Human adenovirus C, complete genome

NCBI Reference Sequence: NC_001405.1

FASTA Graphics

Go to:

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LOCUS       NC_001405            35937 bp    DNA     linear   VRL 13-AUG-2018
DEFINITION  Human adenovirus C, complete genome.
ACCESSION   NC_001405
VERSION     NC_001405.1
DBLINK      BioProject: PRJNA485481
KEYWORDS    RefSeq.
SOURCE      Human mastadenovirus C
  ORGANISM  Human mastadenovirus C
            Viruses; Varidnaviria; Bamfordvirae; Preplasmiviricota;
            Tectiliviricetes; Rowavirales; Adenoviridae; Mastadenovirus.
REFERENCE   1  (sites)
  AUTHORS   Roberts,R.J., Akusjaervi,G., Alestroem,P., Gelinas,R.E.,
            Gingeras,T.R., Sciaky,D. and Pettersson,U.
  TITLE     A consensus sequence for the adenovirus-2 genome
  JOURNAL   (in) Doerfler,W. (Ed.);
            ADENOVIRUS DNA: 1-51;
            Martinus Nijhoff Publishing, Boston (1986)
REFERENCE   2  (bases 1 to 35937)
  CONSRTM   NCBI Genome Project
  TITLE     Direct Submission
  JOURNAL   Submitted (30-SEP-2004) National Center for Biotechnology
            Information, NIH, Bethesda, MD 20894, USA
COMMENT     PROVISIONAL REFSEQ: This record is based on preliminary
annotation
            provided 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 J01917.
            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
            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
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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.

ACCURACY: No potential sequence errors are noted.

COMPLETENESS: full length.

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/old_locus_tag="HAdVCgp12"
/function="DNA encapsidation"
/function="capsid morphogenesis"
/note="genus-common"
/codon_start=1
/product="encapsidation protein 52K"
/protein_id="NP_040519.1"
/db_xref="GeneID:2652993"
/translation="MHPVLRQMRPPPQQRQEQEQRQTCRAPSPSPTASGGATSAADAA
ADGDYEPPRRRARHYLDLEEGEGLARLGAPSPERHPRVQLKRDTREAYVPRQNLFRDR
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EQTVNQEINFQKSFNNHVRTLVAREEVAIGLMHLWDFVSALEQNPNSKPLMAQLFLIV
QHSRDNEAFRDALLNIVEPEGRWLLDLINILQSIVVQERSLSLADKVAAINYSMLSLG
KFYARKIYHTPYVPIDKEVKIEGFYMRMALKVLTLSDDLGVYRNERIHKAVSVSRRRE
LSDRELMHSLQRALAGTGSGDREAESYFDAGADLRWAPSRRALEAAGAGPGLAVAPAR
AGNVGGVEEYDEDDEYEPEDGEY"

CDS 12308..14065
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/old_locus_tag="HAdVCgp12"
/function="capsid morphogenesis"
/note="genus-common"
/codon_start=1
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/protein_id="NP_040520.1"
/db_xref="GeneID:2652993"
/translation="MMQDATDPAVRAALQSQPSGLNSTDDWRQVMDRIMSLTARNPDA
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YTNFVSALRLMVTETPQSEVYQSGPDYFFQTSRQGLQTVNLSQAFKNLQGLWGVRAPT
GDRATVSSLLTPNSRLLLLLIAPFTDSGSVSRDTYLGHLLTLYREAIGQAHVDEHTFQ
EITSVSRALGQEDTGSLEATLNYLLTNRRQKIPSLHSLNSEEERILRYVQQSVSLNLM
RDGVTPSVALDMTARNMEPGMYASNRPFINRLMDYLHRAAAVNPEYFTNAILNPHWLP
PPGFYTGGFEVPEGNDGFLWDDIDDSVFSPQPQTLLELQQREQAEAALRKESFRRPSS
LSDLGAAAPRSDASSPFPSLIGSFTSTRTTRPRLLGEEEYLNNSLLQPQREKNLPPAF
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LGGSGNPFAHLRPRLGRMF"

regulatory 14092..14097
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/gene="L1"
/locus_tag="HAdVC_gp10"
/old_locus_tag="HAdVCgp12"

