

(1) 1 10 20 38
 AM282986 (1) T TCCAC TGC C T TCCACCAAGCTC T GCA G GATCCC A A AG
 Source(1..3215): Source_1
 CDS(2307..1623): CDS POLYMERASE (P)
 Mature Peptide(2847..129): Domain of ...
 CDS(2854..835): CDS LARGE (L) SURFACE
 CDS(3211..835): CDS MIDDLE (M) SURFAC...
 mRNA(2835..1930): mRNA Large S
 mRNA(3185..1930): mRNA Middle S

gi_59439_emb_X65259.1_HBVAYWE (1) CTCCAC AAC CT TCCACCAA A CTCT GCAAGATCCC A G AG
 gi_221497_dbj_D00329.1_HPBADW1 (1) CTCCAC CACT TCCACCAA A CTCT TCAAGATCCC A G AG
 gi_59422_emb_X69798.1_HBVADW4A (1) CTC AAC CCAG T TCCACCAAGCTC T GTTG GATCCC A G GG
 NC_001484 (1) CTG CAG GG GAT T TGCAG - AG GGACT GAGAGC TC TA ACCA
 NC_001719 (1) CT T CAG GG GCT T TGC GG - AG GGACT GAGAGC T TTA A C AA
 NC_004107 (1) CTCCAG GG GT T C G TAG - AC GGAT TAC GAGA C TTG A C AA
 OHVHEPBA (1) CTCCAG GG GT T C G TAG - AC GGAT TAC GAGA C TTG A C AA
 NC_001896 (1) C A C GT C T C T TCCAGAGTTA T C T T CAGAATCCA A AGG
 NC_002168 (1) CTCCAC GGT T TCCACCAAGCTC T GCA G GATCCC A G AG
 gi_452617_emb_X75657.1_HHVBBAS (1) T TCCAC AAC AT TCCACCAAGCTC T GCA G GATCCC A G AG
 gi_6983934_gb_AF160501.1_AF160501 (1) CTCTAC A GC AT TCCACCAAGCTC T ACAA AATCCC A A AG
 Consensus (1) CTCCAC GCTTTCCACCAAGCTCTGCAAGATCCCA AG

(39) 39 50 60 76
 AM282986 (39) T CAGG GGT C TGT A T T T C C T G C T G G T G G C T C C A G T T C A
 Source(1..3215): Source_1
 CDS(2307..1623): CDS POLYMERASE (P)
 Mature Peptide(2847..129): Domain of ...
 CDS(2854..835): CDS LARGE (L) SURFACE
 CDS(3211..835): CDS MIDDLE (M) SURFAC...
 mRNA(2835..1930): mRNA Large S
 mRNA(3185..1930): mRNA Middle S

gi_59439_emb_X65259.1_HBVAYWE (39) T G A G A G G C C T G T A T T T C C C T G C T G G T G G C T C C A G T T C A
 gi_221497_dbj_D00329.1_HPBADW1 (39) T C A G G G C T C T G T A C T T T C C T G C T G G T G G C T C C A G T T C A
 gi_59422_emb_X69798.1_HBVADW4A (39) T A A G G G C T C T G T A C T T C C C T G C T G G T G G C T C C A G T T C A
 NC_001484 (38) C C T C A G A T C A T C A C A A C T C T G C C T A T G G A G A T C C T T T T
 NC_001719 (38) C A C C G G A A C A T C A A C A T T C T G C T A T G G A G A T C C T T T T
 NC_004107 (38) C A A C G G A A C G C C A A C A C A A T G C C T A T G G A G A T C C T T T T
 OHVHEPBA (38) C A A C G G A A C G C C A A C A C A A T G C C T A T G G A G A T C C T T T T
 NC_001896 (39) T C A G A G G C C T C T A C T T T C C T G C T G G T G G C T C A A C T T C A
 NC_002168 (39) T A A G G G G T C T G T A T T T C C C T G C T G G T G G C T C C A G T T C A
 gi_452617_emb_X75657.1_HHVBBAS (39) T A A G A G G C C T G T A T T T C C C T G C T G G T G G C T C C A G T T C C
 gi_6983934_gb_AF160501.1_AF160501 (39) T C A G G G G C C T G T A T T T C C C T G C T G G T G G C T C C A G T T C A
 Consensus (39) T A A G G G G C T G T A T T T C C C T G C T G G T G G C T C C A G T T C A

AM282986 (77) 77 90 100 114
 (77) GGAACAGTAAACCCTGCTCCGAAATATGCGCTCTCACAT

Source(1..3215): Source_1
 CDS(2307..1623): CDS POLYMERASE (P)
 Mature Peptide(2847..129): Domain of ...

CDS(2854..835): CDS LARGE (L) SURFACE
 CDS(3211..835): CDS MIDDLE (M) SURFAC...

mRNA(2835..1930): mRNA Large S
 mRNA(3185..1930): mRNA Middle S

gi_59439_emb_X65259.1_HBVAYWE (77) GGAACAGTAAACCCTGTTCTGACTACTGCGCTCTCCCTT
 gi_221497_dbj_D00329.1_HPBADW1 (77) GGAACAGTAAAGCCCTGCTCAGAACTACTGTCTCAGCCAT
 gi_59422_emb_X69798.1_HBVADW4A (77) GGGACACAGAAACCCTGCTCCGACTATGCGCTCTCTCAC
 NC_001484 (76) ACTACACTAAGCCCTGTGGTACCTACTGTCTCCACCAC
 NC_001719 (76) ACAACACTGAGCCCTGTGGTGCCTACTGTCTCCACCAC
 NC_004107 (76) ACAACACTAAGCCCTGCGGTTCTACTGTATCCACCAT
 OHVHEPBA (76) ACAACACTAAGCCCTGCGGTTCTACTGTATCCACCAT
 NC_001896 (77) AGCATTGTCAAACCCTGTTCCGACCACTGCGCTCCACCAC
 NC_002168 (77) GGGACAGTGAAGCCCTGTTCCGACTACTGCGCTCTCCCAT
 gi_452617_emb_X75657.1_HHVBBAS (77) GGAACAGTGAACCCTGTTCCGACTACTGCGCTCACTCAT
 gi_6983934_gb_AF160501.1_AF160501 (77) GGGATAGTGAACCCTGTTCCGACTATGCGCTCTCACAT
 Consensus (77) GGAACAGTAAAGCCCTGTTCCGACTACTGCGCTC CCCAT

AM282986 (115) 115 120 130 140 152
 (115) CTCGTCAATCTCCGCGAGGACTGGGGACCCTGTGACGA

Source(1..3215): Source_1
 CDS(2307..1623): CDS POLYMERASE (P)
 Mature Peptide(2847..129): Domain of ... Mature Peptide(137..1161): Domain of ...
 Mature Peptide(137..1161): Domain of ...

CDS(2854..835): CDS LARGE (L) SURFACE
 CDS(3211..835): CDS MIDDLE (M) SURFAC...

mRNA(2835..1930): mRNA Large S
 mRNA(3185..1930): mRNA Middle S

gi_59439_emb_X65259.1_HBVAYWE (115) ATCGTCAATCTCCGCGAGGACTGGGGACCCTGCACTGA
 gi_221497_dbj_D00329.1_HPBADW1 (115) ATCGTCAATCTTATCGAAGACTGGGGACCCTGTGCCGA
 gi_59422_emb_X69798.1_HBVADW4A (115) ATCATCAATCTTCTCGAAGACTGGGGGCCCTGCTATGA
 NC_001484 (114) ATTGTCTCCTCCAATGACGATGTTGGGGACCCTGTACTTT
 NC_001719 (114) ATTGTCTCCTCCCTTGAAGATGTTGGGGACCCTGTACAAAT
 NC_004107 (114) ATTGTCTCCTCCCTCGACGACTGGGGACCCTGCACTGT
 OHVHEPBA (114) ATTGTCTCCTCCCTCGACGACTGGGGACCCTGCACTGT
 NC_001896 (115) ATCGTCAAGCTTCTCGACGACTGGGGTCCCTGTCAGCA
 NC_002168 (115) ATCGTCAACCTTCTTGAAGACTGGGGACCCTGCACTGA
 gi_452617_emb_X75657.1_HHVBBAS (115) CTCGTCAATCTTCTCGAAGACTGGGGACCCTGCACCGA
 gi_6983934_gb_AF160501.1_AF160501 (115) CTCGTCAATCTTCTCAGGACTGGGGACCCTGCACCGA
 Consensus (115) ATCGTCAATCTTCTCGA GACTGGGGACCCTGCACTGA

		(153)	153	160	170	180	190
AM282986	(153)	A T A T G G A G A A C A T C A C A T C A G G A T T C C T A G G A C C C C T G					
		Source(1..3215): Source_1					
		CDS(2307..1623): CDS POLYMERASE (P)					
		Mature Peptide(137..1161): Domain of ...					
		Mature Peptide(137..1161): Domain of ...					
		CDS(2854..835): CDS LARGE (L) SURFACE					
		CDS(3211..835): CDS MIDDLE (M) SURFAC...					
		CDS(155..835): CDS SMALL (S) SURFACE ...					
		mRNA(2835..1930): mRNA Large S					
		mRNA(3185..1930): mRNA Middle S					
gi_59439_emb_X65259.1_HBVAYWE	(153)	A C A T G G A G A A C A T C A C A T C A G G A T T C C T A G G A C C C C T G					
gi_221497_dbj_D00329.1_HPBADW1	(153)	A C A T G G A G A A C A T C G C A T C A G G A C T C C T A G G A C C C C T G					
gi_59422_emb_X69798.1_HBVADW4A	(153)	A C A T G G A C A A C A T T A C A T C A G G A C T C C T A G G A C C C C T G					
NC_001484	(152)	C G A C G G A G A T G T C A C C A T C A G G T C T C C T A G G A C T C C T C					
NC_001719	(152)	C A G C G G A G A T G T C A C C A T C A G G T C T C C T A G G A C T C C T C					
NC_004107	(152)	C A C C G G A G A T G T C A C C A T C A A G T C T C C T A G G A C T C C T C					
OHVHEPBA	(152)	C A C C G G A G A T G T C A C C A T C A A G T C T C C T A G G A C T C C T C					
NC_001896	(153)	C C A T G G A C A T C A C T T C A T C A G G A T T C C T A G G A C C C C T T					
NC_002168	(153)	A C A T G G A G A G C A T C T C A T C A G G A T T C C T A G G A C C C C T G					
gi_452617_emb_X75657.1_HHVBBAS	(153)	A C A T G G A A A G C A T C A C A T C A G G A T T C C T A G G A C C C C T G					
gi_6983934_gb_AF160501.1_AF160501	(153)	A C A T G G A G A A C A T C A C A T C A G G A T T C C T A G G A C C C C T G					
Consensus	(153)	A C A T G G A G A C A T C A C A T C A G G A T T C C T A G G A C C C C T G					

		(191)	191	200	210	228	
AM282986	(191)	C T C G T G T T A C A G G C G G G T T T T T C T T G T T G A C A A G A A T					
		Source(1..3215): Source_1					
		CDS(2307..1623): CDS POLYMERASE (P)					
		Mature Peptide(137..1161): Domain of ...					
		Mature Peptide(137..1161): Domain of ...					
		CDS(2854..835): CDS LARGE (L) SURFACE					
		CDS(3211..835): CDS MIDDLE (M) SURFAC...					
		CDS(155..835): CDS SMALL (S) SURFACE ...					
		mRNA(2835..1930): mRNA Large S					
		mRNA(3185..1930): mRNA Middle S					
gi_59439_emb_X65259.1_HBVAYWE	(191)	C T C G T G T T A C A G G C G G G T T T T T C T T G T T G A C A A G A A T					
gi_221497_dbj_D00329.1_HPBADW1	(191)	C T C G T G T T A C A G G C G G G T T T T T C T T G T T G A C A A A A A T					
gi_59422_emb_X69798.1_HBVADW4A	(191)	C T C G T G T T A C A G G C G G T G T G T T T T C T T G T T G A C A A A A A T					
NC_001484	(190)	G C A G G A T T A C A G G T G G T A T A T T T C T T G T G G A C A A A A A T					
NC_001719	(190)	G C G G A T T A C A G G T G G T G T A T T T C T T G T G G A C A A A C A T					
NC_004107	(190)	G C A G G A T T A C A G G T G G T G T A T T T C T T G T G G A C A A A A A T					
OHVHEPBA	(190)	G C A G G A T T A C A G G T G G T G T A T T T C T T G T G G A C A A A A A T					
NC_001896	(191)	C T C G C A T T A C A G G C G G T G T T T T T C T T G T T G A C A A A A A T					
NC_002168	(191)	C T C G T G T T A C A G G C G G G T T T T T C T T G T T G A C A A A A A T					
gi_452617_emb_X75657.1_HHVBBAS	(191)	C T C G T G T T A C A G G C G G G T T T T T C T T G T T G A C A A A A A T					
gi_6983934_gb_AF160501.1_AF160501	(191)	C T C G T G T T A C A G G C G G G T T T T T C T T G T T G A C A A G A A T					
Consensus	(191)	C T C G T G T T A C A G G C G G T G T T T T T C T T G T T G A C A A A A A T					

(229) 229 240 250 266
 AM282986 (229) CCTCACAATACCGCAGAGTCTAGACTCGTGGTGGACTT
 Source(1..3215): Source_1
 CDS(2307..1623): CDS POLYMERASE (P)
 Mature Peptide(137..1161): Domain of ...
 Mature Peptide(137..1161): Domain of ...
 CDS(2854..835): CDS LARGE (L) SURFACE
 CDS(3211..835): CDS MIDDLE (M) SURFAC...
 CDS(155..835): CDS SMALL (S) SURFACE ...
 mRNA(2835..1930): mRNA Large S
 mRNA(3185..1930): mRNA Middle S

gi_59439_emb_X65259.1_HBVAYWE (229) CCTCACAATACCGCAGAGTCTAGACTCGTGGTGGACTT
 gi_221497_dbj_D00329.1_HPBADW1 (229) CCTCACAATACCA CAGAGTCTAGACTCGTGGTGGACTT
 gi_59422_emb_X69798.1_HBVADW4A (229) CCTCACAATACCA CAGAGTCTAGACTCGTGGTGGACTT
 NC_001484 (228) CCTTACAATAGCTCAGAGTCTAGACTG GTGGTGGACTT
 NC_001719 (228) CCTCACAATAGCTCAGAGTCTCGATTG GTGGTGGACTT
 NC_004107 (228) CCTAACAAATAGCTCAGAA TCTAGATTG GTGGTGGACTT
 OHVHEPBA (228) CCTAACAAATAGCTCAGAA TCTAGATTG GTGGTGGACTT
 NC_001896 (229) CCTCACAATGCCA CAGAGTCTAGACTCGTT GTGGACTT
 NC_002168 (229) CCTCACAATTCCTCAGAGTCTAGACTCGTGGTGGACTT
 gi_452617_emb_X75657.1_HHVBBAS (229) CCTCACAATACCGCAGAGTCTAGACTCGTGGTGGACTT
 gi_6983934_gb_AF160501.1_AF160501 (229) CCTCACAATACCGCAGAGTCTAGACTCGTGGTGGACTT
 Consensus (229) CCTCACAATACC CAGAGTCTAGACTCGTGGTGGACTT

(267) 267 280 290 304
 AM282986 (267) CTCTCAATTTTCTAGGGGAACTACCCGTGTGTCCTGGC
 Source(1..3215): Source_1
 CDS(2307..1623): CDS POLYMERASE (P)
 Mature Peptide(137..1161): Domain of ...
 Mature Peptide(137..1161): Domain of ...
 CDS(2854..835): CDS LARGE (L) SURFACE
 CDS(3211..835): CDS MIDDLE (M) SURFAC...
 CDS(155..835): CDS SMALL (S) SURFACE ...
 mRNA(2835..1930): mRNA Large S
 mRNA(3185..1930): mRNA Middle S

gi_59439_emb_X65259.1_HBVAYWE (267) CTCTCAATTTTCTAGGGGAACTACCCGTGTGTCCTGGC
 gi_221497_dbj_D00329.1_HPBADW1 (267) CTCTCAATTTTCTAGGGGAACTACCCGTGTGTCCTGGC
 gi_59422_emb_X69798.1_HBVADW4A (267) CTCTCAATTTTCTAGGGGAACTACCCGTGTGTCCTGGC
 NC_001484 (266) CTCTCAGTTTTCAGGGGCACTACCCAGTGCACTGGC
 NC_001719 (266) CTCTCAGTTTTCAGGGGCACTACCCAGTGCACTGGC
 NC_004107 (266) CTCTCAGTTTTCAGGGGCACTACCCAGTGCACTGGC
 OHVHEPBA (266) CTCTCAGTTTTCAGGGGCACTACCCAGTGCACTGGC
 NC_001896 (267) CTCTCAATTTTCTAGGGGAACTACCCAGCTGTGTCCTGGC
 NC_002168 (267) CTCTCAATTTTCTAGGGGAGCTACCCGTGTGTCCTGGC
 gi_452617_emb_X75657.1_HHVBBAS (267) CTCTCAATTTTCTAGGGGAGCTACCCGTGTGTCCTGGC
 gi_6983934_gb_AF160501.1_AF160501 (267) CTCTCAATTTTCTAGGGGAGCTACCCGTGTGTCCTGGC
 Consensus (267) CTCTCAATTTTCTAGGGGAACTACCCGTGTGTCCTGGC

(305) 305 310 320 330 342
 AM282986 (305) CAAAATT CGCAGT C CCAA CCT CCAAT CACT CACCAAC

Source(1..3215): Source_1

CDS(2307..1623): CDS POLYMERASE (P)

Mature Peptide(137..1161): Domain of ...

Mature Peptide(137..1161): Domain of ...

CDS(2854..835): CDS LARGE (L) SURFACE

CDS(3211..835): CDS MIDDLE (M) SURFAC...

CDS(155..835): CDS SMALL (S) SURFACE ...

mRNA(2835..1930): mRNA Large S

mRNA(3185..1930): mRNA Middle S

gi_59439_emb_X65259.1_HBVAYWE (305) CAAAATT CGCAGT C CCAA CCT CCAAT CACT CACCAAC

gi_221497_dbj_D00329.1_HPBADW1 (305) CAAAATT CGCAGT C CCAA TCT CAGT CACT CACCAAC

gi_59422_emb_X69798.1_HBVADW4A (305) CAAAATT CGCAGT C CCAA CCT CCAAT CACT TACCAAC

NC_001484 (304) CAAAATT TGCAGT T CCAA CCT GCAA CACT TGCCAAC

NC_001719 (304) CAAAATT TGCAGT T CTTAACT TGCAAG CACT TGCCAAC

NC_004107 (304) CAAAATT CGCAGT T CCAA ACT TGCAA CACT TGCCAAC

OHVHEPBA (304) CAAAATT CGCAGT T CCAA ACT TGCAA CACT TGCCAAC

NC_001896 (305) CTAAATT CGCAGT C CCAA CCT CAGT CACT CACCAAC

NC_002168 (305) CAAAATT CGCAGT C CTTAACT CCAAT CACT CACCAAC

gi_452617_emb_X75657.1_HHVBBAS (305) CAAAATT CGCAGT C CCAA CCT CAGT CACT CACCAAC

gi_6983934_gb_AF160501.1_AF160501 (305) CTAAATT CGCAGT C CCAA CCT CCAAT CACT CACCAAT

Consensus (305) CAAAATT CGCAGT C CCAA CCT CCAAT CACT CACCAAC

(343) 343 350 360 370 380
 AM282986 (343) CTCCTGTCTCCAATTTGTCCTGGTTATCGCTGGATGT

Source(1..3215): Source_1

CDS(2307..1623): CDS POLYMERASE (P)

Mature Peptide(137..1161): Domain of ...

Mature Peptide(137..1161): Domain of ...

CDS(2854..835): CDS LARGE (L) SURFACE

CDS(3211..835): CDS MIDDLE (M) SURFAC...

CDS(155..835): CDS SMALL (S) SURFACE ...

mRNA(2835..1930): mRNA Large S

mRNA(3185..1930): mRNA Middle S

gi_59439_emb_X65259.1_HBVAYWE (343) CTCCTGTCTCCAACTTGTCTGGTTATCGCTGGATGT

gi_221497_dbj_D00329.1_HPBADW1 (343) CTGTTGTCTCCAATTTGTCCTGGTTATCGCTGGATGT

gi_59422_emb_X69798.1_HBVADW4A (343) CTCCTGTCTCCAACTTGTCTGGTTATCGCTGGATGT

NC_001484 (342) CTCCTGTCTCCAACCTGCAA TGGCTTTCGCTGGATGT

NC_001719 (342) CTCCTGTCTCCAACCTGCAA TGGCTTTCGCTGGATGT

NC_004107 (342) CTCCTGTCTCCAACTTGC AA TGGCTTTCGCTGGATGT

OHVHEPBA (342) CTCCTGTCTCCAACTTGC AA TGGCTTTCGCTGGATGT

NC_001896 (343) CTGCTGTCTCCA GACTTGTCTGGTTATCGCTGGATGT

NC_002168 (343) CTCCTGTCTCCAATTTGTCCTGGTTATCGCTGGATGT

gi_452617_emb_X75657.1_HHVBBAS (343) CTCCTGTCTCCAATTTGTCCTGGTTATCGCTGGATGT

gi_6983934_gb_AF160501.1_AF160501 (343) CTCCTGTCTCCAACTTGTCTGGTTATCGCTGGATGT

Consensus (343) CTCCTGTCTCCAACTTGTCTGGTTATCGCTGGATGT

(381) 381 390 400 418
 AM282986 (381) **GTCTGCGGCGTTTATCATATTCTCTTCATCCTGCTG**
 Source(1..3215): Source_1
 CDS(2307..1623): CDS POLYMERASE (P)
 Mature Peptide(137..1161): Domain of ...
 Mature Peptide(137..1161): Domain of ...
 CDS(2854..835): CDS LARGE (L) SURFACE
 CDS(3211..835): CDS MIDDLE (M) SURFAC...
 CDS(155..835): CDS SMALL (S) SURFACE ...
 mRNA(2835..1930): mRNA Large S
 mRNA(3185..1930): mRNA Middle S

gi_59439_emb_X65259.1_HBVAYWE (381) **GTCTGCGGCGTTTATCATCTTCTCTTCATCCTGCTG**
 gi_221497_dbj_D00329.1_HPBADW1 (381) **GTCTGCGGCGTTTATCATCTTCTCTTCATCCTGCTG**
 gi_59422_emb_X69798.1_HBVADW4A (381) **GTCTGCGGCGTTTATCATCTTCTCTTCATCCTGCTG**
 NC_001484 (380) **ATCTGCGGCGTTTATCATATACCTGTTAGTCCTGCTG**
 NC_001719 (380) **ATCTGCGGCGTTTATCATATACCTGTTAGTCCTGCTG**
 NC_004107 (380) **ATCTGCGGCGTTTATCATATACCTATTAGTCCTGCTG**
 OHVHEPBA (380) **ATCTGCGGCGTTTATCATATACCTATTAGTCCTGCTG**
 NC_001896 (381) **GTCTGCGGCGTTTATCATCTTCTCTTCATCCTGCTT**
 NC_002168 (381) **GTCTGCGGCGTTTATCATCTTCTCTTCATCCTGCTG**
 gi_452617_emb_X75657.1_HHVBBAS (381) **GTCTGCGGCGTTTATCATCTTCTCTTCATCCTGCTG**
 gi_6983934_gb_AF160501.1_AF160501 (381) **GTCTGCGGCGTTTATCATATTCTCTTCATCCTGCTG**
 Consensus (381) **GTCTGCGGCGTTTATCATCTTCTCTTCATCCTGCTG**

