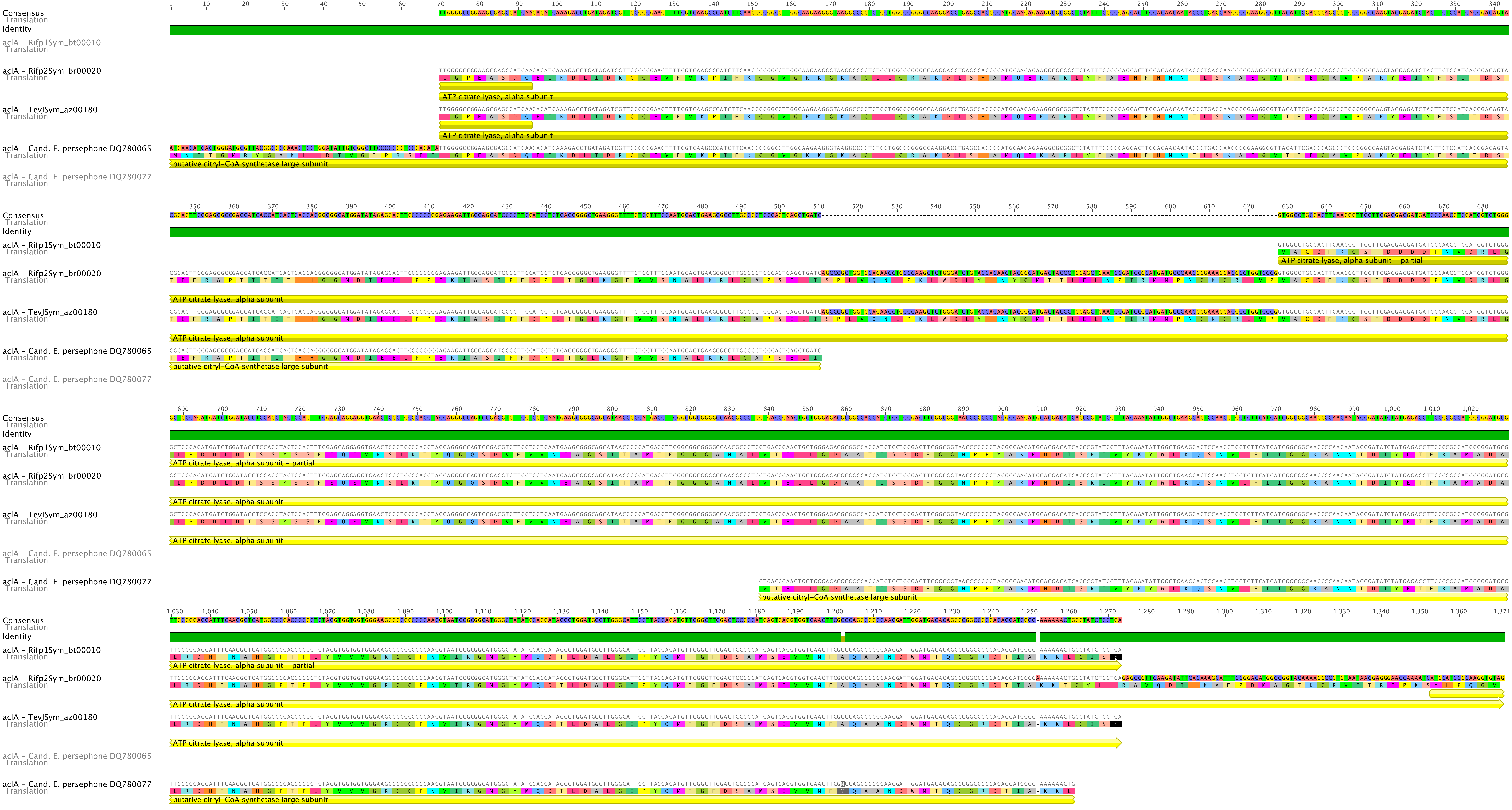
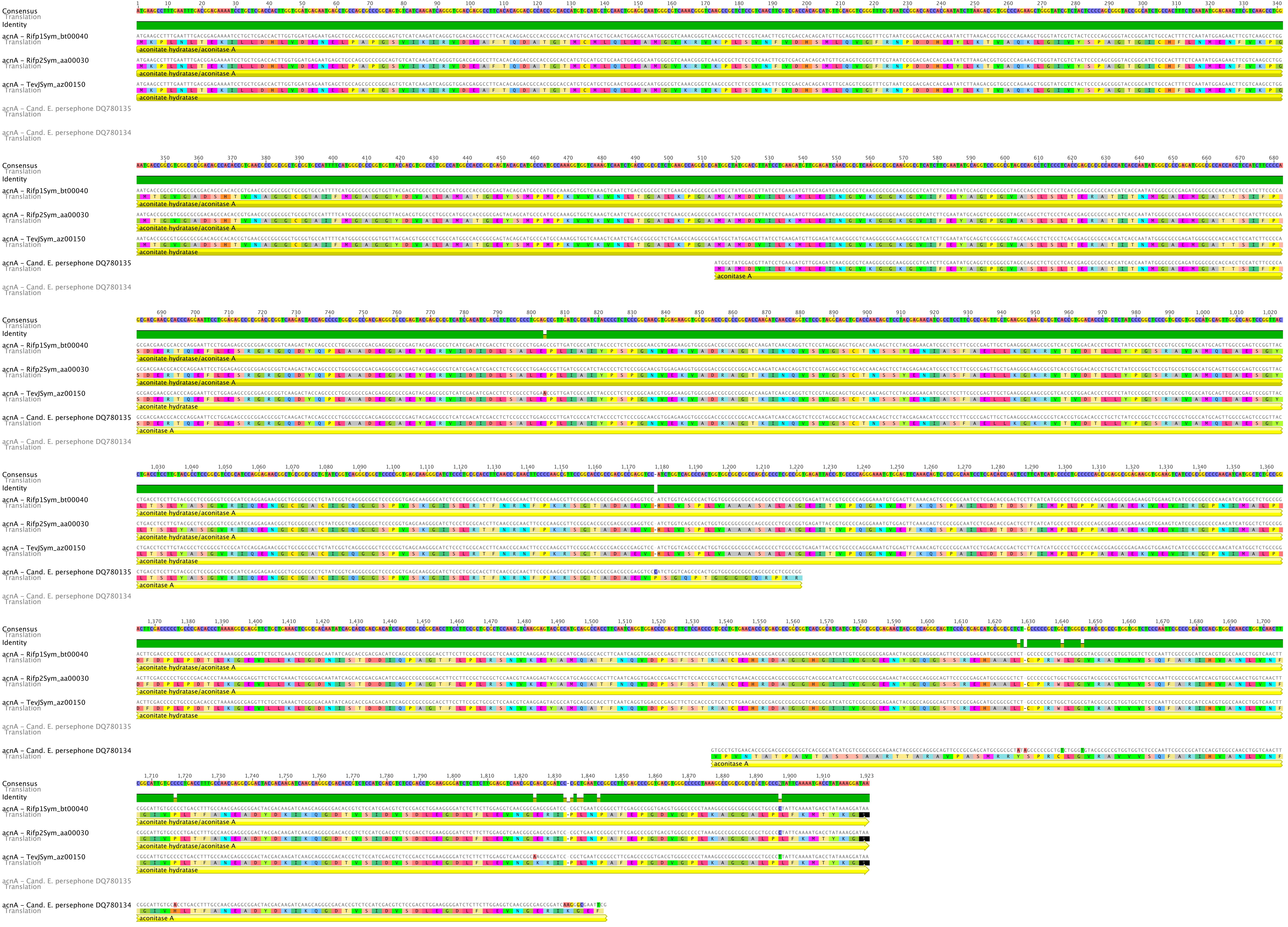
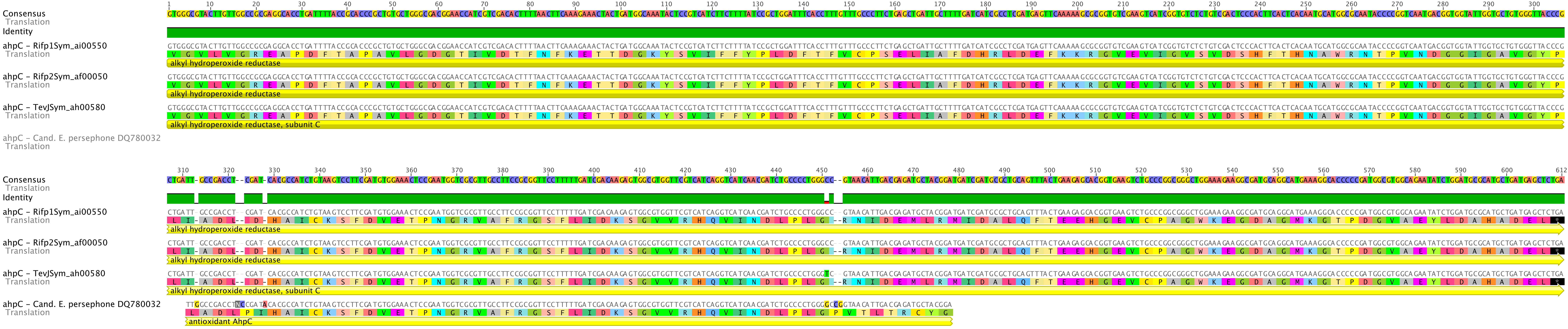
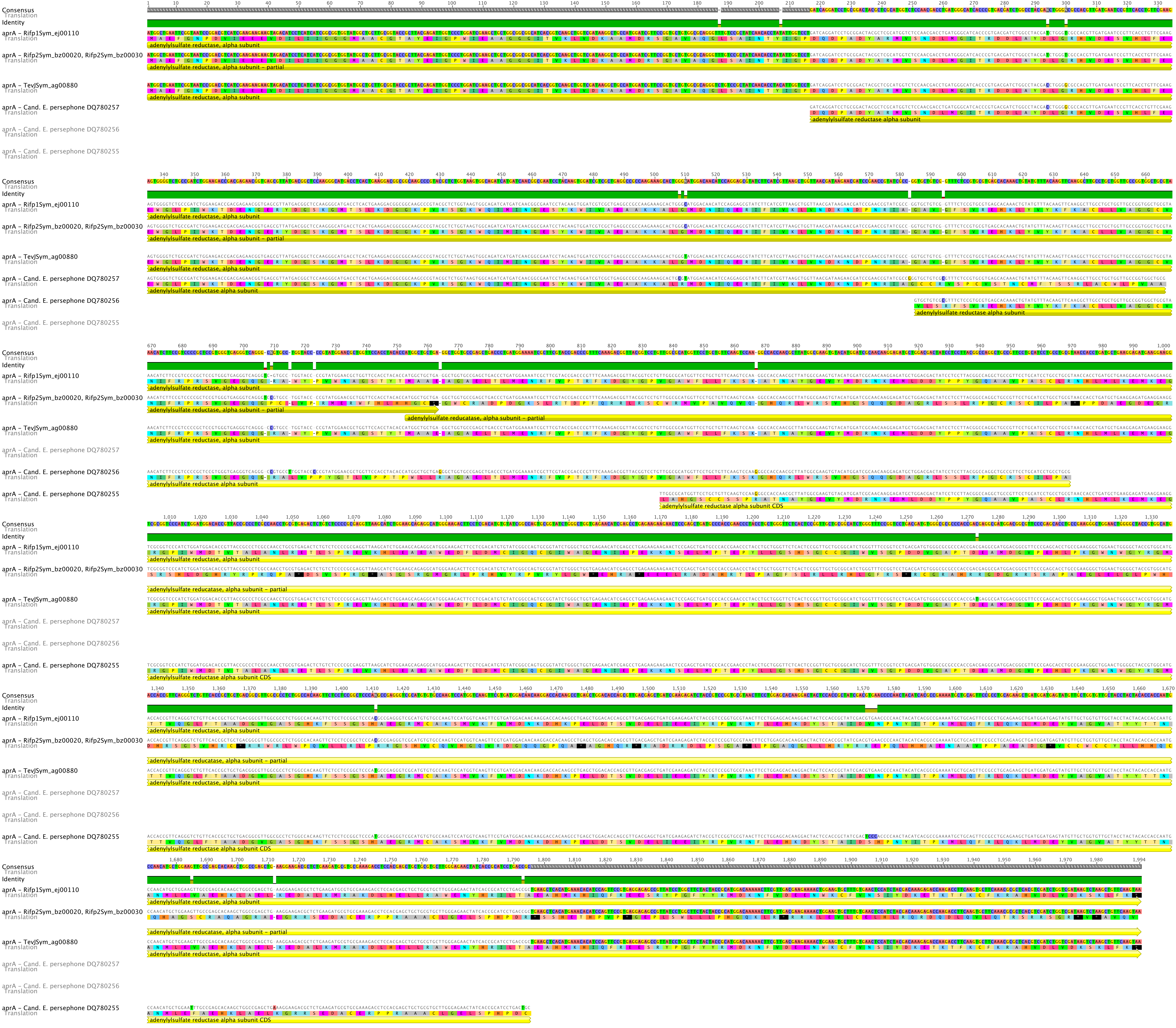
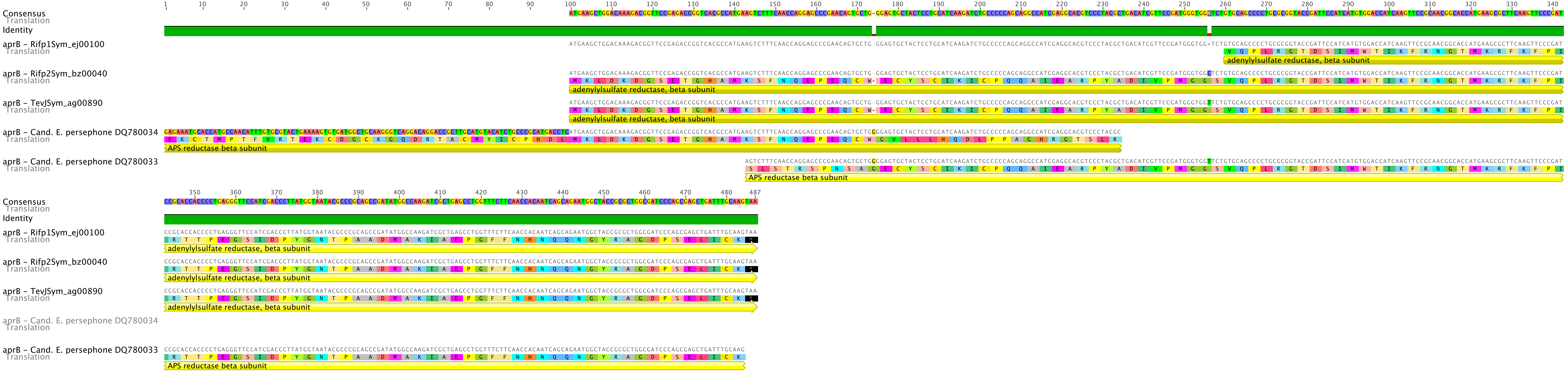

