

ITS-2 rRNA secondary structure model of
Elliptochloris bilobata
strain SAG 245.80 (OG-1) HG972969

Barcode OG-1

5.8S/LSU stem

---00000-000-0111-11
---12345-678-9012-34
---23442-184-2453-26

BC

GCC C G G C
UGCCU A C UCGG UU->
||||| | | | | • | •
ACGGA U G AGUC AG<-
AGA C A - C

->CACCCC

Helix I

11111
56789
64414

BC

- C U - U
UCCAC UCCCU UGC UG GUCU C
• |||| • |||| • || | || | |
GGGUG GGGGA GCG AC CAGA U
C A U A C

AUC

Helix II

2222222223
01234567890
63363374641

BC

U C
UGGUGG CUCAGCUUUC U
• || • || | • |||| • || |
GCCGCC GGGUCGGAAG C
U G

AAGCACAGA

Helix III

333333---333444444444-----45555-5555--5566-666666667777
123456---789012345678-----90123-4567--8901-234567890123
334884---134383384448-----33341-4136--3361-343188888888

BC

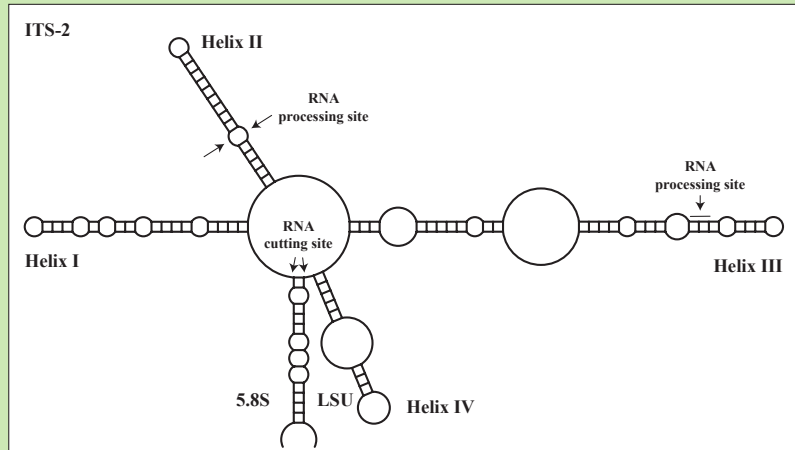
CG-- - A AUCACUCGAU A CU G U
GGC--C AGCG-GG CCC GGGCA CAGU GGUA GCGA U
||| | |||| || ||| |||| | • || • |||| |
CCG--G UCGC-CC GGG CCCGU GUCG CCGU CGCU C
CACG - A C----- G -- A G

CGCA

Helix IV

----- UCC
GGAAGU UGGC A
| • |||| |||| |
CUUUCA ACCG U
AACUAA CUG

->



Barcode legend:

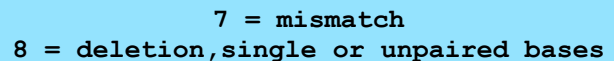
- 1 = A-U
- 2 = U-A
- 3 = G-C
- 4 = C-G
- 5 = G•U
- 6 = U•G
- 7 = mismatch
- 8 = deletion, single or unpaired bases

Barcode OG-2

BC

BC

CAACACUCAACAUC->



ITS-2 rRNA secondary structure model of
Coccoomyxa subellipsoidea
strain NIES 2166 (BC-1a) AGSI00000000

Barcode 1a
ITS2-A1

5.8S/LSU stem

---00000-000-0111-11
---12345-678-9012-34
---23442-154-2453-26

BC

GUC C G C
UGCCU AGC UCGG UU->
|||| |•| ||•| |•
ACGGA UUG AGUC AG<-
AGA C - C

->UACCC

Helix I

1111-1
5678-9
6414-4

BC

C A
UCAC CCCCC A
•||| ||||| |
GGUG GGGGG U
C C

ACC

Helix II

2222222223
01234567890
65347774443

BC

AGU G
UGGC CCCGGUCG C
••|| ||||| |
GUCC GGGCCAGC A
CCU A

AAGACCAGA

Helix III

333-333-333444444-444---455--555555--5566-666666667777
123-456-789012345-678---901--234567--8901-234567890123
334-284-134181388-448---333--114132--3361-363884488884

BC

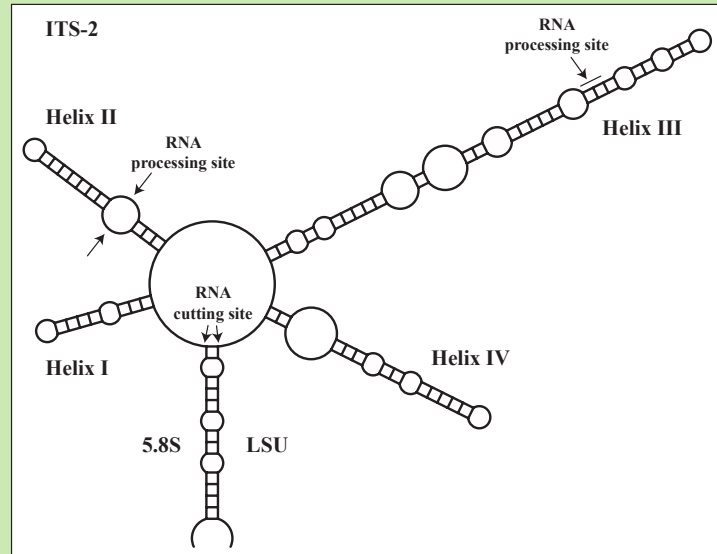
- G GAC ACAU AA CU G A G
GGC U-C AGCA-AG CC GGG AACAGU GGUA GUG -CC---C C
||| | | ||| || || ||| ||||| ||•| |• || |
CCG A-G UCGU-UC GG CCC UUGUCA CCGU CGC -GG---G G
A G AGA ---- GC -- A - A

GGC

Helix IV

AA--- - U U
AGG UCGC CGG CGCCCU A
||| |||| ||| |||||• |
UCC AGCG GCC GCGGGG G
CACAC U C C

UUUC->



Barcode legend:

- 1 = A-U
- 2 = U-A
- 3 = G-C
- 4 = C-G
- 5 = G•U
- 6 = U•G
- 7 = mismatch
- 8 = deletion, single or unpaired bases

ITS-2 rRNA secondary structure model of
Coccoomyxa subellipsoidea
strain NIES 2353 (BC-1a) HG972971

Barcode 1a
ITS2-A1

5.8S/LSU stem

---00000-000-0111-11
---12345-678-9012-34
---23442-154-2453-26

BC

GUC C G C
UGCCU AGC UCGG UU->
|||| |•| ||•| |•
ACGGA UUG AGUC AG<-
AGA C - C

->UACCC

Helix I

1111-1
5678-9
6414-4

BC

C A
UCAC CCCCC A
•||| ||||| |
GGUG GGGGG U
C C

ACC

Helix II

2222222223
01234567890
65347774443

BC

AGU G
UGGC CCCGGUCG C
••|| ||||| |
GUUG GGGCCAGC A
CCU A

AAGACCAGA

Helix III

333-333-333444444-444---455--555555--5566-666666667777
123-456-789012345-678---901--234567--8901-234567890123
334-284-134181388-448---333--114132--3361-363884488884

BC

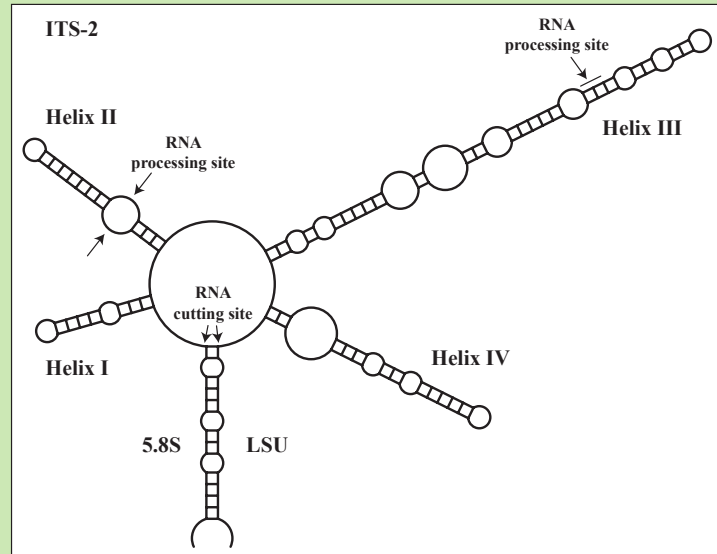
- G GAC ACAU AA CU G A G
GGC U-C AGCA-AG CC GGG AACAGU GGUA GUG -CC---C C
||| | | ||| || || ||| ||||| ||•| |•| || |
CCG A-G UCGU-UC GG CCC UUGUCA CCGU CGC -GG---G G
A G AGA ---- GC -- A - A

GGC

Helix IV

AA--- - U U
AGG UCGC CGG CGCCCU A
||| |||| | | ||||• |
UCC AGCG GCC GCGGGG G
CACAC U C C

UUUC->



Barcode legend:

- 1 = A-U
- 2 = U-A
- 3 = G-C
- 4 = C-G
- 5 = G•U
- 6 = U•G
- 7 = mismatch
- 8 = deletion, single or unpaired bases

ITS-2 rRNA secondary structure model of
Coccoomyxa subellipsoidea
strain CCAP 812/3 (BC-1a) HG972972

Barcode 1a
ITS2-A1

5.8S/LSU stem

---00000-000-0111-11
---12345-678-9012-34
---23442-154-2453-26

BC

GUC C G C
UGCCU AGC UCGG UU->
|||| |•| ||•| |•
ACGGA UUG AGUC AG<-
AGA C - C

->UACCC

Helix I

1111-1
5678-9
6414-4

BC

C A
UCAC CCCCC A
•||| ||||| |
GGUG GGGGG U
C C

ACC

Helix II

2222222223
01234567890
65347774443

BC

AGU G
UGGC CCCGGUCG C
••|| ||||| |
GUCC GGGCCAGC A
CCU A

AAGACCAGA

Helix III

333-333-333444444-444---455--555555--5566-666666667777
123-456-789012345-678---901--234567--8901-234567890123
334-284-134181388-448---333--114132--3361-363884488884

BC

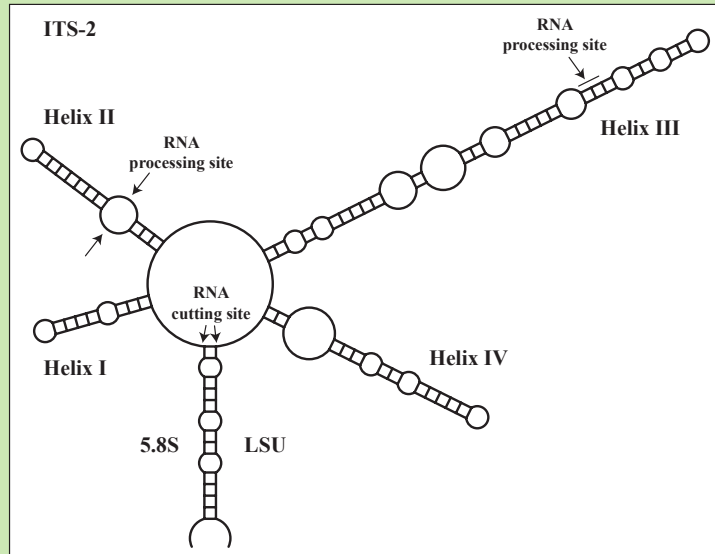
- G GAC ACAU AA CU G A G
GGC U-C AGCA-AG CC GGG AACAGU GGUA GUG -CC---C C
||| | | ||| | | || | ||||| ||•| |•| | | | |
CCG A-G UCGU-UC GG CCC UUGUCA CCGU CGC -GG---G G
A G AGA ---- GC -- A - A

GGC

Helix IV

AA--- - U U
AGG UCGC CGG CGCCCU A
||| |||| | | ||||| • |
UCC AGCG GCC GCGGGG G
CACAC U C C

UUUC->



Barcode legend:

- 1 = A-U
- 2 = U-A
- 3 = G-C
- 4 = C-G
- 5 = G•U
- 6 = U•G
- 7 = mismatch
- 8 = deletion, single or unpaired bases

ITS-2 rRNA secondary structure model of
Coccomyxa subellipsoidea
strain NIES 2252 (BC-1a) HG972973

Barcode 1a
ITS2-A2

5.8S/LSU stem

---00000-000-0111-11
---12345-678-9012-34
---23442-154-2453-26

BC

GUC C G C
UGCCU AGC UCGG UU->
|||| |•| ||•| |•
ACGGA UUG AGUC AG<-
AGA C - C

->UACCC

Helix I

1111-1
5678-9
6414-4

BC

C A
UCAC CCCCC A
•||| ||||| |
GGUG GGGGG U
C C

ACC

Helix II

2222222223
01234567890

65347774443

BC

AGU G
UGGC CCCGGUCG C
••|| ||||| |
GU CG GGGCCAGC A
CCU A

AAGACCAGA

Helix III

333-333-333444444-444---455--555555--5566-666666667777
123-456-789012345-678---901--234567--8901-234567890123

334-284-134181388-448---333--114132--3361-363884488884

BC

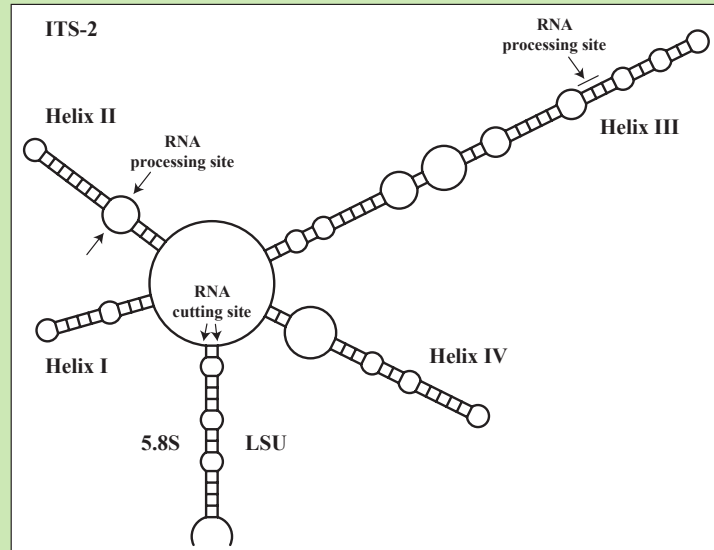
- G GAC ACAU AA CU G A G
GGC U-C AGCA-AG CC GGG AACAGU GGUA GUG -CC---C C
||| | | |||| | || ||| ||||| ||•| |• || |
CCG A-G UCGU-UC GG CCC UUGUCA CCGU CGC -GG---G G
A G AGA ---- GC -- A - A

GGC

Helix IV

AA--- - U U
AGG UCGU CGG CGCCCU A
||| |||• ||| |||||• |
UCC AGCG GCC GCGGGG G
CACAC U C C

UUUC->



Barcode legend:

- 1 = A-U
- 2 = U-A
- 3 = G-C
- 4 = C-G
- 5 = G•U
- 6 = U•G
- 7 = mismatch
- 8 = deletion, single or unpaired bases

ITS-2 rRNA secondary structure model of
Coccoomyxa subellipsoidea
strain CAUP H5105 (BC-1b) HG972974

Barcode 1b
ITS2-A3

5.8S/LSU stem

---00000-000-0111--11
---12345-678-9012--34
---23442-154-2453--26

BC

GUC C G CC
UGCCU AGC UCGG UU->
|||| |•| ||•| |•
ACGGA UUG AGUC AG<-
AGA C - C-

->ACCC

Helix I

1111-1
5678-9
6414-4

BC

C A
UCAC CCCCC A
•||| ||||| |
GGUG GGGGG U
C C

ACC

Helix II

2222222223
01234567890

65347774443

BC

AGU G
UGGC CCCGGUCG C
••|| ||||| |
GU CG GGGCCAGC A
CCU A

AAGACCAGA

Helix III

333-333-333444444--444---455--555555--5566-666666667777
123-456-789012345--678---901--234567--8901-234567890123

334-284-154181383--448---333--114136--3361-363884488884

BC

- G AC ACAU AA CU G A G
GGC U-C AGCA-AG-G CC GGG AACAGU GGUA GUG -CC----C A
||| | |•|| | | || ||| |||||• ||•| |•| || | |
CCG A-G UUGU-UC-C GG CCC UUGUCG CCGU CGC -GG----G A
A G AA ---- GC -- A - A

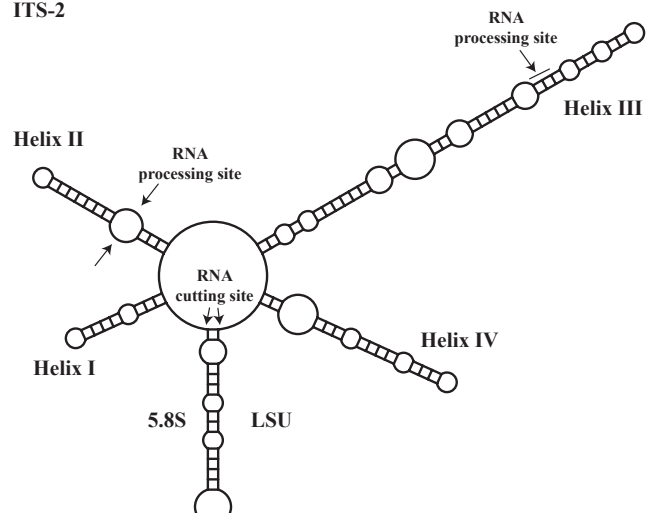
GGC

Helix IV

AA-- - G U
AGG UCGU CGGUC CCCU A
||| |||• |||• |||• |
UCC AGCG GCCGG GGGG G
CACA U A C

UUUC->

ITS-2



Barcode legend:

- 1 = A-U
- 2 = U-A
- 3 = G-C
- 4 = C-G
- 5 = G•U
- 6 = U•G
- 7 = mismatch
- 8 = deletion, single or unpaired bases

ITS-2 rRNA secondary structure model of
Coccomyxa subellipsoidea
strain Wien C20 (BC-1c) HG972975

Barcode 1c
ITS2-A4

5.8S/LSU stem

---00000-000-0111-11
---12345-678-9012-34
---23442-154-2453-26

BC

GUC C G C
UGCCU AGC UCGG UU->
|||| |•| ||•| |•
ACGGA UUG AGUC AG<-
AGA C - C

->UACCC

Helix I

1111-1
5678-9
6414-4

BC

- - A
UCAC CC CCC A
•||| || ||| |
GGUG GG GGG C
C A C

ACC

Helix II

2222222223
01234567890
65347774443

BC

AGU G
UGGC CCCGGUCG C
••|| ||||| |
GU CG GGGCCAGC A
CCU A

AAGACCAGA

Helix III

333-333-333444444--444---455--555555--5566-666666667777
123-456-789012345--678---901--234567--8901-234567890123
334-284-134181383--448---333--114136--3361-363884488884

BC

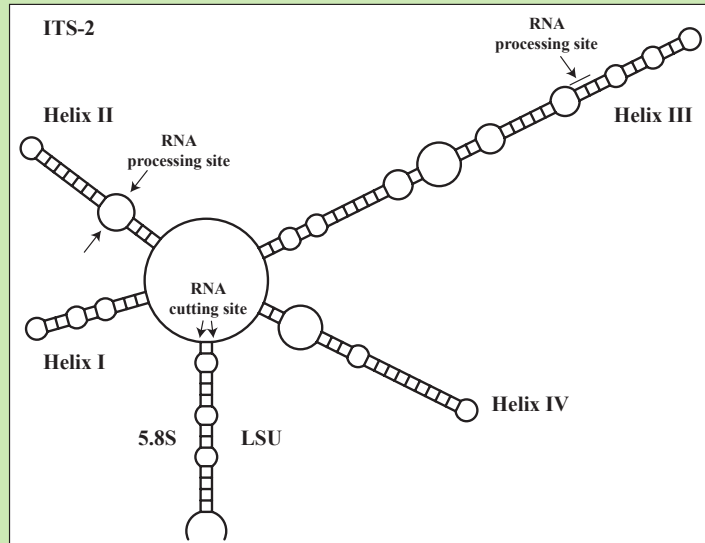
- G AC GCAU AA CU G A G
GGC U-C AGCA-AG-G CC GGG AACAGU GGUA GUG -CC---C A
||| | | ||| | | || ||| ||||• ||•| |•| || | |
CCG A-G UCGU-UC-C GG CCC UUGUCG CCGU CGC -GG---G A
A G GA ---- GC -- A - A