(419) 419 430 440 456
 AM282986 (419) **CTATGCCTCATCTTCTTGTGGTTCTTCTGGATTATCA**
 Source(1..3215): Source_1
 CDS(2307..1623): CDS POLYMERASE (P)
 Mature Peptide(137..1161): Domain of ...
 Mature Peptide(137..1161): Domain of ...
 CDS(2854..835): CDS LARGE (L) SURFACE
 CDS(3211..835): CDS MIDDLE (M) SURFAC...
 CDS(155..835): CDS SMALL (S) SURFACE ...
 mRNA(2835..1930): mRNA Large S
 mRNA(3185..1930): mRNA Middle S

gi_59439_emb_X65259.1_HBVAYWE (419) **CTATGCCTCATCTTCTTGTGGTTCTTCTGGACTATCA**
 gi_221497_dbj_D00329.1_HPBADW1 (419) **CTATGCCTCATCTTCTTGTGGTTCTTCTGGACTATCA**
 gi_59422_emb_X69798.1_HBVADW4A (419) **CTATGCCTCATCTTCTTGTGGTTCTTCTGGACTATCA**
 NC_001484 (418) **CTGTTCTTCATCTTCTTGTGGTTCTTCTGGATTGGAA**
 NC_001719 (418) **CTGTTCTTCATCTTCTTGTGGTTCTTCTGGACTGGAA**
 NC_004107 (418) **CTGTTCTTCATCTTCTTGTGGTTCTTCTGGACTGGAA**
 OHVHEPBA (418) **CTGTTCTTCATCTTCTTGTGGTTCTTCTGGACTGGAA**
 NC_001896 (419) **CTATGCCTCATCTTCTTGTGGTTCTTCTGGACTACA**
 NC_002168 (419) **CTATGCCTCATCTTCTTGTGGTTCTTCTGGATTACCG**
 gi_452617_emb_X75657.1_HHVBBAS (419) **CTATGCCTCATCTTCTTGTGGTTCTTCTGGACTATCA**
 gi_6983934_gb_AF160501.1_AF160501 (419) **CTATGCCTCATCTTCTTGTGGTTCTTCTGGACTATCA**
 Consensus (419) **CTATGCCTCATCTTCTTGTGGTTCTTCTGGACTATCA**

(457) 457 470 480 494
 AM282986 (457) AGGTATGTTGCCCGTTGTCCCTCTAATTCCAGGAAC --
 Source(1..3215): Source_1
 CDS(2307..1623): CDS POLYMERASE (P)
 Mature Peptide(137..1161): Domain of ...
 Mature Peptide(137..1161): Domain of ...
 CDS(2854..835): CDS LARGE (L) SURFACE
 CDS(3211..835): CDS MIDDLE (M) SURFAC...
 CDS(155..835): CDS SMALL (S) SURFACE ...
 mRNA(2835..1930): mRNA Large S
 mRNA(3185..1930): mRNA Middle S

gi_59439_emb_X65259.1_HBVAYWE (457) AGGTATGTTGCCCGTTGTCCCTCTAATTCCAGGAATC --
 gi_221497_dbj_D00329.1_HPBADW1 (457) AGGTATGTTGCCCGTTGTCCCTCTAATTCCAGGAATC --
 gi_59422_emb_X69798.1_HBVADW4A (457) AGGTATGTTGCCCGTTGTCCCTCTACTTCCAGGAATC --
 NC_001484 (456) AGGTTTGCCTTCTGTATGTCCCATGATGCCA --G----
 NC_001719 (456) AGGTTTACTCCAGTATGTCCCATACAACCA --T----
 NC_004107 (456) AGGTTTAAATACCTGTCTGTCCCTTTC AACCC --A----
 OHVHEPBA (456) AGGTTTAAATACCTGTCTGTCCCTTTC AACCC --A----
 NC_001896 (457) AGGTATGTTGCCCGTTGTCCCTTCTTCTA CCAACAGTTA
 NC_002168 (457) AGGTATGTTGCCCGTTGTCCCTCTACTTCCAGGAAC --
 gi_452617_emb_X75657.1_HHVBBAS (457) AGGTATGTTGCCCGTTGTCCCTCTAATTCCAGGAATC --
 gi_6983934_gb_AF160501.1_AF160501 (457) AGGTATGTTGCCCGTTGTCCCTCTGATTCAGGAATC --
 Consensus (457) AGGTATGTTGCCCGTTGTCCCTCTACTTCCAGGA C

(495) 495 500 510 520 532
 AM282986 (493) ----AA CAACAACCAAGTACGGGACCA TGCATAAACCTGCTGC
 Source(1..3215): Source_1
 CDS(2307..1623): CDS POLYMERASE (P)
 Mature Peptide(137..1161): Domain of ...
 Mature Peptide(137..1161): Domain of ...
 CDS(2854..835): CDS LARGE (L) SURFACE
 CDS(3211..835): CDS MIDDLE (M) SURFAC...
 CDS(155..835): CDS SMALL (S) SURFACE ...
 mRNA(2835..1930): mRNA Large S
 mRNA(3185..1930): mRNA Middle S

gi_59439_emb_X65259.1_HBVAYWE (493) ----TT CAACAACCAAGCACGGGACCA TGCAGAACCTGCTGC
 gi_221497_dbj_D00329.1_HPBADW1 (493) ----AT CAACCAACCAAGCACGGGACCA TGCAGAACCTGCTGC
 gi_59422_emb_X69798.1_HBVADW4A (493) ----CA CAGACCAACCAAGCACGGGACCA TGCAGAACCTGCTGC
 NC_001484 (488) ----CA CAACAACCAAGCAACAGTAAAT TGCAGACAATGCTGC
 NC_001719 (488) ----CA CACGGAACAACAGTAAAT TGCAGACAATGCTGC
 NC_004107 (488) ----CA CAACAACCAAGCAACAGTCAAT TGCAGACAATGCTGC
 OHVHEPBA (488) ----CA CAACAACCAAGCAACAGTCAAT TGCAGACAATGCTGC
 NC_001896 (495) CAGGAA CAACAACCAAGCACGGGACCA TGCAGACCTGCTGC
 NC_002168 (493) ----CA CACCAACCAAGCGTGGGACCA TGCAGAACCTGCTGC
 gi_452617_emb_X75657.1_HHVBBAS (493) ----AT CAACCAACCAAGTACGGGACCA TGCAGAACCTGCTGC
 gi_6983934_gb_AF160501.1_AF160501 (493) ----CT CAGACCAACCAAGTACGGGACCA TGCAGAACCTGCTGC
 Consensus (495) CAACAACCAAGCACGGGACCA TGCAGAACCTGCTGC

	(533)	533	540	550	560	570
AM282986	(527)	ACGACTCCTG	CTCAAGGCA	ACTCTATGT	TTCCTCA	TG
		Source(1..3215): Source_1				
		CDS(2307..1623): CDS POLYMERASE (P)				
		Mature Peptide(137..1161): Domain of ...				
		Mature Peptide(137..1161): Domain of ...				
		CDS(2854..835): CDS LARGE (L) SURFACE				
		CDS(3211..835): CDS MIDDLE (M) SURFAC...				
		CDS(155..835): CDS SMALL (S) SURFACE ...				
		mRNA(2835..1930): mRNA Large S				
		mRNA(3185..1930): mRNA Middle S				
gi_59439_emb_X65259.1_HBVAYWE	(527)	ACGACTCCTG	CTCAAGGAA	ACTCTATGT	ATCCCTCCTG	
gi_221497_dbj_D00329.1_HPBADW1	(527)	ACA	ACTCCTG	CTCAAGGAA	ACTCTATGT	TTCCTCA
gi_59422_emb_X69798.1_HBVADW4A	(527)	ACA	ACTCT	TGCA	CAAGGAA	ACTCTATGT
NC_001484	(520)	ACC	ATATCT	GTCTCA	AGACAC	CTTTACAACA
NC_001719	(520)	ACA	ATCTCT	GTCTCA	AGACAC	CTTTCAACT
NC_004107	(520)	ACA	ATCTCT	GTCA	CAAGAC	ATGTA
OHVHEPBA	(520)	ACA	ATCTCT	GTCA	CAAGAC	ATGTA
NC_001896	(533)	ACGCC	AATGT	TTC	CAGGCAT	CTTTCGT
NC_002168	(527)	ACG	ATTCT	GTCTC	AGGAA	CTTTTGT
gi_452617_emb_X75657.1_HHVBBAS	(527)	ACGACTC	TGCTCA	AGGAA	ACTCTATGT	TTCCTCA
gi_6983934_gb_AF160501.1_AF160501	(527)	ACGACTC	CTGCTCA	AGGCA	ACTCTATGT	ATCCCTCA
Consensus	(533)	ACGACTCCTG	CTCAAGGC	ACTCTATGT	TTCCTCCTG	

	(571)	571	580	590	608	
AM282986	(565)	TTGCTGT	ACAAAACC	TTCGGAT	GGAAAT	TGCAC
		Source(1..3215): Source_1				
		CDS(2307..1623): CDS POLYMERASE (P)				
		Mature Peptide(137..1161): Domain of ...				
		Mature Peptide(137..1161): Domain of ...				
		CDS(2854..835): CDS LARGE (L) SURFACE				
		CDS(3211..835): CDS MIDDLE (M) SURFAC...				
		CDS(155..835): CDS SMALL (S) SURFACE ...				
		mRNA(2835..1930): mRNA Large S				
		mRNA(3185..1930): mRNA Middle S				
gi_59439_emb_X65259.1_HBVAYWE	(565)	TTGCTGT	ACAAAACC	TTCGGAC	GGAAAT	TGCAC
gi_221497_dbj_D00329.1_HPBADW1	(565)	TTGCTGT	ACAAAACC	TATGGAT	GGAAAC	TGCAC
gi_59422_emb_X69798.1_HBVADW4A	(565)	TTGCTGT	TCAAACC	TTCGGAC	GGAAAC	TGCAC
NC_001484	(558)	CTG	TGTTT	AAAACC	TACGG	CAGGAAAT
NC_001719	(558)	TTG	TGTTT	AAAACC	TACGG	CAGGAAAT
NC_004107	(558)	TTG	TGTTT	AAAACC	TACGG	CAGGAAAT
OHVHEPBA	(558)	TTG	TGTTT	AAAACC	TACGG	CAGGAAAT
NC_001896	(571)	TTGCTGT	ACAAAACC	TTCGGAC	GGAAAC	TGCAC
NC_002168	(565)	TTGCTGT	ACAAAACC	TTCGGAC	GGAAAT	TGCAC
gi_452617_emb_X75657.1_HHVBBAS	(565)	TTGCTGT	TCAAACC	TTCGGAC	GGAAAT	TGCAC
gi_6983934_gb_AF160501.1_AF160501	(565)	TTGCTGT	ACAAAACC	TTCGGAC	GGAAAT	TGCAC
Consensus	(571)	TTGCTGT	TCAAACC	TTCGGAC	GGAAAT	TGCAC

	(609)	609	620	630	646		
AM282986	(603)	TT	CCCATCCC	ATCGTCT	TGGGCTTTC	CGAAAA	TACCTA
		Source(1..3215): Source_1					
		CDS(2307..1623): CDS POLYMERASE (P)					
		Mature Peptide(137..1161): Domain of ...					
		Mature Peptide(137..1161): Domain of ...					
		CDS(2854..835): CDS LARGE (L) SURFACE					
		CDS(3211..835): CDS MIDDLE (M) SURFAC...					
		CDS(155..835): CDS SMALL (S) SURFACE ...					
		mRNA(2835..1930): mRNA Large S					
		mRNA(3185..1930): mRNA Middle S					
gi_59439_emb_X65259.1_HBVAYWE	(603)	TT	CCCATCCC	ATCATCT	TGGGCTTTC	CGAAAA	TTCCTA
gi_221497_dbj_D00329.1_HPBADW1	(603)	TT	CCCATCCC	ATCATCT	TGGGCTTTC	CGAAAA	TACCTA
gi_59422_emb_X69798.1_HBVADW4A	(603)	TT	CCCATCCC	ATCATCC	TGGGCTTTA	GGAAAA	TACCTA
NC_001484	(596)	GG	CCCATCCC	TTCATCAT	TGGGCTTTA	GGAA	GCTACCTA
NC_001719	(596)	GG	CCCATCCC	TTCATCAT	TGGGCTTTA	GGAA	GCTACCTA
NC_004107	(596)	GG	CCCATCCC	TTCATCAT	TGGGCTTTA	GGAA	TACCTA
OHVHEPBA	(596)	GG	CCCATCCC	TTCATCAT	TGGGCTTTA	GGAA	TACCTA
NC_001896	(609)	TT	CCCATCCC	TCATCAT	TGGGCTTTC	CGAAA	TTCCTA
NC_002168	(603)	TT	CCCATCCC	ACATCAT	TGGGCTTTC	CGAAAA	TTCCTA
gi_452617_emb_X75657.1_HHVBBAS	(603)	TT	CCCATCCC	ATCATCA	TGGGCTTTC	CGAAAA	TTCCTA
gi_6983934_gb_AF160501.1_AF160501	(603)	TT	CCCATCCC	ATCATCT	TGGGCTTTC	CGAAAA	TACCTA
Consensus	(609)	TT	CCCATCCC	ATCATCAT	TGGGCTTTC	CGAAAA	TACCTA

	(647)	647	660	670	684		
AM282986	(641)	TGGGAG	TGGGCCT	CAGT	CCGTTTCTC	TGGCTCAG	TTT
		Source(1..3215): Source_1					
		CDS(2307..1623): CDS POLYMERASE (P)					
		Mature Peptide(137..1161): Domain of ...					
		Mature Peptide(137..1161): Domain of ...					
		CDS(2854..835): CDS LARGE (L) SURFACE					
		CDS(3211..835): CDS MIDDLE (M) SURFAC...					
		CDS(155..835): CDS SMALL (S) SURFACE ...					
		mRNA(2835..1930): mRNA Large S					
		mRNA(3185..1930): mRNA Middle S					
gi_59439_emb_X65259.1_HBVAYWE	(641)	TGGGAG	TGGGCCT	CAGC	CCGTTTCTC	TGGCTCAG	TTT
gi_221497_dbj_D00329.1_HPBADW1	(641)	TGGGAG	TGGGCCT	CAGT	CCGTTTCTC	TGGCTCAG	TTT
gi_59422_emb_X69798.1_HBVADW4A	(641)	TGGGAG	TGGGCCT	CAGC	CCGTTTCTC	TGGCTCAG	TTT
NC_001484	(634)	TGGGAG	TGGGCCT	TAGC	CCGTTTCTC	TGGCTCAG	TTT
NC_001719	(634)	TGGGAG	TGGGCCT	TAGT	CCGTTTCTC	TGGCTCAG	TTT
NC_004107	(634)	TGGGAG	TGGGCCT	TAGC	CCGTTTCTC	TGGCTCA	AFTT
OHVHEPBA	(634)	TGGGAG	TGGGCCT	TAGC	CCGTTTCTC	TGGCTCA	AFTT
NC_001896	(647)	TGGGAC	TGGGCCT	TAGC	CCGTTTCTC	TGGCTCA	AFTC
NC_002168	(641)	TGGGG	TGGGCCT	CAGT	CCGTTTCTC	TGGCTCA	AFTT
gi_452617_emb_X75657.1_HHVBBAS	(641)	TGGGAG	TGGGCCT	CAGC	CCGTTTCTC	TGGCTCAG	TTT
gi_6983934_gb_AF160501.1_AF160501	(641)	TGGGAG	TGGGCCT	CAGT	CCGTTTCTC	TGGCTCAG	TTT
Consensus	(647)	TGGGAG	TGGGCCT	CAGC	CCGTTTCTC	TGGCTCAG	TTT

(685) 685 690 700 710 722
 AM282986 (679) ACTAGTGC CATTGTTCAGTGGTTCG TAGGGC TTTCCC

Source(1..3215): Source_1

CDS(2307..1623): CDS POLYMERASE (P)

Mature Peptide(137..1161): Domain of ...

Mature Peptide(137..1161): Domain of ...

CDS(2854..835): CDS LARGE (L) SURFACE

CDS(3211..835): CDS MIDDLE (M) SURFAC...

CDS(155..835): CDS SMALL (S) SURFACE ...

mRNA(2835..1930): mRNA Large S

mRNA(3185..1930): mRNA Middle S

gi_59439_emb_X65259.1_HBVAYWE (679) ACTAGTGC CATTGTTCAGTGGTTCG TAGGGC TTTCCC
 gi_221497_dbj_D00329.1_HPBADW1 (679) ACTAGTGC CATTGTTCAGTGGTTCG TAGGGC TTTCCC
 gi_59422_emb_X69798.1_HBVADW4A (679) ACTAGTGC AATTGTTCAGTGGTTCG TAGGGC TTTCCC
 NC_001484 (672) ACTAGTGC CTTACTTCAATGGTTAGGAGGAA TTTCCC
 NC_001719 (672) ACTAGTGC CTTGCTTCAATGGTTAGGAGGAA TTTCCC
 NC_004107 (672) ACTAGTGC CTTGCTTCAATGGTTAGGAGGAA TTTCCC
 OHVHEPBA (672) ACTAGTGC CTTGCTTCAATGGTTAGGAGGAA TTTCCC
 NC_001896 (685) ACTTC TGC CATTGTTCAGTGGTTCG CAGGGC TTTCCC
 NC_002168 (679) ACTAGTGC CTTTGTTCAGTGGTTCG CAGGGC TTTCCC
 gi_452617_emb_X75657.1_HHVBBAS (679) ACTAGTGC CATTGTTCAGTGGTTCG CAGGGC TTTCCC
 gi_6983934_gb_AF160501.1_AF160501 (679) ACTAGTGC CATTGTTCAGTGGTTCG TAGGGC TTTCCC
 Consensus (685) ACTAGTGC CATTGTTCAGTGGTTCG AGGGC TTTCCC

(723) 723 730 740 750 760
 AM282986 (717) CCACTGTTGGCTTT CAGCTATATGGATGATGTGGTAT

Source(1..3215): Source_1

CDS(2307..1623): CDS POLYMERASE (P)

Mature Peptide(137..1161): Domain of ...

Mature Peptide(137..1161): Domain of ...

CDS(2854..835): CDS LARGE (L) SURFACE

CDS(3211..835): CDS MIDDLE (M) SURFAC...

CDS(155..835): CDS SMALL (S) SURFACE ...

mRNA(2835..1930): mRNA Large S

mRNA(3185..1930): mRNA Middle S

gi_59439_emb_X65259.1_HBVAYWE (717) CCACTGTTGGCTTT CAGCTATATGGATGATGTGGTAT
 gi_221497_dbj_D00329.1_HPBADW1 (717) CCACTGTTGGCTTT CAGCTATATGGATGATGTGGTAT
 gi_59422_emb_X69798.1_HBVADW4A (717) CCACTGTTGGCTTT TAGTTATATGGATGATGTGGTAT
 NC_001484 (710) TCACTGTTGGCTTTTGCTTATATGGATGATGTGGTAT
 NC_001719 (710) TCACTGTTGGCTTTTGCTTATATGGATGATGTGGTAT
 NC_004107 (710) TCAATTGCGTGGTTTTTGCTTATATGGATGATGTGGTAT
 OHVHEPBA (710) TCAATTGCGTGGTTTTTGCTTATATGGATGATGTGGTAT
 NC_001896 (723) CCACTGTTATGGCTTTTAGTTATATGGATGATGTGGTATC
 NC_002168 (717) CCACTGTTGGCTTT CAGCTATATGGATGATGTGGTAT
 gi_452617_emb_X75657.1_HHVBBAS (717) CCACTGTTGGCTTT CAGCTATATGGATGATGTGGTAT
 gi_6983934_gb_AF160501.1_AF160501 (717) CCACTGTTGGCTTT CAGCTATATGGATGATGTGGTAT
 Consensus (723) CCACTGTTGGCTTTTAGTTATATGGATGATGTGGTAT

(761) 761 770 780 798
 AM282986 (755) TGGGGGGCC AAGTCTGTACAGCATCGTGAGTCCCTTTAT

Source(1..3215): Source_1
 CDS(2307..1623): CDS POLYMERASE (P)
 Mature Peptide(137..1161): Domain of ...
 Mature Peptide(137..1161): Domain of ...
 CDS(2854..835): CDS LARGE (L) SURFACE
 CDS(3211..835): CDS MIDDLE (M) SURFAC...
 CDS(155..835): CDS SMALL (S) SURFACE ...

mRNA(2835..1930): mRNA Large S
 mRNA(3185..1930): mRNA Middle S

gi_59439_emb_X65259.1_HBVAYWE (755) TGGGGGGCC AAGTCTGTACAGCATCGTGAGTCCCTTTAT
 gi_221497_dbj_D00329.1_HPBADW1 (755) TGGGGGGCC AAGTCTGTACAGCATCGTGAGTCCCTTTAT
 gi_59422_emb_X69798.1_HBVADW4A (755) TGGGGGGCC AAATCTGTGCAGCATCGTGAGTCCCTTTAT
 NC_001484 (748) TGGGGGGCC CGTCTTATGAGCATCTTACCGCCGTTTAT
 NC_001719 (748) TGGGGGGCC CGTACTCATGAGCATCTTACCGCCATTTAT
 NC_004107 (748) TGGGGGGCC CGCACTTCTGAGCATCTTACCGCCATTTAT
 OHVHEPBA (748) TGGGGGGCC CGCACTTCTGAGCATCTTACCGCCATTTAT
 NC_001896 (761) TGGGGGGCC AAGTCTGTT CAGCATCGTGAGTCCCTTCTT
 NC_002168 (755) TGGGGGGCC AAGTCTGTACAGCATCGTGAGTCCCTTTAT
 gi_452617_emb_X75657.1_HHVBBAS (755) TGGGGGGCC AAGTCTGTACAGCATCGTGAGTCCCTTTAT
 gi_6983934_gb_AF160501.1_AF160501 (755) TGGGGGGCC AAATCTGTACAGCATCGTGAGTCCCTTTAT
 Consensus (761) TGGGGGGCC AAGTCTGTACAGCATCGTGAGTCCCTTTAT

(799) 799 810 820 836
 AM282986 (793) ACCGCTGTTACCAATTTTCTTTTGTCTCTGGGTATACA

Source(1..3215): Source_1
 CDS(2307..1623): CDS POLYMERASE (P)
 Mature Peptide(137..1161): Domain of ...
 Mature Peptide(137..1161): Domain of ...
 CDS(2854..835): CDS LARGE (L) SURFACE
 CDS(3211..835): CDS MIDDLE (M) SURFAC...
 CDS(155..835): CDS SMALL (S) SURFACE ...