Consensus
Translation
Identity
aclA – Rifp1Sym_bt00010
Translation
aclA – Rifp2Sym_br00020
Translation
aclA – TevJSym_az00180
Translation
aclA – Cand. E. persephone DQ780065
Translation
aclA – Cand. E. persephone DQ780077
Translation
ATP citrate lyase, alpha subunit
ATP citrate lyase, alpha subunit – partial
putative citryl-CoA synthetase large subunit
1
10
340
350
680
690
1,020
1,030
1,371


Consensus
Translation
Identity
aclB - Rifp1Sym_bt00020
Translation
ATP citrate lyase, beta subunit
aclB - Rifp2Sym_aa00010
Translation
ATP citrate lyase, beta subunit - partial
aclB - Rifp2Sym_br00010
Translation
aclB - TevJSym_az00170
Translation
ATP citrate lyase, beta subunit
2,718


Consensus
Translation
Identity
acnA – Rifp1Sym_bt00040
Translation
aconitate hydratase/aconitase A
acnA – Rifp2Sym_aa00030
Translation
aconitate hydratase/aconitase A
acnA – TevJSym_az00150
Translation
aconitate hydratase
acnA – Cand. E. persephone DQ780135
Translation
aconitase A
acnA – Cand. E. persephone DQ780134
Translation
aconitase A
1
340
350
680
690
1,020
1,030
1,360
1,370
1,700
1,710
1,923


Consensus
Translation
Identity
ahpC – Rifp1Sym_ai00550
Translation
alkyl hydroperoxide reductase
ahpC – Rifp2Sym_af00050
Translation
alkyl hydroperoxide reductase
ahpC – TevJSym_ah00580
Translation
alkyl hydroperoxide reductase, subunit C
ahpC – Cand. E. persephone DQ780032
Translation
1
10
20
30
40
50
60
70
80
90
100
110
120
130
140
150
160
170
180
190
200
210
220
230
240
250
260
270
280
290
300
Consensus
Translation
Identity
ahpC – Rifp1Sym_ai00550
Translation
alkyl hydroperoxide reductase
ahpC – Rifp2Sym_af00050
Translation
alkyl hydroperoxide reductase
ahpC – TevJSym_ah00580
Translation
alkyl hydroperoxide reductase, subunit C
ahpC – Cand. E. persephone DQ780032
Translation
antioxidant AhpC
310
320
330
340
350
360
370
380
390
400
410
420
430
440
450
460
470
480
490
500
510
520
530
540
550
560
570
580
590
600
612


Consensus
Translation
Identity
aprA – Rifp1Sym_ej00110
aprA – Rifp2Sym_bz00020, Rifp2Sym_bz00030
aprA – TevJSym_ag00880
aprA – Cand. E. persephone DQ780257
aprA – Cand. E. persephone DQ780256
aprA – Cand. E. persephone DQ780255
adenylylsulfate reductase, alpha subunit
adenylylsulfate reductase, alpha subunit – partial
adenylylsulfate reducatase, alpha subunit – partial
adenylylsulfate reductase alpha subunit
adenylylsulfate reductase alpha subunit CDS



Consensus
Translation
ATGAAGCTGGACAAAGACGGTTCCGAGACCGGTCACGCCATGAAGTCTTTCAACCAGGAGCCCGAACAGTGCTG-GGAGTGCTACTCCTGCATCAAGATCTGCCCCCAGCAGGCCATCGAGGCACGTCCCTACGCTGACATCGTTCCGATGGGTGGNTCTGTGCAGCCCCTGCGCGGTACCGATTCCATCATGTGGACCATCAAGTTCCGCAACGGCACCATGAAGCGCTTCAAGTTCCCGAT

Identity

aprB – Rifp1Sym_ej00100
Translation
ATGAAGCTGGACAAAGACGGTTCCGAGACCGGTCACGCCATGAAGTCTTTCAACCAGGAGCCCGAACAGTGCTG-GGAGTGCTACTCCTGCATCAAGATCTGCCCCCAGCAGGCCATCGAGGCACGTCCCTACGCTGACATCGTTCCGATGGGTGG-TCTGTGCAGCCCCTGCGCGGTACCGATTCCATCATGTGGACCATCAAGTTCCGCAACGGCACCATGAAGCGCTTCAAGTTCCCGAT
V Q P L R G T D S I M W T I K F R N G T M K R F K F P I
adenylylsulfate reductase, beta subunit

aprB – Rifp2Sym_bz00040
Translation
ATGAAGCTGGACAAAGACGGTTCCGAGACCGGTCACGCCATGAAGTCTTTCAACCAGGAGCCCGAACAGTGCTG-GGAGTGCTACTCCTGCATCAAGATCTGCCCCCAGCAGGCCATCGAGGCACGTCCCTACGCTGACATCGTTCCGATGGGTGGCTCTGTGCAGCCCCTGCGCGGTACCGATTCCATCATGTGGACCATCAAGTTCCGCAACGGCACCATGAAGCGCTTCAAGTTCCCGAT
M K L D K D G S E T G H A M K S F N Q E P E Q C W - E C Y S C I K I C P Q Q A I E A R P Y A D I V P M G G S V Q P L R G T D S I M W T I K F R N G T M K R F K F P I
adenylylsulfate reductase, beta subunit

aprB – TevJSym_ag00890
Translation
ATGAAGCTGGACAAAGACGGTTCCGAGACCGGTCACGCCATGAAGTCTTTCAACCAGGAGCCCGAACAGTGCTG-GGAGTGCTACTCCTGCATCAAGATCTGCCCCCAGCAGGCCATCGAGGCACGTCCCTACGCTGACATCGTTCCGATGGGTGGTTCTGTGCAGCCCCTGCGCGGTACCGATTCCATCATGTGGACCATCAAGTTCCGCAACGGCACCATGAAGCGCTTCAAGTTCCCGAT
M K L D K D G S E T G H A M K S F N Q E P E Q C W - E C Y S C I K I C P Q Q A I E A R P Y A D I V P M G G S V Q P L R G T D S I M W T I K F R N G T M K R F K F P I
adenylylsulfate reductase, beta subunit

aprB – Cand. E. persephone DQ780034
Translation
GAGAAATGCACCATGCCAACATTTGTGCGTACTGAAAAGTGTGATGGCTGCAAGGGTCAGGACAGGACCGCTTGCATGTACATCTGCCCGCATGACCTCATGAAGCTGGACAAAGACGGTTCCGAGACCGGTCACGCCATGAAGTCTTTCAACCAGGAGCCCGAACAGTGCTGGGGAGTGCTACTCCTGCATCAAGATCTGCCCCCAGCAGGCCATCGAGGCACGTCCCTACGC
E K C T M P T F V R T E K C D G C K G Q D R T A C M Y I C P H D L M K L D K D G S E T G H A M K S F N Q E P E Q C W G V L L L H Q D L P P A G H R G T S L R
APS reductase beta subunit

aprB – Cand. E. persephone DQ780033
Translation
AGTCTTTCAACCAGGAGCCCGAACAGTGCTGGGGAGTGCTACTCCTGCATCAAGATCTGCCCCCAGCAGGCCATCGAGGCACGTCCCTACGCTGACATCGTTCCGATGGGTGGTTCTGTGCAGCCCCTGCGCGGTACCGATTCCATCATGTGGACCATCAAGTTCCGCAACGGCACCATGAAGCGCTTCAAGTTCCCGAT
S L S T R S P N S A G E C Y S C I K I C P Q Q A I E A R P Y A D I V P M G G S V Q P L R G T D S I M W T I K F R N G T M K R F K F P I
APS reductase beta subunit

Consensus
Translation
CCGCACCACCCCTGAGGGTTCCATCGACCCTTATGGTAATACGCCCGCAGCCGATATGGCCAAGATCGCTGAGCCTGGTTTCTTCAACCACAATCAGCAGAATGGCTACCGCGCTGGCGATCCCAGCGAGCTGATTTGCAAGTAA

