

Supplementary Item 1A: The output from cmsearch showing all 63 relevant matches to the three ectomycorrhizal lineages

```
# cmsearch :: search CM(s) against a sequence database
# INFERNAL 1.1.1 (July 2014)
# Copyright (C) 2014 Howard Hughes Medical Institute.
# Freely distributed under the GNU General Public License (GPLv3).
# -----
# query CM file:                ../basidio_latest_1.1.1.cm
# target sequence database:     ITS1_accOnly.fasta
# number of worker threads:    16
# -----
```

Query: srp3 [CLEN=291]

Hit scores:

rank	E-value	score	bias	sequence	start	end	mdl	trunc	gc	description
(1) !	9.7e-55	162.3	0.0	HE681772	23	293	+	cm	no 0.55	-
(2) !	9.7e-55	162.3	0.0	HE681773	27	297	+	cm	no 0.55	-
(3) !	9.7e-55	162.3	0.0	HE681774	47	317	+	cm	no 0.55	-
(4) !	9.7e-55	162.3	0.0	HE681775	22	292	+	cm	no 0.55	-
(5) !	2.3e-51	153.0	0.0	AB848536	30	299	+	cm	no 0.55	-
(6) !	9.2e-50	148.6	0.0	KC791081	5	271	+	cm	no 0.55	-
(7) !	2e-49	147.6	0.0	AB571500	44	311	+	cm	no 0.55	-
(8) !	2.7e-49	147.3	0.0	DQ093852	12	281	+	cm	no 0.57	-
(9) !	4.4e-49	146.7	0.0	KJ742409	45	314	+	cm	no 0.58	-
(10) !	4.8e-49	146.6	0.0	KJ742410	45	314	+	cm	no 0.58	-
(11) !	6.9e-49	146.1	0.0	KJ742392	53	322	+	cm	no 0.58	-
(12) !	6.9e-49	146.1	0.0	KJ742393	45	314	+	cm	no 0.58	-
(13) !	6.9e-49	146.1	0.0	KJ742411	45	314	+	cm	no 0.58	-
(14) !	7.3e-49	146.1	0.0	FJ596848	59	325	+	cm	no 0.56	-
(15) !	1.1e-48	145.6	0.0	KJ705210	34	303	+	cm	no 0.56	-
(16) !	1.2e-48	145.5	0.0	AB588960	33	302	+	cm	no 0.58	-
(17) !	1.9e-48	144.9	0.0	KJ742395	45	314	+	cm	no 0.58	-
(18) !	3.6e-48	144.1	0.0	UDB016000	129	400	+	cm	no 0.57	-
(19) !	3.6e-48	144.1	0.0	UDB011195	131	402	+	cm	no 0.57	-
(20) !	3.7e-48	144.1	0.0	KJ742390	36	305	+	cm	no 0.58	-
(21) !	9.7e-48	143.0	0.0	KJ742402	45	314	+	cm	no 0.58	-
(22) !	9.7e-48	143.0	0.0	KJ742403	56	325	+	cm	no 0.58	-
(23) !	9.7e-48	143.0	0.0	KJ742404	62	331	+	cm	no 0.58	-
(24) !	9.7e-48	143.0	0.0	KJ742405	45	314	+	cm	no 0.58	-
(25) !	9.7e-48	143.0	0.0	KJ742406	45	314	+	cm	no 0.58	-
(26) !	9.7e-48	143.0	0.0	KJ742407	59	328	+	cm	no 0.58	-
(27) !	9.7e-48	143.0	0.0	UDB023551	44	313	+	cm	no 0.58	-
(28) !	9.7e-48	143.0	0.0	UDB023493	46	315	+	cm	no 0.58	-
(29) !	9.7e-48	143.0	0.0	KM576498	50	319	+	cm	no 0.58	-
(30) !	9.7e-48	143.0	0.0	KF241547	45	314	+	cm	no 0.58	-
(31) !	9.7e-48	143.0	0.0	JX625292	45	314	+	cm	no 0.58	-
(32) !	1.2e-47	142.7	0.0	UDB019724	46	315	+	cm	no 0.59	-
(33) !	1.4e-47	142.5	0.0	UDB011691	45	314	+	cm	no 0.58	-

(34)	!	1.8e-47	142.2	0.0	UDB000354	90	357	+	cm	no	0.59	-
(35)	!	1.8e-47	142.2	0.0	UDB000322	126	393	+	cm	no	0.59	-
(36)	!	2.1e-47	142.1	0.0	JX425382	120	386	+	cm	no	0.60	-
(37)	!	2.7e-47	141.8	0.0	GU234059	12	281	+	cm	no	0.57	-
(38)	!	9.6e-47	140.2	0.0	GU184028	11	280	+	cm	no	0.58	-
(39)	!	1.4e-46	139.8	0.0	HQ204707	115	382	+	cm	no	0.56	-
(40)	!	1.7e-46	139.5	0.0	GU234088	51	320	+	cm	no	0.58	-
(41)	!	6.6e-46	137.9	0.0	UDB000323	130	396	+	cm	no	0.60	-
(42)	!	1.1e-45	137.3	0.0	GU234051	45	314	+	cm	no	0.58	-
(43)	!	4.2e-45	135.7	0.0	AB973750	122	388	+	cm	no	0.60	-
(44)	!	4.4e-45	135.6	0.0	GU184027	7	277	+	cm	no	0.58	-
(45)	!	1e-44	134.6	0.0	JX425373	118	384	+	cm	no	0.60	-
(46)	!	1.4e-44	134.2	0.1	UDB013274	127	393	+	cm	no	0.61	-
(47)	!	1.4e-44	134.2	0.0	HF674530	117	383	+	cm	no	0.59	-
(48)	!	1.4e-44	134.2	0.0	KM576534	117	383	+	cm	no	0.59	-
(49)	!	1.4e-44	134.2	0.0	HF674531	117	383	+	cm	no	0.59	-
(50)	!	1.4e-44	134.2	0.0	HF674533	117	383	+	cm	no	0.59	-
(51)	!	1.4e-44	134.2	0.0	HF674534	117	383	+	cm	no	0.59	-
(52)	!	1.4e-44	134.2	0.0	HF674549	117	383	+	cm	no	0.59	-
(53)	!	1.4e-44	134.2	0.0	HF674551	117	383	+	cm	no	0.59	-
(54)	!	1.4e-44	134.2	0.0	HF674569	117	383	+	cm	no	0.59	-
(55)	!	1.4e-44	134.2	0.0	HF674570	117	383	+	cm	no	0.59	-
(56)	!	1.4e-44	134.2	0.0	HF674572	117	383	+	cm	no	0.59	-
(57)	!	1.4e-44	134.2	0.0	HF674578	117	383	+	cm	no	0.59	-
(58)	!	1.4e-44	134.2	0.0	HF674592	117	383	+	cm	no	0.59	-
(59)	!	1.4e-44	134.2	0.0	HF674638	117	383	+	cm	no	0.59	-
(60)	!	1.4e-44	134.2	0.0	FR852106	125	391	+	cm	no	0.59	-
(61)	!	3.3e-44	133.2	0.0	UDB013255	125	391	+	cm	no	0.60	-
(62)	!	3.9e-41	124.7	0.0	EF218785	5	275	+	cm	no	0.58	-
(63)	!	5.6e-39	118.8	0.0	KJ705211	25	294	+	cm	no	0.56	-
----- inclusion threshold -----												
(64)	?	0.057	16.5	0.0	KF484427	1	89	+	cm	5'	0.62	-
(65)	?	0.25	14.7	0.0	JX136121	116	130	+	cm	no	0.67	-
(66)	?	0.25	14.7	0.0	HM015714	116	130	+	cm	no	0.67	-
(67)	?	0.25	14.7	0.0	HM015727	116	130	+	cm	no	0.67	-
(68)	?	0.6	13.7	0.0	FJ237206	45	171	+	cm	3'	0.41	-
(69)	?	2.9	11.8	0.0	HM015695	169	183	+	cm	no	0.73	-
(70)	?	3.2	11.7	0.0	UDB000658	1	94	+	cm	5'	0.54	-
(71)	?	3.5	11.6	0.0	DQ131633	1	96	+	cm	5'	0.56	-
(72)	?	4.4	11.3	0.0	UDB019779	1	95	+	cm	5'	0.55	-
(73)	?	4.4	11.3	0.0	UDB000646	1	93	+	cm	5'	0.56	-
(74)	?	4.9	11.2	0.0	DQ112615	125	139	+	cm	no	0.60	-
(75)	?	4.9	11.2	0.0	EU915074	126	140	+	cm	no	0.60	-
(76)	?	4.9	11.2	0.0	EU915075	126	140	+	cm	no	0.60	-
(77)	?	6.2	10.9	0.0	KM576321	1	95	+	cm	5'	0.55	-
(78)	?	6.2	10.9	0.0	UDB022819	1	95	+	cm	5'	0.55	-
(79)	?	6.2	10.9	0.0	HM146797_duplic1	1	95	+	cm	5'	0.55	-
(80)	?	6.2	10.9	0.0	HM146797	1	95	+	cm	5'	0.55	-
(81)	?	6.2	10.9	0.0	UDB001523	1	95	+	cm	5'	0.55	-

(82) ? 9.3 10.4 0.0 HM347643 1 93 + cm 5' 0.52 -

Hit alignments:

>> HE681772

rank	E-value	score	bias	mdl	mdl from	mdl to	seq from	seq to	acc trunc	gc
(1) !	9.7e-55	162.3	0.0	cm	1	291 []	23	293 + ..	0.90	no 0.55

```

v          v v          vv          v v          v          v          NC
<<<<_____>>>>--.((((((((((((((((----((((-----.--((((((((-----((((-----((((----- CS
srp3 1 cgGCUGUAAUGGCcguAa.agcgGGAAGcGcucuGuucaaacuCAag.GA.cuccgcUCuauuGcGCGCUGgUUcGcgacuccgcGgccccagacgucca 98
GGCUGUAAUGGCC UAA :C:GGAUGCG:: G U+::+CUCA GA :C :+C +U+G+GCGCUGGUUC+ GAC :::CC:C:CC GA:::C::
HE681772 23 CGGCUGUAAUGGCCUAAaCUCGGGAAUGCGAGGCGGUUGCUCUCAGCgGAaAACUGUCCAUUAGUGCGCUGGUUCAAGAC-UGUCCCUCCAGAAAACUU 122
*****98753899999999*****99999*****886346999*****.***** PP

```

```

v vv          vv v          v          v          v          NC
(((,.<<<.<<<<-<<<<<<<<_____>>>>>>>-->>>>>>.<<_____>><<<<<<<<<-----<<<<-<<<<_____>>>>-->>>>>>)) CS
srp3 99 GGuuc.cac..gcccgccccccccGCAaggggguggggUcgggcgug.gaUAAuuggacgugGUcugggguAGuGgGCAACcGAGCACcccgccagcuccag 195
GG:: CA: G:C CG:C:CGCAAG:G:UG GG:C:UG :AUAAU:GG:C:U:G C :GG +AG+:::GCAA:::GCA CC:G:A:G:CC::
HE681772 123 GGUAGuCAAuuGUC-CUUCGACACGCAAGUGUUGUCU--GGACUUGgAAUAAUCGGUCCUUGAC-UGGUCAGGGAAGCAAUCCGCAUCCAGCAGGACCUA 219
*****955411444.5*****98..77776667*****.***** PP

```

```

v          v          v v          vv          v          NC
)))))))-))--))---)))))---.)))))---.))))---)))))-----)))-)-----)))))-----)))))-----)))))::: CS
srp3 196 CCuggacgcucuUaggggAUacGgcgggc..gucgGuu.CguggagggaGuCuucgggCaauaagaugUcacauCugugCcgagCgCAAACcuucu.UUU 291
CC::G::+UC UAGG:GAU+:GG:::+ GUC G C:: G: G++ C:: C:::CGCAAACC:U: U U
HE681772 220 CCGAGUUAGUCGUAGGAGAUCCGGGGCAUGucGUCGGCCgCGCUGUGGAUCGCGC-----CUCUCGCAAACCCUACcUCU 293
*****9999999999995555555555555555.....6*****999999988*** PP

```

>> HE681773

rank	E-value	score	bias	mdl	mdl from	mdl to	seq from	seq to	acc trunc	gc
(2) !	9.7e-55	162.3	0.0	cm	1	291 []	27	297 + ..	0.90	no 0.55

```

v          v v          vv          v v          v          v          NC
<<<<_____>>>>--.((((((((((((((((----((((-----.--((((((((-----((((-----((((----- CS
srp3 1 cgGCUGUAAUGGCcguAa.agcgGGAAGcGcucuGuucaaacuCAag.GA.cuccgcUCuauuGcGCGCUGgUUcGcgacuccgcGgccccagacgucca 98
GGCUGUAAUGGCC UAA :C:GGAUGCG:: G U+::+CUCA GA :C :+C +U+G+GCGCUGGUUC+ GAC :::CC:C:CC GA:::C::
HE681773 27 CGGCUGUAAUGGCCUAAaCUCGGGAAUGCGAGGCGGUUGCUCUCAGCgGAaAACUGUCCAUUAGUGCGCUGGUUCAAGAC-UGUCCCUCCAGAAAACUU 126
*****98753899999999*****99999*****886346999*****.***** PP

