S1 Alignment. Sequence alignment of MAAP proteins from representative strains, in FASTA format

The sequence features of this alignment are presented in detail in Fig 3.

```
>AAV2|NC_001401_2:2203-4410/1-2208_AAV2|NC_001401.2:2203-4410/1-
2208_Adeno-associated_virus_-_2,_complete_genome/28-146
-------------------------
MAHHHQSPQSGIRTTAGVLCFLGTSTSDPSTDSTRESRSTRQTPRPS
STTKPTTGSSTAETTRTSSTTTPTRSFRSALKKIRLLGATSDEQSSRRKRGFLNLWAWLRNLLRRLRE
K-R-
GR
>AAVhu_32|AY530597_1/1-2211_AAVhu.32|AY530597.1/1-2211_Adeno-
associated_virus_isolate_hu.32_capsid_protein_VP1_cap_gene,_complete
_cds/28-146
-------------------------
MAHHHQSPQSGIRTTAGVLCFLGTSTSDPATDSTRGSRSTQQTRRPS
STTRPTTSSSRPETTRTSSTTTPTPSSRSGSKKIRLLGATSGEQSSRPKRGFLNLLVWLRKRLRRLLE
R-R-
GL
>AAVch_5|AY243021_1/1-2208_AAVch.5|AY243021.1/1-2208_Non-
human_primate_Adeno-
associated_virus_isolate_AAVch.5_capsid_protein_VP1_gene,_complete_c
ds/26-144
-------------------------
MAHHRRNLTNNTGTTVGVLCFLGTSTSDPSTDSTKESRSTRQTPRPS
STTKPTTTSSSKGTTRTSNTTTRTLNFRSVFKKIRLSGATSGEQSSRPKRGYSSLLVWLRKLLRRLLE
K-R-
DL
>AAVrh_23|AY243005_1/1-2058_AAVrh.23|AY243005.1/1-2058_Non-
human_primate_Adeno-
associated_virus_isolate_AAVrh.23_capsid_protein_VP1_gene,_complete_
cds/28-146
-------------------------
MEPRNPKPTSKSRTTAGVWCFLATSTSDPSTDSTRESRSTRQTPRPS
STTRPTTSSSSRGTTRTSSTTTPTPSFRSVFKKIRLLGATSGEQSSRPRSGFSNLSVWLRKALRRLLE
R-R-
DR
>AAV12|DQ813647_1:1985-4213/1-2229_AAV12|DQ813647.1:1985-4213/1-
2229_Adeno-associated_virus_12_Rep78_and_VP1_genes,_complete_cds/28-
146
-------------------------
MELHNPRPTNSIRTTAGVLCFLGTSTSDPSTDSTRESRSTRQTPRPS
STTRPTTSSSSRGTTRISSTTTPTPSSSSAWRPTPLLGATSGEQSSRPKRGFSSLWVWLKRALKRLLE
R-N-
AH
>AAV13|EU285562_1:1948-4149/1-2202_AAV13|EU285562.1:1948-4149/1-
2202_Adeno-
associated_virus_13_nonstructural_protein_and_capsid_protein_genes,_
complete_cds/28-146
-------------------------
MEPLNPRQINNIRTTLGVLCFRVTNTSDPATDLTRGNPSTQRTRQPS
```

```
NTTRPTTSSSRPVTTPTSSTTTPTPSFRSVFKKIRLLGATSDEQSSRPKRGSLSLWVWLRKRLRRLLE
K-R-
DL
>AAV3B|AF028705_1:2208-4418/1-2211_AAV3B|AF028705.1:2208-4418/1-
2211_Adeno-associated_virus_3B,_complete_genome/28-146
-------------------------
MESLNPKRTNNTRTTVGVLCFRVTNTSDPVTDSTKESRSTRRTRQPS
NTTKLTTSSSRPVTTRTSSTTTPTPSFRSVFKKIRLLGATLAEQSSRPKRGSLSLLVWLRKQLKRLLE
R-R-
GL
>AVpo1|FJ688147_1/27-144
-------------------------
MAHPNRSPTSRSKTTPVVLYCLDIITWDPETVSTAENLSTGLTRSRE
STTSRTTSSSRRETTPTSSTTTRTPSFRRSSRTTPPSGATSARQSFRPKKGFSNLLAWLRSLLRRLLK
A-S-
G-
>AAVpo4|JX896667_1/1-2184_AAVpo4|JX896667.1/1-2184_Adeno-
associated_virus_isolate_AAVpo4_capsid_protein_VP1_gene,_complete_cd
s/25-143
-------------------------
MAHPNRSPTSRSRTTPVVLYCLDIIIWDPSTDSTRESPSTERTLLRE
STTSRTTSSFRRETTPTSSTTTRTPSFRRSSRTTPPLGATSERQSFRPRKGFSNLLAWLKRLLRRLQP
R-S-
GR
>AAVpo8|KM349849_1/27-145
-------------------------
MAHPNRSPISKNKTTPVVLYCLDIIIWDPSTDSTRESPSTERTLLRE
STISRTTSSSRRETTPTSSTTTRTPSFRRSSPTTPPLGATSERQSFRPRRGFSNLLAWLKSLLRRLRQ
R-R-
GL
>BovineAAV|NC_005889_1_cds_YP_024971_1/2-144
LLTTLQIGWN-R-
SATAFVNFSALRRVPRNPRPINRSKITLEVLCFLGTSILVLGTALIRAILSILLTRLPE
STTSPTRNSLRRAITLTSSTTTRTQSFRRNSLLTLLLGETLGRLFSRLKRGFSNLLAWLRRRIKRRLR
QK-R
GL
>AAV5|NC_006152_1_cds_YP_068409/2-142
LLITLQIGWK-K-
LVKVFASFWALKRAHRNQNPISSIKIKPVVLCCLVITISDPETVSIEESLSTGQTRSRE
STTSRTTSSLRRETTPTSSTTTRTPSFRRSSPTTHPSGETSERQSFRPRKGFSNLLAWLKRVLRRPLP
E-S-
G-
```

S2 Alignment: MAAP contains no internal methionines and no or few tyrosines

This file contains the sequence alignments S2A, S2B, and S2C, corresponding respectively to the protein MAAP of dependoparvoviruses A, dependoparvoviruses B, and porcine AAVs.

S2A Alignment. MAAP contains no tyrosine or internal methionine in most strains of *dependoparvovirus A*

Sequence alignment of MAAP in *dependoparvovirus A*, in PFAM format. The first aa is represented as L but could be M, since translation starts from a non-canonical CTG codon (see main text).

MAAP contains a Tyrosine (Y, in magenta) only in 10 sequences out of 125 non-redundant ones available. Their name and accession number are highlighted in magenta to the left of the alignment.