Identity

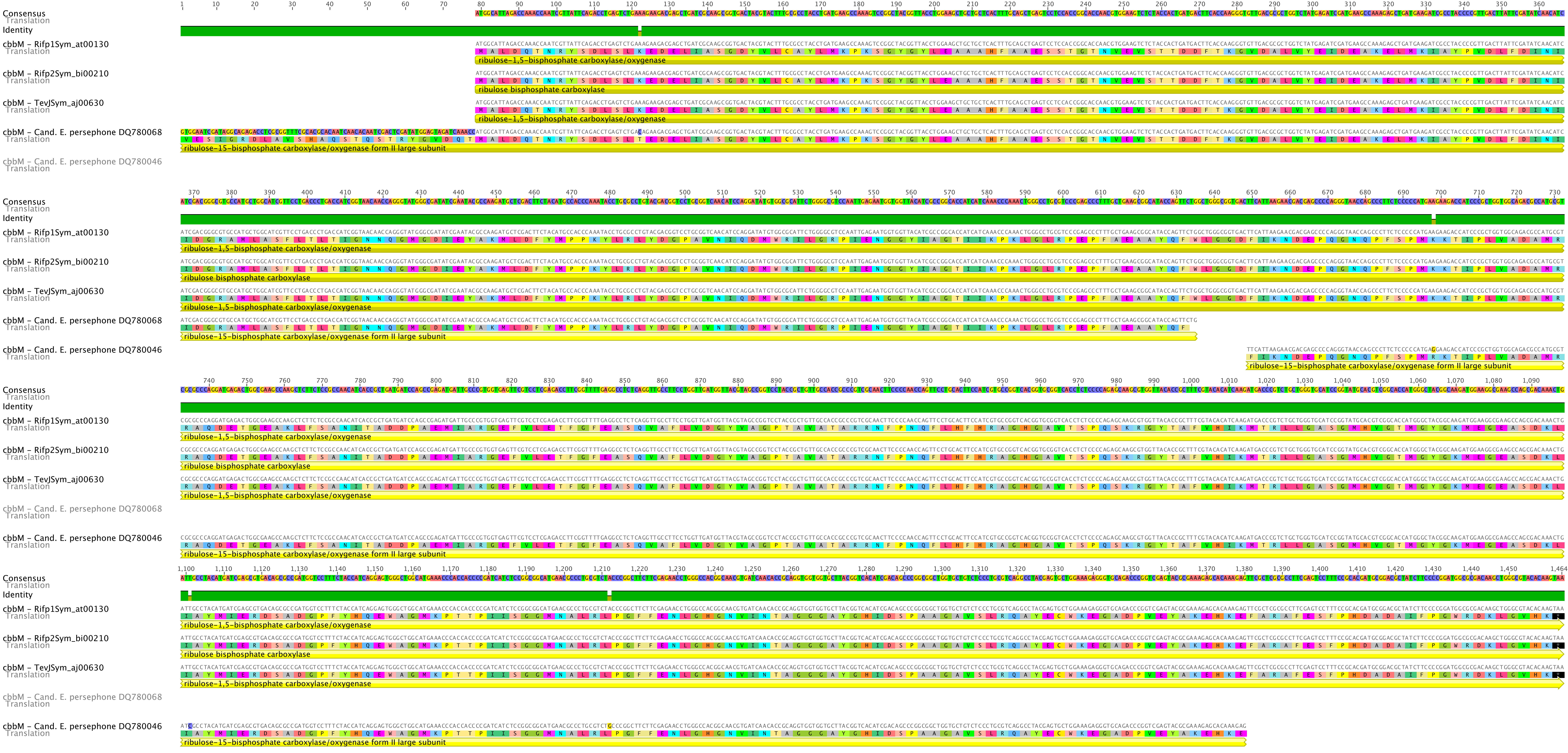
aprB – Rifp1Sym_ej00100
Translation
CCGCACCACCCCTGAGGGTTCCATCGACCCTTATGGTAATACGCCCGCAGCCGATATGGCCAAGATCGCTGAGCCTGGTTTCTTCAACCACAATCAGCAGAATGGCTACCGCGCTGGCGATCCCAGCGAGCTGATTTGCAAGTAA
R T T P E G S I D P Y G N T P A A D M A K I A E P G F F N H N Q Q N G Y R A G D P S E L I C K *
adenylylsulfate reductase, beta subunit

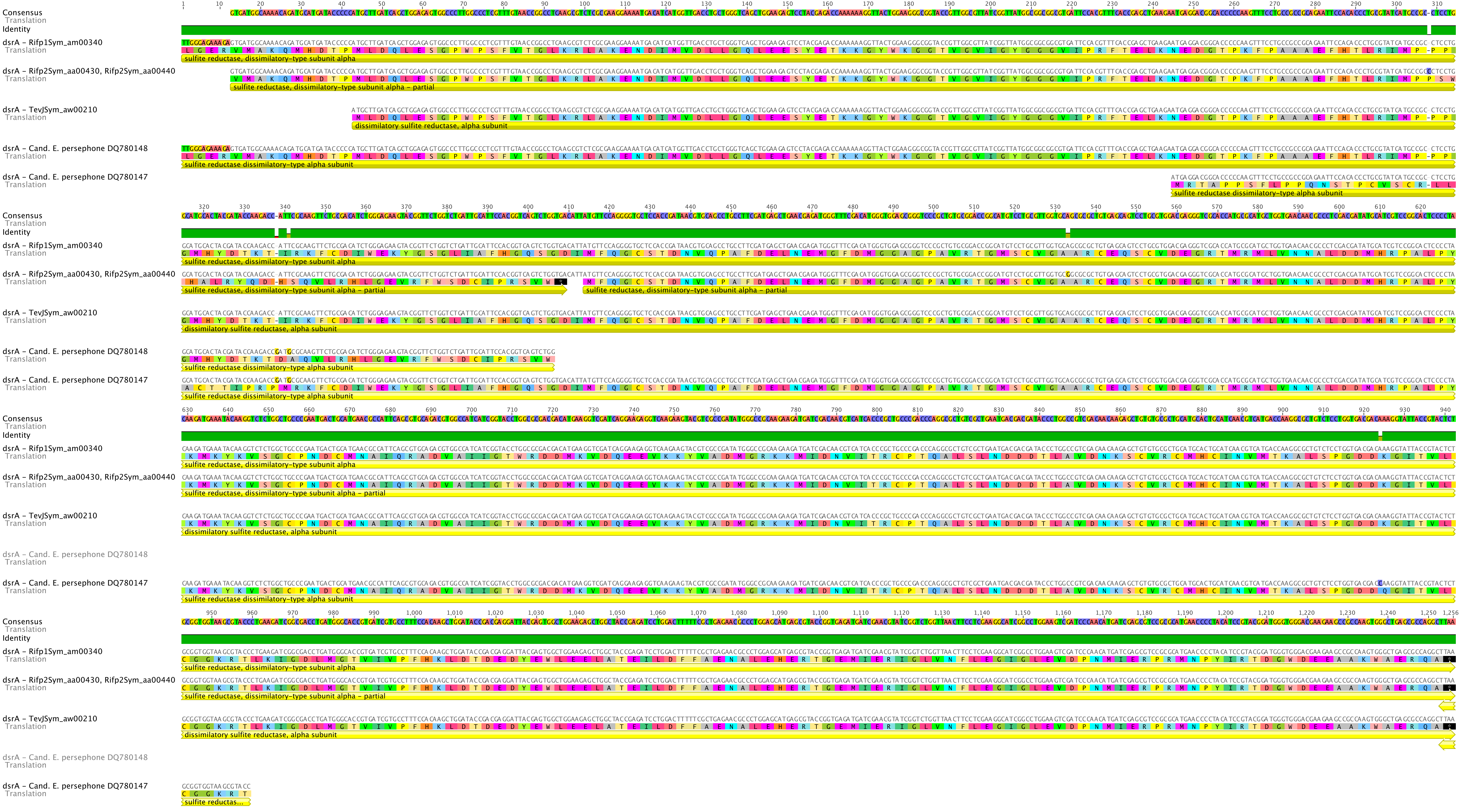
aprB – Rifp2Sym_bz00040
Translation
CCGCACCACCCCTGAGGGTTCCATCGACCCTTATGGTAATACGCCCGCAGCCGATATGGCCAAGATCGCTGAGCCTGGTTTCTTCAACCACAATCAGCAGAATGGCTACCGCGCTGGCGATCCCAGCGAGCTGATTTGCAAGTAA
R T T P E G S I D P Y G N T P A A D M A K I A E P G F F N H N Q Q N G Y R A G D P S E L I C K *
adenylylsulfate reductase, beta subunit

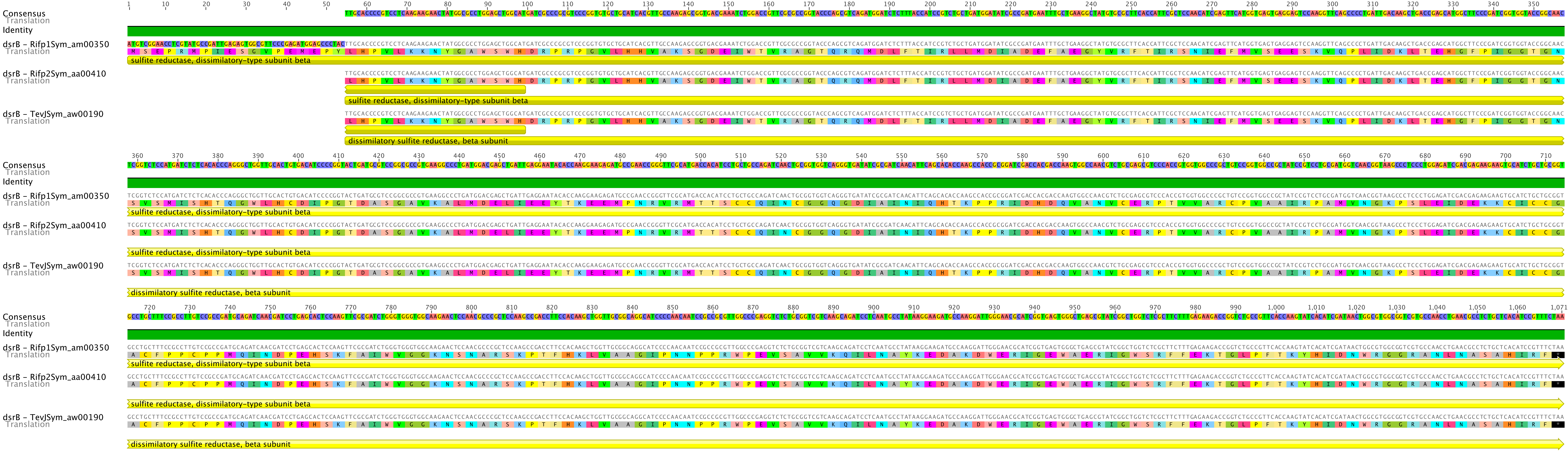
aprB – TevJSym_ag00890
Translation
CCGCACCACCCCTGAGGGTTCCATCGACCCTTATGGTAATACGCCCGCAGCCGATATGGCCAAGATCGCTGAGCCTGGTTTCTTCAACCACAATCAGCAGAATGGCTACCGCGCTGGCGATCCCAGCGAGCTGATTTGCAAGTAA
R T T P E G S I D P Y G N T P A A D M A K I A E P G F F N H N Q Q N G Y R A G D P S E L I C K *
adenylylsulfate reductase, beta subunit

