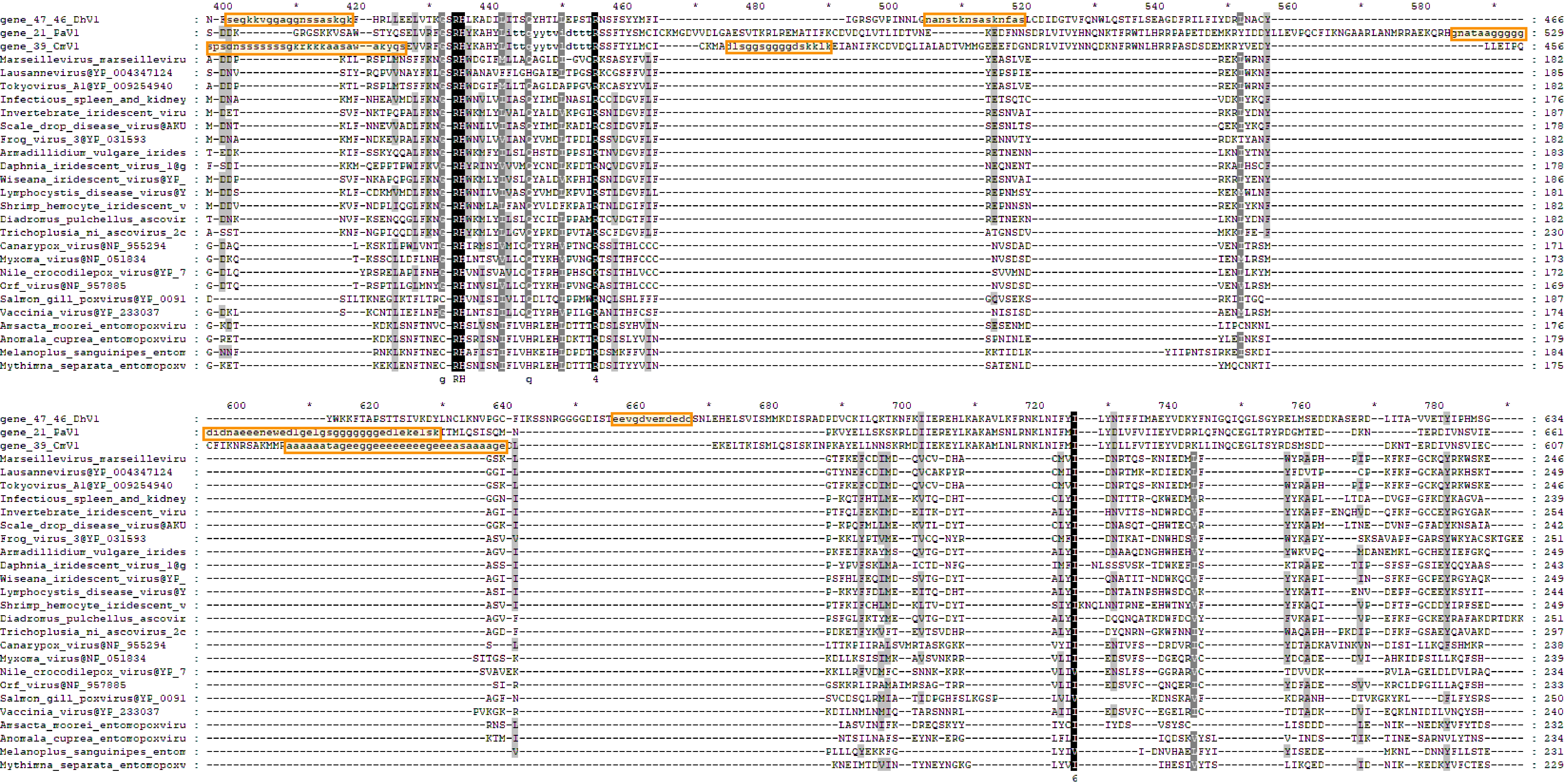
packaging ATPase

cluster PaV1_21 aligned with representative Pitho-, Irido, Marseille-, and Poxviruses


frameshift
gene_47_46_DhV1
gene_21_PaV1
gene_39_CmV1
Marseillevirus_marseilleviru
Lausannevirus@YP_004347124
Tokyovirus_A1@YP_009254940
Infectious_spleen_and_kidney
Invertebrate_iridescent_viru
Scale_drop_disease_virus@AKU
Frog_virus_3@YP_031593
Armadillidium_vulgare_irides
Daphnia_iridescent_virus_1@g
Wiseana_iridescent_virus@YP_
Lymphocystis_disease_virus@Y
Shrimp_hemocyte_iridescent_v
Diadromus_pulchellus_ascovir
Trichoplusia_ni_ascovirus_2c
Canarypox_virus@NP_955294
Myxoma_virus@NP_051834
Nile_crocodilepox_virus@YP_7
Orf_virus@NP_957885
Salmon_gill_poxvirus@YP_0091
Vaccinia_virus@YP_233037
Amsacta_moorei_entomopoxviru
Anomala_cuprea_entomopoxviru
Melanoplus_sanguinipes_entom
Mythimna_separata_entomopoxv
g g GK3
P
6 DD


gene_47_46_DhV1
gene_21_PaV1
gene_39_CmV1
Marseillevirus_marseilleviru
Lausannevirus@YP_004347124
Tokyovirus_A1@YP_009254940
Infectious_spleen_and_kidney
Invertebrate_iridescent_viru
Scale_drop_disease_virus@AKU
Frog_virus_3@YP_031593
Armadillidium_vulgare_irides
Daphnia_iridescent_virus_1@g
Wiseana_iridescent_virus@YP_
Lymphocystis_disease_virus@Y
Shrimp_hemocyte_iridescent_v
Diadromus_pulchellus_ascovir
Trichoplusia_ni_ascovirus_2c
Canarypox_virus@NP_955294
Myxoma_virus@NP_051834
Nile_crocodilepox_virus@YP_7
Orf_virus@NP_957885
Salmon_gill_poxvirus@YP_0091
Vaccinia_virus@YP_233037
Amsacta_moorei_entomopoxviru
Anomala_cuprea_entomopoxviru
Melanoplus_sanguinipes_entom
Mythimna_separata_entomopoxv
400
420
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640
660
680
700
720
740
760
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g RH
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Thymidylate or Deoxyguanosine kinase

cluster PaV1_15 aligned with nearest Pitho-, Irido, Marseilleviruses

taken from: ftp://ftp.ncbi.nih.gov/pub/yutinn/Loki_Castle_NCLDV_2018/PIM_clusters/PIM_afa/pim0066.afa

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                                *        20         *        40         *        60         *        80         *       100         *       120         *       140         *       160         *
gene_39_DhV1         : MNLIPSSTLPIYQINSKPRYS--------------------------------------NVDLNGTGDGG-------------------------YVKMNMNEPTLPSRRGCWGGASRANKSLSLGTPRDNLANRYQRLGL--------SERGNSKLSEHGCLS------- :  93
gene_15_PaV1         : LNG--------------------------------------------------------GILPPdggggggggrsgssdgdddAPAtvtettttitteittqrtttstkrrrteDLLRETNDESGAppppppsssssFAATPRLPEENEEPSSIagvgengaaaaaatgdg : 115
gene_45_CmV1         : MGGHRSaaaaaaRIGFLLRWVFVIISTLSIISIWEAELIPILHVAHLVYNFIHIYFAVRGISLNGRVGGGGe----eaeeeeeefpttttkktttttt-itttttstkttrfrt----raakeeaattptaaaaaeeeaat--------tptaaaaaaeeeaattptt--- : 151
gene_22_LCMAC101_5   : --------------------------------------------------------------------------------------------------------------------------------------------------------------------------- :   -
gene_23_LCPAC101_1   : ----------------------------------------------------------------------------------------------MSAFFKNKSIDGKNIND------------------------------------------------------------ :  17
gene_44_LCPAC202_1   : ----------------------------------------------------------------------------MTERLSNGDSYKTVEENEIMYQFKVGLTNGKNHSM-SYKLKYDIPLGDDPKWMTGLKGTFVRMSN------------------------------ :  64