CDS 14151..15866
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/function="capsid morphogenesis"
/function="cell attachment"
/function="cell entry"
/note="capsid protein III; genus-common"
/codon_start=1
/product="penton base"
/protein_id="NP_040521.1"
/db_xref="GeneID:2652996"
/translation="MQRAAMYEEGPPPSYESVVSAAPVAAALGSPFDAPLDPPFVPPR
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LKYEWVEFTLPEGNYSETMTIDLMNNAIVEHYLKVGRQNGVLESDIGVKFDTRNFRLG
FDPVTGLVMPGVYTNEAFHPDIILLPGCGVDFTHSRLSNLLGIRKRQPFQEGFRITYD
DLEGGNIPALLDVDAYQASLKDDTEQGGDGAGGGNNSGSGAEENSNAAAAAMQPVEDM
NDHAIRGDTFATRAEEKRAEAEAAAEAAAPAAQPEVEKPQKKPVIKPLTEDSKKRSYN
LISNDSTFTQYRSWYLAYNYGDPQTGIRSWTLLCTPDVTCGSEQVYWSLPDMMQDPVT
FRSTSQISNFPVVGAELLPVHSKSFYNDQAVYSQLIRQFTSLTHVFNRFPENQILARP
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SSRTF"

intron complement(14293..24714)
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/old_locus_tag="HAdVCgp06"
/note="precedes DNA polymerase and terminal protein
precursor pTP CDSs"

CDS 15873..16469
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/locus_tag="HAdVC_gp09"
/function="capsid morphogenesis"
/note="genus-common"
/codon_start=1
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/protein_id="NP_040522.1"
/db_xref="GeneID:2652996"
/translation="MSILISPSNNTGWGLRFPSKMFGGAKKRSDQHPVRVRGHYRAPW

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RRVARRHRRRPGTAAQRAAAALLNRARRTGRRAAMRAARRLAAGIVTVPPRSRRRAAA
AAAAAISAMTQGRRGNVYWVRDSVSGLRVPVRTRPPRN"

CDS 16539..17648
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/locus_tag="HAdVC_gp09"
/function="capsid morphogenesis"
/note="genus-specific"
/codon_start=1
/product="core protein V"
/protein_id="NP_040523.1"
/db_xref="GeneID:2652996"
/translation="MSKRKIKEEMLQVIAPEIYGPPKKEEQDYKPRKLKRVKKKKKDD
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GLKRESGDLAPTVQLMVPKRQRLEDVLEKMTVEPGLEPEVRVRPIKQVAPGLGVQTVD
VQIPTTSSTSIATATEGMETQTSPVASAVADAAVQAAAAAASKTSTEVQTDPWMFRVS
APRRPRRSRKYGTASALLPEYALHPSIAPTPGYRGYTYRPRRRATTRRRTTTGTRRRR
RRRQPVLAPISVRRVAREGGRTLVLPTARYHPSIV"

CDS 17676..17918
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/locus_tag="HAdVC_gp09"
/function="capsid morphogenesis"
/note="putative type 2 membrane protein; product Mu;
genus-common"
/codon_start=1
/product="core protein precursor pX"
/protein_id="YP_001551766.1"
/db_xref="GeneID:2652996"
/translation="MALTCRLRFPVPGFRGRMHRRRGMAGHGLTGGMRRAHHRRRRAS
HRRMRGGILPLLIPLIAAAIGAVPGIASVALQAQRH"

regulatory 17949..17954
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CDS 18001..18753
/gene="L3"
/locus_tag="HAdVC_gp08"
/function="capsid morphogenesis"
/note="cleaved peptide stimulates protease; genus-common"
/codon_start=1
/product="capsid protein precursor pVI"
/protein_id="NP_040524.1"
/db_xref="GeneID:2652998"

/translation="MEDINFASLAPRHGSRPFMGNWQDIGTSNMSGGAFSWGSLWSGI
KNFGSTIKNYGSKAWNSSTGQMLRDKLKEQNFQQKVVDGLASGISGVVDLANQAVQNK
INSKLDPRPPVEEPPPAVETVSPEGRGEKRPRPDREETLVTQIDEPPSYEEALKQGLP
TTRPIAPMATGVLGQHTPVTLDLPPPADTQQKPVLPGPSAVVVTRPSRASLRRAASGP
RSMRPVASGNWQSTLNSIVGLGVQSLKRRRCF"