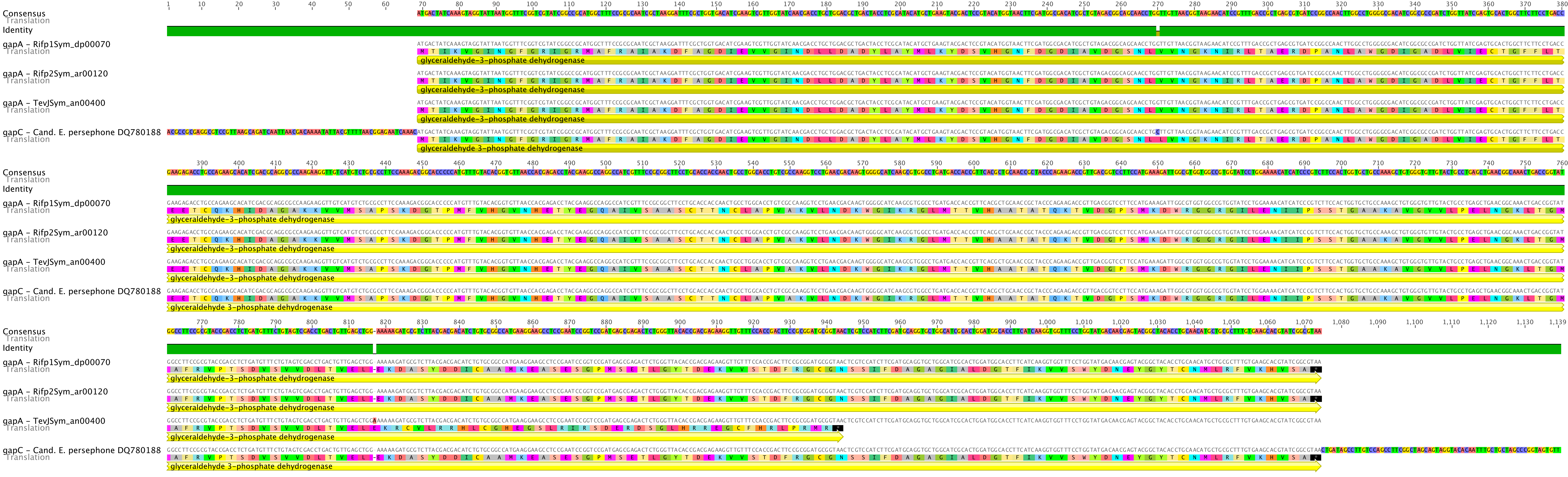
aprB – Cand. E. persephone DQ780034
Translation

aprB – Cand. E. persephone DQ780033
Translation
CCGCACCACCCCTGAGGGTTCCATCGACCCTTATGGTAATACGCCCGCAGCCGATATGGCCAAGATCGCTGAGCCTGGTTTCTTCAACCACAATCAGCAGAATGGCTACCGCGCTGGCGATCCCAGCGAGCTGATTTGCAAG
R T T P E G S I D P Y G N T P A A D M A K I A E P G F F N H N Q Q N G Y R A G D P S E L I C K
APS reductase beta subunit


Consensus
Translation
Identity
cbbM – Rifp1Sym_at00130
cbbM – Rifp2Sym_bi00210
cbbM – TevJSym_aj00630
cbbM – Cand. E. persephone DQ780068
cbbM – Cand. E. persephone DQ780046
ribulose-1,5-bisphosphate carboxylase/oxygenase
ribulose bisphosphate carboxylase
ribulose-15-bisphosphate carboxylase/oxygenase form II large subunit
1
1,464


Consensus
Translation
Identity
dsrA – Rifp1Sym_am00340
Translation
sulfite reductase, dissimilatory-type subunit alpha
dsrA – Rifp2Sym_aa00430, Rifp2Sym_aa00440
Translation
sulfite reductase, dissimilatory-type subunit alpha – partial
dsrA – TevJSym_aw00210
Translation
dissimilatory sulfite reductase, alpha subunit
dsrA – Cand. E. persephone DQ780148
Translation
sulfite reductase dissimilatory-type alpha subunit
dsrA – Cand. E. persephone DQ780147
Translation
sulfite reductase dissimilatory-type alpha subunit
sulfite reductas...
1
10
310
320
620
630
940
950
1,250
1,256


Consensus
Translation
Identity
dsrB – Rifp1Sym_am00350
Translation
sulfite reductase, dissimilatory-type subunit beta
dsrB – Rifp2Sym_aa00410
Translation
sulfite reductase, dissimilatory-type subunit beta
dsrB – TevJSym_aw00190
Translation
dissimilatory sulfite reductase, beta subunit
1
360
720
1,071


Consensus
Translation
Identity
gapA – Rifp1Sym_dp00070
gapA – Rifp2Sym_ar00120
gapA – TevJSym_an00400
gapC – Cand. E. persephone DQ780188
glyceraldehyde-3-phosphate dehydrogenase
glyceraldehyde 3-phosphate dehydrogenase
1
10
20
30
40
50
60
70
80
90
100
110
120
130
140
150
160
170
180
190
200
210
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790
800
810
820
830
840
850
860
870
880
890
900
910
920
930
940
950
960
970
980
990
1,000
1,010
1,020
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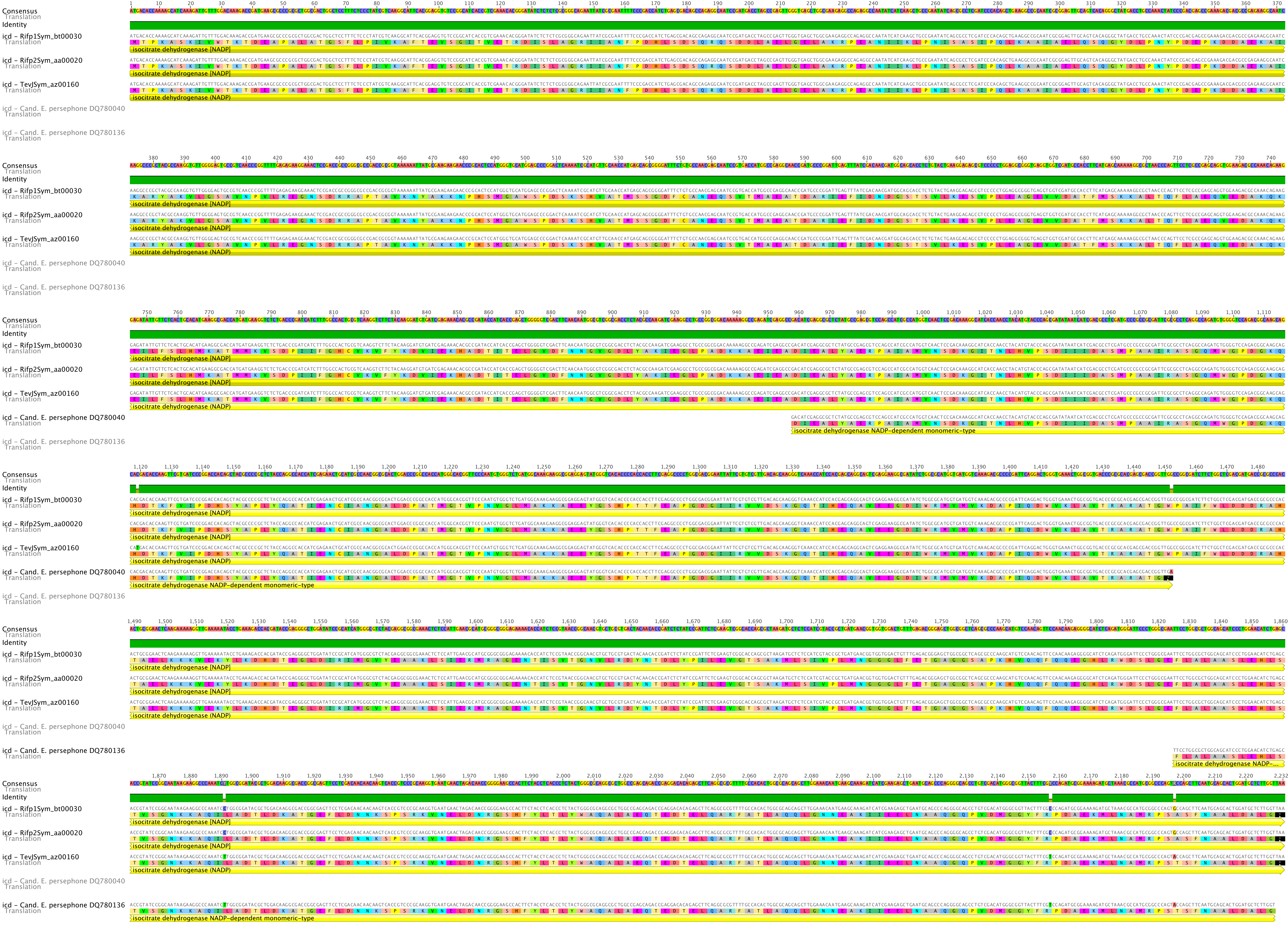
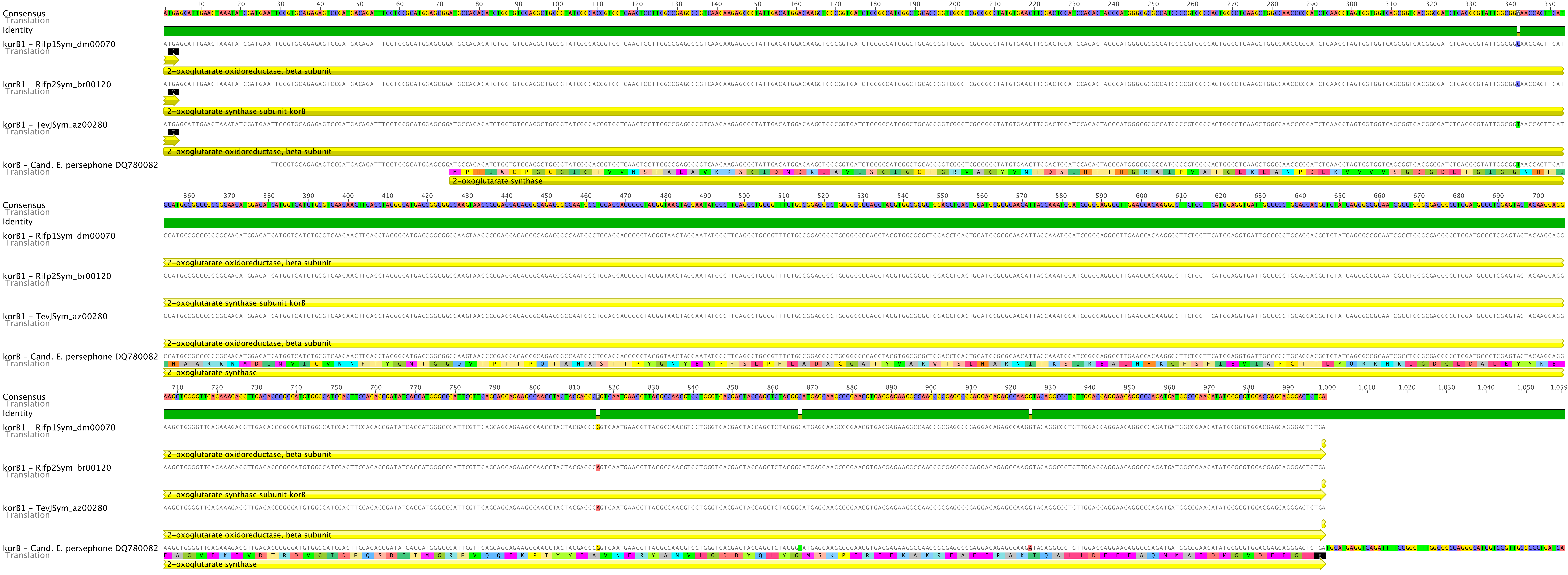
1,110
1,120
1,130
1,139


Consensus
Translation
Identity
icd – Rifp1Sym_bt00030
Translation
isocitrate dehydrogenase [NADP]
icd – Rifp2Sym_aa00020
Translation
isocitrate dehydrogenase [NADP]
icd – TevJSym_az00160
Translation
isocitrate dehydrogenase (NADP)
icd – Cand. E. persephone DQ780040
Translation
isocitrate dehydrogenase NADP-dependent monomeric-type
icd – Cand. E. persephone DQ780136
Translation
isocitrate dehydrogenase NADP-...