```

```

v vv          vv v          v          v          v          NC
(((,.<<<.<<<<-<<<<<<<<_____>>>>>>>-->>>>>>.<<_____>><<<<<<<<-----<<<<-<<<<_____>>>>-->>>>>>)) CS
srp3 99 GGuuc.cac..gcccgccccccccGCAaggggguggggUcgggcgug.gaUAAuuggacgugGUcugggguAGuGgGCAACcGAGCACcccgccagcuccag 195
GG:: CA: G:C CG:C:CGCAAG:G:UG GG:C:UG :AUAAU:GG:C:U:G C :GG +AG+:::GCAA:::GCA CC:G:A:G:CC::
HE681773 127 GGUAGuCAAuuGUC-CUUCGACACGCAAGUGUUGUCU--GGACUUGgAAUAAUCGGUCCUUGAC-UGGUCAGGGAAGCAAUCCGCAUCCAGCAGGACCUA 223
*****955411444.5*****98..77776667*****.***** PP

```



```

srp3 1 cgGCUGUAAUGGCcguAaagcgGAAUGcGcuc.uGuucaaacuCAagGAcuccgcUCuauGcGCGCUG.gUUCGcgacuccgcCgccccagacguc.ca 98
:GGCUGUAA GGCC:+AA::CGGGAAU CG:: U::: C CAA G C:C U G+GCGC+G GUUC+:GA C::CC:C:C: GA ::C ::
KJ742410 45 UGGCUGUAAUGGCCCAAAGUCGGGAAUGCGAGGuGAUGUUCACACAACGGAAUCACGUGCUCGUGCGCYGaGUUCAAGAC-CGCCCCUCUGGAAAACuUU 144
*****655666788888888999*****999*****999.***** PP

```

```

vv vv NC
(((, .<<<<<<-<<<<<<<<____>>>>>>--->>>>>><<____>><<<<<<-<<<-<<<-<<<____>>--->>>>->>>>>>))))) CS
srp3 99 GGuuc.cacgcccgcgcccGCAagggguggggUcgggcguggaUAAuuggacgugGUcugggggAGuGgGCAACcGAGCAccccgcacguccagCCu 198
GG::+ C: :C : CGC::CG AAG::GUG :+ G:: :G::UAA:: G:C:U:G C ::G:+AG+:::G+AA:::+GCA:C::G:A:G:C ::CC:
KJ742410 145 GGUGUcCAUCAUCCUCGCGGCGUAAGCUGUGGCC-GGAUUUGGAGUAAUCGGCCUUGAC-UAGCCAGGAAGUAAUCCGAGCUAGCAGGGCUCACCG 243
*****866655556*****9.56666667*****.***** PP

```

```

v v vv NC
))))-)))--)))))---)))))--..)))))----)))))-----))-))-----)))))::: CS
srp3 199 ggacgcucuUaggggAUacGcgggc.gucgGuuGugggagggaGuCuucgggCaauaagaugUcacauCugugCcgagCgCAAACCuucuUUU 291
:G:: +UC UA:G:GAU+:GG::G++ UC:GU G:G G+ C::+: C:::CG AAACCUU:: U
KJ742410 244 AGUUGGUCUAGGAGAUCAGGGCGUGucAUCUGUC-GCGCGGUGCGCCGUGU-----CCUCGUAAACCUUUCGUG 314
*****9999999999.666665455555433.....6***** PP

```

>> KJ742392

rank	E-value	score	bias	mdl	mdl from	mdl to	seq from	seq to	acc trunc	gc
(11)	!	6.9e-49	146.1	0.0	cm	1	291	[]	53	322 + .. 0.91 no 0.58

```

v v vv v v NC
<<<<____>>>>---(((((((((((((((.--((((-----((((-----,-----((((-----((((-----((((-----((((-----(( CS
srp3 1 cgGCUGUAAUGGCcguAaagcgGAAUGcGcuc.uGuucaaacuCAagGAcuccgcUCuauGcGCGCUG.gUUCGcgacuccgcCgccccagacguc.ca 98
GGCUGUAAUGGCC AA::CGGGAAU CG::: U::: C CAA G C:C U G+GCGCUG GUUC+:GA C::CC:C:C: GA ::C ::
KJ742392 53 CGGCUGUAAUGGCCCAAAGUCGGGAAUGCGAGGuGAUGUUCACACAACGGAAUCACGUGCUCGUGCGCYGaGUUCAAGAC-CGUCCUCUGGAAAACuUU 152
*****655666788888888999*****9*****999.***** PP

```

```

vv vv v v NC
(((, .<<<<<<-<<<<<<<<____>>>>>>--->>>>>><<____>><<<<<<-<<<-<<<-<<<____>>--->>>>->>>>>>))))) CS
srp3 99 GGuuc.cacgcccgcgcccGCAagggguggggUcgggcguggaUAAuuggacgugGUcugggggAGuGgGCAACcGAGCAccccgcacguccagCCu 198
GG::+ C: :C : CGC::CG AAG::GUG :+ G:: :G::UAA:: G C:U:G C ::G:+AG+:::GCAA:::+GCA:C::G:A:G C ::CC:
KJ742392 153 GGUGUcCAUCAUCCUCGCGGCGUAAGCUGUGGCC-GGAUUUGGAGUAAUCGGCCUUGAC-UAGCCAGGAAGCAAUCCGAGCUAGCAGGACUCACCG 251
*****866655556*****9.56666667*****.***** PP

```

```

v v vv NC
))))-)))--)))))---)))))--..)))))----)))))-----))-))-----)))))::: CS
srp3 199 ggacgcucuUaggggAUacGcgggc.gucgGuuGugggagggaGuCuucgggCaauaagaugUcacauCugugCcgagCgCAAACCuucuUUU 291
:G:: +UC UA:G:GAU+:GG::G++ UC:GU G:G G+ C::+: C:::CG AAACCUU:: U
KJ742392 252 AGUUGGUCUAGGAGAUCAGGGCGUGucAUCUGUC-GCGCGGUGCGCCGUGU-----CCUCGUAAACCUUUCGUG 322
*****9999999999.666665455555433.....6***** PP

```

>> KJ742393

rank	E-value	score	bias	mdl	mdl from	mdl to	seq from	seq to	acc trunc	gc
(12)	!	6.9e-49	146.1	0.0	cm	1	291	[]	45	314 + .. 0.91 no 0.58

*****999999999855555544322..22.....3336***** PP

>> AB588960

rank	E-value	score	bias	mdl	mdl from	mdl to	seq from	seq to	acc trunc	gc
(16) !	1.2e-48	145.5	0.0	cm	1	291 []	33	302 + ..	0.91	no 0.58

```

v          v          vvv          v          v          NC
<<<<_____>>>>---(((((((((((((((((.---((((-----((((-----(.-----((((-----((((-----((((-----(( CS
srp3  1  cgGUCGUAAUGGCcguAaagcgGGAUUGcGcuc.uGuucaaaacuCAAGAcuccgcUCuauuGcGCGCUg.gUUCGcgacuccgcCgcccagacguc.ca 98
GGCUGUAA GGCC AA::CGGAAU CG:: U::: C CAA G C:C U G+GCGCUG GUUC+:GA C::CC:C:C: GA ::C ::
AB588960 33 CGGCGUAAACGGCCCCAAGUCGGGAAUGCGAGGUGAUGUUCCACAACGGAAUCACGUGCUCGUGCGCUGaGUUCAAGAC-CGUCCCCUCUGGAAAACuUU 132
*****655666788888888999*****9*****999.***** PP

```

```

vv          vv          v          v          NC
(((, .<<<<<<<<<<<<_____>>>>>>>--->>>>>>><<<<<<<<_____>>>>--->>>>>>>))))) CS
srp3  99 GGuuc.cacgcccgcggcccccGAagggguggggUcgggcguggaUAAuuggacgugGUcuggggguAGuGcGGCAACcGAGCAccccgcacguccagCCu 198
G::+ C: ::C : CGC::CG AAG::GUG :+ G:: :G::UAA::GG C:U:G C ::G:+AG+:::G+AA:::GCA:C::G:A:G CC::CC:
AB588960 133 GGUGUCcCAUCAUCCUCGCGGGCGUAAGCUGUGGCC-GGAUUUGGAGUAAUCGGCCCUUGAC-UAGCCAGGGAAGUAAUCCGCAGCUAGCAGGACCCACCG 231
*****866655556*****9.56666667*****.***** PP

```

```

v          v          vvv          NC
))))-)))--)))))---)))))--..)))))----)))))-----)))))-)))))-----)))))::: CS
srp3  199 ggagcucUaggggAUacGgcccgc.gucgGuuGguggagggGuCuucgggCaauaagaugUcacaucugugCcgagCgCAAACCuucuuUU 291
:G::+UC UA:G:GAU+:GG::G++ UC:GU G+ G+:::: C:::CG AAACCUU:: U
AB588960 232 AGUUGGUCUUAAGGAGAUACAGGGCGUGucAUCUGUC-GCGCGGGUGCGCCGUGU-----CCCUCGUAACCUUUCGUG 302
*****9999999999.6666655455555433.....6***** PP

```

>> KJ742395

rank	E-value	score	bias	mdl	mdl from	mdl to	seq from	seq to	acc trunc	gc
(17) !	1.9e-48	144.9	0.0	cm	1	291 []	45	314 + ..	0.91	no 0.58

```

v          v          vvv          v          v          NC
<<<<_____>>>>---(((((((((((((((((.---((((-----((((-----(.-----((((-----((((-----((((-----(( CS
srp3  1  cgGUCGUAAUGGCcguAaagcgGGAUUGcGcuc.uGuucaaaacuCAAGAcuccgcUCuauuGcGCGCUg.gUUCGcgacuccgcCgcccagacguc.ca 98
:GGCUGUAA+GGCC: AA::CGGAAU CG:: U::: C CAA G C:C U G+GCGCUG GUUC+:GA C::CC:C:C: GA ::C ::
KJ742395 45 YGGCUGUAAAYGGCCMAAGUCGGGAAUGCGAGGUGAUGUUCCACAACGGAAUCACGUGCUCGUGCGCUGaGUUCAAGAC-CGYCCCCUCUGGAAAACuUU 144
*****655666788888888999*****9*****999.***** PP

```

```

vv          vv          v          v          NC
(((, .<<<<<<<<<<<<_____>>>>>>>--->>>>>>><<<<<<<<_____>>>>--->>>>>>>))))) CS
srp3  99 GGuuc.cacgcccgcggcccccGAagggguggggUcgggcguggaUAAuuggacgugGUcuggggguAGuGcGGCAACcGAGCAccccgcacguccagCCu 198
GG::+ C: ::C : CGC::CG AAG::GUG :+ G:: :G::UAA:: G C:U:G C ::G:+AG+:::G+AA:::GCA:C::G:A:G C ::CC:
KJ742395 145 GGUGUCcCAUCAUCCUCGCGGGCGUAAGCUGUGGCC-GGAUUUGGAGUAAUCGGCCCUUGAC-UAGCCAGGGAAGYAAUCCGCAGCUAGCAGGACUCACCG 243
*****866655556*****9.56666667*****.***** PP

```

```

v          v          vvv          NC
))))-)))--)))))---)))))--..)))))----)))))-----)))))-)))))-----)))))::: CS

```

srp3 199 ggacgcucuUaggggAUacGgcgggc..gucgGuuCguggaggggaGuCuucgggCaauaagaugUcacauCugugCcgagCgCAAACCuucuUUU 291
:G::+UC UA:G:GAU+:GG::G++ UC:GU G:G G+ C::+: C::CG AAACCUU:: U
KJ742395 244 AGUUGGUCUUAAGGAGAUACAGGCGUGucAUCUGUC-GCGCGGGUGCCGUGU-----CCCUCGUAACCUUUCGUG 314
*****9999999999.666665455555433.....6***** PP

>> UDB016000

rank	E-value	score	bias	mdl	mdl from	mdl to	seq from	seq to	acc trunc	gc
(18) !	3.6e-48	144.1	0.0	cm	1	291 []	129	400 + ..	0.92	no 0.57

srp3 1 cgGCUGUAAUGGCcguAaagcgGGAUGcGcuc...uGuucaaacuCAagGAcuccgcUCuauuGcGCGCUG.gUUCGcgacuccgcCgcccagacguc 96
:GGCUGUAAUGGCC: AA G GGA:U CG:: UGU C:: CUCAA G ++ C:C UUG+GCGC G GUUC+:GA :::CC:C:CCAGA:::C

UDB016000 129 UGGCUGUAAUGGCCCAAGGUGGGAAUGCGAGGcgaUGUUCUCCUCAACGGAGUCACGUGCUUGUGCGCCGAGUUC AAGAC-UGUCCCCUCCAGAAAAC 227
*****98888888888899999999*****8889*****999.***** PP

srp3 97 .caGGuuc.cacgccccgcccccGCAagggggugggUcgggcguggaUAAuuggacgugGUCugggggAGuGcGGCAACcGAGCAcccgcacgucca 194
::GG::+ C: : :C : CGC::CG A G::GUG :+ G: : :G::UAA:::G C:U:GUC ::G:+AG+:::G AA:::GCA:C::G:A:G C::

UDB016000 228 uUUGGUGUcCAUAGUCCUCGCAGCGUAGGCUGUGGCC-GGAUUUGGAGUAAUCAGCCUUGUC-UAGCCAGGGAAGAAUCCGCAGCUAGCAGGACUC 325
*****77777779*****9.89999999***** PP

srp3 195 gCCuggacgcucuUaggggAUacGgcgggc..gucgGuu.CguggaggggaGuCuucgggCaauaagaugUcacauCugugCcgagCgCAAACCuucuUUU 291
:CC::G:::UCUUAAG:GAU+:GG::: + UC:GU CG:G ::+G GC+ UG C:::CG A:ACCU C U

UDB016000 326 ACCGAGUAGUCUUAAGGAGAUACAGGCAGGcAUCUGUCGCG-----GGUGCGCG-----UGUCCCUCGUAGACCUUCAUAC 400
*****99988888888884444.....33433344.....5557***** PP