mRNA(2835..1930): mRNA Large S
 mRNA(3185..1930): mRNA Middle S

gi_59439_emb_X65259.1_HBVAYWE (793) ACCGCTGTTACCAATTTTCTTTTGTCTCTGGGTATACA
 gi_221497_dbj_D00329.1_HPBADW1 (793) GCCGCTGTTACCAATTTTCTTTTGTCTCTGGGTATACA
 gi_59422_emb_X69798.1_HBVADW4A (793) ACCGCTGTTACCAATTTTCTGTTATCTGTTGGGTATACA
 NC_001484 (786) TCCCAATAATTGCTCTGTTTTCCTTGATTGGGCATACA
 NC_001719 (786) TCCCAATAATTGCTCTGTTTTCCTTGATTGGGCATACA
 NC_004107 (786) TCCCAATAATTGTTCTGTTTTCCTTGATTGGGTATACA
 OHVHEPBA (786) TCCCAATAATTGTTCTGTTTTCCTTGATTGGGTATACA
 NC_001896 (799) GCCCTGTTACCACTTTTCTTTTGGCTTTGGGCATACA
 NC_002168 (793) ACCGCTGTTACCAATTTTCTTTTGTCTCTGGGTATACA
 gi_452617_emb_X75657.1_HHVBBAS (793) ACCGCTGTTACCAATTTTCTTTTGTCTCTGGGTATACA
 gi_6983934_gb_AF160501.1_AF160501 (793) ACCGCTGTTACCAATTTTCTTTTGTCTCTGGGTATACA
 Consensus (799) ACCGCTGTTACCAATTTTCTTTTGTCTCTGGGTATACA

(837) 837 850 860 874
 AM282986 (831) TTTAAA C CCTAAC AAAACA AAAA GATGGGG T TATTCCC
 Source(1..3215): Source_1
 CDS(2307..1623): CDS POLYMERASE (P)
 Mature Peptide(137..1161): Domain of ...
 Mature Peptide(137..1161): Domain of ...
 CDS(2854..835): CDS LARGE (L) SURFACE
 CDS(3211..835): CDS MIDDLE (M) SURFAC...
 CDS(155..835): CDS SMALL (S) SURFACE ...
 mRNA(2835..1930): mRNA Large S
 mRNA(3185..1930): mRNA Middle S

gi_59439_emb_X65259.1_HBVAYWE (831) TTTAAA C CCTAAC AAAACA AAAA GATGGGG T TATTCCC
 gi_221497_dbj_D00329.1_HPBADW1 (831) TTTAAA C CCTAAC AAAACA AAAA GATGGGG AT TATTCCC
 gi_59422_emb_X69798.1_HBVADW4A (831) TTTAAA TAC TCT AAAACA AAAA GATGGGG T TACTCCC
 NC_001484 (824) TCTAAA TGTGG AAAAAC TAAAT GGTGGGG TCACACTT
 NC_001719 (824) TTTAAAT GTAGC CAAAAC TAAAT GGTGGGG ACATCATT
 NC_004107 (824) TTTGAA TGTCAAT AAAACA AAAA GGTGGGG CAATCATC
 OHVHEPBA (824) TTTGAA TGTCAAT AAAACA AAAA GGTGGGG CAATCATC
 NC_001896 (837) TTTGAA C CCTG AAAAGAC CAAA GATGGGG AA AAGCCT
 NC_002168 (831) TTTAAA C CCTGG CAAAAC CAAA GATGGGG CT TATTCCC
 gi_452617_emb_X75657.1_HHVBBAS (831) TTTAAA TCC AAC AAAACA AAAA GATGGGG CT TATTCCC
 gi_6983934_gb_AF160501.1_AF160501 (831) TCTAAA C CCTAAC AAAACA AAAA GATGGGG T TATTCCCT
 Consensus (837) TTTAAATCCTAACAAAACAAAAGATGGGG TATTCCC

(875) 875 880 890 900 912
 AM282986 (869) TAAAC TTT CATGGG T TACAT AATTGGAAG TTGGGGAACG
 Source(1..3215): Source_1
 CDS(2307..1623): CDS POLYMERASE (P)
 Mature Peptide(137..1161): Domain of ...
 Mature Peptide(137..1161): Domain of ...
 Enhancer(900..1310): DNA enhancer 1
 mRNA(2835..1930): mRNA Large S
 mRNA(3185..1930): mRNA Middle S

gi_59439_emb_X65259.1_HBVAYWE (869) TAAAC TTT CATGGG T TACAT AATTGGAAG TTGGGGAACG
 gi_221497_dbj_D00329.1_HPBADW1 (869) TTAAC TTT CATGGG A TATGT AATTGGGAG TTGGG CACA
 gi_59422_emb_X69798.1_HBVADW4A (869) TACAT TTT ATGGG T TATGT CATTGGTAG TTGGG ATCA
 NC_001484 (862) TACACTT CATGGG C TATACC ATTAAATGG TGCAGGAGTG
 NC_001719 (862) TACAT TTT CATGGG T TATGT TATTACTGG AGCA GGAA TT
 NC_004107 (862) TACAT TTT CATGGG A TATGT GATTACTAG TTCA GG TGTA
 OHVHEPBA (862) TACAT TTT CATGGG A TATGT GATTACTAG TTCA GG TGTA
 NC_001896 (875) TAAAT TTT ATGGG A TATGT CATTGGAGG GTATGG TTCT
 NC_002168 (869) TACAT TTT CATGGG C TATGT GATTGGAAG TTGGG AAC
 gi_452617_emb_X75657.1_HHVBBAS (869) TTAAT TTT CATGGG T TATGT AATTGGAAG TTGGG CTCA
 gi_6983934_gb_AF160501.1_AF160501 (869) TAAAT TTT ATGGG A TATGT AATTGGAAG TTGGG TACT
 Consensus (875) TACATTTT CATGGG TATGT ATTGGAAGTTGGGGAAC

(913) 913 920 930 940 950
 AM282986 (907) TTGCCACAAGATCAATTGTACAAAATCAAACACTG

Source(1..3215): Source_1
 CDS(2307..1623): CDS POLYMERASE (P)
 Mature Peptide(137..1161): Domain of ...
 Mature Peptide(137..1161): Domain of ...

Enhancer(900..1310): DNA enhancer 1 (...)

mRNA(2835..1930): mRNA Large S
 mRNA(3185..1930): mRNA Middle S

gi_59439_emb_X65259.1_HBVAYWE (907) TTGCCACAAGATCAATTGTACAAAATCAAAGAAATG
 gi_221497_dbj_D00329.1_HPBADW1 (907) TTGCCACAAGATCAATTGTACAAAATCAAACAATG
 gi_59422_emb_X69798.1_HBVADW4A (907) TTACCACAAGATCAATTGTACAAAATCAAAGAAATG
 NC_001484 (900) TTACCTCAAGATCAACAATGTACATAAAGTAAACAACATA
 NC_001719 (900) TTACCACAAGATCAACAATGTGCAAAAATGATCAACATA
 NC_004107 (900) TTGCCACAAGACAACAATGTTAAGAAAATTTCCCGTTA
 OHVHEPBA (900) TTGCCACAAGACAACAATGTTAAGAAAATTTCCCGTTA
 NC_001896 (913) CTTCCCAACAACAATTATTAGAGATAAGATTGCTTTGTG
 NC_002168 (907) CTACCACAAGACCAATTATTGTACAAAATCAAACAATG
 gi_452617_emb_X75657.1_HHVBBAS (907) TTACCACAAGACCAATCAATACAAAATCAAAGACTG
 gi_6983934_gb_AF160501.1_AF160501 (907) TTGCCACAAGACCAATCACACAGAAAATTTAAGCAATG
 Consensus (913) TTGCCACAAGATCA ATTGTACAAAAAATCAAACAATG

(951) 951 960 970 988
 AM282986 (945) TTTTAGAAAACCTCCGTAAACAGGCCATTGATTGGA

Source(1..3215): Source_1
 CDS(2307..1623): CDS POLYMERASE (P)
 Mature Peptide(137..1161): Domain of ...
 Mature Peptide(137..1161): Domain of ...

Enhancer(900..1310): DNA enhancer 1 (...)

mRNA(2835..1930): mRNA Large S
 mRNA(3185..1930): mRNA Middle S
 Promoter Eukaryotic(950..1310): DNA X...

gi_59439_emb_X65259.1_HBVAYWE (945) TTTTAGAAAACCTCCGTAAACAGGCCATTGATTGGA
 gi_221497_dbj_D00329.1_HPBADW1 (945) TTTTAGAAAACCTCCGTAAACAGGCCATTGATTGGA
 gi_59422_emb_X69798.1_HBVADW4A (945) CTTTCGAAAACCTCCGTAAATCGTCCATTGATTGGA
 NC_001484 (938) CTTAAAACTCTATTCCATTAAATCAACCCTTAGATTATA
 NC_001719 (938) TTTGAAATCCAATCCACTCAACAAACCTTTAGATTATA
 NC_004107 (938) TTTGCGCTCTGTTCCGTAAATCAACCCTCTGATTACA
 OHVHEPBA (938) TTTGCGCTCTGTTCCGTAAATCAACCCTCTGATTACA
 NC_001896 (951) CTTCCAGAAATTAACATGTAATCGACCTATTGATTGGA
 NC_002168 (945) TTTTCGGAAACCTCCGTCAACAGGCCATTGATTGGA
 gi_452617_emb_X75657.1_HHVBBAS (945) TTTTAGAAAACCTCCGTAAACAGGCCATTGATTGGA
 gi_6983934_gb_AF160501.1_AF160501 (945) TTTTCGGAAACCTCCGTAAACAGGCCATTGATTGGA
 Consensus (951) TTTTCGAAAACCTCCGTAAACAGGCCATTGATTGGA

(989) 989 1000 1010 1026
 AM282986 (983) AAGTATGTCAAAGAATTGTGGGTCCTTTGGGCTTTGCT

Source(1..3215): Source_1

CDS(2307..1623): CDS POLYMERASE (P)

Mature Peptide(137..1161): Domain of ...

Mature Peptide(137..1161): Domain of ...

Enhancer(900..1310): DNA enhancer 1 (...)

mRNA(2835..1930): mRNA Large S

mRNA(3185..1930): mRNA Middle S

Promoter Eukaryotic(950..1310): DNA X...

gi_59439_emb_X65259.1_HBVAYWE (983) AAGTATGTCAAACGAATTGTGGGTCCTTTGGGCTTTGCT
 gi_221497_dbj_D00329.1_HPBADW1 (983) AAGTTTGTCAACGAATTGTGGGTCCTTTGGGCTTTGCT
 gi_59422_emb_X69798.1_HBVADW4A (983) AAGTTTGTCAACGCATAGTGGGTCCTTTGGGCTTTGCT
 NC_001484 (976) AAATATGTGAAAGGTGACGGGCATTCTTAATATATGTT
 NC_001719 (976) AAATC TGTGAAAGGTAAACAGGCATTCTGAATATATGTT
 NC_004107 (976) AAATTGTGAAAGATGACTGGTATTCTTAACATATGTT
 OHVHEPBA (976) AAATTGTGAAAGATGACTGGTATTCTTAACATATGTT
 NC_001896 (989) AAGTC TGTCAAGAGAA TTGTTGGTTTATTGGGCTTTGTT
 NC_002168 (983) AAGTATGTCAAACGAATTGTAGGACTATTGGGCTTTGCC
 gi_452617_emb_X75657.1_HHVBBAS (983) AAGTATGTCAAAGAATTGTGGGTCCTTTGGGCTTTGCT
 gi_6983934_gb_AF160501.1_AF160501 (983) AAGTC TGTCAACGAATAACTGGTCGTGGGTTTCGCT
 Consensus (989) AAGT TGTCAAAGAATTGTGGGTCCTTTGGGCTTTGCT

(1027) 1027 1040 1050 1064
 AM282986 (1021) GCTCCA TTTACACAATGTGGATATCCTGCC TTAATGCC

Source(1..3215): Source_1

CDS(2307..1623): CDS POLYMERASE (P)

Mature Peptide(137..1161): Domain of ...

Mature Peptide(137..1161): Domain of ...

Protein Binding Site(1027..1036): DNA...

Enhancer(900..1310): DNA enhancer 1 (...)

Protein Binding Site(1026..1035): DNA...

mRNA(2835..1930): mRNA Large S

mRNA(3185..1930): mRNA Middle S

Promoter Eukaryotic(950..1310): DNA X...

gi_59439_emb_X65259.1_HBVAYWE (1021) GCTCCA TTTACACAATGTGGATATCCTGCC TTAATGCC
 gi_221497_dbj_D00329.1_HPBADW1 (1021) GCCCCTTTTACGCAATGTGGATATCCTGCC TTAATGCC
 gi_59422_emb_X69798.1_HBVADW4A (1021) GCCCCTTTTACCAATGCGGTATCCTGCC TTAATGCC
 NC_001484 (1014) GCTCCTTTTACCAATGTGGTATGCTGCTTTACTGCC
 NC_001719 (1014) GCTCCTTTTACTAAATGTGGTATGCTGCTCTCC TCC
 NC_004107 (1014) GCTCCTTTTACGCTATGTGGATACGCTGCTTTAATGCC
 OHVHEPBA (1014) GCTCCTTTTACGCTATGTGGATACGCTGCTTTAATGCC
 NC_001896 (1027) GCTCCCTTTTACACAATGTGGATACGCTGCTTTAATGCC
 NC_002168 (1021) GCTCCTTTTACTCAATGTGGCTATCCTGCC TTAATGCC
 gi_452617_emb_X75657.1_HHVBBAS (1021) GCCCCTTTTACACAATGTGGATATCCTGCC TTAATGCC
 gi_6983934_gb_AF160501.1_AF160501 (1021) GCTCCTTTTACCAATGTGGTATCCTGCC TTAATGCC
 Consensus (1027) GCTCCTTTTAC CAATGTGGATATCCTGCC TTAATGCC

(1065) 1065 1070 1080 1090 1102
 AM282986 (1059) TTTGTATGCCTGTATACAA GCTAAACAGGCTTTCACTT

Source(1..3215): Source_1
 CDS(2307..1623): CDS POLYMERASE (P)
 Mature Peptide(137..1161): Domain of ...
 Mature Peptide(137..1161): Domain of ...
 Protein Binding Site(1088..1098): DNA...
 Enhancer(900..1310): DNA enhancer 1 (...)
 Protein Binding Site(1081..1087): p53...

mRNA(2835..1930): mRNA Large S
 mRNA(3185..1930): mRNA Middle S
 Promoter Eukaryotic(950..1310): DNA X...

gi_59439_emb_X65259.1_HBVAYWE (1059) TTTGTATGCCTGTATACAA GCTAAACAGGCTTTCACTT
 gi_221497_dbj_D00329.1_HPBADW1 (1059) TTTATATGCATGTATACAA GCAAACAGGCTTTTACTT
 gi_59422_emb_X69798.1_HBVADW4A (1059) TCTGTATGCCTGTATTACTGCTAAACAGGCTTTTGTC
 NC_001484 (1052) TTTATATCAAGCTATTGCTTCTCATACTGCTTTTGT
 NC_001719 (1052) TTTGTATCAAGCTA---CTTCCGGTACGGCATTTGTGT
 NC_004107 (1052) TTTGTATCATGCTATTACTTCCCGTACGGCTTTCA
 OHVHEPBA (1052) TTTGTATCATGCTATTGCTTCCCGTATGGCTTTCA
 NC_001896 (1065) TATATATACATGCATCCAA AAACATCAGGCCTTTACTT
 NC_002168 (1059) TTTGTATAACTGTATACACAA TCGTCAGGCTTTTACTT
 gi_452617_emb_X75657.1_HHVBBAS (1059) TCTGTATGCATGTACTCAA TCTAAGCAGGCTTTCACTT
 gi_6983934_gb_AF160501.1_AF160501 (1059) TTTATATGCATGTATACAA GCTAAGCAGGCTTTTACTT
 Consensus (1065) TTTGTATGCATGTAT CAA CTCATCAGGCTTTTACTT

(1103) 1103 1110 1120 1130 1140
 AM282986 (1097) TCTCGCCAACTTACAAGGCCTTTCCTAA GTAAACAGTAC

Source(1..3215): Source_1
 CDS(2307..1623): CDS POLYMERASE (P)
 Mature Peptide(137..1161): Domain of ...
 Mature Peptide(137..1161): Domain of ...
 Protein Binding Site(1088..1098): DNA...
 Protein Binding Site(1121..1130): DNA...
 Enhancer(900..1310): DNA enhancer 1 (...)
 Protein Binding Site(1121..1130): HNF...

mRNA(2835..1930): mRNA Large S
 mRNA(3185..1930): mRNA Middle S
 Promoter Eukaryotic(950..1310): DNA X...

gi_59439_emb_X65259.1_HBVAYWE (1097) TCTCGCCAACTTACAAGGCCTTTCCTAA GTAAACAGTAC
 gi_221497_dbj_D00329.1_HPBADW1 (1097) TCTCGCCAACTTACAAGGCCTTTCCTAGTAAACAGTAT
 gi_59422_emb_X69798.1_HBVADW4A (1097) TCTCGCCAACCTACAAGGCCTTTCCTGTGTAAACAATAC
 NC_001484 (1090) TCTCCTCCTTA TATAAAA CTGGT TACTGTCACTTTAT
 NC_001719 (1087) TTTCTTCTCTC TACACAG CTGGT TCGTCCCTTTAT
 NC_004107 (1090) TCTCCTCCTTG TATAAATC CTGGT TCGTCTCTTTAT
 OHVHEPBA (1090) TCTCCTCCTTG TATAAATC CTGGT TCGTCTCTTTAT
 NC_001896 (1103) TCTCTCTTGTG TACAAGACCTTTTGTAAAGATCAATAC
 NC_002168 (1097) TCTCGCCAACTTACAAGGCCTTTCCTGCTACACAATAT
 gi_452617_emb_X75657.1_HHVBBAS (1097) TCTCGCCAACTTACAAGGCCTTTCCTGTGTAAACAATAC
 gi_6983934_gb_AF160501.1_AF160501 (1097) TCTCGCCAACTTATAAGGCCTTTCCTGTAAACAATAC
 Consensus (1103) TCTCGCCAACTTACAAGGCCTTTCCTG GTAAACA TAT

(1141) 1141 1150 1160 1178
 AM282986 (1135) ATGAACCTTTTACCCCGTTGCTCGGCAACGGCC TGGTCT

Source(1..3215): Source_1
 CDS(2307..1623): CDS POLYMERASE (P)
 Mature Peptide(137..1161): Domain of ...
 Mature Peptide(137..1161): Domain of ...
 Protein Binding Site(1136..1148): DNA... Mature Peptide(1162..1623): Domain of ...
 Enhancer(900..1310): DNA enhancer 1 (...
 RNA - Misc.(1151..1684): RNA PRE Pos...
 Protein Binding Site(1150..1162): DNA...
 Protein Binding Site(1150..1162): RFX...
 mRNA(2835..1930): mRNA Large S
 mRNA(3185..1930): mRNA Middle S
 Promoter Eukaryotic(950..1310): DNA X...

gi_59439_emb_X65259.1_HBVAYWE (1135) ATGAACCTTTTACCCCGTTGCTCGGCAACGGCC TGGTCT
 gi_221497_dbj_D00329.1_HPBADW1 (1135) ATGACCTTTTACCCCGTTGCTCGGCAACGGCC TGGTCT
 gi_59422_emb_X69798.1_HBVADW4A (1135) ATGAACCTTTTACCCGTTGCTCGGCAACGGCCAGGCCT
 NC_001484 (1128) GGTGAGTGTGGCCGTTGCCAGACAACAGTGGTGTGGT
 NC_001719 (1125) GCTGAGTGTGGCCGTTGCCAGACAACAGTGGTGTGGT
 NC_004107 (1128) GAGGAGTGTGGCCGTTGTCAGACAACAGTGGTGTGGT
 OHVHEPBA (1128) GAGGAGTGTGGCCGTTGTCAGACAACAGTGGTGTGGT
 NC_001896 (1141) ATGCACCTTTTACCCCGTTGCTAGGCAACGAGCTGGGCA
 NC_002168 (1135) CTGACCTTTTACCCCGTTGCTCGGCAACGACCGGGACT
 gi_452617_emb_X75657.1_HHVBBAS (1135) CTGAACCTTTTACCCCGTTGCCCGGCAACGGCCAGGTCT
 gi_6983934_gb_AF160501.1_AF160501 (1135) ATGAACCTTTTACCCCGTTGCTAGGCAACGGCCCGGTCT
 Consensus (1141) ATGAACCTTTTACCCCGTTGCTCGGCAACGGCC GG CT

(1179) 1179 1190 1200 1216
 AM282986 (1173) GTGCCAAGTGT TTGCTGACGCAACCCCCACTGGCTGGG

Source(1..3215): Source_1
 CDS(2307..1623): CDS POLYMERASE (P)
 Protein Binding Site(1188..1196): AP1...
 Mature Peptide(1162..1623): Domain of...
 Enhancer(900..1310): DNA enhancer 1 (...
 RNA - Misc.(1151..1684): RNA PRE Pos...
 mRNA(2835..1930): mRNA Large S
 mRNA(3185..1930): mRNA Middle S
 Promoter Eukaryotic(950..1310): DNA X...

gi_59439_emb_X65259.1_HBVAYWE (1173) GTGCCAAGTGT TTGCTGACGCAACCCCCACTGGCTGGG
 gi_221497_dbj_D00329.1_HPBADW1 (1173) GTGCCAAGTGT TTGCTGACGCAACCCCCACTGGT TGGG
 gi_59422_emb_X69798.1_HBVADW4A (1173) GTGCCAAGTGT TTGCTGACGCAACCCCCACTGGT TGGG
 NC_001484 (1166) GTGCTCT GTGT -- CTGACGCAAC TCCCCACTGGT TGGG
 NC_001719 (1163) GTGCTCT GTGT -- CTGACGCAAC CCCCCACTGGT TGGG
 NC_004107 (1166) GTGCACT GTGT TTGCTGACGCAAC CCCCCACTGGT TGGG
 OHVHEPBA (1166) GTGCACT GTGT TTGCTGACGCAAC CCCCCACTGGT TGGG
 NC_001896 (1179) CTGCCAAGTGT TTGCTGACGCAAC CCCCCACTGGCTGGG
 NC_002168 (1173) GTGCCAAGTGT TTGCTGACGCAAC CCCCCACTGGCTGGG
 gi_452617_emb_X75657.1_HHVBBAS (1173) GTGCCAAGTGT TTGCTGATGCAAC CCCCCACTGGCTGGG
 gi_6983934_gb_AF160501.1_AF160501 (1173) GTGCCAAGTGT TTGCTGACGCAAC CCCCCACTGGT TGGG
 Consensus (1179) GTGCCAAGTGT TTGCTGACGCAACCCCCACTGGT TGGG

(1217) 1217 1230 1240 1254
 AM282986 (1211) GCTTGGCCATAGGCCATCAGCGCATGCGTGGAAACCTTT

Source(1..3215): Source_1

CDS(2307..1623): CDS POLYMERASE (P)

Misc. Feature(1220..1235): NF1 bindin...

Mature Peptide(1162..1623): Domain of...

Enhancer(900..1310): DNA enhancer 1 (...)

