Human adenovirus B1, complete genome

NCBI Reference Sequence: NC_011203.1

FASTA Graphics

Go to:

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LOCUS       NC_011203             35343 bp    DNA     linear   VRL 20-DEC-2020
DEFINITION  Human adenovirus B1, complete genome.
ACCESSION   NC_011203
VERSION     NC_011203.1
DBLINK      BioProject: PRJNA485481
KEYWORDS    RefSeq.
SOURCE      Human mastadenovirus B (HAdV-B)
  ORGANISM  Human mastadenovirus B
            Viruses; Varidnaviria; Bamfordvirae; Preplasmiviricota;
            Tectiliviricetes; Rowavirales; Adenoviridae; Mastadenovirus.
REFERENCE   1  (bases 1 to 35343)
  AUTHORS   Sirena,D., Ruzsics,Z., Schaffner,W., Greber,U.F. and Hemmi,S.
  TITLE     The nucleotide sequence and a first generation gene transfer
vector
            of species B human adenovirus serotype 3
  JOURNAL   Virology 343 (2), 283-298 (2005)
   PUBMED   16169033
REFERENCE   2  (bases 1 to 35343)
  CONSRTM   NCBI Genome Project
  TITLE     Direct Submission
  JOURNAL   Submitted (04-SEP-2008) National Center for Biotechnology
            Information, NIH, Bethesda, MD 20894, USA
REFERENCE   3  (bases 1 to 35343)
  AUTHORS   Hemmi,S., Greber,U.F., Schaffner,W. and Sirena,D.
  TITLE     Direct Submission
  JOURNAL   Submitted (06-JUN-2005) Institute of Molecular Biology,
University
            of Zurich, Winterthurerstrasse 190, Zurich 8057, Switzerland
COMMENT     REVIEWED REFSEQ: This record has been curated by Dr Andrew
Davison
            (MRC Virology Unit, Glasgow, UK) and Dr Balazs Harrach (Veterinary
            Medical Research Institute, Budapest, Hungary). The reference
            sequence was derived from DQ086466.
            CURATION:
                Proteins: A standard nomenclature has been applied so that
            orthologs have the same name. Functional information may have been
            propagated from other adenovirus species.
                Protein-coding regions: The initiation codon for each CDS is
            assigned with as much confidence as possible. CDSs presumably
            inherited from the last common ancestor of all adenoviruses are
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indicated as genus-common, and all other CDSs as genus-specific. CDSs that have paralogues in one or more genomes are listed as members of named families. The evolutionary history of E3 and E4 is complex, frequently involving generation or loss of paralogues in whole or in part, accompanied by rapid sequence divergence. In E3, this is evident in a set of tandemly arranged CDSs encoding transmembrane proteins. All of these are listed as members of the MP family, regardless of whether sequence conservation is detectable.

Transcripts: In mastadenoviruses, transcription arises from the early genes (E1A, E1B, E2A, E2B, E3 and E4), the intermediate genes (IX and IVa2) and the late genes (L, U and E2A-L). Certain transcriptional features are supported by experimental data for some of these genes in a few adenoviruses (particularly human adenovirus C). All transcriptional features not marked as experimentally supported are predictions made on the basis of conservation and relevance to CDS expression. The degree of confidence in each prediction depends on the feature under consideration. In primate adenoviruses, predictions for E3, E4 and the 5'-regions of E2A and E2B are generally the least certain. In non-primate mastadenoviruses, this trend is accentuated to the degree that predictions for introns in E3 and E4 are not provided, and those for the 5'-regions of E2A, E2B and IVa2 and for the intron separating the protein-coding exons of 33K are particularly tentative. In human adenovirus C, rightward-oriented transcripts from the late genes (L1-L5) are polyadenylated close downstream from polyadenylation signals at five locations (the 3'-ends of the pIIIa, pX, protease, control protein E3 12.5K and fiber CDSs), and those from the E3 genes (E3A and E3B) at two locations (the 3'-ends of the membrane protein E3 CR1-beta and control protein E3 14.7K CDSs). Only the polyadenylation signals for L3, E3B and L5 are conserved among all mastadenoviruses, whereas those for L1 and L2 are conserved in most mastadenoviruses and those for L4 and E3A in a few. In addition, potential additional polyadenylation signals exist at the 3'-ends of the penton base, pVII, V, pVI and fiber-2 CDSs in some mastadenoviruses, particularly those with non-primate hosts; the corresponding genes are listed as L1A, L1B, L1C, L2A and L5A, respectively. The gene corresponding to E3B is termed E3 in genomes lacking the E3A polyadenylation signal. In some instances where a TATA signal is not convincingly evident (particularly for E2A/E2B), a tentative assignment is made and marked as nominal.

