100%	0.0	99%	KF525844.1
☐	Phoma tropica strain M4639 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spa	845	845	99%	0.0	99%	JF923817.1
☐	Didymella sp. ATT063 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2,	845	845	99%	0.0	99%	HQ607826.1
☐	Pleosporales sp. E-000535869 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed	843	843	99%	0.0	99%	JN578637.1
☐	Didymellaceae sp. PGP8 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene and internal transcribed spacer 2, complete sequence; an	841	841	100%	0.0	98%	JX243825.1
☐	Stagonosporopsis cucurbitacearum genes for 18S rRNA, ITS1, 5.8S rRNA, ITS2, 28S rRNA, complete and partial sequence, isolate: SE7	841	841	100%	0.0	98%	AB714986.1
☐	Stagonosporopsis cucurbitacearum genes for 18S rRNA, ITS1, 5.8S rRNA, ITS2, 28S rRNA, complete and partial sequence, isolate: SE5	841	841	100%	0.0	98%	AB714984.1
☐	Stagonosporopsis cucurbitacearum isolate OTU450 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene and internal transcribed spacer	841	841	100%	0.0	98%	GU934518.1
☐	Didymella bryoniae strain MA71 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed	841	841	100%	0.0	98%	GU592001.1
☐	Stagonosporopsis cucurbitacearum genes for 18S rRNA, ITS1, 5.8S rRNA, ITS2, 28S rRNA, complete and partial sequence, isolate: SE6	839	839	99%	0.0	98%	AB714985.1
☐	Uncultured fungus genomic DNA sequence containing 18S rRNA gene, ITS1, 5.8S rRNA gene, ITS2 and 28S rRNA gene, clone F12_P_4_D7	839	839	99%	0.0	98%	FN397422.1
☐	Ascomycete sp. HKC7 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2,	839	839	99%	0.0	98%	EF029826.1
☐	Fungal endophyte MS2 IS83 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene and internal transcribed spa	839	839	96%	0.0	99%	AF413038.1
☐	Fungal endophyte MS2 IS37 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene and internal transcribed spa	839	839	96%	0.0	99%	AF413036.1
☐	Phoma sp. CY107 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, con	837	837	100%	0.0	98%	HQ607960.1

19. 0DL5



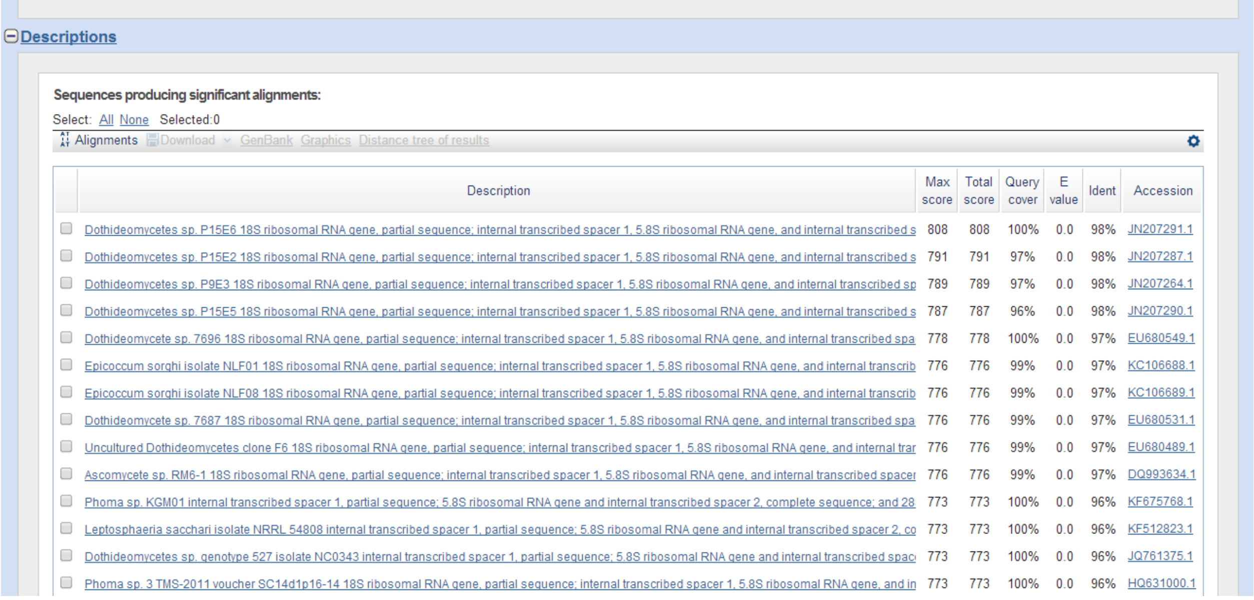
Descriptions

Sequences producing significant alignments:

Select: All None Selected:0

	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	Colletotrichum sp. CRPL1 mitochondrial genomic DNA containing 16S-23S intergenic spacer region, isolate CRPL1	811	811	95%	0.0	99%	HG938365.1
☐	Colletotrichum gloeosporioides strain CG60 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and interr	811	811	95%	0.0	99%	KJ632430.1
☐	Colletotrichum gloeosporioides strain CG14 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and interr	811	811	95%	0.0	99%	KJ632428.1
☐	Colletotrichum gloeosporioides strain CG40 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and interr	811	811	95%	0.0	99%	KJ632415.1
☐	Colletotrichum gloeosporioides strain CG04 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and interr	811	811	95%	0.0	99%	KJ632405.1
☐	Colletotrichum gloeosporioides strain CG20 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and interr	811	811	95%	0.0	99%	KJ632402.1
☐	Colletotrichum gloeosporioides strain CG03 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and interr	811	811	95%	0.0	99%	KJ632401.1
☐	Colletotrichum gloeosporioides strain NF68 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and intern	811	811	95%	0.0	99%	KJ588251.1
☐	Colletotrichum gloeosporioides strain NF52 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and intern	811	811	95%	0.0	99%	KJ588250.1
☐	Colletotrichum gloeosporioides strain NF31 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and intern	811	811	95%	0.0	99%	KJ588249.1
☐	Colletotrichum gloeosporioides strain NF25 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and intern	811	811	95%	0.0	99%	KJ588248.1
☐	Colletotrichum gloeosporioides strain NF21 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and intern	811	811	95%	0.0	99%	KJ588247.1
☐	Colletotrichum sp. 2 MJ-2014 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene and internal transcribed spacer 2, complete sequen	811	811	95%	0.0	99%	KJ572160.1
☐	Colletotrichum sp. GM151 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spa	811	811	95%	0.0	99%	KF214634.1
☐	Colletotrichum sp. GM149 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spa	811	811	95%	0.0	99%	KF214633.1

20. CCL1



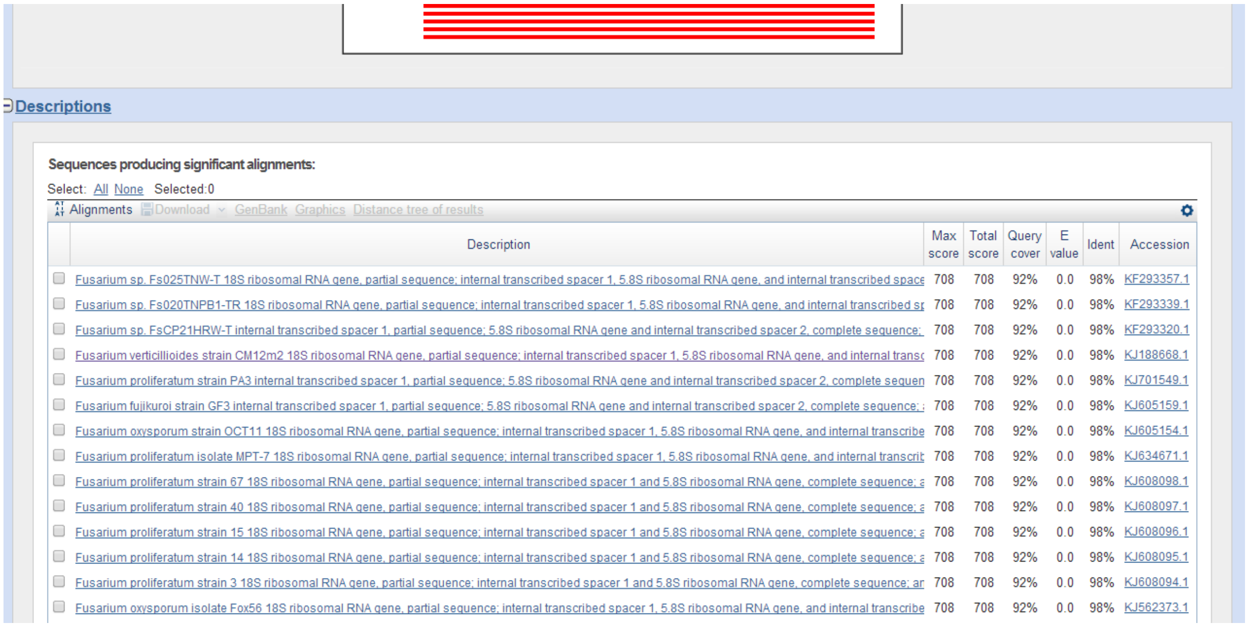
Descriptions

Sequences producing significant alignments:

Select: All None Selected:0

	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	Dothideomycetes sp. P15E6 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed s	808	808	100%	0.0	98%	JN207291.1
☐	Dothideomycetes sp. P15E2 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed s	791	791	97%	0.0	98%	JN207287.1
☐	Dothideomycetes sp. P9E3 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed sp	789	789	97%	0.0	98%	JN207264.1
☐	Dothideomycetes sp. P15E5 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed s	787	787	96%	0.0	98%	JN207290.1
☐	Dothideomycete sp. 7696 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spa	778	778	100%	0.0	97%	EU680549.1
☐	Epicoccum sorghi isolate NLF01 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcrib	776	776	99%	0.0	97%	KC106688.1
☐	Epicoccum sorghi isolate NLF08 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcrib	776	776	99%	0.0	97%	KC106689.1
☐	Dothideomycete sp. 7687 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spa	776	776	99%	0.0	97%	EU680531.1
☐	Uncultured Dothideomycetes clone F6 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal trar	776	776	99%	0.0	97%	EU680489.1
☐	Ascomycete sp. RM6-1 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer	776	776	99%	0.0	97%	DQ993634.1
☐	Phoma sp. KGM01 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene and internal transcribed spacer 2, complete sequence; and 28	773	773	100%	0.0	96%	KF675768.1
☐	Leptosphaeria sacchari isolate NRRL 54808 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene and internal transcribed spacer 2, co	773	773	100%	0.0	96%	KF512823.1
☐	Dothideomycetes sp. genotype 527 isolate NC0343 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene and internal transcribed spac	773	773	100%	0.0	96%	JQ761375.1
☐	Phoma sp. 3 TMS-2011 voucher SC14d1p16-14 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and in	773	773	100%	0.0	96%	HQ631000.1

21. CCL2



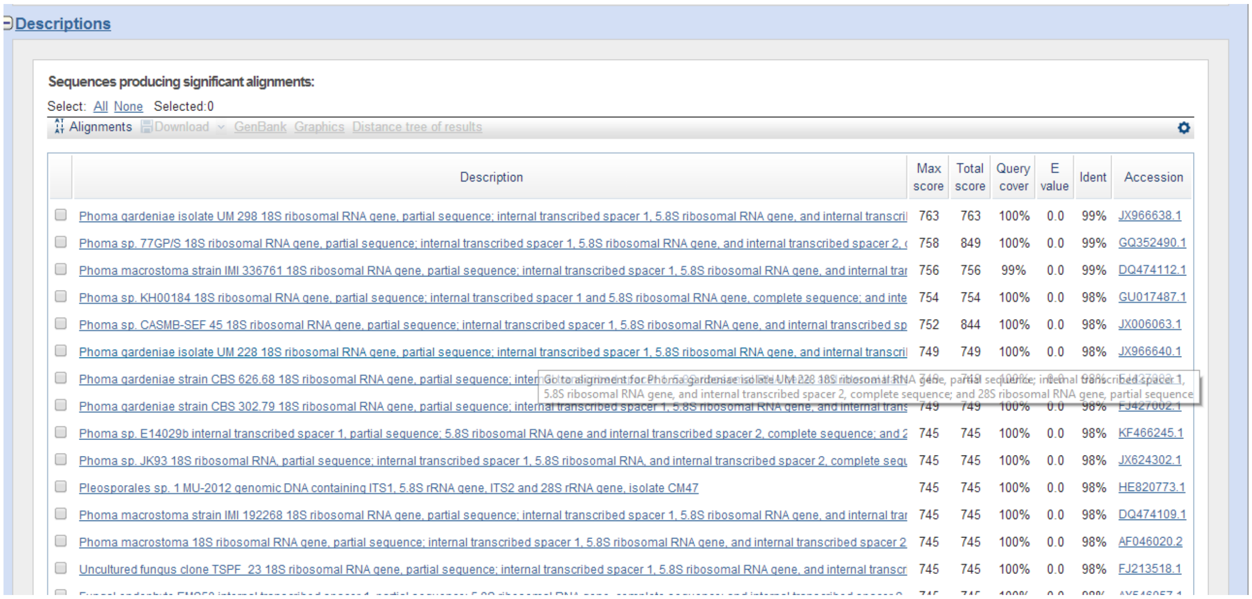
Descriptions

Sequences producing significant alignments:

Select: All None Selected:0

	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	Fusarium sp. Fs025TNW-T 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed space	708	708	92%	0.0	98%	KF293357.1
☐	Fusarium sp. Fs020TNPB1-TR 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed sp	708	708	92%	0.0	98%	KF293339.1
☐	Fusarium sp. FsCP21HRW-T internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene and internal transcribed spacer 2, complete sequence;	708	708	92%	0.0	98%	KF293320.1
☐	Fusarium verticillioides strain CM12m2 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transc	708	708	92%	0.0	98%	KJ188668.1
☐	Fusarium proliferatum strain PA3 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene and internal transcribed spacer 2, complete sequen	708	708	92%	0.0	98%	KJ701549.1
☐	Fusarium fujikuroi strain GF3 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene and internal transcribed spacer 2, complete sequence;	708	708	92%	0.0	98%	KJ605159.1
☐	Fusarium oxysporum strain OCT11 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribe	708	708	92%	0.0	98%	KJ605154.1
☐	Fusarium proliferatum isolate MPT-7 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcrit	708	708	92%	0.0	98%	KJ634671.1
☐	Fusarium proliferatum strain 67 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1 and 5.8S ribosomal RNA gene, complete sequence; a	708	708	92%	0.0	98%	KJ608098.1
☐	Fusarium proliferatum strain 40 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1 and 5.8S ribosomal RNA gene, complete sequence; a	708	708	92%	0.0	98%	KJ608097.1
☐	Fusarium proliferatum strain 15 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1 and 5.8S ribosomal RNA gene, complete sequence; a	708	708	92%	0.0	98%	KJ608096.1
☐	Fusarium proliferatum strain 14 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1 and 5.8S ribosomal RNA gene, complete sequence; a	708	708	92%	0.0	98%	KJ608095.1
☐	Fusarium proliferatum strain 3 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1 and 5.8S ribosomal RNA gene, complete sequence; ar	708	708	92%	0.0	98%	KJ608094.1
☐	Fusarium oxysporum isolate Fox56 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribe	708	708	92%	0.0	98%	KJ562373.1

22. CCL3



Descriptions

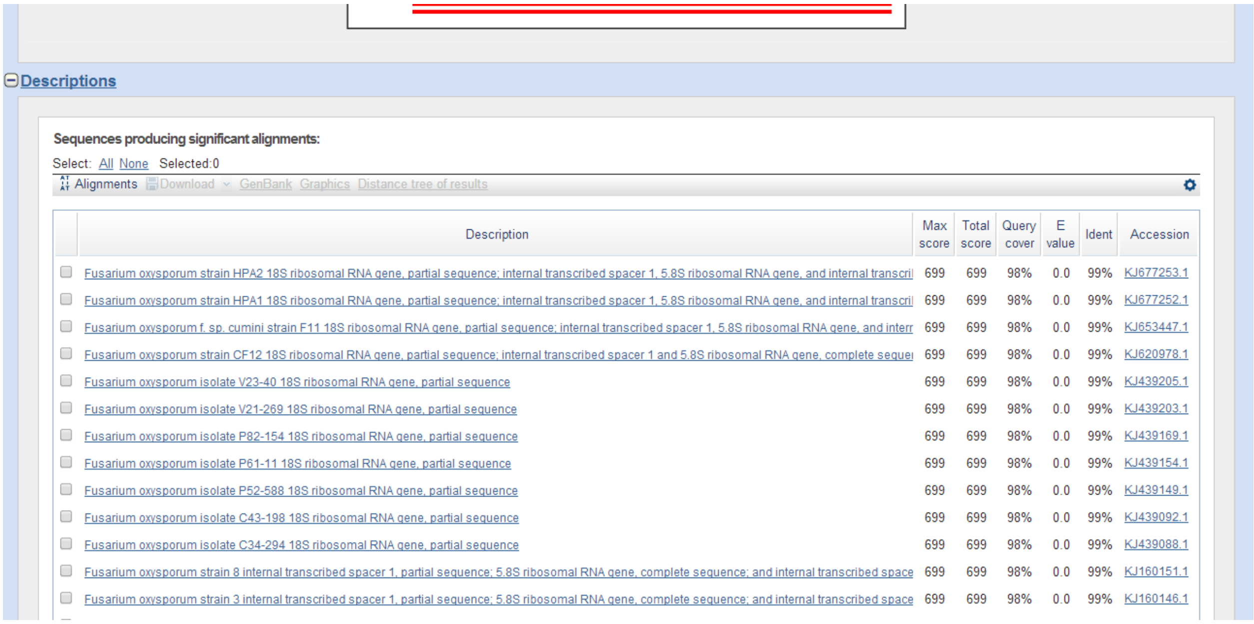
Sequences producing significant alignments:

Select: All None Selected:0

	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	Phoma gardeniae isolate UM 298 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcri	763	763	100%	0.0	99%	JX966638.1
☐	Phoma sp. 77GP/S 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, c	758	849	100%	0.0	99%	GQ352490.1
☐	Phoma macrostoma strain IMI 336761 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal trai	756	756	99%	0.0	99%	DQ474112.1
☐	Phoma sp. KH00184 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1 and 5.8S ribosomal RNA gene, complete sequence; and inte	754	754	100%	0.0	98%	GU017487.1
☐	Phoma sp. CASMB-SEF 45 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed sp	752	844	100%	0.0	98%	JX006063.1
☐	Phoma gardeniae isolate UM 228 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcri	749	749	100%	0.0	98%	JX966640.1
☐	Phoma gardeniae strain CBS 626.68 18S ribosomal RNA gene, partial sequence; inter	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
☐	Phoma gardeniae strain CBS 302.79 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal trans	749	749	100%	0.0	98%	FJ427002.1
☐	Phoma sp. E14029b internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene and internal transcribed spacer 2, complete sequence; and 2	745	745	100%	0.0	98%	KF466245.1
☐	Phoma sp. JK93 18S ribosomal RNA, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA, and internal transcribed spacer 2, complete sequ	745	745	100%	0.0	98%	JX624302.1
☐	Pleosporales sp. 1 MU-2012 genomic DNA containing ITS1, 5.8S rRNA gene, ITS2 and 28S rRNA gene, isolate CM47	745	745	100%	0.0	98%	HE820773.1
☐	Phoma macrostoma strain IMI 192268 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal trai	745	745	100%	0.0	98%	DQ474109.1
☐	Phoma macrostoma 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2	745	745	100%	0.0	98%	AF046020.2
☐	Uncultured fungus clone TSPF_23 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcr	745	745	100%	0.0	98%	FJ213518.1

Go to alignment for Phoma gardeniae isolate UM 228 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence

23. MKS1



Sequences producing significant alignments:

	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	Fusarium oxysporum strain HPA2 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcri	699	699	98%	0.0	99%	KJ677253.1
☐	Fusarium oxysporum strain HPA1 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcri	699	699	98%	0.0	99%	KJ677252.1
☐	Fusarium oxysporum f. sp. cumini strain F11 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and inter	699	699	98%	0.0	99%	KJ653447.1
☐	Fusarium oxysporum strain CF12 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1 and 5.8S ribosomal RNA gene, complete seque	699	699	98%	0.0	99%	KJ620978.1
☐	Fusarium oxysporum isolate V23-40 18S ribosomal RNA gene, partial sequence	699	699	98%	0.0	99%	KJ439205.1
☐	Fusarium oxysporum isolate V21-269 18S ribosomal RNA gene, partial sequence	699	699	98%	0.0	99%	KJ439203.1
☐	Fusarium oxysporum isolate P82-154 18S ribosomal RNA gene, partial sequence	699	699	98%	0.0	99%	KJ439169.1
☐	Fusarium oxysporum isolate P61-11 18S ribosomal RNA gene, partial sequence	699	699	98%	0.0	99%	KJ439154.1
☐	Fusarium oxysporum isolate P52-588 18S ribosomal RNA gene, partial sequence	699	699	98%	0.0	99%	KJ439149.1
☐	Fusarium oxysporum isolate C43-198 18S ribosomal RNA gene, partial sequence	699	699	98%	0.0	99%	KJ439092.1
☐	Fusarium oxysporum isolate C34-294 18S ribosomal RNA gene, partial sequence	699	699	98%	0.0	99%	KJ439088.1
☐	Fusarium oxysporum strain 8 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed space	699	699	98%	0.0	99%	KJ160151.1
☐	Fusarium oxysporum strain 3 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed space	699	699	98%	0.0	99%	KJ160146.1