>> UDB011195

rank	E-value	score	bias	mdl	mdl from	mdl to	seq from	seq to	acc trunc	gc
(19) !	3.6e-48	144.1	0.0	cm	1	291 []	131	402 + ..	0.92	no 0.57

srp3 1 cgGCUGUAAUGGCcguAaagcgGGAUGcGcuc...uGuucaaacuCAagGAcuccgcUCuauuGcGCGCUG.gUUCGcgacuccgcCgcccagacguc 96
:GGCUGUAAUGGCC: AA G GGA:U CG:: UGU C:: CUCAA G ++ C:C UUG+GCGC G GUUC+:GA :::CC:C:CCAGA:::C

UDB011195 131 UGGCUGUAAUGGCCCAAGGUGGGAAUGCGAGGcgaUGUUCUCCUCAACGGAGUCACGUGCUUGUGCGCCGAGUUC AAGAC-UGUCCCCUCCAGAAAAC 229
*****98888888888899999999*****8889*****999.***** PP

srp3 97 .caGGuuc.cacgccccgcccccGCAagggggugggUcgggcguggaUAAuuggacgugGUCugggggAGuGcGGCAACcGAGCAcccgcacgucca 194
::GG::+ C: : :C : CGC::CG A G::GUG :+ G: : :G::UAA:::G C:U:GUC ::G:+AG+:::G AA:::GCA:C::G:A:G C::

UDB011195 230 uUUGGUGUcCAUAGUCCUCGCAGCGUAGGCUGUGGCC-GGAUUUGGAGUAAUCAGCCUUGUC-UAGCCAGGGAAGAAUCCGCAGCUAGCAGGACUC 327
*****77777779*****9.89999999***** PP

GG::+ C: :C : CGC::CG AAG::GUG :+ G:: :G::UAA:: G C:U:G C :G:+AG+:::GCAA::+GCA:C::G:A:G C ::CC:
KJ742402 145 GGUGUcCAUCAUCCUCGCGGCGUAAGCUGUGGCC-GGAUUUGGAGUAAUCGGCCCUUGAC-UAGCCAGGGAAGCAAUCCGCAGCUAGCAGGACUCACCG 243
*****866655556*****9.56666667*****.***** PP

v v vvv NC
))))-)))--)))))---)))))--..)))))----)))))-----))-))-----)))))::: CS
srp3 199 ggacgcucuUaggggAUacGgcgggc..gucgGuuCguggaggggaGuCuucgggCaauaagaugUcacauCugugCcgagCgCAAACCuucuUUU 291
:G::+UC UA:G:GAU+:GG::G++ UC:GU G:G G+ C::+: C:::CG A:ACCUU:: U

KJ742402 244 AGUUGGUCUUAGGAGAUCAGGGCGUGucAUCUGUC-GCGCGGGUGCGCCGUGU-----CCUCGUAGACCUUUCGUG 314
*****9999999999.666665455555433.....6***** PP

>> KJ742403

rank	E-value	score	bias	mdl	mdl from	mdl to	seq from	seq to	acc	trunc	gc
(22) !	9.7e-48	143.0	0.0	cm	1	291 []	56	325 + ..	0.91	no	0.58

v v vvv v NC
<<<<____>>>>---((((((((((((((((((---((((-----((((-----..-----((((-----((((-----((((-----((((-----((CS
srp3 1 cgGCGUAAUGGCcguAaagcgGAAUGcGcuc.uGuucaaacuCAagGAcuccgcUCuauuGcGCGCUG.gUUCGcgacuccgcGgcccagacguc.ca 98
GGCUGUAAUGGCC AA::CGGA:U CG::: U::: C CAA G C:C U G+GCGCUG GUUC+:GA C::CC:C:C: GA ::C ::
KJ742403 56 CGGCGUAAUGGCCCAAGUCGGGAAUGCGAGGuGAUGUUCCACAACGGAAUCACGUGCUCGUGCGCUGaGUUCAAGAC-CGUCCCCUCUGGAAACuUU 155
*****655666788888888999*****9*****999.***** PP

v v v v NC
(((, .<<<<<<<<<<<<<<<<____>>>>>>>--->>))))) CS
srp3 99 GGuuc.cacgcccgcgccgccccGCAagggguggggUcgggcguggaUAAuuggacgugGUcuggggguAGUcGgCAACcGAGCAccccgcacguccagCCu 198
GG::+ C: :C : CGC::CG AAG::GUG :+ G:: :G::UAA:: G C:U:G C :G:+AG+:::GCAA::+GCA:C::G:A:G C ::CC:
KJ742403 156 GGUGUcCAUCAUCCUCGCGGCGUAAGCUGUGGCC-GGAUUUGGAGUAAUCGGCCCUUGAC-UAGCCAGGGAAGCAAUCCGCAGCUAGCAGGACUCACCG 254
*****866655556*****9.56666667*****.***** PP

v v vvv NC
))))-)))--)))))---)))))--..)))))----)))))-----))-))-----)))))::: CS
srp3 199 ggacgcucuUaggggAUacGgcgggc..gucgGuuCguggaggggaGuCuucgggCaauaagaugUcacauCugugCcgagCgCAAACCuucuUUU 291
:G::+UC UA:G:GAU+:GG::G++ UC:GU G:G G+ C::+: C:::CG A:ACCUU:: U
KJ742403 255 AGUUGGUCUUAGGAGAUCAGGGCGUGucAUCUGUC-GCGCGGGUGCGCCGUGU-----CCUCGUAGACCUUUCGUG 325
*****9999999999.666665455555433.....6***** PP

>> KJ742404

rank	E-value	score	bias	mdl	mdl from	mdl to	seq from	seq to	acc	trunc	gc
(23) !	9.7e-48	143.0	0.0	cm	1	291 []	62	331 + ..	0.91	no	0.58

v v vvv v NC
<<<<____>>>>---((((((((((((((((((---((((-----((((-----..-----((((-----((((-----((((-----((((-----((CS
srp3 1 cgGCGUAAUGGCcguAaagcgGAAUGcGcuc.uGuucaaacuCAagGAcuccgcUCuauuGcGCGCUG.gUUCGcgacuccgcGgcccagacguc.ca 98
GGCUGUAAUGGCC AA::CGGA:U CG::: U::: C CAA G C:C U G+GCGCUG GUUC+:GA C::CC:C:C: GA ::C ::
KJ742404 62 CGGCGUAAUGGCCCAAGUCGGGAAUGCGAGGuGAUGUUCCACAACGGAAUCACGUGCUCGUGCGCUGaGUUCAAGAC-CGUCCCCUCUGGAAACuUU 161
*****655666788888888999*****9*****999.***** PP

srp3 99 GGuuc.cacgcccgccccGCAaggguggggUcgggcguggaUAAuuggacgugGUcugggguAGuCgGGCAACcGAGCAccccgcacguccagCCu 198
GG::+ C: :C : CGC::CG AAG::GUG :+ G:: :G::UAA:: G C:U:G C :G:+AG+:::GCAA:::GCA:C::G:A:G C ::CC:
KJ742404 162 GGUGUcCAUCAUCCUCGCGGCGUAAGCUGUGGCC-GGAUUUGGAGUAAUCGGCCUUGAC-UAGCCAGGGAAGCAAUCCGACGUCAGCAGGACUCACCG 260
*****866655556*****9.56666667*****.***** PP

srp3 199 ggacgcucuUaggggAUacGgcgggc.gucgGuuCguggagggaGuCuucgggCaauaagaugUcacaUCugugCcgagCgCAAACCuucuUUU 291
:G::+UC UA:G:GAU+:GG::G++ UC:GU G:G G+ C::+: C:::CG A:ACCUU:: U
KJ742404 261 AGUUGGUCUUAGGAGAUCAGGCGUGucAUCUGUC-GCGCGGGUGCGCCGUGU-----CCCUCGUAGACCUUUCUGUG 331
*****9999999999.666665455555433.....6***** PP

>> KJ742405

rank	E-value	score	bias	mdl	mdl	from	mdl	to	seq	from	seq	to	acc	trunc	gc
(24) !	9.7e-48	143.0	0.0	cm		1	291	[]	45		314	+	..	0.91	no 0.58

srp3 1 cgGCUGUAAUGGCcguAaagcgGGAUUGcGcuc.uGuucaaacuCAAGGAcuccgcUCuauUGcGCUGg.gUUCGcgacuccgcCgcccagacguc.ca 98
GGCUGUAAUGGCC AA::CGGGA:U CG::: U::: C CAA G C:C U G+GCGCUG GUUC+:GA C::CC:C:C: GA ::C :
KJ742405 45 CGGCUGUAAUGGCCAAAGUCGGAAUGCGAGGuGAUGUUCCACAACGGAAUCACGUGCUCGUGCGCUGAGUUCAAGAC-CGUCCCCUCUGGAAACuUU 144
*****65566678888888999*****9*****999.***** PP

srp3 99 GGuuc.cacgcccgccccGCAaggguggggUcgggcguggaUAAuuggacgugGUcugggguAGuCgGGCAACcGAGCAccccgcacguccagCCu 198
GG::+ C: :C : CGC::CG AAG::GUG :+ G:: :G::UAA:: G C:U:G C :G:+AG+:::GCAA:::GCA:C::G:A:G C ::CC:
KJ742405 145 GGUGUcCAUCAUCCUCGCGGCGUAAGCUGUGGCC-GGAUUUGGAGUAAUCGGCCUUGAC-UAGCCAGGGAAGCAAUCCGACGUCAGCAGGACUCACCG 243
*****866655556*****9.56666667*****.***** PP

srp3 199 ggacgcucuUaggggAUacGgcgggc.gucgGuuCguggagggaGuCuucgggCaauaagaugUcacaUCugugCcgagCgCAAACCuucuUUU 291
:G::+UC UA:G:GAU+:GG::G++ UC:GU G:G G+ C::+: C:::CG A:ACCUU:: U
KJ742405 244 AGUUGGUCUUAGGAGAUCAGGCGUGucAUCUGUC-GCGCGGGUGCGCCGUGU-----CCCUCGUAGACCUUUCUGUG 314
*****9999999999.666665455555433.....6***** PP

>> KJ742406

rank	E-value	score	bias	mdl	mdl	from	mdl	to	seq	from	seq	to	acc	trunc	gc
(25) !	9.7e-48	143.0	0.0	cm		1	291	[]	45		314	+	..	0.91	no 0.58

srp3 1 cgGCUGUAAUGGCcguAaagcgGGAUUGcGcuc.uGuucaaacuCAAGGAcuccgcUCuauUGcGCUGg.gUUCGcgacuccgcCgcccagacguc.ca 98
GGCUGUAAUGGCC AA::CGGGA:U CG::: U::: C CAA G C:C U G+GCGCUG GUUC+:GA C::CC:C:C: GA ::C :
KJ742406 145 GGUGUcCAUCAUCCUCGCGGCGUAAGCUGUGGCC-GGAUUUGGAGUAAUCGGCCUUGAC-UAGCCAGGGAAGCAAUCCGACGUCAGCAGGACUCACCG 243
*****866655556*****9.56666667*****.***** PP

KJ742406 45 CGGCUGUAAUGGCCCAAGUCGGGAAUGCGAGGuGAUGUUCCACAACGGAAUCACGUGCUCGUGCGCUGaGUUCAAGAC-CGUCCCCUCUGGAAAACuUU 144
*****655666788888888999*****9*****999.***** PP

srp3 99 GGuuc.cacgcccgcgcccGCAagggguggggUcggguggggUAAuuggacgugGUcuggggguAGuGgGCAACcGAGCAccccgcacguccagCCu 198
GG::+ C: :C : CGC::CG AAG::GUG :+ G:: :G::UAA:: G C:U:G C :G:+AG+:::GCAA::+GCA:C::G:A:G C ::CC:

KJ742406 145 GGUGUcCAUCAUCCUCGCGGCGUAAGCUGUGGCC-GGAUUUGGAGUAAUCGGCCCUUGAC-UAGCCAGGGAAGCAAUCCGCAGCUAGCAGGACUCACCG 243
*****866655556*****9.56666667*****.***** PP

srp3 199 ggagcgcucuUaggggAUacGgcgggc.gucgGuuGgugggggaGuCuucgggCaauaagaugUcacauCugugCcgagCgCAAACCuucuuUUU 291
:G:: +UC UA:G:GAU+:GG::G++ UC:GU G:G G+ C::+:: C:::CG A:ACCUU:: U

KJ742406 244 AGUUGGUCUAGGAGAUCAGGGCGUGucAUCUGUC-GCGCGGGUGCGCCGUGU-----CCUCUGUAGACCUUUCGUG 314
*****9999999999.666665455555433.....6***** PP

>> KJ742407

rank	E-value	score	bias	mdl	mdl from	mdl to	seq from	seq to	acc	trunc	gc
(26) !	9.7e-48	143.0	0.0	cm	1	291 []	59	328 + ..	0.91	no	0.58

srp3 1 cgGUCUGUAAUGGCcguAaagcgGAAUGcGcuc.uGnucaaacuCAagGAcuccgcUCuauuGcGCGCUG.gUUCGcgacuccgcCgcccagacguc.ca 98
GGCUGUAAUGGCC AA::CGGGA:U CG::: U::: C CAA G C:C U G+GCGCUG GUUC+:GA C::CC:C:C: GA ::C ::

KJ742407 59 CGGCUGUAAUGGCCCAAGUCGGGAAUGCGAGGuGAUGUUCCACAACGGAAUCACGUGCUCGUGCGCUGaGUUCAAGAC-CGUCCCCUCUGGAAAACuUU 158
*****655666788888888999*****9*****999.***** PP

srp3 99 GGuuc.cacgcccgcgcccGCAagggguggggUcggguggggUAAuuggacgugGUcuggggguAGuGgGCAACcGAGCAccccgcacguccagCCu 198
GG::+ C: :C : CGC::CG AAG::GUG :+ G:: :G::UAA:: G C:U:G C :G:+AG+:::GCAA::+GCA:C::G:A:G C ::CC:

KJ742407 159 GGUGUcCAUCAUCCUCGCGGCGUAAGCUGUGGCC-GGAUUUGGAGUAAUCGGCCCUUGAC-UAGCCAGGGAAGCAAUCCGCAGCUAGCAGGACUCACCG 257
*****866655556*****9.56666667*****.***** PP

srp3 199 ggagcgcucuUaggggAUacGgcgggc.gucgGuuGgugggggaGuCuucgggCaauaagaugUcacauCugugCcgagCgCAAACCuucuuUUU 291
:G:: +UC UA:G:GAU+:GG::G++ UC:GU G:G G+ C::+:: C:::CG A:ACCUU:: U

KJ742407 258 AGUUGGUCUAGGAGAUCAGGGCGUGucAUCUGUC-GCGCGGGUGCGCCGUGU-----CCUCUGUAGACCUUUCGUG 328
*****9999999999.666665455555433.....6***** PP

>> UDB023551

rank	E-value	score	bias	mdl	mdl from	mdl to	seq from	seq to	acc	trunc	gc
(27) !	9.7e-48	143.0	0.0	cm	1	291 []	44	313 + ..	0.91	no	0.58

v v vvv v v NC

(29) ! 9.7e-48 143.0 0.0 cm 1 291 [] 50 319 + .. 0.91 no 0.58

srp3 1 cgGCUGUAAUGGCcguAaagcgGAAUGcGcuc.uGuucaaaacuCAAGAcuccgcUCuauuGcGCGCUG.gUUCGcgacuccgcCgcccagacguc.ca 98
KM576498 50 CGGCUGUAAUGGCC AA::CGGA:U CG:: U::: C CAA G C:C U G+GCGCUG GUUC+:GA C::CC:C:C: GA ::C ::
*****655666788888888999*****9*****999.***** PP

srp3 99 GGuuc.cacgcccgcgccGCAagggguggggUcgggcguggaUAAuuggacgugGUcuggggguAGuGcGGCAACcGAGCAccccgcacguccagCCu 198
KM576498 150 GGUGUcCAUCAUCCUCGCGGCGUAAGCUGUGGCC-GGAUUUGGAGUAAUCGGCCCUUGAC-UAGCCAGGAAGCAAUCCGCAGCUAGCAGGACUCACCG 248
*****866655556*****9.56666667*****.***** PP

srp3 199 ggacgcucuUaggggAUacGcgggc.gucgGuuGuggaggggaGuCuucgggCaauaagaugUacauCugugCcgagCgCAAACCuucuUUU 291
KM576498 249 AGUUGGUCUAGGAGAUCAGGGCGUGucAUCUGUC-GCGCGGGUGCGCCGUGU-----CCUCGUAGACCUUUCGUG 319
*****9999999999.666665455555433.....6***** PP

>> KF241547

rank E-value score bias mdl mdl from mdl to seq from seq to acc trunc gc
(30) ! 9.7e-48 143.0 0.0 cm 1 291 [] 45 314 + .. 0.91 no 0.58

srp3 1 cgGCUGUAAUGGCcguAaagcgGAAUGcGcuc.uGuucaaaacuCAAGAcuccgcUCuauuGcGCGCUG.gUUCGcgacuccgcCgcccagacguc.ca 98
KF241547 45 CGGCUGUAAUGGCC AA::CGGA:U CG:: U::: C CAA G C:C U G+GCGCUG GUUC+:GA C::CC:C:C: GA ::C ::
*****655666788888888999*****9*****999.***** PP

srp3 99 GGuuc.cacgcccgcgccGCAagggguggggUcgggcguggaUAAuuggacgugGUcuggggguAGuGcGGCAACcGAGCAccccgcacguccagCCu 198
KF241547 145 GGUGUcCAUCAUCCUCGCGGCGUAAGCUGUGGCC-GGAUUUGGAGUAAUCGGCCCUUGAC-UAGCCAGGAAGCAAUCCGCAGCUAGCAGGACUCACCG 243
*****866655556*****9.56666667*****.***** PP

srp3 199 ggacgcucuUaggggAUacGcgggc.gucgGuuGuggaggggaGuCuucgggCaauaagaugUacauCugugCcgagCgCAAACCuucuUUU 291
KF241547 244 AGUUGGUCUAGGAGAUCAGGGCGUGucAUCUGUC-GCGCGGGUGCGCCGUGU-----CCUCGUAGACCUUUCGUG 314
*****9999999999.666665455555433.....6***** PP

>> JX625292

rank	E-value	score	bias	mdl	mdl from	mdl to	seq from	seq to	acc	trunc	gc
(31) !	9.7e-48	143.0	0.0	cm	1	291	45	314 +	0.91	no	0.58

```

                    v          v          vvv          v          v          NC
    <<<<_____>>>>--- (((((((((((((((((-.---(((---(((-----((((-----(.-----(((---(((-----((((-----((((-----((((-----((((-----((
srp3  1 cgGCUGUAUUGGCcguAaagcgGGAAUGcGcuc.uGuucaaacuCAAGGAcuccgcUCuauuGcGCGCUg.gUUCGcgacuccgcCgcccagacguc.ca 98
    GGCUGUAAUGGCC AA::CGGGA:U CG::: U::: C CAA G C:C U G+GCGUG GUUC+:GA C::CC:C:C: GA ::C :
JX625292 45 CGGCUGUAAUGGCCCCAAGUCGGGAUGCGAGGuGAUGUUCCACAACGGAAUCACGUGCUCGUGCGCUgaGUUCAAGAC-CGUCCCCUCUGGAAACuUU 144
    *****655666788888888999*****g*****999.***** PP

```

```

                    vv          vv          v          v          v          NC
    ((((.<<<<<<--<<<<<<_____>>>>>>--->>>>>><<_____>>>><<<<<<-----<<<<-----<<<_____>>>--->>>>->>>>>>)))))) CS
srp3  99 GGuuc.cacgcccgcgccccGCAagggguggggUcggggcguggaUAauuggacgugGucggggguAGUCgGGCAACcGAGCAcccgacguccagCCu 198
    GG::+ C: ::C : CGC::CG AAG::GUG :+ G:: :G::UAA:: G C:U:G C ::G:+AG+:::GCAA::+GCA:C::G:A:G C ::CC:
JX625292 145 GGUGUcCAUCAUCCCUCGCGGCGUAAGCUGUGGCC-GGAUUUGGAGUAAUCGGCCUUGAC-UAGCCAGGGAAGCAAUCCGCAGCUAGCAGGACUCACCG 243
    *****866655556*****9.56666667*****.***** PP

```

```

                    v          v          vvv          v          v          NC
    )))))-))--)))---)))--..)))-)---)))))-----))-))-----)))))::: CS
srp3  199 ggacgcucuUaggggAUacGcgggc.gucgGuuGuggaggggGuCuucgggCaauaagaugUcacauCugugCcgagCgCAAACCuucuUUU 291
    :G::+UC UA:G:GAU+:GG::G++ UC:GU G:G G+ C::+: C:::CG A:ACCUU:: U
JX625292 244 AGUUGGUCUAGGAGUAAGCGCUGUCUCUGUC-GCGCGGUGCGCCUGU-----CCUCUGUAGACCUUCUGUG 314
    *****9999999999.666665455555433.....6***** PP

```

>> UDB019724

rank	E-value	score	bias	mdl	mdl from	mdl to	seq from	seq to	acc	trunc	gc
(32) !	1.2e-47	142.7	0.0	cm	1	291	46	315 +	0.91	no	0.59

```

                    v          v          vvv          v          v          NC
    <<<<_____>>>>--- (((((((((((((((((-.---(((---(((-----((((-----(.-----(((---(((-----((((-----((((-----((((-----((((-----((
srp3  1 cgGCUGUAUUGGCcguAaagcgGGAAUGcGcuc.uGuucaaacuCAAGGAcuccgcUCuauuGcGCGCUg.gUUCGcgacuccgcCgcccagacguc.c 97
    GGCUGUAA GGCC AA::CGGGAAU CG::: U::: C CAA G C:C U G+GCGUG GUUC+:GA C::CC:C:C: GA ::C :
UDB019724 46 CGGCUGUAACGGCCCCAAGUCGGGAUGCGAGGuGAUGUUCCACAACGGAAUCACGUGCUCGUGCGCUgaGUUCAAGAC-CGUCCCCUCUGGAAACuU 144
    *****655666788888888999*****g*****999.***** PP

```

```

                    vv          vv          v          v          v          NC
    ((((.<<<<<<--<<<<<<_____>>>>>>--->>>>>><<_____>>>><<<<<<-----<<<<-----<<<_____>>>--->>>>->>>>>>)))))) CS
srp3  98 aGGuuc.cacgcccgcgccccGCAagggguggggUcggggcguggaUAauuggacgugGucggggguAGUCgGGCAACcGAGCAcccgacguccagC 196
    :GG::+ C: ::C : CGC::CG AAG::GUG :+ G:: :G::UAA::GG C:U:G C ::G:+AG+:::G+ A::+GCA:C::G:A:G CC::C
UDB019724 145 UGGUGUcCAUCAUCCCUCGCGGCGUAAGCUGUGGCC-GGAUUUGGAGUAAUCGGCCUUGAC-UAGCCAGGGAAGUGAUCCGCAGCUAGCAGGACCAC 242
    *****866655556*****9.56666667*****.***** PP

```

```

                    v          v          vvv          v          v          NC
    )))))-))--)))---)))--..)))-)---)))))-----))-))-----)))))::: CS
srp3  197 CuggacgcucuUaggggAUacGcgggc.gucgGuuGuggaggggGuCuucgggCaauaagaugUcacauCugugCcgagCgCAAACCuucuUUU 291
    C::G::+UC UA:G:GAU+:GG::G++ UC:GU G:G G+ C::+: C:::CG AAACCUU:: U

```

UDB019724 243 CGAGUUGGUCUUAGGAGAUCAGGGCGUGucAUCUGUC-GCGCGGGUGCGCCGUGU-----CCCUCGUAACCUUUCGUG 315
*****9999999999.66666554555555433.....6***** PP

>> UDB011691

rank	E-value	score	bias	mdl	mdl from	mdl to	seq from	seq to	acc trunc	gc
(33) !	1.4e-47	142.5	0.0	cm	1	291 []	45	314 + ..	0.91	no 0.58

```
      v          v          vv          v          v          v          v          NC
srp3  1  cgGCUGUAAUGGCcguAaagcgGGAUUGcGcuc.uGuucaaacuCAAGAcuccgcUCuauuGcGCGCUG.gUUCGcgacuccgcCgccccagacguc.c 97
      GGCUGUAAUGGCC AA::CGGGA:U CG:: U+:: C CAA G : :C:C U G+GCGCUG GUUC+:GA C::CC:C:C: GA ::C :
UDB011691 45 CGGCUGUAAUGGCCCAAGUCGCGGAAUGCGAGGUGAUGUUUCCACAACGGAAUCACGUGCUCGUGCGCUGaGUUCAAGAC-CGUCCCCUCUGGAAAACu 143
      *****655556777788888999*****9*****999.***** PP
```

```
      vv          vv          v          v          v          v          v          NC
srp3  98  aGGuuc.cacgcccgcgcccccGCAagggguggggUcgggcguggaUAAuuggacgugGUcuggggguAGuGcGGCAACcGAGCAccccgcacguccagC 196
      :GG::+ C: :C : CGC::CG AAG::GUG :+ G:: :G::UAA:: G C:U:G C ::G:+AG+:::GCAA::+GCA:C::G:A:G C ::C
UDB011691 144 UGGUGUcCAUCAUCCUCGCGGCGUAAGCUGUGGCC-GGAUUUGGAGUAAUCGGCCCUUGAC-UAGCCAGGGAAGCAAUCCGCAGCUAGCAGGACUCAC 241
      *****866655556*****9.56666667*****.***** PP
```

```
      v          v          v          vv          v          v          v          NC
srp3  197 CuggacgcucuUaggggAUacGgcggg..gucgGuu.CguggagggaGuCuucgggCaauaagaugUacauCugugCcgagCgCAAACCuucuUUU 291
      C::G::+UC UA:G:GAU+:GG::G++ UC:GU CG:G: :G+ :: UG C:::CG A:ACCUU:: U
UDB011691 242 CGAGUUGGUCUUAGGAGAUCAGGGCGUGucAUCUGUCgCGCGGGUGUGC--CG-----UGUCCCUCGUAGACCUUUCGUG 314
      *****99999999998656666554333..22.....3336***** PP
```