gene_7_LCPAC201_2    : ----------------------------------------------------------------------------MTEQSSNGNSRKNEKADVVTYKVGLMKFTGDDCLITSYKLKYDMPLNDDLKWMTGLNGTFVRMSN------------------------------ :  65
gene_18_LCPAC001_1   : -------------------------------------------------------------------------------------------------------MSSPNIKI------------------------YNETNE------------------------------ :  14
gene_15_LCPAC104_3   : ---------------------------------------------------------------------------------------------------------MQKIRI------------------------FSVVNE------------------------------ :  12
lym_ir_YP_073536     : --------------------------------------------------------------------------------------------------------------------------------------------------------------------------- :   -
fro_ir_YP_031664     : --------------------------------------------------------------------------------------------------------------------------------------------------------------------------- :   -
sin_ir_YP_164162     : --------------------------------------------------------------------------------------------------------------------------------------------------------------------------- :   -
wis_ir_YP_004732882  : --------------------------------------------------------------------------------------------------------------------------------------------------------------------------- :   -
dia_as_YP_009220694  : --------------------------------------------------------------------------------------------------------------------------------------------------------------------------- :   -
tri_as_YP_803376     : --------------------------------------------------------------------------------------------------------------------------------------------------------------------------- :   -
hel_as_YP_001110907  : --------------------------------------------------------------------------------------------------------------------------------------------------------------------------- :   -
spo_as_YP_762395     : --------------------------------------------------------------------------------------------------------------------------------------------------------------------------- :   -

                             180         *       200         *       220         *       240         *       260         *       280         *       300         *       320         *       340
gene_39_DhV1         : ----HEPEHIYETIKEP----------VPKLTTMKGVEFKHF------------------GHDFLNKTLARNVSKGGEARGFQFL----------------------NTPSLNLKDDA-----VPT---------TNRSIGLGRNYALINVDGVTGSGKSYFIINK-LVDY : 195
gene_15_PaV1         : gRLLEENEEqqqqqqqppppssssAAELPENGPSSSAKETGaaaaaaaDKETAEPLYCKMTCdqddenlddddddqdGNrssrrhhphrfrfqqqqqqqqqqppppppsptqrqqqqqlqryrlppfppalkkllYDPKRE-GANIVFINVDGVTGSGKTVFINNK-LLPA : 284
gene_45_CmV1         : ----ttteeeeeaattp----ttttteveeedtsttaeveaatttptttt----------tteesttSLVEPDNDGMVYRnsnln----------------------stsaaaastnKIGRL-LPT---------YDPKEG-GAIVMFINVDGVVGSGKTIFINDT-LIPG : 270
gene_22_LCMAC101_5   : -----------------------------------------------------------------------------------------------------------------------------------------MASL-ISSFRVIVIDGIIGVGKTSLI-EECLVPL :  32
gene_23_LCPAC101_1   : ------------------------------------------------------------------------------------------------------------------------------------------IYG-ILKGSVICIEGLVGAGKSVAG-FS-VVEY :  47
gene_44_LCPAC202_1   : ---------------------------------------------------------------------------------------------------------------------------------------KARKWA-CLRGHVITIEGLIGAGKSTIG-RT-LVAY :  97