CDS 18838..21744

/gene="L3"
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/function="capsid morphogenesis"
/note="capsid protein II; genus-common"
/codon_start=1
/product="hexon"
/protein_id="NP_040525.1"
/db_xref="GeneID:2652998"
/translation="MATPSMMPQWSYMHISGQDASEYLSPGLVQFARATETYFSLNNK
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IRGVLDRGPTFKPYSGTAYNALAPKGAPNSCEWEQTEDSGRAVAEDEEEEDEDEEEEE
EEQNARDQATKKTHVYAQAPLSGETITKSGLQIGSDNAETQAKPVYADPSYQPEPQIG
ESQWNEADANAAGGRVLKKTTPMKPCYGSYARPTNPFGGQSVLVPDEKGVPLPKVDLQ
FFSNTTSLNDRQGNATKPKVVLYSEDVNMETPDTHLSYKPGKGDENSKAMLGQQSMPN
RPNYIAFRDNFIGLMYYNSTGNMGVLAGQASQLNAVVDLQDRNTELSYQLLLDSIGDR
TRYFSMWNQAVDSYDPDVRIIENHGTEDELPNYCFPLGGIGVTDTYQAIKANGNGSGD
NGDTTWTKDETFATRNEIGVGNNFAMEINLNANLWRNFLYSNIALYLPDKLKYNPTNV
EISDNPNTYDYMNKRVVAPGLVDCYINLGARWSLDYMDNVNPFNHHRNAGLRYRSMLL
GNGRYVPFHIQVPQKFFAIKNLLLLPGSYTYEWNFRKDVNMVLQSSLGNDLRVDGASI
KFDSICLYATFFPMAHNTASTLEAMLRNDTNDQSFNDYLSAANMLYPIPANATNVPIS
IPSRNWAAFRGWAFTRLKTKETPSLGSGYDPYYTYSGSIPYLDGTFYLNHTFKKVAIT
FDSSVSWPGNDRLLTPNEFEIKRSVDGEGYNVAQCNMTKDWFLVQMLANYNIGYQGFY
IPESYKDRMYSFFRNFQPMSRQVVDDTKYKEYQQVGILHQHNNSGFVGYLAPTMREGQ
AYPANVPYPLIGKTAVDSITQKKFLCDRTLWRIPFSSNFMSMGALTDLGQNLLYANSA
HALDMTFEVDPMDEPTLLYVLFEVFDVVRVHQPHRGVIETVYLRTPFSAGNATT"

CDS 21778..22392

/gene="L3"
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/EC_number="3.4.22.39"
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/note="capsid protein 23K; genus-common"
/codon_start=1
/product="protease"
/protein_id="NP_040526.1"
/db_xref="GeneID:2652998"
/translation="MGSSEQELKAIVKDLGCGPYFLGTYDKRFPGFVSPHKLACAIVN
TAGRETGGVHWMAFAWNPRSKTCYLFEPFGFSDQRLKQVYQFEYESLLRRSAIASSPD
RCITLEKSTQSVQGPNSAACGLFCCMFLHAFANWPQTPMDHNPTMNLITGVPNSMLNS

PQVQPTLRRNQEQLYSFLERHSPYFRSHSAQIRSATSFCHLKNM"
regulatory 22418..22423
/regulatory_class="polyA_signal_sequence"
/gene="L3"
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gene complement(22420..27121)
/gene="E2A"
/locus_tag="HAdVC_gp11"
/db_xref="GeneID:5739976"
prim_transcript complement(22420..27092)
/gene="E2A"
/locus_tag="HAdVC_gp11"
/note="5'-end also registered 1 nuc to left; E2A"
gene complement(22420..25985)
/gene="E2A-L"
/locus_tag="HAdVC_gp12"
/db_xref="GeneID:5739977"
prim_transcript complement(22420..25956)
/gene="E2A-L"
/locus_tag="HAdVC_gp12"
/experiment="transcript mapping"
/note="5'-end also registered 2 nuc to left"
regulatory complement(22434..22439)
/regulatory_class="polyA_signal_sequence"
/experiment="transcript mapping"
/note="E2A, E2A-L"
CDS complement(22490..24079)
/gene="E2A"
/locus_tag="HAdVC_gp11"
/function="DNA replication"
/note="DBP; genus-common; DBP family"
/codon_start=1
/product="single-stranded DNA-binding protein"
/protein_id="NP_040527.1"
/db_xref="GeneID:5739976"
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KRLRRRLESEDEEDSSQDALVPRTPSPRPSTSTADLAIASKKKKKRPSPKPERPPSPE
VIVDSEEEREDVALQMVGFSNPPVLIKHGKGGKRTVRRLNEDDPVARGMRTQEEKEES
SEAESESTVINPLSLPIVSAWEKGMEAARALMDKYHVDNDLKANFKLLPDQVEALAAV
CKTWLNEEHRGLQLTFTSNKTFVTMMGRFLQAYLQSFAEVTYKHHEPTGCALWLHRCA
EIEGELKCLHGSIMINKEHVIEMDVTSENGQRALKEQSSKAKIVKNRWGRNVVQISNT
DARCCVHDAACPANQFSGKSCGMFFSEGAKAQVAFKQIKAFMQALYPNAQTGHGHLLM
PLRCECNSKPGHAPFLGRQLPKLTPFALSNAEDLDADLISDKSVLASVHHPALIVFQC
CNPVYRNSRAQGGGPNCDFKISAPDLLNALVMVRSLWSENFTELPRMVVPEFKWSTKH