MAAP contains a Methionine (M, in green) only in 4 strains, whose name and accession number are highlighted in green to the left of the alignment.

```
AAV2|NC_001401.2_cds_YP_680426.1_5/27-145                   LAHHHQSPQSGIRTTAGVLCFLGTSTSDPSTDSTRESRSTRQTPRPSSTTKPTTGSSTAETTRTSSTTTPTRSFRSALKKIRLLGATSDEQSSRRKRGFLNLWAWLRNLLRRLREKRGR
lcl|MK139247.1_cds_QDH44106.1_5/27-145                      LAHHHQSPQSGIRTTAGVLCFLGTSTSDPSTDSTRESRSTRQTPRPSSTTRPTTGSSTAETTRTSSTTTPTRSFRSALKKIRLLGATSDEQSSRRKRGFLNLWAWLRNLLRRLREKRGR
AAVhu.35|AY530599.1 /27-145                                  LAHHHQSPQSGIRTTAGVLCFLGTSTSDPSTDSTRESRSTRQTPRPSSTTKPTTGSSTAETTRTSSTTTPTRSFRSALKKIRLLGATSDEQSSRRKRGYLNLWAWLRNLLRRLREKRGR
AAV_CHC2731_AAV.FL.linear|MK139293.1/27-145                 LAHHHQSPQSGIRTTAGVLCFLGTSTSDPSTDSTRESRSTRQTPRPSSTTRPTTGSSTAETTRTSSTTTPTRSFRSALKKIRLLGATSDEQSSRRKRGFLNLWAWLRNVLRRLREKRGR
lcl|MK139288.1_cds_QDH44387.1_5/27-145                      LAHHHQSPQSGIRTTAGVLCFLGTSTLDPSTDSTRESRSTRQTPRPSSTTRPTTGSSTAETTRTSSTTTPTRSFRSALKKIRLLGATSDEQSSRRKRGFLNLWAWLRNLLRRLREKRGR
lcl|AY530618.1_cds_AAS99303.1_1/27-145                      LAHHHQSPQSGIRTTAGVLCFLDTSTSDPSTDSTRESRSTRQTPRPSSTTRPTTGSSTAETTRTSSTTTPTRSFRSALKKIRLLGATSDEQSSRRKRGFLNLWAWLRNLLRRLREKRGR
lcl|MK139253.1_cds_QDH44148.1_5/27-145                      LAHHHQSPQSGIRTTAGVLCFLGTSTSDPSTDSTRESRSTRQTPRPSSTTKPTTGSSTAETTRTSSTTTPTRSFRSALKKIRLLGATSDEQSSRRKRGFLNLWAWLRNLLRRLLEKRGR
lcl|MK163935.1_cds_QDH44515.1_5/27-145                      LAHHHQSPQSGIRTTAGVLCFLGTSTSDPSTDSTRESRSTRQTPRPSSTTRPTTGSSTAETTRTSSTTTPTRSFRSALKKIRLLGATSDEQSSRQKRGFLNLWAWLRNLLRRLREKRGR
lcl|AY530620.1_cds_AAS99305.1_1/27-145                      LAHHHQSPQSGIRTTAGVLCFLGTSTSDPSTDSTRESRSTRQTPRPSSTTRPTTGSSTAETTRTSSTTTPTRSFRSALKKIRLLGATSDEQSSRQKRGFLNLWAWLRSLLRRLREKRGR
lcl|MK139287.1_cds_QDH44380.1_5/27-145                      LAHHHQSPQSGIRTTAGVLCFLGTSTSDPSTDSTRESRSTRQTPRPSSTTRPTTGSSTAETTRTSSTTTPTRSFRSALKKIRLLGATSDEQSSRRKRGFLNLWAWLRSLLKRLREKRGR
lcl|AY530578.1_cds_AAS99263.1_1/27-145                      LAHHHQSPQSGIRTTAGVLCFLGTSTSDPSTDSTRESRSTRQTPRPSSTTRPTTGSSTAETTRTSSTTTPTRSFRSALKKIRLLGATSDEQSSRQKRGFLNLWAWLRSLLKRLREKRGR
lcl|MK139243.1_cds_QDH44082.1_5/27-145                      LAHHHQSPQSGIRTTAGVLCFLGTSTSDPSTDSTRESRSTRQTPRPSSTTKPTTGSSTAETTRTSSTTTPTRSFRSVLKKIRLLGATSDEQSSRRKRGFLNLWAWLRNLLRRLREKRGR
lcl|MK139289.1_cds_QDH44394.1_5/27-145                      LAHHHQSPQSGIRTTAGVLCFLGTSTSDPSTDSTRESRSTRQTPRPSSTTRPTTGSSTAETTRTSSTTTPTRSFRSVLKKIRLLGATSDEQSSRRKRGFLNLWAWLRNLLRRLREKRGR
lcl|MK139273.1_cds_QDH44284.1_5/27-145                      LAHHHQSPQSGIRTTAGVLCFLGTSTSDPSTDSTRESRSTRQTPRPSSTTRPTTGSSTAETTRTSSTTTPTRSFRSVLKKIRLLGATSDEQSSRRKRGFLNLWAWLRNLLKRLREKRGR
lcl|AY530577.1_cds_AAS99262.1_1/27-145                      LAHHHQSPQSGIRTTAGVLCFLGTSTSDPSTDSTKESRSTRQTPRPSSTTRPTTGSSTAETTRTSSTTTPTRSFRSVLKKIRLLGATSDEQSSRRKRGFLNLWAWLRNLLRRLREKRGR
lcl|MK139298.1_cds_QDH44457.1_5/27-145                      LAHHHQSPQSGTRTTAGVLCFLGTSTSDPSTDSTRESRSTRQTPRPSSTTRPTTGSSTAETTRTSSTTTPTRSFRSVLKKIRLLGATSDEQSSRRKRGFLNLWAWLRNLLRRLREKRGR
lcl|MK139296.1_cds_QDH44443.1_5/27-145                      LAHHHQSPQSGIRTTAGVLCFLGTSTSDPSTDSTRESRSTRQTPRPSSTTRPTTGSSTAETTRTSSTTTPTRSFRSVLKKIRLLGATSDEQSSRRKRGFLNLWAWLRSLLRRLREKRGR
lcl|MK139285.1_cds_QDH44366.1_3/27-145                      LAHHHQSPQSGIRTTAGVLCFLGTSTSDPSTDSTRESRSTRQTPRPSSTTRPTTGSSTAETTRTSSTTTPTRSFRSVLKKIRLLGATSDEQSSRRKRGFLNLWAWLRSLLKRLREKRGR
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lcl|AY530629.1_cds_AAS99314.1_1/27-145                      LAHHHQSPQSGIRTTAGVLCFLGTSTSDPPTDSTKESRSTRQTPRPSSTTRPTTGSSTAETTRTSSTTTPTRSFRSVLKKIRLLGATSDEQSSRRKRGFLNLWAWLRNLLRRLREKRGR
lcl|MK139270.1_cds_QDH44263.1_5/27-145                      LAHHHQSPQSGIRTTAGVLCFLGTSTSDPSTDSTRESRSTRQTPRPSSTTRPTTGSSTAETTRTSSTTTPTRSFRIALKKIRLLGATSDEQSSRRKRGFLNLWAWLRNLLKRLREKRGR
lcl|MK139283.1_cds_QDH44354.1_5/27-145                      LAHHHQSPQSGIRTTAGVLCFLGTSTSDPSTDSTKESRSTRQTPRPSSTTRPTTGSSKAETTRTSSTTTPTRSFRSALKKIRLLGATSDEQSSRRKRGFLNLWAWLRNLLRRLREKRGR
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lcl|AY530576.1_cds_AAS99261.1_1/27-145                      LAHHHQSSQSGIRTTAGVLCFLGTSTSDPSTDSTKESRSTRQTPRPSSTTRPTTGSSTAETTRTSSTTTPTRSFRSVLKKIRLLGATSDEQSSRRKRGFLNLWAWLRNLLRRLREKRGR
lcl|MK139291.1_cds_QDH44408.1_5/26-143                      LAHHHQSPQSGIRTTAGVLCFLGTSTSDPSTDST-ESRSTRQTPRPSNTTRPTTGSSTAETTRTSSTTTPTRSFRSALKKIRLLGATSDEQSSRRKRGFLNLWAWLRNLLRRLREKRGR
AAVhu.34|AY530598.1/27-145                                  LAHHHQSPQSGIRTTAGVLCFLGTSTSDPSTDSTRESRSTRQTPRPSSTTKPTTGSSTAETTRTSSTTTPTRSFRSALKKIRPLGATSDEQSSRRKRGYLNLWAWLRNLLRRLREKRGR
lcl|MK139254.1_cds_QDH44155.1_5/27-145                      LAHRHQSPQSGIRTTTGVLCFLGTSTSDPSTDSTRESRSTRQTPRPSSTTRPTTGSSTAETTRTSSTTTPTRSFRSALKKIRLLGATSDEQSSRRKRGFLNLWAWLRNLLRRLREKRGR
lcl|MK163932.1_cds_QDH44491.1_5/27-145                      LAHHHQSPQSGIRTTAGVLCFLGTSTSDPSTDSTRESRSTRQTPRPSSTTRPTTGSSTAETTRTSSTTTPTRSFRSALKKIRLLGATSDEQSSRRKRGFLNLWAWLRNLLRRLREKRGR
lcl|AY530585.1_cds_AAS99270.1_1/27-145                      LAHHHQSPQSGIRTTAGVLCFLGTSTSDPSTDSTRGSRSTRQTPRPSSTTRPTTGSSTAETTRTSSTTTPTQSFRSALKKIRLLGATSDEQSSRRKRGFLNLWAWLRNLLRRLREKRGR
lcl|AY530602.1_cds_AAS99287.1_1/27-145                      LAHHHQSPQSGIRTTAGVLCFLGTSTSDPSTDSTRGSRSTRQTPRPSSTTRPTTGSSTAETTRTSSTTTPTQSFRSALKKIRLLGATSDEQSSRRKRGFLNLWAWLRSLLRRLREKRGR
lcl|AY530622.1_cds_AAS99307.1_1/27-145                      LAHHHQSPQSGIRTTAGVLCFLGTSTSDPSTDSTRGSRSTRQTPRPSSTTRPTTGSSTAETTRTSSTTTPTRSFRSALKKIRLLGATSDEQSSRQKRGFLNLWAWLRNLLKRLREKRGR
lcl|MK139281.1_cds_QDH44340.1_5/27-145                      LAHHHQSPQSGIRTTAGVLCFLGTSTSDPSTDSTRGSRSTRQTPRPSSTTRPTTGSSTAETTRTSSTTTPTRSFRSVLKKIRLLGATSDEQSSRRKRGFLNLWAWLRNLLRRLREKRGR
lcl|MK139248.1_cds_QDH44113.1_5/27-145                      LAHHHQSPQSGIRTTAGVLCFLGTSTSDPSTDSTRGSRSTRQTPRPSSTTRPTTGSSTAETTRTSSTTTPTRSFRSVLKKIRLLGATSDEQSSRRKRGFLNLWAWLRNLLKRLREKRGR
lcl|AY530628.1_cds_AAS99313.1_1/27-145                      LAHHHQSPQSGIRTTAGVLCFLGTSTSDPSTDSTRGSRSTRQTPRPSSTTRPTTGSSTAETTRTSSTTTPTRSFRSVLKKIRLLGATSDEQSSRRKRGFLNLWAWLRDLLRRLREKRGR
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lcl|AY695372.1_cds_AAU05362.1_2/27-145                      LAHHHQSPQSGTRTTAGVLCFLGTSTSDPSTDSTRGSRSTRQTPRPSSTTRPTTGSSTAETTRTSSTTTPTRSFRSVLKKIRLLGATSDEQSSRRKRGFLNLWAWLRNLLKRLREKRGR
lcl|MK139272.1_cds_QDH44277.1_5/27-145                      LAHHHQSPQSGIRTTAGVLCFLGTSTSDPSTDSTRGSRSTRQTPRPSSTTRPTTGSSTAETTRTSSTTTPTRSFRSALKKIRLLGETSDEQSSRRKRGFLNLWAWLRSLLKRLREKRGR
lcl|MK139274.1_cds_QDH44291.1_5/27-145                      LAHHHQSPQSGIRTTTGVLCFLGTSTSDPSTDSTRGSRSTRQTPRPSSTTRPTTGSSTAETIRTSSTTTPTRSFRSVLKKIRLLGATSDEQSSRRKRGFLNLWAWLRNLLKRLREKRGR
lcl|MK139295.1_cds_QDH44436.1_5/27-145                      LAHHHQSPQSGTRTTVGVLCFLGTSTSDPSTDSTKESRSTRQTPRPSNTTRPTTGSSTAETTRTSSTTTPTRSFRSVLKKIRLLGATSDEQSSRRKRGFLNLWAWLRNLLRRLREKRGR
lcl|MK139259.1_cds_QDH44190.1_5/27-145                      LAHHHQSPQSGTRTTAGVLCFLGTSTSDPSTDSTKESRSTRQTPRPSSTTRPTTGSSTAETTRTSSTTTPTRSFRSVLKKIRLLGATSDEQSSRRKRGFLNLWAWLRSLLKRLREKRGR
lcl|AY530608.1_cds_AAS99293.1_1/27-145                      LAHHHQSPQSGIGTTAGVLCFLGTSTSDPSTDSTRESRSTRQTPRPSSTTKPTTGSSTAETTRTSSTTTPTRSFRSALKKIRLLGATSDEQSSRRKRGFLNLWAWLRNLLRRLREKRGR
lcl|AY530610.1_cds_AAS99295.1_1/27-145                      LAHHHQSPQSGIGTTAGVLCFLGTSTSDPSTDSTRESRSTRQTPRPSSTTKPTTGSSTAETTRTSSTTTPTRSFRSALKKIRLLGATSDEQSSRRKRGFLNLWAWLGNLLRRLREKRGR
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lcl|AY530613.1_cds_AAS99298.1_1/27-145                      LAHHHQSPQSGIRTTAGVLCFLGTSTSDPSTDSTRESRSTRQTPRPSSTTKPTTGSSTAETTRTSSTTTPTRSFRSALKKIRLLGATSDEQSSRRKRGFLNLWAWLGNLSRRLQEKRGR
lcl|AY530584.1_cds_AAS99269.1_1/27-145                      LAHHHQSPQSGIRTTAGVLCFLGTSTSDPSTDSTRESRSTRQTPRPSSTTRPTTGSSTAETTRTSSTTTPTRSFRSVLKKIRLLGATSDEQSSRPKRGFLNLWAWLRNLLRRLREKRGR
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lcl|AY695375.1_cds_AAU05368.1_2/27-145                      LAHHHQSPQSGIRTTAGVLCFLGTSTSDPSTDSTRGSRSTRQTPRPSSTTRPTTGSSTAETTRTSSTTTPTRSFRSVLKKIRLLGATSDEQSSRPKRGFLNLWAWLRSLLRRLREKRGR
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lcl|AY530586.1_cds_AAS99271.1_1/27-145                      LAHHHQSPQSGIRTTAGVLCFLGTGTSDPSTDSTRESRSTRQTPRPSSTTRPTTGSSTAETTRTSSTTTSTRSFRSVLKKIRLLGATSDEQSSRPKRGFLNLWAWLRNLLRRLREKRGR
lcl|AY530581.1_cds_AAS99266.1_1/27-145                      LAHHRQSPQSGIRTTAGVLCFLGTSTSDPSTDSTRESRSTRQTPRPSSTTRPTTGSSTAETTRTSSTTTPARSFRSALKKIRLLGATSDEQSSRPKRGFLNLWAWLRSLLKRLREKRGR
CHC2320_AAV.FL.linear|MK139290.1/26-144                     LAHHHQSPQSGIRTTAGVLCFLGTSTSDPSTDSTRESRSTRQTPRPSSTTRPTTGSSTAETTRTSSTTTPTRSFRSVLKKIRLLGATSDEQSSRRKRGFLKLWAWLRNMLRRLRVKRGR
lcl|AY530625.1_cds_AAS99310.1_1/27-145                      LAHHHQSPQSGIRTTAGVLCFLGTSTLDPSTDSTRESRSTRQTPRPSSTTRPTTGSSTAETTRTSSTTTPTRSSRSVLKKIRLLGATSDEQSSRRKRGFLNLWAWLRNLLRRLREKRGR
lcl|AY530624.1_cds_AAS99309.1_1/27-145                      LAHHHQSPQSGIRTTAGVLCFLGTSTLDPSTDSTRESRSTRQTPRPSSTTRPTTGSSTAETTRTPSTTTPTRSSRSVLKKIRLLGATSDEQSSRRKRGFLNLWAWLRNLLRRLREKRGR
lcl|AY530591.1_cds_AAS99276.1_1/27-145                      LAHHHQSPQSGIRTAAGVLCFLGTSTSDPSTDSTRESRSTRQTPRPSSTTRPTTGSSTAETTRTSSTTTPTRSFRSALKKIRLLGATSDEQSSRQKRGFLNLWAWLRSLLKRLREKRDR
lcl|MK139258.1_cds_QDH44183.1_5/27-145                      LAHHHQSPQSGIKTTAGVLCFLGTSTSDPSTDSTRESRSTRQTPRPSSTTRPTTGNSTAETTRTSSTTTPTRNFRSALKKIRLLGATSDEQSSRQKRGFLNLWAWLRNLLRRLLEKRGR
lcl|AY695376.1_cds_AAU05370.1_2/27-145                      LAHHRQSPQSGIRTTAGVLCFLGTSTSDPSTDSTKESRSTRQTPRPSSTTRPTTGSSTAETTRTSSTTTPTRSFRSVLKKIRLLGATSDEQSSRQKRGFLNLWAWLRSLLRRLLEKRGR
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lcl|EU368915.1_cds_ACB55307.1_1/27-145                      LAHHHQSPQSGIRTTAGVLCFLGTSTSDPSTDSTRESRSTRQTPRPSSTTRPTTGSSTAETTRTSSTTTPTQSFRSALKKIRLLGATSDEQSSRQKRGFWNLWAWLRSLLRRLREKRGR
lcl|MK139264.1_cds_QDH44221.1_3/27-144                      LAHHHQSPQSGIR-TAGVLCFLGTSTSDPSTDSTRENRSTRQTPRPSNTTRPTTGSSTADTSRTSSTTTPTRSFRSALKKIRLLGATSDEQSSRRKRGFLNLWAWLRNLLRRLREKRGR
lcl|MK139252.1_cds_QDH44141.1_5/27-144                      LAHHHQSPQSGIRTTAGVLCFLGTSTSDLSTDSTRESRSTRQTPRPSSTTRPTTGSSTAETTRTSSTTTPTRSFRSVLKKIRLLGATSDEQSSRRKRGFLN-WAWLRNLLRRLREKRGQ
AAVhu.T70|AY695373.1_cds_AAU05364.1_2/27-145                LAHHHQSPQSGIRTTAGVLCFLGTSTSDPSTDSTKESRSTRQTPRPSSTTRPTTGSWKAETTRTSSTTTPTRSFRSVLKKIRLLGATSDEQYSRRKRGFLNLWAWLRSLLRRLREKRGR
lcl|MK139279.1_cds_QDH44326.1_5/27-145                      LAHHHQSPQSGIRTTAGVLCFLGTSTSDPSTDSTKESRSTRQTPRPSSTTRPTTGSSTAETTRTSSTTTPTRSSRSALKKIRLLGATSQEQFSRQKRGFLNLWAWLRNLLRRLREKRGR
lcl|AY530619.1_cds_AAS99304.1_1/27-144                      LAHH-QSPQSGIRTTAGVLCFLDTSTSDPSTDSTRESRSTRQTPRPSSTTRPTTGSSTAETTRTSSTTTPTRSFRSALKKIRLLGATSDEQSSRRKRGFLNLWAWLRNLLRRLREKRGP
lcl|MK139278.1_cds_QDH44319.1_5/27-142                      LAHHHQSPQSGIRTTAGVLCFLGTSTSDPS-DSTKESRSTRQTPRPSSTTRPTTGSSTAETTRTSSTTTPTRSFRSALKKIRLLGATSDEQSSRRKRGFL-LWA-LRNLLRRLREKRGR
lcl|EU368916.1_cds_ACB55308.1_1/27-145                      LAHHHQSPQSGIRTTAGVLCFLGTSTSDPSTDSTRESRSTRQTPRPSSTTKPTTGSSTAETTRTSSTTTPTRSFRSALKKIRLLGATSGEQSSRPRSGFSNLSVWLRKALRRLLERNVR
lcl|AY530609.1_cds_AAS99294.1_1/27-145                      LAHHHQSPQSGIRTTAGVLCFLGTSTSDPSTDSTRESRSTRQTPRPSSTTKPTTGSSTAETTRTSSTTTPTRSFRSALKKIRLLGATSGGQSSRPRSGFSNLSVWLRKALRRLLERNVR
lcl|AY530595.1_cds_AAS99280.1_1/27-145                      LAHHHQSPQSGIRTTAGVLCFLGTSTSDPSTDSTRGSRSTRQTPRPSSTTRPTTGSSTAETTRTSSTTTPTQSFRSALKKIRLLGATSDEQSSRRKRGFLNLCGLV*GNLLRRLREKRG
AAVhu.32|AY530597.1_cds_AAS99282.1_1/27-145                 LAHHHQSPQSGIRTTAGVLCFLGTSTSDPATDSTRGSRSTQQTRRPSSTTRPTTSSSRPETTRTSSTTTPTPSSRSGSKKIRLLGATSGEQSSRPKRGFLNLLVWLRKRLRRLLERRGL
lcl|AY530596.1_cds_AAS99281.1_1/27-145                      LAPHHQSPQSGIRTTAGVLCFLGTSTSDPATDSTRGSRSTQQTRRPSSTTRPTTSSSRPETTRTSSTTTPTPSSRSGSKKIRLLGATSGEQSSRPKRGFLNLLVWLRKRLRRLLERRGL
lcl|AY530579.1_cds_AAS99264.1_1/27-145                      LEPLNPRQINNIKTTLEVLCFRVTNTLDPATDSTRGSRSTQQTRRPSSTTRPTTSSSRPETTRTSSTTTPTPSSRSGSKKIRLLGATSGEQSSRPKRGFLNLLVWLRKRLRRLLERRGL
AAVch.5|AY243021.1_cds_AAO88207.1_1/27-145                  LAHHRRNLTNNTGTTVGVLCFLGTSTSDPSTDSTKESRSTRQTPRPSSTTKPTTTSSSKGTTRTSNTTTRTLNFRSVFKKIRLSGATSGEQSSRPKRGYSSLLVWLRKLLRRLLEKRDL
AAV12|DQ813647.1_cds_ABI16639.1_2/27-145                    LELHNPRPTNSIRTTAGVLCFLGTSTSDPSTDSTRESRSTRQTPRPSSTTRPTTSSSSRGTTRISSTTTPTPSSSSAWRPTPLLGATSGEQSSRPKRGFSSLWVWLKRALKRLLERNAH
lcl|MK139267.1_cds_QDH44242.1_5/27-145                      LEPLNPRQINNIKTTLGVLCFRVTNTLDPATDSTRGSRSTQQTRRPSSTTRHTTSSSRPETTRTSSTTTPTRSFRSVLKKIRLLGATSDEQSSRRKRGFSNLWAWLRNLLRRLREKRGR
AAV13|EU285562.1_cds_ABZ10812.1_2/26-144                    LEPLNPRQINNIRTTLGVLCFRVTNTSDPATDLTRGNPSTQRTRQPSNTTRPTTSSSRPVTTPTSSTTTPTPSFRSVFKKIRLLGATSDEQSSRPKRGSLSLWVWLRKRLRRLLEKRDL
AAV4|NC_001829_1/26-144                                     LEPLNPRQINNIRTTLGVLCFRVTNTSDPATDSTRGNPSTQRTRQPSSTTRPTTSSSRPVTTPTSSTTTPTRSSSSGFRATHRLGATSAEQSSRPKRGFLNLLVWLSKRVRRLLERRDR
AAV3B|AF028705.1_cds_AAB95452.1_2/27-145                    LESLNPKRTNNTRTTVGVLCFRVTNTSDPVTDSTKESRSTRRTRQPSNTTKLTTSSSRPVTTRTSSTTTPTPSFRSVFKKIRLLGATLAEQSSRPKRGSLSLLVWLRKQLKRLLERRGL
AAVrh.23|AY243005.1_cds_AAO88191.1_1/27-145                 LEPRNPKPTSKSRTTAGVWCFLATSTSDPSTDSTRESRSTRQTPRPSSTTRPTTSSSSRGTTRTSSTTTPTPSFRSVFKKIRLLGATSGEQSSRPRSGFSNLSVWLRKALRRLLERRDR
lcl|AY243018.1_cds_AAO88204.1_1/27-145                      LEPRNPKPTSKSRTTAGVWCFLATSTSDPSTDSTRESRSTRQTPRPSSTTRPTTSSSSRGTTRTSSTTTPTPSFRSVFKKIRLLGATSGEQSSRPRSGFSNLSVWLRKALRRLPERRDP
lcl|AY243019.1_cds_AAO88205.1_1/27-145                      LEPRNPKPTSKSRTTAGVWCFLATSTSDPSTDSTRESRSTRQTPRPSSTTRPTTSSSSRGTTRTSSTTTPTPSFRSVFKKIRLLGATSGEQSSRPRSGFSNLSVWLRKSLRRLLERRDP
lcl|AY243014.1_cds_AAO88200.1_1/27-145                      LEPRNPKPTSKSRTTAGVWCFLATSTSDPSTDSTRESRSTRQTPRPSSTTRPTTSSSSRGTTRTSSTTTPTPSFRSVFKKIRLLGATSGEQSSRPRSGFSNLSVWLRKALRRLLERRDP
lcl|EU368913.1_cds_ACB55305.1_1/27-145                      LEPRNPKPTSKSRTTAGVWCFLATGTSDPSTDSTRESRSTRQTPRPSSTTRPTTSSSSRGTTRTSSTTTPTPSFRSVFKKIRLLGATSGEQSSRPRSGFSNLSVWLRKALRRLLERRDP
lcl|AY243010.1_cds_AAO88196.1_1/27-145                      LEPRNPKPTSKSRTTAGVWCFLATSTSDPSTDSTRESRSTRQTPRPSSTTRPTTSSSSRGTTRTSSTTTPTPSFRSVFKKIRLLGATSGEQSSGPRSGFSNLSVWLRKALRRLLERRDP
lcl|AY243016.1_cds_AAO88202.1_1/27-145                      LEPRNPKPTSKSRTTAGVWCFLATSTSDPSTDSTRESRSTRQTPRPSSTTRPTTSSSSRGTTRTSSTTTPTLSFRSVFKKIRLLGATSGEQSSRPRSGFSNLSVWLRKALRRLLERRDP
lcl|AY243023.1_cds_AAO88209.1_1/27-145                      LEPRSPKPTSKSRTTAGVWCFLATSTSDPSTDSTRGSPSTRRTQRPSSTTRPTTSSSKRVTIRTCGITTPTPSFRSVCKKIRLLGATSDEQSSRPRSGFSNLSVWLRKALRRLLERRDR
lcl|EU368921.1_cds_ACB55313.1_1/27-145                      LEPRSPKPTSKSRTTAGVWCFLATSTSDPSTDSTRGSPSTRRTQRPSSTTRPTTSSSKRVTIRTCGITTPTPSFRSVCKKIRLLGATSGEQSSRPRSGFSNLSVWLRKLLRRLLERRDR
lcl|AY530567.1_cds_AAS99252.1_1/27-145                      LEPRNPKPTSRSRTTAGVWCFLATSTSDPSTDSTRGSPSTRRTQRPSSTTRPTTSSSKRVTIRTCGITTPTPSFRSVCKKIRLLGATSGEQSSRPRSGFSNLSVWLRKLLRRLLERRDR
lcl|AY243022.1_cds_AAO88208.1_1/27-145                      LEPRSPKPTSKSRTTAGVWCFLATSTSDPSTDSTRGSPSTRRTQRPSSTTRPTTSSSKRVTIRTCGITTPTPSFRSVCKKIRLLGATSGEQSSRPRSGFSNLSVWLRKALRRLLERRDR
lcl|AY243015.1_cds_AAO88201.1_1/27-145                      LEPRNPKPTSKSRTTAGVWCFLATSTSDPSTDSTRGSPSTRRTQRPSSTTRPTTSSSKRVTIRTCGITTPTPSFRSVCKKIRLLGATSGEQSSRPRSGFSNLSVWLRKALRRLLERRDR
AAVhu.17|AY530582.1_cds_AAS99267.1_1/27-145                 LEPRNPKPTSKSRTTAGVWCFLAASTSDPSTDSTRGSPSTRRTQRPSSTTRPTTSSSKRVTIRTCGITTPTPSFRSVCKKIRLLGATSGEQSSRPRSGFSNLSVWLRKALRRLLERRDR
lcl|AY242997.1_cds_AAO88183.1_1/27-145                      LEPRNPKPTSKSRTTAGVWCFLATSTSDPSTDSTRGSPSTRRTQRPSSTTKPTTSSSKRVTIRTCGIITPTPSFRSVCKKIRLLGATSGEQSSRPRSGFSNLSVWLRKALRRLLERRDR
lcl|AY530565.1_cds_AAS99250.1_1/26-145                      LEPRNPKPTSKSRTTAGVWCFLATSTSDPSTDSTRGSPSTRRTQRPSSTTRPTTSSSKRVTIRTCGIITPTPSFRSVCKKIRLLGATSGEQSSRPRSGFSNLSVWLRKALRRLLERRDR
lcl|AY530572.1_cds_AAS99257.1_1/27-145                      LEPRNPRPTSKSRTTAGVWCFLATSTSDPSTDSTRGSPSTRRTQRPSSTTRPTTSSSKRVTIRTCGIITPTPSFRSVCKKIRLLGATSGEQSSRPRSGFSNLSVWLRKALRRLLERRDR
lcl|AY530560.1_cds_AAS99245.1_1/27-145                      LEPRNPKPTSKSRTTAGAWCFLATSTSDPSTDSTRGSPSTRRTQRPSSTTRPTTSSSKRVTIRTCGITTPTPSFRSVCKKIRLLGATSGEQSSRPRSGFSNLSVWLRKALRRLLERRDQ
lcl|AF513852.1_cds_AAN03857.1_2/27-145                      LEPRSPKPTSKSRTTAGVWCFLATSTSDPSTDSTRGSPSTRRTQRPSSTTRPTTSSCRRVTIRTCGITTPTPSFRSVCKKIRLLGATSGEQSSRPRSGFSNLSVWLRKALRRLLERRDR
lcl|AY530556.1_cds_AAS99241.1_1/27-145                      LEPRSPKPTSKSRTTAGVWCFLATSTSDPSTDSTRGSPSTRRTQRPSSTARPTTSSCRRVTIRTCGITTPTPSFRSVCKKIRLLGATSGEQSSRPRSGFSNLSVWLRKALRRLLERRDR
lcl|AY530569.1_cds_AAS99254.1_1/27-145                      LEPRSPKPTSKSRTTAGVWCFLATSTSDPSTDSTRGSPSTRRTQRPSSTTRPTTSSCRRVTIRTCGIITPTPSFRSVCKKIRLLGATSGEQSSRPRSGFSNLSVWLRKALRRLLERRDR
lcl|AY530564.1_cds_AAS99249.1_1/27-145                      LEPRNPKPTSKSRATAGVWCFLATSTSDPSTDSTRGSPSTRRTQRPSSTTRPTTSSLKRVTIRTCGIITPTPSFRSVCKKIRLLGATSGEQSSRPRSGFSNLSVWLRKALRRLLERRDR
lcl|EU368920.1_cds_ACB55312.1_1/27-145                      LEPRNPKPTSKSRTTAGVWCFLATSTSDPSTDSTRGSPSTRRTQRPSSTTRPTTSSSKRVTIRTCGITTPTPSFRSACKKIRHLGATSGEQSSRPRSGFSNLSVWLRKALRRLLERRDP
lcl|AY243000.1_cds_AAO88186.1_1/27-145                      LEPRNPKPTSKSRTTAGVWCFLATSTSDPSTDSTRGSPSTRRTQRPSSTTRPTTSSSKRVTIRTCGITTPTPSFRSVCKKIRHLGATSGEQSSRPRSGFSNLSVWLRKALRRLLERRDP
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AAVcy.2|AY243020.1 /27-145                    LEPRNPKPTSKSRTTAGVWCFLATSTSDPSTDSTRGSPSTRRTQRPSSTTRPTTSSSMRVTTRTCGITTPTPSFRSVCKKIRHLGATSGEQSSRPRSGFSNLSVWLRKALRRLLQRRDR
AAV7|NC_006260.1_cds_YP_077178.1_2/27-145     LEPRNPKPTSKSRTTAGVWCFLATSTSDPSTDSTRGSPSTRRTQRPSSTTRPTTSSSKRVTIRTCGITTPTPSFRSVCKKIRHLGATSGEQSSRPRSGFSNLSVWLRKALRRLLQRRDR
lcl|AY243006.1_cds_AAO88192.1_1/27-145        LEPRNPKPTSKSRTTAGVWCFLATSTSDPSTDSTRESRSTRRTQRPSSTTRPTTSSSKRVTIRTCGITTPTPSFRSVFKKIRLLGATSGEQSSRPRSGFSNLSVWLRKALRRLLERRDP
lcl|AY243004.1_cds_AAO88190.1_1/27-145        LEPRNPKPTSKSRTTAGVWCFLATSTSDPSTDSTRGSPSTRRTQRPSSTTRPTTSSSKRVTIRTCGITTPTPSFRSVFKKIRLLGATSGEQSSRPRSGFSNLSVWLRKALRRLLERRDP
lcl|KT984498.1_cds_APD78414.1_2/27-145        LEPRNPKPTSKSRTTAGVWCFLATSTSDPSTDSTRGSPSTRRTQRPSSTTRPTTSSSKRVTIRTCGITTPTPSFRSVCKKIRLLGATSGEQSSRPRRGFSNLLVWLRKVLRRLLERNVR
AAV6R2|EU368911.1_cds_ACB55303.1_1/27-145     LEPRNPKPTSKSRTTAGVWCFLATSTSDPSTDSTRGSPSTRRMQRPSSTTRPTTSSSKRVTIRTCGITTPTPSFRSVCKKIRLLGATSGEQSSRPRRGFSNLLVWLRKVLRRLLERNVR
AAV1|NC_002077.1_cds_NP_049542.1_2/27-145     LEPRSPKPTSKSRTTAGVWCFLATSTSDPSTDSTRGSPSTRRTQRPSSTTRPTTSSSKRVTIRTCGITTPTPSFRSVCKKIRLLGATSGEQSSRPRSGFSNLSVWLRKALRRLLERNVR
lcl|DQ180604.1_cds_ABA71699.1_2/27-145        LEPRNPKPTSKSRTTAGVWCFLATSTSDPSTDSTRGSPSTRRTQRPSSTTRPTTSSSKRVTIRTCGITTPTPSFRSVCKKIRLLGATSGEQSSRPRSGFSNLLVWLRKALRRLLERNVR
lcl|AY530606.1_cds_AAS99291.1_1/27-145        LEPPSPRPTSRSRTTAGVWCFLATSTSDPSTDSTRGSPSTRRTQRPSSTTRPTTSSSKRVTIRTRGITTPTPSFRSVCKKIRLLGATSGEQSSRPRSGFSNLSVWLRKLLRRLLERRDR
lcl|EU368923.1_cds_ACB55315.1_1/27-145        LEPPSPRPTSRSRTTAGVWCFLATSTSDPSTDSTRGSPSTRRTQRPSSTTRPTTSSSKRVTIRTCGITTPTPSFRSVCKKIRLLGATSGEQSSRPRSGFSNLSVWLRKLLRRLLERRDR
lcl|AY530605.1_cds_AAS99290.1_1/27-145        LEPPSPRPTSRSRTTAGVWCFLATSTSDPSTDSTRGSPSTRRTQRPSSTTRPTTSSSKRVTIRTCGITTPTPSFRSVCKKIRLLGATSGEQSSRPRSGFSNLSVWLRKRLRRLLERRDR
AAVhu.67|AY530627.1_cds_AAS99312/27-145       LEPPSPRPTSRSRTTAGVWCFLATSTSDPSTDSTRGSPSMRRTQRPSSTTRPTTSSSKRVTIRTCGITTPTPSFRSVCKKIRLLGATSGEQSSRPRSGFSNLSVWLRKLLRRLLERRDR
lcl|AY530570.1_cds_AAS99255.1_1/27-145        LEPPSPRPTSRSRTTAGVWCFLATSTSDPSTDSTRGSPSTRRTQRPSSTTRPTTSSSKRVTIRTCGIITPTPSFRSVCKKIRLLGATSGEQSSRPRSGFSNLSVWLRKLLRRLLERRDR
lcl|AY530573.1_cds_AAS99258.1_1/27-145        LEPPSPRPTSRSRTTAGVWCFLATSTSDPSTDSTRGSPSTRRTQRPSSTTRPTTSSSKRVTIRTCGITTPTPSSRSVCKKIRLLGATSGEQSSRPRSGFSNLSVWLRKLLRRLLERRDR
AAV.rh38AY530558.1_cds_AAS99243.1_1/27-145    LEPPSPRPTSRSRTTAGVWCFLATSTSDPSTDSTRGSPSTRRTQRPSSTTRPTTSSSKRVTIRTCGITTPTPSFRSVYKKIRLLGATSGEQSSRPRSGFSNLSVWLRKLLRRLLERRDR
AAV hu.41|AY530604.1_cds_ /27-145             LEPPSPRPTSRSRTTAGVWCFLATSTSDPSTDSTRGSPSTRRTQRPSSTTRPTTSSSKRVTIRTCGITTPTPSFRSVYKKIRLLGATSGEQSSRPRSGFSNLSVRLRKLLRRLLERRDR
AAVrh32.33|EU368926.1/27-145                  LEPPSPRPTSRSRTTAGVWCFLATSTSDPSTDSTRGSPSTRRTQRPSSTTRPTTSSSKRVTIRTCGITTPTPSFRSVCKKIRLLGATSGEQSSRPRRGYSNLWAWLKKVLRRLLERRDR
AAV11|AY631966.1_cds_AAT46339.1_2/27-145      LEPRSPRPTSRSRTTAGVWCFLATSTSDPSTDSTRGSPSTRRTQRPSSTTRPTTSSSKRVTIRTCGITTPTPSFRSVCKKIRLLGATSGEQSSRPRRGYSNLWAWLKKVLKRLLERRDR
AAVrh.33|AY243002.1_cds_.1_1/27-145           LEPPSSRPTSRSRTTAGVWCFLATSTSDPSTDSTRGSPSTRRTQRPSSTTRPTTSSSKRVTIRTCGITTPTPSFRSVCKKIRLLGATSGEQSSRPRRGYSNHWAWLKKVLRRLLERRDR
AAVpi.2|AY530554.1_cds_AAS99239.1_1/27-145    LEPRNPKPTSKSRTTAGVWCFLATSTSDPSTDSTRGSPSTRRTPRPSSTTRPTTSSSKRVTIRTCGIITPTPSFKSVCKKIRPLGATSGEQSSRPKRGYSSLWVWLRKALRRLLERSGQ
```