GGC

Helix IV

AA-- - U
AGG UCGU CGGUCGCCCU A
||| |||• |||•|||• |
UCC AGCG GCCGGCGGGG G
CACA U C

UUUC->



Barcode legend:

- 1 = A-U
- 2 = U-A
- 3 = G-C
- 4 = C-G
- 5 = G•U
- 6 = U•G
- 7 = mismatch
- 8 = deletion, single or unpaired bases

ITS-2 rRNA secondary structure model of
Coccoomyxa subellipsoidea
strain SAG 216-7 (BC-1c) HG972976

Barcode 1c
ITS2-A4

5.8S/LSU stem

---00000-000-0111-11
---12345-678-9012-34
---23442-154-2453-26

BC

GUC C G C
UGCCU AGC UCGG UU->
|||| |•| ||•| |•
ACGGA UUG AGUC AG<-
AGA C - C

->UACCC

Helix I

1111-1
5678-9
6414-4

BC

- - A
UCAC CC CCC A
•||| || ||| |
GGUG GG GGG C
C A C

ACC

Helix II

2222222223
01234567890

65347774443

BC

AGU G
UGGC CCCGGUCG C
••|| ||||| |
GU CG GGGCCAGC A
CCU A

AAGACCAGA

Helix III

333-333-333444444--444---455--555555--5566-666666667777
123-456-789012345--678---901--234567--8901-234567890123

334-284-134181383--448---333--114136--3361-363884488884

BC

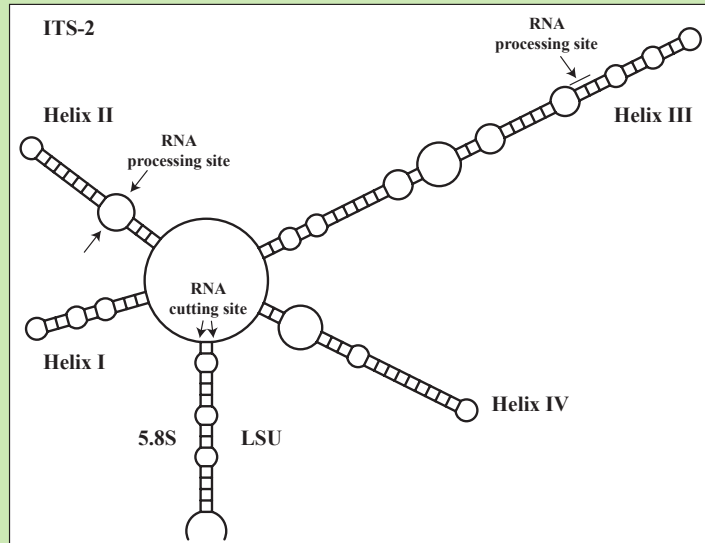
- G AC GCAU AA CU G A G
GGC U-C AGCA-AG-G CC GGG AACAGU GGUA GUG -CC---C A
||| | | ||| | | || ||| ||||• ||•| |•| || | |
CCG A-G UCGU-UC-C GG CCC UUGUCG CCGU CGC -GG---G A
A G GA ---- GC -- A - A

GGC

Helix IV

AA-- - U
AGG UCGU CGGUCGCCCU A
||| |||• |||•|||• |
UCC AGCG GCCGGCGGGG G
CACA U C

UUUC->



Barcode legend:

- 1 = A-U
- 2 = U-A
- 3 = G-C
- 4 = C-G
- 5 = G•U
- 6 = U•G
- 7 = mismatch
- 8 = deletion, single or unpaired bases

ITS-2 rRNA secondary structure model of
Coccomyxa subellipsoidea
strain SAG 216-13 (BC-1c) HG972978

Barcode 1c
ITS2-A4

5.8S/LSU stem

---00000-000-0111-11
---12345-678-9012-34
---23442-154-2453-26

BC

GUC C G C
UGCCU AGC UCGG UU->
|||| |•| ||•| |•
ACGGA UUG AGUC AG<-
AGA C - C

->UACCC

Helix I

1111-1
5678-9
6414-4

BC

- - A
UCAC CC CCC A
•||| || ||| |
GGUG GG GGG C
C A C

ACC

Helix II

2222222223
01234567890

65347774443

BC

AGU G
UGGC CCCGGUCG C
••|| ||||| |
GU CG GGGCCAGC A
CCU A

AAGACCAGA

Helix III

333-333-333444444--444---455--555555--5566-666666667777
123-456-789012345--678---901--234567--8901-234567890123

334-284-134181383--448---333--114136--3361-363884488884

BC

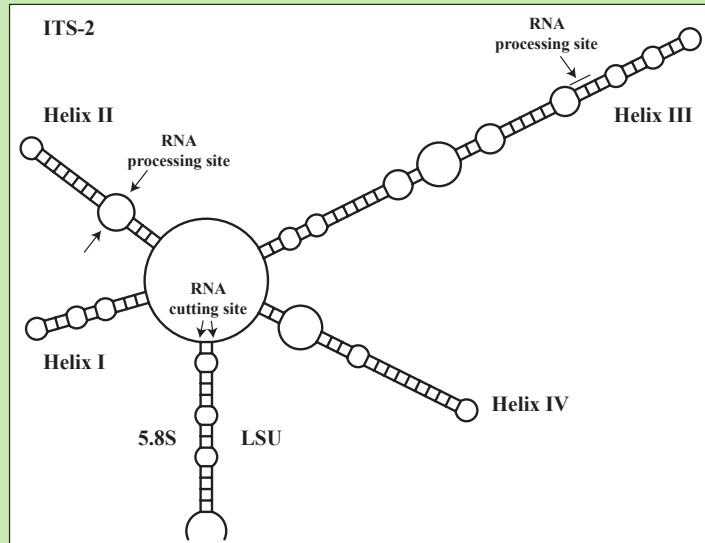
- G AC GCAU AA CU G A G
GGC U-C AGCA-AG-G CC GGG AACAGU GGUA GUG -CC----C A
||| | | ||| | | || | ||| | • || • | • | || | |
CCG A-G UCGU-UC-C GG CCC UUGUCG CCGU CGC -GG----G A
A G GA ---- GC -- A - A

GGC

Helix IV

AA-- - U
AGG UCGU CGGUCGCCCU A
||| ||| • ||| • |||| • |
UCC AGCG GCCGGCGGGG G
CACA U C

UUUC->



Barcode legend:

- 1 = A-U
- 2 = U-A
- 3 = G-C
- 4 = C-G
- 5 = G•U
- 6 = U•G
- 7 = mismatch
- 8 = deletion, single or unpaired bases

ITS-2 rRNA secondary structure model of
Coccomyxa subellipsoidea
strain SAG 69.80 (BC-1c) HG972977

Barcode 1c
ITS2-A5

5.8S/LSU stem

---00000-000-0111-11
---12345-678-9012-34
---23442-154-2453-26

BC

GUC C G C
UGCCU AGC UCGG UU->
|||| |•| ||•| |•
ACGGA UUG AGUC AG<-
AGA C - C

->UACCC

Helix I

1111-1
5678-9
6414-4

BC

- - A
UCAC CC CCC A
•||| || |||| |
GGUG GG GGG A
C A C

ACC

Helix II

2222222223
01234567890
65347774443

BC

AGU G
UGGC CCCGGUCG C
••|| ||||| |
GU CG GGGCCAGC A
CCU A

AAGACCAGA

Helix III

333-333-333444444--444---455--555555--5566-666666667777
123-456-789012345--678---901--234567--8901-234567890123
334-284-134181383--448---333--114136--3361-363884488884

BC

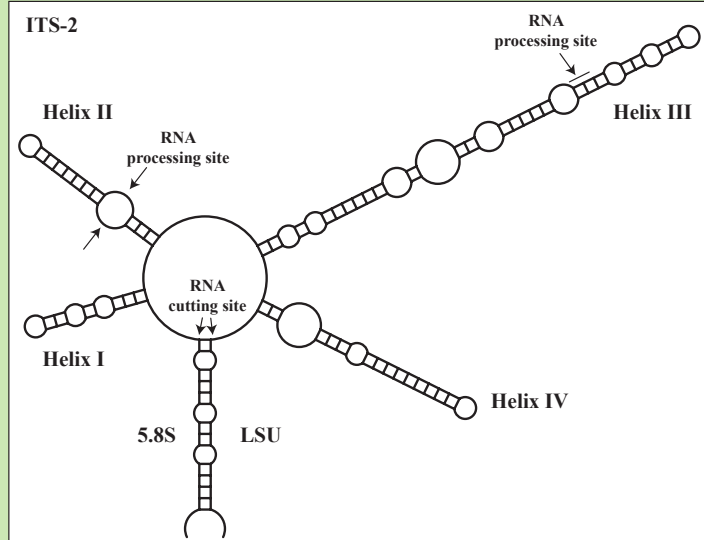
- G AC GCAU AA CU G A G
GGC U-C AGCA-AG-G CC GGG AACAGU GGUA GUG -CC---C A
||| | | |||| | | || ||| ||||• ||• |•| || | |
CCG A-G UCGU-UC-C GG CCC UUGUCG CCGU CGC -GG---G A
A G GA ---- GC -- A - A

GGC

Helix IV

AA-- - U
AGG UCGU CGGUCGCCCU A
||| |||• |||•|||• |
UCC AGCG GCCGGCGGGG G
CACA U C

UUUC->



Barcode legend:

- 1 = A-U
- 2 = U-A
- 3 = G-C
- 4 = C-G
- 5 = G•U
- 6 = U•G
- 7 = mismatch
- 8 = deletion, single or unpaired bases

ITS-2 rRNA secondary structure model of
Coccomyxa polymorpha
strain CAUP H5101 (BC-2) HG972979

Barcode 2
ITS2-B

5.8S/LSU stem

---00000-000-0111-11
---12345-678-9012-34
---23442-154-2453-26

BC

GUC C G C
UGCCU AGC UCGG UU->
|||| |•| ||•| |•
ACGGA UUG AGUC AG<-
GGA C - C

->CACCCC

Helix I

11111
56789
64344

BC

C UU
UCGCCU CUUUCU U
•||||| |||||• |
GGCGGA GAAAGG G
C CU

ACG

Helix II

2222222223
01234567890
65343374643

BC

U UG
UGGCGG CUCGGUCG C
••|||| |•||||| |
GUCGCC GGGCCAGC A
U UC

AAGACCAGA

Helix III

33-3333-33344444--4444---4555--55555--5566-666666667777
12-3456-78901234--5678---9012--34567--8901-234567890123
33-4284-13418138--4448---3338--14136--3361-363182488884

BC

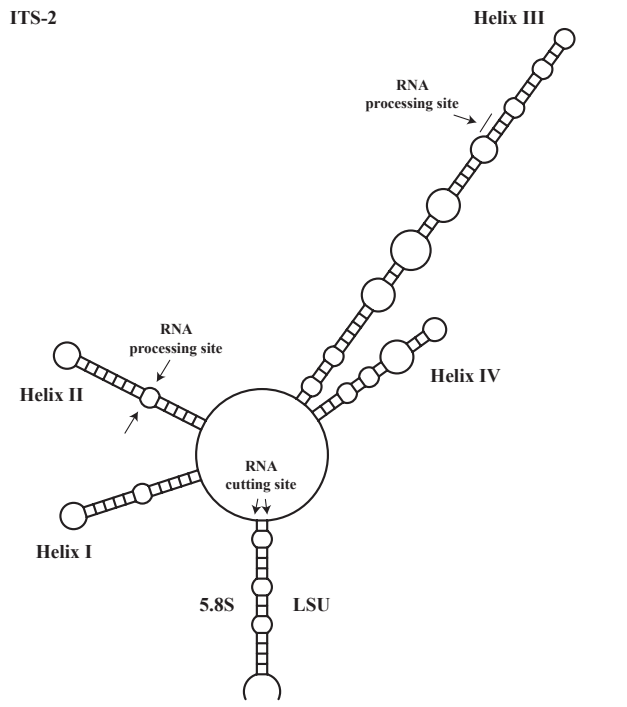
- G GC- AAUC ACA CU G C U
GG CU-C AGCA-AG CCC GGG ACAGU GGUA GUGA UC----C U
|| || | |||| || ||| ||| |•| |•| |•| | | | |
CC GA-G UCGU-UC GGG CCC UGUCG CCGU CGCU AG----G C
G G GCA ---- GGC -- A - G

-

Helix IV

G G C-- AU
GGAA GC CG CCG \
|•|| || || ||| U
CUUU CG GC GGC /
G A CAA CA

UCACCACAUUUC->



Barcode legend:

- 1 = A-U
- 2 = U-A
- 3 = G-C
- 4 = C-G
- 5 = G•U
- 6 = U•G
- 7 = mismatch
- 8 = deletion, single or unpaired bases

ITS-2 rRNA secondary structure model of
Coccomyxa simplex
strain SAG 216-3b (BC-3a) HG972980

Barcode 3a
ITS2-C1

5.8S/LSU stem

---00000-000-0111-11
---12345-678-9012-34
---23442-154-2453-26

BC

GUC C G C
UGCCU AGC UCGG UU->
|||| |•| ||•| |•
ACGGA UUG AGUC AG<-
AGA C - C

->CACCC

Helix I

1111-1
5678-9
6414-4

BC

C C
UCAC CCUCUC A
•||| ||||| |
GGUG GGAGAG U
C C

ACC

Helix II

2222222223
01234567890
63347774443

BC

CGU AA
UGGC CCCGGUU \
•||| ||||| |
GCCG GGGCCAA U
UCU CG

AAGAACAGA

Helix III

333333-333444444444----445-55555555--5566-666666667777
123456-78901234567----890-1234567--8901-234567890123
334288-11431338444----333-4314136--3361-363184488884

BC

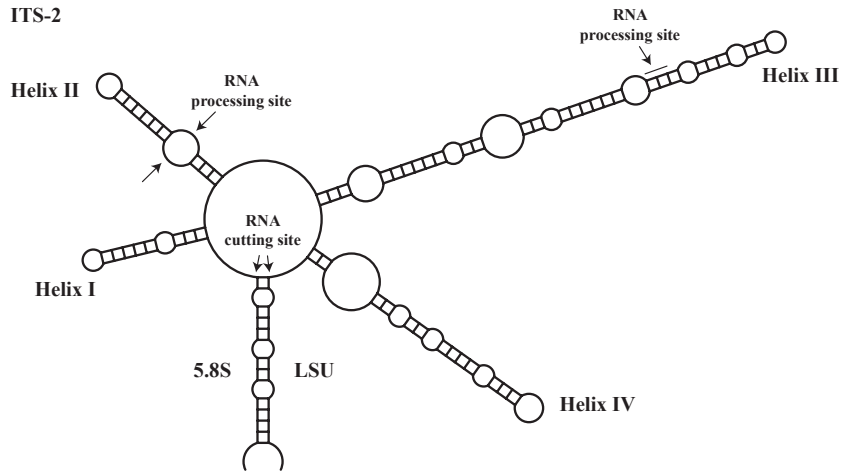
CG- A AUUC A CU G - G
GGCU AACGAGG CCC GGG CGACAGU GGUA GUGA CC----C U
|||| ||||| ||| ||| |||||• ||•| |•|| || |
CCGA UUGCUCG GGG CCC GCUGUCG CCGU CGCU GG----G C
AUG A ---- G -- A A A

GGC

Helix IV

AA---- - U U GU
AGG UCG GCG UCGCU CUUU A
||| ||| ||| •||| ||•| |
UCC AGC CGC GGCGA GAGA A
CCACAG G C U AA

UUC->



Barcode legend:

- 1 = A-U
- 2 = U-A
- 3 = G-C
- 4 = C-G
- 5 = G•U
- 6 = U•G
- 7 = mismatch
- 8 = deletion, single or unpaired bases

ITS-2 rRNA secondary structure model of
Coccomyxa simplex
strain CAUP H5107 (BC-3a) HG972981

Barcode 3a
ITS2-C1

5.8S/LSU stem

---00000-000-0111-11
---12345-678-9012-34
---23442-154-2453-26

BC

GUC C G C
UGCCU AGC UCGG UU->
|||| |•| ||•| |•
ACGGA UUG AGUC AG<-
AGA C - C

->CACCC

Helix I

1111-1
5678-9
6414-4

BC

C C
UCAC CCUCUC A
•||| ||||| |
GGUG GGAGAG U
C C

ACC

Helix II

2222222223
01234567890
63347774443

BC

CGU AA
UGGC CCCGGUU \
•||| ||||| |
GCCG GGGCCAA U
UCU CG

AAGAACAGA

Helix III

333333-333444444444----445-55555555--5566-666666667777
123456-78901234567----890-1234567--8901-234567890123
334288-11431338444----333-4314136--3361-363184488884

BC

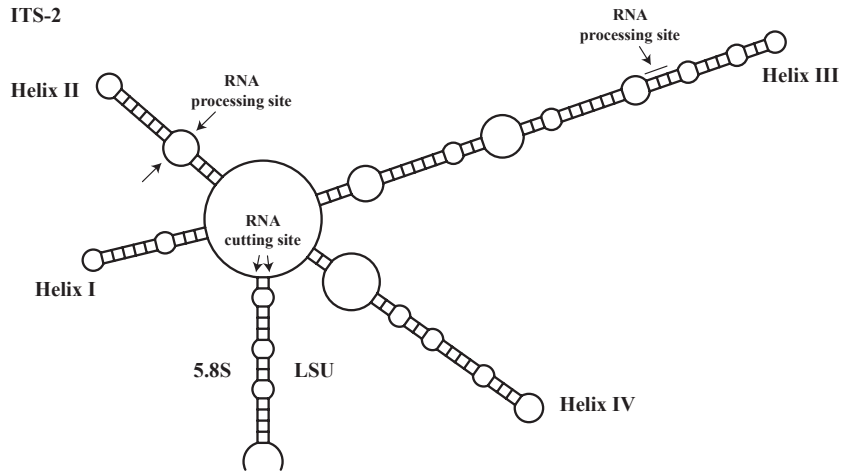
CG- A AUUC A CU G - G
GGCU AACGAGG CCC GGG CGACAGU GGUA GUGA CC----C U
|||| ||||| ||| ||| |||||• ||•| |•|| || |
CCGA UUGCUCG GGG CCC GCUGUCG CCGU CGCU GG----G C
AUG A ---- G -- A A A

GGC

Helix IV

AA---- - U U GU
AGG UCG GCG UCGCU CUUU A
||| ||| ||| •||| ||•| |
UCC AGC CGC GGC GA GAGA A
CCACAG G C U AA

UUC->



Barcode legend:

- 1 = A-U
- 2 = U-A
- 3 = G-C
- 4 = C-G
- 5 = G•U
- 6 = U•G
- 7 = mismatch
- 8 = deletion, single or unpaired bases

ITS-2 rRNA secondary structure model of
Coccomyxa simplex
strain SAG 216-2 (BC-3b) HG972989

Barcode 3b
ITS2-C2

5.8S/LSU stem

---00000-000-0111-11
---12345-678-9012-34
---23442-154-2453-26

BC

GUC C G C
UGCCU AGC UCGG UU->
|||| |•| ||•| |•
ACGGA UUG AGUC AG<-
AGA C - C

->UACCC

Helix I

1111-1
5678-9
6414-4

BC

C U
UCAC CCUCU U
•||| ||||| |
GGUG GGAGA C
C A

ACC

Helix II

2222222223
01234567890
63347774443

BC

CGU A
UGGC CCCGGUUG \
•||| ||||| |• C
GCCG GGGCCAAU /
UCU U

AAGAACAGA

Helix III

333333-33344444444---445-5555555--5566-666666667777
123456-78901234567---890-1234567--8901-234567890123
334288-11431338444---333-4314836--3361-363184488884

BC

CG- A AAUC A A CU G - G
GGCU AACGAGG CCC GGG CGAC GU GGUA GUGA CC---C C
|||| ||||| ||| ||| |||| |• ||•| |•|| || |
CCGA UUGCUC C GGG CCC GCUG CG CCGU CGCU GG---G C
AUG A ---- G C -- A A A