>> UDB000354

rank	E-value	score	bias	mdl	mdl from	mdl to	seq from	seq to	acc trunc	gc
(34) !	1.8e-47	142.2	0.0	cm	1	291 []	90	357 + ..	0.88	no 0.59

```
      vv          vv          vv          vv          v          v          v          NC
srp3  1  cgGCUGUAAUGGCcguAaagcgGGAUUGcGcucuGuucaa..acuCAAGAcuccgcUCuauuGcGCGCUG.gUUCGcgacuccgcCgccccagacguc. 96
      :GGCUGUAAUGGCC: AA G+GGGA:U CG:: G U :: CUCAA G C C U G+GCGC G GUUC+:GA ::CC:C: CAGA ::C
UDB000354 90 UGGCUGUAAUGGCCCAAGGUGGGAAUGCGAGGCGAUGUUCcCUCAACGGAGUCCCGUGCUCGUGCGCCcGUUCAAGAC-UGUCCCUCGAGAAAACu 188
      *****55555440155555567788888888888*****999*****999.***** PP
```

```
      vv          vv          v          v          v          v          v          NC
srp3  97  caGGuuc.cacgcccgcgcccccGCAagggguggggUcgggcguggaUAAuuggacgugGUcuggggguAGuGcGGCAACcGAGCAccccgcacguccag 195
      :GG::+ C: :C:CC:C::CG A G::G:GG:+ G: :G::UAA:::G C:U:GUC ::G:+AG+:::GCAA::+GCA:C::G:A:G C:::
UDB000354 189 UUGGUGUcCAUCGUCCCCCGUAGGCUGGGGUC-GGAUUUGGAGUAAUCAGCCCUUGUC-UAGCCAGGGAAGCAAUCCGCAGCUGGCAGGACUCA 286
      *****76666668*****9.68888888*****.***** PP
```

v v vv vv v v v NC

```
)))))))-))--)))---))))--..)))-.-)))))-----))-))-----)))))))))::: CS
srp3 196 CCuggacgcucuUaggggAUacGgcgggc..gucgGuu.CguggaggggaGuCuucgggCaauaagaugUacauCugugCcgagCgCAAACCuucuUUU 291
CC::G:: +UCUUAG :GAU+:GG::++ UC:GU G G+ :: C+ UG C:::CG A:ACCU UUU
UDB000354 287 CCGAGUUGGUCUUAGGAGAUcAGGGCAUGucAUCUGUCg--CGCGGGUG--CG---CCG-----UGUCCUCGUAGACCU---UUU 357
*****999988888885..43332222...22....222.....4447*****.*** PP
```

>> UDB000322

rank	E-value	score	bias	mdl	mdl from	mdl to	seq from	seq to	acc	trunc	gc
(35) !	1.8e-47	142.2	0.0	cm	1	291 []	126	393 + ..	0.88	no	0.59

```
vvv vv v NC
<<<<_____>>>>---((((((((((((((((((--(((((.-----((((((-----.------(((--(((((((((((((((((((((( CS
srp3 1 cgGCUGUAAUGGCcguAaagcgGGAUGcGcucuGuucaa..acuCAagGAcuccgcUCuauuGcGCGCUG.gUUCGcgacuccgcCgcccagacguc. 96
:GGCUGUAAUGGCC: AA G+GGGA:U CG::: G U :: CUCAA G C C U G+GCGC G GUUC+:GA ::CC:C: CAGA ::C
UDB000322 126 UGGCUGUAAUGGCCCAAGGUGGGAUGCGAGGCGAUGUUCcCCUCAACGGAGUCCCGUGCUGCGCCGcGUUCAAGAC-UGUCCCUUCAGAAAACu 224
*****55555440155555567788888888888*****999*****999.***** PP
```

```
vv vv v NC
(((((.<<<<<<--<<<<<<<_____>>>>>>--->>>>>>><_____>>>><<<<<<<--<<<<--<<<_____>>>--->>>>--->>>>>>)) CS
srp3 97 caGGUuc.cacgcccgcgcccccGCAagggguggggUcggggcguggaUAAuuggacgugGUcuggggguAGuGcGGCAACcGAGCAcccgcacguccag 195
::GG::+ C: :C :CC:C::CG A G::G:GG:+ G: :G::UAA::G C:U:GUC ::G:+AG+:::GCAA::+GCA:C::G:A:G C:::
UDB000322 225 UUGGUGUcCAUCGUCCCCCAGCGUAGGCGUGGGGUC-GGAUUUGGAGUAAUCAGCCCUUGUC-UAGCCAGGGAAGCAAUCCGCAGCUGGCAGGACUCA 322
*****766666668*****9.68888888*****.***** PP
```

```
v vv vv vv v NC
)))))))-))--)))---))))--..)))-.-)))))-----))-))-----)))))))))::: CS
srp3 196 CCuggacgcucuUaggggAUacGgcgggc..gucgGuu.CguggaggggaGuCuucgggCaauaagaugUacauCugugCcgagCgCAAACCuucuUUU 291
CC::G:: +UCUUAG :GAU+:GG::++ UC:GU G G+ :: C+ UG C:::CG A:ACCU UUU
UDB000322 323 CCGAGUUGGUCUUAGGAGAUcAGGGCAUGucAUCUGUCg--CGCGGGUG--CG---CCG-----UGUCCUCGUAGACCU---UUU 393
*****999988888885..43332222...22....222.....4447*****.*** PP
```

>> JX425382

rank	E-value	score	bias	mdl	mdl from	mdl to	seq from	seq to	acc	trunc	gc
(36) !	2.1e-47	142.1	0.0	cm	1	291 []	120	386 + ..	0.88	no	0.60

```
vvvv vv v NC
<<<<_____>>>>---((((((((((((((((((--(((((.-----((((((-----.------(((--(((((((((((((((((((((( CS
srp3 1 cgGCUGUAAUGGCcguAaagcgGGAUGcGcuc.uGuucaaacuCAag..GAcuccgcUCuauuGcGCGCUG.gUUCGcgacuccgcCgcccagacguc. 96
:GGCUGUAA GGCC: AA G+GGGA:U CG::: G U ::++ C ++ G C C U G+GCGC G GUUC+:GA ::CC:C:CCAGA ::C
JX425382 120 UGGCUGUAACGGCCCAAGGUGGGAUGCGAGGc-GAUGUUUCCCAacGGAGUCCCGUGCUGCGCCGaGUUCAAGAC-UGUCCCUCCAGAAAACu 218
*****5.444433333333246677777778888*****8889*****999.***** PP
```

```
vv vv NC
(((((.<<<<<<--<<<<<<<_____>>>>>>--->>>>>>><_____>>>><<<<<<<--<<<<--<<<_____>>>--->>>>--->>>>>>)) CS
srp3 97 caGGUuc.cacgcccgcgcccccGCAagggguggggUcggggcguggaUAAuuggacgugGUcuggggguAGuGcGGCAACcGAGCAcccgcacguccagC 196
::GG::+ C: :C :CC:C::CG A G::G:GG:+ : :G::UAA:: G:C:U:GUC ::G:+AG+:::GCAA::+GCA:C::G:A:G:C :C
JX425382 219 UUGGUGUcCAUUGUCCCCACGGCGUAGGCCGUGGUC-GGAUUUGGAGUAAUCGGCCCUUGUC-UAGCCAGGGAAGCAAUCCGCAGCUAGCAGGGCUCAC 317
```

*****77777779*****.89999999*****.***** PP

```

          v                v          vv vvv          vv          vvvv  NC
  )))))-))--))---)))))---.)))))---.)))))---)))))---)))))---)))))::: CS
srp3 197 CuggacgcucuUaggggAUacGgcgggc..gucgGuu.CuggaggggaGuCuucgggCaauaagaugUcacauCugugCcgagCgCAAACCuucuUUU 291
      C::G::+UCUUAGG:GAU+:GG::+ UC:GU G G+ C:: UG C::CG A:ACC UUU
JX425382 318 CGAGUUGGUCUUAGGAGAUCAGGGCACGucAUCUGUCg--CGCGGGUGCGCCG-----UGUCCUCGUAGACC----UUU 386
      *****9998888888885..444433334433.....3337*****.*** PP

```

>> GU234059

rank	E-value	score	bias	mdl	mdl from	mdl to	seq from	seq to	acc trunc	gc
(37) !	2.7e-47	141.8	0.0	cm	1	291 []	12	281 + ..	0.91	no 0.57

```

                    vvv          v          v          v          v          NC
  <<<<_____>>>>---((((((((((((((((((---((((-----((((-----(.-----((((-----((((-----((((-----((((-----((((-----((((-----((((-----(( CS
srp3 1 cgGCUGUAAUGGCcguAaagcgGGA AUGcGcuc.uGuaacaacuCAagGAcucgcgUCuaauGcGCGCUg.gUucGcgacucgcCgcccagacguc.ca 98
      :GGCUGUAA GGCC:AA::CGGAAU CG:: U::: C CAA G C:C U G+GCGCUG GUUC+:GA C: CC:C:C: GA :C :
GU234059 12 UGGCUGUAAACGGCCAAAGUCGGGAAUGCAGGGuGAUGUUCCACAACGGAAUCACGUGCUCGUGCGCUGaGUUCAAGAC-CGNCCCCUCUGGAAACuUU 111
      *****655666788888888999*****9*****999.***** PP

```

```

          vv          vv          v          v          NC
  ((((.<<<<<<<-----<<<<<<<_____>>>>>>>--->>>>>>>><<<<<<<-----<<<<<<<-----<<<_____>>>--->>>>>>))))) CS
srp3 99 GGuuc.cacgcccgccgccccGCAagggguggggUcgggcguggaUAAuuggacgugGUcugggguAGuCGGCAACcGAGCAccccgcagcuccagCCu 198
      :G::+C : :C : CGC::CG AAG::GUG :+ G:: :G::UAA:: G C:U:G C :G:+AG+::G+AA::+GCA:C::G:A:G C :C:
GU234059 112 GGUGUcCAUCAUCCUCGCGGCGUAAGCUGUGGCC-GGAUUUGGAGUAUUCGCCUUGAC-UAGCCAGGGAAGUAUUCGCAGCUAGCAGGACUCACCG 210
      *****866655556*****9.56666667*****.***** PP

```

```

          v                v          v          vvv          v          v          NC
  )))))-))--))---)))))---.)))))---)))))---)))))---)))))---)))))---)))))::: CS
srp3 199 ggacgcucuUaggggAUacGgcgggc..gucgGuuCguggaggggaGuCuucgggCaauaagaugUcacauCugugCcgagCgCAAACCuucuUUU 291
      :G::+UC UA:G:GAU+:GG :G++ UC:GU G:G G+ C::: C::CG AAACCUU:: U
GU234059 211 AGUUGGUCUUAGGAGAUCAGGGCUGucAUCUGUC-GCGCGGGUGCGCCGUGU-----CCCUCGUAACCUUUCGUG 281
      *****999999999.666665455555433.....6***** PP

```

>> GU184028

rank	E-value	score	bias	mdl	mdl from	mdl to	seq from	seq to	acc trunc	gc
(38) !	9.6e-47	140.2	0.0	cm	1	291 []	11	280 + ..	0.91	no 0.58

```

          v                v                vvv          v          v          NC
  <<<<_____>>>>---((((((((((((((((((---((((-----((((-----((((-----((((-----((((-----((((-----((((-----((((-----((((-----(( CS
srp3 1 cgGCUGUAAUGGCcguAaagcgGGA AUGcGcuc.uGuaacaacuCAagGAcucgcgUCuaauGcGCGCUg.gUucGcgacucgcCgcccagacguc.ca 98
      GGCUGUAA GGCC AA::C:GAAU CG:: U::: C CAA G C:C U G+GCGCUG GUUC+:GA C::CC:C:C: GA ::C :
GU184028 11 CGGCUGUAAACGGCCCAAGUCGGGAAUGCAGGGuGAUGUUCCACAACGGAAUCACGUGCUCGUGCGCUGaGUUCAAGAC-CGUCCUCUGGAAACuUU 110
      *****655666788888888999*****9*****999.***** PP

```

```

          vv          vv          v          v          NC
  ((((.<<<<<<<-----<<<<<<<_____>>>>>>>--->>>>>>><<<<<<<-----<<<<<<<-----<<<_____>>>--->>>>>>))))) CS

```


vv vv v v NC
srp3 99 GGuuc.cacgcccgcgcccccGCAaggggggggUcgggcguggaUAauuggacgugGucuggggguAGuGcGGCAACcGAGCAccccgcacguccagCCu 198
GG::+ C: :C : CGC::CG AAG::GUG :+ G:: :G::UAA:: G C:U:G C : :G:+AG+: : :G+AA:::GCA:C::G:A:G C : :CC:
GU234088 151 GGUGUcCAUCAUCCUCGCGGGGUAAGCUGUGGCC-GGAUUUGGAGUAAUCGCCCUGAC-UAGCCAGGGAAGUAAUCCGCAGCUAGCAGGACUCACCG 249
*****866655556*****9.56666667*****.***** PP

v v vvv v NC
srp3 199 ggacgcucuUaggggAUacGgcgggc.gucgGuuGuggaggggGuCuucgggCaauaagaugUcacauCugugCcgagGcCAAACCuucuUUU 291
:G:: +UC UA:G:GAU+:GG::G++ UC:GU G:G G+ C::+: C::CG AAACCUU:: U
GU234088 250 AGUUGGUCUUAGGAGAUcAGGGGUGucAUCUGUC-GCGCGGGUGCGCCGUGU-----CCCUCGUAACCUUUCGUG 320
*****9999999999.6666655455555433.....6***** PP

>> UDB000323

rank	E-value	score	bias	mdl	mdl from	mdl to	seq from	seq to	acc trunc	gc
(41) !	6.6e-46	137.9	0.0	cm	1	291	130	396 + ..	0.88	no 0.60

vvvv v vvv vv v v NC
srp3 1 cgGCUGUAAUGGCcguAaagcggGAAUGcGcuc..uGuucaaacuCAagGAacuccgcUCuauuGcGCGCUg.gUUCGcgacuccgcGgccccagacguc 96
:GGCUGUAAUGGCC: AA G+GGGA:U CG:: UGU +:: C CAA G C C UUGC CGC G GUUC+:GA : :CC:C:CCAGA : :C
UDB000323 130 UGGCUGUAAUGGCCAACAGGUGGGAAUGCGAGCgaUGU-UCUCCCCAACGGAGUCCCGUGCUUGCGCGCCGaGUUCAAGAC-UGUCCCCCAGAAAAC 227
*****642222.244555555677888888889999999999*****8889*****9999.***** PP

vv v v vv v v v v NC
srp3 97 .caGGuuc.cacgcccgcgcccccGCAagggguggggUcgggcguggaUAauuggacgugGucuggggguAGuGcGGCAACcGAGCAccccgcacgucca 194
:GG::+ C: :C :CC C::CG A G::G GG:+ G: :G::UAA:::G C:U:GUC : :G:+AG+: :G C A:::GCA:C::G:A:G C : :
UDB000323 228 uUUGGUcCAUUGUCCCCACAGGCAUGCUGGGGUC-GGAUUUGGAGUAAUCAGCCCUGUC-UAGCCAGGGAAGCGAUUCCGCAGCUGGCAGGACUC 325
*****87777777999999*****999999.789999999*****.***** PP

v v vv vv v vvv v NC
srp3 195 gCCuggacgcucuUaggggAUacGgcgggc.gucgGuu.CguggagggGGuCuucgggCaauaagaugUcacauCugugCcgagGcCAAACCuucuUUU 291
:CC::G:: +UCUUAGG:GAU+:GG::++ UC:G G G+ : : C+ : : UG C::CG A:ACC UUU
UDB000323 326 ACCGAGUUGGUCUAGGAGAUcAGGGCUGGCG--CGCGGUG--CG---CCG-----UGUCCUCGUAGACC----UUU 396
*****98888888885.33332222...22....333.....4447*****.*** PP

