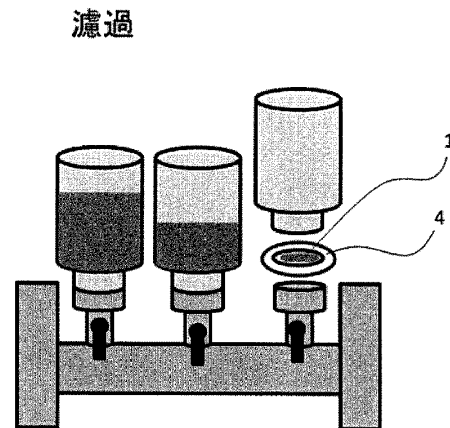
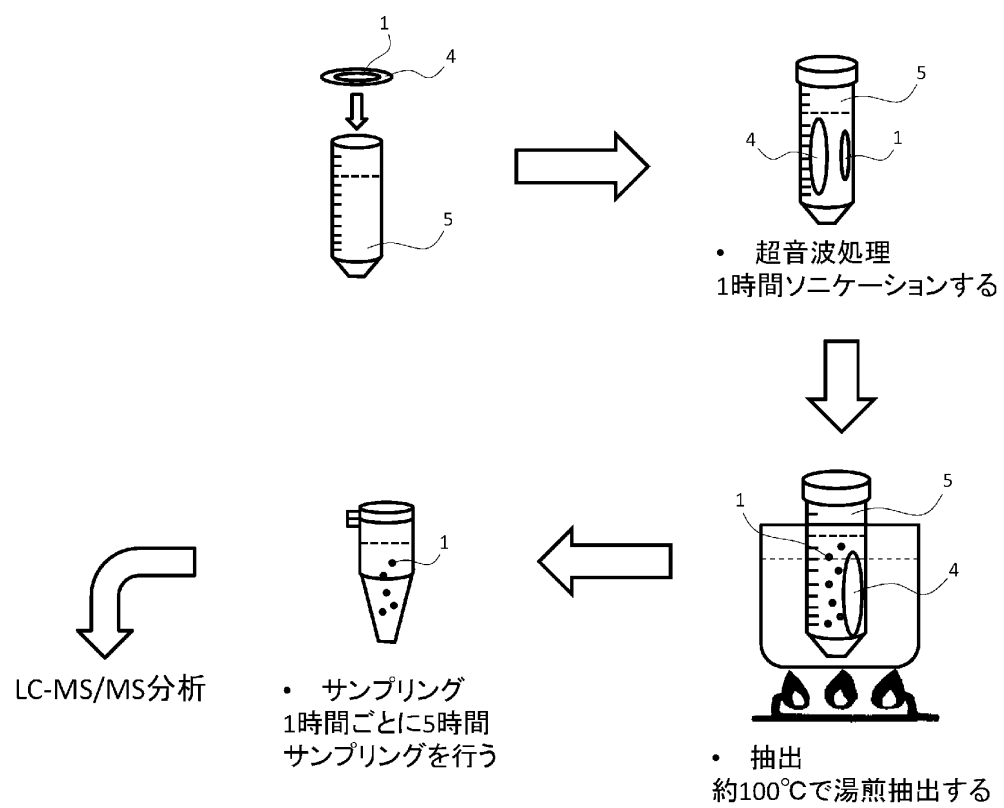


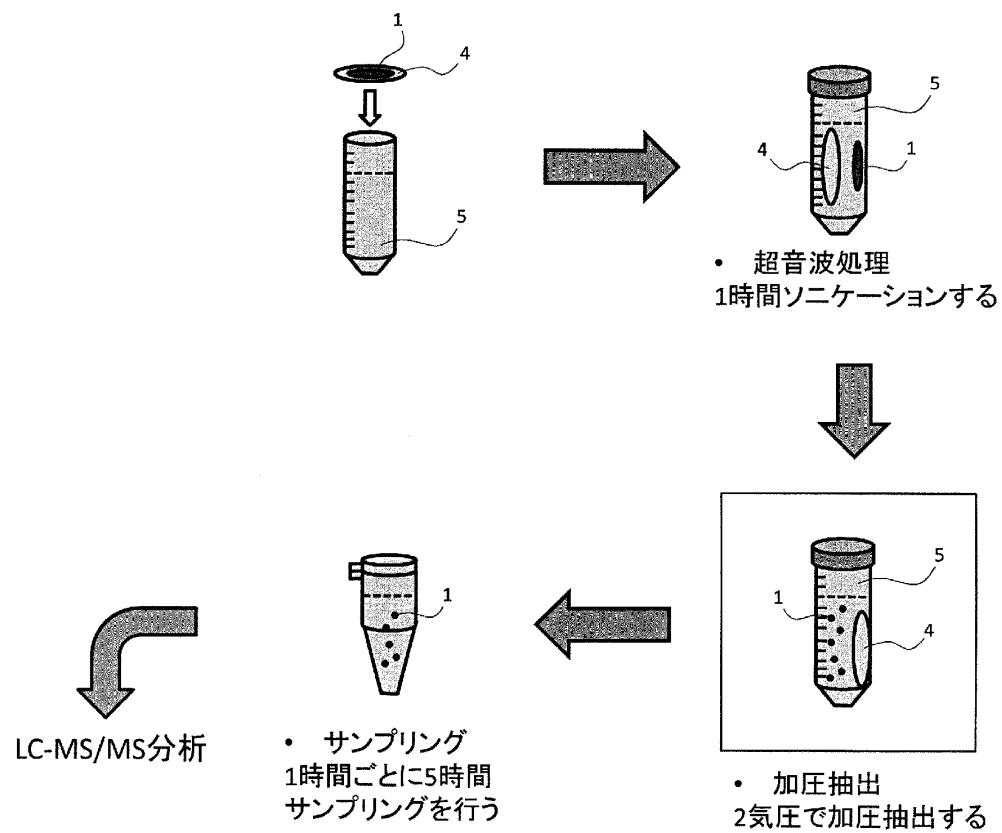
[図1]



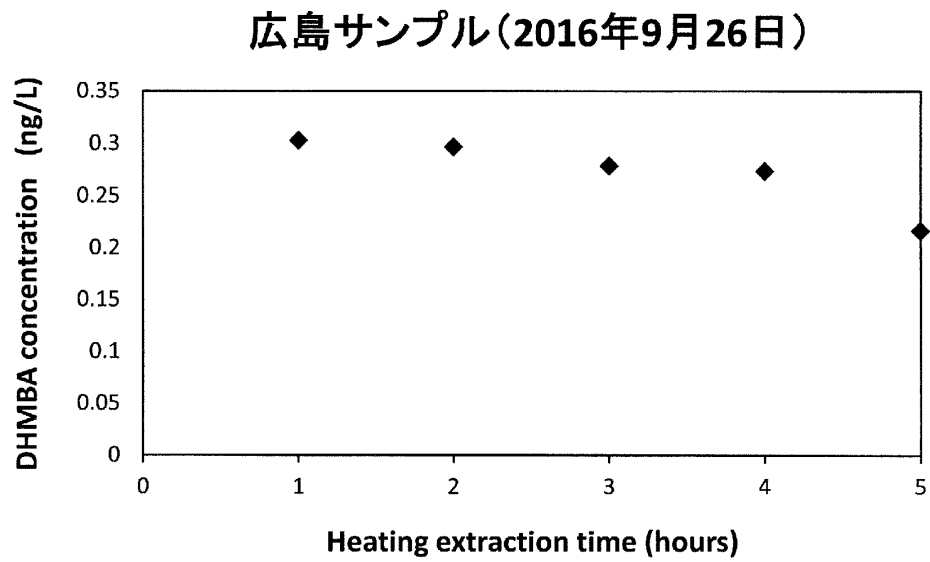
[図2]



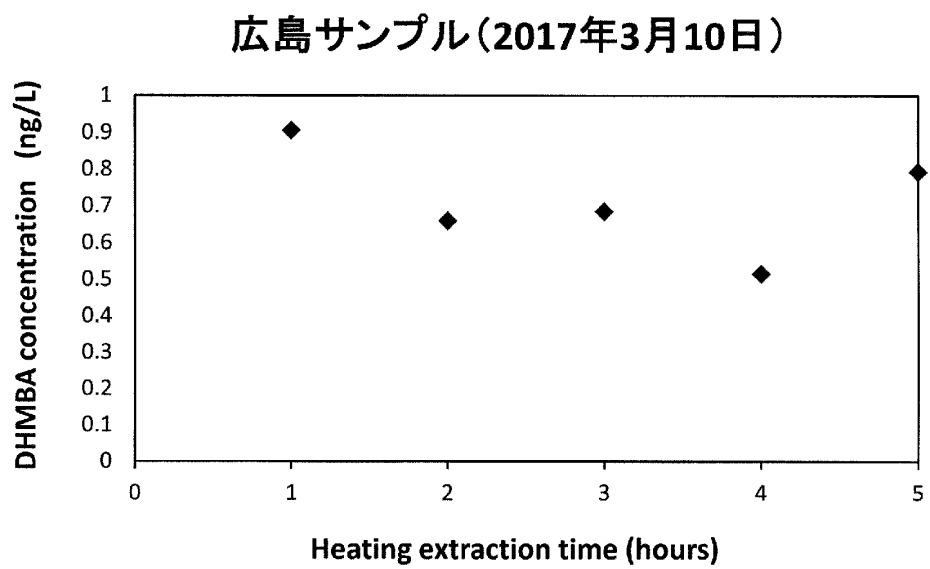
[図3]



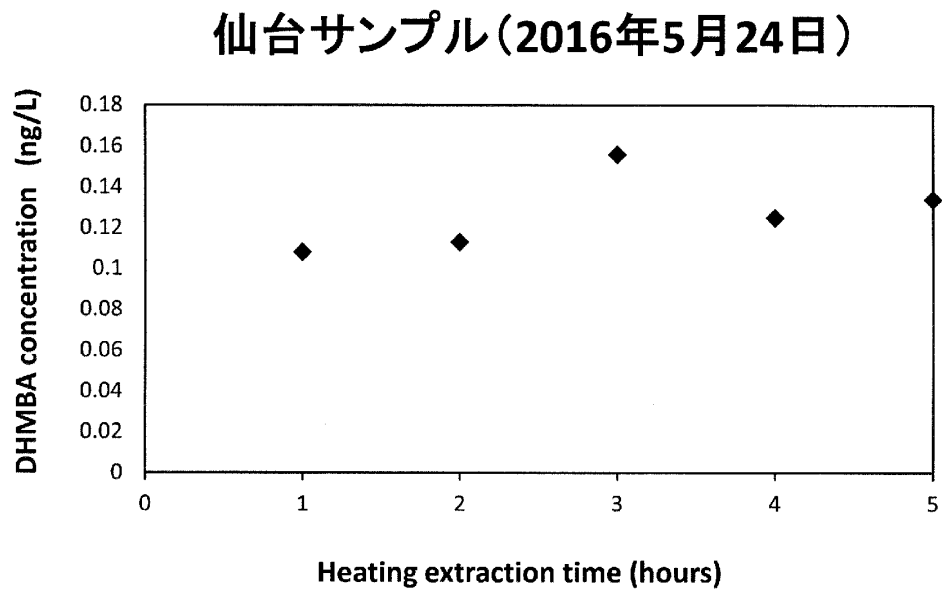
[図4]



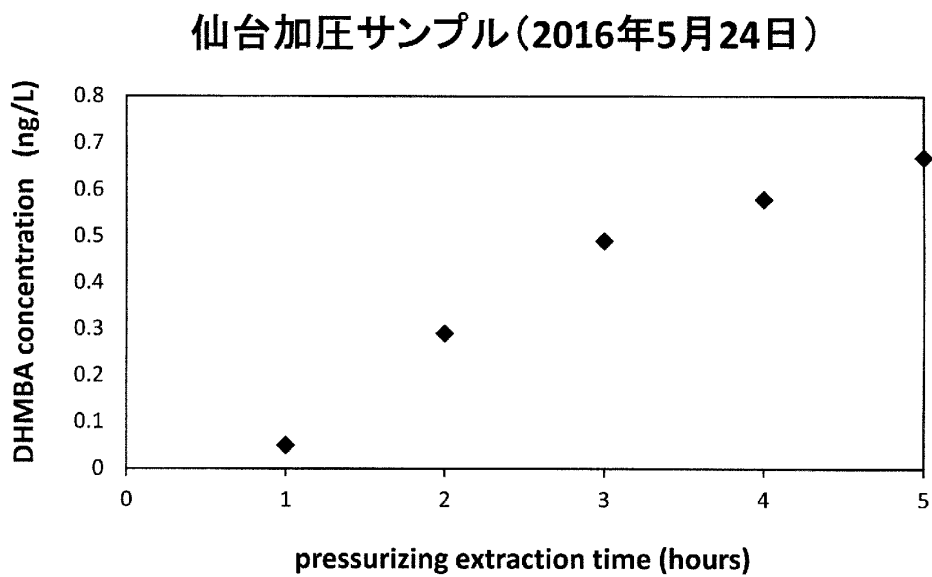
[図5]



[図6]

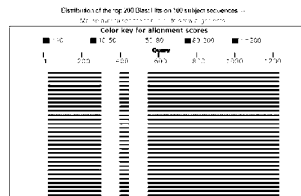


[図7]

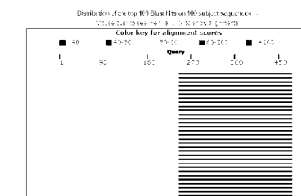


[図8]