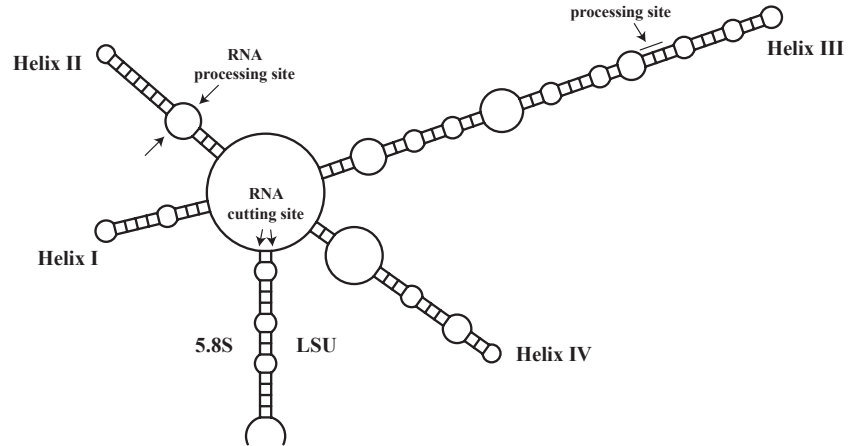
GGC

Helix IV

AA---- - CG U
AGG UCGU CGGC CUC \
||| |||• |||| ||| C
UCC AGCG GCCG GAG /
CCACAC U AA C

UUC->

ITS-2



Barcode legend:

- 1 = A-U
- 2 = U-A
- 3 = G-C
- 4 = C-G
- 5 = G•U
- 6 = U•G
- 7 = mismatch
- 8 = deletion, single or unpaired bases

ITS-2 rRNA secondary structure model of
Coccomyxa simplex
strain SAG 216-3c (BC-3b) HG972990

Barcode 3b
ITS2-C3

5.8S/LSU stem

---00000-000-0111-11
---12345-678-9012-34
---23442-154-2453-26

BC

GUC C G C
UGCCU AGC UCGG UU->
|||| |•| ||•| |•
ACGGA UUG AGUC AG<-
AGA C - C

->UACCC

Helix I

1111-1
5678-9
6414-4

BC

C U
UCAC CCUCU U
•||| ||||| |
GGUG GGAGA C
C A

ACC

Helix II

2222222223
01234567890
63347774443

BC

CGU A
UGGC CCCGGUUG \
•||| |||||• U
GCCG GGGCCAAU /
UCU U

AAAAACAGA

Helix III

333333-333444444444----445-55555555--5566-666666667777
123456-78901234567----890-1234567--8901-234567890123
334288-11431338444----333-4314836--3361-363184488884

BC

CG- A AAUC A A CU G - G
GGCU AACGAGG CCC GGG CGAC GU GGUA GUGA CC----C C
|||| ||||| ||| ||| ||| |• ||•| |•|| || |
CCGA UUGCUC C GGG CCC GCUG CG CCGU CGCU GG----G C
AUG A ---- G C -- A A A

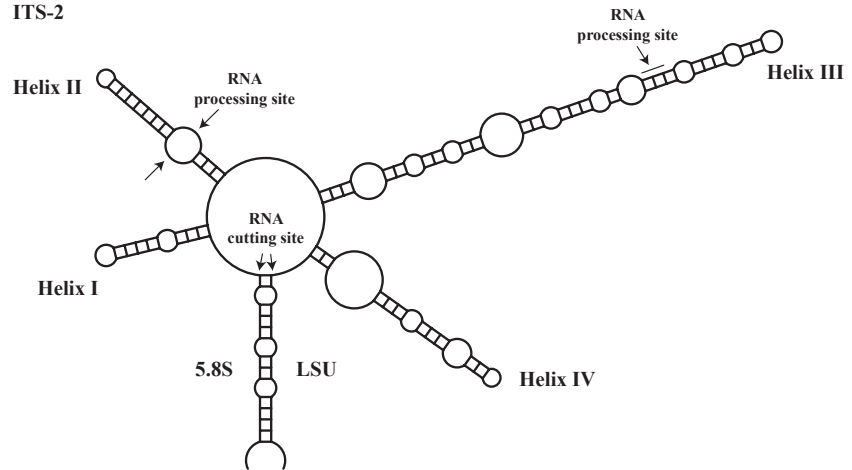
GGC

Helix IV

AA---- - CG U
AGG UCGU CGGC CUC \
||| |||• |||| ||| C
UCC AGCG GCCG GAG /
CCACAC U AA C

UUC->

ITS-2



Barcode legend:

- 1 = A-U
- 2 = U-A
- 3 = G-C
- 4 = C-G
- 5 = G•U
- 6 = U•G
- 7 = mismatch
- 8 = deletion, single or unpaired bases

ITS-2 rRNA secondary structure model of
Coccomyxa simplex
strain SAG 216-8 (BC-3b) HG972991

Barcode 3b
ITS2-C4

5.8S/LSU stem

---00000-000-0111-11
---12345-678-9012-34
---23442-154-2453-26

BC

GUC C G C
UGCCU AGC UCGG UU->
|||| |•| ||•| |•
ACGGA UUG AGUC AG<-
AGA C - C

->UACCC

Helix I

1111-1
5678-9
6414-4

BC

- C
UCAC CCUCU U
•||| ||||| |
GGUG GGAGA C
C A

ACC

Helix II

2222222223
01234567890
63347774443

BC

CGU A
UGGC CCCGGUUA \
•||| ||||| | U
GCCG GGGCCAAU /
UCU U

AAGAACAGA

Helix III

333333-333444444444----445-55555555--5566-666666667777
123456-78901234567----890-1234567--8901-234567890123
334288-11431338444----333-4314836--3361-363184488884

BC

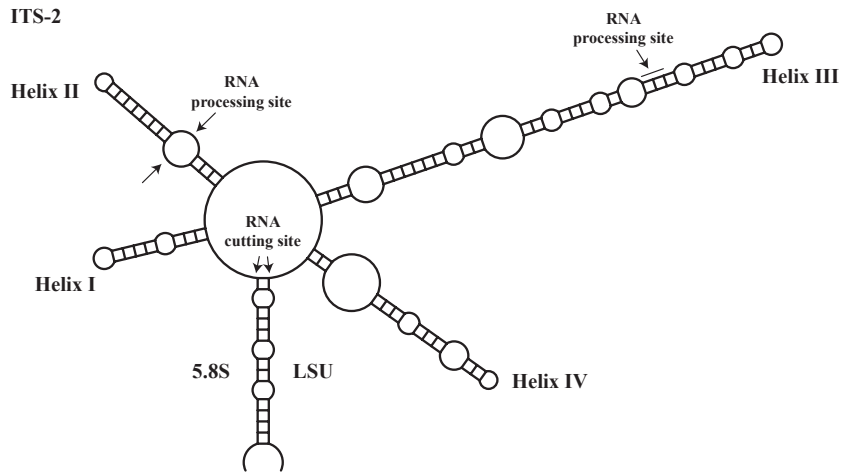
CG- A AAUC A A CU G - G
GGCU AACGAGG CCC GGG CGAC GU GGUA GUGA CC----C C
|||| ||||| ||| ||| ||| |• ||•| |•|| || | |
CCGA UUGCUC C GGG CCC GCUG CG CCGU CGCU GG----G C
AUG A ---- G C -- A A A

GGC

Helix IV

AA---- - CG U
AGG UCGU CGGC CUC \
||| |||• |||| ||| C
UCC AGCG GCCG GAG /
CCACAC U AA C

UUC->



Barcode legend:

- 1 = A-U
- 2 = U-A
- 3 = G-C
- 4 = C-G
- 5 = G•U
- 6 = U•G
- 7 = mismatch
- 8 = deletion, single or unpaired bases

ITS-2 rRNA secondary structure model of
Coccomyxa simplex
strain SAG 216-9a (BC-3b) FN298926

Barcode 3b
ITS2-C4

5.8S/LSU stem

---00000-000-0111-11
---12345-678-9012-34
---23442-154-2453-26

BC

GUC C G C
UGCCU AGC UCGG UU->
|||| |•| ||•| |•
ACGGA UUG AGUC AG<-
AGA C - C

->UACCC

Helix I

1111-1
5678-9
6414-4

BC

- C
UCAC CCUCU U
•||| ||||| |
GGUG GGAGA C
C A

ACC

Helix II

2222222223
01234567890
63347774443

BC

CGU A
UGGC CCCGGUUA \
•||| ||||| | U
GCCG GGGCCAAU /
UCU U

AAGAACAGA

Helix III

333333-333444444444----445-55555555--5566-666666667777
123456-78901234567----890-1234567--8901-234567890123
334288-11431338444----333-4314836--3361-363184488884

BC

CG- A AAUC A A CU G - G
GGCU AACGAGG CCC GGG CGAC GU GGUA GUGA CC----C C
|||| ||||| ||| ||| |||| |• ||•| |•|| || | |
CCGA UUGCUC C GGG CCC GCUG CG CCGU CGCU GG----G C
AUG A ---- G C -- A A A

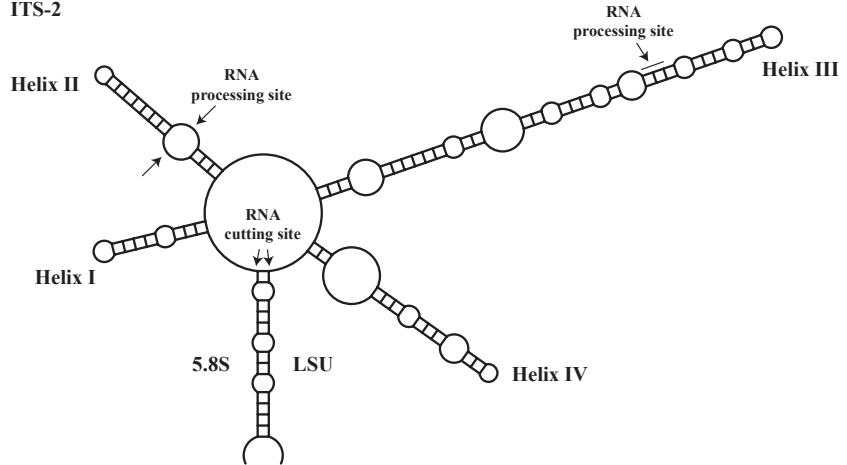
GGC

Helix IV

AA---- - CG U
AGG UCGU CGGC CUC \
||| |||• |||| ||| C
UCC AGCG GCCG GAG /
CCACAC U AA C

UUC->

ITS-2



Barcode legend:

- 1 = A-U
- 2 = U-A
- 3 = G-C
- 4 = C-G
- 5 = G•U
- 6 = U•G
- 7 = mismatch
- 8 = deletion, single or unpaired bases

ITS-2 rRNA secondary structure model of
Coccomyxa simplex
strain SAG 216-5 (BC-3c) HG972982

Barcode 1b
ITS2-C5

5.8S/LSU stem

---00000-000-0111-11
---12345-678-9012-34
---23442-154-2453-26

BC

GUC C G C
UGCCU AGC UCGG UU->
|||| |•| ||•| |•
ACGGA UUG AGUC AG<-
AGA C - C

->CACCC

Helix I

1111-1
5678-9
6414-4

BC

C C
UCAC CCUCUC A
•||| ||||| |
GGUG GGAGAG C
C C

ACC

Helix II

2222222223
01234567890
63347774443

BC

CGU AA
UGGC CCCGGUU \
•||| ||||| | U
GCCG GGGCCAA /
UCU CG

AAGAACAGA

Helix III

333333-333444444444---4555---55555--5566-666666667777
123456-789012345678---9012---34567--8901-234567890123
334288-114313384448---3383---14136--3361-363184488884

BC

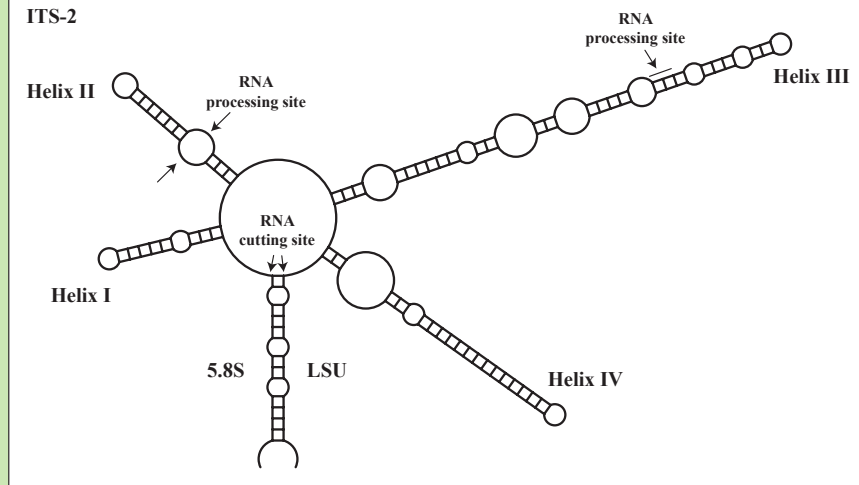
CG- A AAUC ACA CU G - G
GGCU AACGAGG CCC GG-G ACAGU GGUA GUGA CC----C U
|||| ||||| ||| || | |||• ||•| |•|| || | |
CCGA UUGCUC CCG CC-C UGUCG CCGU CGCU GG----G C
AUG A ---- GGC -- A A A

GGC

Helix IV

AA---- - U
AGG UCG GCGGUCGCUUUUUUU A
|•| ||| ||||•|||••||| |
UUC AGC CGCCGGCGAGGAAAA G
CCACAC A A

UUC->



Barcode legend:

- 1 = A-U
- 2 = U-A
- 3 = G-C
- 4 = C-G
- 5 = G•U
- 6 = U•G
- 7 = mismatch
- 8 = deletion, single or unpaired bases

ITS-2 rRNA secondary structure model of
Coccomyxa simplex
strain SAG 216-10 (BC-3c) HG972986

Barcode 3c
ITS2-C5

5.8S/LSU stem

---00000-000-0111-11
---12345-678-9012-34
---23442-154-2453-26

BC

GUC C G C
UGCCU AGC UCGG UU->
||||| |•| ||•| |•
ACGGA UUG AGUC AG<-
AGA C - C

->CACCC

Helix I

1111-1
5678-9
6414-4

BC

C C
UCAC CCUCUC A
•||| ||||| |
GGUG GGAGAG C
C C

ACC

Helix II

2222222223
01234567890
63347774443

BC

CGU AA
UGGC CCCGGUU \
•||| ||||| | U
GCCG GGGCCAA /
UCU CG

AAGAACAGA

Helix III

333333-333444444444---4555---55555--5566-666666667777
123456-789012345678---9012---34567--8901-234567890123
334288-114313384448---3383---14136--3361-363184488884

BC

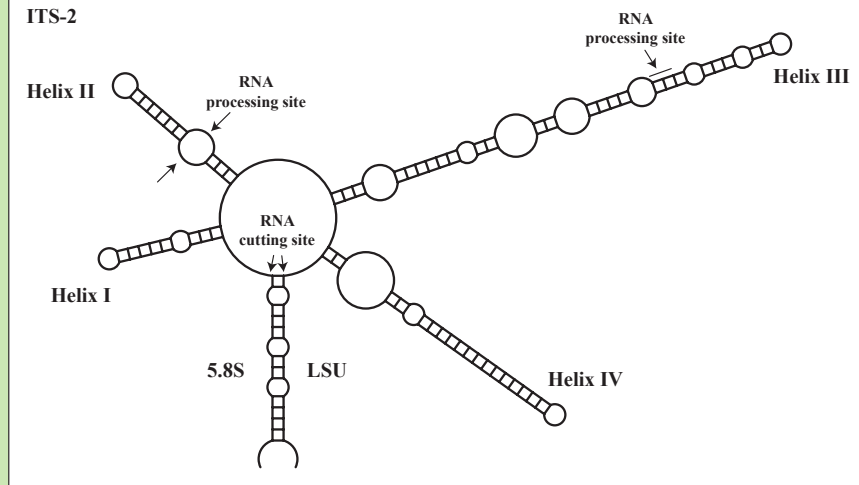
CG- A AAUC ACA CU G - G
GGCU AACGAGG CCC GG-G ACAGU GGUA GUGA CC----C U
||||| ||||| ||| || | ||||• ||•| |•|| || | |
CCGA UUGCUC C GGG CC-C UGUCG CCGU CGCU GG----G C
AUG A --- GGC -- A A A

GGC

Helix IV

AA---- - U
AGG UCG GCGGUCGCUUUUUU A
|•| ||| |||||•|||••||| |
UUC AGC CGCCGCGAGGAAAA G
CCACAC A A

UUC->



Barcode legend:

- 1 = A-U
- 2 = U-A
- 3 = G-C
- 4 = C-G
- 5 = G•U
- 6 = U•G
- 7 = mismatch
- 8 = deletion, single or unpaired bases

ITS-2 rRNA secondary structure model of
Coccomyxa simplex
strain SAG 216-12 (BC-3c) HG972987

Barcode 3c
ITS2-C5

5.8S/LSU stem

---00000-000-0111-11
---12345-678-9012-34
---23442-154-2453-26

BC

GUC C G C
UGCCU AGC UCGG UU->
|||| |•| ||•| |•
ACGGA UUG AGUC AG<-
AGA C - C

->CACCC

Helix I

1111-1
5678-9
6414-4

BC

C C
UCAC CCUCUC A
•||| ||||| |
GGUG GGAGAG C
C C

ACC

Helix II

2222222223
01234567890
63347774443

BC

CGU AA
UGGC CCCGGUU \
•||| ||||| U
GCCG GGGCCAA /
UCU CG

AAGAACAGA

Helix III

333333-333444444444---4555---55555--5566-666666667777
123456-789012345678---9012---34567--8901-234567890123
334288-114313384448---3383---14136--3361-363184488884

BC

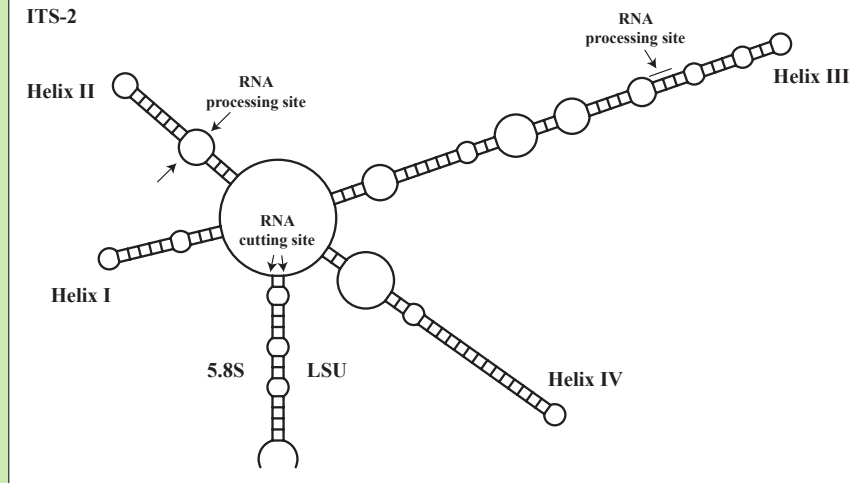
CG- A AAUC ACA CU G - G
GGCU AACGAGG CCC GG-G ACAGU GGUA GUGA CC----C U
|||| ||||| ||| || | |||• ||•| |•|| || | |
CCGA UUGCUC C G G CC-C UGUCG CCGU CGCU GG----G C
AUG A ---- GGC -- A A A

GGC

Helix IV

AA---- - U
AGG UCG GCGGUCGCUUUUUUU A
|•| ||| ||||•|||••||| |
UUC AGC CGCCGGCGAGGAAAA G
CCACAC A A

UUC->



Barcode legend:

- 1 = A-U
- 2 = U-A
- 3 = G-C
- 4 = C-G
- 5 = G•U
- 6 = U•G
- 7 = mismatch
- 8 = deletion, single or unpaired bases

ITS-2 rRNA secondary structure model of
Coccomyxa simplex
strain CCAP 216/15 (BC-3c) HG972985

Barcode 3c
ITS2-C5

5.8S/LSU stem

---00000-000-0111-11
---12345-678-9012-34
---23442-154-2453-26

BC

GUC C G C
UGCCU AGC UCGG UU->
|||| |•| ||•| |•
ACGGA UUG AGUC AG<-
AGA C - C

->CACCC

Helix I

1111-1
5678-9
6414-4

BC

C C
UCAC CCUCUC A
•||| ||||| |
GGUG GGAGAG C
C C

ACC

Helix II

2222222223
01234567890
63347774443

BC

CGU AA
UGGC CCCGGUU \
•||| ||||| U
GCCG GGGCCAA /
UCU CG

AAGAACAGA

Helix III

333333-333444444444---4555---55555--5566-666666667777
123456-789012345678---9012---34567--8901-234567890123
334288-114313384448---3383---14136--3361-363184488884