>> GU234051

rank	E-value	score	bias	mdl	mdl from	mdl to	seq from	seq to	acc trunc	gc
(42) !	1.1e-45	137.3	0.0	cm	1	291	45	314 + ..	0.91	no 0.58

v v vvv v NC
srp3 1 cgGCUGUAAUGGCcguAaagcggGAAUGcGcuc.uGuucaaacuCAagGAacuccgcUCuauuGcGCGCUg.gUUCGcgacuccgcGgccccagacguc.ca 98

GU234051 45 GGCUGU AUGGCC A::CGGAAU CG:: U::: C CAA G C:C U G+GCGUG GUUC+:GA C::CC:C:C: GA ::C ::
CGGCUGUNAUGGCCCGAGUCGGAAUGCGAGGuGAUGUUUCCACAACGGAAUCACGUGCUCGUGCGUGaGUUCAAGAC-CGUCGCCUCUGGAAAACuUU 144
*****6556667888888888999*****9*****999.***** PP

srp3 99 GGuuc.cacgcccggcccccGCAagggguggggUcgggcguggaUAAuuggacgugGUCuggggguAGuGcGGCAACcGAGCAccccgcacguccagCCu 198
GG::+ C: :C : CGC::CG AAG::GUG :+ G:: :G:::UAA:: G C:U:G C :G:+AG+:::G+AA::: GCA:C::G:A:G C ::CC:
GU234051 145 GGUGUcCAUCAUCCUCGCGGGCGUAAGCUGUGGCC-GGAUUUGGAGUAAUCGGCCCUUGAC-UAGCCAGGGAAGUAAUUCGACGCUAGCAGGACUCACCG 243
*****86665556*****9.5666667*****.***** PP

srp3 199 ggacgcucuUaggggAUacGgcgggc.gucgGuuGuggagggGuCuucgggCaauaagaugUcacauCugugCcgagGcCAAACCuucuuUUU 291
:G:: +UC UA:G:GAU+:GG::G++ UC:GU G:G G+ C::+: C:::CG AAACCUU:: U
GU234051 244 AGUUGGUCUUAGGAGAUcAGGGCGUGucAUCUGUC-GCGCGGGUGCGCCGUGU-----CCCUCGUAACCUCUUGUG 314
*****9999999999.666665455555433.....6***** PP

>> AB973750

rank	E-value	score	bias	mdl	mdl from	mdl to	seq from	seq to	acc	trunc	gc
(43) !	4.2e-45	135.7	0.0	cm	1	291 []	122	388 + ..	0.88	no	0.60

srp3 1 cgGCUGUAUUGGCcguAaagcgGAAUGcGcuc.uGuuc..aaacuCAaGAcuccgcUCuauGcGCGUG.gUUCGcgacuccgcCgcccagacguc. 96
:GGCUGUAA GGCC: AA G+GGGA:U CG:: G U :: CUCAA G C C U G+GCG G GUUC+:GA ::CC:C:CCAGA ::C
AB973750 122 UGCUGUAACGGCCCCAAGGUGGAAUGCGAGGc-GAUuuUUCUCAACGGAGUCCGUGCUCGUGCGCCGaGUUCAAGAC-UGUCCCUCCAGAAAACu 220
*****5.554401556666667777788888888888*****8889*****999.***** PP

srp3 97 caGGuuc.cacgcccggcccccGCAagggguggggUcgggcguggaUAAuuggacgugGUCuggggguAGuGcGGCAACcGAGCAccccgcacguccagC 198
::GG::+ C: :C :CC:C::CG A G::G:GG:+ G: :G:::UAA:: G C:U:GUC ::G:+AG+:::GC A:::GCA:C::G:A:G C ::C
AB973750 221 UUGGUGUcCAUCGUCUCCACGGCGUAGCCGUGGUC-GGAUUUGGAGUAAUCGGCCCUUGUC-UAGCCAGGGAAGCGAUCCGACGCUAGCAGGACUCAC 319
*****76666668*****9.68888888*****.***** PP

srp3 197 CuggacgcucuUaggggAUacGgcgggc.gucgGuu.CguggagggGuCuucgggCaauaagaugUcacauCugugCcgagGcCAAACCuucuuUUU 291
C::G:: +UCUAGG:GAU+:GG::: + UC:GU G G+ C::: UG C:::CG A:ACC UUU
AB973750 320 CGAGUUGGUCUUAGGAGAUcGGGGCACGucAUCUGUCg--CGCGGGUGCGCCG-----UGUCCCUcGUGACC----UUU 388
*****999888888888885..4443333333333.....3347*****.*** PP

>> GU184027

rank	E-value	score	bias	mdl	mdl from	mdl to	seq from	seq to	acc	trunc	gc
(44) !	4.4e-45	135.6	0.0	cm	1	291 []	7	277 + ..	0.92	no	0.58

srp3 1 cgGCUGUAAUGGCcguAaagcgGAAUGcGcuc.uGuucaaacuCAagGAcuccgcUCuauuGcGCUCg.gUUCGcgacuccgcCgccccagacguc.ca 98
GGCUGUAA GGCC AA::C:GAAU CG:: U::: C CAA G C:C U G+GCGUG GUUC+:GA +C::CC:C:C: GA ::C ::
GU184027 7 CGGCUGUAAACGGCCCCAAGUCGGGAAUGCGAGGUgAUGUUCCACAACGGAAUCACGUGCUGCGCUGaGUUCAAGACCCGUCGCCUCUGGAAAAcUuu 107
*****65566678888888999*****9***** PP

srp3 99 GGuc.cacgcccgcgcccGCAagggguggggUcgggcguggaUAAuuggacgUGucugggguAGuGcGGCAACcGAGCAccccgcacguccagCCu 198
:G::+C: :C:CGC::CG AAG::GUG: G:: :G::UA :: G C:U G C ::G +AG+:::GCAA::+GCA C::G A:G C ::C:
GU184027 108 GGUGUcCAUCAUCCUCGCGGCGUAAGCUGUGGUc-GGAUUUGGAGUAMUCGGCCCUUGAC-UAGCCAGGGAAGCAAUCCGCASCUGAAGGACUCACCG 206
*****866656667*****9.56666777***** PP

srp3 199 ggagcgcucuUaggggAUacGgcgggc.gucgGuuGgugaggggGuCuucgggCaauaagaugUcacauCugugCcgagCgCAAACCuucuuUUU 291
:G::+UC A:G:GAU+:GG::G++ UC:GU G:G G+ C::: C:::CG AAACC:U:: U
GU184027 207 AGUUGGUCUCAGGAGAUCAGGGCGUGucAUCUGUC-GCGCGGUGCGCCGUGU-----CCCUCGUAACCCUUCUGU 277
*****9.66665455555433.....6***** PP

>> JX425373

rank	E-value	score	bias	mdl	mdl	from	mdl	to	seq	from	seq	to	acc	trunc	gc
(45) !	1e-44	134.6	0.0	cm		1	291	[]	118		384	+ ..	0.87	no	0.60

srp3 1 cgGCUGUAAUGGCcguAaagcgGAAUGcGcuc.uGuucaaacuCAag.GAcuccgcUCuauuGcGCUCg.gUUCGcgacuccgcCgccccagacguc. 96
:GGCUGUAA GGCC: AA G+GGGA:U CG:: G U ::++ C ++ G C C U G+GCG G GUUC+:GA ::CC:C:CCAGA ::C
JX425373 118 UGGCUGUAAACGGCCCCAAGUGGGGAAUGCGAGGc-GAUGUUUCCCAacGGAGUCCCGUGCUCGUGCGCGaGUUCAAGAC-UGUCCCUCCAGAAAACu 216
*****5.44443333333324667777778888*****8889*****999.***** PP

srp3 97 caGGuuc.cacgcccgcgcccGCAagggguggggUcgggcguggaUAAuuggacgUGucugggguAGuGcGGCAACcGAGCAccccgcacguccagC 196
::GG::+C: :C:CC:C::CG A G::G:GG:+ G: :G::UAA:: G C:U:GUC ::G:+AG+:::GC A::+GCA:C::G:A:G C ::C
JX425373 217 UUGGUGUcCAUCGUCCCCACGGCGUAGCCGUGGUC-GGAUUUGGAGUAAUCGGCCCUUGUC-UAGCCAGGGAAGCGAUUCCGCAGCUAGCAGGACUCAC 315
*****766666668*****9.68888888***** PP

srp3 197 CuggagcgcucuUaggggAUacGgcgggc.gucgGuu.CguggagggGuCuucgggCaauaagaugUcacauCugugCcgagCgCAAACCuucuuUUU 291
C::G::+UCUUAGG:GAU+:GG::+ UC:GU G G+ C:: UG C:::CG A:ACC UUU
JX425373 316 CGAGUUGGUCUUAGGAGAUcAGGGCACGucAUCUGUCg--CGCGGGUGCGCG-----UGUCCCUCCAGAAAACu 384
*****999888888888885.4444333334433.....3337***** PP

>> UDB013274

rank	E-value	score	bias	mdl	mdl	from	mdl	to	seq	from	seq	to	acc	trunc	gc
------	---------	-------	------	-----	-----	------	-----	----	-----	------	-----	----	-----	-------	----

(46) ! 1.4e-44 134.2 0.1 cm 1 291 [] 127 393 + .. 0.87 no 0.61

srp3 1 cgGCUGUAAUGGCcguAaagcgGGAUUGcGcuc.uGuucaaacuCAag..GAcuccgcUCuauuGcGCGCUG.gUUCGcgacuccgcCgccccagacguc 96
:GGCUGUAA GGCC: AA G+GGGA:U CG:: G U :++ C ++ G : CC C U G+GCGC G GUUC+:G: ::CC:C:CCAGA :C
UDB013274 127 UGGCUGUAAACGGCCCCAAGGUGGGAAUGCGAGGc-GAUGUUUCCCCAacGGAGCCCCGUGCUCGUGCGCCGaGUUCAAGGC-UGUCCCCUCCAGAAAAC 224
*****5.44443333333246677777778888*****8889*****.***** PP

srp3 97 .caGGuuc.cacgccccccccGCAagggguggggUcggguggggUAAuuggacgugGUcugggggUAGuGcGGCAACcGAGCAccccgcacgucca 194
:GG::+ C: :C :CC: :CG A G:::GG:+ G: :G::UAA::GG C:U:GUC :G:+AG+:::GC A:::+GCA:C::G:A:G CC:
UDB013274 225 uUUGGUGUcCAUCGUCUCCCCACGGCGUAGGCCAUGGUC-GGAUUUGGAGUAAUCGGCCUUGUC-UAGCCAGGGAAGCGAUUCCGCAGCUGGCAGGACCC 322
*****766666668*****9.68888888*****.***** PP

srp3 195 gCCuggacgcucuUaggggAUacGgcgggc..gucgGuu.CguggaggggGuCuucgggCaauaagaugUcacauCugugCcgagCgCAAACCuucuUUU 291
:CC::G:: +UCUUAGG:GAU+:GG::: + :C:GU CG GG : C:: UG C:::CG A:ACC UUU
UDB013274 323 ACCGAGUUGGUCUAGGAGAUACAGGGCAGGucAUCUGUCgCGCGGGU--GCGCCG-----UGUCCCCUGUAGACC----UUU 393
*****999888888888544444333332.....3337*****.*** PP

>> HF674530

rank E-value score bias mdl mdl from mdl to seq from seq to acc trunc gc

(47) ! 1.4e-44 134.2 0.0 cm 1 291 [] 117 383 + .. 0.87 no 0.59

srp3 1 cgGCUGUAAUGGCcguAaagcgGGAUUGcGcuc.uGuucaaacuCAag..GAcuccgcUCuauuGcGCGCUG.gUUCGcgacuccgcCgccccagacguc. 96
:GGCUGUAA GGCC: AA G+GGGA:U CG:: G U :++ C ++ G C C U G+GCGC G GUUC+:GA ::CC:C:CCAGA :C
HF674530 117 UGGCUGUAAACGGCCCCAAGGUGGGAAUGCGAGGc-GAUGUUUCCCCAacGGAGUCCCGUGCUCGUGCGCCGaGUUCAAGAC-UGUCCCCUCCAGAAAACu 215
*****5.44443333333324667777778888*****8889*****999.***** PP

srp3 97 caGGuuc.cacgccccccccGCAagggguggggUcggguggggUAAuuggacgugGUcugggggUAGuGcGGCAACcGAGCAccccgcacgucca 196
:GG::+ C: :C :C:C::CG A G:::G:G :+ G: :G::UAA:: G C:U:GUC :G:+AG+:::GCAA:::+GCA:C::G:A:G C :C
HF674530 216 UUGGUGUcCAUCGUCUCCCCACAGCGUAGGCGUGGUC-GGAUUUGGAGUAAUCGGCCUUGUC-UAGCCAGGGAAGCAAUCCGCAGCUAGCAGGACUCAC 314
*****766666668*****9.68888888*****.***** PP

srp3 197 CuggacgcucuUaggggAUacGgcgggc..gucgGuu.CguggaggggGuCuucgggCaauaagaugUcacauCugugCcgagCgCAAACCuucuUUU 291
C::G:: +UCUUAGG:GAU+:GG::: + UC:GU G G+ C:: UG C:::CG A:ACC UUU
HF674530 315 CGAGUUGGUCUAGGAGAUACAGGGCAGGucAUCUGUCg--CGCGGGUGCGCCG-----UGUCCCCUGUAGACC----UUU 383
*****999888888888854444333334433.....3337*****.*** PP