HW-09-1981 47-49-1981 植物の系統関係と分類学												
Max score	Description	Max score	Total score	Query cover	E value	Ident	Accession	門	亜門	綱	目	科
1112	Acanthamoeba castellanii isolate H90-68118 ribosomal RNA gene, partial sequence	1112	1112	100.0%	0	96.181KJ58760.1	100.0%	Bacillariophyta	Bacillariophyta	Bacillariophyceae	Nitzschiales	ディクタエツキウイ目
1112	Acanthamoeba castellanii isolate H90-68118 ribosomal RNA gene, partial sequence	1112	1112	100.0%	0	96.181KJ58761.1	100.0%	Bacillariophyta	Bacillariophyta	Bacillariophyceae	Nitzschiales	ディクタエツキウイ目
1112	Plasmodium papilioe strain FLB11118 ribosomal RNA gene, partial sequence	1112	1112	100.0%	0	96.181KM1164.1	100.0%	Bacillariophyta	Bacillariophyta	Bacillariophyceae	Goniomonadales	ゴニョモナダ目
1107	Pavlovella taeniata strain COMPT1118 ribosomal RNA gene, partial sequence	1107	1107	100.0%	0	96.835KJ6311.1	100.0%	Bacillariophyta	Bacillariophyta	Bacillariophyceae	Cymbellales	シムベル目
1107	Achnanthes alberta isolate JLDLH1185 ribosomal RNA gene, partial sequence	1107	1107	100.0%	0	96.835KJ6341.1	100.0%	Bacillariophyta	Bacillariophyta	Bacillariophyceae	Goniomonadales	ゴニョモナダ目
1107	Achnanthes montana isolate ANZ1185 ribosomal RNA gene, partial sequence	1107	1107	100.0%	0	96.835KJ63540.1	100.0%	Bacillariophyta	Bacillariophyta	Bacillariophyceae	Goniomonadales	ゴニョモナダ目
1107	Achnanthes montana isolate ANZ1185 ribosomal RNA gene, partial sequence	1107	1107	100.0%	0	96.835KJ63541.1	100.0%	Bacillariophyta	Bacillariophyta	Bacillariophyceae	Goniomonadales	ゴニョモナダ目
1107	Achnanthes montana isolate ANZ1185 ribosomal RNA gene, partial sequence	1107	1107	100.0%	0	96.835KJ63542.1	100.0%	Bacillariophyta	Bacillariophyta	Bacillariophyceae	Goniomonadales	ゴニョモナダ目
1107	Achnanthes montana isolate ANZ1185 ribosomal RNA gene, partial sequence	1107	1107	100.0%	0	96.835KJ63543.1	100.0%	Bacillariophyta	Bacillariophyta	Bacillariophyceae	Goniomonadales	ゴニョモナダ目
1107	Achnanthes montana isolate ANZ1185 ribosomal RNA gene, partial sequence	1107	1107	100.0%	0	96.835KJ63544.1	100.0%	Bacillariophyta	Bacillariophyta	Bacillariophyceae	Goniomonadales	ゴニョモナダ目
1107	Achnanthes montana isolate ANZ1185 ribosomal RNA gene, partial sequence	1107	1107	100.0%	0	96.835KJ63545.1	100.0%	Bacillariophyta	Bacillariophyta	Bacillariophyceae	Goniomonadales	ゴニョモナダ目
1107	Achnanthes montana isolate ANZ1185 ribosomal RNA gene, partial sequence	1107	1107	100.0%	0	96.835KJ63546.1	100.0%	Bacillariophyta	Bacillariophyta	Bacillariophyceae	Goniomonadales	ゴニョモナダ目
1107	Achnanthes montana isolate ANZ1185 ribosomal RNA gene, partial sequence	1107	1107	100.0%	0	96.835KJ63547.1	100.0%	Bacillariophyta	Bacillariophyta	Bacillariophyceae	Goniomonadales	ゴニョモナダ目
1107	Achnanthes montana isolate ANZ1185 ribosomal RNA gene, partial sequence	1107	1107	100.0%	0	96.835KJ63548.1	100.0%	Bacillariophyta	Bacillariophyta	Bacillariophyceae	Goniomonadales	ゴニョモナダ目
1107	Achnanthes montana isolate ANZ1185 ribosomal RNA gene, partial sequence	1107	1107	100.0%	0	96.835KJ63549.1	100.0%	Bacillariophyta	Bacillariophyta	Bacillariophyceae	Goniomonadales	ゴニョモナダ目
1107	Achnanthes montana isolate ANZ1185 ribosomal RNA gene, partial sequence	1107	1107	100.0%	0	96.835KJ63550.1	100.0%	Bacillariophyta	Bacillariophyta	Bacillariophyceae	Goniomonadales	ゴニョモナダ目
1107	Achnanthes montana isolate ANZ1185 ribosomal RNA gene, partial sequence	1107	1107	100.0%	0	96.835KJ63551.1	100.0%	Bacillariophyta	Bacillariophyta	Bacillariophyceae	Goniomonadales	ゴニョモナダ目
1107	Achnanthes montana isolate ANZ1185 ribosomal RNA gene, partial sequence	1107	1107	100.0%	0	96.835KJ63552.1	100.0%	Bacillariophyta	Bacillariophyta	Bacillariophyceae	Goniomonadales	ゴニョモナダ目
1107	Achnanthes montana isolate ANZ1185 ribosomal RNA gene, partial sequence	1107	1107	100.0%	0	96.835KJ63553.1	100.0%	Bacillariophyta	Bacillariophyta	Bacillariophyceae	Goniomonadales	ゴニョモナダ目
1107	Achnanthes montana isolate ANZ1185 ribosomal RNA gene, partial sequence	1107	1107	100.0%	0	96.835KJ63554.1	100.0%	Bacillariophyta	Bacillariophyta	Bacillariophyceae	Goniomonadales	ゴニョモナダ目
1107	Achnanthes montana isolate ANZ1185 ribosomal RNA gene, partial sequence	1107	1107	100.0%	0	96.835KJ63555.1	100.0%	Bacillariophyta	Bacillariophyta	Bacillariophyceae	Goniomonadales	ゴニョモナダ目
1107	Achnanthes montana isolate ANZ1185 ribosomal RNA gene, partial sequence	1107	1107	100.0%	0	96.835KJ63556.1	100.0%	Bacillariophyta	Bacillariophyta	Bacillariophyceae	Goniomonadales	ゴニョモナダ目
1107	Achnanthes montana isolate ANZ1185 ribosomal RNA gene, partial sequence	1107	1107	100.0%	0	96.835KJ63557.1	100.0%	Bacillariophyta	Bacillariophyta	Bacillariophyceae	Goniomonadales	ゴニョモナダ目
1107	Achnanthes montana isolate ANZ1185 ribosomal RNA gene, partial sequence	1107	1107	100.0%	0	96.835KJ63558.1	100.0%	Bacillariophyta	Bacillariophyta	Bacillariophyceae	Goniomonadales	ゴニョモナダ目
1107	Achnanthes montana isolate ANZ1185 ribosomal RNA gene, partial sequence	1107	1107	100.0%	0	96.835KJ63559.1	100.0%	Bacillariophyta	Bacillariophyta	Bacillariophyceae	Goniomonadales	ゴニョモナダ目
1107	Achnanthes montana isolate ANZ1185 ribosomal RNA gene, partial sequence	1107	1107	100.0%	0	96.835KJ63560.1	100.0%	Bacillariophyta	Bacillariophyta	Bacillariophyceae	Goniomonadales	ゴニョモナダ目
1107	Achnanthes montana isolate ANZ1185 ribosomal RNA gene, partial sequence	1107	1107	100.0%	0	96.835KJ63561.1	100.0%	Bacillariophyta	Bacillariophyta	Bacillariophyceae	Goniomonadales	ゴニョモナダ目
1107	Achnanthes montana isolate ANZ1185 ribosomal RNA gene, partial sequence	1107	1107	100.0%	0	96.835KJ63562.1	100.0%	Bacillariophyta	Bacillariophyta	Bacillariophyceae	Goniomonadales	ゴニョモナダ目
1107	Achnanthes montana isolate ANZ1185 ribosomal RNA gene, partial sequence	1107	1107	100.0%	0	96.835KJ63563.1	100.0%	Bacillariophyta	Bacillariophyta	Bacillariophyceae	Goniomonadales	ゴニョモナダ目
1107	Achnanthes montana isolate ANZ1185 ribosomal RNA gene, partial sequence	1107	1107	100.0%	0	96.835KJ63564.1	100.0%	Bacillariophyta	Bacillariophyta	Bacillariophyceae	Goniomonadales	ゴニョモナダ目
1107	Achnanthes montana isolate ANZ1185 ribosomal RNA gene, partial sequence	1107	1107	100.0%	0	96.835KJ63565.1	100.0%	Bacillariophyta	Bacillariophyta	Bacillariophyceae	Goniomonadales	ゴニョモナダ目
1107	Achnanthes montana isolate ANZ1185 ribosomal RNA gene, partial sequence	1107	1107	100.0%	0	96.835KJ63566.1	100.0%	Bacillariophyta	Bacillariophyta	Bacillariophyceae	Goniomonadales	ゴニョモナダ目
1107	Achnanthes montana isolate ANZ1185 ribosomal RNA gene, partial sequence	1107	1107	100.0%	0	96.835KJ63567.1	100.0%	Bacillariophyta	Bacillariophyta	Bacillariophyceae	Goniomonadales	ゴニョモナダ目
1107	Achnanthes montana isolate ANZ1185 ribosomal RNA gene, partial sequence	1107	1107	100.0%	0	96.835KJ63568.1	100.0%	Bacillariophyta	Bacillariophyta	Bacillariophyceae	Goniomonadales	ゴニョモナダ目
1107	Achnanthes montana isolate ANZ1185 ribosomal RNA gene, partial sequence	1107	1107	100.0%	0	96.835KJ63569.1	100.0%	Bacillariophyta	Bacillariophyta	Bacillariophyceae	Goniomonadales	ゴニョモナダ目
1107	Achnanthes montana isolate ANZ1185 ribosomal RNA gene, partial sequence	1107	1107	100.0%	0	96.835KJ63570.1	100.0%	Bacillariophyta	Bacillariophyta	Bacillariophyceae	Goniomonadales	ゴニョモナダ目
1107	Achnanthes montana isolate ANZ1185 ribosomal RNA gene, partial sequence	1107	1107	100.0%	0	96.835KJ63571.1	100.0%	Bacillariophyta	Bacillariophyta	Bacillariophyceae	Goniomonadales	ゴニョモナダ目
1107	Achnanthes montana isolate ANZ1185 ribosomal RNA gene, partial sequence	1107	1107	100.0%	0	96.835KJ63572.1	100.0%	Bacillariophyta	Bacillariophyta	Bacillariophyceae	Goniomonadales	ゴニョモナダ目
1107	Achnanthes montana isolate ANZ1185 ribosomal RNA gene, partial sequence	1107	1107	100.0%	0	96.835KJ63573.1	100.0%	Bacillariophyta	Bacillariophyta	Bacillariophyceae	Goniomonadales	ゴニョモナダ目
1107	Achnanthes montana isolate ANZ1185 ribosomal RNA gene, partial sequence	1107	1107	100.0%	0	96.835KJ63574.1	100.0%	Bacillariophyta	Bacillariophyta	Bacillariophyceae	Goniomonadales	ゴニョモナダ目
1107	Achnanthes montana isolate ANZ1185 ribosomal RNA gene, partial sequence	1107	1107	100.0%	0	96.835KJ63575.1	100.0%	Bacillariophyta	Bacillariophyta	Bacillariophyceae	Goniomonadales	ゴニョモナダ目
1107	Achnanthes montana isolate ANZ1185 ribosomal RNA gene, partial sequence	1107	1107	100.0%	0	96.835KJ63576.1	100.0%	Bacillariophyta	Bacillariophyta	Bacillariophyceae	Goniomonadales	ゴニョモナダ目
1107	Achnanthes montana isolate ANZ1185 ribosomal RNA gene, partial sequence	1107	1107	100.0%	0	96.835KJ63577.1	100.0%	Bacillariophyta	Bacillariophyta	Bacillariophyceae	Goniomonadales	ゴニョモナダ目
1107	Achnanthes montana isolate ANZ1185 ribosomal RNA gene, partial sequence	1107	1107	100.0%	0	96.835KJ63578.1	100.0%	Bacillariophyta	Bacillariophyta	Bacillariophyceae	Goniomonadales	ゴニョモナダ目
1107	Achnanthes montana isolate ANZ1185 ribosomal RNA gene, partial sequence	1107	1107	100.0%	0	96.835KJ63579.1	100.0%	Bacillariophyta	Bacillariophyta	Bacillariophyceae	Goniomonadales	ゴニョモナダ目
1107	Achnanthes montana isolate ANZ1185 ribosomal RNA gene, partial sequence	1107	1107	100.0%	0	96.835KJ63580.1	100.0%	Bacillariophyta	Bacillariophyta	Bacillariophyceae	Goniomonadales	ゴニョモナダ目
1107	Achnanthes montana isolate ANZ1185 ribosomal RNA gene, partial sequence	1107	1107	100.0%	0	96.835KJ63581.1	100.0%	Bacillariophyta	Bacillariophyta	Bacillariophyceae	Goniomonadales	ゴニョモナダ目
1107	Achnanthes montana isolate ANZ1185 ribosomal RNA gene, partial sequence	1107	1107	100.0%	0	96.835KJ63582.1	100.0%	Bacillariophyta	Bacillariophyta	Bacillariophyceae	Goniomonadales	ゴニョモナダ目
1107	Achnanthes montana isolate ANZ1185 ribosomal RNA gene, partial sequence	1107	1107	100.0%	0	96.835KJ63583.1	100.0%	Bacillariophyta	Bacillariophyta	Bacillariophyceae	Goniomonadales	ゴニョモナダ目
1107	Achnanthes montana isolate ANZ1185 ribosomal RNA gene, partial sequence	1107	1107	100.0%	0	96.835KJ63584.1	100.0%	Bacillariophyta	Bacillariophyta	Bacillariophyceae	Goniomonadales	ゴニョモナダ目
1107	Achnanthes montana isolate ANZ1185 ribosomal RNA gene, partial sequence	1107	1107	100.0%	0	96.835KJ63585.1	100.0%	Bacillariophyta	Bacillariophyta	Bacillariophyceae	Goniomonadales	ゴニョモナダ目
1107	Achnanthes montana isolate ANZ1185 ribosomal RNA gene, partial sequence	1107	1107	100.0%	0	96.835KJ63586.1	100.0%	Bacillariophyta	Bacillariophyta	Bacillariophyceae	Goniomonadales	ゴニョモナダ目
1107	Achnanthes montana isolate ANZ1185 ribosomal RNA gene, partial sequence	1107	1107	100.0%	0	96.835KJ63587.1	100.0%	Bacillariophyta	Bacillariophyta	Bacillariophyceae	Goniomonadales	ゴニョモナダ目
1107	Achnanthes montana isolate ANZ1185 ribosomal RNA gene, partial sequence	1107	1107	100.0%	0	96.835KJ63588.1	100.0%	Bacillariophyta	Bacillariophyta	Bacillariophyceae	Goniomonadales	ゴニョモナダ目
1107	Achnanthes montana isolate ANZ1185 ribosomal RNA gene, partial sequence	1107	1107	100.0%	0	96.835KJ63589.1	100.0%	Bacillariophyta	Bacillariophyta	Bacillariophyceae	Goniomonadales	ゴニョモナダ目
1107	Achnanthes montana isolate ANZ1185 ribosomal RNA gene, partial sequence	1107	1107	100.0%	0	96.835KJ63590.1	100.0%	Bacillariophyta	Bacillariophyta	Bacillariophyceae	Goniomonadales	ゴニョモナダ目
1107	Achnanthes montana isolate ANZ1185 ribosomal RNA gene, partial sequence	1107	1107	100.0%	0	96.835KJ63591.1	100.0%	Bacillariophyta	Bacillariophyta	Bacillariophyceae	Goniomonadales	ゴニョモナダ目
1107	Achnanthes montana isolate ANZ1185 ribosomal RNA gene, partial sequence	1107	1107	100.0%	0	96.835KJ63592.1	100.0%	Bacillariophyta	Bacillariophyta	Bacillariophyceae	Goniomonadales	ゴニョモナダ目
1107	Achnanthes montana isolate ANZ1185 ribosomal RNA gene, partial sequence	1107	1107	100.0%	0	96.835KJ63593.1	100.0%	Bacillariophyta	Bacillariophyta	Bacillariophyceae	Goniomonadales	ゴニョモナダ目
1107	Achnanthes montana isolate ANZ1185 ribosomal RNA gene, partial sequence	1107	1107	100.0%	0	96.835KJ63594.1	100.0%	Bacillariophyta	Bacillariophyta	Bacillariophyceae	Goniomonadales	ゴニョモナダ目
1107	Achnanthes montana isolate ANZ1185 ribosomal RNA gene, partial sequence	1107	1107	100.0%	0	96.835KJ63595.1	100.0%	Bacillariophyta	Bacillariophyta	Bacillariophyceae	Goniomonadales	ゴニョモナダ目
1107	Achnanthes montana isolate ANZ1185 ribosomal RNA gene, partial sequence	1107	1107	100.0%	0	96.835KJ63596.1	100.0%	Bacillariophyta	Bacillariophyta	Bacillariophyceae	Goniomonadales	ゴニョモナダ目
1107	Achnanthes montana isolate ANZ1185 ribosomal RNA gene, partial sequence	1107	1107	100.0%	0	96.835KJ63597.1	100.0%	Bacillariophyta	Bacillariophyta	Bacillariophyceae	Goniomonadales	ゴニョモナダ目
1107	Achnanthes montana isolate ANZ1185 ribosomal RNA gene, partial sequence	1107	1107	100.0%	0	96.835KJ63598.1	100.0%	Bacillariophyta	Bacillariophyta	Bacillariophyceae	Goniomonadales	ゴニョモナダ目
1107	Achnanthes montana isolate ANZ1185 ribosomal RNA gene, partial sequence	1107	1107	100.0%	0	96.835KJ63599.1	100.0%	Bacillariophyta	Bacillariophyta	Bacillariophyceae	Goniomonadales	ゴニョモナダ目
1107	Achnanthes montana isolate ANZ1185 ribosomal RNA gene, partial sequence	1107	1107	100.0%	0	96.835KJ63600.1	100.0%	Bacillariophyta	Bacillariophyta	Bacillariophyceae	Goniomonadales	ゴニョモナダ目
1107	Achnanthes montana isolate ANZ1185 ribosomal RNA gene, partial sequence	1107	1107	100.0%	0	96.835KJ63601.1	100.0%	Bacillariophyta	Bacillariophyta	Bacillariophyceae	Goniomonadales	ゴニョモナダ目
1107	Achnanthes montana isolate ANZ1185 ribosomal RNA gene, partial sequence	1107	1107	100.0%	0	96.835KJ63602.1	100.0%	Bacillariophyta	Bacillariophyta	Bacillariophyceae	Goniomonadales	ゴニョモナダ目
1107	Achnanthes montana isolate ANZ1185 ribosomal RNA gene, partial sequence	1107	1107	100.0%	0	96.835KJ63603.1	100.0%	Bacillariophyta	Bacillariophyta	Bacillariophyceae	Goniomonadales	ゴニョモナダ目
1107	Achnanthes montana isolate ANZ1185 ribosomal RNA gene, partial sequence	1107	1107	100.0%	0	96.835KJ63604.1	100.0%	Bacillariophyta	Bacillariophyta	Bacillariophyceae	Goniomonadales	ゴニョモナダ目
1107	Achnanthes montana isolate ANZ1185 ribosomal RNA gene, partial sequence	1107	1107	100.0%	0	96.835KJ63605.1	100.0%	Bacillariophyta	Bacillariophyta	Bacillariophyceae	Goniomonadales	ゴニョモナダ目
1107	Achnanthes montana isolate ANZ1185 ribosomal RNA gene, partial sequence	1107	1107	100.0%	0	96.835KJ63606.1	100.0%	Bacillariophyta	Bacillariophyta	Bacillariophyceae	Goniomonadales	ゴニョモナダ目
1107	Achnanthes montana isolate ANZ1185 ribosomal RNA gene, partial sequence	1107	1107	100.0%	0	96.835KJ63607.1	100.0%	Bacillariophyta	Bacillariophyta	Bacillariophyceae	Goniomonadales	ゴニョモナダ目
1107	Achnanthes montana isolate ANZ1185 ribosomal RNA gene, partial sequence	1107	1107	100.0%	0	96.835KJ63608.1	100.0%	Bacillariophyta	Bacillariophyta	Bacillariophyceae	Goniomonadales	ゴニョモナダ目
1107	Achnanthes montana isolate ANZ1185 ribosomal RNA gene, partial sequence	1107	1107	100.0%	0	96.835KJ63609.1	100.0%	Bacillariophyta	Bacillariophyta	Bacillariophyceae	Goniomonadales	ゴニョモナダ目
1107	Achnanthes montana isolate ANZ1185 ribosomal RNA gene, partial sequence	1107	1107	100.0%	0	96.835KJ63610.1	100.0%	Bacillariophyta	Bacillariophyta	Bacillariophyceae	Goniomonadales	ゴニョモナダ目
1107	Achnanthes montana isolate ANZ1185 ribosomal RNA gene, partial sequence	1107	1107	100.0%	0	96.835KJ63611.1	100.0%	Bacillariophyta	Bacillariophyta	Bacillariophyceae	Goniomonadales	ゴニョモナダ目
1107	Achnanthes montana isolate ANZ1185 ribosomal RNA gene, partial sequence	1107	1107	100.0%	0	96.835KJ63612.1	100.0%	Bacillariophyta	Bacillariophyta	Bacillariophyceae	Goniomonadales	ゴニョモナダ目
1107	Achnanthes montana isolate ANZ1185 ribosomal RNA gene, partial sequence	1107	1107	100.0%	0	96.835KJ63613.1	100.0%	Bacillariophyta	Bacillariophyta	Bacillariophyceae	Goniomonadales	ゴニョモナダ目
1107	Achnanthes montana isolate ANZ1185 ribosomal RNA gene, partial sequence	1107	1107	100.0%	0	96.835KJ63614.1	100.0%	Bacillariophyta	Bacillariophyta	Bacillariophyceae	Goniomonadales	ゴニョモナダ目



[图9]

[illegible]