QYRNVSLPVAHSDARQNPFDF"

intron complement(24089..24714)
/experiment="transcript mapping"
/note="E2A, E2A-L; precedes single-stranded DNA-binding protein CDS"

CDS 24108..26525
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/function="capsid morphogenesis"
/function="translational regulation"
/note="genus-common"
/codon_start=1
/product="hexon assembly protein 100K"
/protein_id="NP_040528.1"
/db_xref="GeneID:2653005"
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IEQDPGFVSEDDEDRSVPTEDKKQDQDDAEANEEQVGRGDQRHGDYLDVGDDVLLKHL
QRQCAIICDALQERSDVPLAIADVSLAYERHLFSPRVPPKRQENGTCEPNPRLNFYPV
FAVPEVLATYHIFFQNCKIPLSCRANRSRADKQLALRQGAVIPDIASLDEVPKIFEGL
GRDEKRAANALQQENSENESHCGVLVELEGDNARLAVLKRSIEVTHFAYPALNLPPKV
MSTVMSELIVRRARPLERDANLQEQTEEGLPAVGDEQLARWLETREPADLEERRKLMM
AAVLVTVELECMQRFFADPEMQRKLEETLHYTFRQGYVRQACKISNVELCNLVSYLGI
LHENRLGQNVLHSTLKGEARRDYVRDCVYLFLCYTWQTAMGVWQQCLEERNLKELQKL
LKQNLKDLWTAFNERSVAAHLADIIFPERLLKTLQQGLPDFTSQSMLQNFRNFILERS
GILPATCCALPSDFVPIKYRECPPPLWGHCYLLQLANYLAYHSDIMEDVSGDGLLECH
CRCNLCTPHRSLVCNSQLLSESQIIGTFELQGPSPDEKSAAPGLKLTPGLWTSAYLRK
FVPEDYHAHEIRFYEDQSRPPNAELTACVITQGHILGQLQAINKARQEFLLRKGRGVY
LDPQSGEELNPIPPPPQPYQQPRALASQDGTQKEAAAAAAAATHGRGGILGQSGRGGFG
RGGGDDGRLGQPRRSFRGRRGVRRNTVTLGRIPLAGAPEIGNRSQHRYNLRSSGAAGT
ACSPTQP"

intron complement(24792..27024)
/experiment="transcript mapping"
/note="E2A, E2B"

intron complement(24792..25885)
/gene="E2A-L"
/locus_tag="HAdVC_gp12"
/experiment="transcript mapping"

regulatory complement(25980..25985)
/regulatory_class="TATA_box"
/gene="E2A-L"
/locus_tag="HAdVC_gp12"

CDS join(26239..26551,26754..27127)
/gene="L4"
/locus_tag="HAdVC_gp07"

