
Aureococcus anophagefferens virus btv-01

NC_024697

370920 nucleotides in sequence

Mean G+C content = 28.7%

1.

```

      t
      g-c
      c-g
      t-a
      t-a
      t-a
      t-a
      g-c      tt
      t      ggcgc a
aa      g      !!!!! g
t      ttcg      ccgcg c
g      !!!!!      t      tt
g      aagc      t
ta      g      a
      a-tag
      c-g
      a-t
      t-a
      c-g
      c      a
      t      a
      agt
```

tRNA-Thr(agt)

72 bases, %GC = 45.8

Sequence c[118324,118395]

Primary sequence for tRNA-Thr(agt)

```
1      .      10      .      20      .      30      .      40      .      50
gcttttgtggcttaatggtaaagcgacatcctagtaagatgtagattccg
cgttcgattcgcggcaaaagct
```

2.

```

      t
      g+t
      c-g
      c-g
      c-g
      t-a
      a-t
      t-a      ct
      t      gaccc a
taaa      g      !!!!! g
t      agcg      ctggg c
g      !!!!!      t      tt
g      tcgc      t
ata      g      a
      t-aag
      c-g
      c-g
      g-c
      c-g
      c      a
      t      a
      tct
```

tRNA-Arg(tct)
74 bases, %GC = 52.7
Sequence c[148317,148390]

Primary sequence for tRNA-Arg(tct)

1	.	10	.	20	.	30	.	40	.	50
gccctattggcgaaattggatatcgcgctccgccttctaagcggaagattc										
tgggttcgatccccagatagggtt										

3.

```

      a
      a-t
      t-a
      c-g
      t-a
      g-c
      t-a
      t-a      ca
      t      t      cgttc      a
tgag      g      !!!!!      g
g      gcg      gcaag      c
g      !!!      tt
t      cgc      c
ctaa      g      t+g
      c-g      c-g
      c-g      t-a
      g-c      c-g
      g-c      t      c
      a      c      aa
      t      c
      t      g
      taa

```

tRNA-Leu(taa)
 82 bases, %GC = 53.7
 Sequence [322252,322333]

Primary sequence for tRNA-Leu(taa)
 1 . 10 . 20 . 30 . 40 . 50
 atctgtttggcggagtggtctaacgcgccggatttaagccccggtctcta
 acgaggcgcaagttcgaaccttgcaacagata

4.

```

      t
      t-a
      t-a
      c-g

```

```

          g-c
          c-g
          c-g
          t-a
          a-t      ta
            t  tacc a
ctaa      a  !!!!! a
t  ctta      atggg c
g  !!!!!      t  tt
g  gaat      a
tta          t
          g+t
          a-t
          c-g
          c-g
          g-c
          t+g
        c  a
        t  a
          tat

```

tRNA-Ile(tat)
 76 bases, %GC = 38.2
 Sequence [322371,322446]

Primary sequence for tRNA-Ile(tat)
 1 . 10 . 20 . 30 . 40 . 50
 ttgcctataattcaatctggttagaatgaccgtcttataagcggtttat
 atgggttcaaattccattaggcgaat

5.

```

          g
          g-c
          a-t
          t-a
          c-g
          t-a
          c-g
          g-c      tt
t  gacac a

```

```

ttaa  a  !!!!! g
g  tacg  ctgtg c
g  :! :  t  tt
t  ttag  gct.t
ctg      g  g.a
          g-c  t+g
          a c  t-a
          a-t  a  a
          t-a  a  g
          g-c      ccg
          g  g
          t  a
          ata

```

tRNA-Tyr(ata)
88 bases, %GC = 45.5
Sequence [322481,322585]

Primary sequence for tRNA-Tyr(ata)
1 . 10 . 20 . 30 . 40 . 50
gatctcgtagcataattggtctgttaggaatggtataaccatcttcccaa
caaatgcatccggctgttaaccggaagattctgtgttcgattcacagcga
gatcg