WO 2020/031720

PCT/JP2019/029201

【図10】

		H7-09-18S 検索条件: Limit to sequences from type material							Max score による 順位	連番	
		Description	Max score	Total score	Query cover	E value	Ident	Accession			
1	1	Fistulifera solaris gene for 18S ribosomal RNA, partial sequence	1027	1027	100.00%	0	93.88%	AB769957.1			注藻
2	2	Pedospumella encystans voucher B 40 0040671 18S ribosomal RNA gene, partial sequence	843	843	100.00%	0	89.06%	AY651083.1			黄金色藻
3	3	Heterococcus fuorenensis partial 18S rRNA gene, strain SAG 835-5	832	832	100.00%	0	88.71%	AM490821.1			黄緑藻
4	3	Heterococcus caespitosus partial 18S rRNA gene, strain SAG 835-2a	832	832	100.00%	0	88.71%	AM490820.1			黄緑藻
5	5	Chlorellidium tetrabotrys strain SAG811-1 18S ribosomal RNA gene, partial sequence	821	821	100.00%	0	88.45%	FJ030892.1			黄緑藻
6	5	Spumella vulgaris isolate 199hm 18S ribosomal RNA gene, partial sequence	821	821	100.00%	0	88.47%	DQ388552.1			黄金色藻
7	7	Sphaerosorus composita partial 18S rRNA gene, strain SAG 53.91	809	809	100.00%	0	88.12%	AJ579333.1			
8	8	Bumilleriopsis pyrenoidosa partial 18S rRNA gene, strain SAG 69.90	802	802	100.00%	0	87.89%	AJ579332.1			
9	9	Pseudotetraedrella kamillae strain SAG 2056 18S ribosomal RNA gene, partial sequence	778	778	100.00%	0	87.39%	EF044311.1			
10	9	Nannochloropsis limnetica strain SAG 18.99 culture-col-ecdon SAG 18.99 18S ribosomal RNA gene, partial sequence	778	778	100.00%	0	87.41%	AF251496.1			
11	11	Monodus unipapilla partial 18S rRNA gene, strain SAG 8.83	767	767	100.00%	0	87.11%	AM490827.1			
12	12	Vischeria helvetica strain SAG 876-1 18S ribosomal RNA gene, complete sequence	763	763	100.00%	0	86.98%	UJ188080.1			
13	13	Eustigmatos vischeri isolate SAG 860-1 18S ribosomal RNA gene, complete sequence	758	758	100.00%	0	86.84%	UJ274590.1			
14	13	Eustigmatos polyphem strain SAG 38.84 18S ribosomal RNA gene, complete sequence	758	758	100.00%	0	86.84%	UJ188077.1			
15	15	Ochromonas danica strain SAG9337 18S ribosomal RNA gene, partial sequence	749	749	100.00%	0	86.62%	UJ281514.1			
16	16	Monodus unipapilla culture SAG 8.83 voucher SAG 8.83 18S ribosomal RNA (ssu) gene, partial sequence	728	728	96.00%	0	86.89%	HQ710565.1			
17	17	Sargassococcus simulans strain CCMP1996 18S ribosomal RNA gene, partial sequence	719	719	100.00%	0	85.88%	MF927481.1			
18	17	Pelagospilus aureus strain CCMP1410 18S ribosomal RNA gene, partial sequence	719	719	100.00%	0	85.90%	MF927480.1			
19	19	Sargassococcus eophyticus strain CCMP1995 18S ribosomal RNA gene, partial sequence	708	708	100.00%	0	85.53%	MF927478.1			
20	20	Lepididion sp. PIML-2010c strain CBS 127042 18S ribosomal RNA gene, partial sequence	686	686	100.00%	0	84.89%	HQ384409.1			
21	21	Geranomyces variabilis voucher MP03 18S small subunit ribosomal RNA gene, partial sequence	682	682	100.00%	0	84.94%	HQ901757.1			
22	21	Geranomyces michiganensis voucher JEL563 18S small subunit ribosomal RNA gene, partial sequence	682	682	100.00%	0	84.94%	HQ901742.1			
23	21	Spumella rivalis strain AR4A6 18S ribosomal RNA gene, partial sequence	682	682	100.00%	0	85.65%	UJ073468.1			
24	24	Fimicolochytrium jonesii JEL 569 18S rRNA gene, partial sequence; from TYPE material	671	671	100.00%	0	84.65%	NC 061114.1			
25	24	Thoreaumyces humboldtii JEL 95 18S rRNA gene, partial sequence; from TYPE material	671	671	100.00%	0	84.63%	NC 061113.1			
26	24	Fimicolochytrium jonesii voucher JEL569 18S small subunit ribosomal RNA gene, partial sequence	671	671	100.00%	0	84.65%	HQ901746.1			
27	24	Thoreaumyces humboldtii voucher JEL95 18S small subunit ribosomal RNA gene, partial sequence	671	671	100.00%	0	84.63%	HQ901727.1			
28	28	Fimicolochytrium alabamense JEL 538 18S rRNA gene, partial sequence; from TYPE material	665	665	100.00%	0	84.51%	NC 062391.1			
29	28	Fimicolochytrium alabamense voucher JEL538 18S small subunit ribosomal RNA gene, partial sequence	665	665	100.00%	0	84.51%	HQ901734.1			
30	29	Myxozyma neglecta 18S rRNA gene, partial sequence; from TYPE material	645	645	99.00%	0	84.03%	NC 062046.1			
31	29	Myxozyma mucilagina 18S rRNA gene, partial sequence; from TYPE material	645	645	99.00%	0	84.03%	NC 062045.1			
32	29	Myxozyma neglecta strain NRRL Y-27508 18S ribosomal RNA gene, partial sequence	645	645	99.00%	0	84.03%	DQ519022.1			
33	29	Myxozyma mucilagina strain NRRL Y-11623 18S ribosomal RNA gene, partial sequence	645	645	99.00%	0	84.03%	DQ519021.1			

【図11】

		H7-09-28S_D2R2 検索条件: Limit to sequences from type material							Max score による 順位	連番	
		Description	Max score	Total score	Query cover	E value	Ident	Accession			
1	1	Chlorellidium tetrabotrys strain SAG811-1 28S ribosomal RNA gene, partial sequence	233	233	48.00%	2.00E-58	84.94%	FJ030881.1			黄緑藻
2	2	Fimicolochytrium jonesii JEL 569 28S rRNA gene, partial sequence; from TYPE material	224	224	48.00%	1.00E-55	84.26%	NC 060391.1			真菌
3	2	Fimicolochytrium jonesii voucher JEL569 28S large subunit ribosomal RNA gene, partial sequence	224	224	48.00%	1.00E-55	84.26%	HQ901681.1			真菌
4	4	Geranomyces variabilis voucher MP03 28S large subunit ribosomal RNA gene, partial sequence	219	219	48.00%	5.00E-54	84.03%	HQ901692.1			真菌
5	5	Thoreaumyces humboldtii JEL 95 28S rRNA gene, partial sequence; from TYPE material	217	217	48.00%	2.00E-53	83.90%	NC 059938.1			真菌
6	5	Thoreaumyces humboldtii voucher JEL95 28S large subunit ribosomal RNA gene, partial sequence	217	217	48.00%	2.00E-53	83.90%	HQ901662.1			真菌
7	5	Spizellomyces acuminatus 28S ribosomal RNA (LSU) gene, partial sequence	217	217	48.00%	2.00E-53	83.83%	JN941010.1			真菌
8	5	Phlyctochytrium africanum voucher CBS 454.65 28S ribosomal RNA gene, partial sequence	217	217	48.00%	2.00E-53	83.83%	FJ827693.1			真菌
9	9	Holtermanniella wettica CBS 9496 28S rRNA gene, partial sequence; from TYPE material	215	215	48.00%	6.00E-53	83.61%	NC 058307.1			
10	9	Holtermanniella wettica culture CBS:9496 large subunit ribosomal RNA gene, partial sequence	215	215	48.00%	6.00E-53	83.61%	KY107874.1			
11	11	Fimicolochytrium alabamense JEL 538 28S rRNA gene, partial sequence; from TYPE material	213	213	48.00%	2.00E-52	83.40%	NC 060390.1			
12	11	Fimicolochytrium alabamense voucher JEL538 28S large subunit ribosomal RNA gene, partial sequence	213	213	48.00%	2.00E-52	83.40%	HQ901669.1			
13	11	Gorgonomyces haynaldii BAF0 ARG 026 28S rRNA, partial sequence; from TYPE material	213	213	48.00%	2.00E-52	83.62%	NC 042448.1			
14	14	Ceriporiopsis semisupina BJFO Cui 10222 28S rRNA gene, partial sequence; from TYPE material	211	211	48.00%	8.00E-52	83.40%	NC 064354.1			
15	14	Ceriporiopsis sp. GLZ-2014 voucher Cui 10222 28S large subunit ribosomal RNA gene, partial sequence	211	211	48.00%	8.00E-52	83.40%	KF845949.1			
16	14	Sonophragmatis ranzonii DAOM BR 060 28S rRNA, partial sequence; from TYPE material	211	211	48.00%	8.00E-52	83.47%	NC 042454.1			
17	17	Basidiobolus undulatus strain CBS 133763 large subunit ribosomal RNA gene, partial sequence	209	209	48.00%	3.00E-51	83.19%	MH877552.1			
18	17	Piskurozyma taiwanensis CBS 9813 28S rRNA gene, partial sequence; from TYPE material	209	209	48.00%	3.00E-51	83.19%	NC 058375.1			
19	17	Goffauezyma gastrica CBS 2288 28S rRNA gene, partial sequence; from TYPE material	209	209	48.00%	3.00E-51	83.19%	NC 058296.1			
20	17	Goffauezyma aciditolerans CBS 10672 28S rRNA gene, partial sequence; from TYPE material	209	209	48.00%	3.00E-51	83.19%	NC 058295.1			
21	17	Solfocozyma aerea culture CBS:155 large subunit ribosomal RNA gene, partial sequence	209	209	48.00%	3.00E-51	83.19%	KY109666.1			
22	17	Piskurozyma taiwanensis culture CBS:9813 large subunit ribosomal RNA gene, partial sequence	209	209	48.00%	3.00E-51	83.19%	KY108934.1			
23	17	Naganishia globosa culture CBS:5106 large subunit ribosomal RNA gene, partial sequence	209	209	48.00%	3.00E-51	83.19%	KY108616.1			
24	17	Naganishia friedmannii culture CBS:7160 large subunit ribosomal RNA gene, partial sequence	209	209	48.00%	3.00E-51	83.19%	KY108613.1			
25	17	Goffauezyma gastrica culture CBS:2288 large subunit ribosomal RNA gene, partial sequence	209	209	48.00%	3.00E-51	83.19%	KY107764.1			
26	17	Goffauezyma aciditolerans culture CBS:10672 large subunit ribosomal RNA gene, partial sequence	209	209	48.00%	3.00E-51	83.19%	KY107763.1			
27	17	Filobasidium wieringae culture CBS:1937 large subunit ribosomal RNA gene, partial sequence	209	209	48.00%	3.00E-51	83.12%	KY107733.1			
28	17	Filobasidium magnum culture CBS:140 large subunit ribosomal RNA gene, partial sequence	209	209	48.00%	3.00E-51	83.12%	KY107722.1			
29	17	Filobasidium globisporum culture CBS:7642 large subunit ribosomal RNA gene, partial sequence	209	209	48.00%	3.00E-51	83.12%	KY107713.1			
30	17	Filobasidium floriforme culture CBS:6241 large subunit ribosomal RNA gene, partial sequence	209	209	48.00%	3.00E-51	83%	KY107703.1			

Substrate Effects on Kinetics in Disrupted Sequences

Query

400 200 100 50

Query

0 100 200 300 400

WO 2020/031720

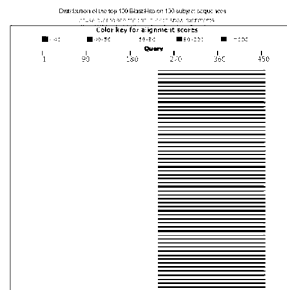
PCT/JP2019/029201

【図14】

H9-05-28S D2R2

種属条件・環境由来配列を除く全体

Max score に基づく 順位	Description	Max score	Total score	Query cover	E value	Ident	Accession	門	亜門	綱	亜綱	目	
1	<i>Pseudo-nitzschia multiseries</i> strain 14D-132 28S ribosomal RNA gene, partial sequence	359	359	43.00%	5.00E-95	96.03%	KX290694.1	法藻	Bacillariophyta	Bacillariophyceae	Bacillariophycidae	Bacillariales	クラシケイノウ目
2	<i>Pseudo-nitzschia areolata</i> strain 22b 28S ribosomal RNA gene, part a sequence	359	359	43.00%	5.00E-95	96.03%	KX290697.1	法藻	Bacillariophyta	Bacillariophyceae	Bacillariophycidae	Bacillariales	クラシケイノウ目
3	<i>Pseudo-nitzschia areolata</i> strain 206b 28S ribosomal RNA gene, part a sequence	359	359	43.00%	5.00E-95	96.03%	KX290695.1	法藻	Bacillariophyta	Bacillariophyceae	Bacillariophycidae	Bacillariales	クラシケイノウ目
4	<i>Pseudo-nitzschia areolata</i> strain 217b 28S ribosomal RNA gene, part a sequence	359	359	43.00%	5.00E-95	96.03%	KX290694.1	法藻	Bacillariophyta	Bacillariophyceae	Bacillariophycidae	Bacillariales	クラシケイノウ目
5	<i>Pseudo-nitzschia areolata</i> strain 423b 28S ribosomal RNA gene, part a sequence	359	359	43.00%	5.00E-95	96.03%	KX290693.1	法藻	Bacillariophyta	Bacillariophyceae	Bacillariophycidae	Bacillariales	クラシケイノウ目
6	<i>Nitzschia radiocarinata</i> voucher NUN2 large subunit ribosomal RNA gene, partial sequence	359	359	43.00%	5.00E-95	96.03%	KX353681.1	法藻	Bacillariophyta	Bacillariophyceae	Bacillariophycidae	Bacillariales	クラシケイノウ目
7	<i>Nitzschia radiocarinata</i> voucher NUN3 large subunit ribosomal RNA gene, partial sequence	359	359	43.00%	5.00E-95	96.03%	KX353680.1	法藻	Bacillariophyta	Bacillariophyceae	Bacillariophycidae	Bacillariales	クラシケイノウ目
8	<i>Nitzschia radiocarinata</i> voucher NUN6 large subunit ribosomal RNA gene, partial sequence	359	359	43.00%	5.00E-95	96.03%	KX353688.1	法藻	Bacillariophyta	Bacillariophyceae	Bacillariophycidae	Bacillariales	クラシケイノウ目
9	<i>Nitzschia radiocarinata</i> voucher NUN5 large subunit ribosomal RNA gene, partial sequence	359	359	43.00%	5.00E-95	96.03%	KX353687.1	法藻	Bacillariophyta	Bacillariophyceae	Bacillariophycidae	Bacillariales	クラシケイノウ目
10	<i>Nitzschia radiocarinata</i> voucher NUN2 large subunit ribosomal RNA gene, partial sequence	359	359	43.00%	5.00E-95	96.03%	KX353686.1	法藻	Bacillariophyta	Bacillariophyceae	Bacillariophycidae	Bacillariales	クラシケイノウ目
11	<i>Nitzschia radiocarinata</i> voucher NUN1 large subunit ribosomal RNA gene, partial sequence	359	359	43.00%	5.00E-95	96.03%	KX353685.1	法藻	Bacillariophyta	Bacillariophyceae	Bacillariophycidae	Bacillariales	クラシケイノウ目
12	<i>Nitzschia radiocarinata</i> voucher NUN3 large subunit ribosomal RNA gene, partial sequence	359	359	43.00%	5.00E-95	96.03%	KX353684.1	法藻	Bacillariophyta	Bacillariophyceae	Bacillariophycidae	Bacillariales	クラシケイノウ目
13	<i>Nitzschia radiocarinata</i> voucher NUN2 large subunit ribosomal RNA gene, partial sequence	359	359	43.00%	5.00E-95	96.03%	KX353683.1	法藻	Bacillariophyta	Bacillariophyceae	Bacillariophycidae	Bacillariales	クラシケイノウ目
14	<i>Pseudo-nitzschia multiseries</i> voucher PNU1 large subunit ribosomal RNA gene, partial sequence	359	359	43.00%	5.00E-95	96.03%	KF021344.1	法藻	Bacillariophyta	Bacillariophyceae	Bacillariophycidae	Bacillariales	クラシケイノウ目
15	<i>Pseudo-nitzschia areolata</i> strain 2b 28S large subunit ribosomal RNA gene, partial sequence	359	359	43.00%	5.00E-95	96.03%	K1189137.1	法藻	Bacillariophyta	Bacillariophyceae	Bacillariophycidae	Bacillariales	クラシケイノウ目
16	<i>Pseudo-nitzschia multiseries</i> isolate GAMB11 28S large subunit ribosomal RNA gene, partial sequence	359	359	43.00%	5.00E-95	96.03%	KJ2795549.1	法藻	Bacillariophyta	Bacillariophyceae	Bacillariophycidae	Bacillariales	クラシケイノウ目
17	<i>Pseudo-nitzschia multiseries</i> strain P553 large subunit ribosomal RNA gene, partial sequence	359	359	43.00%	5.00E-95	96.03%	KO217445.1	法藻	Bacillariophyta	Bacillariophyceae	Bacillariophycidae	Bacillariales	クラシケイノウ目
18	<i>Pseudo-nitzschia multiseries</i> strain P125C large subunit ribosomal RNA gene, partial sequence	359	359	43.00%	5.00E-95	96.03%	KC211480.1	法藻	Bacillariophyta	Bacillariophyceae	Bacillariophycidae	Bacillariales	クラシケイノウ目
19	<i>Pseudo-nitzschia multiseries</i> strain P125C large subunit ribosomal RNA gene, partial sequence	359	359	43.00%	5.00E-95	96.03%	KC211459.1	法藻	Bacillariophyta	Bacillariophyceae	Bacillariophycidae	Bacillariales	クラシケイノウ目
20	<i>Pseudo-nitzschia multiseries</i> strain C163 large subunit ribosomal RNA gene, partial sequence	359	359	43.00%	5.00E-95	96.03%	KC211456.1	法藻	Bacillariophyta	Bacillariophyceae	Bacillariophycidae	Bacillariales	クラシケイノウ目
21	<i>Pseudo-nitzschia multiseries</i> isolate CM2 large subunit ribosomal RNA gene, partial sequence	359	359	43.00%	5.00E-95	96.03%	J150735.1	法藻	Bacillariophyta	Bacillariophyceae	Bacillariophycidae	Bacillariales	クラシケイノウ目
22	<i>Pseudo-nitzschia multiseries</i> voucher COM186 28S ribosomal RNA gene, partial sequence	359	359	43.00%	5.00E-95	96.03%	KJ299845.1	法藻	Bacillariophyta	Bacillariophyceae	Bacillariophycidae	Bacillariales	クラシケイノウ目
23	<i>Pseudo-nitzschia multiseries</i> isolate CM2 large subunit ribosomal RNA gene, partial sequence	359	359	43.00%	5.00E-95	96.03%	EF442761.1	法藻	Bacillariophyta	Bacillariophyceae	Bacillariophycidae	Bacillariales	クラシケイノウ目
24	<i>Pseudo-nitzschia multiseries</i> isolate CM1 large subunit ribosomal RNA gene, partial sequence	359	359	43.00%	5.00E-95	96.03%	EF442761.1	法藻	Bacillariophyta	Bacillariophyceae	Bacillariophycidae	Bacillariales	クラシケイノウ目
25	<i>Pseudo-nitzschia delicatissima</i> strain P23 large subunit ribosomal RNA gene, partial sequence	359	359	43.00%	5.00E-95	96.03%	EF366013.1	法藻	Bacillariophyta	Bacillariophyceae	Bacillariophycidae	Bacillariales	クラシケイノウ目
26	<i>Pseudo-nitzschia areolata</i> strain A-424 large subunit ribosomal RNA gene, partial sequence	359	359	43.00%	5.00E-95	96.03%	DQ013811.1	法藻	Bacillariophyta	Bacillariophyceae	Bacillariophycidae	Bacillariales	クラシケイノウ目
27	<i>Pseudo-nitzschia multiseries</i> isolate SDN-622 large subunit ribosomal RNA gene, partial sequence	359	359	43.00%	5.00E-95	96.03%	AF418753.1	法藻	Bacillariophyta	Bacillariophyceae	Bacillariophycidae	Bacillariales	クラシケイノウ目
28	<i>Pseudo-nitzschia delicatissima</i> strain SDN-616 large subunit ribosomal RNA gene, partial sequence	359	359	43.00%	5.00E-95	96.03%	AF416748.1	法藻	Bacillariophyta	Bacillariophyceae	Bacillariophycidae	Bacillariales	クラシケイノウ目
29	<i>Pseudo-nitzschia delicatissima</i> isolate 2-402 large subunit ribosomal RNA gene, partial sequence	359	359	43.00%	5.00E-95	96.03%	AY193553.1	法藻	Bacillariophyta	Bacillariophyceae	Bacillariophycidae	Bacillariales	クラシケイノウ目
30	<i>Pseudo-nitzschia delicatissima</i> isolate 18-02 large subunit ribosomal RNA gene, partial sequence	359	359	43.00%	5.00E-95	96.03%	AY193548.1	法藻	Bacillariophyta	Bacillariophyceae	Bacillariophycidae	Bacillariales	クラシケイノウ目
31	<i>Nitzschia radiocarinata</i> gene for 28S rRNA, partial sequence, strain BLEC 03-17-2	359	359	43.00%	5.00E-95	95.93%	AB218886.1	法藻	Bacillariophyta	Bacillariophyceae	Bacillariophycidae	Bacillariales	クラシケイノウ目
32	<i>Pseudo-nitzschia areolata</i> strain 14V 18S ribosomal RNA gene, partial sequence, internal transcribed spacer 1, 5.8S ribosomal RNA gene, and 28S ribosomal RNA gene, partial sequence	359	359	43.00%	5.00E-95	95.93%	AB218885.1	法藻	Bacillariophyta	Bacillariophyceae	Bacillariophycidae	Bacillariales	クラシケイノウ目
33	<i>Nitzschia radiocarinata</i> strain VHL587 large subunit ribosomal RNA gene, partial sequence	359	359	43.00%	5.00E-95	95.93%	AF417674.1	法藻	Bacillariophyta	Bacillariophyceae	Bacillariophycidae	Bacillariales	クラシケイノウ目
34	<i>Nitzschia radiocarinata</i> strain 99RG1-16 large subunit ribosomal RNA gene, partial sequence	359	359	43.00%	5.00E-95	95.93%	AF417672.1	法藻	Bacillariophyta	Bacillariophyceae	Bacillariophycidae	Bacillariales	クラシケイノウ目
36	<i>Pseudo-nitzschia multiseries</i> strain Kona1 large subunit ribosomal RNA gene, partial sequence	359	359	43.00%	5.00E-95	95.93%	AF417654.1	法藻	Bacillariophyta	Bacillariophyceae	Bacillariophycidae	Bacillariales	クラシケイノウ目
37	<i>Pseudo-nitzschia multiseries</i> strain VPS-53 large subunit ribosomal RNA gene, partial sequence	359	359	43.00%	5.00E-95	95.93%	AF417648.1	法藻	Bacillariophyta	Bacillariophyceae	Bacillariophycidae	Bacillariales	クラシケイノウ目