Consensus
Translation
Identity
korA1 – Rifp1Sym_dm00080
korA1 – Rifp2Sym_br00160
korA1 – TevJSym_az00290
porA – Cand. E. persephone DQ780126
porA – Cand. E. persephone DQ780069
2-oxoglutarate oxidoreductase, alpha subunit
2-oxoglutarate synthase subunit korA
pyruvate:flavodoxin/ferredoxin oxidoreductase N-terminal
pyruvate:flavodoxin/ferredoxin oxidoreductase N-te...
1
340
350
690
700
1,040
1,050
1,386


Consensus
Translation
Identity
korB1 – Rifp1Sym_dm00070
Translation
2-oxoglutarate oxidoreductase, beta subunit
korB1 – Rifp2Sym_br00120
Translation
2-oxoglutarate synthase subunit korB
korB1 – TevJSym_az00280
Translation
2-oxoglutarate oxidoreductase, beta subunit
korB – Cand. E. persephone DQ780082
Translation
2-oxoglutarate synthase
1
10
20
30
40
50
60
70
80
90
100
110
120
130
140
150
160
170
180
190
200
210
220
230
240
250
260
270
280
290
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310
320
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340
350
360
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760
770
780
790
800
810
820
830
840
850
860
870
880
890
900
910
920
930
940
950
960
970
980
990
1,000
1,010
1,020
1,030
1,040
1,050
1,059

```
1  10  20  30  40  50  60  70  80  90  100  110  120  130  140  150  160  170  180  190  200  210  220  230  240  250  261
Consensus
ATGGCATTCGGCAAAATCAAAGAGATCACCGGCGTTGTCACCATCAACAAGTCTTGGTGCAAGGGATGCGGCTTCTGCGTCAATTATTGCCCGACCGATGCCCTCGCCATGTCATCTGAATATAACGCCAAGGGATATCATCCCCCGTTCGTCAAATCGCCGGATGATTGCAGGAATTGTGATTTCTGCCAGACGATCTGTCCGGAATTCGCCATTTACGTCACCCGCAAGGCGGAACAAGAGGAGAATGAGAATGCGTAA
 Translation
Identity

korD1 - Rifp1Sym_dm00090
ATGGCATTCGGCAAAATCAAAGAGATCACCGGCGTTGTCACCATCAACAAGTCTTGGTGCAAGGGATGCGGCTTCTGCGTCAATTATTGCCCGACCGATGCCCTCGCCATGTCATCTGAATATAACGCCAAGGGATATCATCCCCCGTTCGTCAAATCGCCGGATGATTGCAGGAATTGTGATTTCTGCCAGACGATCTGTCCGGAATTCGCCATTTACGTCACCCGCAAGGCGGAACAAGAGGAGAATGAGAATGCGTAA
 Translation
M A F G K I K E I T G V V T I N K S W C K G C G F C V N Y C P T D A L A M S S E Y N A K G Y H P P F V K S P D D C R N C D F C Q T I C P E F A I Y V T R K A E Q E E N E N A *
2-oxoglutarate oxidoreductase, delta subunit, putative

korD1 - Rifp2Sym_br00140
ATGGCATTCGGCAAAATCAAAGAGATCACCGGCGTTGTCACCATCAACAAGTCTTGGTGCAAGGGATGCGGCTTCTGCGTCAATTATTGCCCGACCGATGCCCTCGCCATGTCATCTGAATATAACGCCAAGGGATATCATCCCCCGTTCGTCAAATCGCCGGATGATTGCAGGAATTGTGATTTCTGCCAGACGATCTGTCCGGAATTCGCCATTTACGTCACCCGCAAGGCGGAACAAGAGGAGAATGAGAATGCGTAA
 Translation
M A F G K I K E I T G V V T I N K S W C K G C G F C V N Y C P T D A L A M S S E Y N A K G Y H P P F V K S P D D C R N C D F C Q T I C P E F A I Y V T R K A E Q E E N E M R
2-oxoglutarate oxidoreductase, delta subunit, putative

korD1 - TevJSym_az00300
ATGGCATTCGGCAAAATCAAAGAGATCACCGGCGTTGTCACCATCAACAAGTCTTGGTGCAAGGGATGCGGCTTCTGCGTCAATTATTGCCCGACCGATGCCCTCGCCATGTCATCTGAATATAACGCCAAGGGATATCATCCCCCGTTCGTCAAATCGCCGGATGATTGCAGGAATTGTGATTTCTGCCAGACGATCTGTCCGGAATTCGCCATTTACGTCACCCGCAAGGCGGAACAAGAGGAGAATGAGAATGCGTAA
 Translation
M A F G K I K E I T G V V T I N K S W C K G C G F C V N Y C P T D A L A M S S E Y N A K G Y H P P F V K S P D D C R N C D F C Q T I C P E F A I Y V T R K A E Q E E N E M R
2-oxoglutarate oxidoreductase, delta subunit
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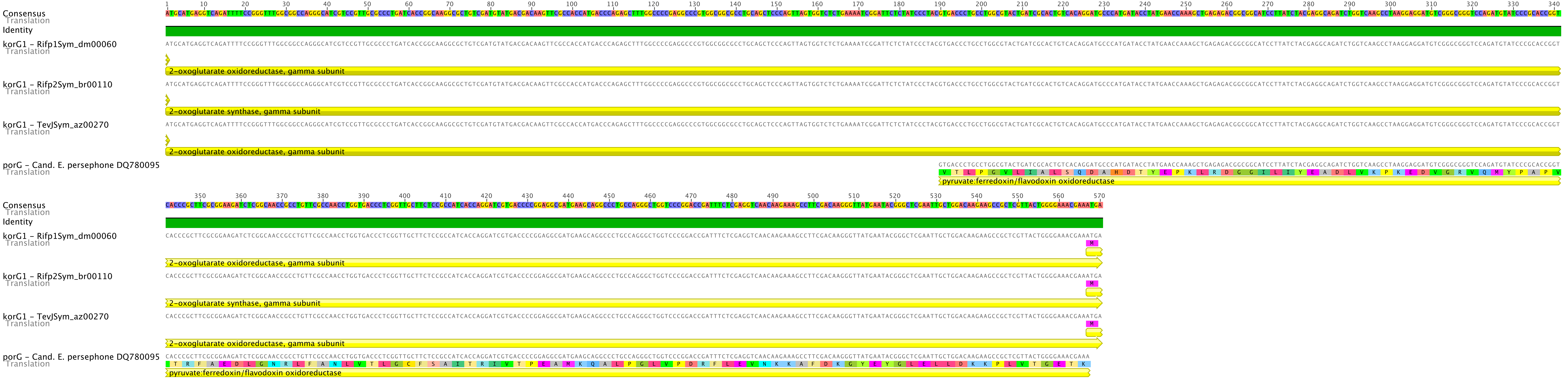

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Consensus                         ATGCATGAGGTCAGATTTTCCGGGTTTGGCGGCCAGGGCATCGTCCGTTGCGCCCTGATCACCGGCAAGGCGCTGTCGATGTATGACGACAAGTTCGCCACCATGACCCAGAGCTTTGGCCCCGAGGCCCGTGGCGGCGCCTGCAGCTCCCAGTTAGTGGTCTCTGAAAATCGGATTCTCTATCCCTACGTGACCCTGCCTGGCGTACTGATCGCACTGTCACAGGATGCCCATGATACCTATGAACCAAAGCTGAGAGACGGCGGCATCCTTATCTACGAGGCAGATCTGGTCAAGCCTAAGGAGGATGTCGGGCGGGTCCAGATGTATCCCGCACCGGT
Translation
Identity
korG1 – Rifp1Sym_dm00060           ATGCATGAGGTCAGATTTTCCGGGTTTGGCGGCCAGGGCATCGTCCGTTGCGCCCTGATCACCGGCAAGGCGCTGTCGATGTATGACGACAAGTTCGCCACCATGACCCAGAGCTTTGGCCCCGAGGCCCGTGGCGGCGCCTGCAGCTCCCAGTTAGTGGTCTCTGAAAATCGGATTCTCTATCCCTACGTGACCCTGCCTGGCGTACTGATCGCACTGTCACAGGATGCCCATGATACCTATGAACCAAAGCTGAGAGACGGCGGCATCCTTATCTACGAGGCAGATCTGGTCAAGCCTAAGGAGGATGTCGGGCGGGTCCAGATGTATCCCGCACCGGT