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            COMPLETENESS: full length.
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                    /rpt_type=inverted
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                    /function="cell cycle regulation"
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                    may produce additional proteins; genus-specific"
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                    HGCKSCEFHRNNTGMKELLCSLCYMRMHCHFIYSPVSDDESPSPDSTTSPPEIQAPAP
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                     EDDWEVAIRNYAKISLRPDKQYRITKKINIRNACYISGNGAEVIIDTQDKAVFRCCMM
                     GMWPGVVGMEAVTLMNIRFKGDGYNGIVFMANTKLILHGCSFFGFNNTCVEAWGQVSV
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regulatory             3419..3424
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regulatory             3909..3914
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regulatory             3913..3918
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                     /note="E1B, IX"
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                     /db_xref="GeneID:6870517"
gene                  complement(3947..5572)
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                     /note="IVa2, E2B"
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                     MADGLKPLKNFSSLQELLSLGGERLLTDLVRENIHVREMMNEVAPLLREDGSCRSLNY
                     HLQPVIGVIYGPTGCGKSQLLRNLLSSQLITPAPETVFFIAPQVDMIPPSELKAWEMQ
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                     IIMDECMENLGGHKGVSKFFHAFPSKLHDKFPKCTGYTVLVVLHNMNPRRDLGGNIAN
                     LKIQSKMHIISPRMHPSQLNRFVNTYTKGLPVAISLLLKDIVQHHALRPCYDWVIYNT
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                     HPVNRCEYCGRLYKHKHECSARRREFYFHHINSHSSNWWQEIQFFPIGSHPRTERLFL
                     TYDVETYTWMGSFGKQLIPFMLVMKLSGDQRLVNIAYDLAIKLKWDRWRQDPQTFYCV
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                     KKLPHVRGTPRFLELYIVGHNINGFDEIVLAAQVINNRAEVPQPFKITRNFMPRAGKI
                     LFNDVTFALPNPAYKKRVDFQLWEQGACDDIDFKYQFLKVMVRDTFALTHTSLRNAAQ
                     AYSLPVEKGCCPYKAVNQFYMLGSYRAEKDGFPLEEYWKDHEEYLLNRELWEKKSQPR
                     YDIIQETLDYCALDVLITAELVAKLQESYAHFIRDSVGLPHAHFNIFQRPTISSNSHA
                     IFRQIVYRAEKPNRTNLGPGLLAPSHELYDYVRASIRGGRCYPTYIGILEEPLYVYDI
                     CGMYASALTHPMPWGTPLNPYERALAVREWQMTLDDPATISYFDKDLLPGIFTIDADP
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             KHGGKLVFDPDEPDLTWLVECETVCASCGADAYSPESIFLAPKLYALKCIYCPACHKT
             SKGKLRAKGHAAEALNYELMVNCYLADMQGANRQRFSTSRMSLKRTLASAQPGAHPFT
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             /note="between L2 and i leaders; precedes protein 13.6K
             CDS"
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                other human mastadenoviruses, but their conservation may
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CDS              complement(join(8422..10389,13848..13856))
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             /note="precedes core protein precursor pVII CDS"
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                ITEPDGRWLYDLINILQSIIVQERSLGLAEKVAAINYSVLSLGKYYARKIYKTPYVPI
                DKEVKIDGFYMRMTLKVLTLSDDLGVYRNDRMHRAVSASRRRELSDRELMHSLQRALT
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CDS             12051..13817
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                DYTNFLSALRLMVAEVPQSEVYQSGPDYFFQTSRQGLQTVNLTQAFKNLKGLWGVHAP
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                IESLVDKMSRWKTYAQDHRDEPRILGATSRPIRRRQRHDRQMGLVWDDEDSADDSSVL
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regulatory        13830..13835
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CDS              13905..15539
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                TEKQKREAAAAEVKKELKIQPLEKDSKSRSYNVLEDKINTAYRSWYLSYNYGNPEKGI
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                /note="precedes DNA polymerase and terminal protein
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               REGEDLYPTMQLMVPKRQRLEDVLEKMKVDADIQPEVKVRPIKEVAPGLGVQTFDIKI
               PTESMEVQTEPAKPTTSIEVQTEPWMPAPVAAPSTTRRSRRKYGPASLLMPNYALHPS
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               /function="capsid morphogenesis"
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               genus-common"
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regulatory       17496..17501
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                     INSRLDPPPATPGEMEVEEELPPLEKRGDKRPRPELEQTLVTRADEPPSYEEAVKLGM
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                     TGNMGVLAGQASQLNAVVDLQDRNTELSYQLLLDSLGDRTRYFSMWNQAVDSYDPDVR
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gene          complement(21950..26643)
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             /locus_tag="HAdVB1_gp11"
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gene          complement(21950..25561)
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             /locus_tag="HAdVB1_gp12"
             /db_xref="GeneID:6870527"
regulatory     complement(21950..21955)
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CDS           complement(22004..23557)
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             PLVSAWEKGMEVMAVLMERYRLDNDLRTSFKLMPEQHEQYKRICHQYVNEEHRGIPLT
             FTSMKTLTTMMGRFMQGLVHYYSEIAHNNWECTGCALWAHGCTDYEGKVKCLHGTIMI
             QKDHIIEMDVASENGQRAMKENPDRAKITQNRWGRNVVQLANNDARCCVNDANCTTNQ
             FSSKSCGMFYTEGSKAQEAFKQYEAFMKAVYPGITPDQARMMLIPIHCDCNHKPGCAP