【図15】

H9-05-18S
検索条件: Limit to sequences from type material

連番	Max score に基づき順位	Description	Max score	Total score	Query cover	E value	Ident	Accession	
1	1	<i>Fistulifera solaris</i> gene for 18S ribosomal RNA, partial sequence	1873	1873	100.00%	0	85.00%	AB769957.1	培養
2	2	<i>Pedospiumella encystans</i> voucher B 40 0040671 18S ribosomal RNA gene, partial sequence	1511	1511	100.00%	0	89.00%	AY651083.1	黄金色藻
3	3	<i>Chloridellidium tetraborys</i> strain SAG3811-1 18S ribosomal RNA gene, partial sequence	1506	1506	100.00%	0	89.00%	FJ030892.1	黄緑藻
4	4	<i>Heterosaccus fuomensis</i> partial 18S rRNA gene, strain SAG 835-5	1495	1495	100.00%	0	89.00%	AM490821.1	黄緑藻
5	4	<i>Heterosaccus caespitosus</i> partial 18S rRNA gene, strain SAG 835-2a	1495	1495	100.00%	0	89.00%	AM490820.1	黄緑藻
6	4	<i>Sphaerosorus composita</i> partial 18S rRNA gene, strain SAG 53.91	1495	1495	100.00%	0	89.00%	AJ579333.1	
7	7	<i>Bumilleriopsis pyrenoidosa</i> partial 18S rRNA gene, strain SAG 69.90	1476	1476	100.00%	0	89.00%	AJ579332.1	
8	8	<i>Nannochloropsis anetii</i> ex strain SAG 18.89 cu functional section SAG 18.89 18S ribosomal RNA gene, partial sequence	1471	1471	100.00%	0	89.00%	AF251496.1	
9	9	<i>Pseudotetraedrella kamillae</i> strain SAG 2056 18S ribosomal RNA gene, partial sequence	1454	1454	100.00%	0	88.00%	EF044311.1	
10	10	<i>Vischeria helvetica</i> strain SAG 876-1 18S ribosomal RNA gene, complete sequence	1450	1450	100.00%	0	88.00%	JX188080.1	
11	11	<i>Eustigmatos vischeri</i> isolate SAG 860-1 18S ribosomal RNA gene, complete sequence	1445	1445	100.00%	0	88.00%	JX274590.1	
12	11	<i>Eustigmatos polyphem</i> strain SAG 38.84 18S ribosomal RNA gene, complete sequence	1445	1445	100.00%	0	88.00%	JX188077.1	
13	11	<i>Scumella vulgaris</i> isolate 189nm 18S ribosomal RNA gene, partial sequence	1445	1445	100.00%	0	88.00%	DG388552.1	
14	14	<i>Monodus unispallia</i> partial 18S rRNA gene, strain SAG 8.93	1443	1443	100.00%	0	88.00%	AM490821.1	
15	15	<i>Ochromonas danica</i> strain SAG9337 18S ribosomal RNA gene, partial sequence	1402	1402	100.00%	0	88.00%	JQ281514.1	
16	16	<i>Bumilleriopsis peterseniana</i> partial 18S rRNA gene, strain SAG 809-3	1380	1380	100.00%	0	87.00%	AJ579331.1	
17	17	<i>Pythium inisidiosum</i> 18S ribosomal RNA gene, partial sequence	1325	1325	100.00%	0	86.00%	AF289981.1	
18	18	<i>Sargassococcus simulans</i> strain CCMP1996 18S ribosomal RNA gene, partial sequence	1317	1317	100.00%	0	86.00%	MF927481.1	
19	18	<i>Pelagospilus aureus</i> strain CCMP1410 18S ribosomal RNA gene, partial sequence	1317	1317	100.00%	0	86.00%	MF927480.1	
20	20	<i>Olpidopsis heterosiphoniae</i> isolate KNU-M-omo4 18S ribosomal RNA gene, partial sequence	1312	1312	100.00%	0	86.00%	MF838767.1	
21	21	<i>Sargassococcus epiphyticus</i> strain CCMP1995 18S ribosomal RNA gene, partial sequence	1306	1306	100.00%	0	86.00%	MF927478.1	
22	22	<i>Pythium grandisporangium</i> strain CBS 286.79 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	1293	1293	100.00%	0	86.00%	AY598692.2	
23	23	<i>Leptididium giganteum</i> f. caninum isolate G13-AK202 small subunit ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and large subunit ribosomal RNA gene, partial sequence	1288	1288	100.00%	0	86.00%	KF915305.2	
24	23	<i>Pythium parvum</i> strain CBS 225.88 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	1288	1288	100.00%	0	86.00%	AY598697.2	
25	23	<i>Pythium aquatile</i> strain CBS 215.80 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	1288	1288	100.00%	0	86.00%	AY598632.2	
26	26	<i>Pythium plurisporum</i> strain CBS 100.630 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	1286	1286	100.00%	0	86.00%	AY598684.2	
27	27	<i>Pythium delense</i> strain CBS 314.33 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	1284	1284	100.00%	0	86.00%	AY598674.2	
28	28	<i>Pythium pyriformis</i> strain CBS 158.64 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	1279	1279	100.00%	0	86.00%	AY598636.2	
29	28	<i>Pythium aphandermatum</i> strain CBS 118.80 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	1279	1279	100.00%	0	86.00%	AY598622.2	
30	30	<i>Pythium rostratiformis</i> voucher CBS115464 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	1262	1262	100.00%	0	85.00%	HQ643761.2	

【図16】

H9-05-28S D2C2
検索条件: Limit to sequences from type material

連番	Max score に基づき順位	Description	Max score	Total score	Query cover	E value	Ident	Accession	
1	1	<i>Nannochloropsis gaditana</i> strain SAG2.99 28S ribosomal RNA gene, partial sequence	193	193	36.00%	3.00E-46	86.00%	FJ030890.1	真正眼点藻
2	2	<i>Fragilium occultum</i> INVAM IA702 28S rRNA gene, partial sequence; from reference material	187	187	64.00%	1.00E-44	78.00%	NG_0271567.1	真菌
3	3	<i>Develepavella elegans</i> strain CCAP1917/1 28S ribosomal RNA gene, partial sequence	183	183	79.00%	2.00E-43	76.00%	FJ030882.1	羽菌
4	4	<i>Sporobolomyces dimmeriae</i> gene for LSU rRNA, partial sequence, strain JCM 8762	169	169	23.00%	5.00E-39	93.00%	AB644404.1	真菌
5	4	<i>Sporobolomyces corollinus</i> genes for 18S rRNA, ITS1, 5.8S rRNA, ITS2, 28S rRNA, partial and complete sequence	169	169	23.00%	5.00E-39	93.00%	AB638335.1	真菌
6	6	<i>Pseudobaeospora vilipactiae</i> SFSU DED 8605 28S rRNA gene, partial sequence; from TYPE material	167	167	33.00%	2.00E-38	86.00%	NG_050108.1	
7	6	<i>Pseudobaeospora vilipactiae</i> voucher DED 8605 28S large subunit ribosomal RNA gene, partial sequence	167	167	33.00%	2.00E-38	86.00%	KC464330.1	
8	8	<i>Afrocastellanella ivoryana</i> OSC 150014 28S rRNA gene, partial sequence; from TYPE material	161	161	33.00%	8.00E-37	85.00%	NG_058595.1	
9	8	<i>Afrocastellanella ivoryana</i> voucher OSC 150014 28S ribosomal RNA gene, partial sequence	161	161	33.00%	8.00E-37	85.00%	KX685720.1	
10	8	<i>Borofutius dhakanus</i> HKAS 73785 28S rRNA, partial sequence; from TYPE material	161	161	33.00%	8.00E-37	85.00%	NG_042663.1	
11	8	<i>Spongiforma squarepantsii</i> voucher LHFB14 28S ribosomal RNA gene, partial sequence	161	161	33.00%	8.00E-37	85.00%	HQ724509.1	
12	8	<i>Spongiforma thailandica</i> BBH DED 7873 28S rRNA, partial sequence; from TYPE material	161	161	33.00%	8.00E-37	85.00%	NG_042464.1	
13	13	<i>Minimedusa polyspora</i> strain CBS 113.16 large subunit ribosomal RNA gene, partial sequence	158	158	33.00%	1.00E-35	84.00%	MH866167.1	
14	13	<i>Malassezia equina</i> CBS 9969 28S rRNA gene, partial sequence; from TYPE material	158	158	34.00%	1.00E-35	84.00%	NG_060248.1	
15	13	<i>Phyllozoma linderiae</i> CBS 7893 28S rRNA gene, partial sequence; from TYPE material	158	158	32.00%	1.00E-35	85.00%	NG_058372.1	
16	13	<i>Phyllozoma coprosimicola</i> CBS 7897 28S rRNA gene, partial sequence; from TYPE material	158	158	32.00%	1.00E-35	85.00%	NG_058371.1	
17	13	<i>Phyllozoma subbrunnea</i> CBS 7196 28S rRNA gene, partial sequence; from TYPE material	158	158	32.00%	1.00E-35	85.00%	NG_057732.1	
18	13	<i>Minimedusa polyspora</i> CBS 113.16 28S rRNA gene, partial sequence; from TYPE material	158	158	33.00%	1.00E-35	84.00%	NG_057640.1	
19	13	<i>Phyllozoma subbrunnea</i> culture CBS:7196 large subunit ribosomal RNA gene, partial sequence	158	158	32.00%	1.00E-35	85.00%	KY108779.1	
20	13	<i>Phyllozoma linderiae</i> culture CBS:7893 large subunit ribosomal RNA gene, partial sequence	158	158	32.00%	1.00E-35	85.00%	KY108777.1	
21	13	<i>Phyllozoma coprosimicola</i> culture CBS:7897 large subunit ribosomal RNA gene, partial sequence	158	158	32.00%	1.00E-35	85.00%	KY108776.1	
22	13	<i>Minimedusa polyspora</i> gene for 28S rRNA, partial sequence, strain: CBS 113.16	158	158	33.00%	1.00E-35	84.00%	AB972779.1	
23	13	<i>Malassezia equina</i> strain MA 146 28S ribosomal RNA gene, partial sequence	158	158	34.00%	1.00E-35	84.00%	AY743621.1	
24	13	<i>Sporobolomyces subbrunneus</i> isolate AFOL-ID 858 25S large subunit ribosomal RNA gene, partial sequence	158	158	32.00%	1.00E-35	85.00%	AY745717.1	
25	13	<i>Phyllozoma subbrunnea</i> strain CBS 7196 26S ribosomal RNA gene, partial sequence	158	158	32.00%	1.00E-35	85.00%	AF189997.1	
26	13	<i>Phyllozoma linderiae</i> strain CBS 7893 26S ribosomal RNA gene, partial sequence	158	158	32.00%	1.00E-35	85.00%	AF189989.1	
27	13	<i>Phyllozoma coprosimicola</i> strain CBS 7897 26S ribosomal RNA gene, partial sequence	158	158	32.00%	1.00E-35	85.00%	AF189981.1	
28	13	<i>Sporobolomyces linderiae</i> 26S ribosomal RNA gene, partial sequence	158	158	32.00%	1.00E-35	85.00%	AF207890.1	
29	29	<i>Hydium berkeleyanum</i> voucher KD-MEH 17-005 large subunit ribosomal RNA gene, partial sequence	156	156	32.00%	4.00E-35	85.00%	MG972970.1	
30	29	<i>Gastrum verrucosum</i> INPA 264956 28S rRNA gene, partial sequence; from TYPE material	156	156	33.00%	4.00E-35	84.00%	NG_060680.1	
31	29	<i>Clavulina ossea</i> URM 89970 28S rRNA gene, partial sequence; from TYPE material	156	156	32.00%	4.00E-35	84.81%	NG_058957.1	
32	29	<i>Clavulina ossea</i> culture URM:GBA>89970 large subunit ribosomal RNA gene, partial sequence	156	156	32.00%	4.00E-35	84.81%	KX811197.1	
33	29	<i>Gastrum verrucosum</i> voucher INPA264956 25S ribosomal RNA gene, partial sequence	156	156	33.00%	4.00E-35	84.38%	KX670831.1	
34	29	<i>Burgella flavoparmellae</i> strain JL192-01 25S large subunit ribosomal RNA gene, partial sequence	156	156	32.00%	4.00E-35	84.81%	DQ915469.1	