C::G::+UCUUAGG:GAU+:GG::+ UC:GU G G+ C:: UG C::CG A:ACC UUU
HF674531 315 CGAGUUGGUCUUAGGAGAUACAGGGCACGucAUCUGUCg--CGCGGGUGCGCCG-----UGUCCUCGUAGACC----UUU 383
*****9998888888888885..4444333334433.....3337*****...** PP

>> HF674533

rank	E-value	score	bias	mdl	mdl from	mdl to	seq from	seq to	acc	trunc	gc
(50) !	1.4e-44	134.2	0.0	cm	1	291 []	117	383 + ..	0.87	no	0.59

srp3 1 cgGCGUAAUGGCcguAaagcgGGAUgCguc.uGuucaaacuCAag..GAcuccgcUCuauuGcGCGCUG.gUUCGcgacuccgcCgccccagacguc. 96
:GGCUGUAA GGCC: AA G+GGGA:U CG:: G U :++ C ++ G C C U G+GCGC G GUUC+:GA ::CC:C:CCAGA ::C
HF674533 117 UGGCUGUAACGGCCCCAAGGUGGGAUgCAGGc-GAUGUUUCCCAacGGAGUCCCGUGCUCGUGCGCCGaGUUCAAGAC-UGUCCCUCCAGAAAACu 215
*****5.444433333333246677777778888*****8889*****999.....** PP

srp3 97 caGGuuc.cacgcccgcgcccccGCAagggguggggUcggguggggUAAuuggacgugGucugggggUAGuCGGGCAACcGAGCAccccgcacguccagC 196
::GG::+ C: :C : C:C::CG A G::G:G :+ G: :G::UAA:: G C:U:GUC ::G:+AG+:::GCAA::+GCA:C::G:A:G C ::C
HF674533 216 UUGGUGUcCAUCGUCCUCACAGCGUAGGCGUGGUC-GGAUUUGGAGUAAUCGGCCCUUGUC-UAGCCAGGGAAGCAAUCCGCAGCUAGCAGGACUCAC 314
*****766666668*****9.68888888*****.....** PP

srp3 197 CuggacgcucuUaggggAUacGgcgggc..gucgGuu.CguggaggggGuCuucgggCaauaagaugUcacauCugugCcgagCgCAAACCuucuUUU 291
C::G::+UCUUAGG:GAU+:GG::+ UC:GU G G+ C:: UG C::CG A:ACC UUU
HF674533 315 CGAGUUGGUCUUAGGAGAUACAGGGCACGucAUCUGUCg--CGCGGGUGCGCCG-----UGUCCUCGUAGACC----UUU 383
*****9998888888888885..4444333334433.....3337*****...** PP

>> HF674534

rank	E-value	score	bias	mdl	mdl from	mdl to	seq from	seq to	acc	trunc	gc
(51) !	1.4e-44	134.2	0.0	cm	1	291 []	117	383 + ..	0.87	no	0.59

srp3 1 cgGCGUAAUGGCcguAaagcgGGAUgCguc.uGuucaaacuCAag..GAcuccgcUCuauuGcGCGCUG.gUUCGcgacuccgcCgccccagacguc. 96
:GGCUGUAA GGCC: AA G+GGGA:U CG:: G U :++ C ++ G C C U G+GCGC G GUUC+:GA ::CC:C:CCAGA ::C
HF674534 117 UGGCUGUAACGGCCCCAAGGUGGGAUgCAGGc-GAUGUUUCCCAacGGAGUCCCGUGCUCGUGCGCCGaGUUCAAGAC-UGUCCCUCCAGAAAACu 215
*****5.444433333333246677777778888*****8889*****999.....** PP

srp3 97 caGGuuc.cacgcccgcgcccccGCAagggguggggUcggguggggUAAuuggacgugGucugggggUAGuCGGGCAACcGAGCAccccgcacguccagC 196
::GG::+ C: :C : C:C::CG A G::G:G :+ G: :G::UAA:: G C:U:GUC ::G:+AG+:::GCAA::+GCA:C::G:A:G C ::C
HF674534 216 UUGGUGUcCAUCGUCCUCACAGCGUAGGCGUGGUC-GGAUUUGGAGUAAUCGGCCCUUGUC-UAGCCAGGGAAGCAAUCCGCAGCUAGCAGGACUCAC 314
*****766666668*****9.68888888*****.....** PP

```

          v          v          vv vvv          vv          vvvv          NC
))))))--))--))---)))))--..)))))---.-)))))-----))---)))))::: CS
srp3 197 CuggacgcucuUaggggAUacGgcgggc..gucgGuu.CguggaggggaGuCuucgggCaauaagaugUcacauCugugCcgagCgCAAACCuucuUUU 291
C::G::+UCUUAGG:GAU+:GG::+ UC:GU G G+ C:: UG C::CG A:ACC UUU
HF674534 315 CGAGUUGGUCUUAGGAGAUACAGGGCACGucAUCUGUCg--CGCGGGUGCGCCG-----UGUCCUCGUAGACC----UUU 383
*****9998888888888885..4444333334433.....3337*****...** PP

```

>> HF674549

rank	E-value	score	bias	mdl	mdl from	mdl to	seq from	seq to	acc trunc	gc
(52) !	1.4e-44	134.2	0.0	cm	1	291 []	117	383 + ..	0.87	no 0.59

```

          vvvv          vv          vvv vv          v          v          NC
<<<<_____>>>>--(((((((((((((((.--((((-----..--((((-----..-----((((-----((((((((((((((((((( CS
srp3 1 cgGCGUAAUGGCcguAaagcgGAAUGcGcuc.uGuucaaacuCAag..GAcuccgcUCuauuGcGCGCUG.gUUCGcgacuccgcCgccccagacguc. 96
:GGCUGUAA GGCC: AA G+GGGA:U CG:: G U :++ C ++ G C C U G+GCGC G GUUC+:GA ::CC:C:CCAGA ::C
HF674549 117 UGGCUGUAACGGCCCCAAGGUGGGAAUGCGAGGc-GAUGUUUCCCCAacGGAGUCCCGUGCUCGUGCGCCGaGUUCAAGAC-UGUCCCUCCAGAAAACu 215
*****5.4444333333333246677777778888*****8889*****999.***** PP

```

```

          vv          vv          v          v          NC
((((((,.<<<<<<<<<<<<<_____>>>>>>>-->>>>>>><_____>><<<<<<<<<<<<<<<<_____>>>>-->>>>>>>)) CS
srp3 97 caGGuuc.cacgcccgcgcccccGCAagggguggggUcggggcguggaUAAuuggacgugGUcuggggguAGuGcGGCAACcGAGCAccccgcacguccagC 196
::GG::+ C: :C :C::CG A G::G:G :+ G: :G::UAA:: G C:U:GUC ::G:+AG+::GCAA::+GCA:C::G:A:G C :C
HF674549 216 UUGGUGUCcAUCGUCCUCACAGCGUAGGcUGUGGUC-GGAUUUGGAGUAAUCGGCCCUUGUC-UAGCCAGGGAAGCAAUCCGCAGCUAGCAGGACUCAC 314
*****766666668*****9.68888888***** PP

```

```

          v          v          vv vvv          vv          vvvv          NC
))))))--))--))---)))))--..)))))---.-)))))-----))---)))))::: CS
srp3 197 CuggacgcucuUaggggAUacGgcgggc..gucgGuu.CguggaggggaGuCuucgggCaauaagaugUcacauCugugCcgagCgCAAACCuucuUUU 291
C::G::+UCUUAGG:GAU+:GG::+ UC:GU G G+ C:: UG C::CG A:ACC UUU
HF674549 315 CGAGUUGGUCUUAGGAGAUACAGGGCACGucAUCUGUCg--CGCGGGUGCGCCG-----UGUCCUCGUAGACC----UUU 383
*****9998888888888885..4444333334433.....3337*****...** PP

```

>> HF674551

rank	E-value	score	bias	mdl	mdl from	mdl to	seq from	seq to	acc trunc	gc
(53) !	1.4e-44	134.2	0.0	cm	1	291 []	117	383 + ..	0.87	no 0.59

```

          vvvv          vv          vvv vv          v          v          NC
<<<<_____>>>>--(((((((((((((((((((.--((((-----..--((((-----..-----((((-----((((((((((((((((((( CS
srp3 1 cgGCGUAAUGGCcguAaagcgGAAUGcGcuc.uGuucaaacuCAag..GAcuccgcUCuauuGcGCGCUG.gUUCGcgacuccgcCgccccagacguc. 96
:GGCUGUAA GGCC: AA G+GGGA:U CG:: G U :++ C ++ G C C U G+GCGC G GUUC+:GA ::CC:C:CCAGA ::C
HF674551 117 UGGCUGUAACGGCCCCAAGGUGGGAAUGCGAGGc-GAUGUUUCCCCAacGGAGUCCCGUGCUCGUGCGCCGaGUUCAAGAC-UGUCCCUCCAGAAAACu 215
*****5.4444333333333246677777778888*****8889*****999.***** PP

```

```

          vv          vv          v          v          NC
((((((,.<<<<<<<<<<<<<_____>>>>>>>-->>>>>>><_____>><<<<<<<<<<<<<<<<_____>>>>-->>>>>>>)) CS
srp3 97 caGGuuc.cacgcccgcgcccccGCAagggguggggUcggggcguggaUAAuuggacgugGUcuggggguAGuGcGGCAACcGAGCAccccgcacguccagC 196
::GG::+ C: :C :C::CG A G::G:G :+ G: :G::UAA:: G C:U:GUC ::G:+AG+::GCAA::+GCA:C::G:A:G C :C

```


*****5.444433333333246677777778888*****8889*****999.***** PP

srp3 97 caGGuuc.cacgcccgcccccGCAagggguggggUcgggcguggaUAAuuggacgugGUcuggggguAGuGcGGCAACcGAGCAccccgcacguccagC 196
HF674578 216 UUGGUGUcCAUCGUCCUCACAGCGUAGGCUGUGGUC-GGAUUUGGAGUAAUCGGCCCUUGUC-UAGCCAGGGAAGCAAUCCGCAGCUAGCAGGACUCAC 314

srp3 197 CuggacgcucuUaggggAUacGgcgggc..gucgGuu.CguggagggGuCuucgggCaauaagaugUcacauCugugCcgagCgCAAACCuucuUUU 291
HF674578 315 CGAGUUGGUCUUAGGAGAUcAGGGCACGucAUCUGUCg--CGCGGGUGCGCCG-----UGUCCUCGUAGACC-----UUU 383

>> HF674592

Table with 11 columns: rank, E-value, score, bias, mdl, mdl from, mdl to, seq from, seq to, acc trunc, gc. Row 1: (58) ! 1.4e-44 134.2 0.0 cm 1 291 [] 117 383 + .. 0.87 no 0.59

srp3 1 cgGCUGUAAUGGCcguAaagcgGGAUUGcGcuc.uGuucaaacuCAag..GAcuccgcUCuauuGcGCGCUg.gUUCGcgacuccgcCgccccagacguc. 96
HF674592 117 UGGCUGUAACGGCCCAAGGUGGAAUGCGAGGc-GAUGUUUCCCAacGGAGUCCCGUGCUCGUGCGCCGaGUUCAAGAC-UGUCCCUCCAGAAAAcU 215

srp3 97 caGGuuc.cacgcccgcccccGCAagggguggggUcgggcguggaUAAuuggacgugGUcuggggguAGuGcGGCAACcGAGCAccccgcacguccagC 196
HF674592 216 UUGGUGUcCAUCGUCCUCACAGCGUAGGCUGUGGUC-GGAUUUGGAGUAAUCGGCCCUUGUC-UAGCCAGGGAAGCAAUCCGCAGCUAGCAGGACUCAC 314

srp3 197 CuggacgcucuUaggggAUacGgcgggc..gucgGuu.CguggagggGuCuucgggCaauaagaugUcacauCugugCcgagCgCAAACCuucuUUU 291
HF674592 315 CGAGUUGGUCUUAGGAGAUcAGGGCACGucAUCUGUCg--CGCGGGUGCGCCG-----UGUCCUCGUAGACC-----UUU 383

>> HF674638

Table with 11 columns: rank, E-value, score, bias, mdl, mdl from, mdl to, seq from, seq to, acc trunc, gc. Row 1: (59) ! 1.4e-44 134.2 0.0 cm 1 291 [] 117 383 + .. 0.87 no 0.59