/function="RNA splicing"
/note="genus-common"
/codon_start=1
/product="protein 33K"
/protein_id="NP_040529.1"
/db_xref="GeneID:2653005"
/translation="MAPKKKLQLPPPPPTDEEEYWDSQAEEVLDEEEEMMEDWDSLDE
ASEAEEVSDETPSPSVAFPSPAPQKLATVPSIATTSAPQAPPALPVRRPNRRWDTTGT
RAAPTAPAAAAAAAATAAVTQKQRRPDSKTLTKPKKSTAAAAAGGGALRLAPNEPVSTR
ELRNRIFPTLYAIFQQSRGQEQELKIKNRSLRSLTRSCLYHKSEDQLRRTLEDAEALF
SKYCALTLKD"
CDS 26239..26826
/gene="L4"
/locus_tag="HAdVC_gp07"
/function="DNA encapsidation"
/function="capsid morphogenesis"
/function="transcriptional control"
/note="genus-common"
/codon_start=1
/product="encapsidation protein 22K"
/protein_id="YP_001551767.1"
/db_xref="GeneID:2653005"
/translation="MAPKKKLQLPPPPPTDEEEYWDSQAEEVLDEEEEMMEDWDSLDE
ASEAEEVSDETPSPSVAFPSPAPQKLATVPSIATTSAPQAPPALPVRRPNRRWDTTGT
RAGKSKQPPPLAQEQQQRQGYRSWRGHKNAIVACLQDCGGNISFARRFLLYHHGVAFP
RNILHYYRHLYSPYCTGGSGSGSNSSGHTEAKATG"
intron 26522..26753
/gene="L4"
/locus_tag="HAdVC_gp07"
/experiment="transcript mapping"
regulatory complement(27116..27121)
/regulatory_class="TATA_box"
/note="E2A, E2B; nominal"
CDS 27215..27898
/gene="L4"
/locus_tag="HAdVC_gp07"
/function="capsid morphogenesis"
/note="genus-common"
/codon_start=1
/product="capsid protein precursor pVIII"
/protein_id="NP_040530.1"
/db_xref="GeneID:2653005"
/translation="MSKEIPTPYMWSYQPQMGLAAGAAQDYSTRINYMSAGPHMISRV
NGIRAHRNRILLEQAAITTTPRNNLNPRSWPAALVYQESPAPTTVVLPRDAQAEVQMT

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                NSGAQLAGGFRHRVRSPGQGITHLKIRGRGIQLNDESVSSSLGLRPDGTFQIGGAGRS
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gene            27580..30864
                /gene="E3B"
                /locus_tag="HAdVC_gp13"
                /old_locus_tag="HAdVCgp27"
                /db_xref="GeneID:2652988"
gene            27580..29804
                /gene="E3A"
                /locus_tag="HAdVC_gp14"
                /old_locus_tag="HAdVCgp28"
                /db_xref="GeneID:2652987"
regulatory      27580..27585
                /regulatory_class="TATA_box"
                /note="E3A, E3B"
prim_transcript 27609..30864
                /gene="E3B"
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                /old_locus_tag="HAdVCgp27"
                /experiment="transcript mapping"
prim_transcript 27609..29804
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                /locus_tag="HAdVC_gp14"
                /old_locus_tag="HAdVCgp28"
                /experiment="transcript mapping"
                /note="3'-ends also registered 3, 5 and 12 nuc to left"
intron          27632..30437
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                /locus_tag="HAdVC_gp13"
                /old_locus_tag="HAdVCgp27"
                /note="precedes control protein E3 14.7K CDS"
intron          27632..30046
                /gene="E3B"
                /locus_tag="HAdVC_gp13"
                /old_locus_tag="HAdVCgp27"
                /note="precedes membrane protein E3 RID-beta CDS"
intron          27632..29764
                /gene="E3A"
                /locus_tag="HAdVC_gp14"
                /old_locus_tag="HAdVCgp28"
                /note="precedes membrane protein E3 RID-alpha CDS"
intron          27632..29465
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/old_locus_tag="HAdVCgp28"
/note="precedes membrane glycoprotein E3 CR1-beta CDS"
intron 27632..28772
/gene="E3A"
/locus_tag="HAdVC_gp14"
/old_locus_tag="HAdVCgp28"
/note="precedes membrane glycoprotein E3 gp19K CDS"
intron 27632..28365
/gene="E3A"
/locus_tag="HAdVC_gp14"
/old_locus_tag="HAdVCgp28"
/note="precedes membrane glycoprotein E3 CR1-alpha CDS"
CDS 27899..28222
/gene="E3A"
/locus_tag="HAdVC_gp14"
/old_locus_tag="HAdVCgp28"
/function="unknown"
/note="genus-specific; 12.5K family"
/codon_start=1
/product="control protein E3 12.5K"
/protein_id="YP_001551768.1"
/db_xref="GeneID:2652987"
/translation="MTSGEAERLRLTHLDHCRRHKCFARGSGEFCYFELPEEHIEGPA
HGVRLTTQVELTRSLIREFTKRPLLVERERGPCVLTVVCNCPNPGLHQDLCCHLCAEY
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intron 27981..28375
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/locus_tag="HAdVC_gp06"
/old_locus_tag="HAdVCgp09"
/experiment="transcript mapping"
regulatory 28205..28210
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/gene="L4"
/locus_tag="HAdVC_gp07"
intron 28560..30437
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/old_locus_tag="HAdVCgp09"
/experiment="transcript mapping"
CDS 28630..28815
/gene="E3A"
/locus_tag="HAdVC_gp14"
/old_locus_tag="HAdVCgp28"