RNA - Misc.(1151..1684): RNA PRE Pos...

mRNA(2835..1930): mRNA Large S

mRNA(3185..1930): mRNA Middle S

Promoter Eukaryotic(950..1310): DNA X...

gi_59439_emb_X65259.1_HBVAYWE (1211) GCTTGGCAATAGGCCAATCAGCGCATGCGTGGAAACCAATT

gi_221497_dbj_D00329.1_HPBADW1 (1211) GCTTGGCCATAGGCCATCAGCGCATGCGTGGAAACCTTT

gi_59422_emb_X69798.1_HBVADW4A (1211) GCTTGGCCATTGGCCATCAGCGCATGCGTGGAAACCTTT

NC_001484 (1204) GCATTTGCAACCACCTGTCAACTCATTTCCGGTACTTTTC

NC_001719 (1198) GCATTTGCAACCACCTATCAACTCATTTCCCGACGGGC

NC_004107 (1204) GCATTTGCCACCACCTATCAACTCCTTTCCGGGACTTTTC

OHVHEPBA (1204) GCATTTGCCACCACCTGTGAGCTCCTTTCCGGGACTTTTC

NC_001896 (1217) GCTTGGTTCATGGGCAATCAGCGCATGCGTGGTACATTTT

NC_002168 (1211) GCTTGGCGCTAGGTCGCCAGCGCATGCGTGGAAACCTTT

gi_452617_emb_X75657.1_HHVBBAS (1211) GCTTGGCCATAGGCCATCAGCGCATGCGCGGAACCTTT

gi_6983934_gb_AF160501.1_AF160501 (1211) GCTTGGCCATCGGCCATCAGCGCATGCGTGGAAACCTTT

Consensus (1217) GCTTGGCCAT GGC ATCAGCGCATGCGTGGAAACCTTT

(1255) 1255 1260 1270 1280 1292
 AM282986 (1249) GTGGCTCCTCTGCCGATCCATACTGCGGAACTCCTAGC

Source(1..3215): Source_1

CDS(2307..1623): CDS POLYMERASE (P)

Splicing Signal(1252..1348): RNA BS S...

Protein Binding Site(1275..1291): RNA...

Mature Peptide(1162..1623): Domain of...

Enhancer(900..1310): DNA enhancer 1 (...)

RNA - Misc.(1151..1684): RNA PRE Pos...

mRNA(2835..1930): mRNA Large S

mRNA(3185..1930): mRNA Middle S

Promoter Eukaryotic(950..1310): DNA X...

RNA - Misc.(1254..1582): RNA Post tra...

gi_59439_emb_X65259.1_HBVAYWE (1249) GTGGCTCCTCTGCCGATCCATACTGCGGAACTCCTAGC

gi_221497_dbj_D00329.1_HPBADW1 (1249) GTGGCTCCTCTGCCGATCCATACTGCGGAACTCCTAGC

gi_59422_emb_X69798.1_HBVADW4A (1249) GTGGCTCCTCTGCCGATCCATACTGCGGAACTCCTAGC

NC_001484 (1242) GGT TTTCTCACTTCCGATGCTTACC GCGGAGCTTATAGC

NC_001719 (1236) GCTTTTGCCCTGCCGATCGCCACCGCGGACGTCATCGC

NC_004107 (1242) GCTTTCCTCCCTCCCTATGACCACGCGGAACTCATTCGC

OHVHEPBA (1242) GCTTTCCTCCCTCCCTATGACCACGCGGAACTCATTCGC

NC_001896 (1255) TTGTCCCGCTGCCATCCATACTGCGGAACTCCTTGC

NC_002168 (1249) GTGGCTCCTCTGCCGATCCATACTGCGGAACTCCTAGC

gi_452617_emb_X75657.1_HHVBBAS (1249) GTGGCTCCTCTGCCGATCCATACTGCGGAACTCCTAGC

gi_6983934_gb_AF160501.1_AF160501 (1249) GTGGCTCCTCTGCCGATCCATACTGCGGAACTCCTAGC

Consensus (1255) GTGTCTCCTCTGCCGATCCATACTGCGGAACTCCTAGC

(1293) 1293 1300 1310 1320 1330
 AM282986 (1287) **C**GCTT**G**TT**T**T**G**CT**C**GC**A**GC**C**GGT**C**TGG**G**GC**A**AA**G**CT**C**A

Source(1..3215): Source_1
 CDS(2307..1623): CDS POLYMERASE (P)
 Splicing Signal(1252..1348): RNA BS S...
 Protein Binding Site(1275..1291): RNA..Misc. Feature(1310..1310): X transcri...
 Mature Peptide(1162..1623): Domain of...
 Enhancer(900..1310): DNA enhancer 1 (...)
 RNA - Misc.(1151..1684): RNA PRE Pos...
 RNA - Misc.(1292..1321): RNA PRE HSL ...
 mRNA(1310..1930): mRNA X
 mRNA(2835..1930): mRNA Large S
 mRNA(3185..1930): mRNA Middle S
 Promoter Eukaryotic(950..1310): DNA X...
 RNA - Misc.(1254..1582): RNA Post tra...

gi_59439_emb_X65259.1_HBVAYWE (1287) **C**GCTT**G**TT**T**T**G**CT**C**GC**A**GC**C**GGT**C**TGG**G**GC**A**AA**G**CT**C**A
 gi_221497_dbj_D00329.1_HPBADW1 (1287) **C**GCTT**G**TT**T**T**G**CT**C**GC**A**GC**A**GGT**C**TGG**A**GC**A**AA**C**CT**C**A
 gi_59422_emb_X69798.1_HBVADW4A (1287) **A**GC**T**T**G**TT**T**T**C**GCT**C**GC**A**GC**A**GGT**C**TGG**A**GC**G**A**C**T**C**T**C**A
 NC_001484 (1280) **C**GC**C**T**G**CC**T**T**G**CT**C**GC**T**GC**T**GG**A**C**A**GG**A**GC**T**CG**G**T**T**GT
 NC_001719 (1274) **C**GC**C**T**G**CC**T**T**G**CT**C**GC**T**GC**T**GG**A**C**A**GG**A**GC**T**CG**G**C**T**GT
 NC_004107 (1280) **C**GC**C**T**G**CC**T**T**G**CC**C**GC**T**GC**T**GG**A**C**A**GG**G**GC**T**CG**G**C**T**GT
 OHVHEPBA (1280) **C**GC**C**T**G**CC**T**T**G**CC**C**GC**T**GC**T**GG**A**C**A**GG**G**GC**T**CG**G**C**T**GT
 NC_001896 (1293) **A**GC**C**T**G**TT**T**T**G**CT**C**GC**T**GC**T**GG**T**C**A**GG**G**GC**A**AA**A**CT**C**A
 NC_002168 (1287) **C**GCTT**G**TT**T**T**G**CT**C**GC**A**GC**A**GGT**C**TGG**A**GC**A**AA**C**AT**T**A
 gi_452617_emb_X75657.1_HHVBBAS (1287) **C**GCTT**G**TT**T**T**G**CT**C**GC**A**GC**A**GGT**C**TGG**A**GC**A**AA**A**CT**T**A
 gi_6983934_gb_AF160501.1_AF160501 (1287) **T**GC**T**T**G**TT**T**T**G**CT**C**GC**A**GC**C**GGT**C**TGG**A**GC**A**AA**A**CT**C**A
 Consensus (1293) **C**GCTT**G**TT**T**T**G**CT**C**GC**A**GCGGT**C**TGG**A**GC**A**AA**G**CT**C**A

(1331) 1331 1340 1350 1368
 AM282986 (1325) **T**CGGA**A**CT**G**AC**A**A**T**T**C**TGT**C**GT**C**CT**C**T**C**GC**G**GA**A**AT**A**T

Source(1..3215): Source_1
 CDS(2307..1623): CDS POLYMERASE (P)
 Splicing Signal(1252..1348): RNA BS S...
 Mature Peptide(1162..1623): Domain of...
 RNA - Misc.(1151..1684): RNA PRE Pos...
 mRNA(1310..1930): mRNA X
 mRNA(2835..1930): mRNA Large S
 mRNA(3185..1930): mRNA Middle S
 RNA - Misc.(1254..1582): RNA Post tra...

gi_59439_emb_X65259.1_HBVAYWE (1325) **T**CGGA**A**CT**G**AC**A**A**T**T**C**TGT**T**GT**C**CT**C**T**C**GC**G**GA**A**AT**A**T
 gi_221497_dbj_D00329.1_HPBADW1 (1325) **T**CGGG**A**CT**G**AC**A**A**T**T**C**TGT**C**GT**A**CT**C**T**C**CC**G**CA**A**AG**T**AT
 gi_59422_emb_X69798.1_HBVADW4A (1325) **T**CGGC**A**CT**G**AC**A**A**T**T**C**TGT**T**GT**C**CT**C**T**C**TAG**G**AA**G**TA**C**
 NC_001484 (1318) **T**GGC**A**CT**G**AT**A**A**C**T**C**CGT**G**GT**C**CT**C**T**C**CG**G**T**A**AG**C**TA
 NC_001719 (1312) **T**GGC**A**CT**G**AC**A**A**C**T**C**CGT**G**GT**T**CT**T**TC**G**GG**C**AA**A**CT**G**
 NC_004107 (1318) **T**GGC**A**CT**G**AC**A**A**T**T**C**CGT**G**GT**GT**T**G**TC**G**GG**G**AA**G**CT**G**
 OHVHEPBA (1318) **T**GGC**A**CT**G**AC**A**A**T**T**C**CGT**G**GT**GT**T**G**TC**G**GG**G**AA**G**CT**G**
 NC_001896 (1331) **T**CGGC**A**CT**G**AC**A**A**CG**CT**G**T**T**GT**G**CT**G**TC**T**CG**GA**AG**T**AT
 NC_002168 (1325) **T**CGGT**A**CT**G**AC**A**A**C**T**C**TGT**T**GT**GT**T**G**TC**G**CG**GA**AA**T**AT
 gi_452617_emb_X75657.1_HHVBBAS (1325) **T**CGGG**A**CT**G**AT**A**A**T**T**C**TGT**C**GT**T**CT**C**T**C**CC**G**AA**G**TA**T**
 gi_6983934_gb_AF160501.1_AF160501 (1325) **T**TGGG**A**CT**G**AC**A**A**T**T**C**TGT**C**GT**C**CT**T**TC**T**CG**GA**AA**T**AT
 Consensus (1331) **T**CGGC**A**CT**G**AC**A**A**T**T**C**TGTGTCT**C**T**C**GC**G**GA**A**AG**T**AT

(1369) 1369 1380 1390 1406
 AM282986 (1363) ACATCGTTTCCATGGCTGCTAGGTTGTTACTGCCAACTG

Source(1..3215): Source_1
 CDS(2307..1623): CDS POLYMERASE (P)
 CDS(1374..1838): CDS X PROTEIN

Mature Peptide(1162..1623): Domain of...

RNA - Misc.(1151..1684): RNA PRE Pos...

mRNA(1310..1930): mRNA X

mRNA(2835..1930): mRNA Large S

mRNA(3185..1930): mRNA Middle S

RNA - Misc.(1254..1582): RNA Post tra...

gi_59439_emb_X65259.1_HBVAYWE (1363) ACATCGTTTCCATGGCTGCTAGGTTGTTACTGCCAACTG
 gi_221497_dbj_D00329.1_HPBADW1 (1363) ACATCGTTTCCATGGCTGCTAGGTTGTTACTGCCAACTG
 gi_59422_emb_X69798.1_HBVADW4A (1363) ACCTCCTTTCCATGGCTGCTCGGATGTTGCTGCAAACTG
 NC_001484 (1356) ACTTCGTTTCCATGGCTGCTCGCTGTGTTGCCAACTG
 NC_001719 (1350) ACTTCCTATCCATGGCTGCTCGCTGTGTTGCCAACTG
 NC_004107 (1356) ACGTCCTTTCCATGGCTGCTCGCTGTGTTGCCAACTG
 OHVHEPBA (1356) ACGTCCTTTCCATGGCTGCTCGCTGTGTTGCCAACTG
 NC_001896 (1369) ACACACTTCCATGGCTGCTAGGCTGTGCTGCTACCTG
 NC_002168 (1363) ACATCGTTTCCATGGCTGCTAGGTTGTTACTGCCAACTG
 gi_452617_emb_X75657.1_HHVBBAS (1363) ACATCCTTTCCATGGCTGCTAGGCTGTGCTGCCAACTG
 gi_6983934_gb_AF160501.1_AF160501 (1363) ACATCCTTTCCATGGCTGCTAGGCTGTGCTGCCAACTG
 Consensus (1369) ACATCCTTTCCATGGCTGCTAGGCTGTGCTGCCAACTG

(1407) 1407 1420 1430 1444
 AM282986 (1401) GATCCTTCGCGGGACGTCCTTTGTTTACGTCCCCTCGG

Source(1..3215): Source_1
 CDS(2307..1623): CDS POLYMERASE (P)
 CDS(1374..1838): CDS X PROTEIN
 RNA - Misc.(1417..1458): RNA PRE HSL ...

Mature Peptide(1162..1623): Domain of...

Promoter Eukaryotic(1403..1626): DNA ...

RNA - Misc.(1151..1684): RNA PRE Pos...

Promoter Eukaryotic(1403..1455): DNA ...

mRNA(1310..1930): mRNA X

mRNA(2835..1930): mRNA Large S

mRNA(3185..1930): mRNA Middle S

RNA - Misc.(1254..1582): RNA Post tra...

gi_59439_emb_X65259.1_HBVAYWE (1401) GATCCTTCGCGGGACGTCCTTTGTTTACGTCCCCTCGG
 gi_221497_dbj_D00329.1_HPBADW1 (1401) GATCCTTCGCGGGACGTCCTTTGTTTACGTCCCCTCGG
 gi_59422_emb_X69798.1_HBVADW4A (1401) GATCCTTCGCGGGACGTCCTTTGTTTACGTCCCCTCGG
 NC_001484 (1394) GATTCTTCGCGGGACGTCCTTCTGTTACGTCCCCTCGG
 NC_001719 (1388) GATTCTTCGCGGGACGTCCTTCTGCTACGTCCCCTCGG
 NC_004107 (1394) GATTCTTCGCGGGACGTCCTTCTGCTACGTCCCCTCGG
 OHVHEPBA (1394) GATTCTTCGCGGGACGTCCTTCTGCTACGTCCCCTCGG
 NC_001896 (1407) GATCCTGAGAGGGACGTGCTTTGTTTACGTCCCCTCA
 NC_002168 (1401) GATACTTCGCGGGACGTCCTTTGTCTACGTCCCCTCGG
 gi_452617_emb_X75657.1_HHVBBAS (1401) GATCCTTCGCGGGACGTCCTTTGTCTACGTCCCCTAG
 gi_6983934_gb_AF160501.1_AF160501 (1401) GATCCTTCGCGGGACGTCCTTTGTTTACGTCCCCTAG
 Consensus (1407) GATCCTTCGCGGGACGTCCTTTGTTTACGTCCCCTCGG

	(1445)	1445	1450	1460	1470	1482			
AM282986	(1439)	CGCTG	AATCC	C	GCGGACGACCC	C	TCTCGGGG	CCG	CTTG
		Source(1..3215): Source_1							
		CDS(2307..1623): CDS POLYMERASE (P)							
		CDS(1374..1838): CDS X PROTEIN							
		RNA - Misc.(1417..1458): RNA PRE HSL ...							
		Mature Peptide(1162..1623): Domain of...							
		Promoter Eukaryotic(1403..1626): DNA ...							
		RNA - Misc.(1151..1684): RNA PRE Pos...							
		Promoter Eukaryotic(1403..1455): DNA ...							
		mRNA(1310..1930): mRNA X							
		mRNA(2835..1930): mRNA Large S							
		mRNA(3185..1930): mRNA Middle S							
		Promoter Eukaryotic(1456..1519): DNA ...							
		RNA - Misc.(1254..1582): RNA Post tra...							
gi_59439_emb_X65259.1_HBVAYWE	(1439)	CGCTG	AATCC	C	GCGGACGACCC	T	TCTCGGGG	CCG	CTTG
gi_221497_dbj_D00329.1_HPBADW1	(1439)	CGCTG	AATCC	C	GCGGACGACCC	T	TCTCGGGG	CCG	CTTG
gi_59422_emb_X69798.1_HBVADW4A	(1439)	CGCTG	AATCC	C	GCGGACGACCC	T	TCTCGGGG	CCG	CTTG
NC_001484	(1432)	CGGAC	AATCC	A	GCGGACGACCC	T	TCTCGGGG	ACTTCT	CTTG
NC_001719	(1426)	CAGCG	AATCC	G	GCGGACGACCC	T	TCTCGGGG	CCCTTCT	CTTG
NC_004107	(1432)	CCCTC	AATCC	A	GCGGACGACCC	T	TCTCGGGG	CCCTGCT	CTTG
OHVHEPBA	(1432)	CCCTC	AATCC	A	GCGGACGACCC	T	TCTCGGGG	CCCTGCT	CTTG
NC_001896	(1445)	AGCTG	AATCC	A	GCGGACGACCC	T	TCTCGGGG	TTGTC	CTTG
NC_002168	(1439)	CGCTG	AATCC	C	GCGGACGACCC	T	TCTCGGGG	T	CTTG
gi_452617_emb_X75657.1_HHVBBAS	(1439)	CGCTG	AATCC	T	GCGGACGACCC	G	TCTCGGGG	T	CTTG
gi_6983934_gb_AF160501.1_AF160501	(1439)	CGCTG	AATCC	A	GCGGACGACCC	C	TCTCGGGG	CCG	CTTG
Consensus	(1445)	CGCTGAATCC	GCGGACGACCC	TCTCGGGGCCG	TTG				

	(1483)	1483	1490	1500	1510	1520			
AM282986	(1477)	GGACTCT	CTCGT	CCCTT	CTCCGT	CTG	CCGTTCC	AGCC	
		Source(1..3215): Source_1							
		CDS(2307..1623): CDS POLYMERASE (P)							
		CDS(1374..1838): CDS X PROTEIN							
		Mature Peptide(1162..1623): Domain of...							
		Promoter Eukaryotic(1403..1626): DNA ...							
		RNA - Misc.(1151..1684): RNA PRE Pos...							
		mRNA(1310..1930): mRNA X							
		mRNA(2835..1930): mRNA Large S							
		mRNA(3185..1930): mRNA Middle S							
		Promoter Eukaryotic(1456..1519): DNA ...							
		RNA - Misc.(1254..1582): RNA Post tra...							
gi_59439_emb_X65259.1_HBVAYWE	(1477)	GGACTCT	CTCGT	CCCTT	CTCCGT	CTG	CCGTTCC	AGCC	
gi_221497_dbj_D00329.1_HPBADW1	(1477)	GGGCTCT	ACCGC	CCCTT	CTCCGT	CTG	CCGTTCC	AGCC	
gi_59422_emb_X69798.1_HBVADW4A	(1477)	GGGCTG	TACCGC	CCCTT	CTCCGT	CTG	CCGTTCC	AGCC	
NC_001484	(1470)	CCGGCTCTC	CGT	CCCTT	CTCCGT	CTG	CCGTTCC	AGCC	
NC_001719	(1464)	CCGGCTCTG	CAT	CCCTT	CTCCGT	CTG	CCGTTCC	AGCC	
NC_004107	(1470)	CCGGT	TCTGCG	CCCTT	CTCCGT	CTG	CCGTTCC	AGCC	
OHVHEPBA	(1470)	CCGGCTCTG	CGG	CCCTT	CTCCGT	CTG	CCGTTCC	AGCC	
NC_001896	(1483)	GGCTGCTGAAA	CCG	CCCTT	CTCCGT	CTG	CCGTTCC	AGCC	
NC_002168	(1477)	GGGCTCT	ACCGC	CCCTT	CTCCGT	CTG	CCGTTCC	AGCC	
gi_452617_emb_X75657.1_HHVBBAS	(1477)	GGGATCT	ATCGT	CCCTT	CTCCGT	CTG	CCGTTCC	AGCC	
gi_6983934_gb_AF160501.1_AF160501	(1477)	GGGCTCT	GTCCG	CCCTT	CTCCGT	CTG	CCGTTCC	AGCC	
Consensus	(1483)	GGGCTCT	CGCC	CTTCTCCGT	CTG	CCGTTCC	CGGCC		

(1521) 1521 1530 1540 1558
 AM282986 (1515) GACCACGGGGCGCACCTCTCTTTACGCGGTCTCCCCGT

Source(1..3215): Source_1
 CDS(2307..1623): CDS POLYMERASE (P)
 CDS(1374..1838): CDS X PROTEIN
 Promoter Eukaryotic(1520..1576): DNA ...
 Mature Peptide(1162..1623): Domain of...
 Promoter Eukaryotic(1403..1626): DNA ...
 RNA - Misc.(1151..1684): RNA PRE Pos...

mRNA(1310..1930): mRNA X
 mRNA(2835..1930): mRNA Large S
 mRNA(3185..1930): mRNA Middle S

Promoter Eukaryotic(1456..1519): DNA ...

gi_59439_emb_X65259.1_HBVAYWE (1515) GACCACGGGGCGCACCTCTCTTTACGCGGTCTCCCCGT
 gi_221497_dbj_D00329.1_HPBADW1 (1515) GACCACGGGGCGCACCTCTCTTTACGCGGACTCCCCGT
 gi_59422_emb_X69798.1_HBVADW4A (1515) GACGACGGGGTCGCACCTCTCTTTACGCGGACTCCCCGT
 NC_001484 (1508) GGT CACCAAGCGGATATCCCTGTGGGCCTCCCCGC
 NC_001719 (1502) GCAGCTGAGTCGCATCTCCCTTTGGGCCTCCCCGC
 NC_004107 (1508) TCAGACGAGTCGGATCTCCCTTTGGGCCTCCCCGC
 OHVHEPBA (1508) TCAGACGAGTCGGATCTCCCTTTGGGCCTCCCCGC
 NC_001896 (1521) TTCCACGGGGCGCACCTCTCTTTACGCGGTCTCCCCTC
 NC_002168 (1515) GACCACGGGGCGCACCTCTCTTTACGCGGTCTCCCCGT
 gi_452617_emb_X75657.1_HHVBBAS (1515) GACCACGGGGCGCACCTCTCTTTACGCGGTCTCCCCGT
 gi_6983934_gb_AF160501.1_AF160501 (1515) GACCACGGGGCGCACCTCTCTTTACGCGGTCTCCCCGT
 Consensus (1521) GACCACGGGGCGCACCTCTCTTTACGCGGTCTCCCCGT

RNA - Misc.(1254..1582): RNA Post tra...

(1559) 1559 1570 1580 1596
 AM282986 (1553) CTGTGCCTTCTCATCTGCCGGTCCGTGTGCACCTTCGCT

Source(1..3215): Source_1
 CDS(2307..1623): CDS POLYMERASE (P)
 CDS(1374..1838): CDS X PROTEIN
 Promoter Eukaryotic(1520..1576): DNA ... Primer Binding Site(1590..1600):
 Mature Peptide(1162..1623): Domain of...
 Promoter Eukaryotic(1403..1626): DNA ...
 RNA - Misc.(1151..1684): RNA PRE Pos...

mRNA(1310..1930): mRNA X
 mRNA(2835..1930): mRNA Large S
 mRNA(3185..1930): mRNA Middle S

gi_59439_emb_X65259.1_HBVAYWE (1553) CTGTGCCTTCTCATCTGCCGGTCCGTGTGCACCTTCGCT
 gi_221497_dbj_D00329.1_HPBADW1 (1553) CTGTGCCTTCTCATCTGCCGGTCCGTGTGCACCTTCGCT
 gi_59422_emb_X69798.1_HBVADW4A (1553) CTGTTCCTTCTCATCTGCCGGTCCGTGTGCACCTTCGCT
 NC_001484 (1546) CTGTTTCTACTCGTCTGCCGGTCCGTGTGCTTGGGCT
 NC_001719 (1540) CTGTTTCTGCCTCGCCGTGCCGGTCCGTGTGCTTGGGCT
 NC_004107 (1546) CTGTTTCTGCCTCGCCGTGCCGGTCCGTGTGCTTGGGCT
 OHVHEPBA (1546) CTGTTTCTGCCTCGCCGTGCCGGTCCGTGTGCTTGGGCT
 NC_001896 (1559) CTGTGCCTTTTCATCTGCCGGTCCGTGTGCTTTCGCT
 NC_002168 (1553) CTGTGCCTTCTCATCTGCCGGTCCGTGTGCACCTTCGCT
 gi_452617_emb_X75657.1_HHVBBAS (1553) CTGTTCTTCTCATCTGCCGGTCCGTGTGCACCTTCGCT
 gi_6983934_gb_AF160501.1_AF160501 (1553) CTGTTCTTCTCATCTGCCGGTCCGTGTGCACCTTCGCT
 Consensus (1559) CTGTTCTTCTCATCTGCCGGTCCGTGTGCACCTTCGCT

RNA - Misc.(1254..1582): RNA Post tra...