BC

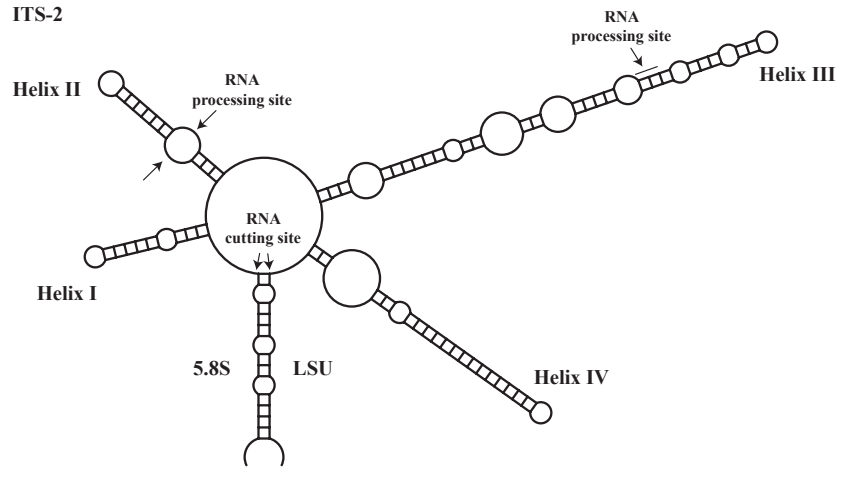
CG- A AAUC ACA CU G - G
GGCU AACGAGG CCC GG-G ACAGU GGUA GUGA CC----C U
|||| ||||| ||| || | |||• ||•| |•|| || | |
CCGA UUGCUC GGG CC-C UGUCG CCGU CGCU GG----G C
AUG A ---- GGC -- A A A

GGC

Helix IV

AA---- - U
AGG UCG GCGGUCGCUUUUUUU A
|•| ||| ||||•|||••||| |
UUC AGC CGCCGGCGAGGAAAA G
CCACAC A A

UUC->



Barcode legend:

- 1 = A-U
- 2 = U-A
- 3 = G-C
- 4 = C-G
- 5 = G•U
- 6 = U•G
- 7 = mismatch
- 8 = deletion, single or unpaired bases

ITS-2 rRNA secondary structure model of
Coccomyxa simplex
strain SAG 216-11a (BC-3c) HG972983

Barcode 3c
ITS2-C6

5.8S/LSU stem

---00000-000-0111-11
---12345-678-9012-34
---23442-154-2453-26

BC

GUC C G C
UGCCU AGC UCGG UU->
|||| |•| ||•| |•
ACGGA UUG AGUC AG<-
AGA C - C

->CACCC

Helix I

1111-1
5678-9
6414-4

BC

C C
UCAC CCUCUC A
•||| ||||| |
GGUG GGAGAG C
C C

ACC

Helix II

2222222223
01234567890
63347774443

BC

CGU AA
UGGC CCCGGUU \
•||| ||||| U
GCCG GGGCCAA /
UCU CG

AAGAACAGA

Helix III

333333-333444444444---4555---55555--5566-666666667777
123456-789012345678---9012---34567--8901-234567890123
334288-114313384448---3383---14136--3361-363184488884

BC

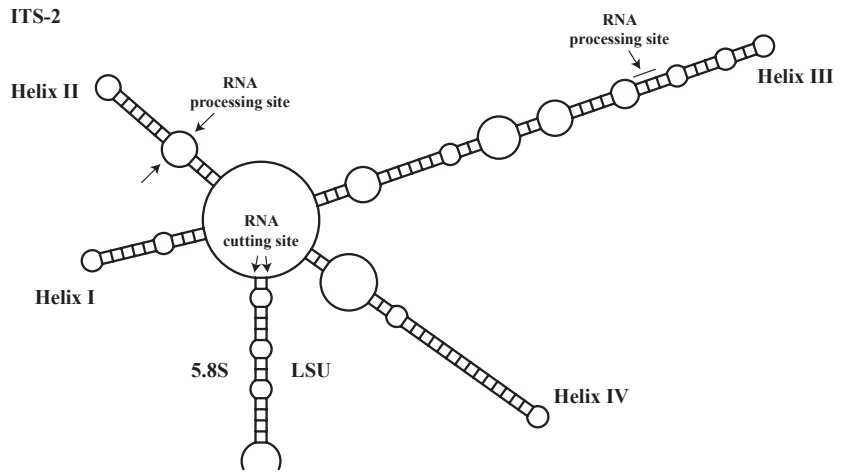
CG- A AAUC ACA CU G - G
GGCU AACGAGG CCC GG-G ACAGU GGUA GUGA CC----C U
|||| ||||| || || | |||• ||•| |•|| || | |
CCGA UUGCUC GGG CC-C UGUCG CCGU CGCU GG----G C
AUG A ---- GGC -- A A A

GGC

Helix IV

AA---- - U
AGG UCG GCGGUCGCUUUUUUU A
|•| ||| ||||•|||••||| |
UUC AGC CGCCGGCGAGGAAAA G
CCACAC A G

UUC->



Barcode legend:

- 1 = A-U
- 2 = U-A
- 3 = G-C
- 4 = C-G
- 5 = G•U
- 6 = U•G
- 7 = mismatch
- 8 = deletion, single or unpaired bases

ITS-2 rRNA secondary structure model of
Coccomyxa simplex
strain SAG 216-11b (BC-3c) HG972984

Barcode 3c
ITS2-C6

5.8S/LSU stem

---00000-000-0111-11
---12345-678-9012-34
---23442-154-2453-26

BC

GUC C G C
UGCCU AGC UCGG UU->
|||| |•| ||•| |•
ACGGA UUG AGUC AG<-
AGA C - C

->CACCC

Helix I

1111-1
5678-9
6414-4

BC

C C
UCAC CCUCUC A
•||| ||||| |
GGUG GGAGAG C
C C

ACC

Helix II

2222222223
01234567890
63347774443

BC

CGU AA
UGGC CCCGGUU \
•||| ||||| U
GCCG GGGCCAA /
UCU CG

AAGAACAGA

Helix III

333333-333444444444---4555---55555--5566-666666667777
123456-789012345678---9012---34567--8901-234567890123
334288-114313384448---3383---14136--3361-363184488884

BC

CG- A AAUC ACA CU G - G
GGCU AACGAGG CCC GG-G ACAGU GGUA GUGA CC----C U
|||| ||||| ||| || | ||||• ||•| |•|| || | |
CCGA UUGCUC CCGG CC-C UGUCG CCGU CGCU GG----G C
AUG A ---- GGC -- A A A

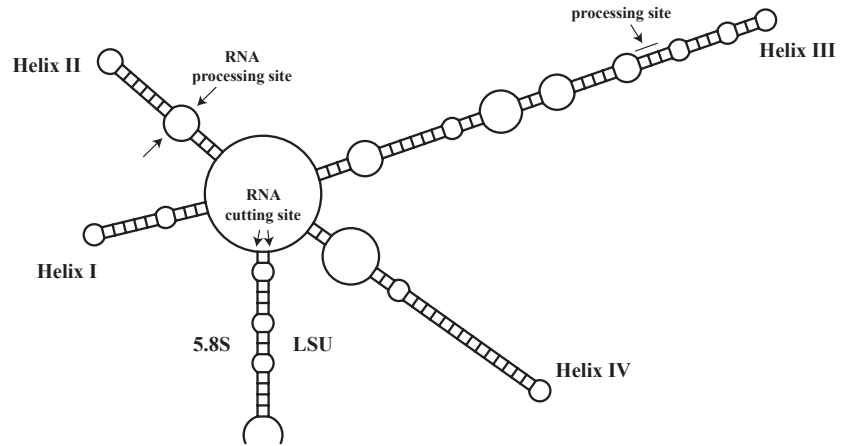
GGC

Helix IV

AA---- - U
AGG UCG GCGGUCGCUUUUUUU A
|•| ||| ||||•|||••||| |
UUC AGC CGCCGGCGAGGAAAA G
CCACAC A G

UUC->

ITS-2



Barcode legend:

- 1 = A-U
- 2 = U-A
- 3 = G-C
- 4 = C-G
- 5 = G•U
- 6 = U•G
- 7 = mismatch
- 8 = deletion, single or unpaired bases

ITS-2 rRNA secondary structure model of
Coccomyxa simplex
strain SAG 216-6 (BC-3c) HG972988

Barcode 3c
ITS2-C6

5.8S/LSU stem

---00000-000-0111-11
---12345-678-9012-34
---23442-154-2453-26

BC

GUC C G C
UGCCU AGC UCGG UU->
|||| |•| ||•| |•
ACGGA UUG AGUC AG<-
AGA C - C

->CACCC

Helix I

1111-1
5678-9
6414-4

BC

C C
UCAC CCUCUC A
•||| ||||| |
GGUG GGAGAG C
C C

ACC

Helix II

2222222223
01234567890
63347774443

BC

CGU AA
UGGC CCCGGUU \
•||| ||||| U
GCCG GGGCCAA /
UCU CG

AAGAACAGA

Helix III

333333-333444444444---4555---55555--5566-666666667777
123456-789012345678---9012---34567--8901-234567890123
334288-114313384448---3383---14136--3361-363184488884

BC

CG- A AAUC ACA CU G - G
GGCU AACGAGG CCC GG-G ACAGU GGUA GUGA CC----C U
|||| ||||| ||| || | |||• ||•| |•|| || | |
CCGA UUGCUCG GGG CC-C UGUCG CCGU CGCU GG----G C
AUG A ---- GGC -- A A A

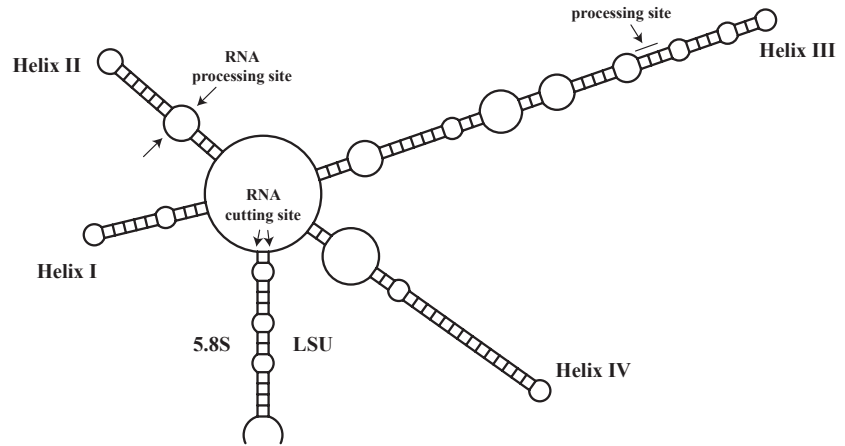
GGC

Helix IV

AA---- - U
AGG UCG GCGGUCGCUUUUUUU A
|•| ||| ||||•|||••||| |
UUC AGC CGCCGGCGAGGAAAA G
CCACAC A G

UUC->

ITS-2



Barcode legend:

- 1 = A-U
- 2 = U-A
- 3 = G-C
- 4 = C-G
- 5 = G•U
- 6 = U•G
- 7 = mismatch
- 8 = deletion, single or unpaired bases

ITS-2 rRNA secondary structure model of
Coccomyxa simplex
strain CCAP 216/24 (BC-3c) FN298927

Barcode 3c
ITS2-C7

5.8S/LSU stem

---00000-000-0111-11
---12345-678-9012-34
---23442-154-2453-26

BC

GUC C G C
UGCCU AGC UCGG UU->
|||| |•| ||•| |•
ACGGA UUG AGUC AG<-
AGA C - C

->CACCC

Helix I

1111-1
5678-9
6414-4

BC

C UU
UCAC CCUCCU A
•||| |||||• |
GGUG GGAGGG C
C CA

ACC

Helix II

2222222223
01234567890
63347774443

BC

CGU GA
UGGC CCCGGUU \
•||| |||||• U
GCCG GGGCCAG /
UCU UC

AAGAACAGA

Helix III

333333-333444444444---4555---55555--5566-666666667777
123456-789012345678---9012---34567--8901-234567890123
334288-114313384448---3383---14136--3361-363184488884

BC

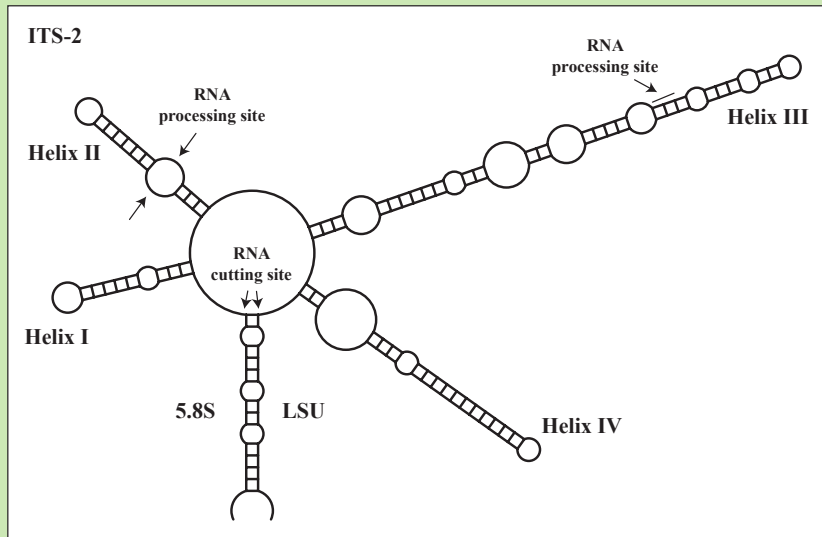
CG- A GAUC ACA CU G - G
GGCU AACGAGG CCC GG-G ACAGU GGUA GUGA CC----C U
|||| ||||| || || | |||• ||•| |•|| || | |
CCGA UUGCUC CCGG CC-C UGUCG CCGU CGCU GG----G C
AUG A ---- GGC -- A A A

GGC

Helix IV

AA---- - C
AGG UCGC CGGUCUUUCUCU A
|•| ||| |||•|||•|| |
UUC AGCG GCCGGAAAGGGA A
CCACAC C C

UUC->



Barcode legend:

- 1 = A-U
- 2 = U-A
- 3 = G-C
- 4 = C-G
- 5 = G•U
- 6 = U•G
- 7 = mismatch
- 8 = deletion, single or unpaired bases

ITS-2 rRNA secondary structure model of
Coccomyxa simplex
strain CCAP 812/2A (BC-3c) HG972992

Barcode 3c
ITS2-C7

5.8S/LSU stem

---00000-000-0111-11
---12345-678-9012-34
---23442-154-2453-26

BC

GUC C G C
UGCCU AGC UCGG UU->
|||| |•| ||•| |•
ACGGA UUG AGUC AG<-
AGA C - C

->CACCC

Helix I

1111-1
5678-9
6414-4

BC

C UU
UCAC CCUCCU A
•||| |||||• |
GGUG GGAGGG C
C CA

ACC

Helix II

2222222223
01234567890
63347774443

BC

CGU GA
UGGC CCCGGUU \
•||| |||||• U
GCCG GGGCCAG /
UCU UC

AAGAACAGA

Helix III

333333-333444444444---4555---55555--5566-666666667777
123456-789012345678---9012---34567--8901-234567890123
334288-114313384448---3383---14136--3361-363184488884

BC

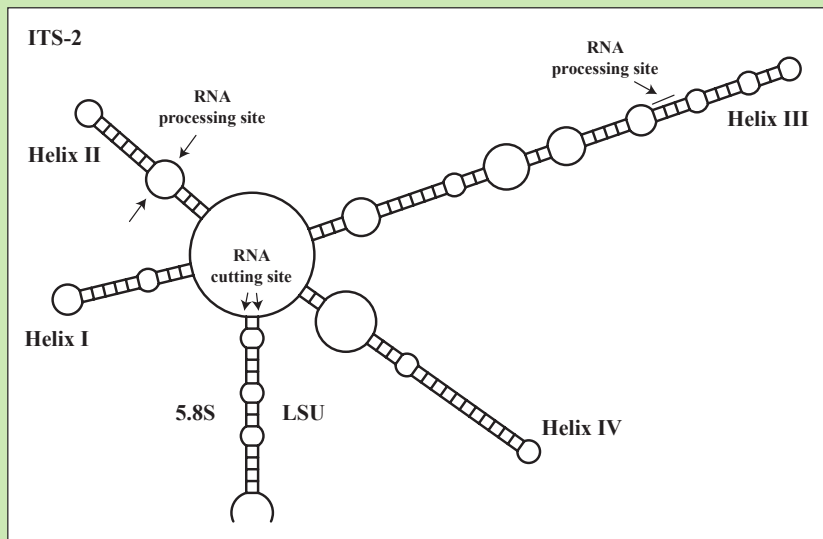
CG- A GAUC ACA CU G - G
GGCU AACGAGG CCC GG-G ACAGU GGUA GUGA CC----C U
|||| ||||| || || | |||• ||• |•|| || | |
CCGA UUGCUC CCGG CC-C UGUCG CCGU CGCU GG----G C
AUG A ---- GGC -- A A A

GGC

Helix IV

AA---- - C
AGG UCGC CGGUCUUUCUCU A
|•| |||| |||•|||•|| |
UUC AGCG GCCGGAAAGGGA A
CCACAC C C

UUC->



Barcode legend:

- 1 = A-U
- 2 = U-A
- 3 = G-C
- 4 = C-G
- 5 = G•U
- 6 = U•G
- 7 = mismatch
- 8 = deletion, single or unpaired bases

ITS-2 rRNA secondary structure model of
Coccomyxa simplex
strain CCAP 812/2B (BC-3c) HG972993

Barcode 3c
ITS2-C7

5.8S/LSU stem

---00000-000-0111-11
---12345-678-9012-34
---23442-154-2453-26

BC

GUC C G C
UGCCU AGC UCGG UU->
|||| |•| ||•| |•
ACGGA UUG AGUC AG<-
AGA C - C

->CACCC

Helix I

1111-1
5678-9
6414-4

BC

C UU
UCAC CCUCCU A
•||| |||||• |
GGUG GGAGGG C
C CA

ACC

Helix II

2222222223
01234567890
63347774443

BC

CGU GA
UGGC CCCGGUU \
•||| |||||• U
GCCG GGGCCAG /
UCU UC

AAGAACAGA

Helix III

333333-333444444444---4555---55555--5566-666666667777
123456-789012345678---9012---34567--8901-234567890123
334288-114313384448---3383---14136--3361-363184488884

BC

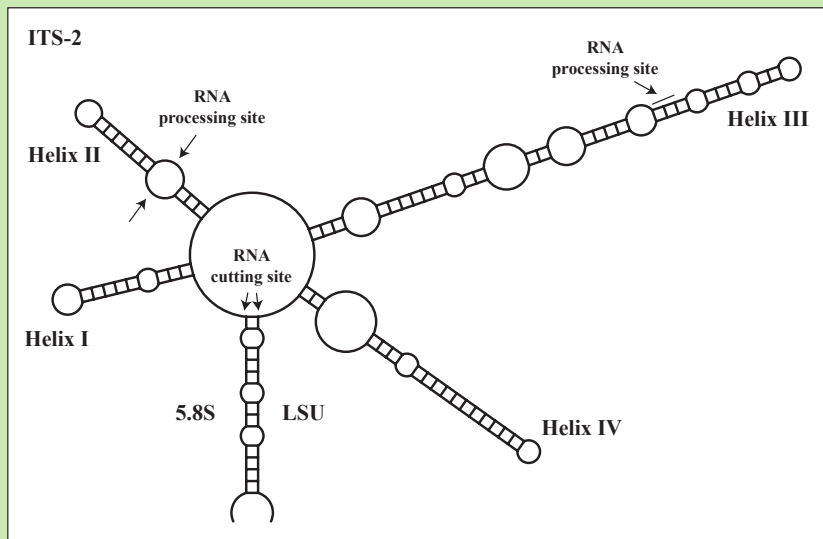
CG- A GAUC ACA CU G - G
GGCU AACGAGG CCC GG-G ACAGU GGUA GUGA CC----C U
|||| ||||| || || | ||||• ||• |•|| || | |
CCGA UUGCUC CCGG CC-C UGUCG CCGU CGCU GG----G C
AUG A ---- GGC -- A A A

GGC

Helix IV

AA---- - C
AGG UCGC CGGUCUUUCUCU A
|•| |||| |||•|||•|| |
UUC AGCG GCCGGAAAGGGA A
CCACAC C C

UUC->



Barcode legend:

- 1 = A-U
- 2 = U-A
- 3 = G-C
- 4 = C-G
- 5 = G•U
- 6 = U•G
- 7 = mismatch
- 8 = deletion, single or unpaired bases