gene_7_LCPAC201_2    : ---------------------------------------------------------------------------------------------------------------------------------------EARKWA-CLRGHVITIEGLIGAGKSTLG-RS-LVAY :  98
gene_18_LCPAC001_1   : ---------------------------------------------------------------------------------------------------------------------------------------HFVKLR-CLGCSIIIVEGLVGAGKTTAG-TS-LKKC :  47
gene_15_LCPAC104_3   : ---------------------------------------------------------------------------------------------------------------------------------------YKKKYR-SISGTIITVEGLIGVGKSTIG-KK-LECF :  45
lym_ir_YP_073536     : ------------------------------------------------------------------------------------------------------------------------------------------------MSKIVCIGGNIGSGKTTLV-------- :  19
fro_ir_YP_031664     : ----------------------------------------------------------------------------------------------------------------------------------------------MSIPTVIAFSGNIGAGKSTLL-------- :  21
sin_ir_YP_164162     : ----------------------------------------------------------------------------------------------------------------------------------------------MALPFLISVSGNIGAGKSSLL-------- :  21
wis_ir_YP_004732882  : ------------------------------------------------------------------------------------------------------------------------------------------------MVYIVTIDAVIGAGKSSLI-SQ----- :  21
dia_as_YP_009220694  : --------------------------------------------------------------------------------------------------------------------------------------------------MYICIEGNIGCGKSSVL-------- :  17
tri_as_YP_803376     : -------------------------------------------------------------------------------------------------------------------------------------------------MIIISIEGNIGSGKSTII-NKLVEEY :  25
hel_as_YP_001110907  : ---------------------------------------------------------------------------------------------------------------------------------------MSSTTE-TESVVYVSVEGNIGSGKSSVM-RSV---- :  30
spo_as_YP_762395     : -------------------------------------------------------------------------------------------------------------------------------------------MT-TDSVVFVSVEGNIGSGKSSVM-RKA---- :  26
                                                                                                                                                                          6   g  G GK3
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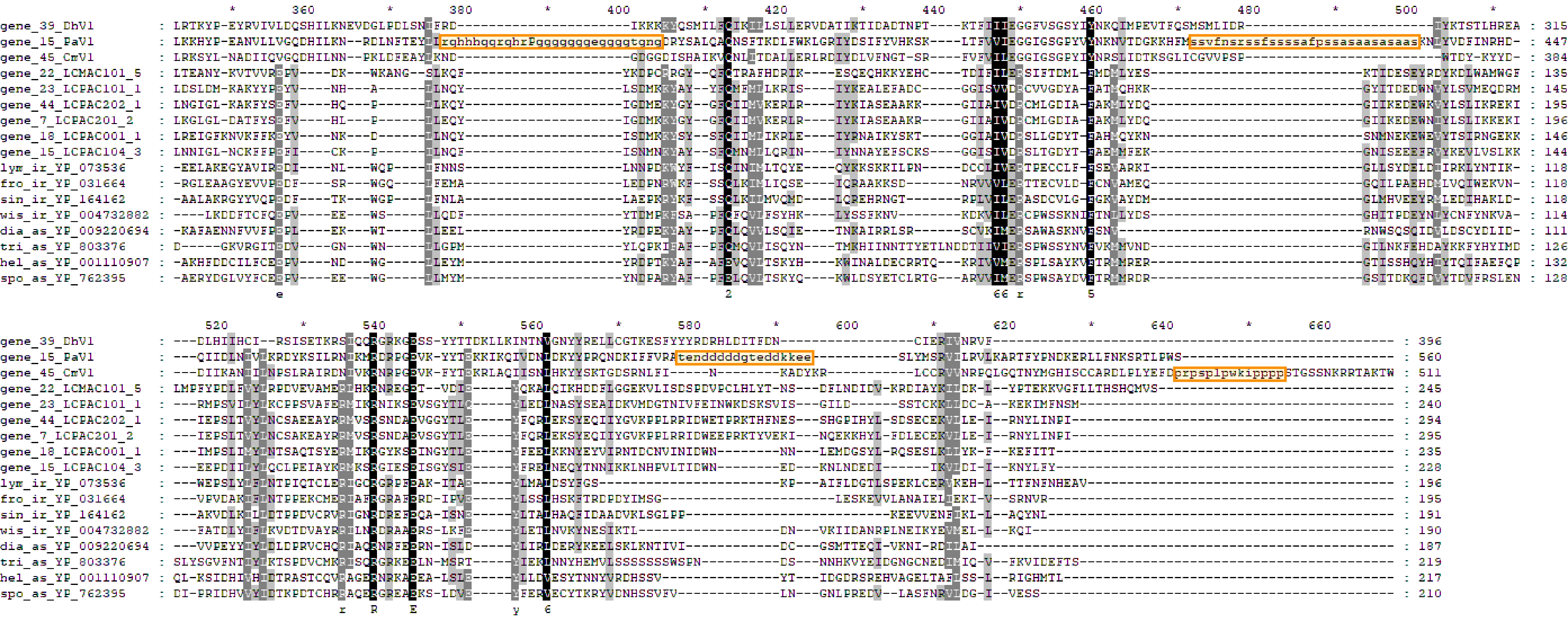

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                            *        360        *        380        *        400        *        420        *        440        *        460        *        480        *        500        *
gene_39_DhV1        : LRTKYP-EYRVIVLDQSHILKNEVDGLPDLSNIFRD----------------------IKKKKYQSMILFQIKIILSLLERVDATIKTIDADTNPT----KTFIIIEGGFVSGSYIYNKQIMPEVTFQSMSMLIDR------------------------IYKTSTLHREA : 315
gene_15_PaV1        : LKKHYP-EANVLLVGQDHILKN--RDLNFTEYIIrghhbggrghrPgggggggeggggtgngDRYSALQAQNSFTKDLFWKLGRIYDSIFYVHKSK----LTFVVIEGGIGSGPYVYNKNVTDGKKHFMssvfnsrssfssssafpssasaasasaasKNIYVDFINRHD- : 447
gene_45_CmV1        : LRKSYL-NADIIQVGQDHILNN--PKLDFEAYIKND----------------------GDGGDISHAIKVQNLITDALLERLRDIYDLVFNGT-SR----FVFVILEGGIGSGPYIYNRSLIDTKSGLICGVVPSP-------------------------WTDY-KYYD- : 384