【図17】

H9-05-28S D2R2
検索条件: Limit to sequences from type material

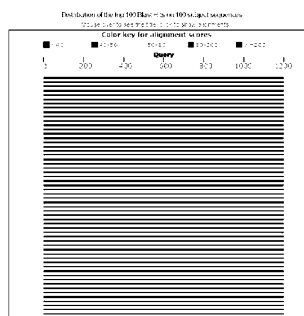
連番	Max scoreに基づく順位	Description	Max score	Total score	Query cover	E value	Ident	Accession	
1	1	Chloroellidium tetrabotrys strain SAG811-1 28S ribosomal RNA gene, partial sequence	215	215	48.00%	6.00E-53	84.21%	FJ030881.1	黄緑藻
2	2	Finiclochytrium jonesii JEL 569 28S rRNA gene, partial sequence; from TYPE material	206	206	48.00%	4.00E-50	83.56%	NG_060391.1	真菌
3	2	Finiclochytrium jonesii voucher JEL569 28S large subunit ribosomal RNA gene, partial sequence	206	206	48.00%	4.00E-50	83.56%	HQ901681.1	真菌
4	4	Gerronomyces variabilis voucher MP03 28S large subunit ribosomal RNA gene, partial sequence	200	200	48.00%	2.00E-48	83.33%	HQ901692.1	真菌
5	5	Thoreauomyces humboldtii JEL 95 28S rRNA gene, partial sequence; from TYPE material	195	195	48.00%	7.00E-48	83.19%	NG_059938.1	真菌
6	5	Thoreauomyces humboldtii voucher JEL95 28S large subunit ribosomal RNA gene, partial sequence	195	195	48.00%	7.00E-48	83.19%	HQ901662.1	
7	5	Spizellomyces acuminatus 28S ribosomal RNA (LSU) gene, partial sequence	195	195	48.00%	7.00E-48	83.11%	JN941010.1	
8	5	Phytocochytrium africanum voucher CBS 454.65 28S ribosomal RNA gene, partial sequence	195	195	48.00%	7.00E-48	83.11%	FJ827693.1	
9	9	Holtermanniella waticca CBS 9496 28S rRNA gene, partial sequence; from TYPE material	195	195	48.00%	2.00E-47	82.89%	NG_058307.1	
10	9	Holtermanniella waticca culture CBS:9496 large subunit ribosomal RNA gene, partial sequence	195	195	48.00%	2.00E-47	82.89%	KY107874.1	
11	11	Finiclochytrium alabamiae JEL 538 28S rRNA gene, partial sequence; from TYPE material	195	195	48.00%	8.00E-47	82.67%	NG_060390.1	
12	11	Finiclochytrium alabamiae voucher JEL538 28S large subunit ribosomal RNA gene, partial sequence	195	195	48.00%	8.00E-47	82.67%	HQ901669.1	
13	11	Gorgonomyces haynaldi BAFG ARG 026 28S rRNA, partial sequence; from TYPE material	195	195	47.00%	8.00E-47	83.11%	NG_042448.1	
14	14	Ceriporiopsis semisupina BJFC Gui 10222 28S rRNA gene, partial sequence; from TYPE material	193	193	48.00%	3.00E-46	82.68%	NG_064354.1	
15	14	Ceriporiopsis sp. CLZ-2014 voucher Cui 10222 28S large subunit ribosomal RNA gene, partial sequence	193	193	48.00%	3.00E-46	82.68%	KF845949.1	
16	14	Sonoraphyctis ransonii DAOM BR 060 28S rRNA, partial sequence; from TYPE material	193	193	48.00%	3.00E-46	82.74%	NG_042454.1	
17	17	Basidiascus undulatus strain CBS 133763 large subunit ribosomal RNA gene, partial sequence	191	191	48.00%	1.00E-45	82.46%	MH877552.1	
18	17	Piskurozyma taiwanensis CBS 9813 28S rRNA gene, partial sequence; from TYPE material	191	191	48.00%	1.00E-45	82.46%	NG_058375.1	
19	17	Goffeauzyma gastrica CBS 2288 28S rRNA gene, partial sequence; from TYPE material	191	191	48.00%	1.00E-45	82.46%	NG_058296.1	
20	17	Goffeauzyma aciditolerans CBS 10872 28S rRNA gene, partial sequence; from TYPE material	191	191	48.00%	1.00E-45	82.46%	NG_058295.1	
21	17	Piskurozyma aerea culture CBS:155 large subunit ribosomal RNA gene, partial sequence	191	191	48.00%	1.00E-45	82.46%	KY109666.1	
22	17	Piskurozyma taiwanensis culture CBS:9813 large subunit ribosomal RNA gene, partial sequence	191	191	48.00%	1.00E-45	82.46%	KY108934.1	
23	17	Piskurozyma cylindrica culture CBS:8880 large subunit ribosomal RNA gene, partial sequence	191	191	48.00%	1.00E-45	82.46%	KY108932.1	
24	17	Naganishia globosa culture CBS:5106 large subunit ribosomal RNA gene, partial sequence	191	191	48.00%	1.00E-45	82.46%	KY108616.1	
25	17	Naganishia friedmannii culture CBS:7100 large subunit ribosomal RNA gene, partial sequence	191	191	48.00%	1.00E-45	82.46%	KY108613.1	
26	17	Goffeauzyma gastrica culture CBS:2288 large subunit ribosomal RNA gene, partial sequence	191	191	48.00%	1.00E-45	82.46%	KY107764.1	
27	17	Goffeauzyma aciditolerans culture CBS:10872 large subunit ribosomal RNA gene, partial sequence	191	191	48.00%	1.00E-45	82.46%	KY107763.1	
28	17	Filobasidium wieringae culture CBS:1937 large subunit ribosomal RNA gene, partial sequence	191	191	48.00%	1.00E-45	82.38%	KY107733.1	
29	17	Filobasidium magnum culture CBS:140 large subunit ribosomal RNA gene, partial sequence	191	191	48.00%	1.00E-45	82.38%	KY107722.1	
30	17	Filobasidium globosum culture CBS:7642 large subunit ribosomal RNA gene, partial sequence	191	191	48.00%	1.00E-45	82.38%	KY107713.1	
31	17	Filobasidium floriforme culture CBS:6241 large subunit ribosomal RNA gene, partial sequence	191	191	48.00%	1.00E-45	82.38%	KY107703.1	
32	17	[Cryptococcus] consartionis culture CBS:7159 large subunit ribosomal RNA gene, partial sequence	191	191	48.00%	1.00E-45	82.46%	KY106961.1	
33	17	[Cryptococcus] albidus var. ovalis culture CBS:5810 large subunit ribosomal RNA gene, partial sequence	191	191	48.00%	1.00E-45	82.46%	KY106965.1	
34	17	[Cryptococcus] albidus var. kuestingii culture CBS:1926 large subunit ribosomal RNA gene, partial sequence	191	191	48.00%	1.00E-45	82.46%	KY106960.1	
35	17	Geminibasidium hirsutum DAOM 241969 28S rRNA, partial sequence; from TYPE material	191	191	48.00%	1.00E-45	82.46%	NG_042695.1	
36	17	Geminibasidium donsium DAOM 241966 28S rRNA, partial sequence; from TYPE material	191	191	48.00%	1.00E-45	82.46%	NG_042694.1	
37	17	Basidiascus magus DAOM 241948 28S rRNA, partial sequence; from TYPE material	191	191	48.00%	1.00E-45	82.46%	NG_042693.1	
38	17	Basidiascus undulatus DAOM 241956 28S rRNA, partial sequence; from TYPE material	191	191	48.00%	1.00E-45	82.46%	NG_042692.1	

【図18】

H9-06-18S

検索条件: 標準由来配列を除く全体

連番	Max scoreに基づく 順位	Description	Max score	Total score	Query cover	E value	Ident	Accession	門	亜門	綱	亜綱	目	
1	1	<i>Entomoneis pakistana</i> isolate 1431 18S ribosomal RNA gene, partial sequence	2121	2121	100.00%	0	99.00%	KX120688.1	注	Bacillariophytina	Bacillariophyceae	Bacillariophycidae	Surirellales	コナンテイク目
2	2	<i>Entomoneis ornata</i> isolate 270 18S ribosomal RNA gene, partial sequence	2104	2104	100.00%	0	98.00%	KX120683.1	注	Bacillariophytina	Bacillariophyceae	Bacillariophycidae	Surirellales	コナンテイク目
3	2	<i>Entomoneis ornata</i> strain MA 18S rDNA subunit ribosomal RNA gene, partial sequence	2104	2104	100.00%	0	98.00%	HQ912411.1	注	Bacillariophytina	Bacillariophyceae	Bacillariophycidae	Surirellales	コナンテイク目
4	3	<i>Entomoneis ornata</i> strain MP03 18S rDNA subunit ribosomal RNA gene, partial sequence	2093	2093	100.00%	0	98.00%	MF000603.1	注	Bacillariophytina	Bacillariophyceae	Bacillariophycidae	Surirellales	コナンテイク目
5	3	<i>Entomoneis cf. alata</i> strain Xmm652 18S ribosomal RNA gene, partial sequence	2093	2093	100.00%	0	98.00%	KY054953.1	注	Bacillariophytina	Bacillariophyceae	Bacillariophycidae	Surirellales	コナンテイク目
6	3	<i>Entomoneis punctulata</i> isolate Dhrm741 18S ribosomal RNA gene, partial sequence	2093	2093	100.00%	0	98.00%	KU561123.1	注	Bacillariophytina	Bacillariophyceae	Bacillariophycidae	Surirellales	コナンテイク目
7	3	<i>Entomoneis punctulata</i> isolate Dhrm741 18S ribosomal RNA gene, partial sequence	2093	2093	100.00%	0	98.00%	KU561111.1	注	Bacillariophytina	Bacillariophyceae	Bacillariophycidae	Surirellales	コナンテイク目
8	3	<i>Entomoneis</i> sp. isolate BSA 18S ribosomal RNA gene, partial sequence	2089	2089	100.00%	0	98.00%	KF869808.1	注	Bacillariophytina	Bacillariophyceae	Bacillariophycidae	Surirellales	コナンテイク目
9	9	<i>Entomoneis</i> sp. strain SA19 Enter-C1 oval subunit ribosomal RNA gene, partial sequence	2087	2087	100.00%	0	98.00%	KX120691.1	注	Bacillariophytina	Bacillariophyceae	Bacillariophycidae	Surirellales	コナンテイク目
10	10	<i>Epithemia argus</i> strain Xmm1153 18S ribosomal RNA gene, partial sequence	2087	2087	100.00%	0	98.00%	KY054960.1	注	Bacillariophytina	Bacillariophyceae	Bacillariophycidae	Rhopileoidales	コナンテイク目
11	10	<i>Entomoneis punctulata</i> strain Xmm751 18S ribosomal RNA gene, partial sequence	2087	2087	100.00%	0	98.00%	KY054959.1	注	Bacillariophytina	Bacillariophyceae	Bacillariophycidae	Surirellales	コナンテイク目
12	10	<i>Entomoneis punctulata</i> strain Xmm28W1 18S ribosomal RNA gene, partial sequence	2087	2087	100.00%	0	98.00%	KY054958.1	注	Bacillariophytina	Bacillariophyceae	Bacillariophycidae	Surirellales	コナンテイク目
13	10	<i>Entomoneis punctulata</i> strain Xmm2151 18S ribosomal RNA gene, partial sequence	2087	2087	100.00%	0	98.00%	KY054957.1	注	Bacillariophytina	Bacillariophyceae	Bacillariophycidae	Surirellales	コナンテイク目
14	10	<i>Entomoneis punctulata</i> strain Xmm552 18S ribosomal RNA gene, partial sequence	2087	2087	100.00%	0	98.00%	KY054956.1	注	Bacillariophytina	Bacillariophyceae	Bacillariophycidae	Surirellales	コナンテイク目
15	10	<i>Entomoneis punctulata</i> strain Xmm1532 18S ribosomal RNA gene, partial sequence	2087	2087	100.00%	0	98.00%	KY054954.1	注	Bacillariophytina	Bacillariophyceae	Bacillariophycidae	Surirellales	コナンテイク目
16	10	<i>Entomoneis ornata</i> strain Xmm551 18S ribosomal RNA gene, partial sequence	2087	2087	100.00%	0	98.00%	KY054952.1	注	Bacillariophytina	Bacillariophyceae	Bacillariophycidae	Surirellales	コナンテイク目
17	10	<i>Entomoneis punctulata</i> isolate Xmm2651 18S ribosomal RNA gene, partial sequence	2087	2087	100.00%	0	98.00%	KU561212.1	注	Bacillariophytina	Bacillariophyceae	Bacillariophycidae	Surirellales	コナンテイク目
18	10	<i>Entomoneis punctulata</i> isolate Xmm353 18S ribosomal RNA gene, partial sequence	2087	2087	100.00%	0	98.00%	KU561203.1	注	Bacillariophytina	Bacillariophyceae	Bacillariophycidae	Surirellales	コナンテイク目
19	10	<i>Entomoneis punctulata</i> isolate Xmm345S 18S ribosomal RNA gene, partial sequence	2087	2087	100.00%	0	98.00%	KU561187.1	注	Bacillariophytina	Bacillariophyceae	Bacillariophycidae	Surirellales	コナンテイク目
20	10	<i>Entomoneis punctulata</i> isolate Xmm11W5 18S ribosomal RNA gene, partial sequence	2087	2087	100.00%	0	98.00%	KU561182.1	注	Bacillariophytina	Bacillariophyceae	Bacillariophycidae	Surirellales	コナンテイク目
21	10	<i>Amphiceros paludosus</i> isolate Xmm1152 18S ribosomal RNA gene, partial sequence	2087	2087	100.00%	0	98.00%	KU561173.1	注	Bacillariophytina	Bacillariophyceae	Bacillariophycidae	Naviculales	コナンテイク目
22	10	<i>Entomoneis punctulata</i> isolate Xmm20W1 18S ribosomal RNA gene, partial sequence	2087	2087	100.00%	0	98.00%	KU561168.1	注	Bacillariophytina	Bacillariophyceae	Bacillariophycidae	Surirellales	コナンテイク目
23	10	<i>Entomoneis ornata</i> isolate Xmm1151 18S ribosomal RNA gene, partial sequence	2087	2087	100.00%	0	98.00%	KU561167.1	注	Bacillariophytina	Bacillariophyceae	Bacillariophycidae	Surirellales	コナンテイク目
24	10	<i>Amphiceros paludosus</i> var. hyalina isolate Xmm3884 18S ribosomal RNA gene, partial sequence	2087	2087	100.00%	0	98.00%	KU561162.1	注	Bacillariophytina	Bacillariophyceae	Bacillariophycidae	Naviculales	コナンテイク目
25	10	<i>Amphiceros paludosus</i> var. hyalina isolate Xmm1354 18S ribosomal RNA gene, partial sequence	2087	2087	100.00%	0	98.00%	KU561161.1	注	Bacillariophytina	Bacillariophyceae	Bacillariophycidae	Naviculales	コナンテイク目
26	10	<i>Entomoneis ornata</i> isolate Xmm451 18S ribosomal RNA gene, partial sequence	2087	2087	100.00%	0	98.00%	KU561144.1	注	Bacillariophytina	Bacillariophyceae	Bacillariophycidae	Surirellales	コナンテイク目
27	10	<i>Amphiceros paludosus</i> var. hyalina isolate Xmm1454 18S ribosomal RNA gene, partial sequence	2087	2087	100.00%	0	98.00%	KU561143.1	注	Bacillariophytina	Bacillariophyceae	Bacillariophycidae	Naviculales	コナンテイク目
28	10	<i>Entomoneis punctulata</i> isolate Dhrm742 18S ribosomal RNA gene, partial sequence	2087	2087	100.00%	0	98.00%	KU561113.1	注	Bacillariophytina	Bacillariophyceae	Bacillariophycidae	Surirellales	コナンテイク目
29	11	<i>Entomoneis cf. alata</i> 18S rRNA gene, clone p540	2085	2085	100.00%	0	98.00%	AJ535160.1	注	Bacillariophytina	Bacillariophyceae	Bacillariophycidae	Surirellales	コナンテイク目