ITS-2 rRNA secondary structure model of
Coccomyxa vinatzeri
strain ASIB V16 (BC-4) HG972994

Barcode 4
ITS2-E

5.8S/LSU stem

---00000-000-0111-11
---12345-678-9012-34
---23442-154-2453-26

BC

GUC C G C
UGCCU AGC UCGG UU->
|||| |•| ||•| |•
ACGGA UUG AGUC AG<-
AGA C - C

->UACCC

Helix I

1111-1
5678-9
6414-2

BC

C - UU
UCAC UUUCCU AUUC U
•||| |•|||• ||| |
GGUG AGAGGG UAAG G
- C UU

AUC

Helix II

2222222223
01234567890
65347774443

BC

AGU G
UGGC CCCGGUUA G
••|| |||||•|| |
GUCC GGGCCGAU A
CCU A

AAGACCAGA

Helix III

333333-333444444444---4555---55555--5566-6666-66667777
123456-789012345678---9012---34567--8901-2345-67890123
334288-114313384448---3383---14136--3361-3635-14443226

BC

CG- A AAUC ACA CU G - GU
GGCU AACGAGG CCC GG-G ACAGU GGUA GUGG ACCCGUUU \
|||| ||||| ||| || | |||• ||•| |••| |||||• U
CCGA UUGCUC GGG CC-C UGUCG CCGU CGCU UGGGCAAG /
AUG A ---- GGC -- A G UA

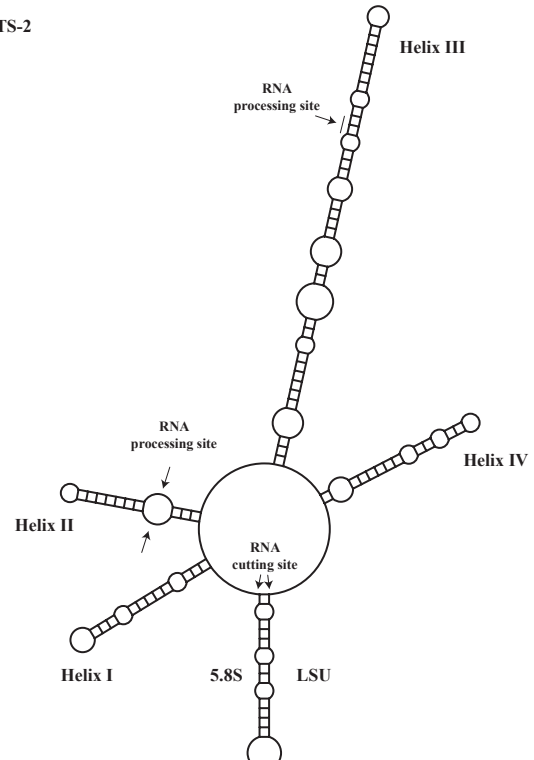
GGCA

Helix IV

AA - - U
GG UCGUUUG GUG GUG G
|| ||||| ||| |•| |
CC AGCAAAC CAC CGC U
-- A A U

AAAUAUAUUUC->

ITS-2



Barcode legend:

- 1 = A-U
- 2 = U-A
- 3 = G-C
- 4 = C-G
- 5 = G•U
- 6 = U•G
- 7 = mismatch
- 8 = deletion, single or unpaired bases

ITS-2 rRNA secondary structure model of
Coccomyxa galuniae
strain CCAP 211/97 (BC-5) FN298928

Barcode 5
ITS2-E

5.8S/LSU stem

---00000-000-0111-11
---12345-678-9012-34
---23442-154-2453-26

BC

GUC C G C
UGCCU AGC UCGG UU->
|||| |•| ||•| |•
ACGGA UUG AGUC AG<-
AGA C - C

->CACCC

Helix I

11111
56789
64141

BC

CA- U
UCACA CCCGC C
•|||| | |||| |
GGUGU GGGCG G
AGC A

AUC

Helix II

2222222223
01234567890
65347774443

BC

AGU CA
UGGC CCCGGUUC \
••|| | ||||| U
GUCC GGGCCAAG /
CCU AC

AAGACCAGA

Helix III

333333-333444444444---4555---55555--5566-666666667777
123456-789012345678---9012---34567--8901-234567890123
334288-134383384448---3383---14136--3361-363226448888

BC

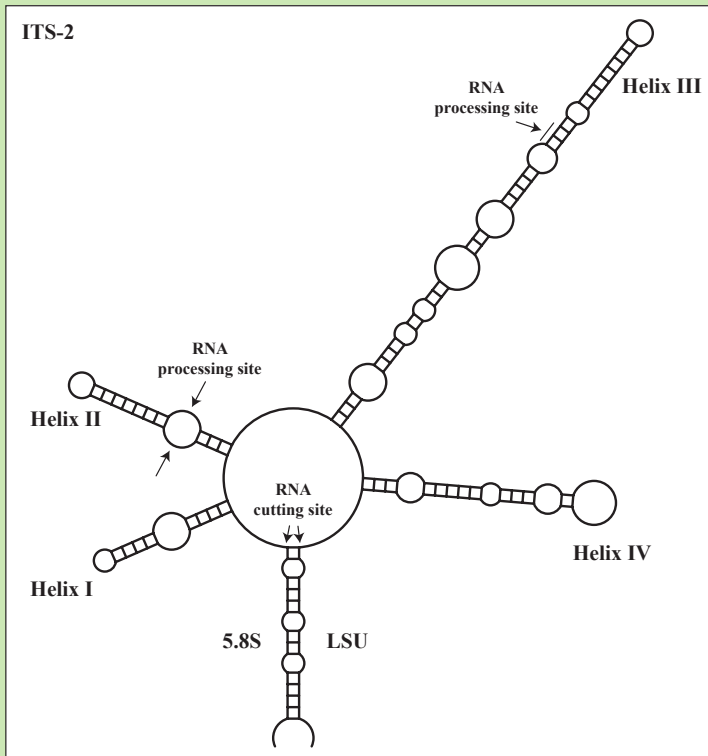
CG- A A GAUC ACA CU G CC
GGCU AGCG GG CCC GG-G ACAGU GGUA GUGUUUCC \
|||| | ||| || || | |||• ||•| |•|||•|| A
CCGA UCGC CC GGG CC-C UGUCG CCGU CGCAAGGG /
AUG C A ---- GGC -- A CC

GGCA

Helix IV

U- - U- GCCG
GGAA UUUGGUU UCG GC U
|•|| | |||||• ||| || |
CUUU AAACCAG AGC CG G
CC G UC AAAA

AACAUUC->



Barcode legend:

- 1 = A-U
- 2 = U-A
- 3 = G-C
- 4 = C-G
- 5 = G•U
- 6 = U•G
- 7 = mismatch
- 8 = deletion, single or unpaired bases

ITS-2 rRNA secondary structure model of
Coccomyxa galuniae
strain CCAP 812/5 (BC-5) HG972995

Barcode 5
ITS2-E

5.8S/LSU stem

---00000-000-0111-11
---12345-678-9012-34
---23442-154-2453-26

BC

GUC C G C
UGCCU AGC UCGG UU->
|||| |•| ||•| |•
ACGGA UUG AGUC AG<-
AGA C - C

->CACCC

Helix I

11111
56789
64141

BC

CA- U
UCACA CCCGC C
•|||| | |||| |
GGUGU GGGCG G
AGC A

AUC

Helix II

2222222223
01234567890
65347774443

BC

AGU CA
UGGC CCCGGUUC \
••|| | ||||| U
GUCC GGGCCAAG /
CCU AC

AAGACCAGA

Helix III

333333-333444444444---4555---55555--5566-666666667777
123456-789012345678---9012---34567--8901-234567890123
334288-134383384448---3383---14136--3361-363226448888

BC

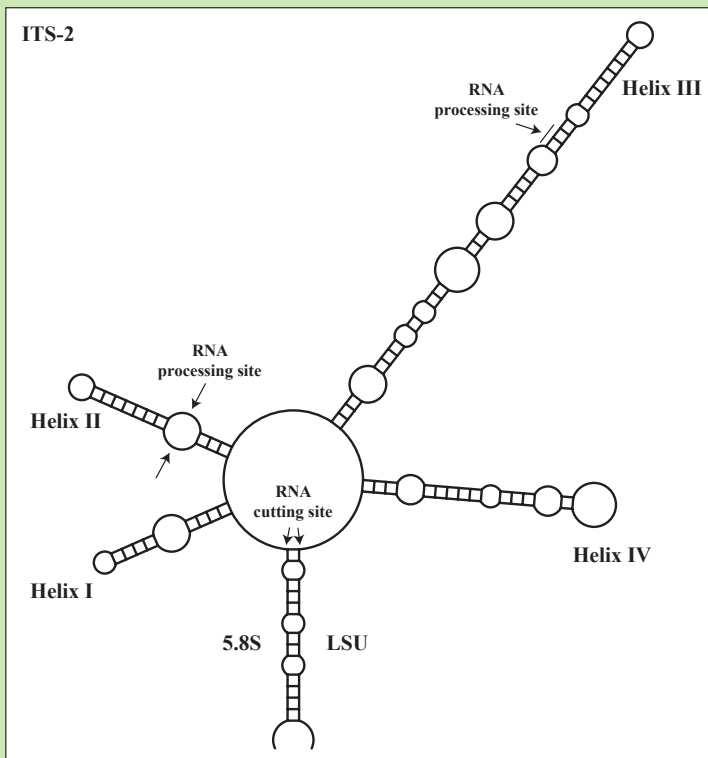
CG- A A GAUC ACA CU G CC
GGCU AGCG GG CCC GG-G ACAGU GGUA GUGUUUCC \
|||| | ||| || | |||• ||•| |•|||•|| A
CCGA UCGC CC GGG CC-C UGUCG CCGU CGCAAGGG /
AUG C A ---- GGC -- A CC

GGCA

Helix IV

U- - U- GCCG
GGAA UUUGGUU UCG GC U
|•|| | |||||• ||| || |
CUUU AAACCAG AGC CG G
CC G UC AAAA

AACAUUC->



Barcode legend:

- 1 = A-U
- 2 = U-A
- 3 = G-C
- 4 = C-G
- 5 = G•U
- 6 = U•G
- 7 = mismatch
- 8 = deletion, single or unpaired bases

ITS-2 rRNA secondary structure model of
Coccomyxa galuniae
strain SAG 2253 (BC-5) HG972996

Barcode 5
ITS2-E

5.8S/LSU stem

---00000-000-0111-11
---12345-678-9012-34
---23442-154-2453-26

BC

GUC C G C
UGCCU AGC UCGG UU->
|||| |•| ||•| |•
ACGGA UUG AGUC AG<-
AGA C - C

->CACCC

Helix I

11111
56789
64141

BC

CA- U
UCACA CCCGC C
•|||| | |||| |
GGUGU GGGCG G
AGC A

AUC

Helix II

2222222223
01234567890
65347774443

BC

AGU CA
UGGC CCCGGUUC \
••|| | ||||| U
GUCC GGGCCAAG /
CCU AC

AAGACCAGA

Helix III

333333-333444444444---4555---55555--5566-666666667777
123456-789012345678---9012---34567--8901-234567890123
334288-134383384448---3383---14136--3361-363226448888

BC

CG- A A GAUC ACA CU G CC
GGCU AGCG GG CCC GG-G ACAGU GGUA GUGUUUCC \
|||| | ||| || || | |||• ||•| |•|||•|| A
CCGA UCGC CC GGG CC-C UGUCG CCGU CGCAAGGG /
AUG C A ---- GGC -- A CC

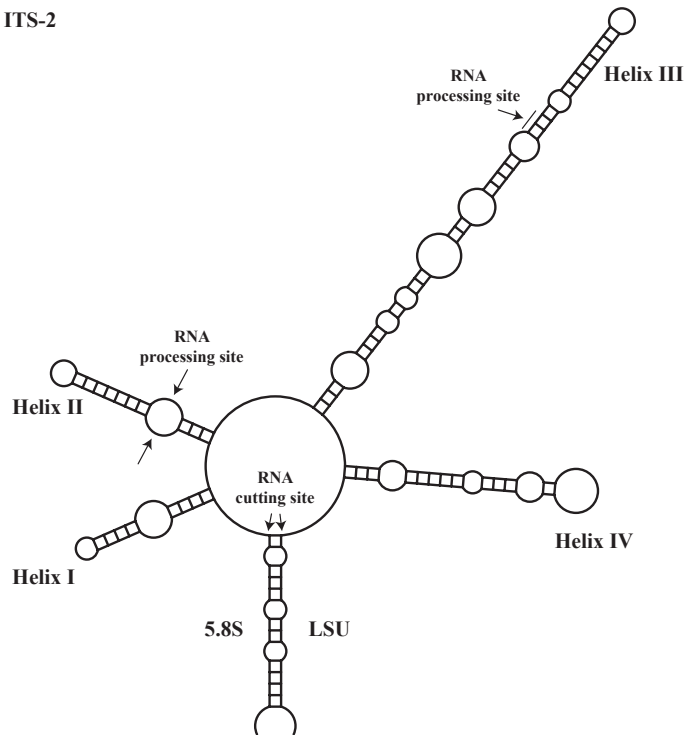
GGCA

Helix IV

U- - U- GCCG
GGAA UUUGGUU UCG GC U
|•|| | |||||• ||| || |
CUUU AAACCAG AGC CG G
CC G UC AAAA

AACAUUC->

ITS-2



Barcode legend:

- 1 = A-U
- 2 = U-A
- 3 = G-C
- 4 = C-G
- 5 = G•U
- 6 = U•G
- 7 = mismatch
- 8 = deletion, single or unpaired bases

ITS-2 rRNA secondary structure model of
Coccomyxa galuniae
strain SAG 2254 (BC-5) HG972997

Barcode 5
ITS2-E

5.8S/LSU stem

---00000-000-0111-11
---12345-678-9012-34
---23442-154-2453-26

BC

GUC C G C
UGCCU AGC UCGG UU->
|||| |•| ||•| |•
ACGGA UUG AGUC AG<-
AGA C - C

->CACCC

Helix I

11111
56789
64141

BC

CA- U
UCACA CCCGC C
•|||| | |||| |
GGUGU GGGCG G
AGC A

AUC

Helix II

2222222223
01234567890
65347774443

BC

AGU CA
UGGC CCCGGUUC \
••|| | ||||| U
GU CG GGGCCAAG /
CCU AC

AAGACCAGA

Helix III

333333-333444444444---4555---55555--5566-666666667777
123456-789012345678---9012---34567--8901-234567890123
334288-134383384448---3383---14136--3361-363226448888

BC

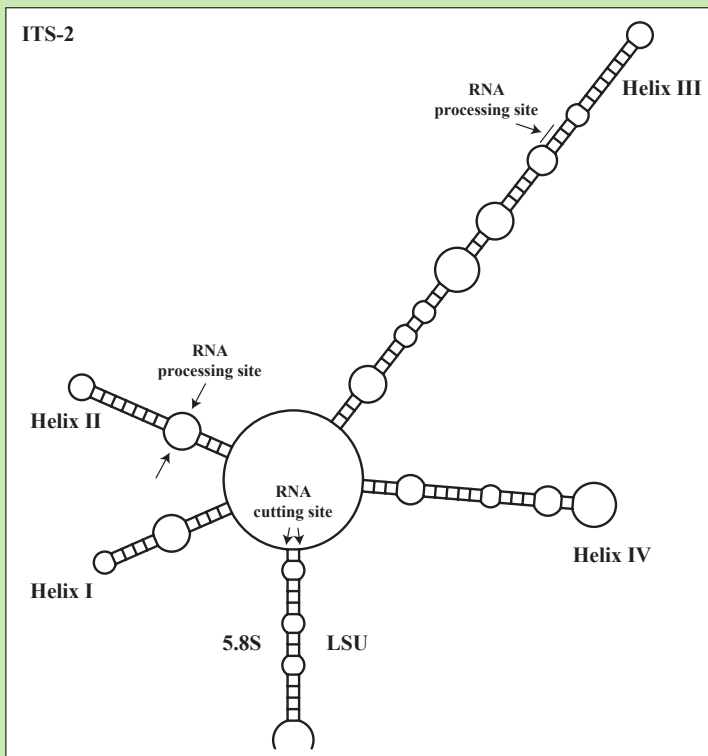
CG- A A GAUC ACA CU G CC
GGCU AGCG GG CCC GG-G ACAGU GGUA GUGUUUCC \
|||| | ||| || || | |||• ||•| |•|||•|| A
CCGA UCGC CC GGG CC-C UGUCG CCGU CGCAAGGG /
AUG C A ---- GGC -- A CC

GGCA

Helix IV

U- - U- GCCG
GGAA UUUGGUU UCG GC U
|•|| | |||||• ||| || |
CUUU AAACCAG AGC CG G
CC G UC AAAA

AACAUUC->



Barcode legend:

- 1 = A-U
- 2 = U-A
- 3 = G-C
- 4 = C-G
- 5 = G•U
- 6 = U•G
- 7 = mismatch
- 8 = deletion, single or unpaired bases

ITS-2 rRNA secondary structure model of
Coccomyxa dispar
strain SAG 49.84 (BC-6) HG972998

Barcode 6
ITS2-F

5.8S/LSU stem

---00000-000-0111-11
---12345-678-9012-34
---23442-154-2453-26

BC

GCC C G U
UGCCU AGC UCGG UU->
|||| |•| ||•| |•
ACGGA UUG AGUC AG<-
AGA C - C

->ACACCC

Helix I

11111
56789
64224

BC

- U
UCUUCU ACCAU U
•|||| |•| |
GGAAGA UGGUG U
G U

ACC

Helix II

2222222223
01234567890
65347774443

BC

UGU CG
UGGC CCCGAUUGUU \
••|| | ||||| U
GU CG GGGCUAACAA /
CCU CG

AAGAACAGA

Helix III

333--333-3334-444-444-44----45-5555555--5566-666666667777
123--456-7890-123-456-78----90-1234567--8901-234567890123
334--484-1343-233-444-42----33-4114136--3361-343122888384

BC

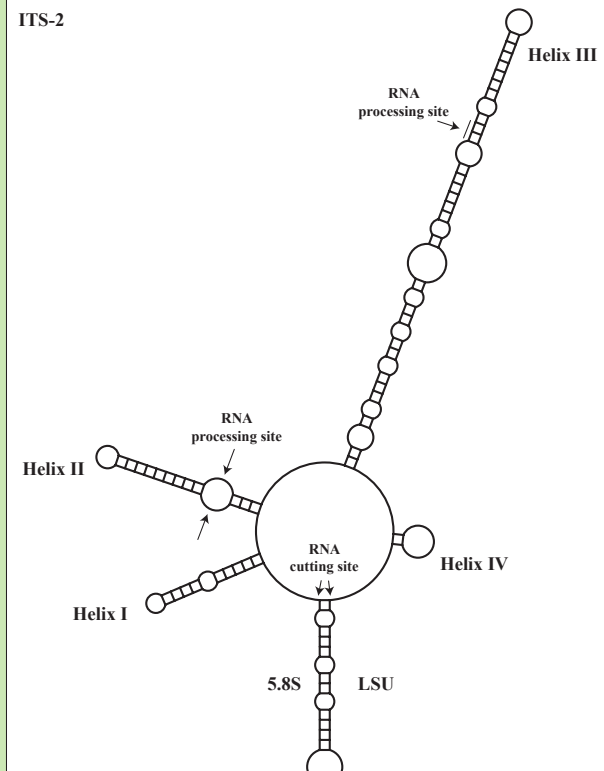
-- G - A A CCAC G CU G UA
GGC C-C AGCG UGG CCC CU GG CAACAGU GGUA GCGAUU---G-C C
||| | | |||| | || | || |||||• ||•| ||||| | | |
CCG G-G UCGC ACC GGG GA CC GUUGUCG CCGU CGCUAA---C-G A
AA - U A - ---- G -- A UA

GCAAGCA

Helix IV

AAA
GG C
|| |
CC C
AAA

AAACAUUC->



Barcode legend:

- 1 = A-U
- 2 = U-A
- 3 = G-C
- 4 = C-G
- 5 = G•U
- 6 = U•G
- 7 = mismatch
- 8 = deletion, single or unpaired bases

ITS-2 rRNA secondary structure model of
Coccomyxa viridis
strain SAG 216-1 (BC-7a) HG972999