Intron from tRNA-Tyr(ata)
1 . 10 . 20 . 30 . 40 . 50
ccatcttcccaacaaat

Intron Length: 17
Intron Insertion Position(38-39): tataa-Intron-gcatc

6.

```

t
g-c
a-t
t-a
a-t
c-g

```

```

      t-a
      g-c      tg
      t      ctgc a
taag  g      !!!!! g
t      gta      gagcg c
g      !!!      t      tt
g      cat      g
taga      g-c
      g+t c-g
      t.t c-g
      c-g c      g
      a-t      gat
      g-c
      a-t
      c      a
      t      a
      tga

```

tRNA-Ser(tga)
 83 bases, %GC = 49.4
 Sequence [322625,322707]

Primary sequence for tRNA-Ser(tga)
 1 . 10 . 20 . 30 . 40 . 50
 gatactgtgatggaattggtagacatgtcagacttgaaatctgttgcccg
 atgggcgtgagcgttcgagtcgctccagtatct

7.

```

      a
      c-g
      c-g
      g-c
      t-a
      c-g
      t-a
      a-t      tg
      t      cgacc a
ga      a      !!!!! a
t      cttg      gctgg c

```

```

t    !!!!    c    tg
a    gaac    t
gaa    g    g
      t-aag
      t-a
      c-g
      g-c
      a-t
      c    a
      t    a
      gta

```

tRNA-Tyr(gta)
 73 bases, %GC = 47.9
 Sequence [322727,322812]

Primary sequence for tRNA-Tyr(gta)
 1 . 10 . 20 . 30 . 40 . 50
 ccgtctatagttcagttagaagaacgttcgactgtaatggttaagcatat
 atcgaaaggctcgctggtgcaagtccagctagacgga

Intron from tRNA-Tyr(gta)
 1 . 10 . 20 . 30 . 40 . 50
 tggttaagcatat

Intron Length: 13
 Intron Insertion Position(37-38): tgtaa-Intron-atcga

8.

```

      t
      g-c
      c-g
      t-a
      c-g
      a-t
      t-a
      a-t      tt
t    aagtc    a

```

```

aa      g      !!!!! g
t  tgtg      ttcag c
g  +!!!!      t      tt
g  gcac      a
ta      t      a
          a-tc
          a-t
          a-t
          g-c
          a-t
          t      t
          t      a
          ttg

```

tRNA-Gln(ttg)
 71 bases, %GC = 33.8
 Sequence [322836,322906]

Primary sequence for tRNA-Gln(ttg)
 1 . 10 . 20 . 30 . 40 . 50
 gctcatatggtgtaatggtagcactaaagatTTTgattctttcaatttca
 gttcgaattctgaatatgagct

tRNA anticodon frequency

AAA Phe	AGA Ser	ATA Tyr 1	ACA Cys
GAA Phe	GGA Ser	GTA Tyr 1	GCA Cys
TAA Leu 1	TGA Ser 1	TTA Stop	TCA SeC
CAA Leu	CGA Ser	CTA Pyl	CCA Trp
AAG Leu	AGG Pro	ATG His	ACG Arg
GAG Leu	GGG Pro	GTG His	GCG Arg
TAG Leu	TGG Pro	TTG Gln 1	TCG Arg
CAG Leu	CGG Pro	CTG Gln	CCG Arg
AAT Ile	AGT Thr 1	ATT Asn	ACT Ser
GAT Ile	GGT Thr	GTT Asn	GCT Ser
TAT Ile 1	TGT Thr	TTT Lys	TCT Arg 1
CAT Met	CGT Thr	CTT Lys	CCT Arg
AAC Val	AGC Ala	ATC Asp	ACC Gly

GAC Val	GGC Ala	GTC Asp	GCC Gly
TAC Val	TGC Ala	TTC Glu	TCC Gly
CAC Val	CGC Ala	CTC Glu	CCC Gly

tRNA codon frequency

TTT Phe	TCT Ser	TAT Tyr 1	TGT Cys
TTC Phe	TCC Ser	TAC Tyr 1	TGC Cys
TTA Leu 1	TCA Ser 1	TAA Stop	TGA SeC
TTG Leu	TCG Ser	TAG Pyl	TGG Trp
CTT Leu	CCT Pro	CAT His	CGT Arg
CTC Leu	CCC Pro	CAC His	CGC Arg
CTA Leu	CCA Pro	CAA Gln 1	CGA Arg
CTG Leu	CCG Pro	CAG Gln	CGG Arg
ATT Ile	ACT Thr 1	AAT Asn	AGT Ser
ATC Ile	ACC Thr	AAC Asn	AGC Ser
ATA Ile 1	ACA Thr	AAA Lys	AGA Arg 1
ATG Met	ACG Thr	AAG Lys	AGG Arg
GTT Val	GCT Ala	GAT Asp	GGT Gly
GTC Val	GCC Ala	GAC Asp	GGC Gly
GTA Val	GCA Ala	GAA Glu	GGA Gly
GTG Val	GCG Ala	GAG Glu	GGG Gly