S2B Alignment. MAAP contains no tyrosine or internal methionine *dependoparvovirus B*

Sequence alignment of MAAP in *dependoparvovirus B*. Conventions are the same as in S2A Alignment. The exact first aa is unknown and translation may proceed from a non-canonical start codon (see Figure 3 and main text).

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AAV5|NC_006152_1_cds_YP_068409       LLITLQIGWKKLVKVFASFWALKRAHRNQNPISSIKIKPVVLCCLVITISDPETVSIEESLSTGQTRSRESTTSRTTSSLRRETTPTSSTTTRTPSFRRSSPTTHPSGETSERQSFRPRKGFSNLLAWLKRVLRRP-L-PESG-
AAV-Go_1|DQ335246_2_cds_ABC69726     LLITLQIGWKKLVKVFASFWALKRAHRNRNPISSIKIKPVVLCCLVITISDPETVSIEESLSTGQTRSRESTTSRTTSSLRRETTPTSSTTTRTPSFRRSSPTTHPSGETSERQSFRPRKGFSNLLAWLKRVLRRP-L-PESG-
BovineAAV_BSRI1|KP264981             LLTTLQIGWNRSATAFVNFSALRRVPRNPRPINRSKITLEVLCFLGTSILVLGTALIRAILSILLTRLPESTTSPTRNSLRRAITLTSSTTTRTQSFRRNSLLTLLLEETLGRLFSRLKRGFSNLLAWLRRRIKRRL-RQKRGL
BovineAAV|NC_005889_YP_024971        LLTTLQIGWNRSATAFVNFSALRRVPRNPRPINRSKITLEVLCFLGTSILVLGTALIRAILSILLTRLPESTTSPTRNSLRRAITLTSSTTTRTQSFRRNSLLTLLLGETLGRLFSRLKRGFSNLLAWLRRRIKRRL-RQKRGL
```

S2C Alignment. MAAP contains a single tyrosine in each porcine AAV, and no internal methionine

Sequence alignment of MAAP. Conventions are the same as in S2A Alignment. The first aa is represented as L but could be M, since translation probably starts from a non-canonical CTG codon (see main text).

MAAP contains no Methionine, but contains one Tyrosine (Y, highlighted in magenta) in each of the 20 non-redundant sequence available for porcine AAVs.

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AAVpo8|KM349849.1_cds_AIU56933.1_1/26-145     LAHPNRSPISKNKTTPVVLYCLDIIIWDPSTDSTRESPSTERTLLRESTISRTTSSSRRETTPTSSTTTRTPSFRRSSPTTPPLGATSERQSFRPRRGFSNLLAWLKSLLRRLRQRRGL
AAVpo7|KM349848.1_cds_AIU56932.1_1/27-146     LAHPNRSPTSRSRTTPVVLYCLDIIIWDPSTDSTRESPSTERTLLRESTISRTTSSFRRATTPTSSTTTRTPSFRRSSRTTPPLGATSERQSFRPRKGFSNLLAWLKRLIRRLRQRRGL
lcl|KM349840.1_cds_AIU56924.1_1/27-146        LAHPNRSPTSRSRTTPVVLYCLDIIIWDPSTDSTRESPSTERTLLRESTISRTTSSSRRETTPTSSTTTRTPSFRRSSRTTPPLGATSERQSFRPRRGFSNLLAWLKRLIRRLRQRRGL
lcl|KM349841.1_cds_AIU56925.1_1/27-146        LAHPNRSPTSRSRTTPVVLYCLDIIIWDPSTDSTRESPSTERTLLRESTTSRTTSSSRRETTPTSSTTTRTPSFRKSSRTTPPLGATSERQSFRQRRGFSNLLAWLKSLLRRLRQRRGL
lcl|KM349839.1_cds_AIU56923.1_1/27-146        LAHPNRSPTSRSRTTPVVLYCLDIIIWDPSTDSTRESPSTERTLLRESTTSRTTSSSRRETTPTSSTTTRTPSFRRSSPTTPPLGATSERQSFRPRRGFSNLLAWLKSLLRRLRQRRGL
lcl|KM349844.1_cds_AIU56928.1_1/27-146        LAHPNRNPISRSRTTPVVLYCLDIIIWDPSTDSTRESPSTERTLLRESTTSRTTSSSRRETTPTSSTTTRTPSFRRSSRTTPPLGATSARQSFRPRRGFSNLLAWLKRLLRRLRERRGP
lcl|KM349842.1_cds_AIU56926.1_1/27-146        LAPPNRSPTSRSRTTPVVLYCLDIIIWDPSTDSTRESPSTERTLLRESTTSRTTSSSRRETTPTSSTTTRTPSFRRSSRTTPPLGATSARQSFRPRRGFSNLLAWLKRLLRRLRERRGP
AAVpo4|JX896667_1/1-2184_AAVpo4|JX896667      LAHPNRSPTSRSRTTPVVLYCLDIIIWDPSTDSTRESPSTERTLLRESTTSRTTSSFRRETTPTSSTTTRTPSFRRSSRTTPPLGATSERQSFRPRKGFSNLLAWLKRLLRRLQPRSGR
lcl|JX896665.1_cds_AGA15925.1_1/27-146        LAHPNRSPTSRSRTTPVVLYCLDIIIWDPSTDSTRESPSTERTLLRESTTSRTTSSSRRETTPTSSTTTRTPSFRRSSRTTPPLGATSERQSFRPRKGFSNLLAWLRHLLRRLQPRSGR
lcl|KM349838.1_cds_AIU56922.1_1/27-146        LAHPNRSPTSRSKTTPVVLYCLDIITWDPSTDSTRESLSTERTPLRESTTSRTTSSSRWETTPTSSTTTRTPSFRRSSRTTPPLGATSERQSFRPRKGFSNLLAWLRHLLRRLQPRSGR
lcl|KM349837.1_cds_AIU56921.1_1/27-146        LAHPNRSPTSRSRTTPVVLYCLDIIIWDPSTDSTRESLSTERTPLRESTTSRTTSSSRWETTPTSSTTTRTPSFRRSSRTTPPLGATSERQSFRPRKGFSNLLAWLRHLLRRLRQRRGL
lcl|KM349836.1_cds_AIU56920.1_1/27-146        LAHPNRSPISKNKTTPVVLYCLDIIIWDPSTDSTRESPSTELTRSRESTTSRTTSSSRREITLISSTTTRTPSFRRSSPTTPPLGATSERQSFRPRRGFSNLLAWLKSLLRRLRQRRGL
AVpo5|JX896666_1/26-145                       LAHPNRSPTSRSKTTPVVLYCLDIITWDPATVSTAENLSTGPTRSRESTTSRTTSSSRRETTPTSSTTTRTPSFKRSSRTTPPSGATSARQSFRPRKGFSNLLAWLRILLRRLLKASG-
AVpo1|FJ688147_1/27-146                       LAHPNRSPTSRSKTTPVVLYCLDIITWDPETVSTAENLSTGLTRSRESTTSRTTSSSRRETTPTSSTTTRTPSFRRSSRTTPPSGATSARQSFRPKKGFSNLLAWLRSLLRRLLKASG-
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lcl|KM349834.1_cds_AIU56918.1_1/27-146        LAHPNRSPTSRSKTTPVVLYCLDIITWDPETVSTAENLSTGPTRSRESTTSRTTSSSRRETTPTSSTTTRTPSFKRSSRTIPPSGATSARQSFRPRKGFSNLLAWLRSLLRRLLQESG-
lcl|KM349831.1_cds_AIU56915.1_1/27-146        LAHPNRSPTSRSKTTPVVLYCLDIITWDPETVSTVENLSTGPTRSRESTTSRTTSSSRRETTPTSSTTTRTPSFRRSSRTTPPSGATSARQSFRPRKGFSNLLAWLRSLLRRLLQESG-
lcl|KM349833.1_cds_AIU56917.1_1/27-146        LAHPNRSPTSRSKTTPVVLYCLDIITWDPETVSTAENLSTGQTRSRESTTSRTTSSSRRETTPTSSTTTRTPSFRRSSRTTPPSGATSARQSFRPRKGFSNLLAWLRSLLRRLLKESG-
lcl|KM349830.1_cds_AIU56914.1_1/27-146        LAHPNRSPTSRSKTTPVVLYCLDIITWDPETVSTVENLSTGQTKSRESTTSRTTSSSRRETTPTSSTTTRTPSFKRSSRTTPPSGATSARQSFRPRKGFSNLLAWLRSLLRRLLKESG-
lcl|KM349829.1_cds_AIU56913.1_1/27-146        LAHPNRSPTSRSKTTPVVLYCLDIITWDPATVSTVENLSTGQTRSRESTTFRTTSSSRRETTPTSSTTTRTPSFRRSSQTTPPSGATSARQSFRPRKGFSNLLAWLRSLLRRLLKASG-
lcl|KM349843.1_cds_AIU56927.1_1/27-145        LAHPNRSPTSRSKTTPVV-YCLDIITWDPETVSTVENLSTGQTRSRESTTSRTTSSSRRETTPTSSTTTRTPSFRRSSRTTPPSGATSARQSFRPRKEFSNLLAWLRSLLRRLLKASG-
```

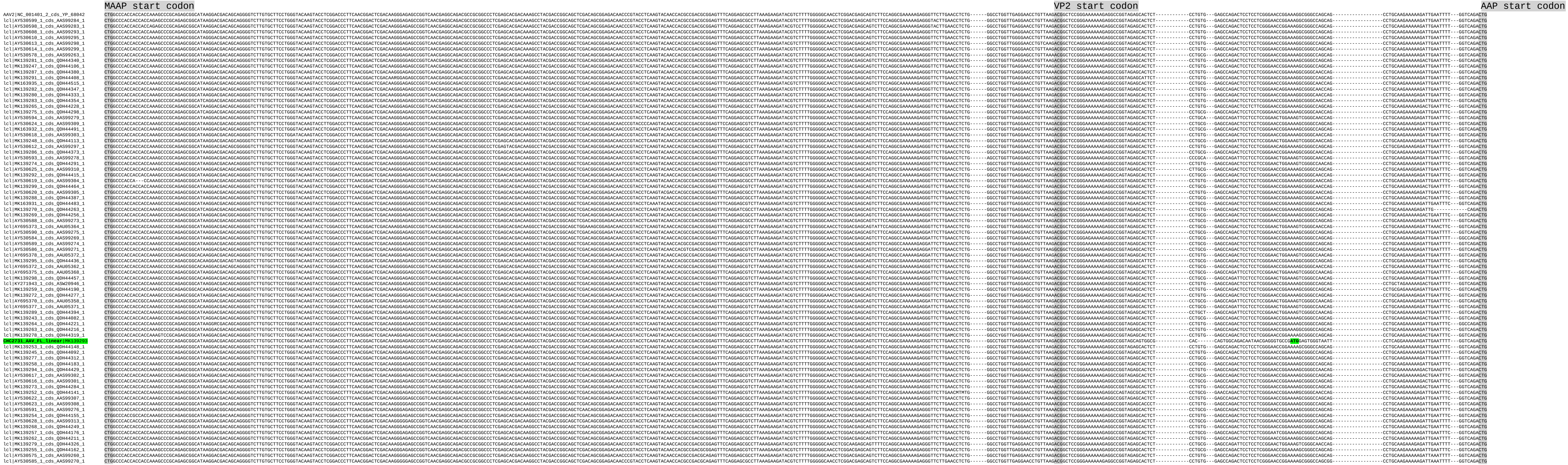
S3 Alignment. The VP1 gene contains no ATG in the region between the start codons of MAAP and AAP

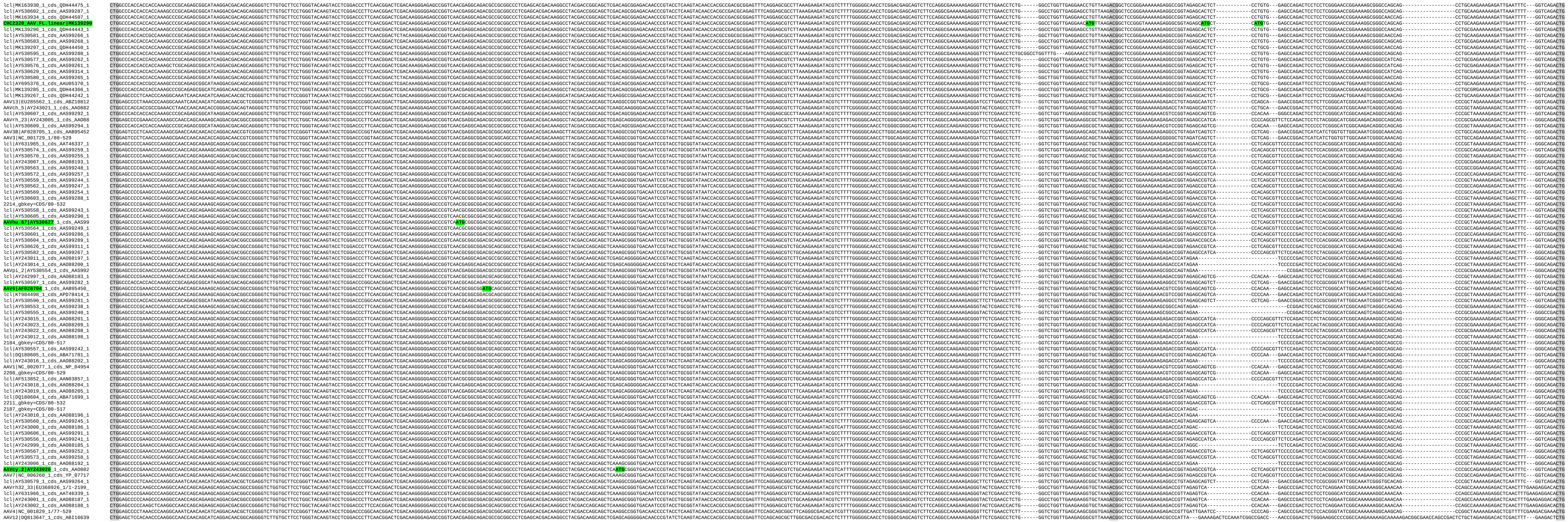
This file contains the nucleotide alignments S3A, S3B, and S3C, corresponding to the region of VP1 located between the start codons of MAAP and AAP in dependoparvoviruses A, dependoparvoviruses B, and porcine AAVs, respectively.

The alignment can be examined in detail by zooming in in any sequence editor.

