

## Bovine herpesvirus type 1.1 complete genome

GenBank: AJ004801.1

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LOCUS AJ004801 135301 bp DNA linear VRL 02-JUN-2010  
DEFINITION Bovine herpesvirus type 1.1 complete genome.  
ACCESSION AJ004801  
VERSION AJ004801.1  
KEYWORDS complete genome.  
SOURCE Bovine herpesvirus type 1.1  
ORGANISM [Bovine herpesvirus type 1.1](#)  
Viruses; Duplodnaviria; Heunggongvirae; Peploviricota;  
Herviviricetes; Herpesvirales; Herpesviridae; Alphaherpesvirinae;  
Varicellovirus.  
REFERENCE 1 (bases 99702 to 103033)  
AUTHORS Wirth,U.V., Fraefel,C., Vogt,B., Vlcek,C., Paces,V. and Schwyzer,M.  
TITLE Immediate-early RNA 2.9 and early RNA 2.6 of bovine herpesvirus 1  
are 3' coterminous and encode a putative zinc finger transactivator  
protein  
JOURNAL J. Virol. 66 (5), 2763-2772 (1992)  
PUBMED [1313901](#)  
REFERENCE 2 (bases 103034 to 111027; 127191 to 135300)  
AUTHORS Schwyzer,M., Vlcek,C., Menekse,O., Fraefel,C. and Paces,V.  
TITLE Promoter, spliced leader, and coding sequence for BICP4, the  
largest of the immediate-early proteins of bovine herpesvirus 1  
JOURNAL Virology 197 (1), 349-357 (1993)  
PUBMED [8212570](#)  
REFERENCE 3 (bases 111028 to 114234; 123984 to 127190)  
AUTHORS Schwyzer,M., Wirth,U.V., Vogt,B. and Fraefel,C.  
TITLE BICP22 of bovine herpesvirus 1 is encoded by a spliced 1.7 kb RNA  
which exhibits immediate early and late transcription kinetics  
JOURNAL J. Gen. Virol. 75 (PT 7), 1703-1711 (1994)  
PUBMED [8021599](#)  
REFERENCE 4 (bases 66900 to 96900)  
AUTHORS Vlcek,C., Benes,V., Lu,Z., Kutish,G.F., Paces,V., Rock,D.,  
Letchworth,G.J. and Schwyzer,M.  
TITLE Nucleotide sequence analysis of a 30-kb region of the bovine  
herpesvirus 1 genome which exhibits a colinear gene arrangement  
with the UL21 to UL4 genes of herpes simplex virus  
JOURNAL Virology 210 (1), 100-108 (1995)  
PUBMED [7793062](#)  
REFERENCE 5 (bases 1 to 31444)  
AUTHORS Schwyzer,M., Styger,D., Vogt,B., Lowery,D.E., Simard,C.,  
LaBoissiere,S., Misra,V., Vlcek,C. and Paces,V.

TITLE Gene contents in a 31-kb segment at the left genome end of bovine herpesvirus-1

JOURNAL Vet. Microbiol. 53 (1-2), 67-77 (1996)

PUBMED [9010999](#)

REMARK Accession# Z54206

REFERENCE 6 (bases 114235 to 122983)

AUTHORS Goltz,M., Buhk,H.J., Broll,H., Lewin,M., Mankertz,A., Boerner,B., Borchers,K. and Weigelt,W.

TITLE Nucleotide sequence of the HindIII O and K fragments located in the US region of the bovine herpesvirus 1 genome

JOURNAL Unpublished

REMARK Accession# Z98199

REFERENCE 7 (bases 96901 to 99695)

AUTHORS Letchworth,G.J. and Kutish,G.F.

TITLE DNA sequence of the BHV-1 UL1 to UL3.5 genes

JOURNAL Unpublished

REFERENCE 8 (bases 121402 to 123983)

AUTHORS Schwyzer,M.

TITLE Glycoprotein E and US9 genes of BHV1

JOURNAL Unpublished

REFERENCE 9 (bases 1 to 135301)

AUTHORS Schwyzer,M., Paces,V., Letchworth,G.J., Misra,V., Buhk,H.J., Lowery,D.E., Simard,C., Bello,L.J., Thiry,E. and Vlcek,C.

TITLE Complete DNA sequence of bovine herpesvirus 1

JOURNAL Unpublished

REFERENCE 10 (bases 30801 to 67800)

AUTHORS Schwyzer,M., Vlcek,C., Lowery,D.E., Bello,L.J., Meyer,G. and Misra,V.

TITLE Gene contents in a 37-kb segment centered in the UL part of the bovine herpesvirus 1 genome: the last gap

JOURNAL Unpublished

REMARK Accession# Z78205

REFERENCE 11 (bases 1 to 135301)

AUTHORS Schwyzer,M.