gene_22_LCMAC101_5  : LTEANY-KVTVVREFV----DK---WKANG--SLKQF--------------------YKDPCERGY--QFQTRAFHDRIK----ESQEQHKKYEHC----TDIFILERSIFTDML-EMDMLYES---------------------------KTIDESEYRDYKDLWAMWGF : 135
gene_23_LCPAC101_1  : LDSLDM-KAKYYPEYV----NH---A------ILNQY--------------------LSDMKKYAY--YFQMFMLLKRIS----IYKEALEFADC-----GGISVVDRCVVGDYA-EATMQHKK---------------------------GYITDEDWNVYLSVMEQDRM : 145
gene_44_LCPAC202_1  : LNGIGL-KAKFYSEFV----HQ---P------ILKQY--------------------IGDMEKYGY--GFQIIMVKERLR----IYKIASEAAKK-----GIIAIVDRCMLGDIA-EAKMLYDQ---------------------------GIIKEDEWKVYLSLIKREKI : 195
gene_7_LCPAC201_2   : LKGLGL-DATFYSEFV----HL---P------ILEQY--------------------IGDMKKYGY--GFQIIMVKERLR----IYKIASEAAKR-----GIIAIVDRCMLGDIA-EAKMLYDQ---------------------------GIIKEDEWNIYLSLIKKEKI : 196
gene_18_LCPAC001_1  : LREIGFKNVKFFKEYV----NK---D------ILNQY--------------------ISDMKKYSY--SFQIIMLIKRLE----IYRNAIKYSKT-----GGIAIVDRSLLGDYT-EAHMQYKN---------------------------SNMNEKEWEVYTSIRNGEKK : 146
gene_15_LCPAC104_3  : LNNIGL-NCKFFPEFI----CK---P------ILNQF--------------------ISNMNKYAY--SFQMNMLLQRIN----IYNNAYEFSCKS----GGISIVDRSLTGDYT-EAEMMFEK---------------------------GNISEEEFRVYKEVLVSLKK : 144
lym_ir_YP_073536    : -EELAKEGYAVIREDI----NL---WQP----IFNNS--------------------LNNPDKWYF--ISQINIMLTQYE----QYKKSKKILPN-----DCCLIVERTPECCLF-ESEVARKI---------------------------GLLSYDELDIIRKLYNTIK- : 118
fro_ir_YP_031664    : -RGLEAAGYEVVPEDF----SR---WGQ----IFEMA--------------------LEDPNRWKF--SSQLKIMLIQSE----IQRAAKKSD-------NRVVVLERTTECVLD-ECNVAMEQ---------------------------GQILPAEHDMLVQIWEKVN- : 118
sin_ir_YP_164162    : -AALAKRGYYVQPEDF----TK---WGP----IFNLA--------------------LAEPKRYKF--SSQLKIIMVQMD----LQREHRNGT-------RPLVILERASDCVLG-EGKVAYDM---------------------------GLMHVEEYRMLEDIHAKLD- : 118
wis_ir_YP_004732882 : ----LKDDFTCFQEPV----EE---WS-----ILQDF--------------------YTDMPKFSA--PFQFQVLFSYHK----LYSSFKNV--------KDKVILERCPWSSKNIETNILYDS---------------------------GHITPDEYNIYCNFYNKVA- : 114
dia_as_YP_009220694 : -KAFAENNFVVFPEPL----EK---WT-----ILEEL--------------------YRDPEKYAY--PFQLQVVLSQIE----TNKAIRRLSR------SCVKIMERSAWASKNVESNV-------------------------------RNWSQSQIDVLDSCYDLID- : 111
tri_as_YP_803376    : D-----GKVRGITEDV----GN---WN-----ILGPM--------------------YLQPKIFAF--PFQMQVLISQYN----TMKHIINNTTYETLNDDTIIVIERSPWSSYNVEVKMMVND---------------------------GILNKFEHDAYKKFYHYIMD : 126
hel_as_YP_001110907 : -AKHFDDCILFCEEPV----ND---WG-----ILEYM--------------------YRDPTKYAF--AFEVQVLTSKYH----KWINALDECRRTQ---KRIVVMERSPLSAYKVETRMMRER---------------------------GTISSHQYHIYTQIFAEFQP : 132
spo_as_YP_762395    : -AERYDGLVYFCEEPV----EE---WG-----ILMYM--------------------YNDPARYAF--PFELQVLTSKYQ----KWLDSYETCLRTG---ARVVIMERSPWSAYDVETRMMRDR---------------------------GSITDKQFDVYTDVFRSLEN : 128
                                   e                                                        2                                 66 r        5

                          520        *        540        *        560        *        580        *        600        *        620        *        640        *        660
gene_39_DhV1        : ---DLHIIHCI--RSISETKRSIQQRGRKGESS-YYTTDKLLKINTNVGNYYRELLCGTKESFYYYRDRHLDITFDN-----------------CIERIVNRVF--------------------------------------------------- : 396
gene_15_PaV1        : ---QIIDLNIVLKRDYKSILRNIKMRDRPGEVK-YYTEKKIKQIVDNLDKYYPRQNDKIFFVRAtendddddgteddkkee-----------SLYMSRVILRVLKARTFYPNDKERLLFNKSRTLPWS--------------------------- : 560