S3A Alignment. In *dependoparvovirus A*, the VP1 gene contains no ATG in the region between the start codons of MAAP and AAP

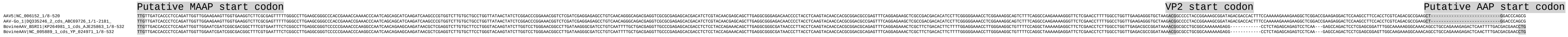
Alignment of the nucleotide sequence coding for the region of VP1 located between the start codons of MAAP and AAP in *dependoparvovirus A*, in PFAM format. The alignment was derived from the VP1 protein sequence alignment by using TranslatorX (see Methods). The MAAP, VP2 and AAP start codons are highlighted in grey and indicated above the alignment. The region considered contains ATG codons (in green) only in 5 sequences (out of 165 non-redundant sequences available in *dependoparvovirus A*), whose strain and accession number are indicated in green to the left of the alignment.





S3B Alignment. The VP1 gene of *dependoparvovirus B* contains no ATG in the region between the start codons of MAAP and AAP

Alignment of the nucleotide sequence coding for the region of VP1 located between the start codons of MAAP and AAP in *dependoparvovirus B*, in PFAM format. Conventions are the same as in Fig S3A.



S3C Alignment. The VP1 gene of porcine AAVs contains no ATG in the region between the start codons of MAAP and AAP

Alignment of the nucleotide sequence coding for the region of VP1 located between the start codons of MAAP and AAP in porcine AAVs, in PFAM format. Conventions are the same as in Fig S3A.