TITLE Direct Submission

JOURNAL Submitted (08-SEP-1997) Institute of Virology, Faculty of Veterinary Medicine, University of Zurich, Winterthurerstrasse 266A, Zurich CH-8057, Switzerland

FEATURES Location/Qualifiers

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CDS complement(96914..97294)  
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gene complement(97958..98863)  
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CDS complement(97958..98863)  
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RGVPVPPSLQNIIYAVQKNFPGAPRPSHGCL<sup>E</sup>DWARRGVLLNTSLTVRSGAPGSHSS  
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gene complement(98866..99342)  
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CDS complement(98866..99342)  
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LADTPVYRD<sup>L</sup>AIQVLN<sup>S</sup>AFGLPHEVRA<sup>L</sup>PPP<sup>R</sup>GCVLPPRYHTGPCPGDGIYR"  
gene 99239..99532  
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CDS 99239..99532  
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CDS 99827..100090  
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gene 100132..100137  
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/gene="BICP0"  
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CDS 100489..101034  
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PAGGRRQGRGRRETGSGLGWK"  
CDS complement(100670..102700)  
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/codon\_start=1  
/product="immediate-early transactivator protein with Zn  
finger (cell nucleus)"  
/protein\_id="[CAA06138.1](#)"  
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MAMLAECGFDDDGLADAMEPLIGEDDAPAFVRSLLFVAARCCTVGPSPHLIPQQSAPPG
GRGVVFLDTSDSEGSEDDSWSESEESSGLSTSDLTAIDDTEPETDAEVESRRT
RGASGAARARRPAERQYVSTRGRQTPAVQPAPRSLARRPCGRAAAVSAPPSSRSRGGR
RDPRILPAAPRAAPAAQARACSPEPREEGRGAGLGVAAGETAGWGAGSEEGRGERRARL
LGEAGPPRVQARRRRTELDRAPTPAPAPAPAPISTVIDLTANAPARPADPAPAAA
PGPASAGAQIGTPAAAAAVTAAAAPSVARSSAPSPAVTAAATSTAAISTRAPTPSP
AGRAPAADPRRAGAPALAGAARAEVGRNGNPGRERRPASAMARGDLDPGPESSAQKRR
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regulatory    102209..102214
/regulatory_class="polyA_signal_sequence"
/gene="LRORF2"

intron        complement(102705..108190)
/note="alternative intron spliced out to produce
immediate-early RNA 2.9 and BICP0"

misc_feature  102918..114234
/note="internal repeat of the short segment IRS"

gene          complement(103627..107704)
/gene="BICP4"

regulatory    complement(103627..103632)
/regulatory_class="polyA_signal_sequence"
/gene="BICP4"

CDS            complement(103673..107704)
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/codon_start=1
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nucleus)"
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/db_xref="GOA:Q4LDG6"
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EAREGSTDADAEEAEAEAGTGAGTRTKAAPREAGAGPGAPRGRAPGPPAPSPPETAP
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PPASTARAARERLRELADRCAVACREALEAARRAAGAAGLPVLSSAAGRGLPAAACAP  
DALAAHPERVLRAAELLGAARDAAVERARLQRAAAPAALRAEAAAALAAARTVAPL  
ARYSTRGAAARASAWALARALFSPPAEVPARLAAALAALEAAGGGAGAGAAAPGRGPV  
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intron complement(107731..108190)  
/note="alternative intron spliced out to produce immediate-early RNA 4.2 and BICP4"

misc\_feature 111080..111300  
/note="origin of DNA replication (ori s), duplicated"

intron 111681..111802  
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/number=1

intron 112069..112745  
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/number=2

gene 112768..113737  
/gene="BICP22"

CDS 112768..113670  
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gene complement(114213..114944)  
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misc\_feature 114235..123983  
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gene complement(115001..115663)  
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CDS complement(115001..115663)  
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gene 115796..117202  
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CDS 115796..117202  
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AHRDVKTENVFLNGPGDVCLGDFGAAGHPVTEPRYYLAGTLETNSPELLARARYDCR
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gene      117337..118671
/gene="US4"

CDS       117337..118671
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gene      118717..118722
/gene="US3"
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regulatory 118717..118722
/regulatory_class="polyA_signal_sequence"
/gene="US3"
/gene_synonym="US4"

gene      118896..120149
/gene="US6"

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CDS 118896..120149  
/gene="US6"  
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gene 120287..121435  
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CDS 120287..121435  
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gene 121431..121436  
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regulatory 121431..121436  
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gene 121714..123506  
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CDS 121714..123441  
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TRPEAAAADAPEPGPPLTSEPAGAPTGPAPWLVLVGLAGLGLVGIAALAVRVCARR
ASQKRTYDILNPFGPVYTSLPTNEPLDVVVPVSDEFSLDEDSFADDSDDDGPASNP
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AARLKSILR"

regulatory      123501..123506
/regulatory_class="polyA_signal_sequence"
/gene="US8"
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gene            123548..124429
/gene="US9"

CDS             123548..123982
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misc_feature    123984..135300
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/gene="US9"

gene            complement(124481..125450)
/gene="BICP22"

regulatory      complement(124481..124486)
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/gene="BICP22"

CDS             complement(124548..125450)

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intron complement(125472..126149)
/note="for immediate-early RNA 1.7 encoding BICP22"
/number=2
intron complement(126416..126537)
/note="for immediate-early RNA 1.7 encoding BICP22"
/number=1
misc_feature complement(126918..127138)
/note="origin of DNA replication (ori s), duplicated"
intron 130028..>135301
/note="5'part of intron spliced out from transcript over
covalently joined genome ends, leading to immediate-early
RNA 1.5 and circ protein"
intron 130028..130487
/note="alternative intron spliced out to produce
immediate-early RNA 4.2 and BICP4"
gene 130514..134591
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nucleus)"
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/db_xref="UniProtKB/TrEMBL:Q4LDG6"
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 TREGILWDCPEIREAAARYAAAAGPAAVF VPEMDAGKQYAALVDLVYARRDAMAWLQS  
 AKLAGPDLQLARLLQRRVQGCRGHSSFITGSVTAPLPPVG DAMA A QNALW ALPHVAAC  
 VAMS RRYDCDQKLFL LQSLR RAYAPMAYPEAGAGGSGARAAL AELRAVLAGRAAPAPL  
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 /note="In the linear genome, G 135301 forms a single base  
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ORIGIN

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