gene_45_CmV1        : ---DIIKANIIINPSLRAIRDNIVKRNRPGEVK-FYTEKRLAQIISNLHKYYSKTGDSRNLFI-----N--------KADYKR-----------LCCRVVNRPQLGQTNYMGHISCCARDLPLYEFDprpsplpwkippppSTGSSNKRRTAKTW : 511
gene_22_LCMAC101_5  : LMPFYPDLFVYLRPDVEVAMERLHKRNREGET--VDIE-----YQKAIQIKHDDFLGGEKVLISDSPDVPCLHLYT-NS---DFLNDIDV-KRDIAYKIIDK-I--YPTEKKVGFLLTHSHQMVS------------------------------ : 245
gene_23_LCPAC101_1  : ---RMPSVILYLKCPPSVAFERMIKRNIKSEVSGYTLQ-----YLEDINASYSEAIDKVMDGTNIVFEINWKDSKSVIS---GILD------SSTCKKLIDC-A--KEKIMFNSM---------------------------------------- : 240
gene_44_LCPAC202_1  : ---IEPSLTVYINCSAEEAYRRMVSRSNDAEVGGYTLE-----YFQRIEKSYEQIIYGVKPPLRRIDWETPRKTHFNES---SHGPIHYL-SDSECEKVILE-I--RNYLINPI----------------------------------------- : 294
gene_7_LCPAC201_2   : ---IEPSLTVYINCSAKEAYRRMVSRSNDAEVSGYTLE-----YFQRIEKSYEQIIYGVKPPLRRIDWEEPRKTYVEKI---NQEKKHYL-FDLECEKVILE-I--RNYLINPI----------------------------------------- : 295
gene_18_LCPAC001_1  : ---IMPSLIMYINTSAQTSYERMIKRGYKSEINGYTLE-----YFEEIKKNYEYVIRNTDCNVINIDWN--------NN---LEMDGSYL-RQSESLKLIYK-F--KEFITT------------------------------------------- : 235
gene_15_LCPAC104_3  : ---EEPDIILYIQCLPEIAYKRMKSRGIESEISGYSIE-----YFREINEQYTNNIKKLNHPVLTIDWN--------ED---KNLNDEDI------IKVIDI-I--KNYLFY------------------------------------------- : 228
lym_ir_YP_073536    : ---WEPSLYIFINTPIQTCLERIGCRGRPFEAK-ITAE-----YLMAIDSYFGS-----------------------KP---AIFLDGTLSPEKLCERVKEH-L--TTFNFNHEAV--------------------------------------- : 196
fro_ir_YP_031664    : ---VPVDAKIFINTPPEKCMERIAFRGRAFERD-IPVE-----YLSSIHSKFTRDPDYIMSG----------------------LESKEVVLANAIELIEKI-V--SRNVR-------------------------------------------- : 195
sin_ir_YP_164162    : ---AKVDLKILIDTPPDVCRVRIGNRDREFEQA-ISNE-----YLTAIHAQFIDAADVKLSGLPP--------------------------KEEVVENFIKL-L--AQYNL-------------------------------------------- : 191
wis_ir_YP_004732882 : ---FATDLYIFLKVDTDVAYRRILNRDRAAERS-LKFE-----YLETINVKYNESIKTL------------------DN---VKIIDANRPLNEIKYEVMEL-L--KQI---------------------------------------------- : 190
dia_as_YP_009220694 : ---VVPEYYIYLDLDPRVCHQRIAQRNRFEERN-ISLD-----YLIRIDERYKEELSKLKNTIVI------------DC---GSMTTEQI-VKNI-RDIIAI----------------------------------------------------- : 187
tri_as_YP_803376    : SLYSGVFNTIYLKTSPDVCMKRISQRGRKEELN-MSRT-----YIEKINNYHEMVLSSSSSSSWSPN----------DS---NNHKVYEIDGNGCNEDIMIQ-V--FKVIDEFTS---------------------------------------- : 219
hel_as_YP_001110907 : QL-KSIDHIVHIDTRASTCQVRAGERNRKAEEA-LSLE-----YLLDVESYTNNYVRDHSSV---------------YT---IDGDRSREHVAGELTAFISS-L--RIGHMTL------------------------------------------ : 217
spo_as_YP_762395    : DI-PRIDHVVYIDTKPDTCHRRAQERGREAEKS-LDVE-----YFERVECYTKRYVDNHSSVFV-------------LN---GNLPREDV--LASFNRVIDG-I--VESS--------------------------------------------- : 210
                                            r  R    E            y   6
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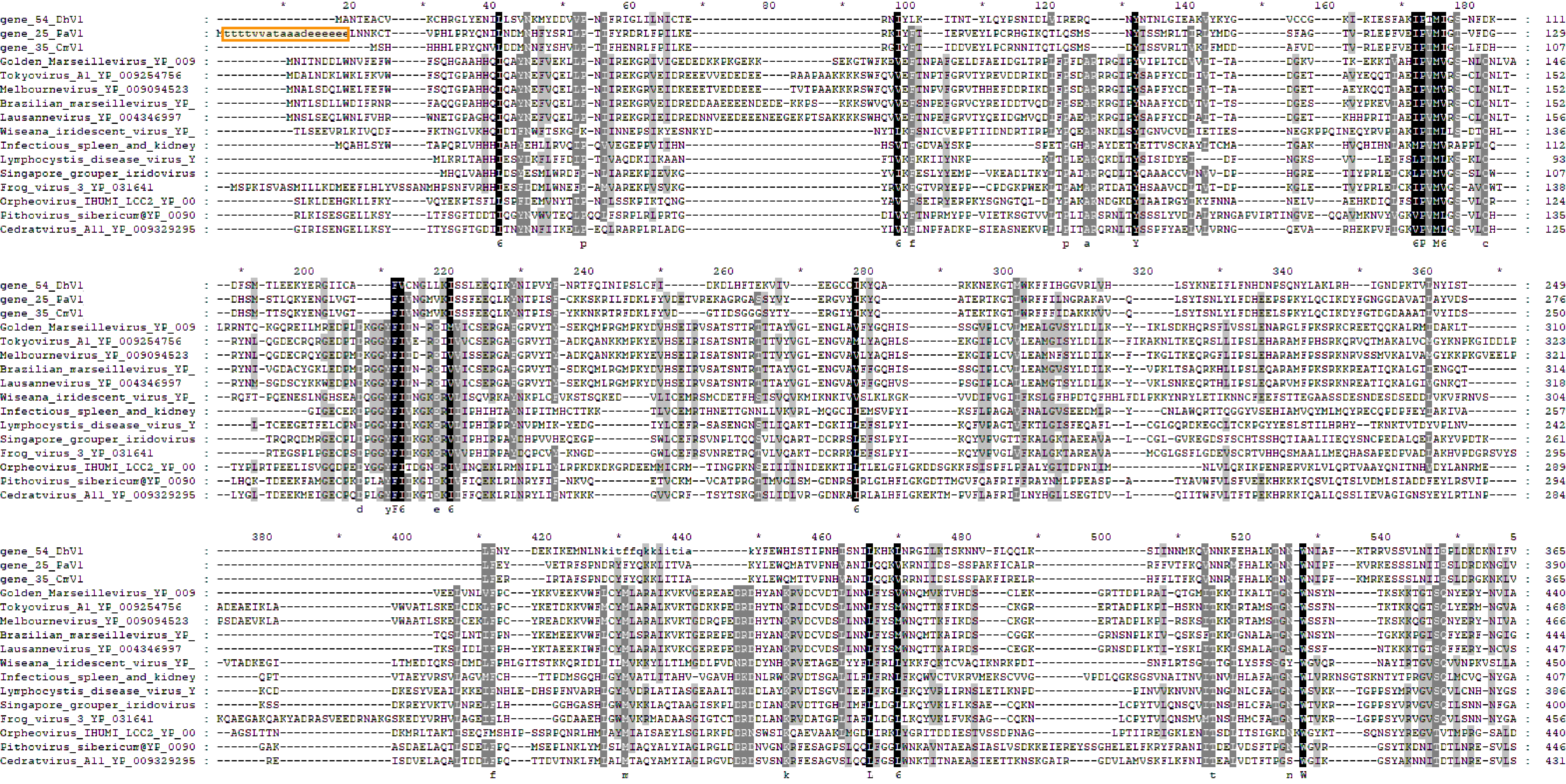
RNApB; DNA-dependent RNA polymerase subunit RPB2

cluster PaV1_25 aligned with representative Pitho-, Irido, Marseilleviruses



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                                         *        20         *        40         *        60         *        80         *       100         *       120         *       140         *       160         *       180
gene_54_DhV1                  : -----------------MANTEACV-----KCHRGLYENIILSVNKMYDDVVP-NIFRIGLIINICTE------------------------------RNIYLK---ITNT-YLQYPSNIDLVIRERQ-----NYNTNLGIEAKVYKYG-------VCCG----KI-KIESFAKIPTMIGS-NFDK--- :  111