Putative MAAP start codon

VP2 start codon

Putative AAP start codon

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AAVpo4|JX896667_1/1-2184_AAVpo4|JX896667_  CTGGCCCACCCAAACCGAAGCCCAACCAGCAGAAGCAGGACAACGCCCGTGGTCTTGTACTGCCTGGATATAATTATCTGGGACCCTTCAACGGACTCGACAAGGGAGAGCCCGTCAACCGAGCGGACGCTGTTGCGCGAGAGCACGACATCTCGTACAACGAGCAGCTTCAGGCGGGAGACAACCCCTACCTCAAGTACAACCACGCGGACGCCGAGTTTCAGGAGAAGCTCAAGGACGACACCTCCTTTGGGGGCAACCTCGGAAAGGCAATCTTTCAGGCCAAGAAAAGGGTTCTCGAACCTTTTGGCCTGGTTGAAGCGCCTGTTAAGACGGCTCCA---GCCAAGAAGCGGCCGATAGAGAAGTCTCCGGCG---GAACCGAGCTCTTCGAAGGGCATCGGCAAGGCGGGCCAGCAGCCTGCGAGAAAGCGGCTCAACTTTGGTCAGACTGGAGACACCGACT
AAVpo7|KM349848_1_cds_AIU56932_1_1/1-2178  CTGGCCCACCCAAACCGAAGCCCAACCAGCAGAAGCAGGACAACGCCCGTGGTCTTGTACTGCCTGGATATAATTATCTGGGACCCTTCAACGGACTCGACAAGGGAGAGCCCGTCAACCGAGCGGACGCTGTTGCGCGAGAGCACGATATCTCGTACAACGAGCAGCTTCAGGCGGGCGACAACCCCTACCTCAAGTACAACCACGCGGACGCCGAGTTTCAGGAGAAGCTCAAGGACGACACCTCCTTTGGGGGCAACCTCGGAAAGGCAATCTTTCAGGCCAAGAAAAGGGTTCTCGAACCTTTTGGCCTGGTTGAAGCGCCTGATAAGACGGCTCCG---GCAAAGAAGAGGCCTGTAGAGCAGTCTCCTGCG---GAACCGGGCTCCTCCTCTGGCATCGGAAAGGCGGGCAATCAGCCTGCGAGAAAGCGACTAAACTTTGGTCAGACTGGAGACGCCGACT
AAVpo8|KM349849_1_cds_AIU56933_1_1/1-2187  CTGGCCCACCCAAACCGAAGCCCAATCAGCAAAAACAAGACAACGCCCGTGGTCTTGTACTGCCTGGATATAATTATCTGGGACCCTTCAACGGACTCGACAAGGGAGAGCCCGTCAACCGAGCGGACGCTGTTGCGCGAGAGCACGATATCTCGTACAACGAGCAGCTCCAGGCGGGAGACAACCCCTACCTCAAGTACAACCACGCGGACGCCGAGTTTCAGGAGAAGCTCGCCGACGACACCTCCTTTGGGGGCAACCTCGGAAAGGCAATCTTTCAGGCCAAGAAGAGGGTTCTCGAACCTTTTGGCCTGGTTGAAGAGCCTGTTAAGACGGCTCCG---GCAAAGAAGAGGCCTGTAGAGCAGTCTCCTGCG---GAACCGGGCCCATCCTCTGGCATCGGAAAGGCGGGCGATCAGCCTGCGAGAAAGCGACTAAACTTTGGTCAGACTGGAGACGCCGACT
AAVp06|JX896664_1_cds_AGA15924_1_1/1-2181  CTGGCCCACCCAAACCGAAGCCCAACCAGCAGAAGCAGGACAACGCCCGTGGTCTTGTACTGCCTGGATATAATTATCTGGGACCCTTCAACGGACTCGACAAGGGAGAGCCCGTCAACCGAGCGGACGCTGTTGCGCGAGAGCACGACATCTCGTACAACGAGCAGCTCCAGGCGGGAGACAACCCCTACCTCAAGTACAACCACGCGGACGCCGAGTTTCAGGAGAAGCTCAAGGACGACACCTCCTTTGGGGGCAACCTCGGAAAGGCAATCTTTCAGGCCAAGAAAAGGGTTCTCGAACCTTTTGGCCTGGTTGAGGCACCTGTTAAGACGGCTCCA---GCCAAGAAGCGGCCGATAGAGAAGTCTCCGGCG---GAACCGAGCTCTTCGAAGGGCATCGGCAAGGCGGGCCAGCAGCCTGCGAGGAAGCGACTCAACTTTGGTCAGACTGGAGACACCGACT
AVpo1|FJ688147_1/77-484                    CTGGCCCACCCAAACCGAAGCCCAACCAGCAGAAGCAAGACGACGCCCGTGGTCTTGTACTGCCTGGATATAATTACCTGGGACCCGGAAACGGTCTCGACCGCGGAGAACCTGTCAACCGGGCTGACGAGGTCGCGCGAGAGCACGACATCTCGTACAACGAGCAGCTCCAGGCGGGAGACAACCCCTACCTCAAGTACAACCACGCGGACGCCGAGTTTCAGGAGAAGCTCGCGGACGACACCTCCTTCGGGGGCAACCTCGGCAAGGCAGTCTTTCAGGCCAAAAAAAGGGTTCTCGAACCTTTTGGCCTGGTTGAGGAGCCTGTTAAGACGGCTGCT---AAAGGCGAGCGGATAGACGACCACTAT---------------------------------------------------CCCAAAAAGAAGAAGGCTCGGATCGAAGAGACCGAAGCT------G
AVpo5|JX896666_1/77-498                    CTGGCCCACCCAAACCGAAGCCCAACCAGCAGAAGCAAGACAACGCCCGTGGTCTTGTACTGCCTGGATATAATTACCTGGGACCCGGCAACGGTCTCGACCGCGGAGAACCTGTCAACCGGGCCGACGAGGTCGCGCGAGAGCACGACATCTCGTACAACGAGCAGCTCCAGGCGGGAGACAACCCCTACCTCAAGTACAACCACGCGGACGCCGAGTTTCAAGAGAAGCTCGCGGACGACACCTCCTTCGGGGGCAACCTCGGCAAGGCAGTCTTTCAGGCCAAGAAAAGGGTTCTCGAACCTTTTGGCCTGGTTGAGGATCCTGTTAAGACGGCTGCTAAAGGCGAGCGGATA---------------GACGACCACTATCCCAAGAAGAAGAAGGCTCGGGTTGAAGAAACCGAAGCT------------------------GGAACCAGCGGAGCC-------
```

S4 Alignment. The VP1-unique region (VP1u) lacks cysteine in all dependoparvoviruses

Sequence alignment of *dependoparvovirus* VP1u in PFAM format.

VP1u contains no Cysteine (C, highlighted in blue), except in one strain of *dependoparvovirus A* (AAVhu.17) and the species *Desmodus rotundus dependoparvovirus*. Their name and accession number are indicated in blue to the left of the alignment.

Dependoparvoviruses A

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AAV2|NC_001401.2_cds_YP_680426.1_5/1      -----MA-ADGYLPDWLED--------TLSEGIRQWWKLKPGPP-PPKPAERHKD------------DSRGLVLPGYKYLGPFNGLDKGEPVNEADAAALEHDKAYDRQLDSGDNPYLKYNHADAEFQERLKEDTSFGGNLGRAVFQAKKRVLEPL--GLVEE--------PVK
lcl|AY530599.1_cds_AAS99284.1_1/1-13      -----MA-ADGYLPDWLED--------TLSEGIRQRWKLKPGPP-PPEPAERHKD------------DSRGLVLPGYKYLGPFNGLDKGEPVNEADAAALEHDKAYDRQLDSGDNPYLKYNHADAEFQERLKEDTSFGGNLGRAVFQAKKRVLEPL--GLVEE--------PVK
lcl|AY530608.1_cds_AAS99293.1_1/1-13      -----MA-ADGYLPDWLED--------TLSEGIRQWWKLKPGPP-PPKPAERHRD------------DSRGLVLPGYKYLGPFNGLDKGEPVNEADAAALEHDKAYDRQLDSGDNPYLKYNHADAEFQERLKEDTSFGGNLGRAVFQAKKRVLEPL--GLVEE--------PVK
lcl|AY530613.1_cds_AAS99298.1_1/1-13      -----MA-ADGYLPDWLED--------TLSEGIRQWWKLKPGPP-PPKPAERHKD------------DSRGLVLPGYKYLGPFNGLDKGEPVNEADAAALEHDKAYDRQLDSGDNPYLKYNHADAEFQERLKEDTSFGGNLGRAVFQAKKRVLEPL--GLVGE--------PVK
lcl|AY530610.1_cds_AAS99295.1_1/1-13      -----MA-ADGYLPDWLED--------TLSEGIRQWWKLKPGPP-PPKPAERHRD------------DSRGLVLPGYKYLGPFNGLDKGEPVNEADAAALEHDKAYDRQLDSGDNPYLKYNHADAEFQERLKEDTSFGGNLGRAVFQAKKRVLEPL--GLVGE--------PVK
lcl|MK139283.1_cds_QDH44354.1_5/1-13      -----MA-ADGYLPDWLED--------TLSEGIRQWWKLKPGPP-PPKPAERHQD------------DSRGLVLPGYKYLGPFNGLDKGEPVNEADAAALEHDKAYDRQLESGDNPYLKYNHADAEFQERLKEDTSFGGNLGRAVFQAKKRVLEPL--GLVEE--------PVK
lcl|MK139275.1_cds_QDH44298.1_5/1-13      -----MA-ADGYLPDWLED--------TLSEGIRQWWKLKPGPP-PPKPAERHQD------------DSRGLVLPGYKYLGPFNGLDKGEPVNEADAAALEHDKAYDRQLDSGDNPYLKYNHADAEFQERLKEDTSFGGNLGRAVFQAKKRVLEPL--GLVEE--------PVK
lcl|AY530624.1_cds_AAS99309.1_1/1-13      -----MA-ADGYLPDWLED--------TLSEGIRQWWKLKPGPP-PPKPAERHKD------------DSRGLVLPGYKYLGPFNGLDKGEPVNEADAAALEHDKAYDRQLDSGDNPYPKYNHADAEFQERLKEDTSFGGNLGRAVFQAKKRVLEPL--GLVEE--------PVK
lcl|AY530612.1_cds_AAS99297.1_1/1-13      -----MA-ADGYLPDWLKD--------TLSEGIRQWWKLKPGPP-PPKPAERHKD------------DSGGLVLPGYKYLGPFNGLDKGEPVNEADAAALEYDKAYDRQLDSGDNPYLKYNHADAEFQERLKEDTSFGGNLGRAVFQAKKRVLEPL--GLVEE--------PVK
lcl|MK139274.1_cds_QDH44291.1_5/1-13      -----MA-ADGYLPDWLED--------TLSEGIRQWWKLKPGPP-PPKPAERHKD------------DNRGLVLPGYKYLGPFNGLDKGEPVNEADAAALEHDKAYDRQLDSGDNPYLKYNHADAEFQERLKEDTSFGGNLGRAVFQAKKRVLEPL--GLVEE--------PVK
lcl|AY530593.1_cds_AAS99278.1_1/1-13      -----MA-ADGYLPDWLED--------TLSEGIRQWWKLKPGPP-PPKPAERHKD------------DSRGLVLPGYKYLGPFNGLDKGEPVNEADAAALEHDKAYDRQLDSGDNPYLKYNHADAEFQERLKEDTSFGGNLGRAVFQAKKRVLEPL--SLVEE--------PVK
lcl|AY530625.1_cds_AAS99310.1_1/1-13      -----MA-ADGYLPDWLED--------TLSEGIRQWWKLKPGPP-PPKPAERHKD------------DSRGLVLPGYKYLGPFNGLDKGEPVNEADAAALEHDKAYDRQLDGGDNPYLKYNHADAEFQERLKEDTSFGGNLGRAVFQAKKRVLEPL--GLVEE--------PVK
lcl|AY530620.1_cds_AAS99305.1_1/1-13      -----MA-ADGYLPDWLED--------TLSEGIRQWWKLKPGPP-PPKPAERHKD------------DSRGLVLPGYKYLGPFNGLDKGEPVNEADAAALEHDKAYDRQLDSGDNPYLKYDHADAEFQERLKEDTSFGGNLGRAVFQAKKRVLEPL--GLVEE--------PVK
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lcl|AY695373.1_cds_AAU05364.1_2/1-13      -----MA-ADGYLPDWLED--------TLSEGIRQWWKLKPGPP-PPKPAERHKD------------DSRGLVLPGYKYLGPFNGLDKGEPVNEADAAALEHDKAYDRQLESGDNPYLKYNHADAEFQERLKEDTSFGGNLGRAVFQAKKRVLEPL--GLVEE--------PVK
lcl|AY530588.1_cds_AAS99273.1_1/1-13      -----MA-ADGYLPDWLED--------TLSEGIRQWWKLKPGPP-PPKPAERHKD------------DSRGLVLPGYKYLGPFNGLDKGEPVNEADAAALEHDKAYDRQLDSGDNPYLKYNHADAEFQERLKGDTSFGGNLGRAVFQAKKRILEPL--GLVEE--------PVK
lcl|AY530590.1_cds_AAS99275.1_1/1-13      -----MA-ADGYLPDWLED--------TLSEGIRQWWKLKPGPP-PPKPAERHKD------------DSRGLVLPGYKYLGPFNGLDKGEPVNEADAAALEHDKAYDRQLDSGDNPYLKYNHADAEFQERLKEDTSFGGNLGRAVFQAKKRILEPL--GLVEE--------PVK
lcl|AY530586.1_cds_AAS99271.1_1/1-13      -----MA-ADGYLPDWLED--------TLSEGIRQWWKLKPGPP-PPKPAERHKD------------DSRGLVLPGYRYLGPFNGLDKGEPVNEADAAALEHDKAYDRQLDSGDNPYLKYNHVDAEFQERLKEDTSFGGNLGRAVFQAKKRILEPL--GLVEE--------PVK
lcl|KY271943.1_cds_ASW20946.1_5/1-13      -----MA-ADGYLPDWLED--------TLSEGIRQWWKLKPGPP-PPKPAERHKD------------DSRGLVLPGYKYLGPFNGLDKGEPVNEADAAALEHDKAYDRQLDSGDNPYLKYNHADSEFQERLKEDTSFGGNLGRAVFQAKKRVLEPL--GLVEE--------PVK
lcl|AY695377.1_cds_AAU05371.1_1/1-13      -----MA-ADGYLPDWLED--------TLSEGIRQWWKLKPGPP-PPKPAERHKD------------DSRGLVLPGYKYLGPFNGLDKGEPVNEADAAALEHDKAYDRQLDSGDNPYLKYNHADAKFQERLKEDTSFGGNLGRAVFQAKKRILEPL--GLVEE--------PVK
lcl|MK139263.1_cds_QDH44216.1_3/1-13      -----MA-ADGYLPDWLED--------TPSAGISQWWKLKPGPP-PPKPAERHKD------------DSRGLVLPGYKYLGPFNGLDKGEPVNEADAAALEHDKAYDRQLDSGDNPYLKYNHADAEFQERLKEDTSFGGNLGRAVFQAKKRVLEPL--GLVEE--------PVK
lcl|MK139264.1_cds_QDH44221.1_3/1-13      -----MA-ADGYLPDWLGE--------TLSQGIRQWWKLKPGPP-PPKPAERHKD-------------SRGLVLPGYKYLGPFNGLDKGEPVNEADAAALEHDKAYDRQLDSGHIPYLKYNHADAEFQERLKEDTSFGGNLGRAVFQAKKRVLEPL--GLVEE--------PVK
lcl|MK139278.1_cds_QDH44319.1_5/1-13      -----MA-ADGYLPDWLED--------TLSEGIRQWWKLKPGPP-PPKSAERHKD------------DSRGLVLPGYKYLGPF-GLDKGEPVNEADAAALEHDKAYDRQLDSGDNPYLKYNHADAEFQERLKEDTSFGGNLGRAVFQAKKRVL-PL--G-VEE--------PVK
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lcl|AY530591.1_cds_AAS99276.1_1/1-13      -----MA-ADGYLPDWLED--------TLSEGIRQWWKLKPGPP-PPKPAERHKD------------GSRGLVLPGYKYLGPFNGLDKGEPVNEADAAALEHDKAYDRQLNSGDNPYLKYNHADAEFQERLKEDTSFGGNLGRAVFQAKKRVLEPL--GLVEE--------PVK
lcl|AY530628.1_cds_AAS99313.1_1/1-13      -----MA-ADGYLPDWLED--------TLSEGIRQWWKLKPGPP-PPKPAERHKD------------DSRGLVLPGYKYLGPFNGLDKGEPVNEADAAALEHDKAYDRQLDSGDNPYLKYNHADAEFQERLKEDTSFGGNLGRAVFQAKKRVLEPL--GLVEG--------PVK
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lcl|AY530585.1_cds_AAS99270.1_1/1-13      -----MA-ADGYPPDWLED--------TLSEGIRQWWKLKPGPP-PPKPAERHKD------------DSRGLVLPGYKYLGPFNGLDKGEPVNEADAAALEHDKAYDRQLDSGDNPYLKYNHADAEFQERLKEDTSFGGNLGRAVFQAKKRVLEPL--GLVEE--------PVK
CHC2320_AAV.FL |MK139290.1_cds            -----MA-ADGYLPDWLED--------TLSEGIRQWWKLKPGPP-PPKPAERHKD------------DSRGLVLPGYKYLGPFNGLDKGEPVNEADAAALEHDKAYDRQLDSGDNPYLKYNHADAEFQERLKEDTSFGGNLGRAVFQAKKRVLETL--GLVEE--------HVK
lcl|AY530581.1_cds_AAS99266.1_1/1-13      -----MA-ADGYLPDWLED--------TLSEGIRQWWKLKPGPP-PPKPAERHKD------------DSRGLVLPGYKYLGPFNGLYKGEPVNEADAAALEHDKAYDRQLDSGDNPYLKYNHAGAEFQERLKEDTSFGGNLGRAVFQAKKRVLEPL--GLVEE--------PVK
lcl|AY530576.1_cds_AAS99261.1_1/1-13      -----MA-ADGYLPDWLED--------TLSEGIRQWWKLKPGPP-PPKLAERHQD------------DSRGLVLPGYKYLGPFNGLDKGEPVNEADAAALEHDKAYDRQLDSGDNPYLKYNHADAEFQERLKEDTSFGGNLGRAVFQAKKRVLEPL--GLVEE--------PVK
lcl|AY530580.1_cds_AAS99265.1_1/1-13      -----MA-ADGYLPDWLED--------TLSEGIRQWWKLKPGPP-PPKPAERHKD------------DSRGLVLPGYKYLGPFNGLYKGEPVDEADAAALEHDKAYDRQLDSGDNPYLKYNHADAEFQERLKEDTSFGGNLGRAVFQAKKRVLEPL--GLVGE--------PVK
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AAVch.5|AY243021.1_cds_AAO88207.1_1/      -----MA-ADGYLPDWLED--------TLSEGIRQWWKLKPGPP-PPKPNQQHRD------------DSRGLVLPGYKYLGPFNGLDKGEPVNEADAAALEHDKAYDHQLKQGDNPYLKYNHADAEFQERLQEDTSFGGNLGRAVFQAKKRVLEPL--GLVEE--------AVK
lcl|MK139285.1_cds_QDH44366.1_3/1-13      -----MA-ADGYLPDWLQE--------NLFFDIRQWWKLKPGPP-PPKPAERHQD------------NSRGLVLPGYKYLGPFNGLDKGEPVNEADAAALEHDKAYDRQLDSGDNPYLKYNHADAEFQERLKEDTSFGGNLGRAVFQAKKRVLEPL--GLVEE--------PVK
lcl|MK139252.1_cds_QDH44141.1_5/1-13      -----MA-ADGYLPDWLED--------TLSEGIRQWWKLKPGPP-PPKPAERHKD------------DSRGLVLPGYKYLGPFNGLDKGEPVNEADAAAIEHDKAYDRQLDSGDNPYLKYNHADAEFQERLKEDTSFGGNLGRAVFQAKKRVLE----GLVEE--------PVK
lcl|MK139267.1_cds_QDH44242.1_5/1-13      -----MA-ADGYLPDWLED--------NLSEGIREWWALKPGAP-QPKANQQHQD------------NARGLVLPGYKYLGPGNGLDKGEPVNAADAAALEHDKAYDKQLKAGDNPYLKYNHADAEFQERLKEDTSFGGNLGRAVFQAKKRVLEPL--GLVEE--------PVK
AAV3B|AF028705.1_cds_AAB95452.1_2/1-      -----MA-ADGYLPDWLED--------NLSEGIREWWALKPGVP-QPKANQQHQD------------NRRGLVLPGYKYLGPGNGLDKGEPVNEADAAALEHDKAYDQQLKAGDNPYLKYNHADAEFQERLQEDTSFGGNLGRAVFQAKKRILEPL--GLVEE--------AAK
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lcl|AY530579.1_cds_AAS99264.1_1/1-13      -----MA-ADGYLPDWLED--------NLSEGIREWWALKPGAP-QPKANQQHQD------------NARGLVLPGYKYLGPGNGLDKGEPVNAADAAALEHDKAYDQQLKAGDNPYLKYNHADAEFQERLKEDTSFGGNLGRAVFQAKKRLLEPL--GLVEE--------AAK
AAV12|DQ813647.1_cds_ABI16639.1_2/1-      -----MA-ADGYLPDWLED--------NLSEGIREWWALKPGAP-QPKANQQHQD------------NGRGLVLPGYKYLGPFNGLDKGEPVNEADAAALEHDKAYDKQLEQGDNPYLKYNHADAEFQQRLATDTSFGGNLGRAVFQAKKRILEPL--GLVEE--------GVK
lcl|AY530571.1_cds_AAS99256.1_1/1-13      -----MA-ADGYLPDWLED--------NLSEGIHEWWDPKPGAP-KPKANQQKQD------------DGRGLVLPGYKYLGPFNGLDKGEPVNAADAAALEHDKAYDQQLKAGDNPYLRYNHADAEFQERLQEDTSFGGNLGRAVFQAKKRVLEPL--GLVEE--------GAK
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CHC2731_AAV.FL.linear|MK139293.1          -----MA-ADGYLPDWLED--------TLSEGIRQWWKLKPGPP-PPKPAERHKD------------DSRGLVLPGYKYLGPFNGLDKGEPVNEADAAALEHDKAYDRQLDSGDNPYLKYNHADAEFQERLKEDTSFGGNLGRAVFQAKKRVLEPL--GLVEE--------RVK
lcl|AY243014.1_cds_AAO88200.1_1/1-13      -----MA-ADGYLPDWLED--------NLSEGIREWWDLRPGAP-KPKANQQKQD------------DGRGLVLPGYKYLGPFNGLDKGEPVNEADAAALEHDKAYDKQLEQGDNPYLKYNHADAEFQERLQEDTSFGGNLGRAVFQAKKRVLEPL--GLVEE--------GAK
lcl|AY243012.1_cds_AAO88198.1_1/1-13      -----MA-ADGHLPDWLED--------NLSEGIREWWDLKPGAP-KPKANQQKQD------------DGRGLVLPGYKYLGPFNGLDKGEPVNAADAAALEHDKAYDQQLKAGDNPYLRYNHADAEFQERLQEDTSFGGNLGRAVFQAKKRVLEPL--GLVEE--------GAK
lcl|AY530595.1_cds_AAS99280.1_1/1-13      -----MA-ADGYLPDWLED--------TLSEGIRQWWKLKPGPP-PPKPAERHKD------------DSRGLVLPGYKYLGPFNGLDKGEPVNEADAAALEHDKAYDRQLDSGDNPYLKYNHADAEFQERLKEDTSFGGNLGRAVFQAKKRVLEPLRPGL-RK--------PVK
lcl|AY530606.1_cds_AAS99291.1_1/1-13      -----MA-ADGYLPDWLED--------NLSEGIREWWDLKPGAP-KPKANQQKQD------------DGRGLVLPGYKYLGPFNGLDKGEPVNAADAAALEHDKAYDQQLKAGDNPYPRYNHADAEFQERLQEDTPFGGNLGRAVFQAKKRVLEPL--GLVEE--------AAK
lcl|AY243019.1_cds_AAO88205.1_1/1-13      -----MA-ADGYLPDWLED--------NLSEGIREWWDLKPGAP-KPKANQQKQD------------DGRGLVLPGYKYLRPFNGLDKGEPVNEADAAALEHDKAYDKQLEQGDNPYLKYNHADAEFQERLQEDTSFGGNLGRAVFQAKKRVLEPL--GLVEE--------VAK
lcl|EU368913.1_cds_ACB55305.1_1/1-13      -----MA-ADGYLPDWLED--------NLSEGIREWWDLKPGAP-KPKANQQKQD------------DGRGLVLPGYRYLGPFNGLDKGEPVNEADAAALEHDKAYDKQLEQGDNPYLKYNHADAEFQERLQEDTSFGGNLGRAVFQAKKRVLEPL--GLVEE--------GAK
lcl|AY243017.1_cds_AAO88203.1_1/1-13      -----MA-ADGYLPDWLEG--------NLSEGIREWWDLKPGAP-KPKANQQKQD------------DGRGLVLPGYRYLGPFNGLDKGEPVNEADAAALEHDKAYDKQLEQGDNPYLKYNHADAEFQERLQEDTSFGGNLGRAVFQAKKRVLEPL--GLVEE--------GAK
lcl|AY530567.1_cds_AAS99252.1_1/1-13      -----MA-ADGYLPDWLED--------NLSEGIREWWDLKPGAP-KPKANQQKQD------------DGRGLVLPGYKYLGPFNGLDKGEPVNAADAAALEHDKAYDQQLKAGDNPYLRYNHADAEFQERLQEDTSFGGNLGRAVFQAKKRVLEPL--GLVEE--------AAK
lcl|AY243010.1_cds_AAO88196.1_1/1-13      -----MA-ADGYLPDWLED--------NLSEGIREWWDLKPGAP-KPKANQQKQD------------DGRGLVLPGYKYLGPFNGLDKGEPVNEADAAALEHDKAYDKQLEQGDNPYLKYNHADAEFQERLQEDTSFGGNLGRAVFRAKKRVLEPL--GLVEE--------GAK
lcl|AY530573.1_cds_AAS99258.1_1/1-13      -----MA-ADGYLPDWLED--------NLSEGIREWWDLKPGAP-KPKANQQKQD------------DGRGLVLPGYKYLGPFNGLDKGEPVNAADAAALEHDKAYDQQLKAGDNPYLRYNHADAEFQERLQEDTSFGGNLGRAVFQAKKRVLEPL--GLAEE--------AAK
lcl|AY243001.1_cds_AAO88187.1_1/1-13      -----MA-ADGYLPDWLED--------NLSEGIREWWDLKPGAP-KPKANQQKQD------------DGRGLVLPGYEYLGPFNGLDKGEPVNAADAAALEHDKAYDQQLKAGDNPYLRYNHADAEFQERLQEDTSFGGNLGRAVFQAKKRVLEPL--GLVEE--------GAK
lcl|AY243020.1_cds_AAO88206.1_1/1-13      -----MA-ADGYLPDWLED--------NLSEGIREWWDLKPGAP-KPKANQQKQD------------NGRGLVLPGYKYLGPFNGLDKGEPVNAADAAALEHDKAYDQQLNAGDNPYLRYNHADAEFQERLQEDTSFGGNLGRAVFQAKKRVLEPL--GLVEE--------GAK
lcl|AY243002.1_cds_AAO88188.1_1/1-13      -----MA-ADGYLPDWLED--------NLSEGIREWWDLKPGAP-KLKANQQKQD------------DGRGLVLPGYKYLGPFHGLDKGEPVNAADAAALEHDKAYDQQLKAGDNPYLRYNHADAEFQERLQEDTSFGGNLGRAVFQAKKRVLEPL--GLVEE--------GAK
AAVpi.2|AY530554.1_cds_AAS99239.1_1/      -----MA-ADGYLPDWLED--------NLSEGIREWWALKPGAP-QPKANQQKQD------------DGRGLVLPGYKYLGPFNGLDKGEPVNEADAAALEHDKAYDQQLKAGDNPYLRYNHADAEFQERLQEDTSFGGNLGRAVFQAKKRVLEPL--GLVEE--------GAK
AAV7|NC_006260.1_cds_YP_077178.1_2/1      -----MA-ADGYLPDWLED--------NLSEGIREWWDLKPGAP-KPKANQQKQD------------NGRGLVLPGYKYLGPFNGLDKGEPVNAADAAALEHDKAYDQQLKAGDNPYLRYNHADAEFQERLQEDTSFGGNLGRAVFQAKKRVLEPL--GLVEE--------GAK
lcl|AY530556.1_cds_AAS99241.1_1/1-13      -----MA-ADGYLPDWLED--------NLSEGIREWWALKPGAP-KPKANQQKQD------------DGRGLVLPGYKYLGPFNGLDKGEPVNAADAAALEHGKAYDQQLQAGDNPYLRYNHADAEFQERLQEDTSFGGNLGRAVFQAKKRVLEPL--GLVEE--------GAK
lcl|AY243022.1_cds_AAO88208.1_1/1-13      -----MA-ADGYLPDWLED--------NLSEGIREWWALKPGAP-KPKANQQKQD------------DGRGLVLPGYKYLGPFNGLDKGEPVNAADAAALEHDKAYDQQLKAGDNPYLRYNHADAEFQERLQEDTSFGGNLGRAVFQAKKRVLEPL--GLVEE--------GAK
AAVhu.17|AY530582.1_cds_AAS99267.1_1      -----MA-ADGYLPDWLED--------NLSEGIREWWDLKPGAP-KPKANQQKQD------------DGRGLVLPGCKYLGPFNGLDKGEPVNAADAAALEHDKAYDQQLKAGDNPYLRYNHADAEFQERLQEDTSFGGNLGRAVFQAKKRVLEPL--GLVEE--------GAK
lcl|AY530562.1_cds_AAS99247.1_1/1-13      -----MA-ADGYLPDWLED--------NLSEGIREWWDLKPGAP-KPKANQQKQD------------DGRGLVLPGYKYLGPFNGLDKGEPVNAADAAALEHDKAYDQQLKAGDNPHLRYNHADAEFQERLQEDTSFGGNLGRAVFQAKKRVLEPL--GLVEE--------GAK
lcl|AY530569.1_cds_AAS99254.1_1/1-13      -----MA-ADGYLPDWLED--------NLSEGIREWWALKPGAP-KPKANQQKQD------------DGRGLVLPGYKYLGPFNGLDKGEPVNAADAAALEHDKAYDQQLQAGDNPYLRYNHADAEFQERLQEDTSFGGNLGRAVFQAKKRVLEPL--GLVEE--------GAK
lcl|AY530564.1_cds_AAS99249.1_1/1-13      -----MV-ADGYLPDWLED--------NLSEGIREWWDLKPGAP-KPKANQQKQG------------DGRGLVLPGYKYLGPFNGLDKGEPVNAADAAALEHDKAYDQQLKAGDNPYLRYNHADAELQERLQEDTSFGGNLGRAVFQAKKRVLEPL--GLVEE--------GAK
