

A.
68.8% identity in 141 nt overlap
A. cinerea tRNA^{Pro}-ND6
A. cinerea NC1 (26-157)

tRNA^{Pro} | |ND6

CAACTCCCAAAGCTGGCATTTTATACTAACTACTTTC-TGAACTCCGTACCAA-CCTAACTGCCGAAGAGCCCCACGA
.....C.....-.....CC.....-.....C...CA.C.A...A.AC.T...A...C...CA...-...TA...A.A..

A. cinerea tRNA^{Pro}-ND6
A. cinerea NC1 (26-157)

GATAACCCCGCCTAACTCTAACACAACAAAGTTAACAGTAAACCCTCAACCTCCCA
A...A.T.A.....C--.....G.....G.C..C..-C.T..C..C...A.A.

85.7% identity in 42 nt overlap
A. cinerea ND6
A. cinerea NC1 (176-217)

ND6|

CACAAAGCATAGCCCTAAAAAATTACAAAGTAAGTCATAGC
.T...CT.T.A.....C.....

72.3% identity in 148 nt overlap
A. cinerea Cytb-tRNA^{Thr}
A. cinerea NC2 (13-154)

AGCCTCCATTACCTACTTCAATCCTCCTAATCCTATTCC-CCATTACTGGAGCCCTAGAAAACAAAATACTAAATTAC
.T..A..TCCG..C.....-...CC...CTC...T...C.....A...-.....C...CC..

Cytb | |tRNA^{Thr}

TAAACCACCTCTAATAGTTTATTAAAAACATTGGTCTTGTAACCAAGAATGAAGACTATACCCCTTC
C...T...-...C.A...C...G.G...AAC.C..CT.....A...C...A.C.

A. cinerea Cytb-tRNA^{Thr}
A. cinerea NC2 (13-154)

B.
63.0% identity in 208 nt overlap
A. purpurea ND6
A. purpurea NC1 (25-218)

CACAAAACTACTAATCCACCCAGATACACCAGAAACAGCACCAGCGAAATAAAGAAACCCCAAACTCAACAACC
.....CT.C..ATCA.GC...T.CC.G..G..C-...G.A.C.ACA.A.C.G.C..C.CC..A...C.AAA.TA..A.

A. purpurea ND6
A. purpurea NC1 (25-218)

ACCCACACCCTACAACAGATGCCAGAATAAACCAACAACC--CCATAATAGGGTGACGGGTTGGAAGCAACCGCTAGTC
.T...-.....-.....T...C..CTT..AG..CT..AA..GA..C.....A.AC.....A...T.C..CT

ND6 |

CACCTAACACAAAACATAACCCCTAAAAAACTACAAAATAAGTCATAG
...C.....-.....C.....-.....C...C..

68.0% identity in 153 nt overlap
A. purpurea Cytb-tRNA^{Thr}
A. purpurea NC2 (12-152)

AACTA-GCCTCCGTACCTACTTTCATAATCCTCCTGATCTATTCCCCATTACTGGAGCCCTAGAAAACAAAATACTAA
..A..T...T.A...C...CC..C..A..-.....C...C.A.....-.....T...C

Cytb | |tRNA^{Thr}

CTACTAAATTACTCTAATAGTTTACTAAAAACATTGGTCTTGTA-ACCAAAGGATGAAGACTATACCCCTTC
...C...CC..C...C.AC.....-.....AAC.C...T.G...A..AC..CCAC.CT...A..

A. purpurea Cytb-tRNA^{Thr}
A. purpurea NC2 (12-152)

C.
76.3% identity in 76 nt overlap
A. modesta tRNA^{Pro}
A. modesta NC1 (39-114)

tRNA^{Pro} |

AGAAAGAGAGAGCTCAAACCTCCATCTCCAACCTCCAAAGCTGGTATTTTATACT--AACTACTTTCTGAACCTC
..GG.A.....T.....C.....A...C.CC....TG...CG..CC..T.C.C..