*****5.444433333333246677777778888*****8889*****999.***** PP

srp3 1 cgGCUGUAAUGGCcguAaagcgGAAUGcGcuc.uGuucaaacuCAag..GAcuccgcUCuauGcGCGcUg.gUUCGcgacuccgcGgccccagacguc. 96
:GGCUGUAA GGCC: AA G+GGGA:U CG:: G U ::++ C ++ G C C U G+GCGC G GUUC+:GA :::CC:C:CCAGA ::C
HF674638 117 UGGCUGUAAACGGCCCAAGGUGGGAAUGCGAGGc-GAUGUUUCCCCAacGGAGUCCCUGCUCGUGCGCCGaGUUCAAGAC-UGUCCCUCCAGAAAACu 215
*****5.444433333333246677777778888*****8889*****999.***** PP

vv vv v v NC
(((((((.<<<<<<<<<<<<<<<<<_____>>>>>>>--->>>>>>><<<<<<<<<<_____>>>>>>>--->>>>>>>))) CS
srp3 97 caGGuuc.cacgccccgccccGCAagggguggggUcgggcguggaUAAuuggacgugGUcuggggguAGuCgGGCAACcGAGCAccccgcacguccagC 196
::GG::+ C: :C : C:C::CG A G::G:G :+ G: :G::UAA:: G C:U:GUC ::G:+AG+:::GCAA:::GCA:C::G:A:G C ::C
HF674638 216 UUGGUGUcCAUCGUCCUCACAGCGUAGGCGUGGUC-GGAUUUGGAGUAAUCGGCCUUGUC-UAGCCAGGGAAGCAAUCCGCGAGCUAGCAGGACUCAC 314
*****766666668*****9.68888888*****.***** PP

v v vv vv vv vvvv NC
))))))--)))--)))---))))---.))))---.)))))-----))--))-----)))))))))::: CS
srp3 197 CuggacgcucuUaggggAUacGgcgggc.gucgGuu.CguggaggggaGuCuucgggCaauaagaugUcacauCugugCcgagCgCAAACCuucuUUU 291
C::G::+UCUUAGG:GAU+:GG::+ UC:GU G G+ C:: UG C:::CG A:ACC UUU
HF674638 315 CGAGUUGGUCUUAGGAGAUAGGACGAGGCGCUCUCGUCG--CGCGGGUGCGCCG-----UGUCCUCGUAGACC---UUU 383
*****9998888888888885..44443333334433.....3337*****...** PP

>> FR852106

rank	E-value	score	bias	mdl	mdl	from	mdl	to	seq	from	seq	to	acc	trunc	gc
(60) !	1.4e-44	134.2	0.0	cm		1	291]		125		391 + ..	0.87	no	0.59

vvvv vv vvv vv v v NC
<<<<_____>>>>---(((((((-----(((((-----..--(((((((-----..-----(((((((-----(((((((----- CS
srp3 1 cgGCUGUAAUGGCcguAaagcgGAAUGcGcuc.uGuucaaacuCAag..GAcuccgcUCuauGcGCGcUg.gUUCGcgacuccgcGgccccagacguc. 96
:GGCUGUAA GGCC: AA G+GGGA:U CG:: G U ::++ C ++ G C C U G+GCGC G GUUC+:GA :::CC:C:CCAGA ::C
FR852106 125 UGGCUGUAAACGGCCCAAGGUGGGAAUGCGAGGc-GAUGUUUCCCCAacGGAGUCCCUGCUCGUGCGCCGaGUUCAAGAC-UGUCCCUCCAGAAAACu 223
*****5.4444333333333246677777778888*****8889*****999.***** PP

vv vv v v NC
(((((((.<<<<<<<<<<<<<<<<<_____>>>>>>>--->>>>>>><<<<<<<<<<_____>>>>>>>--->>>>>>>))) CS
srp3 97 caGGuuc.cacgccccgccccGCAagggguggggUcgggcguggaUAAuuggacgugGUcuggggguAGuCgGGCAACcGAGCAccccgcacguccagC 196
::GG::+ C: :C : C:C::CG A G::G:G :+ G: :G::UAA:: G C:U:GUC ::G:+AG+:::GCAA:::GCA:C::G:A:G C ::C
FR852106 224 UUGGUGUcCAUCGUCCUCACAGCGUAGGCGUGGUC-GGAUUUGGAGUAAUCGGCCUUGUC-UAGCCAGGGAAGCAAUCCGCGAGCUAGCAGGACUCAC 322
*****766666668*****9.68888888*****.***** PP

v v vv vv vv vvvv NC
))))))--)))--)))---))))---.))))---.)))))-----))--))-----)))))))))::: CS
srp3 197 CuggacgcucuUaggggAUacGgcgggc.gucgGuu.CguggaggggaGuCuucgggCaauaagaugUcacauCugugCcgagCgCAAACCuucuUUU 291
C::G::+UCUUAGG:GAU+:GG::+ UC:GU G G+ C:: UG C:::CG A:ACC UUU
FR852106 323 CGAGUUGGUCUUAGGAGAUAGGACGAGGCGCUCUCGUCG--CGCGGGUGCGCCG-----UGUCCUCGUAGACC---UUU 391
*****9998888888888885..44443333334433.....3337*****...** PP

>> UDB013255

rank	E-value	score	bias	mdl	mdl	from	mdl	to	seq	from	seq	to	acc	trunc	gc
(61) !	3.3e-44	133.2	0.0	cm		1	291]		125		391 + ..	0.88	no	0.60

srp3 1 cgGCUGUAAUGGCcguAaagcgGAAUGcGcuc.uGuuc..aaacuCAagGAcuccgcUCuauuGcGCGCUg.gUUCGegacuccgcCgccccagacguc 96
:GGCUGUAA GGCC: AA G+GGGA:U CG:: G U :: CUCAA G C C U G+GCGC G GUUC+:GA ::CC:C:CCAGA ::C
UDB013255 125 UGGCUGUAAACGGCCCCAAGGUGGGAAUGCGAGGc-GAUGuuUUCUCAACGGAGUCCCGUGCUCUGCGCCGaGUUCAAGAC-UGUCCCCUCCAGAAAAC 222
*****5.55440155666666777778888888888*****8889*****999.***** PP

srp3 97 .caGGuuc.cacgcccgcggccccGCAagggguggggUcgggcguggaUAAuuggacgugGUcugggggAGuGcGGCAACcGAGCAccccgcacgucca 194
:GG::+ C: :C :CC:C::CG A G::G:GG: G: :G::UAA:: G C:U GUC ::G:+AG+:::GCAA:::GCA:C::G A:G C :
UDB013255 223 uUUGGUGUcCAUCGUCUUAGGAGUAGCGGCGUAGGCCGUGGUU-GGAUUUGGAGUAAUCGGCCUCGUC-UAGCCAGGGAAGCAAUCCGCAGCUAGCAGGACUC 320
*****766666668*****9.78888888***** PP

srp3 195 gCCuggacgcucuUaggggAUacGgcgggc.gucgGuu.CguggagggAGuCuucgggCaauaagaugUcacauCugugCcgagCgCAAACCuucuUUU 291
:CC::G:: +UCUUAAGG:GAU+:GG::+ UC:GU G G+ C:: UG C::CG A:ACC UUU
UDB013255 321 ACCGAGUUGGUCUUAGGAGAUcGGGGCAGcAUCUGUCg--CGCGGGUGCGCG--UGUCCCCUGUAGACC---UUU 391
*****99988888888885..444333333333.....3347***** PP

>> EF218785

rank	E-value	score	bias	mdl	mdl from	mdl to	seq from	seq to	acc	trunc	gc
(62) !	3.9e-41	124.7	0.0	cm	1	291 []	5	275 + ..	0.91	no	0.58

srp3 1 cgGCUGUAAUGGCcguAaagcgGAAUGcGcuc.uGuuc..aaacuCAagGAcuccgcUCuauuGcGCGCUg.gUUCGegacuccgcCgccccagacguc.ca 98
:GGCUGUAA GGCC:+AA::CGGGAAU G::: U::: C CAA G C:C U G+GCGCUG UUC+:GA C::CC:C:C: GA ::C ::
EF218785 5 UGGCUGUAAACGGCCCCAAGGUGGGAAUGCGAGGGuGAUGUUUCCACAACGAAUCACGUCGUCGCGCUGaNUUCAAGAC-CGCCCCUCUGGAAAACuUU 104
*****655666788888888899999999*****9*****999.***** PP

srp3 99 GGuuc.cacgcccgcggccccGCAagggguggggUcgggcguggaUAAuuggacgugGUcugggggAGuGcGGCAACcGAGCAccccgcacguccagCC 197
GG::+ C: :C :CGC::CG AAG::GUG + G:: :G::UAA:: G C:U:G C ::G:+ G+:::G+AA:::GCA:C::G:A:G:C :C
EF218785 105 GGUGUcCAUCAUCCUCGCGCGUAAGCUGUGGCC-GGAUUUGGAGUAAUCGGCCUCGUC-UAGCCAGGGAAGCAAUCCGCAGCUAGCAGGACUC 203
*****866655556*****9.56666667*****.***96349***** PP

srp3 198 uggacgcucuUaggggAUacGgcgggc.gucgGuuCguggagggAGuCuucgggCaauaagaugUcacauCugugCcgagCgCAAACCuucuUUU 291
:G::+ UC UA:G:GAU+:GG::G++ UC:GU G:G G+ C::+:: C:::C AAACCUU:: U
EF218785 204 GAGUUGGUCUARGAGAUcAGGGCUGucAUCUGUC-GCGUGGUGCGCGUGU-----CCUCGUAACCUUUCGUG 275
*****9999999998.666665555555433.....6***** PP

>> KJ705211

rank	E-value	score	bias	mdl	mdl from	mdl to	seq from	seq to	acc trunc	gc
(63) !	5.6e-39	118.8	0.0	cm	1	291 []	25	294 + ..	0.90	no 0.56
srp3	1	cgGCUGUAAUGGCcguAaagcgGAAUGcGcuc.uGuucaaacuCAagGAcuccgcUCuauuGcGCGCUG.gUUCGcgacuccgcGgcccagacguc.ca								NC
KJ705211	25	UGGCUGGAAAAGCCCCNNUCNGGAAUGCNAGGuGAUGUUCCACAACGGAAUCACAUGCUCGUGCGCUGaGUUCAAGAC-CGUCCCCUCCGGAAAACuUU								CS
		*****88888*****655566777888888999*****9*****999*****								PP
srp3	99	GGuuc.cacgcccgcggcgcccGCAagggguggggUcggcguggaUAAuuggacgugGUcuggggguAGuGgGCAACcGAGCAccccgcacguccagCCu								NC
KJ705211	125	GGUGUcCAUCAUCCUCGCAGCGUAAGCUGUGGCC-GGAUUUGGAGUAAUCGGUCCUUGAC-UAGCCAGGGAAGCAAUCCACAGCUGGCAGGACUCACCG								CS
		*****866655556*****9.56666667*****.*****3336*****								PP
srp3	199	ggacgcucuUaggggAUacGgcggg..gucGGuu.CguggagggGuCuucgggCaauagaugUcacauCugugCcgagCgCAAACCuucuUUU								NC
KJ705211	224	AGUUAGUCUUAGGAGAUcAGGGCGUGucAUCUGUCgCGUGGGUGUGC--CG-----UGUCCUCGUAAACCUCGUGCA								CS
		*****99999999985555544322..22.....3336*****								PP

//

Internal CM pipeline statistics summary:

Query model(s):	1	(291 consensus positions)
Target sequences:	422981	(154151640 residues searched)
Target sequences re-searched for truncated hits:	422981	(462063624 residues re-searched)
Windows passing local HMM SSV filter:	58310	(0.01852); expected (0.35)
Windows passing local HMM Viterbi filter:	37298	(0.01123); expected (0.15)
Windows passing local HMM Viterbi bias filter:	34730	(0.01043); expected (0.15)
Windows passing local HMM Forward filter:	4105	(0.00137); expected (0.003)
Windows passing local HMM Forward bias filter:	3999	(0.001334); expected (0.003)
Windows passing glocal HMM Forward filter:	755	(0.0003149); expected (0.003)
Windows passing glocal HMM Forward bias filter:	741	(0.0003106); expected (0.003)
Envelopes passing glocal HMM envelope defn filter:	728	(0.0002483); expected (0.003)
Envelopes passing local CM CYK filter:	276	(0.0001382); expected (0.0001)
Total CM hits reported:	82	(3.161e-05); includes 19 truncated hit(s)

CPU time: 225.16u 5.66s 00:03:50.82 Elapsed: 00:00:18.98

//

[ok]

Supplementary Item 1B: Detail of the primers used to re-amplify the specimens.

Forward primers (aligned):

```
ITS1-F  CTT GGT CAT TTA GAG GAA GTA A           [ = 1735-1756 (18S) (Tedersoo et al. 2015)]
ITS5      G GAA GTA AAA GTC GTA ACA AGG        [ = 1749-1770 (18S) (Tedersoo et al. 2015)]
ITS0F A  CTT GGT CAT TTA GAG GAA GT           [ = 1734-1754 (18S) (Tedersoo et al. 2008)]
```

Reverse primers (not aligned):

```
LB-w  CTTTTTCATCTTTCCTCACGG                   [ = AB973750_Russula_sp pos 1775-1795 in alignment (Tedersoo et al. 2008)]
ITS4b CAGGAGACTTGTTACACGGTCCAG                [ = AB973750_Russula_sp pos 1588-1610 in alignment (Gardes & Bruns 1993)]
```

ITS4b is thus located 187 bases upstream of LB-W.

References

Gardes M, Bruns TD (1993) ITS primers with enhanced specificity for basidiomycetes - application to the identification of mycorrhizas and rusts. *Molecular Ecology* 2: 113-118.

Tedersoo L, Jairus T, Horton BM, Abarenkov K, Suvi T, Saar I, Kõljalg U (2008) Strong host preference of ectomycorrhizal fungi in a Tasmanian wet sclerophyll forest as revealed by DNA barcoding and taxon-specific primers. *New Phytologist* 180: 479-490.

Tedersoo L, Anslan S, Bahram M et al. (2015) Shotgun metagenomes and multiple primer pair-barcode combinations of amplicons reveal biases in metabarcoding analyses of fungi. *MycKeys* 10: 1-43.