WO 2020/031720

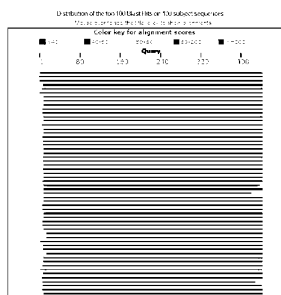
PCT/JP2019/029201

【図19】

H9-06-285_D2C2

最高条件で選出された配列を抜く全体

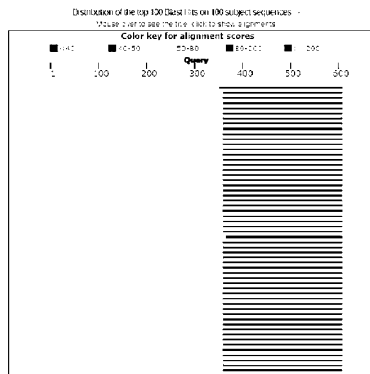
順番	max score に基づく順	Description	Max score	Total score	Query cover	E value	Ident	Accession	門	亜門	綱	亜綱	目	
1	1	Entomoneis omata isolate 270 28S ribosomal RNA gene, partial sequence	604	604	100.00%	#####	91.00%	KX120381.1	担菌	Bacillariophyta	Bacillariophyceae	Bacillariophycidae	Surirellales	コバンケイソウ目
2	1	Entomoneis omata isolate 14A 28S ribosomal RNA gene, partial sequence	604	604	100.00%	#####	91.00%	KX120381.1	担菌	Bacillariophyta	Bacillariophyceae	Bacillariophycidae	Surirellales	コバンケイソウ目
3	1	Entomoneis paubosa isolate L431 28S ribosomal RNA gene, partial sequence	593	593	100.00%	#####	91.00%	KX120381.1	担菌	Bacillariophyta	Bacillariophyceae	Bacillariophycidae	Surirellales	コバンケイソウ目
4	1	Entomoneis sp. isolate 3354-E1 1 28S ribosomal RNA gene, partial sequence	598	598	98.00%	#####	90.00%	KX120381.1	担菌	Bacillariophyta	Bacillariophyceae	Bacillariophycidae	Surirellales	コバンケイソウ目
5	5	Protokellia bassoni isolate 3554-A20 28S ribosomal RNA gene, partial sequence	564	564	99.00%	#####	90.00%	KX120350.1	担菌	Bacillariophyta	Bacillariophyceae	Bacillariophycidae	Rhopodiales	クシガタケイソウ目
6	6	Entomoneis sp. isolate C08 28S ribosomal RNA gene, partial sequence	582	582	100.00%	#####	89.00%	KX120381.1	担菌	Bacillariophyta	Bacillariophyceae	Bacillariophycidae	Surirellales	コバンケイソウ目
7	7	Surirella cf. phanta isolate 342 28S ribosomal RNA gene, partial sequence	558	558	98.00%	#####	90.00%	KX120394.1	担菌	Bacillariophyta	Bacillariophyceae	Bacillariophycidae	Surirellales	コバンケイソウ目
8	8	Surirella brightwellii isolate CCMP1912 28S ribosomal RNA gene, partial sequence	553	553	98.00%	#####	89.00%	KX120391.1	担菌	Bacillariophyta	Bacillariophyceae	Bacillariophycidae	Surirellales	コバンケイソウ目
9	8	Surirella brightwellii isolate L1763 28S ribosomal RNA gene, partial sequence	553	553	98.00%	#####	89.00%	KX120391.1	担菌	Bacillariophyta	Bacillariophyceae	Bacillariophycidae	Surirellales	コバンケイソウ目
10	8	Entomoneis sp. strain 958A2-4 type culture ribosomal RNA gene, partial sequence	553	553	98.00%	#####	89.00%	KX120391.1	担菌	Bacillariophyta	Bacillariophyceae	Bacillariophycidae	Surirellales	コバンケイソウ目
11	11	Entomoneis sp. isolate B3A 28S ribosomal RNA gene, partial sequence	549	549	98.00%	#####	89.00%	KX120391.1	担菌	Bacillariophyta	Bacillariophyceae	Bacillariophycidae	Surirellales	コバンケイソウ目
12	12	Surirella arguata isolate neoSur 28S ribosomal RNA gene, partial sequence	547	547	98.00%	#####	89.00%	KX120400.1	担菌	Bacillariophyta	Bacillariophyceae	Bacillariophycidae	Surirellales	コバンケイソウ目
13	12	Surirella sp. isolate 1B 2 28S ribosomal RNA gene, partial sequence	547	547	98.00%	#####	89.00%	KX120391.1	担菌	Bacillariophyta	Bacillariophyceae	Bacillariophycidae	Surirellales	コバンケイソウ目
14	12	Campylodiscus sp. isolate G02130 28S ribosomal RNA gene, partial sequence	547	547	99.00%	#####	89.00%	KX120375.1	担菌	Bacillariophyta	Bacillariophyceae	Bacillariophycidae	Surirellales	コバンケイソウ目
15	12	Surirella arguata strain WC2 28S ribosomal RNA gene, partial sequence	547	547	98.00%	#####	89.00%	JX032944.1	担菌	Bacillariophyta	Bacillariophyceae	Bacillariophycidae	Surirellales	コバンケイソウ目
16	16	Surirella brabisonii isolate K01 28S ribosomal RNA gene, partial sequence	542	542	98.00%	#####	89.00%	KX120397.1	担菌	Bacillariophyta	Bacillariophyceae	Bacillariophycidae	Surirellales	コバンケイソウ目
17	16	Entomoneis cf. colludosa isolate CCAP1963.4 28S ribosomal RNA gene, partial sequence	542	542	98.00%	#####	89.00%	KX120559.1	担菌	Bacillariophyta	Bacillariophyceae	Bacillariophycidae	Surirellales	コバンケイソウ目
18	18	Surirella cf. lineata isolate 0960 28S ribosomal RNA gene, partial sequence	543	543	98.00%	#####	89.00%	KX120423.1	担菌	Bacillariophyta	Bacillariophyceae	Bacillariophycidae	Surirellales	コバンケイソウ目
19	18	Surirella sp. ECR-2011 isolate L0218 28S ribosomal RNA gene, partial sequence	538	538	98.00%	#####	89.00%	JX032866.1	担菌	Bacillariophyta	Bacillariophyceae	Bacillariophycidae	Surirellales	コバンケイソウ目
20	20	Surirella ovalis var. apiculata isolate L295 28S ribosomal RNA gene, partial sequence	536	536	98.00%	#####	89.00%	KX120386.1	担菌	Bacillariophyta	Bacillariophyceae	Bacillariophycidae	Surirellales	コバンケイソウ目
21	20	Surirella minuta isolate J0015 28S ribosomal RNA gene, partial sequence	536	536	98.00%	#####	89.00%	KX120397.1	担菌	Bacillariophyta	Bacillariophyceae	Bacillariophycidae	Surirellales	コバンケイソウ目
22	22	Surirella helmsella isolate LO130 28S ribosomal RNA gene, partial sequence	534	534	98.00%	#####	88.00%	JX032882.1	担菌	Bacillariophyta	Bacillariophyceae	Bacillariophycidae	Surirellales	コバンケイソウ目
23	23	Surirella icone la isolate LO189 28S ribosomal RNA gene, partial sequence	532	532	98.00%	#####	88.00%	JX032883.1	担菌	Bacillariophyta	Bacillariophyceae	Bacillariophycidae	Surirellales	コバンケイソウ目
24	24	Surirella sp. isolate L51 28S ribosomal RNA gene, partial sequence	531	531	98.00%	#####	88.00%	KX120399.1	担菌	Bacillariophyta	Bacillariophyceae	Bacillariophycidae	Surirellales	コバンケイソウ目
25	24	Campylodiscus sp. isolate G0216 28S ribosomal RNA gene, partial sequence	531	531	98.00%	#####	88.00%	KX120372.1	担菌	Bacillariophyta	Bacillariophyceae	Bacillariophycidae	Surirellales	コバンケイソウ目
26	26	Cymatopleura solis isolate B484 28S ribosomal RNA gene, partial sequence	525	525	98.00%	#####	88.00%	KX120418.1	担菌	Bacillariophyta	Bacillariophyceae	Bacillariophycidae	Surirellales	コバンケイソウ目
27	26	Surirella sp. isolate 27G 28S ribosomal RNA gene, partial sequence	525	525	98.00%	#####	88.00%	KX120393.1	担菌	Bacillariophyta	Bacillariophyceae	Bacillariophycidae	Surirellales	コバンケイソウ目
28	28	Surirella cf. squimia isolate 0569 28S ribosomal RNA gene, partial sequence	523	523	98.00%	#####	89.00%	KX120422.1	担菌	Bacillariophyta	Bacillariophyceae	Bacillariophycidae	Surirellales	コバンケイソウ目
29	29	Cymatopleura solis strain L1346 28S ribosomal RNA gene, partial sequence	521	521	97.00%	#####	88.00%	JX032942.1	担菌	Bacillariophyta	Bacillariophyceae	Bacillariophycidae	Surirellales	コバンケイソウ目
30	30	Cymatopleura solis isolate L1453 28S ribosomal RNA gene, partial sequence	520	520	98.00%	#####	88.00%	KX120381.1	担菌	Bacillariophyta	Bacillariophyceae	Bacillariophycidae	Surirellales	コバンケイソウ目



[図20]

H9-06-28S_D2R2
検索条件: 環境由来配列を除く全体

連番	Max score に達する 順位	Description	Max score	Total score	Query cover	E value	Ident	Accession	
1	1	<i>Vannella seotentrionalis</i> 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.	311	311	42.00%	1.00E-80	88.00%	GU001161.1	アメーバ
2	2	<i>Glomus</i> sp. MUCL 43205 28S rRNA gene, strain MUCL 43205, clone 11	165	165	41.00%	1.00E-36	79.00%	AJ854611.1	真菌
3	3	<i>Rhizoglyphus irregularis</i> partial 28S rRNA gene, strain DAOM229458, isolate spore 3, clone 63L2.19.9	159	159	41.00%	5.00E-35	79.00%	HF969006.1	真菌
4	3	<i>Rhizoglyphus irregularis</i> partial 28S rRNA gene, strain DAOM229458, isolate spore 3, clone 63L2.16.6	159	159	41.00%	5.00E-35	79.00%	HF969005.1	真菌
5	3	<i>Rhizoglyphus irregularis</i> partial 28S rRNA gene, strain DAOM229458, isolate spore 3, clone 63L2.16.7	159	159	41.00%	5.00E-35	79.00%	HF969004.1	真菌
6	3	<i>Rhizoglyphus irregularis</i> partial 28S rRNA gene, strain DAOM229458, isolate spore 2, clone 63L2.7.22	159	159	41.00%	5.00E-35	79.00%	HF968997.1	真菌
7	3	<i>Rhizoglyphus irregularis</i> partial 28S rRNA gene, strain DAOM229458, isolate spore 2, clone 63L2.7.3	159	159	41.00%	5.00E-35	79.00%	HF968996.1	真菌
8	3	<i>Rhizoglyphus irregularis</i> partial 28S rRNA gene, strain DAOM229458, isolate spore 2, clone 63L2.7.14	159	159	41.00%	5.00E-35	79.00%	HF968994.1	真菌
9	3	<i>Glomus</i> sp. MUCL 41833 28S rRNA gene, strain MUCL 41833, clone 11	159	159	41.00%	5.00E-35	79.00%	AJ854654.1	真菌
10	3	<i>Glomus</i> sp. MUCL 41833 28S rRNA gene, strain MUCL 41833, clone 10	159	159	41.00%	5.00E-35	79.00%	AJ854653.1	真菌
11	3	<i>Glomus</i> sp. MUCL 41833 28S rRNA gene, strain MUCL 41833, clone 2	159	159	41.00%	5.00E-35	79.00%	AJ854641.1	真菌
12	3	<i>Glomus</i> sp. MUCL 41833 28S rRNA gene, strain MUCL 41833, clone 1	159	159	41.00%	5.00E-35	79.00%	AJ854640.1	真菌
13	3	<i>Glomus</i> sp. MUCL 43207 28S rRNA gene, strain MUCL 43207, clone 3	159	159	41.00%	5.00E-35	79.00%	AJ854625.1	真菌
14	3	<i>Glomus</i> sp. MUCL 43206 28S rRNA gene, strain MUCL 43206, clone 10	159	159	41.00%	5.00E-35	79.00%	AJ854622.1	真菌
15	3	<i>Glomus</i> sp. MUCL 43206 28S rRNA gene, strain MUCL 43206, clone 9	159	159	41.00%	5.00E-35	79.00%	AJ854621.1	真菌
16	3	<i>Glomus</i> sp. MUCL 43206 28S rRNA gene, strain MUCL 43206, clone 6	159	159	41.00%	5.00E-35	79.00%	AJ854618.1	真菌
17	3	<i>Glomus</i> sp. MUCL 43206 28S rRNA gene, strain MUCL 43206, clone 5	159	159	41.00%	5.00E-35	79.00%	AJ854617.1	真菌
18	3	<i>Glomus</i> sp. MUCL 43206 28S rRNA gene, strain MUCL 43206, clone 2	159	159	41.00%	5.00E-35	79.00%	AJ854614.1	真菌
19	3	<i>Glomus</i> sp. MUCL 43206 28S rRNA gene, strain MUCL 43206, clone 1	159	159	41.00%	5.00E-35	79.00%	AJ854613.1	真菌
20	3	<i>Glomus</i> sp. MUCL 43205 28S rRNA gene, strain MUCL 43205, clone 8	159	159	41.00%	5.00E-35	79.00%	AJ854606.1	真菌
21	3	<i>Glomus</i> sp. MUCL 43205 28S rRNA gene, strain MUCL 43205, clone 2	159	159	41.00%	5.00E-35	79.00%	AJ854602.1	真菌
22	3	<i>Glomus</i> sp. MUCL 43205 28S rRNA gene, strain MUCL 43205, clone 1	159	159	41.00%	5.00E-35	79.00%	AJ854601.1	真菌
23	3	<i>Glomus</i> sp. MUCL 43204 28S rRNA gene, strain MUCL 43204, clone 5	159	159	41.00%	5.00E-35	79.00%	AJ854597.1	真菌
24	3	<i>Glomus</i> sp. MUCL 43204 28S rRNA gene, strain MUCL 43204, clone 3	159	159	41.00%	5.00E-35	79.00%	AJ854596.1	真菌
25	3	<i>Glomus</i> sp. MUCL 43204 28S rRNA gene, strain MUCL 43204, clone 2	159	159	41.00%	5.00E-35	79.00%	AJ854595.1	真菌
26	3	<i>Glomus</i> sp. MUCL 43203 28S rRNA gene, strain MUCL 43203, clone 11	159	159	41.00%	5.00E-35	79.00%	AJ854593.1	真菌
27	3	<i>Glomus</i> sp. MUCL 43203 28S rRNA gene, strain MUCL 43203, clone 8	159	159	41.00%	5.00E-35	79.00%	AJ854591.1	真菌
28	3	<i>Glomus</i> sp. MUCL 43203 28S rRNA gene, strain MUCL 43203, clone 7	159	159	41.00%	5.00E-35	79.00%	AJ854590.1	真菌
29	3	<i>Glomus</i> sp. MUCL 43203 28S rRNA gene, strain MUCL 43203, clone 1	159	159	41.00%	5.00E-35	79.00%	AJ854584.1	真菌
30	30	<i>Oxetolthylales</i> sp. TRN489 isoate TRN 489 large subunit ribosomal RNA gene, partial sequence	156	156	39.00%	7.00E-34	79.00%	FJ358262.1	真菌
31	30	<i>Glomus</i> sp. MUCL 43205 28S rRNA gene, strain MUCL 43205, clone 4	156	156	41.00%	1.00E-33	78.57%	AJ854604.1	真菌



[図21]

H9-96-18S
検索条件: Limit to sequences from type material

Max score に基づいて 順番	Max score	Total score	Query cover	E value	Ident	Accession	
番号	Description	score	score				
1 1	<i>Fistulifera solaris</i> gene for 18S ribosomal RNA, partial sequence	1866	1866	100.00%	0	95.00%	AB789957.1 注葉
2 2	<i>Pedospumella encystans</i> voucher B 40 0040671 18S ribosomal RNA gene, partial sequence	1524	1524	100.00%	0	90.00%	AY651083.1 真金色藻
3 3	<i>Chlorocidium tetraobryon</i> strain SAG811-1 18S ribosomal RNA gene, partial sequence	1519	1519	100.00%	0	89.00%	FJ030892.1 真緑藻
4 4	<i>Heterococcus fuernbergensis</i> partial 18S rRNA gene, strain SAG 835-5	1507	1507	100.00%	0	89.00%	AM490821.1 真緑藻
5 4	<i>Heterococcus caespitosus</i> partial 18S rRNA gene, strain SAG 835-2a	1507	1507	100.00%	0	89.00%	AM490820.1
6 4	<i>Sphaerosorus composita</i> partial 18S rRNA gene, strain SAG 53.81	1507	1507	100.00%	0	89.00%	AJ573333.1
7 7	<i>Bumilleriopsis pyrenoidosa</i> partial 18S rRNA gene, strain SAG 69.90	1489	1489	100.00%	0	89.00%	AJ578332.1
8 8	<i>Neurospora leucospora</i> strain SAG 18.39 culture collection SAG 18.39 18S ribosomal RNA gene, partial sequence	1483	1483	100.00%	0	89.00%	AF251496.1
9 9	<i>Pseudotetrastadrella kamillae</i> strain SAG 2056 18S ribosomal RNA gene, partial sequence	1467	1467	100.00%	0	89.00%	EF043111.1
10 10	<i>Vischeria helvetica</i> strain SAG 876-1 18S ribosomal RNA gene, complete sequence	1463	1463	100.00%	0	89.00%	JX188080.1
11 11	<i>Eustigmatos vischeri</i> isolate SAG 860-1 18S ribosomal RNA gene, complete sequence	1458	1458	100.00%	0	89.00%	JX274590.1
12 11	<i>Eustigmatos polychem</i> strain SAG 38.24 18S ribosomal RNA gene, complete sequence	1458	1458	100.00%	0	89.00%	JX168077.1
13 11	<i>Squawella vulgaris</i> isolate 199hm 18S ribosomal RNA gene, partial sequence	1458	1458	100.00%	0	89.00%	DO386552.1
14 14	<i>Monodus uripapilla</i> partial 18S rRNA gene, strain SAG 8.83	1456	1456	100.00%	0	89.00%	AM490827.1
15 15	<i>Ochromonas danica</i> strain SAG933.7 18S ribosomal RNA gene, partial sequence	1415	1415	100.00%	0	88.00%	JQ281514.1
16 16	<i>Bumilleriopsis peterseniana</i> partial 18S rRNA gene, strain SAG 809-3	1393	1393	100.00%	0	87.00%	AJ578331.1
17 17	<i>Pythium insidiosum</i> 18S ribosomal RNA gene, partial sequence	1338	1338	100.00%	0	87.00%	AF269981.1
18 18	<i>Sargassococcus simulans</i> strain COMP196 18S ribosomal RNA gene, partial sequence	1330	1330	100.00%	0	87.00%	MF927481.1
19 18	<i>Phragmites australis</i> strain COMP1410 18S ribosomal RNA gene, partial sequence	1330	1330	100.00%	0	87.00%	MF927480.1
20 20	<i>Disiopsis heteropoda</i> strain KNU-MH-9805 18S ribosomal RNA gene, partial sequence	1325	1325	100.00%	0	87.00%	MF928771.1
21 21	<i>Sargassococcus spathulatus</i> strain COMP196 18S ribosomal RNA gene, partial sequence	1319	1319	100.00%	0	87.00%	MF927478.1
22 22	<i>Pythium grandisporangium</i> strain CBS 286.79 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	1306	1306	100.00%	0	86.00%	AY598692.2
23 23	<i>Leguminaria gigantea</i> f. caninum isolate C13-AK202 small subunit ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and large subunit ribosomal RNA gene, partial sequence	1301	1301	100.00%	0	86.00%	KF915305.2
24 23	<i>Pythium parvum</i> strain CBS 225.08 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	1301	1301	100.00%	0	86.00%	AY598697.2
25 23	<i>Pythium aquaticum</i> strain CBS 215.80 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	1301	1301	100.00%	0	86.00%	AY598632.2
26 26	<i>Pythium plurisporum</i> strain CBS 100530 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	1299	1299	100.00%	0	86.00%	AY598684.2
27 27	<i>Pythium delense</i> strain CBS 314.33 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	1297	1297	100.00%	0	86.00%	AY598674.2
28 28	<i>Pythium pyriformis</i> strain CBS 158.64 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	1291	1291	100.00%	0	86.00%	AY598636.2
29 28	<i>Pythium aphanidermatum</i> strain CBS 118.80 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	1291	1291	100.00%	0	86.00%	AY598622.2
30 30	<i>Pythium rostratum</i> strain CBS15464 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	1275	1275	100.00%	0	86.00%	HO643761.2

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[図22]