68.5% identity in 143 nt overlap
A. modesta Cytb-tRNA^{Thr}
A. modesta NC2 (14-145)

AACTAGCCTCCATCACCTACTTTCATAATCCTACTAATCCT-AT-TC-CCCATCACTGGAGCCCTAGAAAATAAAATACTA
...ACA.....TC..-..C...C.....-..C.GC...T..G..T...C..A.A.....C.....-.....AA.

Cytb | |tRNA^{Thr}

AACTACTAAACCACTCTAATAGTTTACCAAAAACATTGGTCTTGTAAGCAAGAAATGAAGGC
C.....-...C...C..C...T.....A.C.C.AC.AG.....C..A..A..

A. modesta Cytb-tRNA^{Thr}
A. modesta NC2 (14-145)

D.
63.6% identity in 231 nt overlap

|tRNA^{Pro} | |tRNA^{Pro}|

A. intermedia tRNA^{Pro}-ND6
A. intermedia NC1 (18-243)

ACTCAGAAAGAGAGAGCTCAAACCTCCATCTC---CAACTCCCAAAGCTGGCTATTTTACTACTAACTACTTTCTGAAC
.G...A.....A.CT.....T...ATCT.....A...-...C.....T..C..CA.T.

|ND6

A. intermedia tRNA^{Pro}-ND6
A. intermedia NC1 (18-243)

TCCACACTAAACCTAAGTCCGGAAGAGCCCCACGAGATAACCCCGCCTAACTCTAACACGACAACAGAG--TTAAC
.T...TC.....TCA..TA...A.T...A.A.C.....A.C.AT..AAGC.GCAC...C..TGTCC.C..G

A. intermedia tRNA^{Pro}-ND6
A. intermedia NC1 (18-243)

AACAGCCC--CCAACCTCCTACTAAA-----AACATCCCACCTCCATGCGAATAAAAACATAGCTACACCTC
...A..TAA.A..GAG.A...T..CCCCC..T.A..T...AGGCCT.C.T...C.....-...T..A...

63.6% identity in 129 nt overlap
A. intermedia Cytb-tRNA^{Thr}
A. intermedia NC2 (16-137)

Cytb | |tRNA^{Thr}

TTCCCATCACTGGAGCCTTAGAAAATAAAATACTAACTACTAAACCACTCTAATAGTTTACTAAAAACATTGGTCTTG
.A...T...TCCCA..CC.C..CTCC.G.A.AC.....-..G.....C.C..C...G.CA.AC---C.A

tRNA^{Thr}|

A. intermedia Cytb-tRNA^{Thr}
A. intermedia NC2 (16-137)

TAAACCAAGAATGAAGACTATACCCCTTCTTAGAGT-TAGACACCCAC
C.....G...A..C.-.....-.....ACC..A.....

E.
60.5% identity in 162 nt overlap
A. ibis ND6 (324-482)
A. ibis NC1 (2-156)

AACTACTAATCCACCCAAGTACACCAAAAACAACCCAATGAGATAAAAGAAACACCCAAGCTCAACAACCATCCA
.....T.C.C.CAG...T...AAG.C...CTC.ACC...AC.GC...C...TC.TTA...-CT.....-...G...

A. ibis ND6 (324-482)
A. ibis NC1 (2-156)

CACCCA-AC--AACAGACGCCAAAACCAACCAACCCCATAGTAAGGTGACGGATTGGAAGCAACTGCCAACCCACCTA
T.A...C..TG...TT..A.--CT...G.T.C.....-...AC.GAA.CG..A.GCT...-T.....T.....C..

62.6% identity in 131 nt overlap
A. ibis Cytb-tRNA^{Thr}
A. ibis NC2 (33-146)

Cytb | |tRNA^{Thr}

CTACTTTACGATCCTCCTAGTCTTATCCCTATCACTGGGGCCTTAGAGAACAAAGATACTAACTACTAACCCTCTAAT
.....-.....C.AC.....-.....A---A.TCC.A.A...AGC...-...C.....T..C..C..

A. ibis Cytb-tRNA^{Thr}
A. ibis NC2 (33-146)

-AGTTTATTAAAAACATTGGTCTTGTAACCAAGAATGAAGACTATACCC
C.A..C.CC.....CAAA.-...-G.....-...A..A..C.CG...