gene_25_PaV1                  : MttttvvataaadeeeeeLNNKCT-----VPHLPRYQNIINDMNHFYSRILP-TIFYRDRLFPILKE------------------------------RKIYFT---IERVEYLPCRHGIKQTLQSMS-----NYTSSMRLTIRIYMDG-------SFAG----TV-RLEPFVEIPVMIGT-VFDG--- :  129
gene_35_CmV1                  : -----------------------MSH-----HHHLPRYQNVIDDMNNFYSHVLP-TIFHENRLFPILKE------------------------------RGIYFT---IDDVEYLPCRNNITQTLQSMS-----DYTSSVRLTVKIFMDD-------AFVD----TV-RLEPFVEIPIMIGT-LFDH--- :  107
Golden_Marseillevirus_YP_009  : ----------MNITNDDLWNVFEFW-----FSQHGAAHHQIQAYNEFVEKLLP-NIIREKGRIVIGEDEDKKPKGEKK----------SEKGTWFKEVEFTNPAFGELDFAEIDGLTRPLFPFDAPTRGIPYVIPLTCDVVIT-TA-------DGKV----TK-EKKTVAHIPVMVGS-NLCNLVA :  146
Tokyovirus_A1_YP_009254756    : ----------MDALNDKLWKLFKVW-----FSQTGPAHHQIQAYNEFVQELLP-NIIREKGRVEIDREEEVVEDEDEE----RAAPAAKKKKSWFQVVEFTNPTFGRVTYREVDDRIKDIFPSDAPRRGIPYSAPFYCDIIVT-TA-------DGET----AVYEQQTIAEIPVMVRS-CLCNLT- :  152
Melbournevirus_YP_009094523   : ----------MNALSDQLWELFEFW-----FSQTGPAHHQIQAYNEFVQELLP-NIIREKGRVEIDKEEETVEDDEEE----TVTPAAKKKRSWFQVVEFTNPVFGRVTHHEFDDRIKDIFPSDAPRRGIPYSAPFYCDIFVT-TA-------DGET----AEYKQQTIAEIPVMVRS-CLCNLT- :  152
Brazilian_marseillevirus_YP_  : ----------MNTLSDLLWDIFRNR-----FAQQGPAHHQIQAYNEFVQELLP-NIIREKGRVEIDREDDAAEEEENDEDE-KKPS---KKKSWVQVVEFSNPEFGRVCYREIDDTVQDIFPSEAPKRGIPYNAAFYCDVTVT-TS-------DGES----KVYPKEVIAEIPVMVRS-CLCNLT- :  152
Lausannevirus_YP_004346997    : ----------MNSLSEQLWNLFVHR-----WNETGPAGHQIQAYNEFVQELLP-NIIREKGRIEIDREDNNVEEDEEENEEGEKPTSAKKKKSWHQVVEFTNPEFGRVTYQEIDGMVQDIFPAEAPKRGIPYSAPFYCDIAIT-TA-------DGET----KHHPRITIAEIPVMVRS-CLCNLT- :  156
Wiseana_iridescent_virus_YP_  : -----------TLSEEVRLKIVQDF-----FKTNGLVKHQIDTFNWFTSKGIK-NIINNEPSIKYESNKYD---------------------------NYTIKFSNICVEPPTIIDNDRTIRPIYPQEAPNKDLSYIGNVCVDIIETIES-------NEGKPPQINEQYRVPIAKIPIMILS-DTCHL-- :  136
Infectious_spleen_and_kidney  : -----------------MQAHLSYW-----TAPQRLVHHHIAHYEHLIRVQIP-QVVEGEPPVIIHN------------------------------HSVTFGDVAYSKP----------SPETPGHAPAYDETYETTVSCKAYITCMA-------TGAK----HVQHIHNIAKMPVMVRAPPLCQ-- :  112
Lymphocystis_disease_virus_Y  : -----------------------------MLKRLTAHHIESYIKFLFFDIP-TIVAQDKIIKAAN-----------------------------FTVKFKKIIYNKP----------KITPLEAPQKDLTYSISIDYEI----DF-------NGKS----VV---LEIFSLPIMIKS-KLC----- :   93
Singapore_grouper_iridovirus  : ------------------------------MHQLVAHHLDSYESMIWRDFP-NIIAREKPIEVKG-----------------------------YVIKFESLYYEMP--VKEADLTKYITPAIAPRQDLTYQAAACCVINVV-DP-------HGRE----TIYPRLEICKLPVMVGS-SLCW--- :  107
Frog_virus_3_YP_031641        : --MSPKISVASMILLKDMEEFLHLYVSSANMHPSNFVRHHIESFIDMIWNEFP-AIVAREKPVSVKG-----------------------------YRVKFGTVRYEPP--CPDGKPWEKITPAMAPRTDATYHSAAVCDITVT-DP-------KGLE----TVYPRLEICKIPVMVGS-AVCWT-- :  138
Orpheovirus_IHUMI_LCC2_YP_00  : -----------SLKLDEHGKLLFKY-----VQYEKPTSFILSPFIEMVNYTIP-NILSSKPIKTQNG-----------------------------YAV-FSEIRYERPKYSGNGTQL-DIYPAKAPNDGKDYTAAIRGYIKYFNNA-------NELV----AEHKDIQIFSIPVMVGS-VLCR--- :  124
Pithovirus_sibericum@YP_0090  : -----------RLKISESGELLKSY-----LTFSGFTDDTIQGYNVWVTEQLPQQIFSRPLRIPRTG-----------------------------DLVYFTNPRMYPP-VIETKSGTVVITPLIAPSRNLTYSSSLYVDIAIYRNGAPVIRTINGVE--QQAVMKNVYVGKVPVMIGS-VLCH--- :  135
Cedratvirus_A11_YP_009329295  : -----------GIRISENGELLKSY-----ITYSGFTGDIITNYNNFIIKELP-EQIRARPLRLADG-----------------------------YLVYFLNPFADKP-SIEASNEKVPILPITAPQRNLTYSSPFYAEIVIVRNG-------QEVA----RHEKPVFIGKVPVMIGS-VLCH--- :  125