Barcode 7a
ITS2-G1

5.8S/LSU stem

---00000-000-0111-11
---12345-678-9012-34
---23442-156-2453-26

BC

GCC C G U
UGCCU AGU UCGG UU->
|||| |•• ||•| |•
ACGGA UUG AGUC AG<-
GGA C - C

->CACCC

Helix I

1111---1
5678---9
6434---4

BC

CCA A-- U
UCGC CCCUUCU UUCUC C
•||| ||||•||| |||||
GGCG GGGAGAGA AAGAG A
AG- CAC C

AUC

Helix II

2222222223
01234567890
65347774443

BC

CGU U
UGGC CCCGGUC C
••|| ||||| |
GUCC GGGCCAG A
UCU C

AAGCGCAGA

Helix III

333-333-3334444-4444-----4-455--55-555--55566-6666--66667777
123-456-7890123-4567-----8-901--23-456--78901-2345--67890123
334-286-1343833-2444-----3-333--41-413--43361-3631--44822424

BC

- G A UAUAGAU U AA A AC G GC U
GGC U-U AGCG-GG UCCC G GGG CA CAG CGGUA GUGA CC-UUCUC C
||| |• |||| | |||| | ||| ||| ||| |||•| |•|| || ||||| |
CCG A-G UCGC-CC AGGG C CCC GU GUC GCCGU CGCU GG-AAGAG C
C G - ----- - AG C -- A A- G

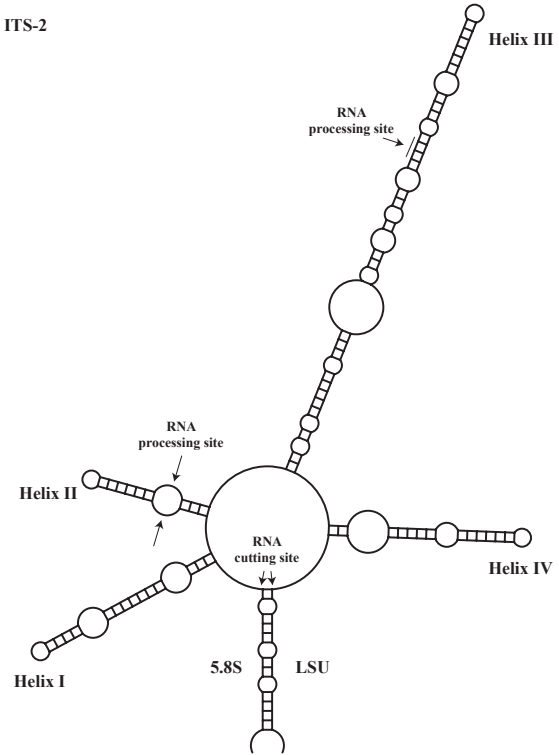
CAGCAG

Helix IV

A--- GA U
GAG CGGUGU CCGGUCC C
||| |||||• ||||| |
CUC GCCACG GGCCAGG G
AUAC AA C

AACCAUUC->

ITS-2



Barcode legend:

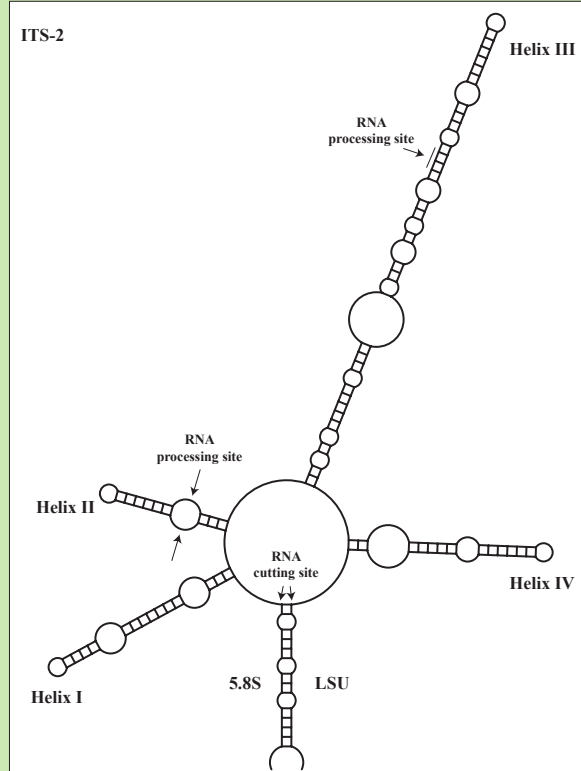
- 1 = A-U
- 2 = U-A
- 3 = G-C
- 4 = C-G
- 5 = G•U
- 6 = U•G
- 7 = mismatch
- 8 = deletion, single or unpaired bases

Barcode 7a
ITS2-G2



BC

AACCAUUC->



8 = deletion, single or unpaired bases

ITS-2 rRNA secondary structure model of
Coccoomyxa viridis
strain SAG 216-4 (BC-7a) HG973001

Barcode 7a
ITS2-G3

5.8S/LSU stem

---00000-000-0111-11
---12345-678-9012-34
---23442-156-2453-26

BC

GCC C G U
UGCCU AGU UCGG UU->
|||| |•• ||•| |•
ACGGA UUG AGUC AG<-
GGA C - C

->CACCC

Helix I

1111--1
5678--9
6434--4

BC

CA - U
UCGC CCCCUUUC UCUGUC C
•||| |||||•||| |
GGCG GGGGAAAG AGACAG C
C- C G

AUC

Helix II

22222222223
01234567890
65347774443

BC

CGU UU
UGGC CCCGGUC \
••|| ||||•|| U
GUUC GGGCUAG /
UCU UC

AAGCGCAGA

Helix III

333-333-3334444--4444-----4-455--55-555--55566-6666--66667777
123-456-7890123--4567-----8-901--23-456--78901-2345--67890123
334-286-1343833--2444-----3-333--41-413--43361-3631--44822424

BC

- G AU UUCUAAU U AA A AC G GC C
GGC U-U AGCG-GG UCCC G GGG CA CAG CGGUA GUGA CC-UUCUC \
||| | • |||| || |||| | ||| || ||| |||•| |•|| || ||||| U
CCG A-G UCGC-CC AGGG C CCC GU GUC GCCGU CGCU GG-AAGAG /
C G -- ----- - AG C -- A A- C

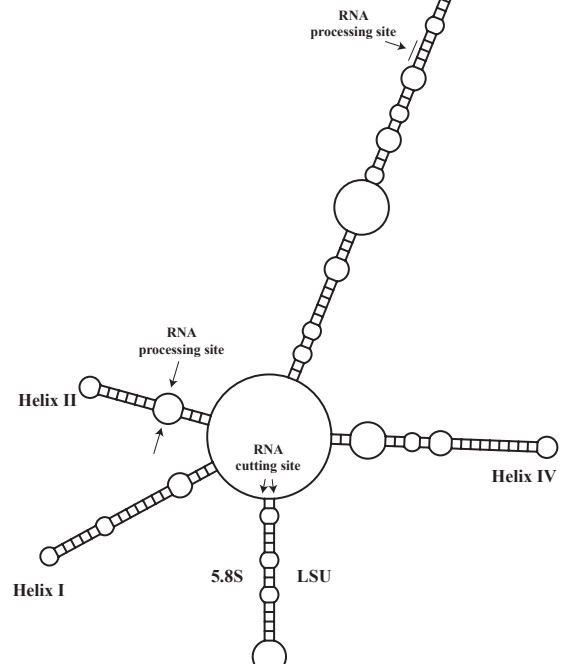
CAGCAG

Helix IV

A--- U GA CA
GAG CGG GU CGGUGGUUCC \
||| ||| || ||•||| ||| C
CUC GCC CA GCUACCAAGG /
ACUA C AA AG

AACCAUUC->

ITS-2



Barcode legend:

- 1 = A-U
- 2 = U-A
- 3 = G-C
- 4 = C-G
- 5 = G•U
- 6 = U•G
- 7 = mismatch
- 8 = deletion, single or unpaired bases

ITS-2 rRNA secondary structure model of
Coccothryxa viridis
strain SAG 216-14 (BC-7a) HG973002

Barcode 7a
ITS2-G3

5.8S/LSU stem

---00000-000-0111-11
---12345-678-9012-34
---23442-156-2453-26

BC

GCC C G U
UGCCU AGU UCGG UU->
|||| |•• ||•| |•
ACGGA UUG AGUC AG<-
GGA C - C

->CACCC

Helix I

1111--1
5678--9
6434--4

BC

CA - U
UCGC CCCCUUUC UCUGUC C
•||| |||||•||| |
GGCG GGGGAAAG AGACAG C
C- C G

AUC

Helix II

22222222223
01234567890
65347774443

BC

CGU UU
UGGC CCCGGUC \
••|| ||||•|| U
GUUC GGGCUAG /
UCU UC

AAGCGCAGA

Helix III

333-333-3334444--4444-----4-455--55-555--55566-6666--66667777
123-456-7890123--4567-----8-901--23-456--78901-2345--67890123
334-286-1343833--2444-----3-333--41-413--43361-3631--44822424

BC

- G AU UUCUAAU U AA A AC G GC C
GGC U-U AGCG-GG UCCC G GGG CA CAG CGGUA GUGA CC-UUCUC \
||| | • |||| || |||| | ||| || ||| |||•| |•|| || ||||| U
CCG A-G UCGC-CC AGGG C CCC GU GUC GCCGU CGCU GG-AAGAG /
C G -- ----- - AG C -- A A- C

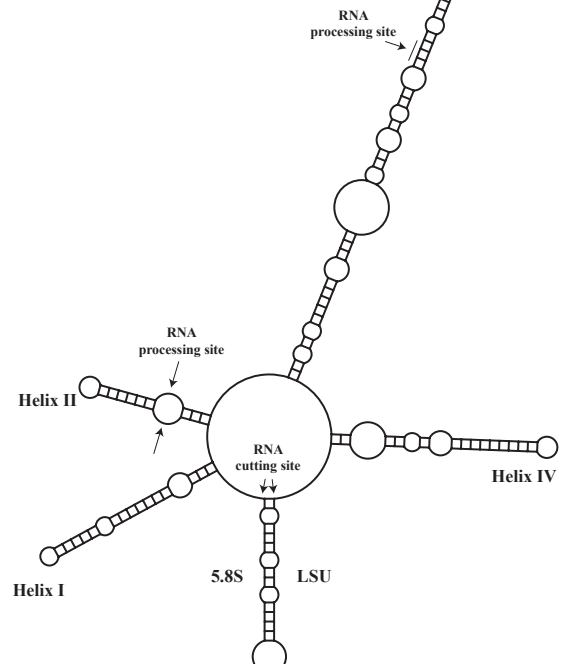
CAGCAG

Helix IV

A--- U GA CA
GAG CGG GU CGGUGGUUCC \
||| ||| || ||•||| ||| C
CUC GCC CA GCUACCAAGG /
ACUA C AA AG

AACCAUUC->

ITS-2



Barcode legend:

- 1 = A-U
- 2 = U-A
- 3 = G-C
- 4 = C-G
- 5 = G•U
- 6 = U•G
- 7 = mismatch
- 8 = deletion, single or unpaired bases

ITS-2 rRNA secondary structure model of
Coccomyxa viridis
strain SAG 2104 (BC-7a) HG973003

Barcode 7a
ITS2-G3

5.8S/LSU stem

---00000-000-0111-11
---12345-678-9012-34
---23442-156-2453-26

BC

GCC C G U
UGCCU AGU UCGG UU->
|||| |•• ||•| |•
ACGGA UUG AGUC AG<-
GGA C - C

->CACCC

Helix I

1111--1
5678--9
6434--4

BC

CA - U
UCGC CCCCUUUC UCUGUC C
•||| |||||•||| |
GGCG GGGGAAAG AGACAG C
C- C G

AUC

Helix II

22222222223
01234567890
65347774443

BC

CGU UU
UGGC CCCGGUC \
••|| ||||•|| U
GUUC GGGCUAG /
UCU UC

AAGCGCAGA

Helix III

333-333-3334444--4444-----4-455--55-555--55566-6666--66667777
123-456-7890123--4567-----8-901--23-456--78901-2345--67890123
334-286-1343833--2444-----3-333--41-413--43361-3631--44822424

BC

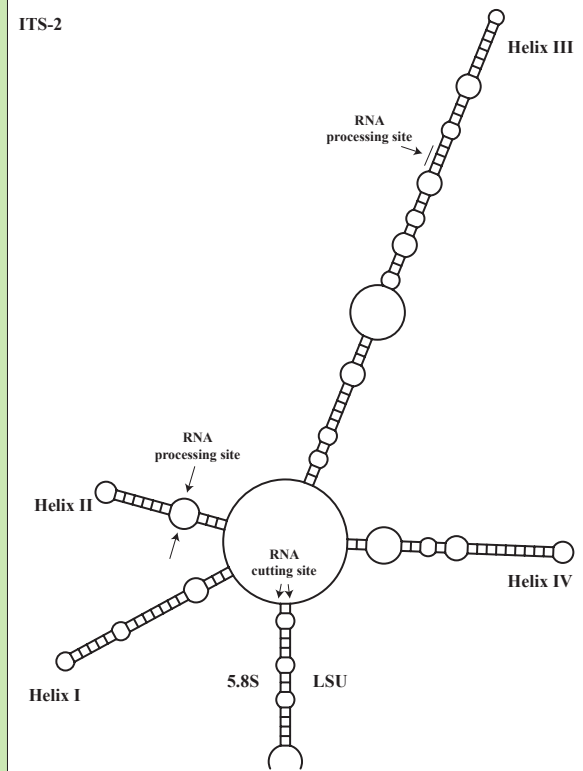
- G AU UUCUAAU U AA A AC G GC C
GGC U-U AGCG-GG UCCC G GGG CA CAG CGGUA GUGA CC-UUCUC \
||| | • |||| || |||| | ||| || ||| |||•| |•|| || ||||| U
CCG A-G UCGC-CC AGGG C CCC GU GUC GCCGU CGCU GG-AAGAG /
C G -- ----- - AG C -- A A- C

CAGCAG

Helix IV

A--- U GA CA
GAG CGG GU CGGUGGUUCC \
||| ||| || ||•||| ||| C
CUC GCC CA GCUACCAAGG /
ACUA C AA AG

AACCAUUC->



Barcode legend:

- 1 = A-U
- 2 = U-A
- 3 = G-C
- 4 = C-G
- 5 = G•U
- 6 = U•G
- 7 = mismatch
- 8 = deletion, single or unpaired bases

ITS-2 rRNA secondary structure model of
Coccomyxa viridis
strain SAG 2040 (BC-7b) HG973004

Barcode 7b
ITS2-G4

5.8S/LSU stem

---00000-000-0111-11
---12345-678-9012-34
---23442-156-2453-26

BC

GCC C G U
UGCCU AGU UCGG UU->
|||| |•• ||•| |•
ACGGA UUG AGUC AG<-
GGA C - C

->CACCC

Helix I

1111-1
5678-9
6434-4

BC

C U - U C
UCGC C CCCUUC UUUU UC U
•||| | ||||| |•• |||
GGCG G GGGAAAG AAAG AG C
U - U C G

AUC

Helix II

2222222223
01234567890
65347774443

BC

CGU UC
UGGC CCCGGUC \
••|| ||||| C
GUUC GGGCCAG /
UCU UU

AAGCGCAGA

Helix III

333-3333334444--4444-----4-455--55-555--55566-6666--66667777
123-4567890123--4567-----8-901--23-456--78901-2345--67890123
334-2661343833--2444-----3-333--41-413--43361-3631--44822424

BC

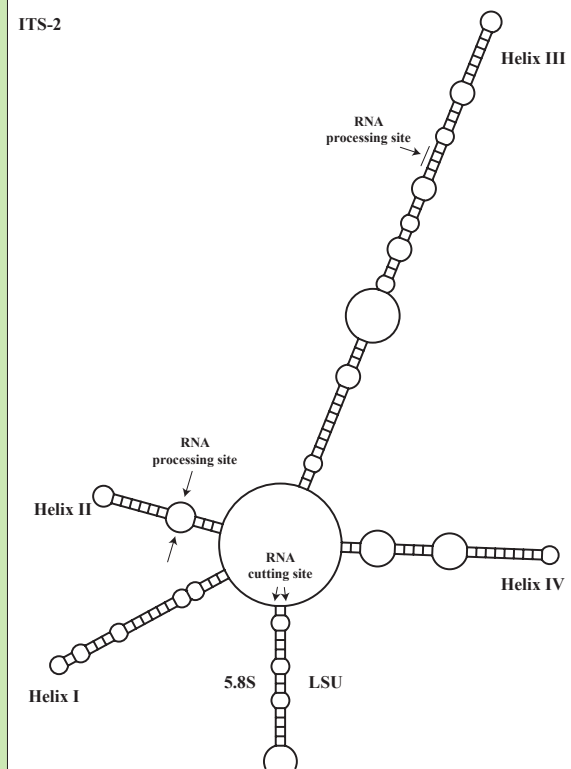
- AU UUCUAAU U AA A AC G GC CU
GGC UUUAGCG-GG UCCC G GGG CA CAG CGGUA GUGA CC-UUCUC \
||| |••||| || ||| | ||| |||•| |•|| || ||||| C
CCG AGGUCGC-CC AGGG C CCC GU GUC GCCGU CGCU GG-AAGAG /
C -- - - - - AG C -- A A- AG

CAGCAG

Helix IV

A--- GUAA U
GAG CGGUG UGAUGGGUC C
||| |||| |•||| |||
CUC GCCAC AUUACCCAG A
ACUA AACA C

AACCAUUC->



Barcode legend:

- 1 = A-U
- 2 = U-A
- 3 = G-C
- 4 = C-G
- 5 = G•U
- 6 = U•G
- 7 = mismatch
- 8 = deletion, single or unpaired bases

ITS-2 rRNA secondary structure model of
Coccomyxa viridis
strain SAG 2127 (BC-7b) HG973005

Barcode 7b
ITS2-G4

5.8S/LSU stem

---00000-000-0111-11
---12345-678-9012-34
---23442-156-2453-26

BC

GCC C G U
UGCCU AGU UCGG UU->
|||| |•• ||•| |•
ACGGA UUG AGUC AG<-
GGA C - C

->CACCC

Helix I

1111-1
5678-9
6434-4

BC

C U - U C
UCGC C CCCUUC UUUU UC U
•||| | ||||| |•• || |
GGCG G GGGAAAG AAAG AG C
U - U C G

AUC

Helix II

2222222223
01234567890
65347774443

BC

CGU UC
UGGC CCCGGUC \
••|| ||||| C
GUCC GGGCCAG /
UCU UU

AAGCGCAGA

Helix III

333-3333334444--4444-----4-455--55-555--55566-6666--66667777
123-4567890123--4567-----8-901--23-456--78901-2345--67890123
334-2661343833--2444-----3-333--41-413--43361-3631--44822424

BC

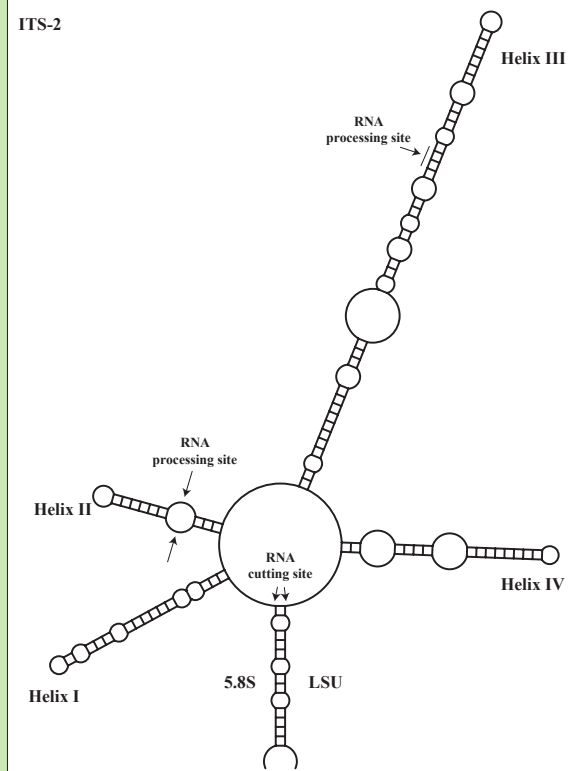
- AU UUCUAAU U AA A AC G GC CU
GGC UUUAGCG-GG UCCC G GGG CA CAG CGGUA GUGA CC-UUCUC \
||| |••||| || ||| | ||| ||| |•• |••| || ||||| C
CCG AGGUCGC-CC AGGG C CCC GU GUC GCCGU CGCU GG-AAGAG /
C -- - - - - AG C -- A A- AG

CAGCAG

Helix IV

A--- GUAA U
GAG CGGUG UGAUGGGUC C
||| |||| |•||| || |
CUC GCCAC AUUACCCAG A
ACUA AACA C

AACCAUUC->



Barcode legend:

- 1 = A-U
- 2 = U-A
- 3 = G-C
- 4 = C-G
- 5 = G•U
- 6 = U•G
- 7 = mismatch
- 8 = deletion, single or unpaired bases

ITS-2 rRNA secondary structure model of
Coccomyxa viridis
strain SAG 2325 (BC-7b) HG973006

Barcode 7b
ITS2-G4

5.8S/LSU stem

---00000-000-0111-11
---12345-678-9012-34
---23442-156-2453-26

BC

GCC C G U
UGCCU AGU UCGG UU->
|||| |•• ||•| |•
ACGGA UUG AGUC AG<-
GGA C - C

->CACCC

Helix I

1111-1
5678-9
6434-4

BC

C U - U C
UCGC C CCCUUUC UUUU UC U
•||| | ||||| |•• || |
GGCG G GGGAAAG AAAG AG C
U - U C G

AUC

Helix II

2222222223
01234567890
65347774443

BC

CGU UC
UGGC CCCGGUC \
••|| ||||| C
GUUC GGGCCAG /
UCU UU

AAGCGCAGA

Helix III

333-3333334444--4444-----4-455--55-555--55566-6666--66667777
123-4567890123--4567-----8-901--23-456--78901-2345--67890123
334-2661343833--2444-----3-333--41-413--43361-3631--44822424

BC

- AU UUCUAAU U AA A AC G GC CU
GGC UUUAGCG-GG UCCC G GGG CA CAG CGGUA GUGA CC-UUCUC \
||| |••||| || ||| | ||| |||•| |•|| || ||||| C
CCG AGGUCGC-CC AGGG C CCC GU GUC GCCGU CGCU GG-AAGAG /
C -- - - - - AG C -- A A- AG

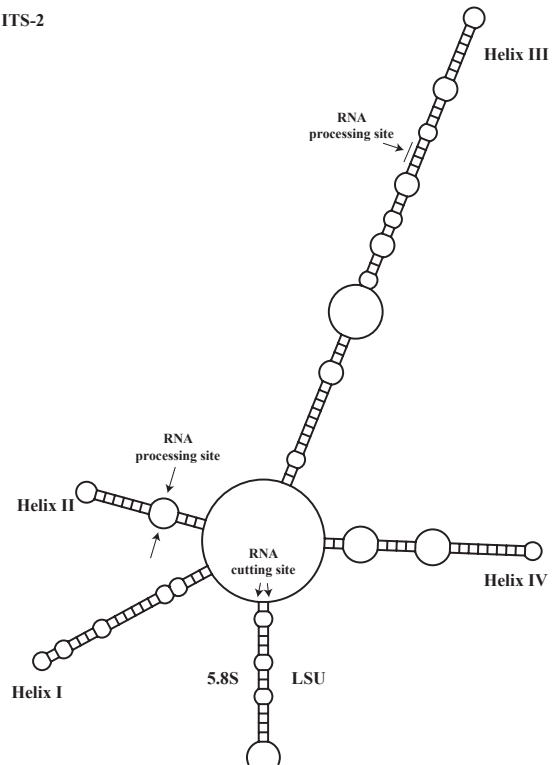
CAGCAG

Helix IV

A--- GUAA U
GAG CGGUG UGAUGGGUC C
||| |||| |•||| || |
CUC GCCAC AUUACCCAG A
ACUA AACA C

AACCAUUC->

ITS-2



Barcode legend:

- 1 = A-U
- 2 = U-A
- 3 = G-C
- 4 = C-G
- 5 = G•U
- 6 = U•G
- 7 = mismatch
- 8 = deletion, single or unpaired bases

Barcode 7b
ITS2-G5

```
---00000-000-0111-11
---12345-678-9012-34
---23442-156-2453-26
```


1111-1
5678-9
6434-4



22222222223
01234567890
65347774443

BC

Helix III

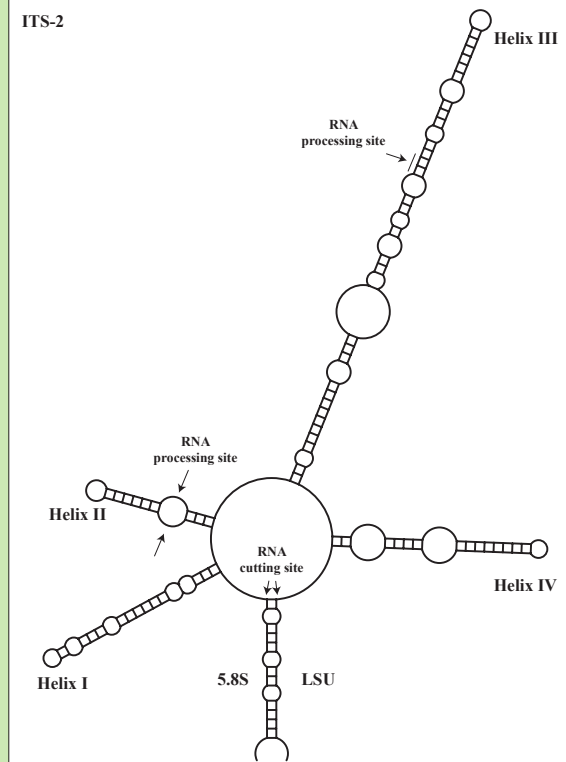
333-3333334444--4444-----4-455--55-555--55566-6666--66667777
123-4567890123--4567-----8-901--23-456--78901-2345--67890123
334-2661343833--2444-----3-333--41-413--43361-3631--44822424

BC

Helix IV

A---	GUAA	U
GAG	CGGUG	UGAUGGGUC C
		•
CUC	GCCAC	AUUACCCAG A
ACUA	AACA	C

AACCAUUC->		



- 1 = A-U
- 2 = U-A
- 3 = G-C
- 4 = C-G
- 5 = G•U
- 6 = U•G

```
7 = mismatch
```

8 = deletion, single or unpaired bases

ITS-2 rRNA secondary structure model of
Coccoomyxa subellipsoidea
uncultured (BC-1d) AY293946 *

Barcode 1d
ITS2-A4

5.8S/LSU stem

---00000-000-0111-11
---12345-678-9012-34
---23442-154-2453-26

BC

GUC C G C
UGCCU AGC UCGG UU->
|||| |•| ||•| |•
acgga uug aguC AG<-
aga c - C

->UACCC

Helix I

1111-1
5678-9
6414-4

BC

- C A
UCAC CC CCC A
•||| || ||| |
GGUG GG GGG U
C A C

ACC

Helix II

2222222223
01234567890

65347774443

BC

AGU G
UGGC CCCGGUCG C
••|| ||||| |
GU CG GGGCCAGC A
CCU A

AAGACCAGA

Helix III

333-333-333444444--444---455--555555--5566-666666667777
123-456-789012345--678---901--234567--8901-234567890123

334-284-134181383--448---533--114136--3361-363884488884

BC

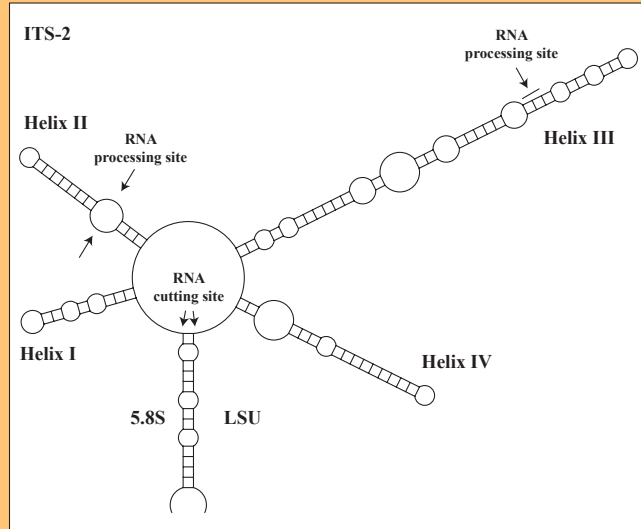
- G AC GCAU AA CU G A G
GGC U-C AGCA-AG-G CC GGG AACAGU GGUA GUG -CC---C C
||| | | ||| | | || •|| |||| • ||•| |•| || | |
CCG A-G UCGU-UC-C GG UCC UUGUCG CCGU CGC -GG---G A
A G GA ---- GC -- A - A

GGC

Helix IV

AA-- - U
AGG UCGU CGGUCGCCCCU A
||| |||• |||•|||• |
UCC AGCG GCCGGCGGGG G
CACA U C

UUUC->



Barcode legend:

- 1 = A-U
- 2 = U-A
- 3 = G-C
- 4 = C-G
- 5 = G•U
- 6 = U•G
- 7 = mismatch
- 8 = deletion, single or unpaired bases

ITS-2 rRNA secondary structure model of
Coccomyxa simplex
strain GSE4G (BC-3c) HE586518 *

Barcode 3c
ITS2-C8

5.8S/LSU stem

---00000-000-0111-11
---12345-678-9012-34
---23442-154-2453-26

BC

GUC C G C
UGCCU AGC UCGG UU->
|||| |•| ||•| |•
acgga uug aguc ag<-
aga c - c

->CACCC

Helix I

1111-1
5678-9
6414-4

BC

C C
UCAC CCUCCU A
•||| |||||• |
GGUG GGAGGG C
C C

ACC

Helix II

2222222223
01234567890
63347774443

BC

CGU U
UGGC CCCGGUCG \
•||| ||||| U
GCCG GGGCCAGC /
CCU G

AAGAACAGA

Helix III

333333-333444444444---4555---55555--5566-666666667777
123456-789012345678---9012---34567--8901-234567890123
334288-114313384448---3383---14136--3361-363184488884

BC

CG- A AAUC ACA CU G - G
GGCU AACGAGG CCC GG-G ACAGU GGUA GUGA CC----C C
|||| ||||| || || | |||• ||•| |•|| || | |
CCGA UUGCUC C GGG CC-C UGUCG CCGU CGCU GG----G G
AUG A ---- GGC -- A A A

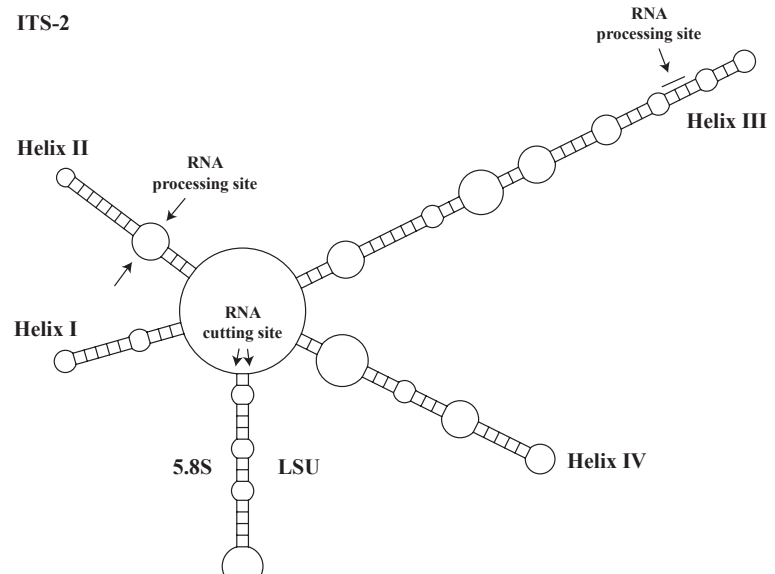
GGC

Helix IV

AA--- - CGA CU
AGG UCGC CGGU CCUUUC G
||| |||| |||| ||||| |
UCC AGCG GCCA GGAAAG A
CACAC C AC- CC

Uuuc->

ITS-2



Barcode legend:

- 1 = A-U
- 2 = U-A
- 3 = G-C
- 4 = C-G
- 5 = G•U
- 6 = U•G
- 7 = mismatch
- 8 = deletion, single or unpaired bases

ITS-2 rRNA secondary structure model of
Coccoomyxa viridis
strain CR-2 (BC-7a) HE586519

Barcode 7a
ITS2-G6

5.8S/LSU stem

---00000-000-0111-11
---12345-678-9012-34
---23442-156-2453-26

BC

GCC C G U
UGCCU AGU UCGG UU->
|||| |•• ||•| |•
ACGGA UUG AGUC AG<-
GGA C - C

->CACCC

Helix I

1111-1
5678-9
6434-4

BC

C U UU U
UCGC CUCCC UYC UUAUC U
•||| |•||| ||| ||||| |
GGCG GGGGG AAG AAUAG C
U C CU G

Y = C or U
(should be a U)

AUC

Helix II

2222222223
01234567890
65347774443

BC

CGU CA
UGGC CCCGAUU \
••|| | ||||| U
GUUC GGGCUAA /
UCU CC

AAGCGCAGA

Helix III

333-333-3334444--4444-----4-455--55-555--55566-6666--66667777
123-456-7890123--4567-----8-901--23-456--78901-2345--67890123
334-286-1343833--2444-----3-333--41-413--43361-3631--44822424

BC

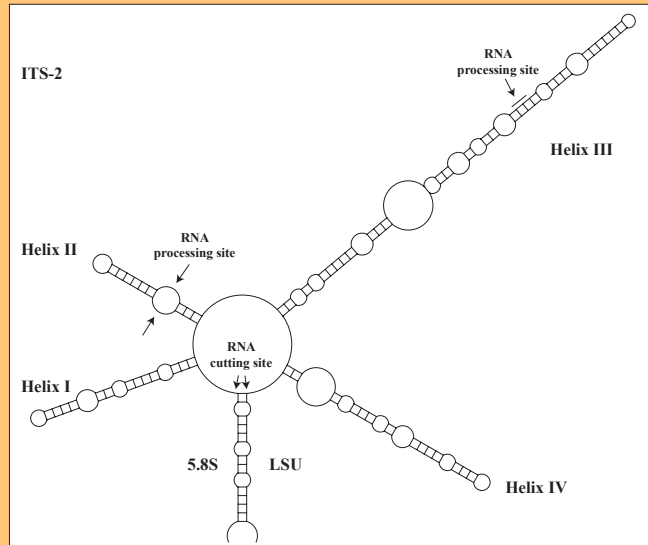
- G AU UUCUGAU C AA A AC G GC C
GGC U-U AGCG-GG UCCC G GGG CA CAG CGGUA GUGA CC-UUCUC \
||| | • |||| || ||| ||| ||| • | • || || ||||| U
CCG A-G UCGC-CC AGGG C CCC GU GUC GCCGU CGCU GG-AAGAG /
C G -- - - - - AG C -- A A- C

CAGCA

Helix IV

----- - - GA A U
GGA GA CGGU GU CUGGG GGUC C
||| || |•| || ||||| |•|| |
CCU CU GCUA CA GACCC CUAG A
ACUCA A C AG C C

AUUC->



Barcode legend:

- 1 = A-U
- 2 = U-A
- 3 = G-C
- 4 = C-G
- 5 = G•U
- 6 = U•G
- 7 = mismatch
- 8 = deletion, single or unpaired bases

ITS-2 rRNA secondary structure model of
Coccomyxa viridis
strain C9 (BC-7a) HE586536 *

Barcode 7a
ITS2-G7

5.8S/LSU stem

---00000-000-0111-11
---12345-678-9012-34
---23442-156-2453-26

BC

GCC C G U
UGCCU AGU UCGG UU->
|||| |•• ||•| |•
acgga uug aguc AG<-
gga c - C

->CACCC

Helix I

1111--1
5678--9
6434--4

BC

CA - U
UCGC CCCCUUUCUC UGUC C
•||| ||||| |||||
GGCG GGGGAAAGAG ACAG C
C- U G

AUC

Helix II

22222222223
01234567890
65347774443

BC

CUU GU
UGGC CCCGGUC \
••|| ||||| A
GUCC GGGCCAG /
UCU UU

AAGCGCAGA

Helix III

333-333-3334444--4444-----4-455--55-555--55566-6666--66667777
123-456-7890123--4567-----8-901--23-456--78901-2345--67890123
334-286-1343833--2444-----3-333--41-413--43361-3631--44822424

BC

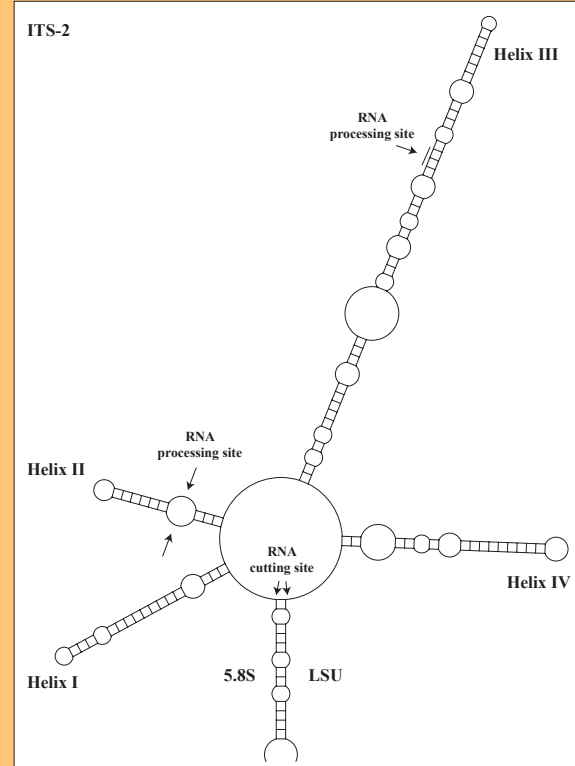
- G AU UUCUAAU U AA A UC G GC C
GGC U-U AGCG-GG UCCC G GGG CA CAG CGGUA GUGA CC-UUCUC \
||| | • |||| | |||| | ||| ||| ||| • | • || || ||||| U
CCG A-G UCGC-CC AGGG C CCC GU GUC GCCGU CGCU GG-AAGAG /
C G -- - - - - - AG C -- A A- C

CAGCAG

Helix IV

A--- C GA CA
GAG CGG GU CGGUGGUUCC A
||| ||| || ||•||| |||
CUC GCC CA GCUACCAAGG U
ACUA C AA AA

AACCAUUC->



Barcode legend:

- 1 = A-U
- 2 = U-A
- 3 = G-C
- 4 = C-G
- 5 = G•U
- 6 = U•G
- 7 = mismatch
- 8 = deletion, single or unpaired bases

Barcode 8
ITS2-J

```

---00000-000-0111-11
---12345-678-9012-34
---63442-154-2453-26

```


->ACACCC

11111
56789

ACC

22222222223
01234567890

AAGAACAGA

333--333-3334-444---44444---45-5555555--5566-666666667777
123--456-7890-123---45678---90-1234567--8901-234567890123
354--484-1343-233---42442---33-4114136--3361-343124888381

BC

GCAAGC

AUGAAACAUC->


$$1 = A - U$$
$$2 = U - A$$

3 = G-C

4 = C-G

$$5 = G \bullet U$$
$$6 = U \bullet G$$

7 = mismatch

8 = deletion, single or unpaired bases

ITS-2 rRNA secondary structure model of
Coccomyxa sp.
strain T4 (BC-9a) HE586516

Barcode 9a
ITS2-K1

5.8S/LSU stem

---00000-000-0111-11
---12345-678-9012-34
---23442-154-2453-26

BC

GUC C G C
UGCCU AGC UCGG UU->
|||| |•| ||•| |•
ACGGA UUG AGUC AG<-
GGA C - C

->CACCCCC

Helix I

11111
56789
64344

BC

- C- UU
UCGCC UCC CUUUGUUU U
•|||| | |•||||| |
GGCGG AGG GGAACAAG A
U AA CC

ACG

Helix II

2222222223
01234567890

65343374443

BC

U GAA C
UGGCGG CCCGGU CUUUC U
••|||| | | | | | | | | | |
GUCGCC GGGCCA GAAAG U
U ACA C

AAGACCAGA

Helix III

33-3333-333444444444---4555---5555--5566-666-666667777
12-3456-789012345678---9012---34567--8901-234-567890123
33-4284-134115384448---3338---14136--3361-313-382488888

- G A AUUC ACAA CU G C GU
GG CU-C AGCAAGG CCC MGG ACAGU GGUA GAG G-UC C
|| || | |||||•| ||| |||• ||•| ||| | || |
CC GA-G UCGUUUC GGG CCC UGUCG CCGU CUC C-AG U
G G A ---- GGC- C- A - AC