Translation
                                  2–oxoglutarate oxidoreductase, gamma subunit
korG1 – Rifp2Sym_br00110           ATGCATGAGGTCAGATTTTCCGGGTTTGGCGGCCAGGGCATCGTCCGTTGCGCCCTGATCACCGGCAAGGCGCTGTCGATGTATGACGACAAGTTCGCCACCATGACCCAGAGCTTTGGCCCCGAGGCCCGTGGCGGCGCCTGCAGCTCCCAGTTAGTGGTCTCTGAAAATCGGATTCTCTATCCCTACGTGACCCTGCCTGGCGTACTGATCGCACTGTCACAGGATGCCCATGATACCTATGAACCAAAGCTGAGAGACGGCGGCATCCTTATCTACGAGGCAGATCTGGTCAAGCCTAAGGAGGATGTCGGGCGGGTCCAGATGTATCCCGCACCGGT
Translation
                                  2–oxoglutarate synthase, gamma subunit
korG1 – TevJSym_az00270            ATGCATGAGGTCAGATTTTCCGGGTTTGGCGGCCAGGGCATCGTCCGTTGCGCCCTGATCACCGGCAAGGCGCTGTCGATGTATGACGACAAGTTCGCCACCATGACCCAGAGCTTTGGCCCCGAGGCCCGTGGCGGCGCCTGCAGCTCCCAGTTAGTGGTCTCTGAAAATCGGATTCTCTATCCCTACGTGACCCTGCCTGGCGTACTGATCGCACTGTCACAGGATGCCCATGATACCTATGAACCAAAGCTGAGAGACGGCGGCATCCTTATCTACGAGGCAGATCTGGTCAAGCCTAAGGAGGATGTCGGGCGGGTCCAGATGTATCCCGCACCGGT
Translation
                                  2–oxoglutarate oxidoreductase, gamma subunit
porG – Cand. E. persephone DQ780095                                                                                                                                                                                                   GTGACCCTGCCTGGCGTACTGATCGCACTGTCACAGGATGCCCATGATACCTATGAACCAAAGCTGAGAGACGGCGGCATCCTTATCTACGAGGCAGATCTGGTCAAGCCTAAGGAGGATGTCGGGCGGGTCCAGATGTATCCCGCACCGGT
Translation                                                                                                                                                                                                                           V  T  L  P  G  V  L  I  A  L  S  Q  D  A  H  D  T  Y  E  P  K  L  R  D  G  G  I  L  I  Y  E  A  D  L  V  K  P  K  E  D  V  G  R  V  Q  M  Y  P  A  P  V
                                                                                                                                                                                                                                      pyruvate:ferredoxin/flavodoxin oxidoreductase

Consensus                         CACCCGCTTCGCGGAAGATCTCGGCAACCGCCTGTTCGCCAACCTGGTGACCCTCGGTTGCTTCTCCGCCATCACCAGGATCGTGACCCCGGAGGCGATGAAGCAGGCCCTGCCAGGGCTGGTCCCGGACCGATTTCTCGAGGTCAACAAGAAAGCCTTCGACAAGGGTTATGAATACGGGCTCGAATTGCTGGACAAGAAGCCGCTCGTTACTGGGGAAACGAAATGA
Translation
Identity
korG1 – Rifp1Sym_dm00060           CACCCGCTTCGCGGAAGATCTCGGCAACCGCCTGTTCGCCAACCTGGTGACCCTCGGTTGCTTCTCCGCCATCACCAGGATCGTGACCCCGGAGGCGATGAAGCAGGCCCTGCCAGGGCTGGTCCCGGACCGATTTCTCGAGGTCAACAAGAAAGCCTTCGACAAGGGTTATGAATACGGGCTCGAATTGCTGGACAAGAAGCCGCTCGTTACTGGGGAAACGAAATGA
Translation                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    M
                                  2–oxoglutarate oxidoreductase, gamma subunit
korG1 – Rifp2Sym_br00110           CACCCGCTTCGCGGAAGATCTCGGCAACCGCCTGTTCGCCAACCTGGTGACCCTCGGTTGCTTCTCCGCCATCACCAGGATCGTGACCCCGGAGGCGATGAAGCAGGCCCTGCCAGGGCTGGTCCCGGACCGATTTCTCGAGGTCAACAAGAAAGCCTTCGACAAGGGTTATGAATACGGGCTCGAATTGCTGGACAAGAAGCCGCTCGTTACTGGGGAAACGAAATGA
Translation                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    M
                                  2–oxoglutarate synthase, gamma subunit
korG1 – TevJSym_az00270            CACCCGCTTCGCGGAAGATCTCGGCAACCGCCTGTTCGCCAACCTGGTGACCCTCGGTTGCTTCTCCGCCATCACCAGGATCGTGACCCCGGAGGCGATGAAGCAGGCCCTGCCAGGGCTGGTCCCGGACCGATTTCTCGAGGTCAACAAGAAAGCCTTCGACAAGGGTTATGAATACGGGCTCGAATTGCTGGACAAGAAGCCGCTCGTTACTGGGGAAACGAAATGA
Translation                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    M
                                  2–oxoglutarate oxidoreductase, gamma subunit
porG – Cand. E. persephone DQ780095  CACCCGCTTCGCGGAAGATCTCGGCAACCGCCTGTTCGCCAACCTGGTGACCCTCGGTTGCTTCTCCGCCATCACCAGGATCGTGACCCCGGAGGCGATGAAGCAGGCCCTGCCAGGGCTGGTCCCGGACCGATTTCTCGAGGTCAACAAGAAAGCCTTCGACAAGGGTTATGAATACGGGCTCGAATTGCTGGACAAGAAGCCGCTCGTTACTGGGGAAACGAAA
Translation                          T  R  F  A  E  D  L  G  N  R  L  F  A  N  L  V  T  L  G  C  F  S  A  I  T  R  I  V  T  P  E  A  M  K  Q  A  L  P  G  L  V  P  D  R  F  L  E  V  N  K  K  A  F  D  K  G  Y  E  Y  G  L  E  L  L  D  K  K  P  L  V  T  G  E  T  K