Number of tRNA genes with no introns = 6

Number of tRNA genes with C-loop introns = 2

tRNA GC range = 33.8% to 53.7%

Number of tmRNA genes = 0

Paramecium bursaria Chlorella virus

NC_024697

370920 nucleotides in sequence

Mean G+C content = 28.7%

1.

t
g-c
c-g
t-a
t-a
t-a

```

      t-a
      g-c      tt
      t      ggcgc a
aa      g      !!!!! g
t ttcg      ccgcg c
g !!!!!      t      tt
g aagc      t
ta      g      a
      a-tag
      c-g
      a-t
      t-a
      c-g
      c      a
      t      a
      agt

```

tRNA-Thr(agt)
 72 bases, %GC = 45.8
 Sequence c[118324,118395]

Primary sequence for tRNA-Thr(agt)
 1 . 10 . 20 . 30 . 40 . 50
 gcttttgtggcttaatggtaaagcgacatcctagtaagatgtagattccg
 cgttcgaattcgcggcaaaagct

2.

```

      t
      g+t
      c-g
      c-g
      c-g
      t-a
      a-t
      t-a      ct
      t      gaccc a
taa      g      !!!!! g
t agcg      ctggg c

```

```

g   !!!!   t   tt
g   tcgc   t
ata   g   a
      t-aag
      c-g
      c-g
      g-c
      c-g
      c   a
      t   a
      tct

```

tRNA-Arg(tct)
74 bases, %GC = 52.7
Sequence c[148317,148390]

Primary sequence for tRNA-Arg(tct)
1 . 10 . 20 . 30 . 40 . 50
gccctattggcgaaattggatatcgcgctccgccttctaagcggaagattc
tgggttcgatccccagatagggtt

3.

```

      a
      a-t
      t-a
      c-g
      t-a
      g-c
      t-a
      t-a   ca
      t   t   cgttc   a
tgag   g   !!!!   g
g   gcg   gcaag   c
g   !!!   tt
t   cgc   c
ctaa   g   t+g
      c-g   c-g
      c-g   t-a

```

```

      g-c   c-g
      g-c   t   c
      a c       aa
t      c
t      g
      taa

```

tRNA-Leu(taa)
82 bases, %GC = 53.7
Sequence [322252,322333]

Primary sequence for tRNA-Leu(taa)
1 . 10 . 20 . 30 . 40 . 50
atctgtttggcggagtggtctaacgcgccggatttaagccccggtctcta
acgaggcgcaagttcgaaccttgcaacagata

4.

```

      t
      t-a
      t-a
      c-g
      g-c
      c-g
      c-g
      t-a
      a-t      ta
      t      tacc a
ctaa a      !!!!! a
t      ctta      atggg c
g      !!!!!      t      tt
g      gaat      a
      tta      t
      g+t
      a-t
      c-g
      c-g
      g-c
      t+g

```

```

c   a
t   a
tat

```

```

tRNA-Ile(tat)
76 bases, %GC = 38.2
Sequence [322371,322446]

```

```

Primary sequence for tRNA-Ile(tat)
1   .   10   .   20   .   30   .   40   .   50
ttcgcctataattcaatctggttagaatgaccgtcttataagcggtttat
atgggttcaaattcccattaggcgaat

```

5.

```

          g
        g-c
        a-t
        t-a
        c-g
        t-a
        c-g
        g-c      tt
      t      gacac a
ttaa      a      !!!!! g
g      tacg      ctgtg c
g      :! :      t      tt
t      ttag      gct.t
ctg      g      g.a
      g-c      t+g
      a c      t-a
      a-t      a      a
      t-a      a      g
      g-c      ccg
g      g
t      a
ata