             VMGRQTCKMTPFGMANAEDLDVTTISDPTVLASVRHPALIVFQCCNPVYRNSRVQNAG
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                /note="genus-common"
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                VYQEAGIRDHVADYLTGLGGEDVLLKHLARQSIIVKDALLDLTEVPISVEELSRAYEL
                NLFSPQVPPKRQPNGTCEANPRLNFYPAFTIPEVLATYHIFFKNQKIPVSCRANRTRA
                DALLNLGPGARLPDIASLEEVPKIFEGLGSDETRAANALQQGENDMDEHHSALVELEG
                DNARIAVLKRSIVVTHFAYPAVNLPPKVMSAVMDHLLIKRARPLSENQNMQDPDASDE
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                GAAVAPRGYEGRLGQSGRGGDGRLGQPGRGGGQPGGRQFGGGRRGGRGGGRSNRRQTV
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intron           complement(24356..26546)
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intron           complement(24356..25455)
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regulatory        complement(25556..25561)
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CDS              join(25776..26124,26294..26649)
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              EPAQTRELRNRIFPTLYAIFQQSRGQEQELKVKNRSLRSLTRSCLYHKSEDQLQRTLE
              DAEALFNKYCALTLKE"
CDS            25776..26375
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              /function="DNA encapsidation"
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              /function="transcriptional control"
              /note="genus-common"
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              /protein_id="YP_002213784.1"
              /db_xref="GeneID:6870520"
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intron          26125..26293
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regulatory      complement(26638..26643)
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              /gene="E2A"
              /locus_tag="HAdVB1_gp11"
              /note="E2A, E2B; nominal"
CDS            26720..27403
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              /function="capsid morphogenesis"
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intron           27137..30714
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intron           27137..30043
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intron           27137..29781
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intron           27137..28076
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                /note="precedes membrane glycoprotein E3 gp19K CDS"
intron           27137..27600
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CDS             27403..27723
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                     AHGVRITIEGGIDSRLHRIFSQRPVLIERDQGNTTISIYCICNHPGLHESLCCLVCAE
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     CDS              27677..28117
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                     /note="0 CR1 domains; genus-specific; MP family"
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                     /protein_id="YP_002213787.1"
                     /db_xref="GeneID:6870528"
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                     PFIQDSNSTLPAPSTTNLPETNKLASHLQHRLSRSLLSANTTTPKTGGELRGLPTDDP
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     regulatory        27712..27717
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                     /gene="L4"
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     CDS              28102..28620
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                     /locus_tag="HAdVB1_gp13"
                     /function="immune regulation"
                     /note="binds to MHC-I and inhibits transport;
                     genus-specific; MP family"
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                     PRQSNEEKEKMP"
     CDS              28650..29189
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                     /function="unknown"
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     CDS              29202..29771
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                     /function="unknown"
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                     /function="unknown"
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                     /db_xref="GeneID:6870528"
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                     IQQPLALVQYENEPQPSLPPAISYFNLTGGDD"
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                     /function="apoptosis"
                     /note="genus-specific; 12.5K family"
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                     /db_xref="GeneID:6870528"
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                     /gene="E3"
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                     /locus_tag="HAdVB1_gp14"
                     /db_xref="GeneID:6870529"
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                     DKDCIADF"
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                     LQIEQNKLCSKLGNGLTFDSSNSIALKNNTLWTGPKPEANCIIEYGKQNPDSKLTLIL
                     VKNGGIVNGYVTLMGASDYVNTLFKNKNVSINVELYFDATGHILPDSSSLKTDLELKY
                     KQTADFSARGFMPSTTAYPFVLPNAGTHNENYIFGQCYYKASDGALFPLEVTVMLNKR
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     gene             complement(32352..35040)
                     /gene="E4"
                     /locus_tag="HAdVB1_gp15"
                     /db_xref="GeneID:6870530"
     regulatory        complement(32352..32357)
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                     /gene="E4"
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