H9-06-28S; D2C2

検索条件: Limit to sequences from type material

連番	Max scoreに基づく順位	Description	Max score	Total score	Query cover	E value	Ident	Accession	
1	1	Nannochloropsis gaditana strain SAG299 28S ribosomal RNA gene, partial sequence	189	189	40.00%	3.00E-45	86.00%	FJ030880.1	真正眼点藻 卵菌 真菌 真菌
2	2	Deleopayella elegans strain CCAP1917/1 28S ribosomal RNA gene, partial sequence	172	172	59.00%	3.00E-40	79.00%	FJ030882.1	
3	3	Sporobolomyces dimmenae gene for LSU rRNA, partial sequence, strain: JCM 8762	169	169	26.00%	4.00E-39	93.00%	AB644404.1	
4	3	Sporobolomyces corallinus genes for 18S rRNA, ITS1, 5.8S rRNA, ITS2, 28S rRNA, partial and complete sequence	169	169	26.00%	4.00E-39	93.00%	AB638335.1	
5	5	Paraglomus occultum INVAM IA702 28S rRNA gene, partial sequence; from reference material	167	167	41.00%	2.00E-38	83.00%	NG_027567.1	
6	6	Pseudobaeospora wipacabae SF5U DED 8605 28S rRNA gene, partial sequence; from TYPE material	163	163	25.00%	2.00E-37	93.00%	NG_060108.1	
7	6	Pseudobaeospora wipacabae voucher DED 8605 25S large subunit ribosomal RNA gene, partial sequence	163	163	25.00%	2.00E-37	93.00%	KC464330.1	
8	8	Afrocastellanota ivoryana OSC 150014 28S rRNA gene, partial sequence; from TYPE material	158	158	25.00%	1.00E-35	92.00%	NG_058595.1	
9	8	Afrocastellanota ivoryana voucher OSC 150014 28S ribosomal RNA gene, partial sequence	158	158	25.00%	1.00E-35	92.00%	KX685720.1	
10	8	Borofutys dhakanus HKAS 73785 28S rRNA, partial sequence; from TYPE material	158	158	25.00%	1.00E-35	92.00%	NG_042663.1	
11	8	Spongiforma squarepantsii voucher LHF814 28S ribosomal RNA gene, partial sequence	158	158	25.00%	1.00E-35	92.00%	HQ724509.1	
12	8	Spongiforma thailandica RBH DFD 7873 28S rRNA, partial sequence; from TYPE material	158	158	25.00%	1.00E-35	92.00%	NG_042464.1	
13	13	Phyllozoma linderiae CBS 7893 28S rRNA gene, partial sequence; from TYPE material	156	156	25.00%	3.00E-35	92.00%	NG_058372.1	
14	13	Phyllozoma coprosomicola CBS 7897 28S rRNA gene, partial sequence; from TYPE material	156	156	25.00%	3.00E-35	92.00%	NG_058371.1	
15	13	Phyllozoma subbrunnea CBS 7196 28S rRNA gene, partial sequence; from TYPE material	156	156	25.00%	3.00E-35	92.00%	NG_057732.1	
16	13	Phyllozoma subbrunnea culture CBS:7196 large subunit ribosomal RNA gene, partial sequence	156	156	25.00%	3.00E-35	92.00%	KY108779.1	
17	13	Phyllozoma linderiae culture CBS:7893 large subunit ribosomal RNA gene, partial sequence	156	156	25.00%	3.00E-35	92.00%	KY108777.1	
18	13	Phyllozoma coprosomicola culture CBS:7897 large subunit ribosomal RNA gene, partial sequence	156	156	25.00%	3.00E-35	92.00%	KY108776.1	
19	13	Sporobolomyces subbrunneus isolate AFTOL ID 889 28S large subunit ribosomal RNA gene, partial sequence	156	156	25.00%	3.00E-35	92.00%	AY745717.1	
20	13	Phyllozoma subbrunnea strain CBS 7196 26S ribosomal RNA gene, partial sequence	156	156	25.00%	3.00E-35	92.00%	AF189997.1	
21	13	Phyllozoma linderiae strain CBS 7893 26S ribosomal RNA gene, partial sequence	156	156	25.00%	3.00E-35	92.00%	AF189989.1	
22	13	Phyllozoma coprosomicola strain CBS 7897 26S ribosomal RNA gene, partial sequence	156	156	25.00%	3.00E-35	92.00%	AF189981.1	
23	13	Sporobolomyces linderiae 26S ribosomal RNA gene, partial sequence	156	156	25.00%	3.00E-35	92.00%	AF207890.1	
24	24	Minimedusa polyspora strain CBS 113.16 large subunit ribosomal RNA gene, partial sequence	154	154	25.00%	1.00E-34	91.00%	MH866167.1	
25	24	Hydnum berkeleyanum voucher KO-MEH 17-005 large subunit ribosomal RNA gene, partial sequence	154	154	25.00%	1.00E-34	91.00%	MG972970.1	
26	24	Gastrum verrucosum INPA 264956 28S rRNA gene, partial sequence; from TYPE material	154	154	25.00%	1.00E-34	91.00%	NG_060680.1	
27	24	Malassezia equina CBS 9969 28S rRNA gene, partial sequence; from TYPE material	154	154	37.00%	1.00E-34	84.00%	NG_060248.1	
28	24	Clavulina ossea URM 89970 28S rRNA gene, partial sequence; from TYPE material	154	154	25.00%	1.00E-34	91.00%	NG_058957.1	
29	24	Anthracoidea pamirolaica KRA F-2012-146 28S rRNA gene, partial sequence; from TYPE material	154	154	25.00%	1.00E-34	92.00%	NG_058578.1	
30	24	Minimedusa polyspora CBS 113.16 28S rRNA gene, partial sequence; from TYPE material	154	154	25.00%	1.00E-34	91.00%	NG_057640.1	
31	24	Clavulina ossea culture URM:BR-89970 large subunit ribosomal RNA gene, partial sequence	154	154	25.00%	1.00E-34	91.15%	KX811197.1	
32	24	Gastrum verrucosum voucher INPA284956 25S ribosomal RNA gene, partial sequence	154	154	25.00%	1.00E-34	91.15%	KX670831.1	
33	24	Anthracoidea pamirolaica voucher KRA large subunit ribosomal RNA gene, partial sequence	154	154	25.00%	1.00E-34	91.82%	KT008854.1	
34	24	Minimedusa polyspora gene for 28S rRNA, partial sequence, strain: CBS 113.16	154	154	25.00%	1.00E-34	91.15%	AB927779.1	
35	24	Burgella flavoparmellae strain JL192-01 25S large subunit ribosomal RNA gene, partial sequence	154	154	25.00%	1.00E-34	91.15%	DQ915469.1	
36	24	Malassezia equina strain MA 146 26S ribosomal RNA gene, partial sequence	154	154	37.00%	1.00E-34	83.64%	AY743821.1	

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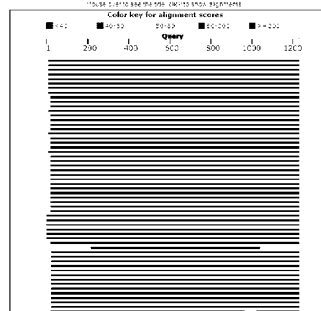
PCT/JP2019/029201

[図23]

H9-08-28S, D2R2 検索条件: Limit to sequences from type material									
通番	Max scoreに基づく順位	Description	Max score	Total score	Query cover	E value	Ident	Accession	
1	1	Conidobolus terrestris CBS 345.65 28S rRNA gene, partial sequence; from TYPE material	150	150	39.00%	2.00E-33	79.00%	NG_064046.1	真菌
2	1	Conidobolus terrestris strain CBS 345.65 large subunit ribosomal RNA gene, partial sequence	150	150	39.00%	2.00E-33	79.00%	MH870240.1	真菌
3	1	Cladophialophora sylvestris strain CBS 350.83 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	150	150	39.00%	2.00E-33	78.00%	EU035413.1	真菌
4	4	Nulliomyces eucalypti culture CPC:32942 28S ribosomal RNA gene, partial sequence	145	145	39.00%	1.00E-31	78.00%	MH327843.1	真菌
5	4	Gromochytrium marmkævae strain CALU x-51 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	145	145	39.00%	1.00E-31	78.00%	KF586842.1	真菌
6	6	Cladophialophora sylvestris strain CBS 350.83 large subunit ribosomal RNA gene, partial sequence	143	143	39.00%	3.00E-31	78.00%	MH873324.1	
7	7	Diplococcium mirabile strain CBS 184.58 large subunit ribosomal RNA gene, partial sequence	139	139	39.00%	4.00E-30	78.00%	MH869282.1	
8	7	Diplococcium mirabile CBS 184.58 28S rRNA gene, partial sequence; from TYPE material	139	139	39.00%	4.00E-30	78.00%	NG_059075.1	
9	7	Salpingoeca dolichonecata strain ATCC 30656 28S large subunit ribosomal RNA gene, partial sequence	139	139	39.00%	4.00E-30	77.00%	KT757473.1	
10	7	Cladophialophora minutissima strain CBS 121.758 28S ribosomal RNA gene, partial sequence	139	139	39.00%	4.00E-30	78.00%	KJ636047.1	
11	7	Batrachochytrium salamandrivorans CBS 135/44 28S rRNA, partial sequence; from TYPE material	139	139	41.00%	4.00E-30	77.00%	NG_042774.1	
12	7	Diplococcium mirabile strain CBS 184.58 28S large subunit ribosomal RNA gene, partial sequence	139	139	39.00%	4.00E-30	78.00%	EF204494.1	
13	13	Suziyamella bullrunensis culture CBS:11640 large subunit ribosomal RNA gene, partial sequence	137	137	39.00%	2.00E-29	78.00%	KY106376.1	
14	14	Varicelladium giganteum strain CBS 508.71 large subunit ribosomal RNA gene, partial sequence	135	135	39.00%	6.00E-29	77.00%	MH872007.1	
15	14	Wickerhamomyces subpelliculosus NRRL Y-1683 28S rRNA gene, partial sequence; from TYPE material	135	135	39.00%	6.00E-29	77.00%	NG_057173.1	
16	14	Wickerhamomyces subpelliculosus culture CBS:5767 large subunit ribosomal RNA gene, partial sequence	135	135	39.00%	6.00E-29	77.00%	KY110142.1	
17	14	Priceomyces haplophilus culture CBS:2028 large subunit ribosomal RNA gene, partial sequence	135	135	41.00%	6.00E-29	77.00%	KY108940.1	
18	14	Priceomyces haplophilus NRRL Y-7860 28S rRNA, partial sequence; from TYPE material	135	135	41.00%	6.00E-29	77.00%	NG_042633.1	
19	14	Wickerhamomyces subpelliculosus strain NRRL Y-1683 26S ribosomal RNA gene, partial sequence	135	135	39.00%	6.00E-29	77.00%	EF550340.1	
20	20	Neomutolodopsonella eucalypti culture CPC:31787 28S ribosomal RNA gene, partial sequence	134	134	39.00%	2.00E-28	77.00%	MH327836.1	
21	20	Helicodendron microsporium strain CBS 100149 large subunit ribosomal RNA gene, partial sequence	134	134	39.00%	2.00E-28	77.00%	MH874296.1	
22	20	Helicodendron websteri strain CBS 745.96 large subunit ribosomal RNA gene, partial sequence	134	134	39.00%	2.00E-28	77.00%	MH874234.1	
23	20	Dinorophospora follicola strain CBS 221.59 large subunit ribosomal RNA gene, partial sequence	134	134	39.00%	2.00E-28	77.00%	MH869385.1	
24	20	Conidobolus rhyosporus ATCC 12588 28S rRNA gene, partial sequence; from TYPE material	134	134	38.00%	2.00E-28	78.00%	NG_058831.1	
25	20	Helicodendron microsporium CBS 100149 28S rRNA gene, partial sequence; from TYPE material	134	134	39.00%	2.00E-28	77.00%	NG_058155.1	
26	20	Citeromyces matritensis culture CBS:2764 large subunit ribosomal RNA gene, partial sequence	134	134	39.00%	2.00E-28	77.00%	KY106924.1	
27	20	Bacillidiolium lobatum genomic DNA sequence contains 18S rRNA gene, ITS1, 5.8S rRNA gene, ITS2, 28S rRNA gene, isolate CCF 5200	134	134	39.00%	2.00E-28	77.00%	LT558703.1	
28	20	Helicodendron microsporium strain CBS 100149 28S ribosomal RNA gene, partial sequence	134	134	39.00%	2.00E-28	77.00%	KR078441.1	
29	20	Citeromyces nyonsensis partial 26S rRNA gene, strain CLJB 1303	134	134	39.00%	2.00E-28	77.00%	HF913858.1	
30	20	Conidobolus rhyosporus strain ATCC 12588 26S ribosomal RNA gene, partial sequence	134	134	38.00%	2.00E-28	78.00%	JN131540.1	
31	20	Helicodendron microsporium CBS 100149 28S rRNA gene, partial sequence; from TYPE material	134	134	39.00%	2.00E-28	77.14%	NG_058155.1	
32	20	Citeromyces matritensis culture CBS:2764 large subunit ribosomal RNA gene, partial sequence	134	134	39.00%	2.00E-28	77.05%	KY106924.1	
33	20	Bacillidiolium lobatum genomic DNA sequence contains 18S rRNA gene, ITS1, 5.8S rRNA gene, ITS2, 28S rRNA gene, isolate CCF 5200	134	134	39.00%	2.00E-28	77.14%	LT558703.1	
34	20	Helicodendron microsporium strain CBS 100149 28S ribosomal RNA gene, partial sequence	134	134	39.00%	2.00E-28	77.14%	KR078441.1	
35	20	Citeromyces nyonsensis partial 26S rRNA gene, strain CLJB 1303	134	134	39.00%	2.00E-28	77.05%	HF913858.1	
36	20	Conidobolus rhyosporus strain ATCC 12588 26S ribosomal RNA gene, partial sequence	134	134	38.00%	2.00E-28	77.73%	JN131540.1	
37	20	Citeromyces matritensis NRRL Y-2407 28S rRNA, partial sequence; from TYPE material	134	134	39.00%	2.00E-28	77.05%	NG_042645.1	
38	20	Clydaea vesicula JEL 369 28S rRNA, partial sequence; from TYPE material	134	134	39.00%	2.00E-28	77.37%	NG_042443.1	
39	20	Citeromyces matritensis strain NRRL Y-2407 26S ribosomal RNA gene, partial sequence	134	134	39.00%	2.00E-28	77.05%	EF550346.1	
40	20	Mitula brevispora strain ZW02-012 25S large subunit ribosomal RNA gene, partial sequence	134	134	39.00%	2.00E-28	77.14%	AY789293.1	

H9-09-18S

Distribution of the top 142 Blast-Hits on 100 subject sequences



HD-03-28S_D002

[illegible]