```

```

tRNA-Tyr(ata)

```

88 bases, %GC = 45.5
Sequence [322481,322585]

Primary sequence for tRNA-Tyr(ata)

```
1   .   10   .   20   .   30   .   40   .   50
gatctcgtagcataattggtctgttaggaatggtataaccatcttcccaa
caaatgcatccggctgttaaccggaagattctgtgttcgattcacagcga
gatcg
```

Intron from tRNA-Tyr(ata)

```
1   .   10   .   20   .   30   .   40   .   50
ccatcttcccaacaaat
```

Intron Length: 17

Intron Insertion Position(38-39): tataa-Intron-gcatc

6.

```

      t
      g-c
      a-t
      t-a
      a-t
      c-g
      t-a
      g-c      tg
      t      ctgc a
taag  g      !!!!! g
t      gta      gagcg c
g      !!!      t      tt
g      cat      g
taga      g-c
      g+t c-g
      t.t c-g
      c-g c      g
      a-t      gat
      g-c
      a-t
c      a
t      a
      tga
```

tRNA-Ser(tga)
 83 bases, %GC = 49.4
 Sequence [322625,322707]

Primary sequence for tRNA-Ser(tga)
 1 . 10 . 20 . 30 . 40 . 50
 gatactgtgatggaattggtagacatgtcagacttgaaatctgttgcccg
 atgggcgtgagcgttcgagtcgctccagtatct

7.

```

      a
      c-g
      c-g
      g-c
      t-a
      c-g
      t-a
      a-t      tg
      t      cgacc a
ga      a      !!!!! a
t      cttg      gctgg c
t      !!!!!      c      tg
a      gaac      t
gaa      g      g
      t-aag
      t-a
      c-g
      g-c
      a-t
      c      a
      t      a
      gta

```

tRNA-Tyr(gta)
 73 bases, %GC = 47.9
 Sequence [322727,322812]

Primary sequence for tRNA-Tyr(gta)

```

1   .   10   .   20   .   30   .   40   .   50
ccgtctatagttcagttagaagaacgttcgactgtaatggttaagcatat
atcgaaaggctcgctggtgcaagtccagctagacgga

```

Intron from tRNA-Tyr(gta)

```

1   .   10   .   20   .   30   .   40   .   50
tggttaagcatat

```

Intron Length: 13

Intron Insertion Position(37-38): tgtaa-Intron-atcga

8.

```

          t
        g-c
        c-g
        t-a
        c-g
        a-t
        t-a
        a-t      tt
      t  aagtc  a
aa  g  !!!!!  g
t  tgtg  ttcag  c
g  +!!!  t  tt
g  gcac  a
ta  t  a
      a-tc
      a-t
      a-t
      g-c
      a-t
      t  t
      t  a
      ttg

```

tRNA-Gln(ttg)

71 bases, %GC = 33.8
Sequence [322836,322906]

Primary sequence for tRNA-Gln(ttg)

1 . 10 . 20 . 30 . 40 . 50
gctcatatggtgtaatggtagcactaaagatTTTgattctttcaatttca
gttcgattctgaatatgagct

tRNA anticodon frequency

AAA Phe	AGA Ser	ATA Tyr 1	ACA Cys
GAA Phe	GGA Ser	GTA Tyr 1	GCA Cys
TAA Leu 1	TGA Ser 1	TTA Stop	TCA SeC
CAA Leu	CGA Ser	CTA Pyl	CCA Trp
AAG Leu	AGG Pro	ATG His	ACG Arg
GAG Leu	GGG Pro	GTG His	GCG Arg
TAG Leu	TGG Pro	TTG Gln 1	TCG Arg
CAG Leu	CGG Pro	CTG Gln	CCG Arg
AAT Ile	AGT Thr 1	ATT Asn	ACT Ser
GAT Ile	GGT Thr	GTT Asn	GCT Ser
TAT Ile 1	TGT Thr	TTT Lys	TCT Arg 1
CAT Met	CGT Thr	CTT Lys	CCT Arg
AAC Val	AGC Ala	ATC Asp	ACC Gly
GAC Val	GGC Ala	GTC Asp	GCC Gly
TAC Val	TGC Ala	TTC Glu	TCC Gly
CAC Val	CGC Ala	CTC Glu	CCC Gly