(1597) 1597 1610 1620 1634
 AM282986 (1591) TCACCTCTGCAC-----GTTGCATGGAGACCACCGTGTG

Source(1..3215): Source_1
 CDS(2307..1623): CDS POLYMERASE (P)
 CDS(1374..1838): CDS X PROTEIN
 Primer Binding Site(1590..1600): DNA ...
 Mature Peptide(1162..1623): Domain of...
 Promoter Eukaryotic(1403..1626): DNA ...
 RNA - Misc.(1151..1684): RNA PRE Pos...

mRNA(1310..1930): mRNA X
 mRNA(2835..1930): mRNA Large S
 mRNA(3185..1930): mRNA Middle S

gi_59439_emb_X65259.1_HBVAYWE (1591) TCACCTCTGCAC-----ATTGCATGGAGACCACCGTGTG
 gi_221497_dbj_D00329.1_HPBADW1 (1591) TCACCTCTGCAC-----GTCGCATGGAGACCACCGTGTG
 gi_59422_emb_X69798.1_HBVADW4A (1591) TCACCTCTGCAC-----GTCGCATGGAGACCACCGTGTG
 NC_001484 (1584) TCACCTGTGCAGACTTGC GAACCATGGATTCCACCGTGTG
 NC_001719 (1578) TCACCTGTGCAGAATTTCG GAGCCATGGTTTCCACCAATG
 NC_004107 (1584) TCACCTGTGCAGAATTTCG GAACCATGGATTCCACCGTGTG
 OHVHEPBA (1584) TCACCTGTGCAGACTTGC GAACCATGGATTCCACCGTGTG
 NC_001896 (1597) TCACCTCTGCACCTGGAGATG CATGGAGACCACCAATG
 NC_002168 (1591) TCACCTCTGCAC-----GTTGCATGGAGACCACCGTGTG
 gi_452617_emb_X75657.1_HHVBBAS (1591) TCACCTCTGCAC-----GTCGCATGGAGACCACCGTGTG
 gi_6983934_gb_AF160501.1_AF160501 (1591) TCACCTCTGCAC-----GTTAATGGAAACCGCCATG
 Consensus (1597) TCACCTCTGCAC GT GCATGGAGACCACCGTGTG

(1635) 1635 1640 1650 1660 1672
 AM282986 (1623) AACGCCCATCAGATCCTGCCCAAGGCTTTACATAAGAG

Source(1..3215): Source_1
 CDS(2307..1623): CDS POLYMERASE (P) Enhancer(1636..1744): DNA Enhancer 2 ...
 CDS(1374..1838): CDS X PROTEIN
 Promoter Eukaryotic(1626..1775): DNA ...
 Mature Peptide(1162..1623): Domain of...
 Promoter Eukaryotic(1403..1626): DNA ...
 RNA - Misc.(1151..1684): RNA PRE Pos...

mRNA(1310..1930): mRNA X
 mRNA(2835..1930): mRNA Large S
 mRNA(3185..1930): mRNA Middle S

gi_59439_emb_X65259.1_HBVAYWE (1623) AACGCCCATCAGATTTATGCCC AAGGCTTTACATAAGAG
 gi_221497_dbj_D00329.1_HPBADW1 (1623) AACGCCCATCCGGAACCTGCCCAAGGCTTTGCATAAGAG
 gi_59422_emb_X69798.1_HBVADW4A (1623) AACGCCCATCTGGAGTTTGC CAAAGGCTTTACATAAGAG
 NC_001484 (1622) AAC TT---TGTACCTTGCA-----TGCT-AAGCG
 NC_001719 (1616) AAC TT---TGTCACTTGCA-----TGCA-AAACG
 NC_004107 (1622) AAC TT---TGTCTCCTTGCA-----TGCA-AAATCG
 OHVHEPBA (1622) AAC TT---TGTCTCCTTGCA-----TGCA-AAATCG
 NC_001896 (1635) AAC TC---TGTCACTTGCC-----TGCGTAAGAG
 NC_002168 (1623) AACGCCCATCCGGAACCTTGCCC AAGGCTTTGCATAAGAG
 gi_452617_emb_X75657.1_HHVBBAS (1623) AACGCCCATCCAAATATGCCC AAGGCTTTACATAAGAG
 gi_6983934_gb_AF160501.1_AF160501 (1623) AACACCTCTCATCATCTGCCAAGGCAGTTATATAAGATG
 Consensus (1635) AACGCCCATGTA CTTGCCCAAGGCTTTGCATAAGAG

(1673) 1673 1680 1690 1700 1710
 AM282986 (1661) GACTCTTGGACTCCAGCAATGTCAACGACCGACCTTG

Source(1..3215): Source_1
 Enhancer(1636..1744): DNA Enhancer 2 ...
 CDS(1374..1838): CDS X PROTEIN
 Promoter Eukaryotic(1626..1775): DNA ...

RNA - Misc.(1151..1684): RNA PRE Pos...

mRNA(1310..1930): mRNA X
 mRNA(2835..1930): mRNA Large S
 mRNA(3185..1930): mRNA Middle S

gi_59439_emb_X65259.1_HBVAYWE (1661) GACTCTTGGACTCCAGCAATGTCAACGACCGACCTTG
 gi_221497_dbj_D00329.1_HPBADW1 (1661) GACTCTTGGACTTTCAGCAATGTCAACGACCGACCTTG
 gi_59422_emb_X69798.1_HBVADW4A (1661) GACTCTTGGACTTTCAGGATGGTCAATGACCTGGATCG
 NC_001484 (1648) ACAGCTGGGCAATGATGCAA-----AAGGACCTT--TGG
 NC_001719 (1642) CCAACTGGGCAATGCCAACA-----AAGGACCTT--TGG
 NC_004107 (1648) TCAACTTGGCAATGCCAAGT-----AAGGACCTT--TGG
 OHVHEPBA (1648) TCAACTTGGCAATGCCAAGT-----AAGGACCTT--TGG
 NC_001896 (1661) GACCCTTGGACTCCGCACTGCACCACTTACCGTGAATGG
 NC_002168 (1661) GACTCTTGGACTGTCAACAATGTCAACGACCGGAATTG
 gi_452617_emb_X75657.1_HHVBBAS (1661) GACTCTTGGACTCTCTGCAATGTCAACGACCGACCTTG
 gi_6983934_gb_AF160501.1_AF160501 (1661) GACTCTTGGACTGTTTGTATGTCAACAACCGGGTGG
 Consensus (1673) GACTCTTGGACTGCCAGCAATGTCAACGACCG TGG

(1711) 1711 1720 1730 1748
 AM282986 (1699) AG-GCCTACTTCAAAGACTGTGTTTAAAGGACTGGGA

Source(1..3215): Source_1
 Enhancer(1636..1744): DNA Enhancer 2 ...
 CDS(1374..1838): CDS X PROTEIN
 Promoter Eukaryotic(1626..1775): DNA ...

mRNA(1310..1930): mRNA X
 mRNA(2835..1930): mRNA Large S
 mRNA(3185..1930): mRNA Middle S

gi_59439_emb_X65259.1_HBVAYWE (1699) AG-GCCTACTTCAAAGACTGTGTTTAAAGGACTGGGA
 gi_221497_dbj_D00329.1_HPBADW1 (1699) AG-GCATACTTCAAAGACTGTGTTTAAATGAGTGGGA
 gi_59422_emb_X69798.1_HBVADW4A (1699) AA-GAATACATCAAAGACTGTGTTTAAAGGACTGGGA
 NC_001484 (1679) ACTGCTTATATAGAGATCAATTAATTAACCTTTATGGGA
 NC_001719 (1673) ACTCTTATGTAGAAATCAATTAATTAACCAAATGGGA
 NC_004107 (1679) ACTCTTATATAAAAGATCAATTAATTAACTAAATGGGA
 OHVHEPBA (1679) ACTCTTATATAAAAGATCAATTAATTAACTAAATGGGA
 NC_001896 (1699) AG-CAATACATCAAAGACTGTTTGTGTTGAAACAGTGGGA
 NC_002168 (1699) AG-ACATACTTCAAAGACTGTGTTTAAAGACTGGGA
 gi_452617_emb_X75657.1_HHVBBAS (1699) AG-GCATACTTCAAAGACTGTGTTTAAAGACTGGGA
 gi_6983934_gb_AF160501.1_AF160501 (1699) AG-AAATACTTCAAAGACTGTGTTTGTGCTGAGTGGGA
 Consensus (1711) AG GCATACTTCAAAGACTGTTTGTGTTAA GA TGGGA

(1749) 1749 1760 1770 1786
 AM282986 (1736) **G G A G C T G G G G G A G G A G A T T A G G T T A A A G G T C T T T G T A T**

Source(1..3215): Source_1

Enhancer(1636..1744): DNA Enhancer 2 ...

CDS(1374..1838): CDS X PROTEIN

Promoter Eukaryotic(1626..1775): DNA ...

mRNA(1310..1930): mRNA X

mRNA(2835..1930): mRNA Large S

mRNA(3185..1930): mRNA Middle S

gi_59439_emb_X65259.1_HBVAYWE (1736) **G G A G C T G G G G G A G G A G A T T A G G T T A A A G G T C T T T G T A T**
 gi_221497_dbj_D00329.1_HPBADW1 (1736) **G G A G C T G G G G G A G G A G A T T A G G T T A A A G G T C T T T G T A C**
 gi_59422_emb_X69798.1_HBVADW4A (1736) **G G A G T T G G G G G A G G A G A T T A G G T T A A A G G T C T T T G T A T**
 NC_001484 (1717) **G G A G G G T A T C A T C G A T C C T A G G C T G A A A T T A T T T G T A T**
 NC_001719 (1711) **G G A G G G T A C T A T T G A T T C T A G A T T A C C A C T G T T T G T A T**
 NC_004107 (1717) **G G A G G G C A G C A T T G A T C C T A G A T T A T C A A T A T T T G T A T**
 OHVHEPBA (1717) **G G A G G G C A G C A T T G A T C C T A G A T T A T C A A T A T T T G T A T**
 NC_001896 (1736) **A G A A C A A G G G G A G G A G C C T A G G T T A A A G G T C T T T G T A T**
 NC_002168 (1736) **G G A G T T A G G G G A G G A G A T C A G G T T A A A G G T C T T T G T A T**
 gi_452617_emb_X75657.1_HHVBBAS (1736) **G G A G T C G G G G G A G G A G A T T A G A T T A A A G G T C T T T G T A C**
 gi_6983934_gb_AF160501.1_AF160501 (1736) **A G A A T T A G G C A A T G A G T C C A G G T T A A T G A C C T T T G T A T**
 Consensus (1749) **G G A G T G G G G A G G A G A T T A G G T T A A A G G T C T T T G T A T**

(1787) 1787 1800 1810 1824
 AM282986 (1774) **T A G G A G G C T G T A G G C A T A A A T T G G T C T G C G C A C C A G C A**

Source(1..3215): Source_1

TATA Signal(1790..1794): DNA PreC mRN...

CDS(1374..1838): CDS X PROTEIN

Promoter Eukaryotic(1626..1775): DNA ...

mRNA(1310..1930): mRNA X

mRNA(2835..1930): mRNA Large S

mRNA(3185..1930): mRNA Middle S

gi_59439_emb_X65259.1_HBVAYWE (1774) **T A G G A G G C T G T A G G C A T A A A T T G G T C T G C G C A C C A G C A**
 gi_221497_dbj_D00329.1_HPBADW1 (1774) **T C G G A G G C T G T A G G C A T A A A T T G G T C T G T T C A C C A G C A**
 gi_59422_emb_X69798.1_HBVADW4A (1774) **T A G G A G G C T G T A G G C A T A A A T T G G T C T G T T C A C C A G C A**
 NC_001484 (1755) **T A G G A G G C T G T A G G C A T A A A T A C A T G T G A A T G C T G G A**
 NC_001719 (1749) **T A G G G G G C T G T A G G C A T A A A T A C A T G T A A C T G C C G C A**
 NC_004107 (1755) **T A G G A G G C T G T A G G C A T A A A T G C A T G C G A C T T C T G T A**
 OHVHEPBA (1755) **T A G G A G G C T G T A G G C A T A A A T G C A T G C G A C T T C T G T A**
 NC_001896 (1774) **T A G G A G G C T G T A G G C A T A A A T T G G T G G G A A C T G C C T C A**
 NC_002168 (1774) **T A G G A G G C T G T A G G C A T A A A T T G G T C T G T T C A C C A G C A**
 gi_452617_emb_X75657.1_HHVBBAS (1774) **T A G G A G G C T G T A G G C A T A A A T T G G T C T G C G C A C C A G C A**
 gi_6983934_gb_AF160501.1_AF160501 (1774) **T A G G A G G C T G T A G G C A T A A A T T G G T C T G C G C A C C A G C A**
 Consensus (1787) **T A G G A G G C T G T A G G C A T A A A T T G G T C T G C A C C A G C A**

(1825) 1825 1830 1840 1850 1862
 AM282986 (1812) CCATGCAACTTTTTTCACCTCTGCCTAATCAT --- CTCT

Source(1..3215): Source_1

Primer Binding Site(1824..1834): DNA ...

CDS(1374..1838): CDS X PROTEIN

CDS(1814..2458): CDS PRECORE HBeAg

mRNA(1310..1930): mRNA X

mRNA(2835..1930): mRNA Large S

mRNA(3185..1930): mRNA Middle S

gi_59439_emb_X65259.1_HBVAYWE (1812) CCATGCAACTTTTTTCACCTCTGCCTAATCAT --- CTCT
 gi_221497_dbj_D00329.1_HPBADW1 (1812) CCATGCAACTTTTTTCACCTCTGCCTAGTCAT --- CTCT
 gi_59422_emb_X69798.1_HBVADW4A (1812) CCATGCAACTTTTTTCACCTCTGCCTAATCAT --- CTCT
 NC_001484 (1793) TCATGTATCTTTTTTCACCTGTGCCTTGT TTT TGC CTGT
 NC_001719 (1787) TCATGTATCTTTTTTCACCTGTGCCTTGT TTT TGC CTGT
 NC_004107 (1793) CCATGTATCTTTTTTCACCTGTGCCTTGT TTT TGC CTGT
 OHVHEPBA (1793) CCATGTATCTTTTTTCACCTGTGCCTTGT TTT TGC CTGT
 NC_001896 (1812) CCATGCATCTTTTTTCACCTCTGCCTGATCAT --- CTTA
 NC_002168 (1812) CCATGCAACTTTTTTCACCTCTGCCTAATCAT --- CTCA
 gi_452617_emb_X75657.1_HHVBBAS (1812) CCATGCAACTTTTTTCACCTCTGCCTAATCAT --- CTCT
 gi_6983934_gb_AF160501.1_AF160501 (1812) CCATGTAACTTTTTTCACCTCTGCCTAATCAT --- CTCT
 Consensus (1825) CCATGCAACTTTTTTCACCTCTGCCTAATCAT CTCT

(1863) 1863 1870 1880 1890 1900
 AM282986 (1847) TGTTCATGTCCCACTGTTCAAGCCTCCAAGCTGTGCCT

Source(1..3215): Source_1

CDS(1852..1908): CDS C0 PEPTIDE

CDS(1814..2458): CDS PRECORE HBeAg

RNA - Misc.(1851..1904): RNA epsilon ...

mRNA(1310..1930): mRNA X

mRNA(2835..1930): mRNA Large S

mRNA(3185..1930): mRNA Middle S

gi_59439_emb_X65259.1_HBVAYWE (1847) TGTTCATGTCCCACTGTTCAAGCCTCCAAGCTGTGCCT
 gi_221497_dbj_D00329.1_HPBADW1 (1847) TGTTCATGTCCCACTGTTCAAGCCTCCAAGCTGTGCCT
 gi_59422_emb_X69798.1_HBVADW4A (1847) TGTTCATGTCCCACTGTTCAAGCCTCCAAGCTGTGCCT
 NC_001484 (1831) GTTCCATGTCCCACTGTTCAAGCCTCCAAGCTGTGCCT
 NC_001719 (1825) GTTTCATGTCCCACTGTTCAAGCCTCCAAGCTGTGCCT
 NC_004107 (1831) GTTCCATGTCCCACTGTTCAAGCCTCCAAGCTGTGCCT
 OHVHEPBA (1831) GTTCCATGTCCCACTGTTCAAGCCTCCAAGCTGTGCCT
 NC_001896 (1847) TGTTCATGTCCCACTGTTCAAGCCTCCAAGCTGTGCCT
 NC_002168 (1847) TGTTCATGTCCCACTGTTCAAGCCTCCAAGCTGTGCCT
 gi_452617_emb_X75657.1_HHVBBAS (1847) TGTTCATGTCCCACTGTTCAAGCCTCCAAGCTGTGCCT
 gi_6983934_gb_AF160501.1_AF160501 (1847) TGTTCATGTCCCACTGTTCAAGCCTCCAAGCTGTGCCT
 Consensus (1863) TGTTCATGTCCCACTGTTCAAGCCTCCAAGCTGTGCCT

(1901) 1901 1910 1920 1938
 AM282986 (1885) TGGGTGGCTTTGGGCATG --- GA ---
 Source(1..3215): Source_1
 CDS(1852..1908): CDS C0 PEPTIDE
 Variation(1896..1896): Variation, G18...
 CDS(1814..2458): CDS PRECORE HBeAg
 CDS(1901..2458): CDS CORE HBeAg
 RNA - Misc.(1851..1904): RNA epsilon ...
 mRNA(1310..1930): mRNA X
 mRNA(2835..1930): mRNA Large S
 mRNA(3185..1930): mRNA Middle S

gi_59439_emb_X65259.1_HBVAYWE (1885) TGGGTGGCTTTAGGGCATG --- GA ---
 gi_221497_dbj_D00329.1_HPBADW1 (1885) TGGGTGGCTTTGGGCATG --- GA ---
 gi_59422_emb_X69798.1_HBVADW4A (1885) TGGGTGGCTTTGGGCATG --- GA ---
 NC_001484 (1869) TGGATGGCTTTGGGA CATG --- GA ---
 NC_001719 (1863) TGGATGGCTTTGGGA CATG --- GA ---
 NC_004107 (1869) TGGATGGCTTTGGGCATG --- GA ---
 OHVHEPBA (1869) TGGATGGCTTTGGGCATG --- GA ---
 NC_001896 (1885) TGGGTGGCTTTTGGGCATG --- GA ---
 NC_002168 (1885) TGGGTGGCTTTTGGGCATG --- GA ---
 gi_452617_emb_X75657.1_HHVBBAS (1885) TGGGTGGCTTTGGGCATG --- GA ---
 gi_6983934_gb_AF160501.1_AF160501 (1885) TGGGTGGCTTTAGGGCATG GATA GAACAACCTTTGCCAT
 Consensus (1901) TGGGTGGCTTTGGGCATG GA

(1939) 1939 1950 1960 1976
 AM282986 (1906) --- --- --- CATTGACCCTTATAAAGAA
 Source(1..3215): Source_1
 CDS(1852..1908): CDS C0 PEPTIDE PolyA Signal(1916..1921): RNA Poly A ...
 CDS(1814..2458): CDS PRECORE HBeAg
 CDS(1901..2458): CDS CORE HBeAg
 mRNA(1310..1930): mRNA X
 mRNA(2835..1930): mRNA Large S
 mRNA(3185..1930): mRNA Middle S

gi_59439_emb_X65259.1_HBVAYWE (1906) --- --- --- CATTGACCCTTATAAAGAA
 gi_221497_dbj_D00329.1_HPBADW1 (1906) --- --- --- CATTGACCCTTATAAAGAA
 gi_59422_emb_X69798.1_HBVADW4A (1906) --- --- --- CATTGACCCTTATAAAGAA
 NC_001484 (1890) --- --- --- CATTGACCCTTATAAAGAA
 NC_001719 (1884) --- --- --- CATTGACCCTTATAAAGAA
 NC_004107 (1890) --- --- --- CATTGACCCTTATAAAGAA
 OHVHEPBA (1890) --- --- --- CATTGACCCTTATAAAGAA
 NC_001896 (1906) --- --- --- CATTGACCCTTATAAAGAA
 NC_002168 (1906) --- --- --- CATTGACCCTTATAAAGAA
 gi_452617_emb_X75657.1_HHVBBAS (1906) --- --- --- CATTGACCCTTATAAAGAA
 gi_6983934_gb_AF160501.1_AF160501 (1923) ATGGCCTTTTGGCTTAGA CATTGACCCTTATAAAGAA
 Consensus (1939) CATTGACCCTTATAAAGAA

(1977) 1977 1990 2000 2014
 AM282986 (1925) TTTGGAGCTACTGTGGAGTTACTCTCGTTTGTGCCTTC

Source(1..3215): Source_1

PolyA Site(1930..1930): RNA PolyA cle...