                                                                 6                   p                                                    6 f                    p   a         Y                                             6P M6     c

                                   *        200         *        220         *        240         *        260         *        280         *        300         *        320         *        340         *        360         *
gene_54_DhV1                  : --DFSM-TLEEKYERGIICA-----FVCNGLLKISSLEEQIKYNIPVYF-NRTFQINIPSLCFI------DKDLHFTEKVIV----EEGCCIKYQA----------RKKNEKGTMWKFFIHGGVRLVH---------LSYKNEIFLFNHDNPSQNYLAKLRH---IGNDPKTVINYIST------- :  249
gene_25_PaV1                  : --DHSM-STLQKYENGLVGT-----FIVNGMVKISSFEEQLKYNTPISF-CKKSKRILFDKLFYVDETVREKAGRGASSYVY----ERGVYIKYQ-----------ATERTKGTIWRFFILNGRAKAV--Q------LSYTSNLYLFDHEEPSPKYLQCIKDYFGNGGDAVATIAYVDS------- :  276
gene_35_CmV1                  : --DHSM-TTSQKYENGLVGT-----FIVNGMVKISSFEEQLKYNTPISF-YKKNKRTRFDKLFYVD----GTIDSGGGSYTY----ERGIYIKYQ-----------ATEKTKGTIWRFFFIDAKKKVV--Q------LSYTSNLYLFDHEELSPKYLQCIKDYFGTDGDAAATIVYIDS------- :  250
Golden_Marseillevirus_YP_009  : LRRNTQ-KGQREILMREDPLIKGGYFIIN-REIMVICSERGAFGRVYTY-SEKQMPRGMPKYDVHSEIRVSATSTTRTTTAYVGL-ENGLAVFYGQHIS-------SSGVPLCVIMEALGVSYLDLLK--Y--IKLSDKHQRSFLVSSLENARGLFPKSRKCREETQQKALRMIDAKLT------- :  310
Tokyovirus_A1_YP_009254756    : --RYNL-QGDECRQRGEDPTIRGGYFIVE-REIIVVCSERGAFGRVYTY-ADKQANKKMPKYEVHSEIRISATSNTRTTTVYVGL-ENGVAMLYAQHLS-------EKGIPLCVVLEAMGISYLDLLK--FIKAKNLTKEQRSLLIPSLEHARAMFPHSRKQRVQTMAKALVCMGYKNPKGIDDLP :  323
Melbournevirus_YP_009094523   : --RYNL-QGDECRQYGEDPMIKGGYFIID-REIVVISSERGAFGRVYTY-ADKQANKKMPKYEVHSEIRISATSNTRTTTVYVGL-ENGVAVLYAQHLS-------EKGIPLCVVLEAMNFSYLDILK--F--TKGLTKEQRGFLIPSLEHARAMFPSSRKNRVSSMVKALVAMGYKKPKGVEELP :  321
Brazilian_marseillevirus_YP_  : --RYNI-VGDACYGKLEDPMIRGGYFIIN-REIVVICSERGAFGRVYTY-SDKQMLRGMPKYDVHSEIRVSATSNTRTTTAYVGL-ENGVAVFFGQHIS-------SSGIPLCVILEAMGVSYLDILK--Y--VPKLTSAQRKHLLIPSLEQARAMFPKSRKKREATIQKALGIIENGQT------- :  314
Lausannevirus_YP_004346997    : --RYNM-SGDSCYKKWEDPNIKGGYFIIN-REIVVICSERGAFGRVYTY-SEKQMLRGMPKYDVHSEIRVSATSNTRTTTAYVGL-ENGVAVFFGQHVS-------PSGIPLCAILEAMGTSYLDLLK--Y--VKLSNKEQRTHLIPSLEQARVMFPKSRKNREATIQKALGIVGNKQT------- :  318
Wiseana_iridescent_virus_YP_  : --RQFT-PQENESLNGHSEAIQGGYFIINGKERVLISQVRKAYNKPLCFVKSTSQKED----VLICEMRSMCDETFHSTSVQVKMIKNKIVVSLKLKGK-------VVDIPVGIIFKSLGFHPDTQFHHLFDLPKKYNRYLETIKNNCFEEFSTTEGAASSDESNDESDSEDDIVKVFRNVS---- :  304
Infectious_spleen_and_kidney  : -------------GIGECEKIPGGYFIVKGKERIIIPHIHTAYNIPITMHCTTKK-------TLVCEMRTHNETTGNNLLVKVRL-MQGCIIEMSVPYI-------KSFLPAGAVFNALGVSEEDMLR--Y----CNLAWQRTTQGGYVSEHIAMVQYMLMQYRECQPDPFEYIAKIVA------- :  257
Lymphocystis_disease_virus_Y  : -----I-TCEEGETFELCPNIPGGYFIVKGKERVLIPHIRPRYNVPMIK-YEDG-------IYLCEFR-SASENGNSTLIQAKT-DGKIILEFSLPYI-------KQFVPAGTVFKTLGISFEQAFL--L--CGLGQRDKEGCLTCKPGYYESLSTILHRHY--TKNKTVTDYVPLNV------- :  242
Singapore_grouper_iridovirus  : -------TRQRQDMRGECPLIPGGYFIIKGKERVLIPHIRPAYDHPVVHEQEGP-------SWLCEFRSVNPLTQQSVLVQART-DCRRSLEFSLPYI-------KQYVPVGTTFKALGKTAEEAVA--L--CGL-GVKEGDSFSCHTSSHQTIAALIIEQYSNCPEDALQEIAKYVPDTK---- :  261
Frog_virus_3_YP_031641        : -------RTEGSPLPGECPSIPGGYFIIKGKERVVVPHIRPAYDQPCVY-KNGD-------GWLCEFRSVNRETRQTVLVQAKT-DCRRKLEFSLPYI-------KQYVPVGLVFKALGKTAREAVA-----MCGLGSFLGDEVSCRTVHHQSMAALLMEQHASAPEDPVADIAKHVPDGRSVYS :  295
Orpheovirus_IHUMI_LCC2_YP_00  : --TYPLRTPEELISVGQDPEIYGGYFITDGNERIVINQEKLRMNIPLIYLRPKDKDKGRDEEMMICRM--TINGPKNSEIIIINIDEKKTILTLELGFLGKDDSGKKFSISPFLPFALYGITDPNIIM-------------NLVLQKIKPENRERVKLVLQRTVAAYQNITNHVDYLANRME---- :  289