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【図26】

HO-09-28S_D2R2
検索条件: 種別由来配列を除く全体

Max score 運番に基づく順	Description	Max score	Total score	Query cover	E value	Ident	Accession	門	亜門	綱	亜綱	目
1	<i>Pseudo-nitzschia multiseta</i> strain H49-132 28S ribosomal RNA gene, partial sequence	329	329	50.0%	3.00E-86	92.0%	KX290844.1	担子菌	Bacillariophytina	Bacillariophyceae	Bacillariophycidae	Bacillariales クサリケイソウ目
2	<i>Pseudo-nitzschia areolaris</i> strain 2714 28S ribosomal RNA gene, partial sequence	329	329	50.0%	3.00E-86	92.0%	KX290853.1	担子菌	Bacillariophytina	Bacillariophyceae	Bacillariophycidae	Bacillariales クサリケイソウ目
3	<i>Pseudo-nitzschia areolaris</i> strain 2714 28S ribosomal RNA gene, partial sequence	329	329	50.0%	3.00E-86	92.0%	KX290855.1	担子菌	Bacillariophytina	Bacillariophyceae	Bacillariophycidae	Bacillariales クサリケイソウ目
4	<i>Pseudo-nitzschia areolaris</i> strain 2714 28S ribosomal RNA gene, partial sequence	329	329	50.0%	3.00E-86	92.0%	KX290854.1	担子菌	Bacillariophytina	Bacillariophyceae	Bacillariophycidae	Bacillariales クサリケイソウ目
5	<i>Pseudo-nitzschia areolaris</i> strain 4226 28S ribosomal RNA gene, partial sequence	329	329	50.0%	3.00E-86	92.0%	KX290853.1	担子菌	Bacillariophytina	Bacillariophyceae	Bacillariophycidae	Bacillariales クサリケイソウ目
6	<i>Nitzschia multiseta</i> "la cocha" H4931 large subunit rDNA gene, partial sequence	329	329	50.0%	3.00E-86	92.0%	KX353591.1	担子菌	Bacillariophytina	Bacillariophyceae	Bacillariophycidae	Bacillariales クサリケイソウ目
7	<i>Nitzschia multiseta</i> "la cocha" H4931 large subunit rDNA gene, partial sequence	329	329	50.0%	3.00E-86	92.0%	KX353590.1	担子菌	Bacillariophytina	Bacillariophyceae	Bacillariophycidae	Bacillariales クサリケイソウ目
8	<i>Nitzschia multiseta</i> "la cocha" H4931 large subunit rDNA gene, partial sequence	329	329	50.0%	3.00E-86	92.0%	KX353588.1	担子菌	Bacillariophytina	Bacillariophyceae	Bacillariophycidae	Bacillariales クサリケイソウ目
9	<i>Nitzschia multiseta</i> "la cocha" H4931 large subunit rDNA gene, partial sequence	329	329	50.0%	3.00E-86	92.0%	KX353587.1	担子菌	Bacillariophytina	Bacillariophyceae	Bacillariophycidae	Bacillariales クサリケイソウ目
10	<i>Nitzschia multiseta</i> "la cocha" H4931 large subunit rDNA gene, partial sequence	329	329	50.0%	3.00E-86	92.0%	KX353586.1	担子菌	Bacillariophytina	Bacillariophyceae	Bacillariophycidae	Bacillariales クサリケイソウ目
11	<i>Nitzschia multiseta</i> "la cocha" H4931 large subunit rDNA gene, partial sequence	329	329	50.0%	3.00E-86	92.0%	KX353585.1	担子菌	Bacillariophytina	Bacillariophyceae	Bacillariophycidae	Bacillariales クサリケイソウ目
12	<i>Nitzschia multiseta</i> "la cocha" H4931 large subunit rDNA gene, partial sequence	329	329	50.0%	3.00E-86	92.0%	KX353584.1	担子菌	Bacillariophytina	Bacillariophyceae	Bacillariophycidae	Bacillariales クサリケイソウ目
13	<i>Nitzschia multiseta</i> "la cocha" H4931 large subunit rDNA gene, partial sequence	329	329	50.0%	3.00E-86	92.0%	KX353583.1	担子菌	Bacillariophytina	Bacillariophyceae	Bacillariophycidae	Bacillariales クサリケイソウ目
14	<i>Pseudo-nitzschia alutacea</i> strain H4931 large subunit rDNA gene, partial sequence	329	329	50.0%	3.00E-86	92.0%	KR021344.1	担子菌	Bacillariophytina	Bacillariophyceae	Bacillariophycidae	Bacillariales クサリケイソウ目
15	<i>Pseudo-nitzschia alutacea</i> strain H4931 large subunit rDNA gene, partial sequence	329	329	50.0%	3.00E-86	92.0%	KJ188137.1	担子菌	Bacillariophytina	Bacillariophyceae	Bacillariophycidae	Bacillariales クサリケイソウ目
16	<i>Pseudo-nitzschia alutacea</i> strain H4931 large subunit rDNA gene, partial sequence	329	329	50.0%	3.00E-86	92.0%	J077649.1	担子菌	Bacillariophytina	Bacillariophyceae	Bacillariophycidae	Bacillariales クサリケイソウ目
17	<i>Pseudo-nitzschia alutacea</i> strain H4931 large subunit rDNA gene, partial sequence	329	329	50.0%	3.00E-86	92.0%	KG017445.1	担子菌	Bacillariophytina	Bacillariophyceae	Bacillariophycidae	Bacillariales クサリケイソウ目
18	<i>Pseudo-nitzschia alutacea</i> strain H4931 large subunit rDNA gene, partial sequence	329	329	50.0%	3.00E-86	92.0%	KG017440.1	担子菌	Bacillariophytina	Bacillariophyceae	Bacillariophycidae	Bacillariales クサリケイソウ目
19	<i>Pseudo-nitzschia alutacea</i> strain H4931 large subunit rDNA gene, partial sequence	329	329	50.0%	3.00E-86	92.0%	KG017439.1	担子菌	Bacillariophytina	Bacillariophyceae	Bacillariophycidae	Bacillariales クサリケイソウ目
20	<i>Pseudo-nitzschia alutacea</i> strain H4931 large subunit rDNA gene, partial sequence	329	329	50.0%	3.00E-86	92.0%	KG017458.1	担子菌	Bacillariophytina	Bacillariophyceae	Bacillariophycidae	Bacillariales クサリケイソウ目
21	<i>Pseudo-nitzschia alutacea</i> strain H4931 large subunit rDNA gene, partial sequence	329	329	50.0%	3.00E-86	92.0%	KJ150735.1	担子菌	Bacillariophytina	Bacillariophyceae	Bacillariophycidae	Bacillariales クサリケイソウ目
22	<i>Pseudo-nitzschia alutacea</i> strain H4931 large subunit rDNA gene, partial sequence	329	329	50.0%	3.00E-86	92.0%	KJ096845.1	担子菌	Bacillariophytina	Bacillariophyceae	Bacillariophycidae	Bacillariales クサリケイソウ目
23	<i>Pseudo-nitzschia alutacea</i> strain H4931 large subunit rDNA gene, partial sequence	329	329	50.0%	3.00E-86	92.0%	EF642728.1	担子菌	Bacillariophytina	Bacillariophyceae	Bacillariophycidae	Bacillariales クサリケイソウ目
24	<i>Pseudo-nitzschia alutacea</i> strain H4931 large subunit rDNA gene, partial sequence	329	329	50.0%	3.00E-86	92.0%	EF642727.1	担子菌	Bacillariophytina	Bacillariophyceae	Bacillariophycidae	Bacillariales クサリケイソウ目
25	<i>Pseudo-nitzschia alutacea</i> strain H4931 large subunit rDNA gene, partial sequence	329	329	50.0%	3.00E-86	92.0%	EF586013.1	担子菌	Bacillariophytina	Bacillariophyceae	Bacillariophycidae	Bacillariales クサリケイソウ目
26	<i>Pseudo-nitzschia alutacea</i> strain H4931 large subunit rDNA gene, partial sequence	329	329	50.0%	3.00E-86	92.0%	KG013811.1	担子菌	Bacillariophytina	Bacillariophyceae	Bacillariophycidae	Bacillariales クサリケイソウ目
27	<i>Pseudo-nitzschia alutacea</i> strain H4931 large subunit rDNA gene, partial sequence	329	329	50.0%	3.00E-86	92.0%	AF416753.1	担子菌	Bacillariophytina	Bacillariophyceae	Bacillariophycidae	Bacillariales クサリケイソウ目
28	<i>Pseudo-nitzschia alutacea</i> strain H4931 large subunit rDNA gene, partial sequence	329	329	50.0%	3.00E-86	92.0%	AF416746.1	担子菌	Bacillariophytina	Bacillariophyceae	Bacillariophycidae	Bacillariales クサリケイソウ目
29	<i>Pseudo-nitzschia alutacea</i> strain H4931 large subunit rDNA gene, partial sequence	329	329	50.0%	3.00E-86	92.0%	AY519349.1	担子菌	Bacillariophytina	Bacillariophyceae	Bacillariophycidae	Bacillariales クサリケイソウ目
30	<i>Pseudo-nitzschia alutacea</i> strain H4931 large subunit rDNA gene, partial sequence	329	329	50.0%	3.00E-86	92.0%	AY519349.1	担子菌	Bacillariophytina	Bacillariophyceae	Bacillariophycidae	Bacillariales クサリケイソウ目
31	<i>Pseudo-nitzschia alutacea</i> strain H4931 large subunit rDNA gene, partial sequence	329	329	50.0%	3.00E-86	92.34%	AY519349.1	担子菌	Bacillariophytina	Bacillariophyceae	Bacillariophycidae	Bacillariales クサリケイソウ目
32	<i>Nitzschia multiseta</i> "la cocha" H4931 large subunit rDNA gene, partial sequence	329	329	50.0%	3.00E-86	92.31%	AF417845.1	担子菌	Bacillariophytina	Bacillariophyceae	Bacillariophycidae	Bacillariales クサリケイソウ目
33	<i>Nitzschia multiseta</i> "la cocha" H4931 large subunit rDNA gene, partial sequence	329	329	50.0%	3.00E-86	92.34%	AF417845.1	担子菌	Bacillariophytina	Bacillariophyceae	Bacillariophycidae	Bacillariales クサリケイソウ目
34	<i>Pseudo-nitzschia alutacea</i> strain H4931 large subunit rDNA gene, partial sequence	329	329	50.0%	3.00E-86	92.34%	AY476138.1	担子菌	Bacillariophytina	Bacillariophyceae	Bacillariophycidae	Bacillariales クサリケイソウ目
35	<i>Nitzschia multiseta</i> "la cocha" H4931 large subunit rDNA gene, partial sequence	329	329	50.0%	3.00E-86	92.31%	AF417845.1	担子菌	Bacillariophytina	Bacillariophyceae	Bacillariophycidae	Bacillariales クサリケイソウ目
36	<i>Nitzschia multiseta</i> "la cocha" H4931 large subunit rDNA gene, partial sequence	329	329	50.0%	3.00E-86	92.31%	AF417845.1	担子菌	Bacillariophytina	Bacillariophyceae	Bacillariophycidae	Bacillariales クサリケイソウ目
37	<i>Pseudo-nitzschia multiseta</i> strain H4931 large subunit rDNA gene, partial sequence	329	329	50.0%	3.00E-86	92.31%	AF417845.1	担子菌	Bacillariophytina	Bacillariophyceae	Bacillariophycidae	Bacillariales クサリケイソウ目
38	<i>Pseudo-nitzschia multiseta</i> strain H4931 large subunit rDNA gene, partial sequence	329	329	50.0%	3.00E-86	92.31%	AF417845.1	担子菌	Bacillariophytina	Bacillariophyceae	Bacillariophycidae	Bacillariales クサリケイソウ目

【図27】

H9-09-18S
検索条件: Limit to sequences from type material

Max score 運番に基づく順	Description	Max score	Total score	Query cover	E value	Ident	Accession	門	亜門	綱	亜綱	目
1	<i>Pedospumella encystans</i> voucher B 40 0040671 18S ribosomal RNA gene, partial sequence	1170	1427	93.00%	0	89.00%	AY651083.1	黄金色藻				
2	<i>Spumella vulgaris</i> isolate 199hm 18S ribosomal RNA gene, partial sequence	1120	1370	92.00%	0	89.00%	DG388552.1	黄金色藻				
3	<i>Streptothrix capillatum</i> strain SAG 2559 small subunit ribosomal RNA gene, partial sequence	1114	1346	93.00%	0	88.00%	MG652626.1	車軸藻				
4	<i>Fistulifera solaris</i> gene for 18S ribosomal RNA, partial sequence	1112	1350	93.00%	0	88.00%	AB769957.1	珪藻				
5	<i>Eustigmatos vischeri</i> isolate SAG 860-1 18S ribosomal RNA gene, complete sequence	1112	1365	93.00%	0	88.00%	JX274590.1	真正眼点藻				
6	<i>Eustigmatos polyphem</i> strain SAG 38.84 18S ribosomal RNA gene, complete sequence	1112	1365	93.00%	0	88.00%	JX188077.1	真正眼点藻				
7	<i>Vischeria helvetica</i> strain SAG 876-1 18S ribosomal RNA gene, complete sequence	1112	1359	93.00%	0	88.00%	JX188080.1					
8	<i>Pseudotetradlella kamillae</i> strain SAG 2056 18S ribosomal RNA gene, partial sequence	1109	1359	93.00%	0	88.00%	EF044311.1					
9	<i>Monodus unipapilla</i> partial 18S rRNA gene, strain SAG 8.83	1109	1359	93.00%	0	88.00%	AM490827.1					
10	<i>Heterococcus fuernensis</i> partial 18S rRNA gene, strain SAG 835-5	1101	1352	92.00%	0	88.00%	AM490821.1					
11	<i>Heterococcus caespitosus</i> partial 18S rRNA gene, strain SAG 835-2a	1101	1352	92.00%	0	88.00%	AM490820.1					
12	<i>Nannochloropsis limnetica</i> strain SAG 18.95 culture-collection SAG 18.95 18S ribosomal RNA gene, partial sequence	1101	1346	95.00%	0	87.00%	AF251496.1					
13	<i>Oloidiopsis heterosiphonia</i> isolate KNU-M-omc4 18S ribosomal RNA gene, partial sequence	1098	1342	91.00%	0	88.00%	MF838767.1					
14	<i>Saitoella complicata</i> strain NRRL Y-17804 18S ribosomal RNA gene, partial sequence	1098	1309	93.00%	0	88.00%	JQ698935.1					
15	<i>Saitoella complicata</i> IAM 12963 18S rRNA gene, partial sequence: from TYPE material	1098	1309	93.00%	0	88.00%	NG 013154.1					
16	<i>Poteriospumella lacustris</i> voucher B 40 0040673 18S ribosomal RNA gene, partial sequence	1098	1329	92.00%	0	88.00%	AY651074.1					
17	<i>Chloridium tetrabotrys</i> strain SAG811-1 18S ribosomal RNA gene, partial sequence	1096	1357	92.00%	0	88.00%	FJ030892.1					
18	<i>Saitoella complicata</i> gene for 18S rRNA	1096	1313	93.00%	0	88.00%	D12530.1					
19	<i>Ochromonas danica</i> strain SAG833.7 18S ribosomal RNA gene, partial sequence	1088	1315	92.00%	0	88.00%	QJ281514.1					
20	<i>Hydrospidium curvatum</i> SAG 235-1 18S rRNA gene, partial sequence: from reference material	1077	1304	93.00%	0	88.00%	NG 017172.1					
21	<i>Micromonas commoda</i> isolate RCC299 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	1074	1311	92.00%	0	88.00%	KU612123.1					
22	<i>Micromonas</i> sp. RCC299 18S ribosomal RNA gene, partial sequence	1074	1311	92.00%	0	88.00%	HM191693.1					
23	<i>Micromonas</i> sp. RCC299 chromosome 8, complete sequence	1074	3934	92.00%	0	88.00%	CP001575.1					
24	<i>Sphaerosorus composita</i> partial 18S rRNA gene, strain SAG 53.91	1074	1329	92.00%	0	88.00%	AJ579333.1					
25	<i>Taphrina populina</i> CBS 337.55 18S rRNA gene, partial sequence: from TYPE material	1070	1261	92.00%	0	87.00%	NG 062683.1					
26	<i>Taphrina populina</i> gene for 18S rRNA	1070	1261	92.00%	0	87.00%	D14165.1					
27	<i>Endogone corticoides</i> gene for 18S ribosomal RNA, partial sequence, specimen_voucher: A-14002	1068	1270	85.00%	0	88.00%	LC107355.1					
28	<i>Micromonas commoda</i> 18S ribosomal RNA gene, partial sequence	1068	1300	92.00%	0	87.00%	KU244632.1					
29	<i>Klebsormidium elegans</i> 18S rRNA gene, ITS1, 5.8S rRNA gene, ITS2 and 26S rRNA gene (partial), strain: SAG 7.96	1068	1287	93.00%	0	87.00%	AM490840.1					
30	<i>Klebsormidium dissectum</i> strain SAG 2155 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 26S ribosomal RNA gene, partial sequence	1068	1291	93.00%	0	87.00%	EF372518.1					

H9-09-28S_D2C2

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[図29]

H9-09-28S.D2R2

検索条件: Limit to sequences from type material

	Description	Max score	Total score	Query cover	E value	Ident	Accession	
1	Chlorellidium tetrabotrys strain SAG811-1 28S ribosomal RNA gene, partial sequence	196	196	50.00%	2.00E-47	82.00%	FJ030881.1	黄緑藻
2	Geriporiopsis sp. CLZ-2014 voucher Cui 10222 28S large subunit ribosomal RNA gene, partial sequence	185	185	50.00%	4.00E-44	81.00%	KF845949.1	真菌
3	Spizellomyces acuminatus 28S ribosomal RNA (LSU) gene, partial sequence	183	183	50.00%	1.00E-43	81.00%	JN941010.1	真菌
4	Phlyctochytrium africanum voucher CBS 464.65 28S ribosomal RNA gene, partial sequence	183	183	50.00%	1.00E-43	81.00%	FJ827693.1	真菌
5	Fimicolochytrium jonesii JEL 569 28S rRNA gene, partial sequence; from TYPE material	182	182	50.00%	5.00E-43	81.00%	NG_060391.1	真菌
6	Geranomyces variabilis voucher MP03 28S large subunit ribosomal RNA gene, partial sequence	182	182	50.00%	5.00E-43	81.00%	HQ901692.1	真菌
7	Fimicolochytrium jonesii voucher JEL569 28S large subunit ribosomal RNA gene, partial sequence	182	182	50.00%	5.00E-43	81.00%	HQ901681.1	真菌
8	Thoreauomyces humboldtii JEL 95 28S rRNA gene, partial sequence; from TYPE material	180	180	50.00%	2.00E-42	81.00%	NG_059938.1	真菌
9	Thoreauomyces humboldtii voucher JEL95 28S large subunit ribosomal RNA gene, partial sequence	180	180	50.00%	2.00E-42	81.00%	HQ901662.1	
10	Sonoraphytis ranzonii DAOM BR 060 28S rRNA, partial sequence; from TYPE material	180	180	50.00%	2.00E-42	81.00%	NG_042454.1	
11	Basidioascus undulatus strain CBS 133763 large subunit ribosomal RNA gene, partial sequence	178	178	50.00%	6.00E-42	80.00%	MH877552.1	
12	Piskurozyma taiwanensis CBS 9813 28S rRNA gene, partial sequence; from TYPE material	178	178	50.00%	6.00E-42	80.00%	NG_058375.1	
13	Goffeauzyma aciditolerans CBS 10872 28S rRNA gene, partial sequence; from TYPE material	178	178	50.00%	6.00E-42	80.00%	NG_058295.1	
14	Solicoccozyma aerea culture CBS:155 large subunit ribosomal RNA gene, partial sequence	178	178	50.00%	6.00E-42	80.00%	KY109666.1	
15	Piskurozyma taiwanensis culture CBS:9813 large subunit ribosomal RNA gene, partial sequence	178	178	50.00%	6.00E-42	80.00%	KY108934.1	
16	Piskurozyma cylindrica culture CBS:8680 large subunit ribosomal RNA gene, partial sequence	178	178	50.00%	6.00E-42	80.00%	KY108932.1	
17	Naganishia globosa culture CBS:5106 large subunit ribosomal RNA gene, partial sequence	178	178	50.00%	6.00E-42	80.00%	KY108616.1	
18	Naganishia friedmannii culture CBS:7160 large subunit ribosomal RNA gene, partial sequence	178	178	50.00%	6.00E-42	80.00%	KY108613.1	
19	Goffeauzyma aciditolerans culture CBS:10872 large subunit ribosomal RNA gene, partial sequence	178	178	50.00%	6.00E-42	80.00%	KY107763.1	
20	Filobasidium wieringae culture CBS:1937 large subunit ribosomal RNA gene, partial sequence	178	178	50.00%	6.00E-42	80.00%	KY107733.1	
21	Filobasidium magnum culture CBS:140 large subunit ribosomal RNA gene, partial sequence	178	178	50.00%	6.00E-42	80.00%	KY107722.1	
22	Filobasidium globosporum culture CBS:7842 large subunit ribosomal RNA gene, partial sequence	178	178	50.00%	6.00E-42	80.00%	KY107713.1	
23	Filobasidium floriforme culture CBS:6241 large subunit ribosomal RNA gene, partial sequence	178	178	50.00%	6.00E-42	80.00%	KY107703.1	
24	[Cryptococcus] conserlionis culture CBS:7159 large subunit ribosomal RNA gene, partial sequence	178	178	50.00%	6.00E-42	80.00%	KY106981.1	
25	[Cryptococcus] albidus var. ovalis culture CBS:5810 large subunit ribosomal RNA gene, partial sequence	178	178	50.00%	6.00E-42	80.00%	KY106965.1	
26	[Cryptococcus] albidus var. kuetzingii culture CBS:1929 large subunit ribosomal RNA gene, partial sequence	178	178	50.00%	6.00E-42	80.00%	KY106960.1	
27	Geminibasidium hirsutum DAOM 241969 28S rRNA, partial sequence; from TYPE material	178	178	50.00%	6.00E-42	80.00%	NG_042695.1	
28	Geminibasidium donsium DAOM 241966 28S rRNA, partial sequence; from TYPE material	178	178	50.00%	6.00E-42	80.00%	NG_042694.1	
29	Basidioascus magus DAOM 241948 28S rRNA, partial sequence; from TYPE material	178	178	50.00%	6.00E-42	80.00%	NG_042693.1	
30	Basidioascus undulatus DAOM 241956 28S rRNA, partial sequence; from TYPE material	178	178	50.00%	6.00E-42	80.00%	NG_042692.1	