lcl|EU368921.1_cds_ACB55313.1_1/1-13      -----MA-ADGYLPDWLED--------NLSEGIREWWALKPGAP-KPKANQQKQD------------DGRGLVLPGYKYLGPFNGLDKGEPVNAADAAALEHDKAYDQQLKAGDNPYLRYNHADAEFQERLQEDTSFGGNLGRAVFQAKKRVLEPL--GLVEE--------AAK
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lcl|AY530627.1_cds_AAS99312.1_1/1-13          -----MA-ADGYLPDWLED--------NLSEGIREWWDLKPGAP-KPKANQQKQD------------DGRGLVLLGYKYLGPFNGLDKGEPVNAADAAALEHDKAYDQQLKAGDNPYLRYNHADAEFQERLQEDTSFGGNLGRAVFQAKKRVLEPL--GLVEE--------AAK
lcl|AY530604.1_cds_AAS99289.1_1/1-13          -----MA-ADGYLPDWLED--------NLSEGIREWWDLKPGAP-KPKANQQKQD------------DGRGLVLPGYKYLGPFNGLDKGEPVNAADAAALEHDKAYDQQLKAGDNPYLRYNHADAEFQERLQEDTSFGGNLGRAVFQAKKRVLEPL--GPVEE--------AAK
lcl|MH202997.1_cds_AXN94234.1_1/1-12          -----MS-----FFDWIGR--------KYANGAAEFWDLEPGPP-KPK--KARVD------------DSAGFNFPGHKYLGPGNGLDRGDPVDADDAAAQKHDQEYQALLESGENPYLTFNHADRQLQKDLAEDQSFEGNLARGLFEAKKLAAQVV--GVEEP----------E
lcl|MH202993.1_cds_AXN94230.1_1/1-12          -----MS-----FFDWIGR--------KYANGAAEFWDLEPGPP-KPK--KARVD------------DSAGFNFPGHKYLGPGNGLDRGEPVDADDAAAQKHDQEYQALLESGENPYLTFNHADRQLQKDLAEDQSFEGNLARGLFEAKKLAAQVV--GVEEP----------E
lcl|MH203003.1_cds_AXN94240.1_1/1-12          -----MS-----FFDWIGR--------KYANGAAEFWDLEPGPP-KPK--KARVD------------DSAGFNFPGHKYLGPGNGLDRGEPVDVDDAAAQKHDQEYQALLESGENPYLTFNHADRQLQKDLAEDRSFEGNLARGLFEAKKLAAQVV--GVEEP----------E
lcl|MH203001.1_cds_AXN94238.1_1/1-12          -----MS-----FFDWIGR--------KYANGAAEFWDLEPGPP-KPK--KARVD------------DSAGFNFPGHKYLGPGNGLDRGEPVDADDAAAQKHDQEYQALLESGENPYLTFNHADRQLQKDLAEDHSFEGNLARGLFEAKKLAAQVV--GVEEP----------E
AAV13|EU285562.1_cds_ABZ10812.1_2/1-          ------M-TDGYLPDWLED--------NLSEGVREWWALQPGAP-KPKANQQHQD------------NARGLVLPGYKYLGPGNGLDKGEPVNAADAAALEHDKAYDQQLKAGDNPYLKYNHADAEFQERLQEDTSFGGNLGRAVFQAKKRILEPL--GLVEE--------AAK
AAV4|NC_001829_1/1-136                        ------M-TDGYLPDWLED--------NLSEGVREWWALQPGAP-KPKANQQHQD------------NARGLVLPGYKYLGPGNGLDKGEPVNAADAAALEHDKAYDQQLKAGDNPYLKYNHADAEFQQRLQGDTSFGGNLGRAVFQAKKRVLEPL--GLVEQ--------AGE
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Dependoparvoviruses B

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AAV5|NC_006152_1/1-136                        -----MS-FVDHPPDWLEE---------VGEGLREFLGLEAGPP-KPKPNQQHQD------------QARGLVLPGYNYLGPGNGLDRGEPVNRADEVAREHDISYNEQLEAGDNPYLKYNHADAEFQEKLADDTSFGGNLGKAVFQAKKRVLEPF--GLVEE--------GAK
BovineAAV_BSRI1|KP264981_1_cds_AJE25          -----MS-FVDHPPDWLE---------SIGDGFREFLGLEAGPP-KPKANQQKQD------------NARGLVLPGYKYLGPGNGLDKGDPVNFADEVAREHDLSYQKQLEAGDNPYLKYNHADAEFQEKLASDTSFGGNLGKAVFQAKKRLLEPL--GLVET--------PDK
BovineAAV|NC_005889_1_cds_YP_024971_          -----MS-FVDHPPDWLE---------SIGDGFREFLGLEAGPP-KPKANQQKQD------------NARGLVLPGYKYLGPGNGLDKGDPVNFADEVAREHDLSYQKQLEAGDNPYLKYNHADAEFQEKLASDTSFGGNLGKAVFQAKKRILEPL--GLVET--------PDK
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Porcine AAVs

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AAVpo5|JX896666_1/1-136                       -----MS-FVDHPPDWLEE---------IGEGLKEFLGLEPGPP-KPKPNQQKQD------------NARGLVLPGYNYLGPGNGLDRGEPVNRADEVAREHDISYNEQLQAGDNPYLKYNHADAEFQEKLADDTSFGGNLGKAVFQAKKRVLEPF--GLVED--------PVK
AAVpo1|FJ688147_1/1-136                       -----MS-FVDHPPDWLEE---------IGEGLKEFLGLEPGPP-KPKPNQQKQD------------DARGLVLPGYNYLGPGNGLDRGEPVNRADEVAREHDISYNEQLQAGDNPYLKYNHADAEFQEKLADDTSFGGNLGKAVFQAKKRVLEPF--GLVEE--------PVK
AAVpo4|JX896667_1/1-2184_AAVpo4|JX89          -----MS-FVDHPPDWLEE---------VGEGLHEFLELEAGPP-KPKPNQQKQD------------NARGLVLPGYNYLGPFNGLDKGEPVNRADAVAREHDISYNEQLQAGDNPYLKYNHADAEFQEKLKDDTSFGGNLGKAIFQAKKRVLEPF--GLVEA--------PVK
AAVpo8|KM349849.1_cds_AIU56933.1_1/1          -----MS-FVDHPPDWLEE---------VGEGLHEFLELEAGPP-KPKPNQQKQD------------NARGLVLPGYNYLGPFNGLDKGEPVNRADAVAREHDISYNEQLQAGDNPYLKYNHADAEFQEKLADDTSFGGNLGKAIFQAKKRVLEPF--GLVEE--------PVK
AAVpo7|KM349848.1_cds_AIU56932.1_1/1          -----MS-FVDHPPDWLEE---------VGEDLHEFLELEAGPP-KPKPNQQKQD------------NARGLVLPGYNYLGPFNGLDKGEPVNRADAVAREHDISYNEQLQAGDNPYLKYNHADAEFQEKLKDDTSFGGNLGKAIFQAKKRVLEPF--GLVEA--------PDK
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Other dependoparvoviruses

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MHH-05-2015|NC_040671.1_cds_YP_00955          -----MS-AADSVPDWLENF----VRKHIVNPVAEFAHLEAGAP-QPKPNQQHQDR-GG-----TKDDSRGLVLPGYKYLGPFNGLDKGEPVNAADAAALEHDKAYDQQLQAGDNPYLKYNHADAEFQEALKDDTSFGGNLGKAVFQAKKRVLEPF--GLAED------G---K
MarsupialAAV1|MK026553_3472_gbke              -----MS-FLEAFEDWYEK------------AAATWRHLEPGAP-RPKANQQHQEQHHPVPAEEPKDQARGLVLPGYKYLGPFNGLDKGDPVNQADAAALEHDKAYNHLLEEGQNPYLVYNEADKHFQETLQGDTSFGGNLGKAVFQGKKRVLEPF--GLVDEE-------PHE
BatAAV_09YN|MH167452.1_cds_AWW87409.          -----MS-FVDHPPDWLEE---------IGEGLSEFIGLEAGPP-KPKPGYQDR--------------ARGLVVPGYKYLGPFNGLDRGEPVNAADAAAKKHDEEYDRLLKEGDNPYLTYNHADAQFQQDLRGDASLAGNAANALFQAKKRVLEPF--GLVEGEP------EPK
lcl|MH167454.1_cds_AWW87411.1_1/1-13          -----MS-FVDHPPDWLEE---------IGEGLSEFIGLEAGPP-KPKPGYQDR--------------ARGLVVPGYKYLGPFNGLDRGEPVNAADAAAKKHDEEYDRLLKEGDNPYLTYNHADAEFQKDLRGDASLAGNAANALFQAKKRVLEPF--GLVEGEP------EPK
lcl|MH167451.1_cds_AWW87408.1_1/1-13          -----MS-FVDHPPDWLEE---------IGEGLSEFIGLEAGPP-KPKPGYRDR--------------ERGLVVPGYKYLGPFNGLDRGEPVNAADAAAKKHDEEYDRLLKEGDNPYLTYNHADAEFQKDLRGDASLAGNAANALFQAKKRVLEPF--GLVEGEP------EPK
BatAAV_YNM|NC_014468_1/1-136                  -----MS-FVDHPPDWLEE---------IGEGLSEFIGLEAGPP-KPKPGYQDR--------------ARGLVVPGYKYLGPFNGLDRGEPVNAADAAAKKHDEEYDRLLKAGDNPYLAYNHADAEFQKDLSGDSSLAGNAANALFQAKKRVLEPF--GLVEGEP------EPK
AvianAAV_BR_DF12|MN175614.1_cds_QEJ8          -----MA-AEGVVPEWLERFIKRRIF-------------------RPIGSLFHEA------------KQRGAVLPGYKYLGPFNDLDRGEPVNAADAAALEHDRAYDEEIKKGKNPYLTFNKADEKLMRDLKDDKSLGGNLAKALFQAKKRIAEPL--GRVEL-----------
lcl|MH167453.1_cds_AWW87410.1_1/1-13          -----MS-FVDHPPDWLEE---------IGEGLSEFIGLEAGPP-KPKPGYQDR--------------ARGLVVPGYKYLGPFNGLDRGEPVNAADAAAKKHDEEYDRLLKAGDNPYLTYNHADAEFQKDLRGDASLAGNAANALFQAKKRVLEPF--GLVEGEP------EPK
MurineAAV2|MF416384_1/1-129                   -----MS-----FFDWVGK--------KYAQGAAEFWDLKSGPP-APK--KARKD------------GSAGFNFPGHKYLGPGNSLDRGDPVDADDAAAQKHDQAYQEQLEAGDNPYLKYNHADREFQEALKDDTSFEGNLARGLFEAKKLVAEPL--GLVEP----------E
lcl|DQ100362.1_cds_AAZ79672.1_2/1-12          -----MS-----FFDWLGK--------QYAQGAAEFWDLKSGPP-APK--KARKD------------GSAGFNFPGHKYLGPGNSLDRGDPVDADDAAAQKHDQSYQEQLEAGDNPYLKYNHADREFQEALKDDTSFEGNLARGLFEAKKLVAEPL--GLVEP----------E
lcl|AY629583.1_cds_AAT48615.1_2/1-14          -----MSLISDAIPDWLERL----VK-KGVNAAADFYHLESGPP-HPKANQQTQ-------ESPEKDDSRGLVFPGYKYLGPFNGLDKGKPVNEADAAALEHDKAYDLELKDGHNPYFEYNEADRRFQERLKDDTSFGGNLGKAIFQAKKRVLEPF--GLIEQ--------PDN
lcl|KF937794.1_cds_AHK22793.1_2/1-14          -----MSLISDAIPDWLERL----VR-KGVNAAADFYHLESGPP-APKANQQTQ-------ESPEKDDSRGLVFPGYKYLGPFNGLDKGEPVNEADAAALEHDKAYDLEIKDGHNPYFEYNEADRRFQERLKDDTSFGGNLGKAIFQAKKRVLEPF--GLIEQ--------PDN
lcl|GQ368252.1_cds_ACU30842.1_2/1-14          -----MSLISDAIPDWLERL----VR-KGVNAAADFYHLESGPP-APKANQQTQ-------ESPEKDDSRGLVFPGYKYLGPFNGLDKGEPVNEADAAALEHDKAYDLELKDGHNPYFEYNEADRRFQERLKDDTSFGGNLGKAIFQAKKRVLEPF--GLIEQ--------PDN
lcl|MG846444.1_cds_AXL64653.1_2/1-14          -----MSLISDAIPDWLERL----VK-KGVNAAADFYHLESGPP-APKANQQTQ-------ESPEKDDSRGLVFPGYKYLGPFNGLDKGEPVNEADAAALEHDKAYDLELKDGHNPYFEYNEADRRFQERLKDDTSFGGNLGKAIFQAKKRVLEPF--GLIEQ--------PDN
RhinolophusPusillus|MF682926_1/1-213          MIRVVMS-FVDYPPDWLKE---------VAGGLKEFIDLKPGAP-KPKANQQKQD-------------QRGLVLPGYKYLGPFNGLDKGQPVNKADEVAREHDIEYDKLLKEGDNPYVKYNHADQEFQEKLEGDESFGGNLGRAVFQAKKRLLEPF--GLSEETP---------
RhinopholusSiniAAV1|MF682927_1/1-220          MSRVVMS-FVDHPPDWLKE---------AAGGLREFLDLEPGAP-KPKPNQQKQD-------------QRGLVLPGYKYLGPFNGLDKGQPVNKADEVAREHDLEYNKLLEAGDNPYLKYNHADQEFQEKLEGDTSFGGNLGRAVFQAKKRVLEPF--GLAEEAP------A-K
lcl|EU088102.1_cds_ABU50783.1_1/1-14          -----MSTFLDSFEEWYE------------TAAASWRNLKAGAP-QPKPNQQSQSV-SPDREPERRDNNRGFVLPGYKYLGPGNGLDKGPPVNNADSVALEHDKAYDQQLKAGDNPYIKFNHADQDFIDSLQDDQSFGGNLGKAVFQAKKRILEPF--GLVED--------PIN
PygmyChameleon|KP733796_1/1-1132_Pyg          -----MDFLDDFFSNKYKET----VE-------------ELSKPVNPPPVQH--------------GS-RGLVVPGYRYLGPGNSLDRGEPVNQADAAAKKHDIEYDKQLQAGDNPYIKYNHADAEFQKDLQGDTSLAGNAANALFQAKKTLLEPL--GLVEH-PG-----G-N
MurineAAV1|MF416383_1_cds_AWB14638/1          -----MS-----FFDWIGK--------QYAQGAAEFWDLKSGPP-APK--KARKD------------GSAGFNFPGHKYLGPGNSLDRGDPVDADDAAAQKHDQSYQEQLEAGDNPYLKYNHADREFQEALKGDTSFEGNLARGLFEAKKLVAEPL--GLVEP----------E
BeardedDragon|NC_027429_1/1-2178_Bea          -----MDFLDFLLGEKYEET----AK-------------ELGKPINPPPVQQISHA----------DSRRGLVVPGYKYLGPFNGLDKGEPVNAADAAALEHDKAYNELLEAGDNPYIKYNHADAVFQERLQGDTSLGGNAANAVFQFKKRLLEPF--GAVEQ-PQ-----PEK
GooseParvovirus|NC_001701_1/1-2199_G          -----MSTFLDSFEEWYE------------TAAASWRNLKAGAP-QPKPNQQSQSV-SPDREPERKDNNRGFVLPGYKYLGPGNGLDKGPPVNKADSVALEHDKAYDQQLKAGDNPYIKFNHADQDFIDSLQDDQSFGGNLGKAVFQAKKRILEPF--GLVED--------PVN
lcl|U34761.1_cds_AAA75286.1_2/1-145           -----MSTFLDSFEEWYE------------TAAASWRNLKAGAP-QPKPNQQSQSV-SPDREPERKDNNRGFVLPGYKYLGPGNGLDKGPPVNKADSVALEHDKAYDLQLKAGDNPYIKFNHADQDFIDSLQDDHSFGGNLGKAVFQAKKRILEPF--GLVEE--------PIN
lcl|KU684472.1_cds_ANN12566.1_2/1-14          -----MSTFLDSFEEWYE------------TAAASWRNLKAGAP-HPKPNQQSQSV-SPDREPERRDNNRGFVLPGYKYLGPGNGLDKGPPVNKADSVALEHDKAYDLQLKAGDNPYIKFNHADQDFIDSLQDDHSFGGNLGKAVFQAKKRILEPF--GLVEE--------PIN
lcl|KR265070.1_cds_ALH24919.1_1/1-14          -----MSTFLDSFGEWYE------------TAAASWRNLKAGAP-HPKPNQQTQSL-SPAKEPERRDNNRGFVLPGYKYLGPGNGLDKGPPVNKADSVALEHDKAYDQQLKAGDNPYIKFNHADQDFIDSLQDDQSFGGNLGKAVFQAKKRILEPF--GLVED--------PVN
lcl|MF962899.1_cds_AXG65518.1_1/1-14          -----MSTFLDSFEEWYE------------TAAASWRNLKAGAP-HPKPNQQTQSV-SPAREPERRDSNRGFVLPGYKYLGPGNGLDKGPPVNKADSVALEHDKAYDQQLKAGDNPYIKFNHADQDFIDSLQDDRSFGGNLGKAVFQAKKRILEPF--GLVED--------SIN
lcl|MH717784.1_cds_QBS32947.1_2/1-14          -----MSTFLDSFEEWYE------------TAAASWRNLKAGAP-HPKPNQQTQSL-SPAREPERRDNNRGFVLPGYKYLGPGNGLDKGPPVNKADSVALEHDKAYDQQLKAGDNPYIKFNHADQDFIDSLQDDQSFGGNLGKAVFQAKKRILEPF--GLVED--------PVN
lcl|MF441222.1_cds_ATX74763.1_2/1-14          -----MSTFLDSFEEWYE------------TAAASWRNLKAGAP-QPKPNQQSQSV-SPDREPERRDNNRGFVLPDYKYLGPGNGLDKGPPVNKADSVALEHDKAYDLQLKAGDDPYIKFNHADQDFIDSLQHDHSFGGNLGKAVFQAKKRILEPF--GLVEE--------PIN
lcl|AY382888.1_cds_AAR24362.1_1/1-14          -----MSTFLDSFEEWYE------------TAAASWRNLKAGAP-HPKPNQQTQSV-SPAREPGRRDNNRGFVLPGYKYLGPGNGLDKGPPVNKADSVALEHDKAYDQQLKAGDNPYIKFNHADQDFIDSLQDDQSFGGNLGKAVFQAKKRILEPF--GLVED--------PVN
lcl|KT935531.2_cds_AOM63305.2_2/1-14          -----MSTFLDSFEEWYE------------TAAASWRNLKAGAP-QPKPNQQSQSV-SPDREPERRDNNRGFVLPGYKYLGPGNGLDKGPPVNKADSVALEHDKAYDLQLKAGDNPYIKFNHADQDFIDSLQHDHSFGGNLGKAVFQAKKRILEPF--GLVEE--------PIN
lcl|AY382885.1_cds_AAR24359.1_1/1-14          -----MSTFLDSFEEWYE------------TAAASWRNLKAGAP-HPKPNQQTQSV-SPAREPERRDNNRGFVLPGYKYLGPGNGLDKGPPVNKADSVALEHDKAYDQQLKAGDNPYIKFNHADQDFIDSLQDDQSFGGNLGKAVFQAKKRILEPF--GLVED--------PVN
lcl|MF441225.1_cds_ATX74769.1_2/1-14          -----MSTFLDSFEEWYE------------TAAASWRNLKAGAP-QPKPNQQSQSV-SPDREPERRDNNRGFVLPGYKYLGPGNGLDKGPPVNKADSVALEHDKAYDLQLKAGDNPYIKFNHADQDFIDGLQHDHSFGGNLGKAVFQAKKRILEPF--GLVEE--------PIN
lcl|MF441221.1_cds_ATX74761.1_2/1-14          -----MSTFLDSFEEWYE------------TAAASWRNLKAGAP-QPKPNQQSQSV-SPDREPERRDNNRGFVLPGYRYLGPGNGLDKGPPVNKADSVALEHDKAYDLQLKAGDDPYIKFNHADQDFIDSLQHDHSFGGNLGKAVFQAKKRILEPF--GLVEE--------PIN
lcl|KT751090.1_cds_AMK92591.1_2/1-14          -----MSTFLDSFEEWYE------------TAAASWRNLKAGAP-QPKPNQQSQSV-SPDREPERRDNNRGFVLPGYKYLGPGNGLDKGPPVNKADSVALEHDKAYDLQLKAGDNPYTKFNHADQDFIDSLQHDHSFGGNLGKAVFQAKKRILEPF--GLVEE--------PIN
CornSnake|KP733795_1/1-136                    -----MDFVDDFFTDKYKET----YK-------------ELSKPVNPKPVQQISEKHS------EPGS-RGLVLPGYRYLGPGNSLDRGEPVNEADAAAREHDISYNKQLEVGDNPYVKYNHADEKLQSDLQGDVSFGGNAANAVFQAKKRLLEPF--GLVEA-PL-----P-A
lcl|EF515837.1_cds_ABP82770.1_3/1-14          -----MSTFLDSFEEWYE------------TAAASWRHLKAGAP-KPKPNQQSQSV-STDRKPQRKDNNRGFVLPGYKYLGPGNGLDKGPPVNKADSVALEHDKAYDQQLKAGDNPYIKFNHADQEFIDSLQDDRSFGGNLGKAVFQAKKRILEPL--GLVEE--------PVN
lcl|MF942875.1_cds_AXG65513.1_1/1-14          -----MSTFLDSFEEWYE------------TAAASWRNLKAGAP-HPKPNQQTQSV-SPDREPERRDNNRGFVLPGYKYLGPGNGLDKGPPVNKADSVALEHDKAYDLQLKAGDNPYIKFNHADQDFIDSLQHDRSFGGNLGKAVFQAKKRILEPF--GLVED--------PIN
lcl|MF429924.1_cds_AXK47377.1_1/1-14          -----MSTFLDSFEEWYE------------TAAASWRNLKAGAP-HPKPNQQTQSL-SPAREPERRDNNRGFVLPGYKYLGPGNGLDKGPPVNKADSVALEHDKAYDQQLKAGDNPYIKFNHADQDFIDSLQDDQSFGGNLGKAVFQAKKRILEPL--GLVED--------PVN
lcl|KR136258.1_cds_ALI16103.1_2/1-14          -----MSTFLDSFEEWYE------------TAAASVGNLKAGAP-HPKPNQQTQSV-SPAREPERRDNNRGFVLPGYKYLGPGNGLDKGPPVNKADSVALEHDKAYDQQLKAGDNPYIKFNHADQDFIDSLQDDQSFGGNLGKAVFQAKKRILEPF--GLVED--------PVN
lcl|MK736656.1_cds_QDH44605.1_2/1-14          -----MSTFLDSFEEWYE------------TAAASWRNLKAGAP-QPKPNQQSQSV-SPAREPERRDNNRGFVLPGYKYLGPGNGLDKGPPVNNADSVALEHDKAYDQQLKAGDNPYIKFNHADQDFIDSLQDDQSFGGNLGKAVFQAKKRILEPF--GLVED--------PVN
AvianAAV_VR865|NC_004828_1_cds_NP_85          -----MSLISDAIPDWLERL----VK-KGVNAAADFYHLESGPP-RPKANQQTQ-------ESLEKDDSRGLVFPGYNYLGPFNGLDKGEPVNEADAAALEHDKAYDLEIKDGHNPYFEYNEADRRFQERLKDDTSFGGNLGKAIFQAKKRVLEPF--GLVED---------SK
lcl|KT232256.1_cds_AKP07377.1_2/1-14          -----MSTFLDSFEEWYE------------TAAASWRNLKAGAP-HPKPNQQTQSV-SPAREPERRDNNRGFVLPGYKYLGPGNGLDKGPPVNNADSVALEHDKAYDQQLKAGDNPYIKFNHADQDFIDSLQDDQSFGGNLGKAVFQAKKRILEPF--GLVED--------PVN
lcl|KU844283.1_cds_ANX99769.1_2/1-14          -----MSTFLDSFEEWYE------------TAAASWRNLKAGAP-QPKPNQQSQSV-SPDREPERRDNNRGFVLPGYKYLGPGNGLDKGPPVNKADSVALEHDKAYDLQLKSGDNPYIKFNHADQDFIDSLQDDHSFGGNLGKAVFQAKKRILEPF--GLVEE--------PIN
lcl|EU088103.1_cds_ABU50786.1_1/1-14          -----MSTFLDSFEEWYE------------TAAASWRNLKAGAP-HPKPNQQTQSV-SPAREPERRDNNRGFVLPGYRYLGPGNGLDKGPPVNKADSVALEHDKAYDQQLKAGDNPYIKFNHADQDFIDSLQDDQSFGGNLGKAVFQAKKRILEPF--GLVED--------PVN
lcl|KR265066.1_cds_ALH24915.1_1/1-14          -----MSTFLDSFEGWYG------------TAAASWRNLKAGAP-HPKPNQQTQSV-SPAREPERRDNNRGFVLPGYKYLGPGNGLDKGPPVNKADSVALEHDKAYDQQLKAGDNPYIKFNHADQDFIDSLQDDQSFGGNLGKAVFQAKKRILEPF--GLVED--------PVN
lcl|KY411078.1_cds_ATU81352.1_1/1-14          -----MSTFLDSFEEWYE------------TAAASWRNLKAGAP-HPKPNQQTQSV-SPAREPERRDNTRGFVLPGYKYLGPGNGLDKGPPVNKADSVALEHDKAYDQQLKAGDNPYIKFNHADQDFIDSLQDDQSFGGNLGKAVFQAKKRILEPF--GLVED--------PVN
lcl|KR265068.1_cds_ALH24917.1_1/1-14          -----MSTFLDSFREWYE------------TAAASWRNLKAGAP-HPKPNQQTQSV-SPAREPERRDNNRGFVLPGYKYLGPGNGLDKGPPVNKADSVALEHDKAYDQQLKAGDNPYIKFNHADQDFIDSLQDDQSFGGNLGKAVFQAKKRILEPF--GLVED--------PVN
lcl|AY506547.1_cds_AAR91603.1_1/1-14          -----MSTFLDSFEEWYE------------TAAASWRNLKVGAP-HPKPNQQTQSV-SPAREPERRDSNRGFVLPGYKYLGPGNGLDKGPPVNKADSVALEHDKAYDQQLKAGDNPYIKFNHADQDFIDSLQDDRSFGGNLGKAVFQAKKRILEPF--GLVED--------SIN
lcl|KT598506.1_cds_AOG75033.1_2/1-14          -----MSTFLDSFEEWYE------------TAAASWRNLKAGAP-HPKPNQQTQSV-SPAREPERRDNNRGFVLPGYKYLGPGNGLDKGPPVNKADSVALEHDKAYDQQLKAGDNPYIKFNHADQDFIDSLQDDRSFGGNLGKAVFQAKKRILEPF--GLVED--------SIN
lcl|AY382889.1_cds_AAR24363.1_1/1-14          -----MSTFLDSFEEWYE------------TAAASWRNLKAGAP-HPKPNQQTQSV-SPAREPERRDNNRGFVLPGYKYLGPGNGLDKGPPVNKADSVALEHDKAYDQQLKAGDNPYIRFNHADQDFIDSLQDDQSFGGNLGKAVFQAKKRILEPF--GLVED--------PVN
lcl|KY744743.1_cds_ASR91721.1_2/1-14          -----MSTFLEKFEDWYE------------TAAASWRHLKAGAP-KPKSNQQSQSV-STDRKPQRKDNNRGFVLPGYKYLGPGNGLDKGPPVNKADSIALEHDKAYDQQLKAGDNPYIKFNHADQEFIDNLQGDTSFGGNLGKAVFQAKKRILEPL--GLVEE--------PVN
lcl|MH807698.1_cds_QBY91918.1_2/1-14          -----MSTFLEKFEDWYE------------TAAASWRHLKAGAP-KPKSNQQSQSV-STDRKPRRKDNNRGFVLPGYKYLGPGNGLDKGPPVNKADSVALEHDKAYDQQLKAGDNPYIKFNHADQEFIDNLQGDTSFGGNLGKAVFQAKKRILEPL--GLVEE--------PVN
lcl|KC171936.1_cds_AGG53768.1_2/1-14          -----MSTFLEKFEDWYE------------TAAASWRHLKAGAP-KPKSNQQSQSV-STDRKPQRKDNNRGFVLPGYKYLGPGNGLDKGPPVNKADSVALEHDKAYDQQLKAGDNPYIKFNHADQEFIDNLQGDTSFGGNLGKAVFQAKKRILEPL--GLVEE--------PVN
lcl|KR029614.1_cds_AKP07369.1_2/1-14          -----MSTFLEKFEDWYE------------TAAASWRHLKAGAP-KPKSNQQSQSV-STDGKPQRKDNNRGFVLPGYKYLGPGNGLDKGPPVNKADSVALEHDKAYDQQLKAGDNPYIKFNHADQEFIDNLQGDTSFGGNLGKAVFQAKKRILEPL--GLVEE--------PVN
lcl|KR075690.1_cds_AKP07383.1_2/1-14          -----MSNFLEKFEDWYE------------TAAASWRHLKAGAP-KPKSNQQSQSV-STDRKPRRKDNNRGFVLPGYKYLGPGNGLDKGPPVNKADSVALEHDKAYDQQLKAGDNPYIKFNHADQEFIDNLQGDTSFGGNLGKAVFQAKKRILEPL--GLVEE--------PVN
MuscovyDuck|NC_006147_2/1-145                 -----MSTFLEKFEDWYE------------TAAASWRHLKAGAP-KPKSNQQSQSV-STDRKPQRKDNNRGFVLPGYKYVGPGNGLDKGPPVNKADSVALEHDKAYDQQLKAGDNPYIKFKHADQEFIDNLQGDTSFGGNLGKAVFQAKKRILEPL--GLVEE--------PVN
Rhinolophus_Pusillus_BtAAV-CXC1|MK39          MSRVVMS-FVDHPPDWLKE---------VAGGLREFLDLEPGAP-RPKANQQKQD-------------QRGLVVPGYKYLGPFNGLDKGQPVNKADEVAREHDLEYNKLLEAGDNPYLKYNHADSEFQEKLQDDKSWGGNLGKAVFQAKKRVLEPF--GLVEE-------TPAK
lcl|KT865605.1_cds_AMO03313.1_2/1-14          -----MSTFLEKFEDWYE------------TAAASWRHLKAGAP-KPKSNQQSQSV-STDRKPQRKDNNRGFVLPGYKYLGPGNGLDKGPPVNKADSVALEHDKAYDQQLKAGDNPYIKFNHADREFIDNLQGDTSFGGNLGRAVFQAKKRILEPL--GLVEE--------PVN