tRNA codon frequency

TTT Phe	TCT Ser	TAT Tyr 1	TGT Cys
TTC Phe	TCC Ser	TAC Tyr 1	TGC Cys
TTA Leu 1	TCA Ser 1	TAA Stop	TGA SeC
TTG Leu	TCG Ser	TAG Pyl	TGG Trp
CTT Leu	CCT Pro	CAT His	CGT Arg
CTC Leu	CCC Pro	CAC His	CGC Arg
CTA Leu	CCA Pro	CAA Gln 1	CGA Arg
CTG Leu	CCG Pro	CAG Gln	CGG Arg
ATT Ile	ACT Thr 1	AAT Asn	AGT Ser
ATC Ile	ACC Thr	AAC Asn	AGC Ser

ATA Ile 1	ACA Thr	AAA Lys	AGA Arg 1
ATG Met	ACG Thr	AAG Lys	AGG Arg
GTT Val	GCT Ala	GAT Asp	GGT Gly
GTC Val	GCC Ala	GAC Asp	GGC Gly
GTA Val	GCA Ala	GAA Glu	GGA Gly
GTG Val	GCG Ala	GAG Glu	GGG Gly

Number of tRNA genes with no introns = 6
 Number of tRNA genes with C-loop introns = 2
 tRNA GC range = 33.8% to 53.7%
 Number of tmRNA genes = 0

vSAG1.JdFR (Genome from Current Study)

306156 nucleotides in sequence
 Mean G+C content = 24.1%

1.

```

      a
    c-g
    t-a
    c-g
    t-a
    c-g
    t+g
    g-c      ta
      t    ggtcc a
    ga    a    !!!!! g
    t  ctcg    ccagg c
    t    !!!!! c    tt
    g    gagc    t
    gca    g    g
      g+tag
    g-c
    g-c
    g-c
    a-t
    c    a
    t    g
    gta
  
```

tRNA-Tyr(gta)
73 bases, %GC = 58.9
Sequence [20672,20764]

Primary sequence for tRNA-Tyr(gta)
1 . 10 . 20 . 30 . 40 . 50
ctctctgtagctcagttggcagagcgggggactgtagatggtttttagatt
agcagtgatccctaggtcccaggttcgaatcctggcgagagaga

Intron from tRNA-Tyr(gta)
1 . 10 . 20 . 30 . 40 . 50
atggtttttagatttagcagtg

Intron Length: 20
Intron Insertion Position(37-38): tgtag-Intron-atccc
Number of tmRNA genes = 0

vSAG8.JdFR (Genome from Current Study)

300125 nucleotides in sequence
Mean G+C content = 21.2%

1.

```

      a
      c-g
      t-a
      c-g
      t-a
      c-g
      t+g
      g-c      ta
      t      ggtcc a
ga      a      !!!!! g
t      ctcg      ccagg c
t      !!!!!      c      tt
g      gagc      t
gca      g      g
      g+tag
      g-c
```

g-c
g-c
a-t
c a
t g
gta

tRNA-Tyr(gta)
73 bases, %GC = 58.9
Sequence [20161,20253]

Primary sequence for tRNA-Tyr(gta)
1 . 10 . 20 . 30 . 40 . 50
ctctctgtagctcagttggcagagcgggggactgtagatggtttttagatt
agcagtgatccctaggtcccaggttcgaatcctggcgagaga

Intron from tRNA-Tyr(gta)
1 . 10 . 20 . 30 . 40 . 50
atggtttttagattagcagtg

Intron Length: 20
Intron Insertion Position(37-38): tgtag-Intron-atccc
Number of tmRNA genes = 0

ARAGORN v1.2.38 Dean Laslett

Please reference the following paper if you use this
program as part of any published research.

Laslett, D. and Canback, B. (2004) ARAGORN, a
program for the detection of transfer RNA and
transfer-messenger RNA genes in nucleotide sequences.
Nucleic Acids Research, 32;11-16.

Searching for tRNA genes with introns in anticodon loop
Intron length from 0 to 3000 bases
Searching for tmRNA genes
Assuming linear topology, search will not wrap around ends

Searching both strands
Using standard genetic code