CDS(1814..2458): CDS PRECORE HBeAg

CDS(1901..2458): CDS CORE HBeAg

mRNA(1310..1930): mRNA X

mRNA(2835..1930): mRNA Large S

mRNA(3185..1930): mRNA Middle S

gi_59439_emb_X65259.1_HBVAYWE (1925) TTTGGAGCTACTGTGGAGTTACTCTCGTTTGTGCCTTC
 gi_221497_dbj_D00329.1_HPBADW1 (1925) TTTGGAGCTACTGTGGAGTTACTCTCGTTTGTGCCTTC
 gi_59422_emb_X69798.1_HBVADW4A (1925) TTTGGAGCTACTGTGGAGTTACTCTCGTTTGTGCCTTC
 NC_001484 (1909) TTTGGTTCTTCTTATCAGTTGTTGAATTTTCTTCCTTT
 NC_001719 (1903) TTTGGTTCATCCTACCAGTTGTTGAATTTTCTTCCTTT
 NC_004107 (1909) TTTGGTTCATCTTATCAGTTGTTGAATTTTCTTCCTTT
 OHVHEPBA (1909) TTTGGTTCATCTTATCAGTTGTTGAATTTTCTTCCTTT
 NC_001896 (1925) TTTGGCGCTACTGTTGAGTTATTGTCTTTTGTGCCTGC
 NC_002168 (1925) TTTGGAGCTACTGTGGAGTTACTCTCGTTTGTGCCTTC
 gi_452617_emb_X75657.1_HHVBBAS (1925) TTTGGAGCTACTGTGGAGTTACTCTCGTTTGTGCCTTC
 gi_6983934_gb_AF160501.1_AF160501 (1961) TTTGGAGCTACTGTGGAGTTGCTCTCGTTTGTGCCTTC
 Consensus (1977) TTTGGAGCTACTGTGGAGTTACTCTCTTTTGTGCCTTC

(2015) 2015 2020 2030 2040 2052
 AM282986 (1963) TGACTTCTTTCCTTCGTAGAGATCTCTAGACACCG

Source(1..3215): Source_1

CDS(1814..2458): CDS PRECORE HBeAg

CDS(1901..2458): CDS CORE HBeAg

gi_59439_emb_X65259.1_HBVAYWE (1963) TGACTTCTTTCCTTCGTAGAGATCTCTAGACACCG
 gi_221497_dbj_D00329.1_HPBADW1 (1963) TGACTTCTTTCCTTCGTAGAGATCTCTAGACACCG
 gi_59422_emb_X69798.1_HBVADW4A (1963) TGACTTCTTTCCTTCGTAGAGATCTCTAGACACCG
 NC_001484 (1947) GGACTTCTTTCCTTCGTAGAGATCTCTAGACACCG
 NC_001719 (1941) GGACTTCTTTCCTTCGTAGAGATCTCTAGACACCG
 NC_004107 (1947) GGACTTCTTTCCTTCGTAGAGATCTCTAGACACCG
 OHVHEPBA (1947) GGACTTCTTTCCTTCGTAGAGATCTCTAGACACCG
 NC_001896 (1963) TGACTTCTTTCCTTCGTAGAGATCTCTAGACACCG
 NC_002168 (1963) GGACTTCTTTCCTTCGTAGAGATCTCTAGACACCG
 gi_452617_emb_X75657.1_HHVBBAS (1963) TGACTTCTTTCCTTCGTAGAGATCTCTAGACACCG
 gi_6983934_gb_AF160501.1_AF160501 (1999) TGACTTCTTTCCTTCGTAGAGATCTCTAGACACCG
 Consensus (2015) TGACTTCTTTCCTTC GT AG GATCT CT GACACCG

(2053) 2053 2060 2070 2080 2090
 AM282986 (2001) CCTCAGCTCTGTATCGGGAAGCCTTAGAGTCTCCTGAG
 Source(1..3215): Source_1

CDS(1814..2458): CDS PRECORE HBeAg
 CDS(1901..2458): CDS CORE HBcAg

gi_59439_emb_X65259.1_HBVAYWE (2001) CCTCAGCTCTGTATCGGGAAGCCTTAGAGTCTCCTGAG
 gi_221497_dbj_D00329.1_HPBADW1 (2001) TCTCTGCTCTGTATCGGGAAGCCTTAAATCTCCTGAG
 gi_59422_emb_X69798.1_HBVADW4A (2001) CTTCAGCTCTTTATCCGGGATGCTTTAGAGTCACTGAA
 NC_001484 (1985) CTGCTGCTCTTTATGAAGAAGAAATTAACAGGTAGGGAG
 NC_001719 (1979) CTACTGCTCTCTATGAAGAAGAAATTAACAGGTAGGGAG
 NC_004107 (1985) CTACTGCTCTGTATGAAGAAGAGCTAACAGGTAGGGAA
 OHVHEPBA (1985) CTACTGCTCTGTATGAAGAAGAGCTAACAGGTAGGGAA
 NC_001896 (2001) CTTCTGCTCTGTATAGAAGAGCCCTGGAGTCTTCCGAC
 NC_002168 (2001) CATCAGCCCTGTATCGGGAAGCCTTAGAGTCTCCAGAA
 gi_452617_emb_X75657.1_HHVBBAS (2001) CCTCAGCTCTGTATCGGGAAGCCTTAGAGTCTCCTGAG
 gi_6983934_gb_AF160501.1_AF160501 (2037) CTTCAGCTTTGTACCGGGAATCCTTAGAGTCTCTGAT
 Consensus (2053) CTTCTGCTCTGTATCGGGAAGCCTTAGAGTCTCCTGAG

(2091) 2091 2100 2110 2128
 AM282986 (2039) CATTGTCTCACCTCACCATACTGCACTCAGGCAAGCAAT
 Source(1..3215): Source_1

CDS(1814..2458): CDS PRECORE HBeAg
 CDS(1901..2458): CDS CORE HBcAg

gi_59439_emb_X65259.1_HBVAYWE (2039) CATTGTCTCACCTCACCATACTGCACTCAGGCAAGCAAT
 gi_221497_dbj_D00329.1_HPBADW1 (2039) CATTGTCTCACCTCACCATACTGCACTCAGGCAAGCTAT
 gi_59422_emb_X69798.1_HBVADW4A (2039) CATTGTCACTCCCAACCATACTGCTTCTCAGGCAAGCTAT
 NC_001484 (2023) CATTGTCTCTCCTCATCATACTGCTATTAGACAGGCTT
 NC_001719 (2017) CACTGCTCTCTCCTCATCACACAGCTATTCAGACAGCTTT
 NC_004107 (2023) CATTGTCTCTCCGCACATACAGCTATTAGACAGCTTT
 OHVHEPBA (2023) CATTGTCTCTCCGCACATACAGCTATTAGACAGCTTT
 NC_001896 (2039) CACTGTTTCACTCCGCACATACTGCTTGTAGGCAAGCGGT
 NC_002168 (2039) CATTGTCTCACCTAACCATACAGCACTCAGGCAAGCAGT
 gi_452617_emb_X75657.1_HHVBBAS (2039) CATTGTCTCACCTCACCATACTGCACTCAGGCAAGCCTAT
 gi_6983934_gb_AF160501.1_AF160501 (2075) CATTGTCTCGCCTCACCATACAGCACTCAGGCAAGCAAT
 Consensus (2091) CATTGTCTCACCTCACCATACTGCACTCAGGCAAGC AT

(2129) 2129 2140 2150 2166
 AM282986 (2077) TCTCTGCTGGGGGGAATTGATGACTCTAGCTACCTGGG
 Source(1..3215): Source_1

CDS(1814..2458): CDS PRECORE HBeAg
 CDS(1901..2458): CDS CORE HBeAg

gi_59439_emb_X65259.1_HBVAYWE (2077) TCTTTGCTGGGGGGAAC TAATGACTCTAGCTACCTGGG
 gi_221497_dbj_D00329.1_HPBADW1 (2077) TCTGTGCTGGGGGGAATTAATGACTCTAGCTACCTGGG
 gi_59422_emb_X69798.1_HBVADW4A (2077) TTTGTGCTGGGGT GAGTTAATGACTTTGGCTTCTGGG
 NC_001484 (2061) AGTGTGCTGGGAA GAATTA ACTAGATT AATTACATGGA
 NC_001719 (2055) AGTTTGCTGGGAA GAATTA ACAAGATT AATTGCGTGGG
 NC_004107 (2061) AGTATGCTGGGAT GAATTA ACTAAATT GATAGCTTGGG
 OHVHEPBA (2061) AGTATGCTGGGAT GAATTA ACTAAATT GATAGCTTGGG
 NC_001896 (2077) ACTGTGCTGGGGAGA GAATTAATGTCCTTAGCTTCTGGG
 NC_002168 (2077) TCTGTGCTGGGGT GAGTTAATGACTCTGGCTTCTGGG
 gi_452617_emb_X75657.1_HHVBBAS (2077) TCTTTGCTGGGGAGA GAAC TAATGACTCTAGCTACCTGGG
 gi_6983934_gb_AF160501.1_AF160501 (2113) CCTGTGCTGGGGT GAGTTGATGACTCTAGCTACCTGGG
 Consensus (2129) TCTGTGCTGGGG GAATTAATGACTTTAGCTACCTGGG

(2167) 2167 2180 2190 2204
 AM282986 (2115) TGGGTAATAA TTTGGAAGATCCAGCATC CAGGGATCTA
 Source(1..3215): Source_1

CDS(1814..2458): CDS PRECORE HBeAg
 CDS(1901..2458): CDS CORE HBeAg

gi_59439_emb_X65259.1_HBVAYWE (2115) TGGGTGTAA TTTGGAAGATCCAGCATCTAGAGACTTA
 gi_221497_dbj_D00329.1_HPBADW1 (2115) TGGGTAATAA TTTGGAAGATCCAGCATCCCGGATCTA
 gi_59422_emb_X69798.1_HBVADW4A (2115) TGGCAATAA TTTGGAAGGACCTGCAGCTAGGGAATTA
 NC_001484 (2099) TGA GTGAAAATACAA --- CAGAAGAA GTTAGAAGAA TT
 NC_001719 (2093) TGA GTGC TAA CATTA ATTCAGAAGAA GTAAGAAGAG TT
 NC_004107 (2099) TGA GCTC TAA CATTA ACTTTC TGAACAAGTAAGAACAA TC
 OHVHEPBA (2099) TGA GCTC TAA CATTA ACTTTC TGAACAAGTAAGAACAA TC
 NC_001896 (2115) TGGGAAC TAA TTTGGAAGGATCC TGTGCTAGAGAAATTA
 NC_002168 (2115) TGGGTAATAA TTTGGAAGACCCAGCATCTAGGGAAC TG
 gi_452617_emb_X75657.1_HHVBBAS (2115) TGGGTGTAA TTTGGAAGATCCAGCATC CAGGGACCTA
 gi_6983934_gb_AF160501.1_AF160501 (2151) TGGGTAATAA TTTGGAAGATCCAGCATC CAGAGATT TG
 Consensus (2167) TGGGTAATAA TTTGGAAGATCCAGCATC AGAGAA TA

(2205) 2205 2210 2220 2230 2242
 AM282986 (2153) GTAGTCAATTATGTTAATACTAACATGGGTTTAAAGAT
 Source(1..3215): Source_1

CDS(1814..2458): CDS PRECORE HBeAg
 CDS(1901..2458): CDS CORE HBeAg

gi_59439_emb_X65259.1_HBVAYWE (2153) GTAGTCAAGTTATGTTCAACACTAATATGGGCCTAAAGTT
 gi_221497_dbj_D00329.1_HPBADW1 (2153) GTAGTCAATTATGTTAACTACTAACATGGGCCTAAAGAT
 gi_59422_emb_X69798.1_HBVADW4A (2153) GTAGTTAACTATGTTAACTACTAACATGGGCCTAAAAT
 NC_001484 (2134) ATTGTTGATCATGTTCAATAATACTTGGGGACTTAAAGT
 NC_001719 (2131) ATAGTTGCTCATGTTCAATGACACTTGGGGACTTAAAGT
 NC_004107 (2137) ATAGTAAATCATGTTCAATGATACTTGGGGACTTAAAGT
 OHVHEPBA (2137) ATAGTAAATCATGTTCAATGATACTTGGGGACTTAAAGT
 NC_001896 (2153) GTGGTTAGCTATGTTCAATGACAACTGGGGACTGAAGT
 NC_002168 (2153) GTAGTTAATTATGTTCAACAATAATATGGGGCTAAAAT
 gi_452617_emb_X75657.1_HHVBBAS (2153) GTAGTCAAGTTATGTTCAATACTAATATGGGCCTAAAGTT
 gi_6983934_gb_AF160501.1_AF160501 (2189) GTGGTCAATTATGTTAATACTAATATGGGTTTAAAAT
 Consensus (2205) GTAGT AATTATGTTCAATACTAATATGGG CTAAAG T

(2243) 2243 2250 2260 2270 2280
 AM282986 (2191) CAGGCAACTATTGTTGGTTTCATATATCTTGCCTTACTT
 Source(1..3215): Source_1

CDS(1814..2458): CDS PRECORE HBeAg
 CDS(1901..2458): CDS CORE HBeAg

gi_59439_emb_X65259.1_HBVAYWE (2191) CAGGCAACTCTTGTGGTTTCACATTTCTTGTCTCACTT
 gi_221497_dbj_D00329.1_HPBADW1 (2191) CAGGCAACTATTGTTGGTTTCACATTTCTTGTCTTACTT
 gi_59422_emb_X69798.1_HBVADW4A (2191) TAGACAACCTGTTGTGGTTTCACATTTCTTGCCTTACTT
 NC_001484 (2172) AAGACAGACTTTATGGTTTCATTTATCAGTCTTACTT
 NC_001719 (2169) TAGGCAAGAAATTTATGGTTTCATTTATCTTGTCTGACTT
 NC_004107 (2175) GAGACAAGTTTATGGTTTCATTTGTCAAGTCTCACTT
 OHVHEPBA (2175) GAGACAAGTTTATGGTTTCATTTGTCAAGTCTCACTT
 NC_001896 (2191) GAGACAACCTCCTTGGTTTCATATTTCTTGTCTCACTT
 NC_002168 (2191) CAGACAACCTACTGTTGGTTTCACATTTCTTGTCTTACTT
 gi_452617_emb_X75657.1_HHVBBAS (2191) CAGGCAACTATTGTTGGTTTCACATTTCTTGTCTCACTT
 gi_6983934_gb_AF160501.1_AF160501 (2227) CAGGCAACTATTGTTGGTTTCACATTTCTTGTCTTACTT
 Consensus (2243) CAGGCAACT TTGTTGGTTTCACATTTCTTGTCTTACTT

(2281) 2281 2290 2300 2318
 AM282986 (2229) TTGGAAGAGAGACTGTACTTGAAATATTGGTCTCTTTC
 Source(1..3215): Source_1

CDS(1814..2458): CDS PRECORE HBeAg
 CDS(1901..2458): CDS CORE HBeAg

gi_59439_emb_X65259.1_HBVAYWE (2229) TTGGAAGAGAAACAGTTATAGAGTATTTGGTGTCTTTC
 gi_221497_dbj_D00329.1_HPBADW1 (2229) TTGGAAGAGAAACTGTTCTGGAATATTTGGTATCTTTT
 gi_59422_emb_X69798.1_HBVADW4A (2229) TTGGAAGAGAAACAGTTCTAGAGTATTTGGTGTCTTTT
 NC_001484 (2210) TTGGACAACACACAGTTCAGAATTTTTGGTGTAGTTT
 NC_001719 (2207) TTGGGCAACACACAGTGCAGGAATTTTGTAGTCAGCTTT
 NC_004107 (2213) TTGGACAACATACAGTTCAGAATTTTGTAGTAAGTTT
 OHVHEPBA (2213) TCGGACAACATACAGTTCAGAATTTTGTAGTAAGTTT
 NC_001896 (2229) TTGGTAGGAAACTGTTTGGAAATATCTGGTGTCTTTT
 NC_002168 (2229) TTGGAAGAGAAACAGTTTGTAGAAATATTTGGTGTCTTTT
 gi_452617_emb_X75657.1_HHVBBAS (2229) TTGGAAGAGAAACCGTTCATAGAGTATTTGGTGTCTTTT
 gi_6983934_gb_AF160501.1_AF160501 (2265) TTGGGAGAGAAACCGTTCTTGAATATTTGGTGTCTTTT
 Consensus (2281) TTGGAAGAGAAACAGTTCTAGAAATATTTGGT TCTTTT

(2319) 2319 2330 2340 2356
 AM282986 (2267) GGAGTGTGGATTCGCACCTCCTCCAGCTTATAGACCACC
 Source(1..3215): Source_1

CDS(1814..2458): CDS PRECORE HBeAg
 CDS(1901..2458): CDS CORE HBeAg

gi_59439_emb_X65259.1_HBVAYWE (2267) GGAGTGTGGATTCGCACCTCCTCCAGCTTATAGACCACC
 gi_221497_dbj_D00329.1_HPBADW1 (2267) GGAGTGTGGATTCGCACCTCCTCCAGCTTATAGACCACC
 gi_59422_emb_X69798.1_HBVADW4A (2267) GGAGTGTGGATTCGCACCTCCTCCAGCTTATAGACCACC
 NC_001484 (2248) GGAGTATGGATTAGAACTCCAGCTCCTTATAGACCACC
 NC_001719 (2245) GGAGTAAAGGATCAGAACTCCGGCTCCTTATAGACCTCC
 NC_004107 (2251) GGAGTATGGATCAGAACTCCAGCTCCATATAGACCTCC
 OHVHEPBA (2251) GGAGTATGGATCAGAACTCCAGCTCCATATAGACCTCC
 NC_001896 (2267) TGGGTGTGGATACGCCACACCTCCTGCATATAGACCACC
 NC_002168 (2267) GGAGTGTGGATTCGCACCTCCTCCAGCTTATAGACCACC
 gi_452617_emb_X75657.1_HHVBBAS (2267) GGAGTGTGGATTCGCACCTCCTCCAGCTTATAGACCACC
 gi_6983934_gb_AF160501.1_AF160501 (2303) GGAGTGTGGATTCGCACCTCCTCCAGCTTATAGACCACC
 Consensus (2319) GGAGTGTGGATTCGCACCTCCTCCAGCTTATAGACCACC

(2357) 2357 2370 2380 2394
 AM282986 (2305) AAATGCCCTATCTTATCAACACTTCCGGAAACTACTG
 Source(1..3215): Source_1
 CDS(2307..1623): CDS POLYMERASE (P)
 Mature Peptide(2307..2843): Domain of...
 CDS(1814..2458): CDS PRECORE HBeAg
 CDS(1901..2458): CDS CORE HBeAg

gi_59439_emb_X65259.1_HBVAYWE (2305) AAATGCCCTATCTTATCAACACTTCCGGAAACTACTG
 gi_221497_dbj_D00329.1_HPBADW1 (2305) AAATGCCCTATCTTATCAACACTTCCGGAAACTACTG
 gi_59422_emb_X69798.1_HBVADW4A (2305) AAATGCCCTATCTTATCAACACTTCCGGAAACTACTG
 NC_001484 (2286) TAATGCACCCATTTTATCAACTTCCGGAAACTACTG
 NC_001719 (2283) TAATGCACCCATTTCTCAACTTCCGGAAACTACTG
 NC_004107 (2289) TAATGCACCCATTTCTCGAACTTCCGGAAACTACTG
 OHVHEPBA (2289) TAATGCACCCATTTCTCGAACTTCCGGAAACTACTG
 NC_001896 (2305) CAATGCCCTATCTTATCAACACTTCCGGAAACTACTG
 NC_002168 (2305) AAATGCCCTATCTTGTCAACACTTCCGGAAACTACTG
 gi_452617_emb_X75657.1_HHVBBAS (2305) AAATGCCCTATCTTATCAACACTTCCGGAAACTACTG
 gi_6983934_gb_AF160501.1_AF160501 (2341) AAATGCCCTATCTTATCAACACTTCCGGAAACTACTG
 Consensus (2357) AAATGCCCTATCTTATCAACACTTCCGGAAACTACTG

(2395) 2395 2400 2410 2420 2432
 AM282986 (2343) TTGTTAGACGACGGACCG-----AGGCAGGTCC
 Source(1..3215): Source_1
 CDS(2307..1623): CDS POLYMERASE (P)
 Mature Peptide(2307..2843): Domain of...
 CDS(1814..2458): CDS PRECORE HBeAg
 CDS(1901..2458): CDS CORE HBeAg

gi_59439_emb_X65259.1_HBVAYWE (2343) TTGTTAGACGACGGACCG-----AGGCAGGTCC
 gi_221497_dbj_D00329.1_HPBADW1 (2343) TTGTTAGACGACGGACCG-----AGGCAGGTCC
 gi_59422_emb_X69798.1_HBVADW4A (2343) TTGTTAGACGACGGACCG-----AGGCAGGTCC
 NC_001484 (2324) TCAITTAGAGAGAGAGGAGGTTCAAGAGCTGCTAGGTCC
 NC_001719 (2321) TCAITTAGAGAGAGAGGAAGTGCAAGAGTTGTTAGGTCC
 NC_004107 (2327) TCAITTAGAGAGAGAGGAGGTGCAAGAGCTTCTAGGTCC
 OHVHEPBA (2327) TCAITTAGAGAGAGAGGAGGTGCAAGAGCTTCTAGGTCC
 NC_001896 (2343) TTGTTAGACGACGGACCG-----GAGACCC
 NC_002168 (2343) TTGTTAGACGACGGACCG-----AGGCAGGTCC
 gi_452617_emb_X75657.1_HHVBBAS (2343) TTGTTAGACGACGGACCG-----AGGCAGGTCC
 gi_6983934_gb_AF160501.1_AF160501 (2379) TTGTTAGACGACGGACCG-----AGGCAGGTCC
 Consensus (2395) TTGTTAGACGACGGACCG-----AGGCAGGTCC

(2433) 2433 2440 2450 2460 2470
 AM282986 (2372) CCTAGAAGAA GAACTCCCTCGCCTCG CAGACGCAGATC
 Source(1..3215): Source_1
 CDS(2307..1623): CDS POLYMERASE (P)
 Mature Peptide(2307..2843): Domain of...
 CDS(1814..2458): CDS PRECORE HBeAg
 CDS(1901..2458): CDS CORE HBeAg

gi_59439_emb_X65259.1_HBVAYWE (2366) CCTAGAAGAA GAACTCCCTCGCCTCG CAGACCAAGGTC
 gi_221497_dbj_D00329.1_HPBADW1 (2366) CCTAGAAGAA GAACTCCCTCGCCTCG CAGACGAAGGTC
 gi_59422_emb_X69798.1_HBVADW4A (2366) CCTAGAAGAA GAACTCCCTCGCCTCG CAGACGAAGATC
 NC_001484 (2362) CCCGAAGACGC ACTCCCTCTCCTCG CAGGAGAAGGTC
 NC_001719 (2359) CCCAGAAGACGC ACTCCCTCTCCTCG CAGGAGAAGATC
 NC_004107 (2365) CCCAGAAGACGC ACTCCCTCTCCTCG CAGGAGAAGATC
 OHVHEPBA (2365) CCCAGAAGACGC ACTCCCTCTCCTCG CAGGAGAAGATC
 NC_001896 (2363) TCTGGAAGACGC ACTCCCTCGCCTCG CAGACGAAGATC
 NC_002168 (2366) CCTAGAAGAA GAACTCCCTCGCCTCG CAGACGAAGGTC
 gi_452617_emb_X75657.1_HHVBBAS (2366) CCTAGAAGAA GAACTCCCTCGCCTCG CAGACGAAGATC
 gi_6983934_gb_AF160501.1_AF160501 (2402) CCTCGAAGAA GAACTCCCTCGCCTCG CAGACGAAGATC
 Consensus (2433) CCTAGAAGAA GAACTCCCTCGCCTCG CAGACGAAGATC

(2471) 2471 2480 2490 2508
 AM282986 (2410) TCAATCGCCGCGTCGCAGAAGATCTCAATCTC GGGAAAT
 Source(1..3215): Source_1
 CDS(2307..1623): CDS POLYMERASE (P)
 Mature Peptide(2307..2843): Domain of...
 CDS(1814..2458): CDS PRECORE HBeAg
 CDS(1901..2458): CDS CORE HBeAg

gi_59439_emb_X65259.1_HBVAYWE (2404) TCAATCGCCGCGTCGCAGAAGATCTCAATCTC GGGAAAT
 gi_221497_dbj_D00329.1_HPBADW1 (2404) TCAATCA CCGCGTCGCAGAAGATCTCAATCTC GGGAAAT
 gi_59422_emb_X69798.1_HBVADW4A (2404) TCAATCGCCGCGTCGC CAGATCTCAATCTC CAGCTT
 NC_001484 (2400) TCAATCA CCGCGTCGCAGA CACTCTCAATCTC CAGCTT
 NC_001719 (2397) TCAATCA CCGCGTCGCAGGC ---CTCAATCTC CAGCTT
 NC_004107 (2403) TCAATCA CCGCGTCGCAGACGCTCTCAATCTC CATCTG
 OHVHEPBA (2403) TCAATCA CCGCGTCGCAGACGCTCTCAATCTC CATCTG
 NC_001896 (2401) TCAATCGCCGCGTCGCAGAAGGTCTCAATCTC CAGCAT
 NC_002168 (2404) TCAATCA CCGCGTCGCAGAAGATCTCAATCTC CAGCTT
 gi_452617_emb_X75657.1_HHVBBAS (2404) TCAATCGCCGCGTCGCAGAAGATCTCAATCTC CAGCTT
 gi_6983934_gb_AF160501.1_AF160501 (2440) TCAATCGCCGCGTCGCAGAAGATCTGCATCTC CAGCTT
 Consensus (2471) TCAATCGCCGCGTCGCAGAAGATCTCAATCTCCAGCTT