/function="unknown"
/note="protein E3 6.7K; probable relic; apoptosis;
genus-specific; MP family"
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/product="membrane glycoprotein E3 CR1-alpha"
/protein_id="YP_001551769.1"
/db_xref="GeneID:2652987"
/translation="MSNSSNSTSLSNFSGIGVGVILTLVILFILILALLCLRVAACCT
HVCTYCQLFKRWGQHPR"
CDS 28812..29291
/gene="E3A"
/locus_tag="HAdVC_gp14"
/old_locus_tag="HAdVCgp28"
/function="immune regulation"
/note="binds to MHC-I and inhibits transport; protein E3
6.7K; probable relic; apoptosis; genus-specific; MP
family"
/codon_start=1
/product="membrane glycoprotein E3 gp19K"
/protein_id="NP_040531.1"
/db_xref="GeneID:2652987"
/translation="MRYMILGLLALAAVCSAAKKVEFKEPACNVTFKSEANECTTLIK
CTTEHEKLIIRHKDKIGKYAVYAIWQPGDTNDYNVTVFQGENRKTFMYKFPFYEMCDI
TMYMSKQYKLWPPQKCLENTGTFCSTALLITALALVCTLLYLKYKSRRSFIDEKKMP"
CDS 29468..29773
/gene="E3A"
/locus_tag="HAdVC_gp14"
/old_locus_tag="HAdVCgp28"
/function="unknown"
/note="protein E3 11.6K (adenovirus death protein);
probable relic; cell egress; genus-specific; MP family"
/codon_start=1
/product="membrane glycoprotein E3 CR1-beta"
/protein_id="NP_040532.1"
/db_xref="GeneID:2652987"
/translation="MTGSTIAPTTDYRNTTATGLTSALNLPQVHAFVNDWASLDMWWF
SIALMFVCLIIMWLICCLKRRRARPPIYRPIIVLNPHNEKIHRLDGLKPCSLLLQYD"
regulatory 29769..29774
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/gene="E3A"
/locus_tag="HAdVC_gp14"
/old_locus_tag="HAdVCgp28"
CDS 29781..30056
/gene="E3B"

/locus_tag="HAdVC_gp13"
/old_locus_tag="HAdVCgp27"
/function="apoptosis"
/note="genus-specific; MP family"
/codon_start=1
/product="membrane protein E3 RID-alpha"
/protein_id="YP_001551770.1"
/db_xref="GeneID:2652988"
/translation="MIPRVLILLTLVALFCACSTLAAVAHIEVDCIPPFTVYLLYGFV
TLILICSLVTVVIAFIQFIDWVCVRIAYLRHHPQYRDRTIADLLRIL"

CDS 30059..30451
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/old_locus_tag="HAdVCgp27"
/function="apoptosis"
/note="genus-specific; MP family"
/codon_start=1
/product="membrane protein E3 RID-beta"
/protein_id="YP_001551771.1"
/db_xref="GeneID:2652988"
/translation="MKRSVIFVLLIFCALPVLCSQTSAPPKRHISCRFTQIWNIPSCY
NKQSDLSEAWLYAIISVMVFCSTIFALAIYPYLDIGWNAIDAMNHPTFPVPAVIPLQQ
VIAPINQPRPPSPTPTEISYFNLTGGDD"

CDS 30444..30830
/gene="E3B"
/locus_tag="HAdVC_gp13"
/old_locus_tag="HAdVCgp27"
/function="apoptosis"
/note="genus-specific; 12.5K family"
/codon_start=1
/product="control protein E3 14.7K"
/protein_id="NP_597753.1"
/db_xref="GeneID:2652988"
/translation="MTESLDLELDGINTEQRLLERRKAASERERLKQEVEDMVNLHQC
KRGIFCVVKQAKLTYEKTTTGNRLSYKLPTQRQKLVLMVGEKPITVTQHSAETEGCLH
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intron 30583..31029
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