                                   pyruvate:ferredoxin/flavodoxin oxidoreductase
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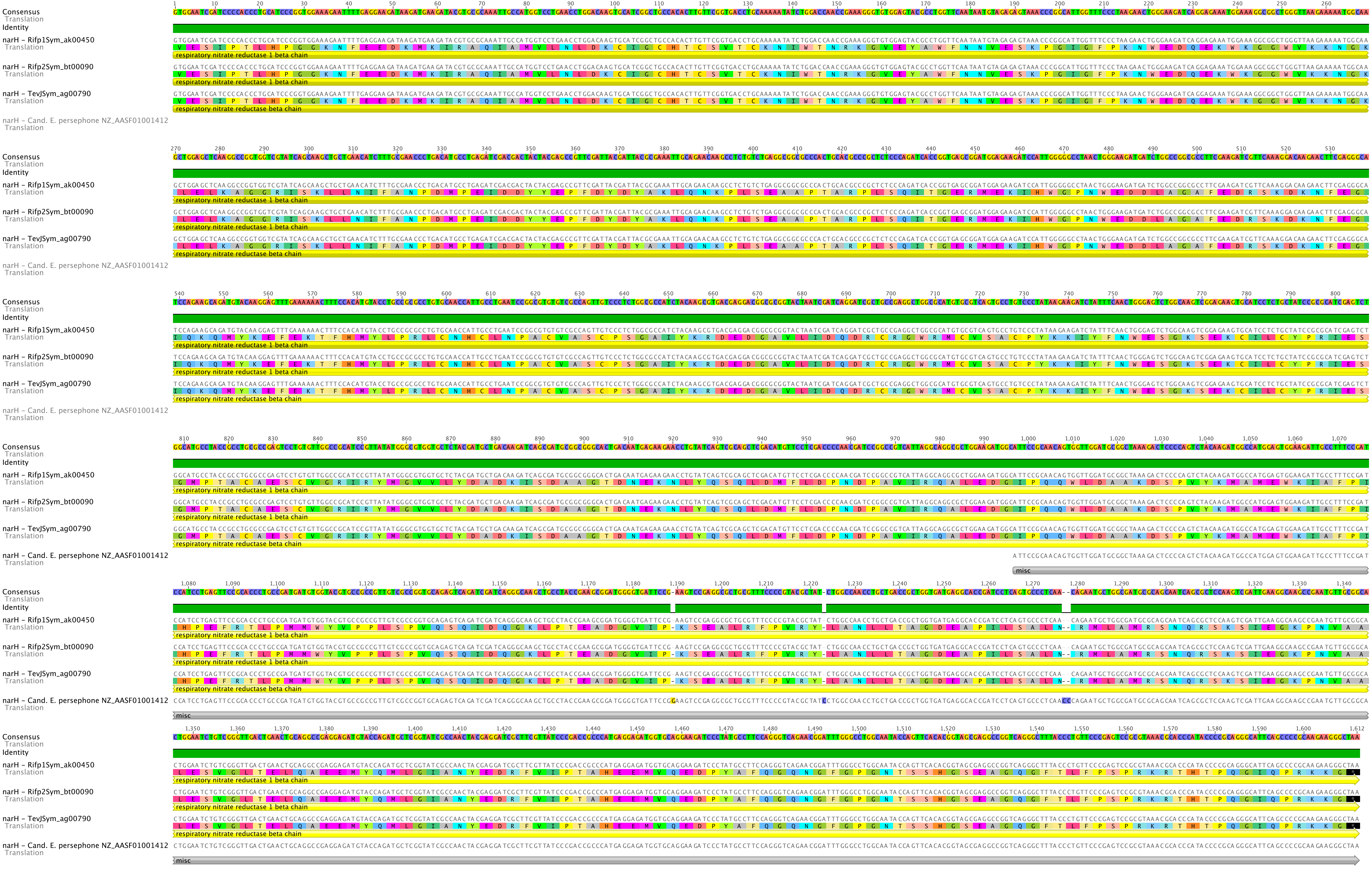
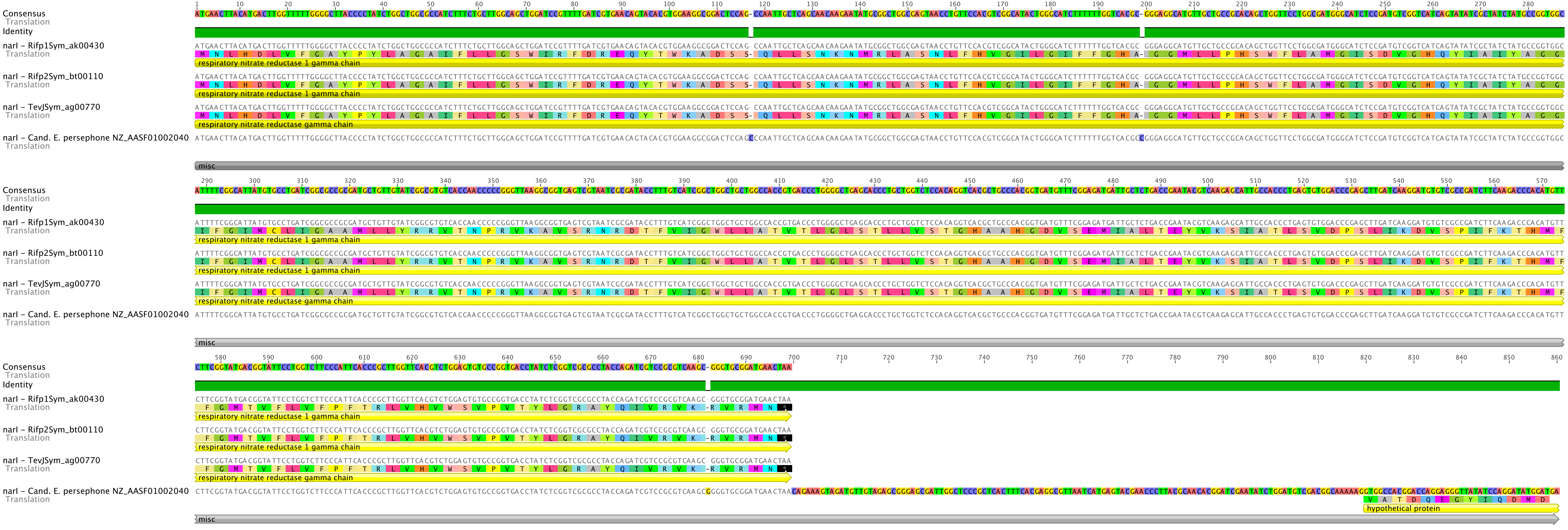
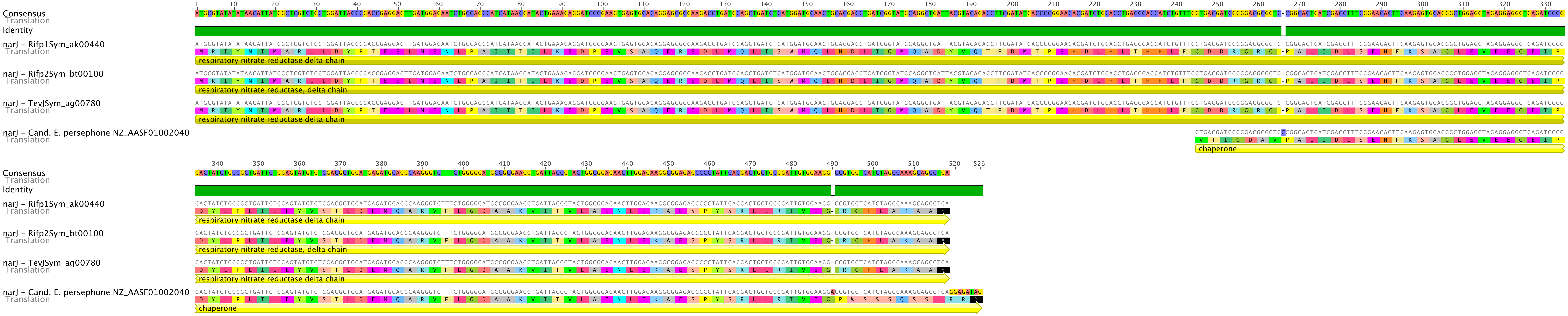

Consensus
Translation
Identity
narH – Rifp1Sym_ak00450
Translation
respiratory nitrate reductase 1 beta chain
narH – Rifp2Sym_bt00090
Translation
respiratory nitrate reductase 1 beta chain
narH – TevJSym_ag00790
Translation
respiratory nitrate reductase beta chain
narH – Cand. E. persephone NZ_AASF01001412
Translation
misc


Consensus
Translation
Identity
narI – Rifp1Sym_ak00430
Translation
respiratory nitrate reductase 1 gamma chain
narI – Rifp2Sym_bt00110
Translation
respiratory nitrate reductase 1 gamma chain
narI – TevJSym_ag00770
Translation
respiratory nitrate reductase gamma chain
narI – Cand. E. persephone NZ_AASF01002040
Translation
misc
hypothetical protein


Consensus
Translation
Identity
narJ - Rifp1Sym_ak00440
Translation
respiratory nitrate reductase delta chain
narJ - Rifp2Sym_bt00100
Translation
respiratory nitrate reductase, delta chain
narJ - TevJSym_ag00780
Translation
respiratory nitrate reductase delta chain
narJ - Cand. E. persephone NZ_AASF01002040
Translation
chaperone
1
10
20
30
40
50
60
70
80
90
100
110
120
130
140
150
160
170
180
190
200
210
220
230
240
250
260
270
280
290
300
310
320
330
340
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360
370
380
390
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410
420
430
440
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460
470
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490
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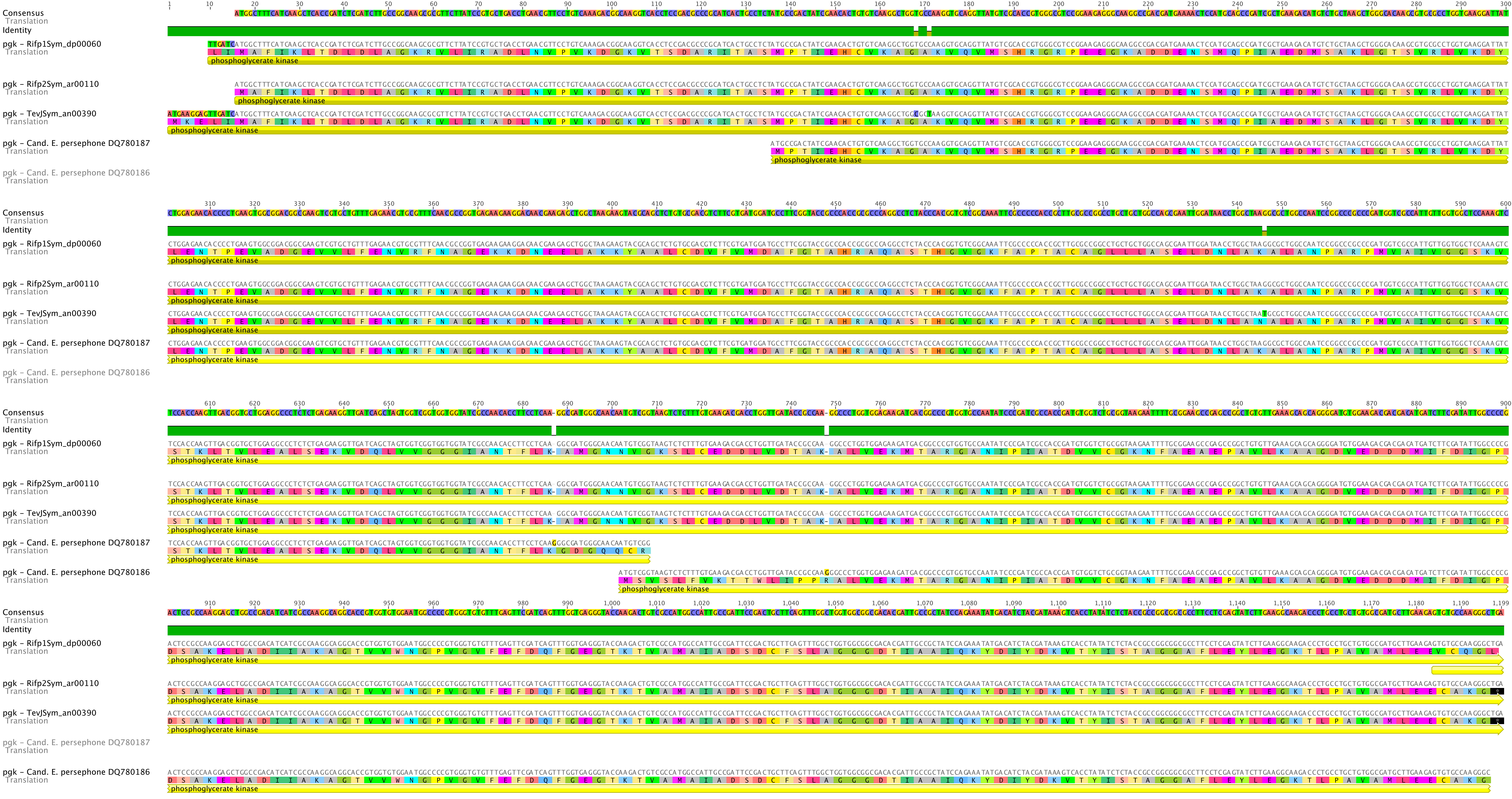
510
520
526


Consensus
Translation
Identity
nosZ - Rifp1Sym_ag00460
Translation
nitrous-oxide reductase
nosZ - Rifp2Sym_au00130, Rifp2Sym_au00140
Translation
nitrous-oxide reductase - partial
nosZ - TevJSym_ac00130
Translation
nitrous-oxide reductase


Consensus
Translation
Identity
pgk – Rifp1Sym_dp00060
Translation
pgk – Rifp2Sym_ar00110
Translation
pgk – TevJSym_an00390
Translation
pgk – Cand. E. persephone DQ780187
Translation
pgk – Cand. E. persephone DQ780186
Translation
phosphoglycerate kinase
1
10
20
30
40
50
60
70
80
90
100
110
120
130
140
150
160
170
180
190
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830
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850
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950
960
970
980
990
1,000
1,010
1,020
1,030
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1,060
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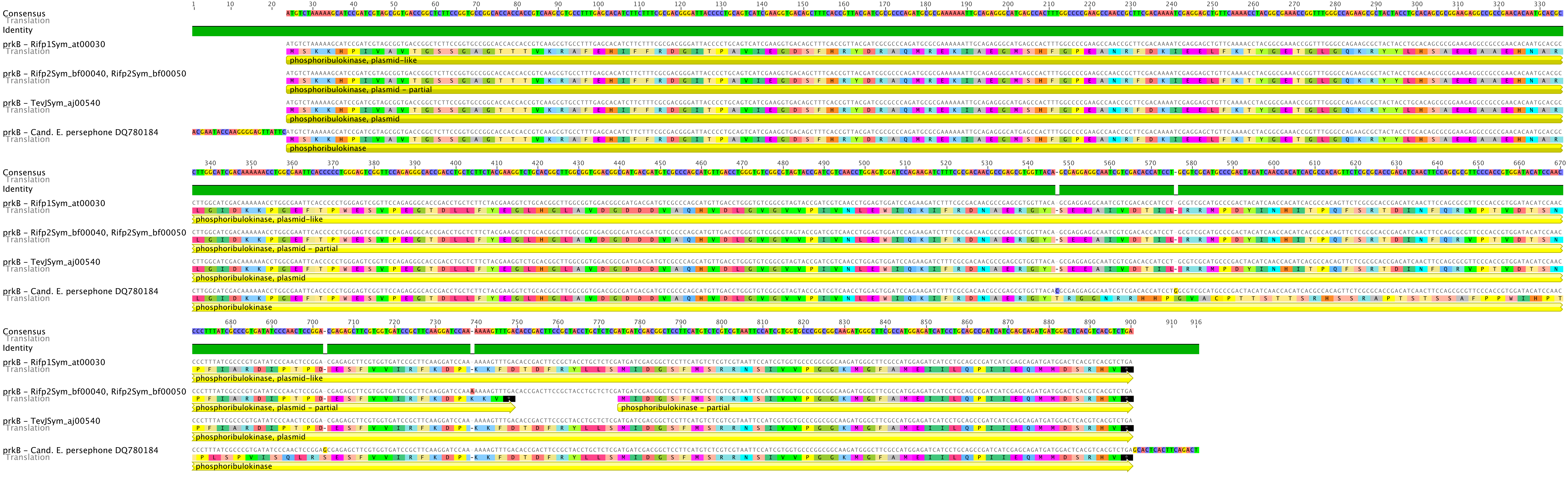
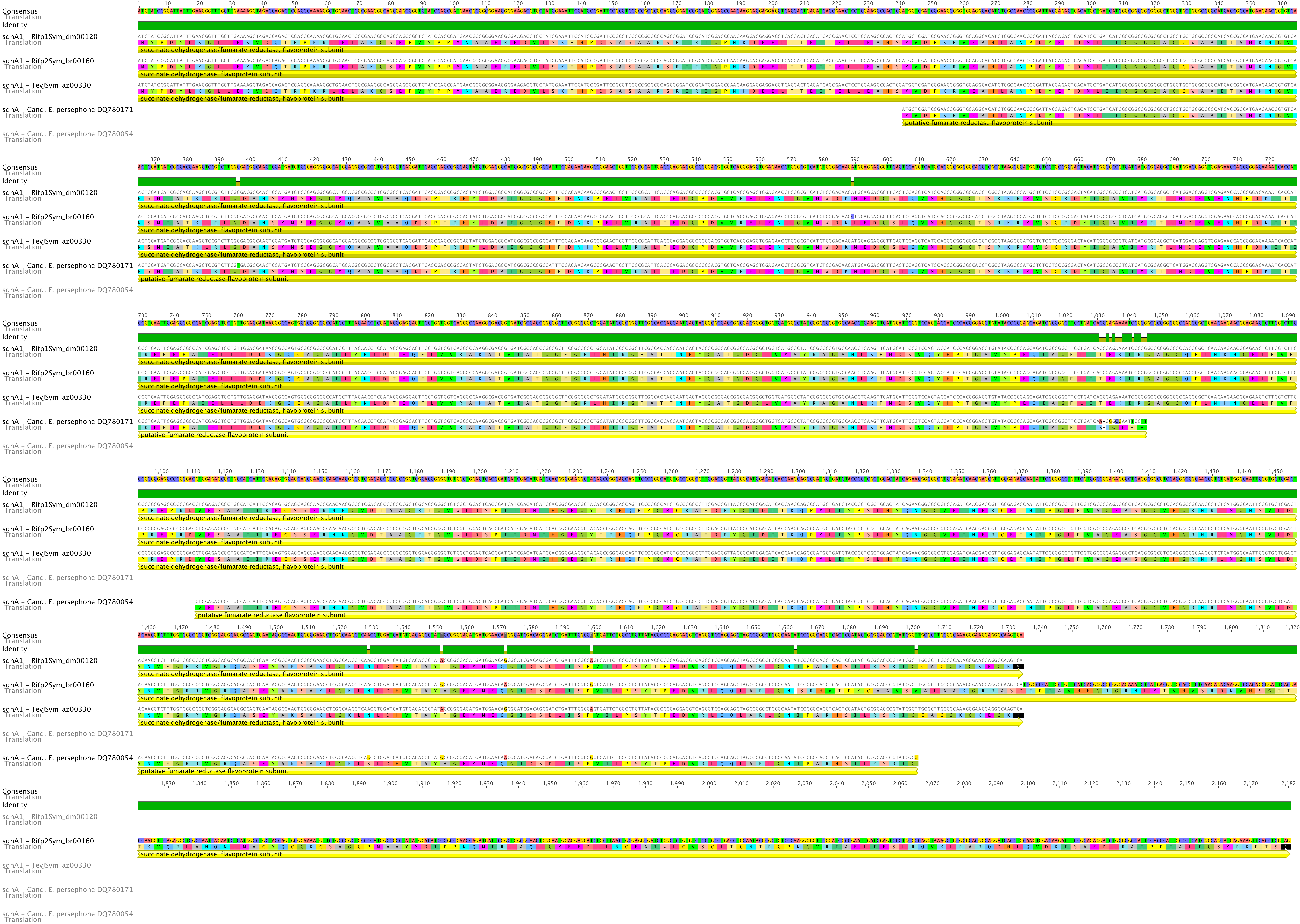
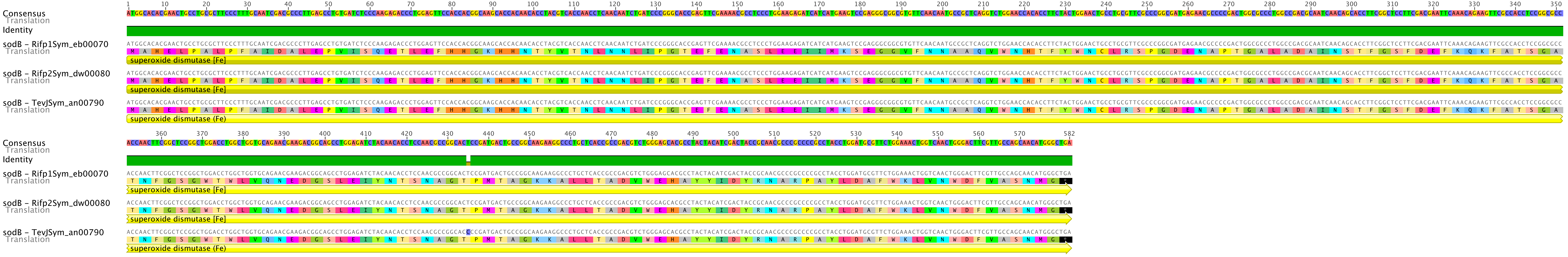
1,190
1,199


Consensus
Translation
Identity
prkB – Rifp1Sym_at00030
Translation
phosphoribulokinase, plasmid-like
prkB – Rifp2Sym_bf00040, Rifp2Sym_bf00050
Translation
phosphoribulokinase, plasmid – partial
prkB – TevJSym_aj00540
Translation
phosphoribulokinase, plasmid
prkB – Cand. E. persephone DQ780184
Translation
phosphoribulokinase
phosphoribulokinase – partial
1
10
20
30
330
340
670
680
900
910
916


Consensus
Translation
Identity
sdhA1 – Rifp1Sym_dm00120
Translation
succinate dehydrogenase/fumarate reductase, flavoprotein subunit
sdhA1 – Rifp2Sym_br00160
Translation
succinate dehydrogenase, flavoprotein subunit
sdhA1 – TevJSym_az00330
Translation
succinate dehydrogenase/fumarate reductase, flavoprotein subunit
sdhA – Cand. E. persephone DQ780171
Translation
putative fumarate reductase flavoprotein subunit
sdhA – Cand. E. persephone DQ780054
Translation
putative fumarate reductase flavoprotein subunit
1
10
360
370
720
730
1,090
1,100
1,450
1,460
1,820
1,830
2,182



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Consensus