(2509) 2509 2520 2530 2546
 AM282986 (2448) C T C A A T G T T A G T A T T C C T T G G A C T C A T A A G G T G G G A A A
 Source(1..3215): Source_1
 CDS(2307..1623): CDS POLYMERASE (P)
 Mature Peptide(2307..2843): Domain of...
 CDS(1814..2458): CDS PRECORE HBeAg
 CDS(1901..2458): CDS CORE HBeAg

gi_59439_emb_X65259.1_HBVAYWE (2442) C T C A A T G T T A G T A T T C C T T G G A C T C A T A A G G T G G G G A A
 gi_221497_dbj_D00329.1_HPBADW1 (2442) C C C A A T G T T A G T A T T C C T T G G A C T C A T A A G G T G G G A A A
 gi_59422_emb_X69798.1_HBVADW4A (2442) C C C A A T G T T A G T A T T C C T T G G A C T C A T A A G G T G G G A A A
 NC_001484 (2438) C C A A C T G C T G A T T T G G A G T G G A T T C A T A A G A C A A A T G T
 NC_001719 (2432) C C A A C T G C T G A T C T T G A T T G G G T G C A T C A A A C T A A T G C
 NC_004107 (2441) C C A A C T G C T G A T C T T C A A T G G G T A C A T A A A A C T A A T G C
 OHVHEPBA (2441) C C A A C T G C T G A T C T T C A A T G G G T A C A T A A A A C T A A T G C
 NC_001896 (2439) C T T C C T G T T A G T A T A C C T T G G A C T C A T A A G G T G G G G C C
 NC_002168 (2442) C C C A A T G T T A G T A T T C C T T G G A C T C A C A A G G T G G G A A A
 gi_452617_emb_X75657.1_HHVBBAS (2442) C C C A A T G T T A G T A T T C C T T G G A C T C A T A A G G T G G G A A A
 gi_6983934_gb_AF160501.1_AF160501 (2478) C C C A A T G T T A G T A T T C C T T G G A C T C A C A A G G T G G G A A A
 Consensus (2509) C C C A A T G T T A G T A T T C C T T G G A C T C A T A A G G T G G G A A A

(2547) 2547 2560 2570 2584
 AM282986 (2486) C T T T A C G T G G G C T T T A T T C C T C T A C A G T A C C T A T C T T T A
 Source(1..3215): Source_1
 CDS(2307..1623): CDS POLYMERASE (P)
 Mature Peptide(2307..2843): Domain of...

gi_59439_emb_X65259.1_HBVAYWE (2480) C T T T A C G G G G C T T T A T T C T T C T A C T G T T C C T G T C T T T A
 gi_221497_dbj_D00329.1_HPBADW1 (2480) C T T T A C G G G G C T T T A T T C T T C T A C A G T A C C T G T C T T T A
 gi_59422_emb_X69798.1_HBVADW4A (2480) C T T T A C G G G G C T T T A C T C T T C T A C T G T G C C T G C T T T A
 NC_001484 (2476) T A T T A C A G G T T T G T A T T C T A C T C A A A C A G A A A A A T T T A
 NC_001719 (2470) T A T A A C G G G T C T T T A T T C T A C T C A G A C A G C T A A G T T T A
 NC_004107 (2479) T A T T A C A G G T C T T T A C T C T A A C C A A G C T G C T C A G T T C A
 OHVHEPBA (2479) A A T T A C A G G T C T T T A C T C T A A C C A A G C T G C T C A G T T C A
 NC_001896 (2477) A T T C T C G G G T T T G T A T T C T G T T T C A C T C T C A C A T T C A
 NC_002168 (2480) C T T T A C G G G G C T T T A T T C T T C T A C C G C A C C T G T C T T T A
 gi_452617_emb_X75657.1_HHVBBAS (2480) T T T T A C G G G G C T T T A C T C T T C T A C T A T A C C T G T C T T T A
 gi_6983934_gb_AF160501.1_AF160501 (2516) C T T T A C G G G G C T G T A T T C T T C T A C T A T A C C T G T C T T T A
 Consensus (2547) C T T T A C G G G G C T T T A T T C T T C T A C G T A C C T G T C T T T A

(2585) 2585 2590 2600 2610 2622
 AM282986 (2524) ATCCTGAAATGGCAAACCTCTTCCTTTCCTAAGATTCAT
 Source(1..3215): Source_1
 CDS(2307..1623): CDS POLYMERASE (P)
 Mature Peptide(2307..2843): Domain of...

gi_59439_emb_X65259.1_HBVAYWE (2518) ATCCTCATTTGGAAAACA CTTCTTTTCCTAATATACAT
 gi_221497_dbj_D00329.1_HPBADW1 (2518) ATCCTGAAATGGCAAACCTCTCTTTTCAGACATTCAT
 gi_59422_emb_X69798.1_HBVADW4A (2518) ATCCTAACTGGTCCACTCTTCTTTTCCTGATATTCAT
 NC_001484 (2514) ATTGTAACTGGAAACAACCTGTATTTCCCAAAATCCAT
 NC_001719 (2508) ATCCTGAAATGGAAACAACCTGATTTTCCAAAAATTCAC
 NC_004107 (2517) ATCCGCATTTGGATTCAA CTTGAGTTTCCTGAAC TTCAT
 OHVHEPBA (2517) ATCCGAAATTTGGATTCAA CTTGAGTTTCCTGAAC TTCAT
 NC_001896 (2515) ATCCACAATTTGGAAAACCTCCAA TTTCTTTGATTCAC
 NC_002168 (2518) ATCCTAACTGGCAAACCTCTCTTTTCCTGACATTCAT
 gi_452617_emb_X75657.1_HHVBBAS (2518) ATCCTAACTGGAAAACCTCATCTTTTCCTGATATTCAT
 gi_6983934_gb_AF160501.1_AF160501 (2554) ATCCTGAAATGGCAAACCTCTCTTTTTCCTGA ATTCAT
 Consensus (2585) ATCCT A TGGAAAACCTCTTCTTTTTCCTGA ATTCAT

(2623) 2623 2630 2640 2650 2660
 AM282986 (2562) TTACATAGAGGACATTAATTAATAGGTGTCAACAATTGTT
 Source(1..3215): Source_1
 CDS(2307..1623): CDS POLYMERASE (P)
 Mature Peptide(2307..2843): Domain of...

gi_59439_emb_X65259.1_HBVAYWE (2556) TTACATCCAGAGCATTATCAAAAATGTGAACAATTGTT
 gi_221497_dbj_D00329.1_HPBADW1 (2556) TTACAGGAGGACATTTGTTGATAGATGTAAGCAATTGTT
 gi_59422_emb_X69798.1_HBVADW4A (2556) TTGCATCAGACCCTGATTTCTAAATGTGAACAATTGTT
 NC_001484 (2552) CTGGATAATAATTATTTCCAAAAGTTGGAGAAATTAATT
 NC_001719 (2546) TTGTCTGAGATTATTTCTAAACTA-C AACAATTTT
 NC_004107 (2555) TTACATAATGATTTAATTCAAAATTTGC AACAGTATTT
 OHVHEPBA (2555) TTACATAATGATTTAATTCAAAATTTGC AACAGTATTT
 NC_001896 (2553) CTTAAGGAGATTTAATTCCTTTTATAGAGTCA TATTT
 NC_002168 (2556) TTACATCCAGGATATCATTAACAAGTGTGAACAATTAGT
 gi_452617_emb_X75657.1_HHVBBAS (2556) TTGCATCCAGGACATTAATTAACAATGTGAACAATTGTT
 gi_6983934_gb_AF160501.1_AF160501 (2592) TTGCATCAGAGCATTATTAACTAAATGTGAACAATTGTT
 Consensus (2623) TTACAT A GATAT ATT A AAATGTGAACAATTGTT

(2661) 2661 2670 2680 2698
 AM282986 (2600) - GGGC CCTCT CACTGTAAATGAAAAGAGAAGATTGAAA
 Source(1..3215): Source_1
 CDS(2307..1623): CDS POLYMERASE (P)
 Mature Peptide(2307..2843): Domain of...

gi_59439_emb_X65259.1_HBVAYWE (2594) - A GGC CCACTCACAGTCAATGAGAAAAGAAGACTGC AA
 gi_221497_dbj_D00329.1_HPBADW1 (2594) - G GGA CCCC TACAGTAAATGAAAACAGGAGACTAAAA
 gi_59422_emb_X69798.1_HBVADW4A (2594) - A GGC CCACTTACTAAAATGAAATTACGAAGATTAAAA
 NC_001484 (2590) - T GGA CCTTTA ACTACTAATGAAAAAAGGAGACTAAAA
 NC_001719 (2583) G TGGT CCTCTTACAGTTAATGAAAAAAGGAAATTAAAA
 NC_004107 (2593) - T GGT CCTTTGACTATAAATGAAAAGAGAAATTGC AA
 OHVHEPBA (2593) - T GGT CCTTTGACTATAAATGAAAAGAGAAATTGC AA
 NC_001896 (2591) - T GGC CCTCTA ACTTAGCAATGAAAAAAGGAGACTCAA
 NC_002168 (2594) - T GGT CCACTTACGTAAATGAAAAAAGGAGATTAAAG
 gi_452617_emb_X75657.1_HHVBBAS (2594) - A GGT CCTCTA ACTGTAAATGAAAACGAAGATTAAAC
 gi_6983934_gb_AF160501.1_AF160501 (2630) - G GGC CCTCTCACAGTAAATGAGAAACGAAGATTAAAA
 Consensus (2661) TGG CCTCT ACTGTAAATGAAAAAGAAGATTAAAA

(2699) 2699 2710 2720 2736
 AM282986 (2637) TTAATTATGCTGCTAGATTTCTATCCTAACCACACTAA
 Source(1..3215): Source_1
 CDS(2307..1623): CDS POLYMERASE (P)
 Mature Peptide(2307..2843): Domain of...

gi_59439_emb_X65259.1_HBVAYWE (2631) TTGATTATGCTGCTAGGTTTATA CCAAATGTC ACCAA
 gi_221497_dbj_D00329.1_HPBADW1 (2631) TTAATAATGCTGCTAGATTTTATA CCAAATGTT ACCAA
 gi_59422_emb_X69798.1_HBVADW4A (2631) TTGGTTATGCTAGCTAGATTTTATA CCAAAGGTT ACCAA
 NC_001484 (2627) CTGTATTTCCAGCTAGATTTCTTCCCAAATGCT ACCAA
 NC_001719 (2621) TTAATTTTCCGCTAGGTTTTC CCAAAGGCTACTAA
 NC_004107 (2630) TTAATTTTCCGCTAGATTTTTC CCAAAGCTACTAA
 OHVHEPBA (2630) TTAATTTTCCGCTAGATTTTTC CCAAAGCTACTAA
 NC_001896 (2628) TTGGTTTACCAGCTAGATTTTATA CCAAAGGCT ACCAA
 NC_002168 (2631) TTAATTATGCTGCTAGATTTCTAT CCAACTCT ACCAA
 gi_452617_emb_X75657.1_HHVBBAS (2631) TTAGTCATGCTGCTAGATTTTTC CCACTCTACTAGAA
 gi_6983934_gb_AF160501.1_AF160501 (2667) CTAGTTATGCTGCTAGATTTTTC CCAA ACTCTACTAA
 Consensus (2699) TTAATTATGCTGCTAGATTTTTC CCAA GCTACCAA

(2737) 2737 2750 2760 2774
 AM282986 (2675) ATATTTG CCCTTAGA CAAAGGAT TAAACCTTAT TATC
 Source(1..3215): Source_1
 CDS(2307..1623): CDS POLYMERASE (P)
 Mature Peptide(2307..2843): Domain of...

gi_59439_emb_X65259.1_HBVAYWE (2669) ATATTTG CCATTGGATAAG GGTATTAAA CTTATTATC
 gi_221497_dbj_D00329.1_HPBADW1 (2669) ATATTTG CCCTTAGATAAA GGTATCAAACCTTATTATC
 gi_59422_emb_X69798.1_HBVADW4A (2669) ATATTTT CCAATGGATAAAGGCATCAAACCTTATTATC
 NC_001484 (2665) ATATTTT CCTTTACTTAAAGGAATAAAA GATAAATATC
 NC_001719 (2659) ATATTTT CCCCCTTTCCAAAAGGAATAAAA AATTAATTATC
 NC_004107 (2668) ATATTTT CCTTTAAT TAAAGGCATAAAA AACAAATTATC
 OHVHEPBA (2668) ATATTTT CCTTTAAT TAAAGGCATAAAA AACAAATTATC
 NC_001896 (2666) ATATTTT CCACTGGAGAAA GGTATTAAA CTTCAATTATC
 NC_002168 (2669) ATATTTT CCCCCTGATAAAGGTATTAAA CTTATTATC
 gi_452617_emb_X75657.1_HHVBBAS (2669) ATATTTG CCCC TAGAGAAA GGTATAAAA CTTATTATC
 gi_6983934_gb_AF160501.1_AF160501 (2705) ATATTTA CCAATTAGACAAA GGTATCAAACCTGATTATC
 Consensus (2737) ATATTT CCCTTAGATAAAGG AT AAACCTTATTATC

(2775) 2775 2780 2790 2800 2812
 AM282986 (2713) CAGATCAGGTAGTTAATCATTACTTCCA AAACCAGACAT
 Source(1..3215): Source_1
 CDS(2307..1623): CDS POLYMERASE (P)
 Mature Peptide(2307..2843): Domain of...
 Promoter Eukaryotic(2716..2834): DNA ...

gi_59439_emb_X65259.1_HBVAYWE (2707) CAGAGCATCTAGTTAATCATTACTTCCA AAACCAGACAT
 gi_221497_dbj_D00329.1_HPBADW1 (2707) CAGAGCATGTAGTTAATCATTACTTCCA GACTAGACAT
 gi_59422_emb_X69798.1_HBVADW4A (2707) CTGAGCATGCAGTTAATCATTACTTTAAA ACCAGACAT
 NC_001484 (2703) CTAAATTTACTATA TAGAACACTTT TTTGCTGCAGCA AAT
 NC_001719 (2697) CTGATTTCTCTA TAGAACACTTT TTTGCTAGCTGCA AACT
 NC_004107 (2706) CTAAATTTTGCTT TAGAACATTTC TTTGCTACC GCA AAT
 OHVHEPBA (2706) CTAAATTTTGCTT TAGAACATTTC TTTGCTACC GCA AAT
 NC_001896 (2704) CTAAATGATGTAGTTAATCATTAT TACCAAGTTCAGCAT
 NC_002168 (2707) CTGAGCATGGGTTAATCATTAT TCCAAGCCAGACAC
 gi_452617_emb_X75657.1_HHVBBAS (2707) CAGATAATGTAGTTAATCATTACTTCCA AAACCAGACAC
 gi_6983934_gb_AF160501.1_AF160501 (2743) CAGAAAATGTAGTTAATCATTACTTCCA GACCAGACAT
 Consensus (2775) CTGAT ATGTAGTTAATCATTACTTCCA AAACCAGACAT

(2813) 2813 2820 2830 2840 2850
 AM282986 (2751) TATTTACATACTCTT TGG AAGGCTGGTATTCTATATAA
 Source(1..3215): Source_1
 CDS(2307..1623): CDS POLYMERASE (P)
 Mature Peptide(2307..2843): Domain of...
 Promoter Eukaryotic(2716..2834): DNA ...

gi_59439_emb_X65259.1_HBVAYWE (2745) TATTTACACACTCTTA TGG AAGGCGGGTATAATTATATAA
 gi_221497_dbj_D00329.1_HPBADW1 (2745) TATTTGCATACTCTT TGG AAGGCGGGTATCTTATATAA
 gi_59422_emb_X69798.1_HBVADW4A (2745) TATTTGCATACTTTA TGG AAGGCGGGAATTTTATATAA
 NC_001484 (2741) TATTTATGGACATTTG TGG AATCAGGAATTCCTATATTT
 NC_001719 (2735) TATTTATGGACTTTG TGG AATCAGGAATCTTTGTATTT
 NC_004107 (2744) TATTTGTGGACTTTA TGG AAGCTGG AATTTTGTATTT
 OHVHEPBA (2744) TATTTGTGGACTTTA TGG AAGCTGG AATTTTGTATTT
 NC_001896 (2742) TATTTACATACCCCT TGG AAGGCGGGAGTCTTATATAA
 NC_002168 (2745) TATTTACATACCTTG TGG AAGGCGGGTGTCTTATATAA
 gi_452617_emb_X75657.1_HHVBBAS (2745) TATTTACATACCCCTA TGG AAGGCGGGCATCTTATATAA
 gi_6983934_gb_AF160501.1_AF160501 (2781) TATTTACATACCCCT TGG AAGGCGGGTATTCTATATAA
 Consensus (2813) TATTTACATACTTT TGG AAGGCGGGAATTTTATATAA

(2851) 2851 2860 2870 2888
 AM282986 (2789) GAGGGA AAC CACACG TAGCGCATCATT TTG CGGGTCAC
 Source(1..3215): Source_1
 CDS(2307..1623): CDS POLYMERASE (P)
 Mature Peptide(2307..2843): Domain of...
 Promoter Eukaryotic(2716..2834): DNA ...

gi_59439_emb_X65259.1_HBVAYWE (2783) GAGGGA AAC AACACATAGCGCCTCATT TTGTGGGTCAC
 gi_221497_dbj_D00329.1_HPBADW1 (2783) AAGGAGGTCAACACATAGCGCCTCATT TTGCGGGTCAC
 gi_59422_emb_X69798.1_HBVADW4A (2783) GAGGGAATCCACACG TAGCGCCTCATT TTGTGGGTCAC
 NC_001484 (2779) AAGAAAATCAGACAACTCTCACTTTTAGAGGTAAAC
 NC_001719 (2773) GAGGAAAATCA AAC TACTCTCACTTTAAGGGTAAAC
 NC_004107 (2782) AAGGAG AATCAACA ACTTTGACTTTTAAAGGTAAAC
 OHVHEPBA (2782) AAGGAG AATCAACA ACTTTGACTTTTAAAGGTAAAC
 NC_001896 (2780) AAGGAGACAACTCACAGTGCCTCATTCTTTGGGACAC
 NC_002168 (2783) GAGGGA AAC AACACG TAGCGCTTCATT TTGTGGGTCAC
 gi_452617_emb_X75657.1_HHVBBAS (2783) AAGGGA AAC TACACG TAGCGCCTCATT TTGTGGGTCAC
 gi_6983934_gb_AF160501.1_AF160501 (2819) GAGGGA AAC ATCCG TAGCGCTTCATT TTGTGGGTCAC
 Consensus (2851) GAGGGA AAC ACAC TAGCGCCTCATT TTGTGGGTCAC

(2889) 2889 2900 2910 2926
 AM282986 (2827) CATATTCTTGGGAACA-----AGAGCTACAGCAT

Source(1..3215): Source_1

CDS(2307..1623): CDS POLYMERASE (P)

Mature Peptide(2307..2843): Domain oMature Peptide(2847..129): Domain of ...

Promoter Eukaryotic(2716..2834): DNA ...

Misc. Feature(2835..2835): S1 transcr...

CDS(2854..835): CDS LARGE (L) SURFACE

mRNA(2835..1930): mRNA Large S

gi_59439_emb_X65259.1_HBVAYWE (2821) CATATTCTTGGGAACA-----AGAGCTACAGCAT
 gi_221497_dbj_D00329.1_HPBADW1 (2821) CTATTCTTGGGAACA-----AGATCTACAGCAT
 gi_59422_emb_X69798.1_HBVADW4A (2821) CATATTCTTGGGAACA-----AGAGCTACAGCAT
 NC_001484 (2817) CATATTCTTGGGAACACAGACAGCTAGAGCAACATAAT
 NC_001719 (2811) CATATTCTTGGGGAACACAGACAGCTAGAGCAACATAAT
 NC_004107 (2820) CATATTCTTGGGAACACAGACAGCTAGTGCACATAAT
 OHVHEPBA (2820) CATATTCTTGGGAACACAGACAGCTAGTGCACATAAT
 NC_001896 (2818) CGTACACTTGGGAACA-----TAAGCTACAGCAT
 NC_002168 (2821) CATATTCTTGGGAACA-----AGAGCTACAGCAT
 gi_452617_emb_X75657.1_HHVBBAS (2821) CTATTCTTGGGAACA-----AGAGCTACATCAT
 gi_6983934_gb_AF160501.1_AF160501 (2857) CATATACTTGGGAACA-----AGATCTACAGCAT
 Consensus (2889) CATATTCTTGGGAACA AGAGCTACAGCAT

(2927) 2927 2940 2950 2964
 AM282986 (2856) GGGAGGTTGGTCTTCCAAACCTCGCAAAGGCATGGGGA

Source(1..3215): Source_1

CDS(2307..1623): CDS POLYMERASE (P)

Mature Peptide(2847..129): Domain of ...

CDS(2854..835): CDS LARGE (L) SURFACE

mRNA(2835..1930): mRNA Large S

gi_59439_emb_X65259.1_HBVAYWE (2850) GGG-----GC--A-----
 gi_221497_dbj_D00329.1_HPBADW1 (2850) GGGAGGTTGGTCTTCCAAACCTCGAAAAGGCATGGGGA
 gi_59422_emb_X69798.1_HBVADW4A (2850) GGGAGCACCTCTCTCAACGACACGAAGAGGCATGGGAC
 NC_001484 (2855) GGG--CAACAAATIAAAGTAACTTCGATCCAACA
 NC_001719 (2849) GGG--CAACAAATGAAGTCACTTCAATCAGAGAA
 NC_004107 (2858) GGG--CAACAAATIAAAGTCACTTCAATCAGACAA
 OHVHEPBA (2858) GGG--CAACAAATIAAAGTCACTTCAATCAGACAA
 NC_001896 (2847) GGGAC--T-----
 NC_002168 (2850) GGG-----GC
 gi_452617_emb_X75657.1_HHVBBAS (2850) GGGGCTTTCTTGGACGGTCCCTCTCGAATG--GGGGA
 gi_6983934_gb_AF160501.1_AF160501 (2886) GGGGCTTTCTTGGACGGTCCCTCTCGAGTGT--GGGAA
 Consensus (2927) GGG C C T AA C C A C G GAA

(2965) 2965 2970 2980 2990 3002
 AM282986 (2894) C G A A T C T T T C T G T T C C C A A C C C T C T G G G A - T T C T T T C C

Source(1..3215): Source_1

CDS(2307..1623): CDS POLYMERASE (P)

Mature Peptide(2847..129): Domain of ...