lcl|AY382891.1_cds_AAR24365.1_1/1-14          -----MSTFLEKFEDWYE------------TAAASWRHLKAGAP-KPKSNQQSQSV-STDRKPQRTDNNRGFVLPGYKYLGPGNGLDKGPPVNKADSVALEHDKAYDQQLKAGDNPYIKFNHADQEFINNLQGDTSFGGNLGKAVFQAKKRILEPL--GLVEE--------PVN
lcl|AY510603.1_cds_AAR92460.1_1/1-14          -----MSTFLEKFEDWYE------------TAAASWRHLKAGAP-KPKSNQQSQSV-STDRKPQRKDNNRGFVLPGYKYLGPGNGLDKGPPVNKADNIALEHDKAYDQQLKAGDNPYIKFNHADQEFIDNLQGDTSFGGNLGKAVFQAKKRILEPL--GLVEE--------PVN
lcl|KU844282.1_cds_ANX99767.1_2/1-14          -----MSTFLEKFEDWYE------------TAAASWRHLKAGAP-KPKSNQQSQSV-STDRKPQRKDNNRGFVLPGYKYLGPGNGLDIGPPVNKADSIALEHDKAYDQQLKAGDNPYIKFNHADQEFIDNLQGDTSFGGNLGKAVFQAKKRILEPL--GLVEE--------PVN
lcl|KR075689.1_cds_AKP07381.1_2/1-14          -----MSTFLEKFEDWYE------------TAAASWRHLKAGAP-KPKSNQQSQSV-STDRKPQRNDNNRGFVLPGYKYLGPGNGLDKGPPVNKADSVALEHDKAYDQQLKAGDNPYIKFNHADQEFIDNLQGDTSFGGNLGKAVFQAKKRILEPL--GLVEE--------PVN
SnakeAAV|NC_006148_1/1-137                    -----MDFLDDFFADKYKET----VN-------------ELGKPVNPKPVKHISEAHS------QPGSRRGFVVPGYRYLGPGNSLDRGKPVNKADEAAKKHDQEYDQQLKAGDNPYIKYNHADEQFQKDLQGDTSLAGNAANALFQGKKTLLAPL--GLVET-PV-----G-K
CaliforniaSeaLion|NC_038539_1/1-2157          -----MS---SLFKEYLQS--------TGLVGI------QSGAP-KPKAGQQKQDT-GSFEWKKKEDTARGLVLPGYKYLGPFNGLERGEPVNAADAAAQRHDRQYDRILQQGGNPYLTYNHADREFQEELQSDESFGGNLGKAVFQAKKRILEPL--GLVEEDPSQPDSSSDN
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DesmodusRotundus|MG745677_1/1-2157_D      -----MT--------WTICPP-----------------FDTNPS-NPFLVEQKSE--GPTQ------KKRGWVWPGYKYLGPGNSLDKGEPVNALDAAARLHDIGYSRLQEKGVNPYLLYSSVDADFQSAIQTDKSFEGNLARGLFQLKRRLFPHT--GVVPEDLG--NQAGVQ
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S5 Alignment. The VP2c region (common to VP1 and VP2) lacks cysteine in all dependoparvoviruses, and lacks tyrosine in dependoparvoviruses A, B, and in some porcine AAVs

Sequence alignment of *dependoparvovirus* VP2c in PFAM format.

VP2c contains no cysteine (C, highlighted in blue), apart from one strain of *dependoparvovirus A* (AAV_CHC2731_AAV.FL.linear), and the strain GXN45 of a species annotated as *duck parvovirus*. Their name and accession number are indicated in blue to the left of the alignment.
The *duck parvovirus* sequence does not in fact contain cysteines, which were artefactually introduced by a frameshift sequencing error (nucleotides 2847-2963 of the genomic sequence [accession number MH717783.1] were translated in the +2 frame instead of the +0 VP1 frame).

VP2c contains no tyrosine (Y, highlighted in magenta) in dependoparvoviruses A, B, and in most porcine AAVs. The name and accession number of porcine AAV sequences that contain a tyrosine are indicated in magenta to the left of the alignment. In contrast, VP2c contains a tyrosine in many other dependoparvoviruses, which we have not indicated to not clutter the alignment.

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Dependoparvoviruses A
AAV2|NC_001401.2_cds_YP_680426.1_5/138-     TAP--GKKR--------------PVE---------HS-------PV-EPDSSSGTGKAG-QQPARKR-------------LNF--GQTGDADSVPDPQPLGQPPAAPSG-LGTNT
lcl|AY530578.1_cds_AAS99263.1_1/138-202     TAP--GKKR--------------PVE---------HS-------PA-EPDSSSGTGKAG-QQPARKR-------------LNF--GQTGDADSVPDPQPLGQPPAAPSG-LGTNT
lcl|MK139281.1_cds_QDH44340.1_5/138-202     TAP--GKKR--------------PVE---------HS-------PV-EPDSSSGTGKAG-QQPARKR-------------LNF--GQTGDADSVPDPQPLGQPPAAPSG-LGTTT
lcl|MK139287.1_cds_QDH44380.1_5/138-202     TAP--GKKR--------------PVE---------HS-------PV-EPDSSSGTGKAG-NQPARKR-------------LNF--GQTGDADSVPDPQPLGQPPAAPSG-LGTNT
lcl|MK163935.1_cds_QDH44515.1_5/138-202     TAP--GKKR--------------PVE---------HS-------PA-EPDSSSGTGKAG-NQPARKR-------------LNF--GQTGDADSVPDPQPLGQPPAAPSG-LGTNT
lcl|EU368915.1_cds_ACB55307.1_1/138-202     TAP--GKKR--------------PVE---------HS-------PA-EPDSSSGTGKSG-NQPARKR-------------LNF--GQTGDSDSVPDPQPLGQPPAAPSG-LGTNT
lcl|AY530618.1_cds_AAS99303.1_1/138-202     TAP--GKKR--------------PVE---------HS-------PV-EPDSSSGTGKAG-NQPARKR-------------LNF--GQTGDADSVPDPQPLGQPPASPSG-LGTNT
lcl|MK139248.1_cds_QDH44113.1_5/138-202     TAP--GKKR--------------PVE---------HS-------PA-EPDSSSGTGKSG-NQPARKR-------------LNF--GQTGDADSVPDPQPLGQPPAAPSG-LGTNT
lcl|MK139274.1_cds_QDH44291.1_5/138-202     TAP--GKKR--------------PVE---------HS-------PV-EPDSSSGTGKSG-QQPARKR-------------LNF--GQTGDADSVPDPQPLGQPPAAPSG-LGTNT
lcl|AY530625.1_cds_AAS99310.1_1/138-202     TAP--GKKR--------------PVE---------HS-------LA-EPDSSSGTGKAG-QQPARRR-------------LNF--GQTGDADSVPDPQPLGQPPAAPSG-LGTNT
lcl|AY530590.1_cds_AAS99275.1_1/138-202     TAP--GKKR--------------PVE---------HS-------PA-EPDSSSGTGKAG-QQPARKR-------------LNF--GQTGDADSVPDPRPLGQPPAAPSG-LGTNT
lcl|AY530584.1_cds_AAS99269.1_1/138-202     TAP--GEKR--------------PVE---------HS-------PA-EPDSSSGTGKAG-QQPARKR-------------LNF--GQTGDADSVPDPQPLGQPPAAPSG-LGTNT
lcl|AY530586.1_cds_AAS99271.1_1/138-202     AAP--GEKR--------------PVE---------HS-------PA-EPDSSSGTGKAG-QQPARKR-------------LNF--GQTGDADSVPDPQPLGQPPAAPSG-LGTNT
lcl|AY695375.1_cds_AAU05368.1_2/138-202     TAP--GKKR--------------PVE---------HS-------PA-EPDSSSGTGKSG-QQPARKR-------------LNF--GQTGDADSVPDPQPLGQPPAAPSG-LGTNT
lcl|MK139289.1_cds_QDH44394.1_5/138-202     TAP--GKKR--------------PVE---------HS-------PA-EPDSSSGTGKSG-QQPARKR-------------LNF--GQTGDADSVPDPQPLGEPPAAPTS-LGSTT
lcl|MK139243.1_cds_QDH44082.1_5/138-202     TAP--GKKR--------------PVE---------HS-------PA-EPDSSSGTGKAG-QQPARKR-------------LNF--GQTGDADSVPDPQPLGQPPAAPTS-LGSTT
lcl|MK139278.1_cds_QDH44319.1_5/135-199     TAP--GKKR--------------PVE---------HS-------PV-EPDSSSGTGKAG-QQPARKR-------------LNF--GQTGDSDSSSRDMRKVFSAAAPTS-LGSTT
lcl|MK139245.1_cds_QDH44092.1_1/138-202     TAP--GKKR--------------PVE---------HS-------PV-EPDSSSGTGKAG-QQPARKR-------------LNF--GQTGDADSVPDPQPLGQPPAAPSG-LGSTT
lcl|MK139277.1_cds_QDH44312.1_5/138-202     TAP--GKKR--------------PVE---------HS-------PA-EPDSSSGTGKAG-QQPARKR-------------LNF--GQTGDADSVPDPQPLGQPPAAPSG-LGSTT
lcl|MK139294.1_cds_QDH44429.1_5/138-202     TAP--GKKR--------------PVE---------HS-------PV-EPDSSSGTGKAG-QQPAKKR-------------LKF--GQTGDADSVPDPQPLGQPPAAPSG-LGSTT
lcl|AY530623.1_cds_AAS99308.1_1/138-202     TAP--GKKR--------------PVE---------HP-------PV-EPDSSSGTGKAG-QQPARKR-------------LNF--GQTGDADSVPDPQPLGQPPAAPSG-LGSTT
lcl|MK139268.1_cds_QDH44249.1_5/138-202     TAP--GKKR--------------PVE---------HS-------PV-EPDSSSGTGKAG-QQPARKR-------------LNF--GQTGDADSVPDPQPLGKPPAAPSG-LGSTT
lcl|MK139257.1_cds_QDH44176.1_5/138-202     TAP--GKKR--------------PVE---------HS-------PA-EPDSSSGIGKAG-QQPARKR-------------LNF--GQTGDADSVPDPQPLGQPPAAPSG-LGSTT
lcl|MK139279.1_cds_QDH44326.1_5/138-202     TAP--GKKR--------------PVE---------HS-------PA-EPDSSSGTGKSG-NQPARKR-------------LNF--GQTGDADSVPDPQPLGQPPAAPSG-LGSTT
lcl|AY530585.1_cds_AAS99270.1_1/138-202     TAP--GKKR--------------PVE---------HS-------PV-EPDSSSGTGKAG-QRPARKR-------------LNF--GQTGDADSVPDPQPLGQPPAAPSG-LGSTT
lcl|MK163934.1_cds_QDH44507.1_5/138-202     TAP--GKKR--------------PVE---------HS-------PV-EPDSSSGTGKAG-NQPARKR-------------LNF--GQTGDADSVPDPQPLGQPPAAPSG-LGSTT
lcl|MK139296.1_cds_QDH44443.1_5/138-202     TAP--GKKR--------------PVE---------HS-------PV-EPDSSSGTGKAG-QQPAKKR-------------LNF--GQTGDADSVPDPQPLGQPPAAPSG-LGSTT
CHC2320_AAV.FL |MK139290.1                  TAP--GKKR--------------AVE---------HA-------HV-EPDSSSGTGKAG-QQPARKR-------------LNF--GQTGDADSVPDPQPLGQPPAAP-G-LGSTT
lcl|MK139297.1_cds_QDH44450.1_5/138-202     TAP--GKKR--------------PVE---------HS-------PA-EPDSSSGTGKAG-NQPARKR-------------LNF--GQTGDADSVPDPQPIGQPPAAPTS-LGSTT
lcl|AY530577.1_cds_AAS99262.1_1/138-202     TAP--GKKR--------------PVE---------HS-------PV-EPDSSSGTGKAG-HQPARKR-------------LNF--GQTGDADSVPDPQPLGQPPAAPTS-LGSTT
lcl|AY695376.1_cds_AAU05370.1_2/138-202     TAP--GKKR--------------PVE---------HS-------PA-EPDSSSGTGKSG-QQPARKR-------------LNF--GQTGDSDSVPDPQPLGEPPAAPTS-LGSTT
AAVch.5|AY243021.1_cds_AAO88207.1_1/138     TAP--GKKR--------------PIE---------QS-------PA-EPDSSSGIGKSG-QQPAKKR-------------LNF--GQTGDTESVPDPQPIGEPPAAPSG-VGSNT
lcl|AY530615.1_cds_AAS99300.1_1/138-202     TAP--GKKR--------------PVE---------HS-------PA-EPDSSSGTGKAG-QQPARKR-------------LNF--GQTGDADSVPDPQPLRQPPAAPTS-LGSTT
lcl|MK139252.1_cds_QDH44141.1_5/136-200     TAP--GKKR--------------PVA---------HS-------PA-EPDSSSGTGKAG-NQPARKR-------------LNF--GQTGDADSVPDPQPLGQPPAAPTS-LGSTT
lcl|MK139267.1_cds_QDH44242.1_5/138-202     TAP--GKKR--------------PVE---------HS-------PA-EPDSSSGTGKSG-QQPARKR-------------LNF--GQTGDADSVPDPQPLGQPPAAPSG-LGSTT
AAV3B|AF028705.1_cds_AAB95452.1_2/138-2     TAP--GKKR--------------PVD---------QS-------PQ-EPDSSSGVGKSG-KQPARKR-------------LNF--GQTGDSESVPDPQPLGEPPAAPTS-LGSNT
AAV3|NC_001729_1/138-202                    TAP--GKKG--------------AVD---------QS-------PQ-EPDSSSGVGKSG-KQPARKR-------------LNF--GQTGDSESVPDPQPLGEPPAAPTS-LGSNT
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lcl|AY243008.1_cds_AAO88194.1_1/138-203     TAP--GKKR--------------PVE---------PS-------PQRSPDSSTGIGKTG-QQPAKKR-------------LNF--GQTGDSESVPDPQPIGEPPAGPSG-LGSGT
lcl|EU368916.1_cds_ACB55308.1_1/138-202     TAP--GKKR--------------PVE---------QS-------PQ-GPDSSSGIGKTG-QQPAKKR-------------LNF--GQTGDSESVPDPQPLGEPPATPAA-VGPTT
lcl|AY530609.1_cds_AAS99294.1_1/138-202     TAP--GKKR--------------PVE---------QS-------PQ-EPDSPSGIGKTG-QQPAKKR-------------LNF--GQTGDSESVPDPQPLGEPPATPAA-VGPTT
lcl|AY530597.1_cds_AAS99282.1_1/138-202     TAP--GKKR--------------PVE---------QS-------PQ-EPDSSAGIGKSG-SQPAKKK-------------LNF--GQTGDTESVPDPQPIGEPPAAPSG-VGSLT
lcl|AY530560.1_cds_AAS99245.1_1/138-202     TAP--GKKR--------------PVE---------QS-------PQ-EPDSSSGIGKKG-QQPARKR-------------LNF--GQTGDSESVPDPQPLGEPPAAPSG-VGPNT
lcl|EU368925.1_cds_ACB55317.1_1/138-202     TAP--GKKR--------------PVE---------QS-------PQ-EPDSSSGIGKTG-QQPAKKR-------------LNF--GQTGDSESVPDPQPLGEPPAAPSG-LGPNT
lcl|KT984498.1_cds_APD78414.1_2/138-202     TAP--GKKR--------------PVE---------QS-------PQ-EPDSSSGIGKSG-QQPAKKR-------------LNF--GQTGDSESVPDPQPLGEPPATPAA-VGPTT
lcl|EU368911.1_cds_ACB55303.1_1/138-202     TAP--GKKR--------------PVE---------QS-------PQ-EPDSSSGIGKTG-QQPAKKR-------------LNF--GQTGDSESVPDPQPLGEPPATPAA-VGPTT
lcl|AY530579.1_cds_AAS99264.1_1/138-202     TAP--GKKR--------------PVE---------QS-------PQ-EPDSSAGIGKSG-AQPAKKR-------------LNF--GQTGDTESVPDPQPIGEPPAAPSG-VGSLT
lcl|DQ180605.1_cds_ABA71701.1_2/138-202     TAP--GKKR--------------PVE---------QS-------PQ-EPDSSSGIGKSG-QQPAKKR-------------LNF--GQTGDSESVPDPQPLGEPPATPAA-LGPTT
AAV12|DQ813647.1_cds_ABI16639.1_2/138-2     TAP--GKKR--------------PL----------EKTPN---RPT-NPDS-------G-KAPAKKKQKDGEPADSARRTLDF--EDSGAGDG-P---PEGSSSGEMSH---DAE
lcl|AY530571.1_cds_AAS99256.1_1/138-203     TAP--GKKR--------------PVE---------PS-------PQRSPDSSTGIGKKG-QQPARKR-------------LNF--GQTGDSESVPDPQPIGEPPAAPSS-VGSGT
AAV_CHC2731_AAV.FL.linear|MK139293.1_cd     TAP--GKKR--------------PVAVAHQWQTITRV-------PM-E----------W-VIPQEKR-------------LNF--GQTGDADWHCDPQPLGQPPAAPSG-LGSTT
lcl|AY243014.1_cds_AAO88200.1_1/138-198     TAP--GKKR--------------PIE---------------------SPDSSTGIGKKG-QQPAKKR-------------LNF--GQTGDSESVPDPQPIGEPPAGPSG-LGSGT
lcl|AY243012.1_cds_AAO88198.1_1/138-198     TAP--GKKR--------------PIE---------------------SPDSSTGIGKKG-QQPAKKK-------------LNF--GQTGDSESVPDPQPIGEPPAGPSG-LGSGT
lcl|AY530606.1_cds_AAS99291.1_1/138-203     TAP--GKKR--------------PVE---------PS-------PQRSPDSSTGIGKKG-QQPAKKR-------------LNF--GQTGDSESVPDPQPIGEPPAGPSG-LGSGT
lcl|AY243016.1_cds_AAO88202.1_1/138-198     TAP--GKKR--------------PIE---------------------SPDSSTGIGKKG-QQPAKKK-------------LNF--GQTGDSESVPDPQPLGEPPAAPSG-LGSGT
lcl|AY243018.1_cds_AAO88204.1_1/138-198     TAS--GKKR--------------PIE---------------------SPDSSTGIGKKG-QQPAKKK-------------LNF--GQTGDSESVPDPQPLGEPPAAPSG-LGSGT
lcl|EU368913.1_cds_ACB55305.1_1/138-198     TAP--GKKR--------------PIE---------------------SPDSSTGIGKNG-QPPAKKK-------------LNF--GQTGDSESVPDPQPLGEPPAAPSG-LGSGT
lcl|AY530567.1_cds_AAS99252.1_1/138-203     TAP--GKKR--------------PVE---------PS-------PQRSPDSSTGIGKKG-QQPARKR-------------LNF--GQTGDSESVPDPQPLGEPPAGPSG-LGSGT
lcl|EU368923.1_cds_ACB55315.1_1/138-203     TAP--GKKR--------------PVE---------PS-------PQRSPDSSTGIGKKG-QQPARKR-------------LNF--GQTGDSESVPDPQPIGEPPAGPSG-LGSGT
lcl|EU368926.1_cds_ACB55318.1_1/138-196     TAP--GKKR--------------PL----------ES-------PQ-EPDSSSGIGKKG-KQPAKKR-------------LNFE-EDTGAGDG-P---PEGSDTSAMSS---DIE
lcl|EU368920.1_cds_ACB55312.1_1/138-198     TAP--GKKR--------------PID---------------------SPDSSTGIGKKG-QQPAKKK-------------LNF--GQTGDSESVPDPQPLGEPPAAPSS-VGSGT
lcl|AY243020.1_cds_AAO88206.1_1/138-203     TAP--AKKR--------------PVE---------PS-------PQRSPDSSTGIGKKG-QQPARKR-------------LNF--GQTGDSESVPDPQPLGEPPAAPSS-VGSGT
lcl|AY242999.1_cds_AAO88185.1_1/138-198     TAP--GKKR--------------PIG---------------------SPDSSTGIGKKG-QQPAKKK-------------LNF--GQTGDSESVPDPQPLGEPPAAPSS-VGSGT
lcl|AY631966.1_cds_AAT46339.1_2/138-196     TAP--GKKR--------------PL----------ES-------PQ-EPDSSSGIGKKG-KQPARKR-------------LNFE-EDTGAGDG-P---PEGSDTSAMSS---DIE
AAVpi.2|AY530554.1_cds_AAS99239.1_1/138     TAP--GKKR--------------PVE----------------------PDSSSGIGKSG-RQPAKKR-------------LNF--GQTGDSESVPDPQPLSEPPAGPSG-LGSGT
lcl|AY530555.1_cds_AAS99240.1_1/138-197     TAP--GKKR--------------PVE----------------------PDSSSGIGKSG-QQPAKKR-------------LNF--GPTGDSESVPDPQPLSEPPAGPSG-LGSGT
lcl|AY530553.1_cds_AAS99238.1_1/138-197     TAP--GKKR--------------PVE----------------------PDSSSGIGKSG-QQPAKKR-------------LNF--GQTGDSESVPDPQPLSEPPAGPSG-LGSGT
lcl|AY530556.1_cds_AAS99241.1_1/138-203     TAP--GKKR--------------PVE---------PS-------PQRSPDSSTGIGKKG-QQPARKR-------------LNF--GQTGDSESVPDPQPLGEPPAAPSG-VGPNT
lcl|AY243023.1_cds_AAO88209.1_1/138-203     TAP--GKKR--------------PVE---------PS-------PQRSPDSTTGIGKKG-QQPAKKR-------------LNF--GQTGDSESVPDPQPIGEPPAGPSG-LGSGT
lcl|AY530601.1_cds_AAS99286.1_1/138-203     TAP--GKKR--------------PVE---------PS-------PQRSPDSSTGIGKKG-QQPARKR-------------LNF--GRTGDSESVPDPQPIGEPPAAPSS-VGSGT
lcl|AY530563.1_cds_AAS99248.1_1/138-203     TAP--GKKR--------------PVE---------PS-------PQRSPDSSTGIGKKG-QQPAGKR-------------LNF--GQTGDSESVPDPQPIGEPPAAPSS-VGSGT
lcl|AY631965.1_cds_AAT46337.1_2/138-203     TAP--GKKR--------------PVE---------PS-------PQRSPDSSTGIGKKG-QQPAKKR-------------LNF--GQTGESESVPDPQPIGEPPAGPSG-LGSGT
lcl|AY530562.1_cds_AAS99247.1_1/138-203     TAP--GKKR--------------PVE---------PS-------PQRSPDSSTGIGKKG-QQPARKR-------------LNF--GQTGDSESVPDPQLIGEPPAAPSS-VGSGT
lcl|AY530626.1_cds_AAS99311.1_1/138-203     TAP--GKKR--------------PVE---------PS-------PQRSPDSSAGIGKKG-QQPAKKR-------------LNF--GQTGDSESVPDPQPIGEPPAGPSG-LGSGT
lcl|EU368919.1_cds_ACB55311.1_1/138-203     TAP--GKKR--------------PVE---------PS-------PQRSPDSSTGIGKKG-HQPARKR-------------LNF--GQTGDSESVPDPQPIGEPPAGPSG-LGSGT
lcl|AY530603.1_cds_AAS99288.1_1/138-203     TAP--GKKR--------------PVE---------PS-------PQRSPDSSTGIGKKG-QQPAKKR-------------LSF--GQTGDSESVPDPQPIGEPPAGPSG-LGSGT
lcl|AY530558.1_cds_AAS99243.1_1/138-203     TAP--GKKR--------------PVE---------PS-------PQRSPDSSTGIGKKG-QRPAKKR-------------LNF--GQTGDSESVPDPQPIGEPPAGPSG-LGSGT
lcl|AY530604.1_cds_AAS99289.1_1/138-203     TAP--GKKR--------------PVE---------PP-------PQRSPDSSTGIGKKG-QQPAKKR-------------LNF--GQTGDSESVPDPQPIGEPPAGPSG-LGSGT
lcl|MH202997.1_cds_AXN94234.1_1/130-195     LAP--------------------PVKRP-------HS-------PEKTPEDQKGQPRPDPRTPAKKR-------------LEFS-DQPGSSADLPASSQQSQPPAGVPG-VVPGT
lcl|MH203003.1_cds_AXN94240.1_1/130-195     LAP--------------------PVKRP-------HS-------PEETPEDQKAQPRPDPRTPAKKR-------------LEFS-DQPGSSADLPASSQQSQPPAGVPG-VVPGT
lcl|MH202992.1_cds_AXN94229.1_1/130-195     LAP--------------------PVKRP-------HS-------PEKTPEDQKGQPRPDPRTPAKKR-------------LEFS-DQPGSAADLRTSSQQSQPPAGVPG-VVSGT
RatAAV1|DQ100363_1_cds_AAZ79676/130-195     LAP--------------------PVKRP-------HS-------PEKTPENQKGQPRPDPRTPAKKR-------------LEFS-DQPGSSADLPASSQQSQPPAGVPG-VVPGT
AAV4|NC_001829_1/137-196                    TAP--GKKR--------------PLI---------ES-------PQ-QPDSSTGIGKKG-KQPAKKK-------------LVFE-DETGAGDG-P---PEGSTSGAMSD---DSE
AAV13|EU285562.1_cds_ABZ10812.1_2/137-2     TAP--GKKR--------------PVE---------QS-------PA-EPDSSSGIGKSG-QQPARKR-------------LNF--GQTGDTESVPDPQPLGQPPAAPSG-VGSTT
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Dependoparvoviruses B

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AAV5|NC_006152_1/137-192                    TAP--TGKR---------IDDHFPKRK--------KARTEEDSKP--STSSDAEAGPSG-SQ-----------------QLQI--------------------PAQPASSLGADT
BovineAAV_BSRI1|KP264981_1_cds_AJE25863     TAP-AAKKR--------------PLE---------QS-------PQ-EPDSSSGFGKKG-KQPARKR-------------LNFD-DEPGAGDGPP---PEGPSSGAMST---ETE
BovineAAV|NC_005889_1_cds_YP_024971_1/1     TAP-AAKKR--------------PLE---------QS-------PQ-EPDSSSGVGKKG-KQPARKR-------------LNFD-DEPGAGDGPP---PEGPSSGAMST---ETE
```