ATGGCACACGAACTGCCTGCGCTTCCCTTTGCAATCGACGCCCTTGAGCCTGTGATCTCCCAAGAGACCCTGGAGTTCCACCACGGCAAGCACCACAACACCTACGTCACCAACCTCAACAATCTGATCCCGGGCACCGAGTTCGAAAACGCCTCCCTGGAAGAGATCATCATGAAGTCCGAGGGCGGCGTGTTCAACAATGCCGCTCAGGTCTGGAACCACACCTTCTACTGGAACTGCCTGCGTTCGCCCGGCGATGAGAACGCCCCGACTGGCGCCCTGGCCGACGCAATCAACAGCACCTTCGGCTCCTTCGACGAATTCAAACAGAAGTTCGCCACCTCCGGCGCC
Translation
Identity

sodB - Rifp1Sym_eb00070
ATGGCACACGAACTGCCTGCGCTTCCCTTTGCAATCGACGCCCTTGAGCCTGTGATCTCCCAAGAGACCCTGGAGTTCCACCACGGCAAGCACCACAACACCTACGTCACCAACCTCAACAATCTGATCCCGGGCACCGAGTTCGAAAACGCCTCCCTGGAAGAGATCATCATGAAGTCCGAGGGCGGCGTGTTCAACAATGCCGCTCAGGTCTGGAACCACACCTTCTACTGGAACTGCCTGCGTTCGCCCGGCGATGAGAACGCCCCGACTGGCGCCCTGGCCGACGCAATCAACAGCACCTTCGGCTCCTTCGACGAATTCAAACAGAAGTTCGCCACCTCCGGCGCC
Translation
M A H E L P A L P F A I D A L E P V I S Q E T L E F H H G K H H N T Y V T N L N N L I P G T E F E N A S L E E I I M K S E G G V F N N A A Q V W N H T F Y W N C L R S P G D E N A P T G A L A D A I N S T F G S F D E F K Q K F A T S G A
superoxide dismutase [Fe]

sodB - Rifp2Sym_dw00080
ATGGCACACGAACTGCCTGCGCTTCCCTTTGCAATCGACGCCCTTGAGCCTGTGATCTCCCAAGAGACCCTGGAGTTCCACCACGGCAAGCACCACAACACCTACGTCACCAACCTCAACAATCTGATCCCGGGCACCGAGTTCGAAAACGCCTCCCTGGAAGAGATCATCATGAAGTCCGAGGGCGGCGTGTTCAACAATGCCGCTCAGGTCTGGAACCACACCTTCTACTGGAACTGCCTGCGTTCGCCCGGCGATGAGAACGCCCCGACTGGCGCCCTGGCCGACGCAATCAACAGCACCTTCGGCTCCTTCGACGAATTCAAACAGAAGTTCGCCACCTCCGGCGCC
Translation
M A H E L P A L P F A I D A L E P V I S Q E T L E F H H G K H H N T Y V T N L N N L I P G T E F E N A S L E E I I M K S E G G V F N N A A Q V W N H T F Y W N C L R S P G D E N A P T G A L A D A I N S T F G S F D E F K Q K F A T S G A
superoxide dismutase [Fe]

sodB - TevJSym_an00790
ATGGCACACGAACTGCCTGCGCTTCCCTTTGCAATCGACGCCCTTGAGCCTGTGATCTCCCAAGAGACCCTGGAGTTCCACCACGGCAAGCACCACAACACCTACGTCACCAACCTCAACAATCTGATCCCGGGCACCGAGTTCGAAAACGCCTCCCTGGAAGAGATCATCATGAAGTCCGAGGGCGGCGTGTTCAACAATGCCGCTCAGGTCTGGAACCACACCTTCTACTGGAACTGCCTGCGTTCGCCCGGCGATGAGAACGCCCCGACTGGCGCCCTGGCCGACGCAATCAACAGCACCTTCGGCTCCTTCGACGAATTCAAACAGAAGTTCGCCACCTCCGGCGCC
Translation
M A H E L P A L P F A I D A L E P V I S Q E T L E F H H G K H H N T Y V T N L N N L I P G T E F E N A S L E E I I M K S E G G V F N N A A Q V W N H T F Y W N C L R S P G D E N A P T G A L A D A I N S T F G S F D E F K Q K F A T S G A
superoxide dismutase (Fe)

Consensus
ACCAACTTCGGCTCCGGCTGGACCTGGCTGGTGCAGAACGAAGACGGCAGCCTGGAGATCTACAACACCTCCAACGCCGGCACTCCGATGACTGCCGGCAAGAAGGCCCTGCTCACCGCCGACGTCTGGGAGCACGCCTACTACATCGACTACCGCAACGCCCGCCCCGCCTACCTGGATGCGTTCTGGAAACTGGTCAACTGGGACTTCGTTGCCAGCAACATGGGCTGA
Translation
Identity

sodB - Rifp1Sym_eb00070
ACCAACTTCGGCTCCGGCTGGACCTGGCTGGTGCAGAACGAAGACGGCAGCCTGGAGATCTACAACACCTCCAACGCCGGCACTCCGATGACTGCCGGCAAGAAGGCCCTGCTCACCGCCGACGTCTGGGAGCACGCCTACTACATCGACTACCGCAACGCCCGCCCCGCCTACCTGGATGCGTTCTGGAAACTGGTCAACTGGGACTTCGTTGCCAGCAACATGGGCTGA
Translation
T N F G S G W T W L V Q N E D G S L E I Y N T S N A G T P M T A G K K A L L T A D V W E H A Y Y I D Y R N A R P A Y L D A F W K L V N W D F V A S N M G *
superoxide dismutase [Fe]

sodB - Rifp2Sym_dw00080
ACCAACTTCGGCTCCGGCTGGACCTGGCTGGTGCAGAACGAAGACGGCAGCCTGGAGATCTACAACACCTCCAACGCCGGCACTCCGATGACTGCCGGCAAGAAGGCCCTGCTCACCGCCGACGTCTGGGAGCACGCCTACTACATCGACTACCGCAACGCCCGCCCCGCCTACCTGGATGCGTTCTGGAAACTGGTCAACTGGGACTTCGTTGCCAGCAACATGGGCTGA
Translation
T N F G S G W T W L V Q N E D G S L E I Y N T S N A G T P M T A G K K A L L T A D V W E H A Y Y I D Y R N A R P A Y L D A F W K L V N W D F V A S N M G *
superoxide dismutase [Fe]

sodB - TevJSym_an00790
ACCAACTTCGGCTCCGGCTGGACCTGGCTGGTGCAGAACGAAGACGGCAGCCTGGAGATCTACAACACCTCCAACGCCGGCACCCCGATGACTGCCGGCAAGAAGGCCCTGCTCACCGCCGACGTCTGGGAGCACGCCTACTACATCGACTACCGCAACGCCCGCCCCGCCTACCTGGATGCGTTCTGGAAACTGGTCAACTGGGACTTCGTTGCCAGCAACATGGGCTGA
Translation
T N F G S G W T W L V Q N E D G S L E I Y N T S N A G T P M T A G K K A L L T A D V W E H A Y Y I D Y R N A R P A Y L D A F W K L V N W D F V A S N M G *
superoxide dismutase (Fe)
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Consensus
Translation
Identity
sopT – Rifp1Sym_cn00110
sopT – Rifp2Sym_az00240
sopT – TevJSym_ad01200
sopT – Cand. E. persephone DQ780113
ATP-sulfurylase
bacterial Atp sulfurylase chain A
1
1,192