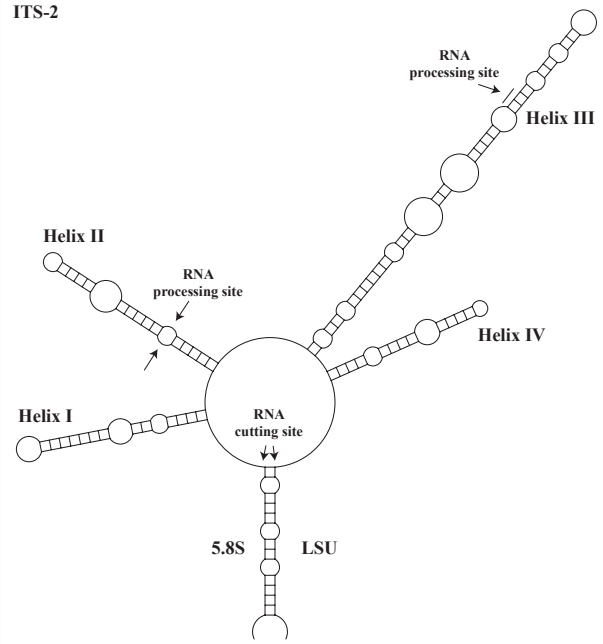
G

Helix IV

C UC U
GAAGG GCUCC GGUUA \
||||• ||||| ||||| G
CUUCU CGAGG CCAAU /
- - G

AUGAAAUAUUC->

ITS-2



Barcode legend:

- 1 = A-U
- 2 = U-A
- 3 = G-C
- 4 = C-G
- 5 = G•U
- 6 = U•G
- 7 = mismatch
- 8 = deletion, single or unpaired bases

BC

M = C or A
(should be a G)

ITS-2 rRNA secondary structure model of
Coccoomyxa sp.
strain CCAP 216/25 (BC-9b) FR850476

Barcode 9b
ITS2-K2

5.8S/LSU stem

---00000-000-0111-11
---12345-678-9012-34
---23442-154-2453-26

BC

GNC C G C *
UGCCU AGC UCGG Uu->
|||| |•| ||•| |•
ACGGA UUG AGUC AG<-
GGA C - C

->CACCCCC

N = here
probably U
* = U is
missing here

Helix I

11111
56789
64344

BC

- C- C CU
UCGCC UCC CUUUGU UC \
•|||| ||| |•|||| | A
GGCGG AGG GGAACA AG /
U AA - CC

ACG

Helix II

2222222223
01234567890

65343374443

BC

U GAA C
UGGCGG CCCGGU CUUUC U
••|||| ||||| |•||| |
GUCGCC GGGCCA GGAAG U
U ACA C

AAGACCAGA

Helix III

33-3333-333444444444---4555---5555--5566-666-666667777
12-3456-789012345678---9012---34567--8901-234-567890123
33-4284-154115384448---3338---14136--3361-313-382488888

BC

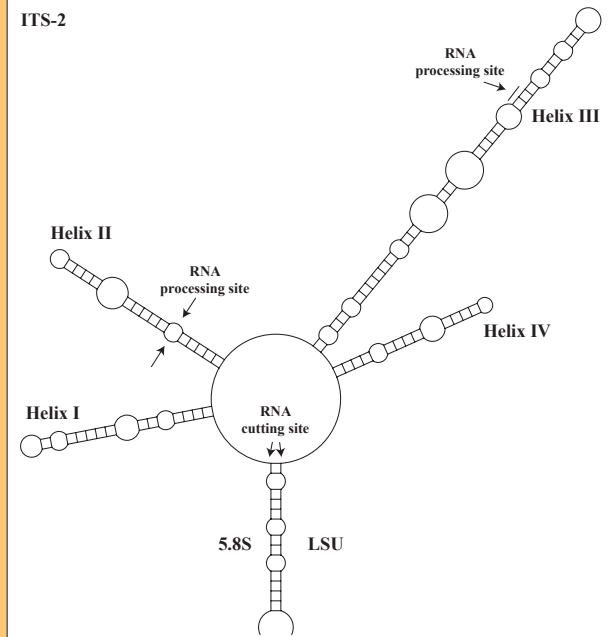
- G A AUUC ACAA CU G C GU
GG CU-C AGCAAGG CCC GGG ACAGU GGUA GAG G-UC C
|| || | |•|||•| ||| |||• ||•| ||| | ||| |
CC GA-G UUGUUUC GGG CCC UGUCG CCGU CUC C-AG U
G G A ---- GGC- C- A - AC

G

Helix IV

C UC U
GAAGG GCUCC GGUUA \
||||• |||| ||||| G
CUUCU CGAGG CCAAU /
- -- G

AUGAAAUAUUC->



Barcode legend:

- 1 = A-U
- 2 = U-A
- 3 = G-C
- 4 = C-G
- 5 = G•U
- 6 = U•G
- 7 = mismatch
- 8 = deletion, single or unpaired bases

ITS-2 rRNA secondary structure model of
Coccomyxa sp.
strain T1 (BC-10) HE586550

Barcode 10
ITS2-L1

5.8S/LSU stem

---00000-000-0111-11
---12345-678-9012-34
---23442-154-2453-26

BC

GUC C G C
UGCCU AGC UCGG UU->
|||| |•| ||•| |•
ACGGA UUG AGUC AG<-
GGA C - C

->CACCCUC

Helix I

11111
56789
64344

BC

C UC
UCGCC CCCC \
•|||| ||||| A
GGCGG GGGGC /
C AC

ACA

Helix II

2222222223
01234567890
65347774443

BC

AGU A
UGGC CCCGGUCG \
••|| ||||| U
GUUG GGGCCAGC /
CCU C

AAGACCAGA

Helix III

33-3333-333444444444---4555--55555--5566-666666667777
12-3456-789012345678---9012--34567--8901-234567890123
33-4284-134115384448---3338--14136--3361-363184488884

BC

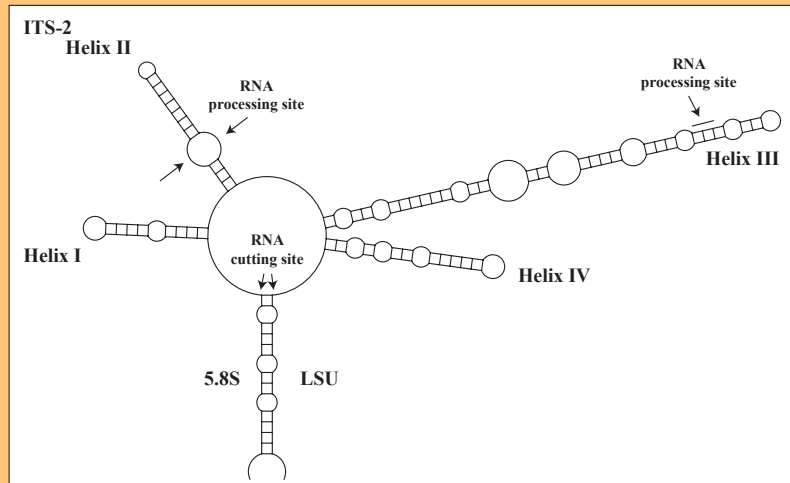
- G A AAUC ACA CU G - G
GG CU-C AGCAAGG CCC GGG ACAGU GGUA GUGA CC----C C
|| || | |||||•||| ||| ||||• ||•| |•|| || | |
CC GA-G UCGUUUC GGG CCC UGUCG CCGU CGCU GG----G A
G G A ---- GGC -- A A A

-

Helix IV

A C G AU
GGU GG GCG CCGGUU \
|•| |•| ||| ||||| G
CUA CU CGC GGCCAA /
- A - GG

UCAUUC->



Barcode legend:

- 1 = A-U
- 2 = U-A
- 3 = G-C
- 4 = C-G
- 5 = G•U
- 6 = U•G
- 7 = mismatch
- 8 = deletion, single or unpaired bases

ITS-2 rRNA secondary structure model of
Coccomyxa sp.
strain T3 (BC-10) HE586515

Barcode 10
ITS2-L1

5.8S/LSU stem

---00000-000-0111-11
---12345-678-9012-34
---23442-154-2453-26

BC

GUC C G C
UGCCU AGC UCGG UU->
|||| |•| ||•| |•
ACGGA UUG AGUC AG<-
GGA C - C

->CACCCUC

Helix I

11111
56789
64344

BC

C UC
UCGCC CCCC \
•|||| ||||| A
GGCGG GGGG /
C AC

ACA

Helix II

2222222223
01234567890
65347774443

BC

AGU A
UGGC CCCGGUCG \
••|| ||||| U
GUCC GGGCCAGC /
CCU C

AAGACCAGA

Helix III

33-3333-333444444444---4555--55555--5566-666666667777
12-3456-789012345678---9012--34567--8901-234567890123
33-4284-134115384448---3338--14136--3361-363184488884

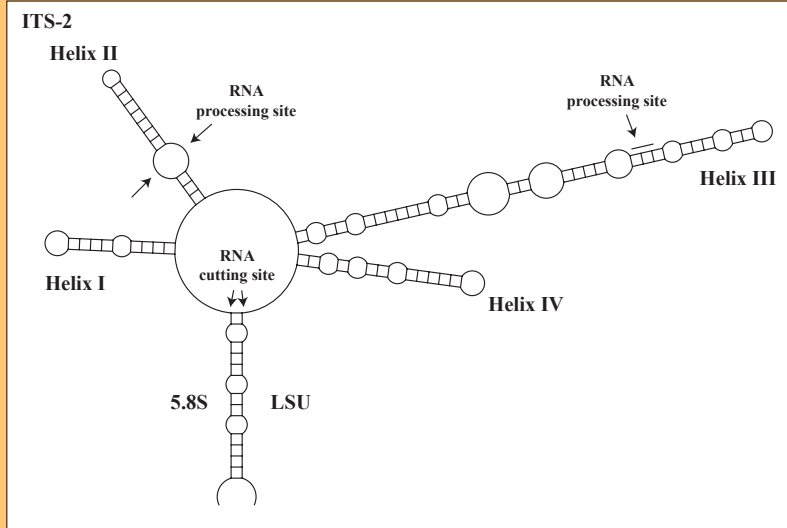
BC

- G A AAUC ACA CU G - G
GG CU-C AGCAAGG CCC GGG ACAGU GGUA GUGA CC----C C
|| || | |||||• ||| ||| ||||• ||•| |•|| || |
CC GA-G UCGUUUC GGG CCC UGUCG CCGU CGCU GG----G A
G G A ---- GGC -- A A A

Helix IV

A C G AU
GGU GG GCG CCGGUU \
|•| |•| ||| ||||| G
CUA CU CGC GGCCAA /
- A - GG

UCAUUC->



Barcode legend:

- 1 = A-U
- 2 = U-A
- 3 = G-C
- 4 = C-G
- 5 = G•U
- 6 = U•G
- 7 = mismatch
- 8 = deletion, single or unpaired bases

ITS-2 rRNA secondary structure model of
Coccomyxa sp.
strain ACCV1 (BC-10) HE617183

Barcode 10
ITS2-L2

5.8S/LSU stem

---00000-000-0111-11
---12345-678-9012-34
---23442-154-2453-26

BC

GUC C G C
UGCCU AGC UCGG UU->
|||| |•| ||•| |•
ACGGA UUG AGUC AG<-
GGA C - C

->CACCCUC

Helix I

11111
56789

64344

BC

C- CU
UCGCC CUCCC U
•|||| ||||| |
GGCGG GAGGG C
CA UG

ACA

Helix II

22222222223
01234567890

65347774443

BC

AGU U
UGGC CCCGGUCGC U
••|| ||||||•| |
GU CG GGGCCAGUG C
CCU G

AAGGCCAGA

Helix III

33-3333-333444444444---4555--55555--5566-666666667777
12-3456-789012345678---9012--34567--8901-234567890123

33-4284-134115384448---3338--14136--3361-363184488884

BC

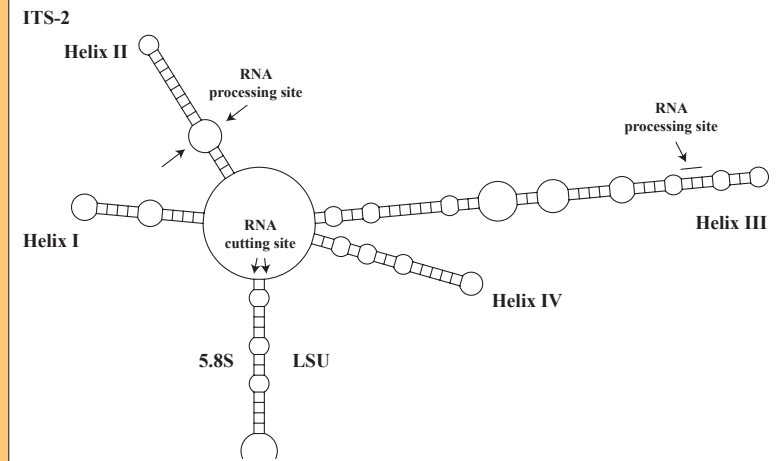
- G A AAUC ACA CU G - G
GG CU-C AGCAAGG CCC GGG ACAGU GGUA GUGA CC----C C
|| || | |||||•| ||| ||| ||||• ||•| |•|| || | |
CC GA-G UCGUUUC GGG CCC UGUCG CCGU CGCU GG----G A
G G A ---- GGC -- A A A

-

Helix IV

A C U AC
GGA GG GCG CCGGUU \
•|| || ||| ||||| G
UCU CC CGC GGCCAA /
A C - GG

CAUUC->



Barcode legend:

- 1 = A-U
- 2 = U-A
- 3 = G-C
- 4 = C-G
- 5 = G•U
- 6 = U•G

7 = mismatch

8 = deletion, single or unpaired bases

ITS-2 rRNA secondary structure model of
Coccomyxa sp.
strain UTEX SNO83 (BC-11) HE586506 *

Barcode 11
ITS2-M

5.8S/LSU stem

---00000-000-0111-11
---12345-678-9012-34
---23442-154-2453-26

BC

GCC C G -
UGCCU AGC UCGG UU->
|||| |•| ||•| |•
acgga uug aguc ag<-
gga c - c

->CCACCC

Helix I

1111-1
5678-9
6434-4

BC

- - - UU
UCGC C UCUC CCAC \
•||| | |||| |||| C
GGCG G AGAG GGUG /
A A U GC

ACC

Helix II

2222222223
01234567890
65344374443

BC

U CA
UGGCCG CCCGAUC \
••||| | ||||| G
GUCGGC GGGCUAG /
U CG

AAGCGCAGA

Helix III

333-333-333444-44444-----4-455--55-555--55566-6666--66667777
123-456-789012-34567-----8-901--23-456--78901-2345--67890123
334-286-134333-32444-----3-333--41-413--43361-3631--43828484

BC

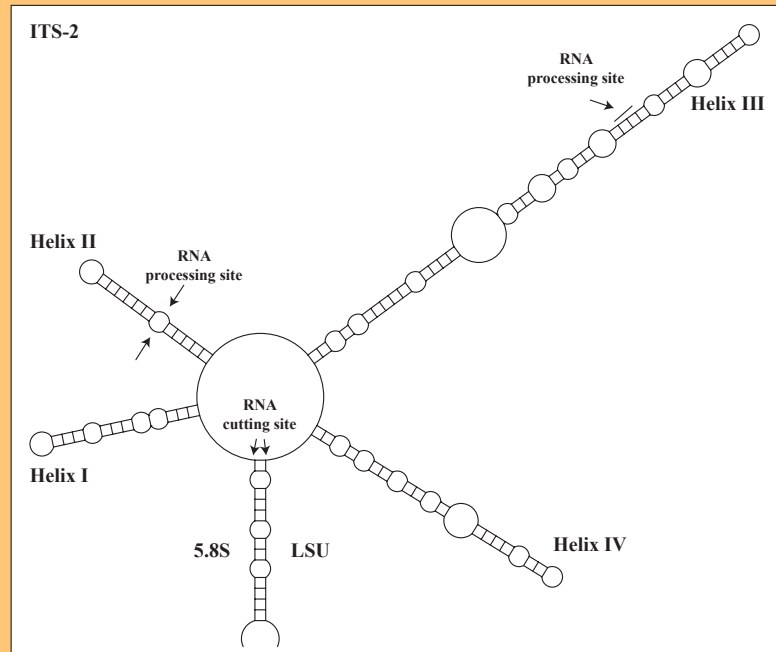
- G A UCCAAU C AA A AC G GC G
GGC U-U AGCGGG GUCCC G GGG CA CAG CGGUA GUGA CG-U-C-C G
||| | • ||||| ||||| | ||| || ||| |||•| •|| ||| | | |
CCG A-G UGCCCC CAGGG C CCC GU GUC GCCGU CGCU GC-A-G-G A
C G - ----- - GG C -- A A- A

GAGCA

Helix IV

- C G C --- G G
GGA GA GGU CGG UC GCGAC GGG C
||| || ||| ||| || ||||| ||| |
CCU CU CCA GCC AG CGCUG CCC G
A A - - CGA A A

AUuc->



Barcode legend:

- 1 = A-U
- 2 = U-A
- 3 = G-C
- 4 = C-G
- 5 = G•U
- 6 = U•G
- 7 = mismatch
- 8 = deletion, single or unpaired bases

ITS-2 rRNA secondary structure model of
Coccomyxa sp.
strain C4 (BC-12) HE586508 *

Barcode 12
ITS2-N

5.8S/LSU stem

---00000-000-0111-11
---12345-678-9012-34
---23442-154-2453-26

BC

GCC C G -
UGCCU AGC UCGG UU->
|||| |•| ||•| |•
acgga uug aguc aG<-
gga c - c

->CCACCC

Helix I

1111-1
5678-9
6434-4

BC

- CUC- A
UCGC CUCAC CC U
•||| ||||| || |
GGCG GAGUG GG C
A CGUU C

ACC

Helix II

2222222223
01234567890
65344374443

BC

U CC
UGGCCG CCCGAUC \
••||| ||||| U
GUCGGC GGGCUAG /
U CG

AAGCGCAGA

Helix III

333-333-333444-44444-----4-455--55-555--55566-6666--6666-7777
123-456-789012-34567-----8-901--23-456--78901-2345--6789-0123
334-286-134333-32444-----3-333--41-413--43361-3631--4324-2424

BC

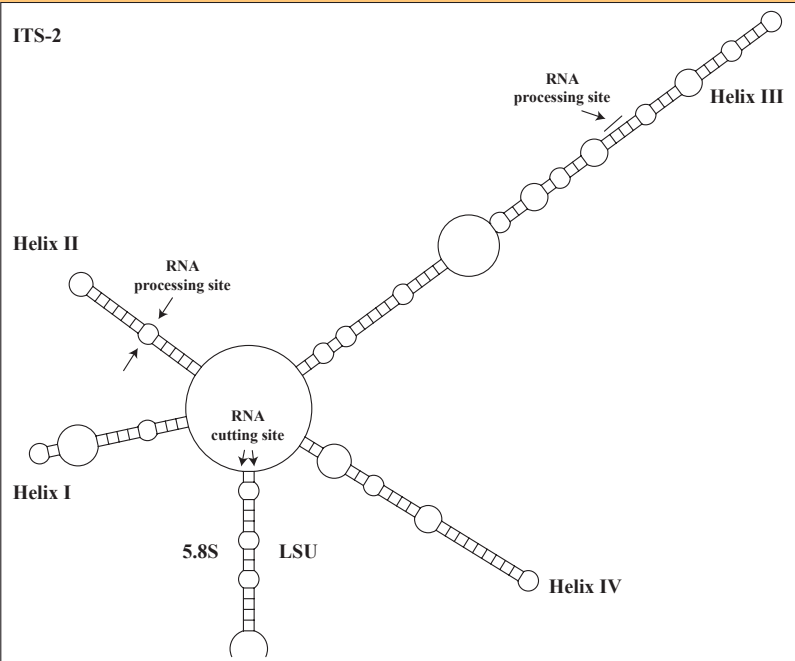
- G A UUCUAAC U AA A AC G GC C U
GGC U-U AGCGGG GUCCC G GGG CA CAG CGGUA GUGA CGUC UCUC C
||| |•| ||||| ||||| | ||| || ||| |||•| |•|| |||| ||||| |
CCG A-G UGCCCC CAGGG C CCC GU GUC GCCGU CGCU GCAG AGAG C
C G - ----- - GG C -- A A- - G

GAGCA

Helix IV

GAC G -- G
GGA GGU CGGCU CGCGACGGGG A
||| |•| |||||•| ||||| ||||| |
CCU CUA GCCGG GCGCUGCCCC G
A-- A CG A

AUUC->



Barcode legend:

- 1 = A-U
- 2 = U-A
- 3 = G-C
- 4 = C-G
- 5 = G•U
- 6 = U•G
- 7 = mismatch
- 8 = deletion, single or unpaired bases