CDS(2854..835): CDS LARGE (L) SURFACE

mRNA(2835..1930): mRNA Large S

gi_59439_emb_X65259.1_HBVAYWE (2856) - G A A T C T T T C C A C C A G C A A T C C T C T G G G A - T T C T T T C C
 gi_221497_dbj_D00329.1_HPBADW1 (2888) C A A A T C T T T C T G T T C C C A A T C C C T G G G A - T T C T T C C C
 gi_59422_emb_X69798.1_HBVADW4A (2888) A G A A T C T C T C T G T G C C A A T C C T C T G G G A - T T C T T T C C
 NC_001484 (2891) A T T A G C T G C A T G G T G G C C A A C A G T G G G A A C T T A T T A T A
 NC_001719 (2885) A G T A G C A G C A T G G T G G C C A G C A G T G G G C A C A T A T T A C A
 NC_004107 (2894) A A T A G C A G C A T G G T G G C T G C A G T G G G C A C T T A T T A C A
 OHVHEPBA (2894) A A T A G C A G C A T G G T G G C T G C A G T G G G C A C T T A T T A C A
 NC_001896 (2853) - C A A C C A G T C A A C G T T C A A C C C G C T G G G A - T T C T T T C C
 NC_002168 (2855) A G A A C C T T T C T G T C A C C A A C C C T T T G G G A - T T C T T C C C
 gi_452617_emb_X75657.1_HHVBBAS (2885) A G A A T A T T T C C A C C A C C A A T C C T C T G G G A - T T T T T T C C
 gi_6983934_gb_AF160501.1_AF160501 (2921) A G A A C C T T T C C G C C A G C A A T C C T C T A G G A - T T C C T T C C
 Consensus (2965) A G A A C T T T C T G G C A A C C T C T G G G A T T C T T T C C

(3003) 3003 3010 3020 3030 3040
 AM282986 (2931) C G A T C A T C A G T - - - - T G G - - - A C C - - - C T G C A T T C G G A

Source(1..3215): Source_1

CDS(2307..1623): CDS POLYMERASE (P)

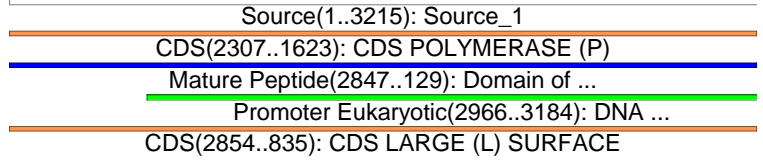
Mature Peptide(2847..129): Domain of ...

CDS(2854..835): CDS LARGE (L) SURFACE

mRNA(2835..1930): mRNA Large S

gi_59439_emb_X65259.1_HBVAYWE (2892) C G A C C A C C A G T - - - - T G G - - - A T C - - - C A G C C T T C A G A
 gi_221497_dbj_D00329.1_HPBADW1 (2925) C G A T C A T C A G T - - - - T G G - - - A C C - - - C T G C A T T C A A A
 gi_59422_emb_X69798.1_HBVADW4A (2925) A G A C C A T C A G C - - - - T G G - - - A T C - - - G C T A T T C A G A
 NC_001484 (2929) C A C C C A C T A C C A C C G T G A C A A A T C A G C A A T A T T C A A A
 NC_001719 (2923) C A A A C A G C A C G C C T C A G G - - - A C C C T C C A G T T T T C A A
 NC_004107 (2932) C A A C C A C T T A T C C T C A G A - - - A T C A G T C A G T G T T T C A A
 OHVHEPBA (2932) C A A C C A C T T A T C C T C A G A - - - A T C A G T C A G T G T T T C A A
 NC_001896 (2889) C A G T C A T C A G C - - - - T G G - - - A C C - - - C C C T G T T C A A G
 NC_002168 (2892) C G A G C A T C A A T - - - - T G G - - - A C C - - - G C T G T T C C G A
 gi_452617_emb_X75657.1_HHVBBAS (2922) C G A C C A C C A G T - - - - T G G - - - A T C - - - C A G C A T T C A G A
 gi_6983934_gb_AF160501.1_AF160501 (2958) C G A T C A C C A G T - - - - T G G - - - A C C - - - C A G C A T T C A G A
 Consensus (3003) C G A C C A C C A G T T G G A T C C A G T A T T C A G A

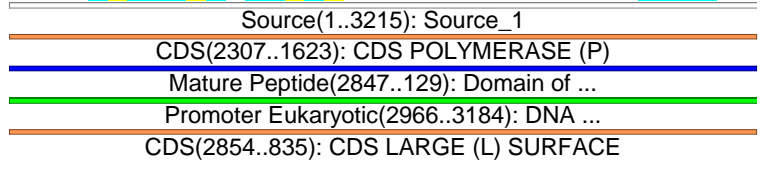
(3041) 3041 3050 3060 3078
 AM282986 (2959) G C A A C T C A A A C A A T C C A G A T T G G G A C T T C A A C C C A T



mRNA(2835..1930): mRNA Large S

gi_59439_emb_X65259.1_HBVAYWE (2920) G C A A A C A C C G C A A A T C C A G A T T G G G A C T T C A A T C C A A
 gi_221497_dbj_D00329.1_HPBADW1 (2953) G C C A A C T C A G A A A A T C C A G A T T G G G A C C T C A A C C C A C A
 gi_59422_emb_X69798.1_HBVADW4A (2953) G C A A A T T C C A G C A G T C C G G A C T T G G G A C T T C A A C A C A A A
 NC_001484 (2967) C C A G G A A T T T A T C A G A C A A C G T C T T T A A A A A A T C C A A A
 NC_001719 (2958) C C A G G G A T T T A C C A A A C A A C T T C T T T G G T G A A T C C C A A
 NC_004107 (2967) C C A G G A A T T T A T C A A A C A A C A T C T C T G A T A A A T C C C A A
 OHVHEPBA (2967) C C A G G A A T T T A T C A A A C A A C A T C T C T G A T A A A T C C C A A
 NC_001896 (2917) G C C A A T G C A G G C T C A G C A G A T T G G G A C A A A A A T C C A A A
 NC_002168 (2920) G C C A A C A C A A A C A A T C C A G A T T G G G A C T T C A A T C C C A A
 gi_452617_emb_X75657.1_HHVBBAS (2950) G C A A A C A C C A G A A A T C C A G A T T G G G A C C A C A A T C C C A A
 gi_6983934_gb_AF160501.1_AF160501 (2986) G C A A A T A C C A A C A A T C C A G A T T G G G A C T T C A A T C C C A A
 Consensus (3041) G C A A A A C A C A A A T C C A G A T T G G G A C T T C A A T C C C A A

(3079) 3079 3090 3100 3116
 AM282986 (2997) - - - - C A A G G A C C A C T G G - - - - - - - - - - C C A G C A



mRNA(2835..1930): mRNA Large S

gi_59439_emb_X65259.1_HBVAYWE (2958) - - - - C A A G G A C A C C T G G - - - - - - - - - - C C A G A C
 gi_221497_dbj_D00329.1_HPBADW1 (2991) - - - - C A A G G A C A A C T G G - - - - - - - - - - C C G G A C
 gi_59422_emb_X69798.1_HBVADW4A (2991) - - - - C A A G G A C A G T G G - - - - - - - - - - C C A A T G
 NC_001484 (3005) G A A T C A A C A A G A G T T A G A T G C T A T A C T T A T G A C A A G A T
 NC_001719 (2996) A A A T C A G C A A G A A C T G G A G G C A G T G T T A G A G A A A A G A T
 NC_004107 (3005) A A A T C A A C A A G A A C T G G A C T C T G T T C T T A T A A A C A G A T
 OHVHEPBA (3005) A A A T C A A C A A G A A C T G G A C T C T G T T C T T A T A A A C A G A T
 NC_001896 (2955) - - - - C A A G G A C C C T G G - - - - - - - - - - C C A C A A
 NC_002168 (2958) - - - - C A A G G A C A C T G G - - - - - - - - - - C C A G A A
 gi_452617_emb_X75657.1_HHVBBAS (2988) - - - - C A A A G A C C A C T G G - - - - - - - - - - A C A G A A
 gi_6983934_gb_AF160501.1_AF160501 (3024) - - - - A A A G G A C C C T G G - - - - - - - - - - C C A G A G
 Consensus (3079) C A A G G A C A A C T G G C C A G A

(3117) 3117 3130 3140 3154
 AM282986 (3016) G C C A A C C -- A G G T A G G -- -- -- -- -- A G T G G G A

Source(1..3215): Source_1
 CDS(2307..1623): CDS POLYMERASE (P)
 Mature Peptide(2847..129): Domain of ...
 Promoter Eukaryotic(2966..3184): DNA ...
 CDS(2854..835): CDS LARGE (L) SURFACE

mRNA(2835..1930): mRNA Large S

gi_59439_emb_X65259.1_HBVAYWE (2977) G C C A A C A -- -- A G G T A G G -- -- -- -- -- A G C T G G A
 gi_221497_dbj_D00329.1_HPBADW1 (3010) G C C C A C A -- -- A G G T G G G -- -- -- -- -- A G T G G G A
 gi_59422_emb_X69798.1_HBVADW4A (3010) G C A A A C A -- -- A G G T A G G -- -- -- -- -- A G T G G G A
 NC_001484 (3043) A C A A A G A A A T A G A T T G G G A C A A T T G G C A A G G A T T C C C T
 NC_001719 (3034) A C A A A C A A A T A G A T T G G -- -- -- -- -- G A T T C C C T
 NC_004107 (3043) A C A A A C A G A T A G A C T G G A A C A C T T G G C A A G G A T T C C C T
 OHVHEPBA (3043) A C A A A C A G A T A G A C T G G A A C A C T T G G C A A G G A T T C C C T
 NC_001896 (2974) G C C C A C G -- -- A C A C G G C -- -- -- -- -- A G T G G G G
 NC_002168 (2977) G C C A C C A -- -- A G G T A G G -- -- -- -- -- A G T G G G A
 gi_452617_emb_X75657.1_HHVBBAS (3007) G C C A A C A -- -- A G G T A G G -- -- -- -- -- A G T G G G A
 gi_6983934_gb_AF160501.1_AF160501 (3043) G C C A A C A -- -- A G G T A G G -- -- -- -- -- A G T G G G A
 Consensus (3117) G C C A A C A A G G T A G G A G T G G G A

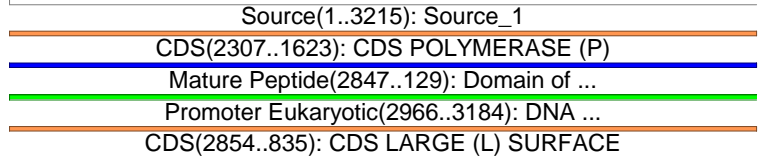
(3155) 3155 3160 3170 3180 3192
 AM282986 (3037) G -- -- -- -- -- C A T T C G G G C -- C A G G G T T C A C C

Source(1..3215): Source_1
 CDS(2307..1623): CDS POLYMERASE (P)
 Mature Peptide(2847..129): Domain of ...
 Promoter Eukaryotic(2966..3184): DNA ...
 CDS(2854..835): CDS LARGE (L) SURFACE

mRNA(2835..1930): mRNA Large S

gi_59439_emb_X65259.1_HBVAYWE (2998) G -- -- -- -- -- C A T T C G G G C -- T G G G T T C A C C
 gi_221497_dbj_D00329.1_HPBADW1 (3031) G -- -- -- -- -- C A T T C G G G C -- C A G G A T T C A C C
 gi_59422_emb_X69798.1_HBVADW4A (3031) G -- -- -- -- -- G C T A C G G T C -- C A G G G T T C A C A
 NC_001484 (3081) G - T G A A T C A A A G G C T C C C A G T G A G C A A C A C A A T C C T C
 NC_001719 (3059) G G T A A A T C A A A A A T T A C C A T T G G T C A G C A G G G T T C C T C
 NC_004107 (3081) G - T G G A T C A A A A A T T A C C A T T G G T C A G C A G G G A T C C T C
 OHVHEPBA (3081) G - T G G A T C A A A A A T T T T C A T T G G T C A G C A G G G A T C C T C
 NC_001896 (2995) G -- -- -- -- -- C C T T T G G T C -- C A G G A C T A G T G
 NC_002168 (2998) G -- -- -- -- -- C A T T T G G G C -- C A G G G T T C A C T
 gi_452617_emb_X75657.1_HHVBBAS (3028) G -- -- -- -- -- C A T T C G G G C -- C T G G G T T C A C T
 gi_6983934_gb_AF160501.1_AF160501 (3064) G -- -- -- -- -- C C T A T G G A C -- C C G G G T T C A C C
 Consensus (3155) G C C T T T G G G C C A G G G T T C A C C

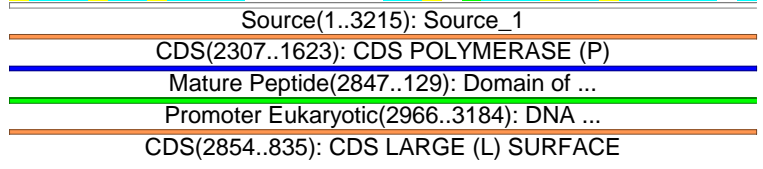
(3193) 3193 3200 3210 3220 3230
 AM282986 (3058) CC-----TCCACACGGCG---GTGTTTT



mRNA(2835..1930): mRNA Large S

gi_59439_emb_X65259.1_HBVAYWE (3019) CC-----ACCGCACGGAG---GTCTTTT
 gi_221497_dbj_D00329.1_HPBADW1 (3052) CC-----TCCCATTGGGG---GACTGTT
 gi_59422_emb_X69798.1_HBVADW4A (3052) CC-----CACAACGGTG---GCTTGCT
 NC_001484 (3118) CC-----TC-----AGGTCAAAGGCGAGACTTTT
 NC_001719 (3097) CC AAGTCTCCTCCCCAAGATCAAAGAGCTCAAACCTTTT
 NC_004107 (3118) CC CCAAACCTTATATAAATCAATCAGCTCAAACCTTTT
 OHVHEPBA (3118) CC CCAAACCTTATATAAATCAATCAGCTCAAACCTTTT
 NC_001896 (3016) CC-----ACCCATTGGAG---GCTTCT
 NC_002168 (3019) CC-----ACCTCACGGAG---GTCTTTT
 gi_452617_emb_X75657.1_HHVBBAS (3049) CC-----CCCACACGGAG---GCTTTT
 gi_6983934_gb_AF160501.1_AF160501 (3085) CC-----TCCAACACGGAG---GCTTTT
 Consensus (3193) CC ACC CACGGAG G CTTTT

(3231) 3231 3240 3250 3268
 AM282986 (3078) GGGGTGGAGCCC-----TCA-GGCTCAGGGCATAIT



mRNA(2835..1930): mRNA Large S

gi_59439_emb_X65259.1_HBVAYWE (3039) GGGGTGGAGCCC-----TCA-GGCTCAGGGCATACT
 gi_221497_dbj_D00329.1_HPBADW1 (3072) GGGGTGGAGCCC-----TCA-GGCTCAGGGCATACT
 gi_59422_emb_X69798.1_HBVADW4A (3072) GGGGTGGAGCCC-----TCA-AGCACAGGTGTGT
 NC_001484 (3144) GAAATCAATCCAGGCCTATAATA GTTCAGGAATAAG
 NC_001719 (3135) GAAATCAAACCCAGGCCTAA TCAATA GTTCCTGGAATCAG
 NC_004107 (3156) GAAATCAAACCTGGGCCTATAATA GTTCCG- AATTCG
 OHVHEPBA (3156) GAAATCAAACCTGGGCCTATAATA GTTCCGGAATTCG
 NC_001896 (3036) GGGGTGGAGTTT-----ACA-AGCTCAGGGTTIGTC
 NC_002168 (3039) GGGGTGGAGCCC-----GCA-GGCTCAGGGCGTAC
 gi_452617_emb_X75657.1_HHVBBAS (3069) GGGGTGGAGCCC-----TCA-GGCTCAGGGCATGCT
 gi_6983934_gb_AF160501.1_AF160501 (3105) GGGGTGGAGCCC-----TCA-GTCTCAGGGCACACT
 Consensus (3231) GGGGTGGAGCCC TCA GGCTCAGGGCATACT

(3269) 3269 3280 3290 3306
 AM282986 (3108) GACCACAGTGTCAAC -- AATCCCTCCTCCTGCCTCCA

Source(1..3215): Source_1
 CDS(2307..1623): CDS POLYMERASE (P)
 Mature Peptide(2847..129): Domain of ...
 Promoter Eukaryotic(2966..3184): DNA ...
 CDS(2854..835): CDS LARGE (L) SURFACE

mRNA(2835..1930): mRNA Large S

gi_59439_emb_X65259.1_HBVAYWE (3069) ACATACCGTGCCAGC -- AATCCGCTCCTGCCTCTA
 gi_221497_dbj_D00329.1_HPBADW1 (3102) ACATCTGTGTCAGC -- AGCTCCTCCTCCTGCCTCCA
 gi_59422_emb_X69798.1_HBVADW4A (3102) AACAACTTGCCAGC -- AGATCCGCTCCTGCCTCCA
 NC_001484 (3182) GGATATACCACGTGGCATAGTACCACCTCAGACTCCAT
 NC_001719 (3173) AGACATCCCACGTGGTATAGTACCACCTCAAAACACCAC
 NC_004107 (3193) GGACATACCACGTGGTTTGTAGTTCCGCTCCTCAAACTCCAA
 OHVHEPBA (3194) GGACATACCACGTGGTTTGTAGTTCCGCTCCTCAAACTCCAA
 NC_001896 (3066) TGTACAGTGCCAGCA -- CACCCTCCTCCTCCATCAA
 NC_002168 (3069) CCAATACCTGCCAGC -- AGTTCTCCTCCTGCCTCCA
 gi_452617_emb_X75657.1_HHVBBAS (3099) AAAAACAATGTCAGC -- AGATCCGCTCCTGCCTCCA
 gi_6983934_gb_AF160501.1_AF160501 (3135) AACAACTT TGCCAGC -- AGATCCGCTCCTGCCTCCA
 Consensus (3269) AA ACA TGCCAGC AGTTCCGCTCCTGCCTCCA

(3307) 3307 3320 3330 3344
 AM282986 (3143) CCAATCGGCAGTCAGGAAGGCAGCCTACTCCCATCTCT

Source(1..3215): Source_1
 CDS(2307..1623): CDS POLYMERASE (P)
 Mature Peptide(2847..129): Domain of ...
 Promoter Eukaryotic(2966..3184): DNA ...
 CDS(2854..835): CDS LARGE (L) SURFACE

mRNA(2835..1930): mRNA Large S

gi_59439_emb_X65259.1_HBVAYWE (3104) CCAATCGGCAGTCAGGAAGGCAGCCTACTCCCTCTGTCT
 gi_221497_dbj_D00329.1_HPBADW1 (3137) CCAATCGGCAGTCAGGACGGCAGCCTACTCCCTATCT
 gi_59422_emb_X69798.1_HBVADW4A (3137) CCAATCGGCAGTCAGGAGGAAAGCCAACCCAGTCTCT
 NC_001484 (3220) CCAATCGGGATCAAAGAAAGAAACCCACACCTCTAACT
 NC_001719 (3211) CCAATCGAGACAAAGGGAGGAAACCTACTTCCCTCAGACT
 NC_004107 (3231) CAAATCGAGATCAAAGGGAGAAAGCCTACTTCCCTCAACT
 OHVHEPBA (3232) CAAATCGAGATCAAAGGGAGAAAGCCTACTTCCCTCAACT
 NC_001896 (3101) CCAATCGCGACAAAGGAAGGAAACCAACACAGCTACT
 NC_002168 (3104) CCAATCGGCAGTCAGGAAGGCAGCCTACTCCCATCTCT
 gi_452617_emb_X75657.1_HHVBBAS (3134) CCAATCGGCAGTCAGGAAGGCAGCCTACTCCCAATCACT
 gi_6983934_gb_AF160501.1_AF160501 (3170) CCAATCGTTCAGTCAGGAGGCAGCCTACTCCCATCTCT
 Consensus (3307) CCAATCGGCAGTCAGGAAGGCAGCCTACTCC CT TCT

(3345) 3345 3350 3360 3370 3382
 AM282986 (3181) CCACCTCTAAGAGACACTCATCCTCAGGCCATGCAGTG
 Source(1..3215): Source_1
 CDS(2307..1623): CDS POLYMERASE (P)
 Mature Peptide(2847..129): Domain of ...
 Promoter Eukaryotic(2966..3184): DNA ...
 CDS(2854..835): CDS LARGE (L) SURFACE
 Misc. Feature(3185..3185): S2 transcr... CDS(3211..835): CDS MIDDLE (M) SURFA
 mRNA(2835..1930): mRNA Large S
 mRNA(3185..1930): mRNA Middle S

gi_59439_emb_X65259.1_HBVAYWE (3142) CCACCTTTGAGAAACACTCATCCTCAGGCCATGCAGTG
 gi_221497_dbj_D00329.1_HPBADW1 (3175) CCACCTCTAAGGGACACTCATCCTCAGGCCATGCAGTG
 gi_59422_emb_X69798.1_HBVADW4A (3175) CCACCTCTAAGAGACACACATCCAAGGCCAATGCAGTG
 NC_001484 (3258) CCTCCTTTGAGAGACACACACCCTCA TTTGA CAATGAA
 NC_001719 (3249) CGCCTTTAAGAGACACTCACCCCTCA TTTGA ACATGAA
 NC_004107 (3269) CCACCTCTAAGAGATACTCACCCCA CTTAA CTATGAA
 OHVHEPBA (3270) CCACCTCTAAGAGATACTCACCCCA CTTAA CTATGAA
 NC_001896 (3139) CCTCCTCTGAGAGACACTCACCCA CAAGCCATGACCTG
 NC_002168 (3142) CCACCTTTGAGAGACACTCATCCTCAGGCCATGCAGTG
 gi_452617_emb_X75657.1_HHVBBAS (3172) CCACCTTTGAGAGACACTCATCCTCAGGCCATGCAGTG
 gi_6983934_gb_AF160501.1_AF160501 (3208) CCACCACTAAGAGACAGTCATCCTCAGGCCATGCAGTG
 Consensus (3345) CCACCTCTAAGAGACACTCATCCTCAGGCCATGCAGTG

(3383) 3383 3399
 AM282986 (3219) GAA-----
 CDS(2307..1623): CDS POLYMERASE (P)
 Mature Peptide(2847..129): Domain.of ...
 CDS(2854..835): CDS LARGE (L) SURFACE
 CDS(3211..835): CDS MIDDLE (M) SURFAC...
 mRNA(2835..1930): mRNA Large S
 mRNA(3185..1930): mRNA Middle S

gi_59439_emb_X65259.1_HBVAYWE (3180) GAA-----
 gi_221497_dbj_D00329.1_HPBADW1 (3213) GAA-----
 gi_59422_emb_X69798.1_HBVADW4A (3213) GAA-----
 NC_001484 (3296) AAA TCAGACAGGTCAC-
 NC_001719 (3287) AAA TCAGAGCCCTCATC
 NC_004107 (3307) AAA TCAGACTTTTCAT-
 OHVHEPBA (3308) AAA TCAGACTTTTCAT-
 NC_001896 (3177) GAA-----
 NC_002168 (3180) GAA-----
 gi_452617_emb_X75657.1_HHVBBAS (3210) GAA-----
 gi_6983934_gb_AF160501.1_AF160501 (3246) GAA-----
 Consensus (3383) GAA