Porcine AAVs

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AAVpo4|JX896667_1/1-2184_AAVpo4|JX896667    TAP--AKKR--------------PIE---------KS-------PA-EPSSSKGIGKAG-QQPARKR-------------LNF--GQTGDTDSAADPQPLGEPPAAPSG-LGTGT
AAVpo8|KM349849.1_cds_AIU56933.1_1/137-     TAP--AKKR--------------PVE---------QS-------PA-EPGPSSGIGKAG-DQPARKR-------------LNF--GQTGDADSEPDPQPLGEAPAANPN-LGSAT
AAVpo7|KM348848.1_cds_AIU56932.1_1/137-     TAP--AKKR--------------PVE---------QS-------PA-EPGSSSGIGKAG-NQPARKR-------------LNF--GQTGDADSEPDPQPLGEAPAANPD-LGSAT
AAVpo5|JX896666_1/137-183                   TAA--KGER---------IDDHYPKKK--------KARVEE-----------TEAGTSG-AQ-----------------QLQI--------------------PAQPASSLGADT
AAVpo1|FJ688147_1/137-183                   TAA--KGER---------IDDHYPKKK--------KARIEE-----------TEAGTSG-AQ-----------------QLQI--------------------PAQPASSLGADT
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Other dependoparvoviruses

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MarsupialAAV1|MK026553_3472_gbkey=C         LAPP-PKKKT-------------KQE----YKDTLEA-----IPPPSREEQTPQKGSSA-SKNGASS---------------------------------SAAAAAPSN-LGSGI
BatAAV_09YN|MH167452.1_cds_AWW87409.1_1     KTP--SVKR-----------------------------------PHASPDSSSGVGKKG-DQPARKR-------------LDFG-TEPASQDGAGR-------AAQATGDMASAE
lcl|MH167454.1_cds_AWW87411.1_1/137-192     KTP--SVKR-----------------------------------PHESPDSSSGVGKKG-DQPARKR-------------LDFG-TEPASQDGAGR-------AAQATGDMASAE
BatAAV_YNM|NC_014468_1/137-192              KTP--SVKR-----------------------------------PHASPDSSSGVGKKG-DQPARKR-------------LDFG-TEPAGQDGAGR-------AAQAAGDMASAE
MHH-05-2015|NC_040671.1_cds_YP_00955282     TAP-TNERRK------ENIDDYYPKR------KKAKAGEE---KPP-STDAVEGAGDG---EPSTST---G--------------GET------------------PSG-TQSNT
AvianAAV_BR_DF12|MN175614.1_cds_QEJ8080     ----AGKDS---------IKDYFPARK--------KAKTGG-GEPPAPPPIEEPKGVGG-AENGNAT---G--------------GGAG-------------AEGSPVS-GAASI
lcl|MH167453.1_cds_AWW87410.1_1/137-192     KTP--SVKR-----------------------------------PHASPDSSSGIGKRG-DQPARKR-------------LDFG-TEPASQDGAGR-------AANAAGDMASAE
MurineAAV2|MF416384_1/130-194               LAP--GKKR--------------PAA----------S-------PVQSPDSSSGIGKKG-AQPSRRR-------------LDF--DQA-DRETAAEAGATGTGSLPPASNLGPVT
lcl|DQ100362.1_cds_AAZ79672.1_2/130-189     LAPPSGRKR--------------PVQ----------S-------SQESGYSSS--------QDKRPN-------------LDV--DEE-DREFAAAAAETETGSAPPTGNLGPGT
lcl|AY629583.1_cds_AAT48615.1_2/147-203     TAG--TGEKR-----PERVDDFFPKK---------KK-------AKTEQGKAPAQTGED-PGEGTSS---------------------------------NAGSSAP-SSVGSSV
lcl|GQ368252.1_cds_ACU30842.1_2/147-203     TAG--TGEKR-----PERVDDFFPKK---------KK-------AKTEQGKTPAQTGED-PGEGTSS---------------------------------NAGSSAP-SSVGSSV
lcl|MG846444.1_cds_AXL64653.1_2/147-203     TAG--TGEKR-----PERVDDFFPKK---------KK-------AKTEQGKAPAQTGED-PGEGTSS---------------------------------NAGSSAP-SGVGSSI
RhinolophusPusillus|MF682926_1/1-2139_R     --P--RKR------------------------------------PASENNQSDVPAKR------RLI-------------LDPE-DNGAAEGEPIE-------QQQPANDMASAE
RhinopholusSiniAAV1|MF682927_1/1-2208_R     TAP--GKKRP------------RPIE---------PP-------PSSENSVDEDLVER---QAQRQR-------------LGFQ-DGPGNSANQV--------QQQPAANMASAE
lcl|EU088102.1_cds_ABU50783.1_1/146-198     TAP--AKKNT-----GKLTD-HYPVV---------KK-------PKLTEEVSAGGGSSA-VEDGGAT---------------------------------AEGT-EP---VAASE
PygmyChameleon|KP733796_1/1-1132_PygmyC     TSD--KRKPPPGLL-------TPPKT------PK-KQKFQI-PAPP---------NQAG-TSSAGSDT------------------------------------------SGTSI
MurineAAV1|MF416383_1_cds_AWB14638/130-     LAPPSGRKR--------------PVQ----------S-------SQESGYSSS--------QDKRPN-------------LDL--DEE-DRELAAAAAETETGSAPPTGNLGPGT
lcl|EU583392.1_cds_ACE95855.1_2/146-198     TAP--AKKNT-----GKLTD-HYPVV---------KK-------PKLTEEVSAGGGSSA-VQDGGAT---------------------------------AEGT-EP---VAASE
BeardedDragon|NC_027429_1/1-2178_Bearde     TAE--KRKTPEEWL-------AQEKT------PT-KQRFQI-PAPGQSGSDSPSTSGSG-GT-AGSSS------------------------------------------SASNT
lcl|KU684472.1_cds_ANN12566.1_2/146-198     TAP--TKKNT-----GKLTD-HYPVV---------KK-------PKLTEEVSAGGGSSV-VQDGGAT---------------------------------AEGT-EP---VAASE
lcl|KR265070.1_cds_ALH24919.1_1/146-198     TAP--AKKNT-----GKLTD-HYPVV---------KK-------PKLTEEVSAGGGTSA-VQDGGAT---------------------------------AEGT-EP---VAASE
lcl|MF962899.1_cds_AXG65518.1_1/146-198     TAP--VKKNT-----GKLTD-HYPVV---------KK-------PKLTEEVSAGGGTSA-VQDGGAT---------------------------------AEGT-EP---VAASE
lcl|MF441222.1_cds_ATX74763.1_2/146-198     TAP--AKKNT-----GKLTD-HYPVV---------KK-------PKLTEEVSAGGGSSV-VQDGGAT---------------------------------AEGT-EP---VAASE
lcl|MF405917.1_cds_ASR73561.1_1/146-198     TAP--AKKNT-----GKLTD-HYPVV---------KK-------AKLTEEVSAGGGTSA-VQDGGAT---------------------------------AEGT-EP---VAASE
lcl|KT751090.1_cds_AMK92591.1_2/146-198     MAP--AKKNT-----GKLTD-HYPVV---------KK-------PKLTEEVSAGGGSSV-VQDGGAT---------------------------------AEGT-EP---VAASE
CornSnake|KP733795_1/137-189                KTD--KGKVDD----------YFPKA------KKAKQTFQI-PPPAKEDPGEGSSAQSG-GSPAGSDT------------------------------------------SGSSV
lcl|EF515837.1_cds_ABP82770.1_3/146-198     TAP--AKKSS-----GKLTD-HYPIV---------KK-------PKLSEENSPSPSNSG-GEASAAA---------------------------------TEGS-EP---VAAPN
lcl|KY679174.1_cds_ARF02874.1_2/146-198     TAP--AKKNT-----GKLTD-HYPVV---------RK-------PKLTEEVSAGGGSSV-VQDGGAT---------------------------------AEGT-EP---VAASE
lcl|MF429924.1_cds_AXK47377.1_1/146-198     TAP--AKKNT-----GKLTD-HYPVV---------KK-------PKLTEEVSAGGGTSA-VQDGGAT---------------------------------AKGT-EP---VAASE
lcl|MK736656.1_cds_QDH44605.1_2/146-198     TAP--AKKNT-----GKLTD-HYPVV---------KK-------PKLTEEVSAGGGTSV-VQDGGAT---------------------------------AEGT-EP---VAASE
lcl|KR265069.1_cds_ALH24918.1_1/146-198     TAP--TKKNT-----GKLTD-HYPVV---------KK-------PKLTEEVSAGGGSSA-VQDGGAT---------------------------------AEGT-EP---VAASE
AvianAAV_VR865|NC_004828_1_cds_NP_85278     TAP--TGDKRKGEDEPRLPDTSSQTP---------KK-------NKKPRKERPSGGAED-PGEGTSS---------------------------------NAGAAAPASSVGSSI
lcl|KR265066.1_cds_ALH24915.1_1/146-198     TAP--AKKNT-----GKLTD-HYPVV---------KK-------PKLTEEVSAGGGSSA-VQDGGAT---------------------------------GEGT-EP---VAASE
lcl|KT898978.1_cds_ALL25608.1_2/146-198     TAP--AKKSS-----GKLTD-HYPIV---------KK-------PKLSEENSPSLSNSG-GEASAAA---------------------------------TEGS-EP---VAAPN
DuckParvovirus GXN45|MH717783.1_cds_        TAP--AKK-------------------------------------KYREAYGPLPSSEE-AETHRGS---------------------------------QCGRWQQ---CRTRR
lcl|MH807445.1_cds_QBZ68882.1_2/146-198     TAP--AKKSS-----GKLTD-HYPIV---------KK-------PKLSEENSPSPSNSG-GEASAAA---------------------------------TEGS-EP---VAASK
lcl|KM093740.1_cds_AIR74894.1_2/146-198     MAP--AKKSS-----GKLTD-HDPIV---------KK-------PKLSEENSPSPSNSG-GEASAAA---------------------------------TEGS-EP---VAAPN
lcl|X75093.1_cds_CAA52984.1_2/146-198       TAP--AKKSS-----GKLTD-HDPIV---------KK-------PKLSEENSPSPSNSG-GEASAAA---------------------------------TEGS-EP---VAAPN
Rhinolophus_Pusillus_BtAAV-CXC1|MK39148     TAP--GKKR--------------PLES-----------------PWRSPDSSTGTGKKG-DQPSRKR-------------LNFDPPQDGSSEAAPSG---GGEGAAPSGNMATDI
lcl|KR029616.1_cds_AKP07373.1_2/146-198     TAP--AKKSS-----GKLTD-HYPVV---------KK-------PKLSEENSPSPSNSG-GEASAAA---------------------------------TEGS-EP---VAAPN
SnakeAAV|NC_006148_1/138-190                TSE--KHKLDE----------YYPKA------KKAKQGLQI-PAPPKGGEEEATSSQSG-GSPAGSDT------------------------------------------SGTSV
CaliforniaSeaLion|NC_038539_1/1-2157_Ca     TAPP-VKKS--------------RLE---------EA------QPIQSPDVSSSTG-----------------------------GGIADVMS------------------GDAE
DesmodusRotundus|MG745677_1/1-2157_Desm     AAG-AGATSG-------------TVE----------------GLPASSS-----------AKVSKRR---G--------DLGGR-GRGGK--------------------RRKIS
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