Pithovirus_sibericum@YP_0090  : --LHQK-TDEEKFAMGECPKIPLAYFIIKGIEKIVFIQEKLRLNRYFIF-NKVQ-------ETVCKM--VCATPRGTTMVGLSM-GDNRSIRLGLHFLGKGDTTMGVFQAFRIFFRAYNMLPPEASP--A------TYAVWFVLSFVEEKHKKKIQSVLQTSLVDMLSIADDFEYLRSVIP---- :  294
Cedratvirus_A11_YP_009329295  : --LYGL-TDEEKMEIGECPQIPLGYFIIKGTEKIIFFQEKLRLNRYLIF-NTKKK-------GVVCRF--TSYTSKGTSLIDLVR-GDNKAIRLALHFLGKEKTM-PVFLAFRIILNYHGLLSEGTDV--L------QIITWFVLTFTPEKHRKKIQALLQSSLIEVAGIGNSYEYLRTLNP---- :  284
                                                    d   yF6   e 6                                                         6

                                       380         *        400         *        420         *        440         *        460         *        480         *        500         *        520         *        540         *        5
gene_54_DhV1                  : ------------------------------------------LFNY---DEKIKEMNLNkitffqkkiitia--------kYFEWHISTIPNHISNIIKHKINRGILKTSKNNV-FLQQLK----------------SIINNMKQVNNKFEHALKINN-WNIAF---KTRRVSSVLNIIEPLDKDKNIFV :  365
gene_25_PaV1                  : ------------------------------------------LFEY-----VETRFSPNDRYFYQKKLITVA--------KYLEWQMATVPNHVANIIQQKVKRNIIDS-SSPAKFICALR----------------RFFVTFKQVNNRMFHALKINN-WNIPF---KVRKESSSLNIIESLDRDKNGLV :  390
gene_35_CmV1                  : ------------------------------------------LFER-----IRTAFSPNDCYFYQKKLITIA--------KYLEWQMTTVPNHVANIIQQKVRRNIIDSLSSPAKFIRELR----------------HFFLTFKQVNNRMFHALKINN-WNIPF---KMRKESSSLNIIESLDRGKNKLV :  365
Golden_Marseillevirus_YP_009  : ---------------------------------VEEIVNLVFPC---YKKVEEKVWFICYMLAPAIKVKVGEREAEDRIHYANKRVDCVDTILNNIFYSVWNQMVKTVHDS----CLEK----------GRTTDPLRAI-QTGMITKKLIKALTTGN-WNSYN------TKSKKTGTSQNYERY-NVIA :  440
Tokyovirus_A1_YP_009254756    : ADEAEIKLA----------------VWVATLSKEICDKLFPC---YKETDKKVWFMCYMLAPALKVKTGDKKPEDRIHYTNKRIDCVDSILNNIFYSMWNQTTKFIKDS----CKGR----------ERTADPLKPI-HSKNITKKIRTAMSTGN-WSSFN------TKTKKQGTSQLYERM-NGVA :  468
Melbournevirus_YP_009094523   : PSDAEVKLA----------------VWAATLSKEICEKLFPC---YREADKKVWFMCYMLAPALKVKTGDRQPEDRIHYTNKRVDCVDSILNNIFYSMWNQTTKFIKDS----CKGK----------ERTADPLKPI-RSKSITKKIRTAMSTGN-WSSFN------TKSKKQGTSQNYERY-NIVA :  466
Brazilian_marseillevirus_YP_  : ---------------------------------TQSILNTIFPN---YKEMEEKVWFICYMLSPAIKVKTGEREPEDRIHYANKRVDCVDSILNNIFYSMWNQMTKAIRDS----CGGK----------GRNSNPLKIV-QSKSFIKKIGNALATGN-WNSYN------TGKKKPGISQFYERF-NGIG :  444
Lausannevirus_YP_004346997    : ---------------------------------TKSIIDLIFPH---YKTAEEKIWFICYMLAPAIKVKCGEREPEDRIHYANKRVDCVDSILNNIFYSMWNQTTKAIRDS----CEGK----------GRNSDPLKTI-YSKLITKKISMALATGN-WSSF-------NTKKKTGTSQFFERY-NCVS :  447
Wiseana_iridescent_virus_YP_  : -VTADKEGI----------------LTMEDIQKSIDMDLFPHLGITSTKKQRIDLIILMVKKYLLTLMGDLPVDNRIDYNHKRVETAGEIYYFIFRLIYKKFQKTCVAQIKNRKPDI-----------------SNFLRTSGITTGILYSFSSGY-WGVQR------NAYIRTGVSQVVNPKVSLLA :  450
Infectious_spleen_and_kidney  : ------QPT----------------VTAEYVRSVIAGVMFCH----TTPDMSGQHIGYMVATLITAHV-VGAVHDRINLRWKRVDTSGAIILFIFRNIFKQWVCTVKRVMEKSCVVG-------VPDLQGKSGSVNAITNVITNVIHLAFATGN-WLVRKNSGTSKNTYTPRGVSQLMCVQ-NYGA :  407
Lymphocystis_disease_virus_Y  : ------KCD----------------DKESYVEAIIKKEIFNHLE-DHSPFNVARHIGYMVDRLATIASGEAALTDRIDLAYKRVDTSGVIIEFIFKGIFKQYVRLIRNSLETLKNPD---------------PINVVKNVNVITNGINLCFATGN-WSVKK---TGPPSYMRVGVSQVLCNH-NYGS :  386
Singapore_grouper_iridovirus  : ------KSS----------------DKREYVKTVINRELFLH------GGHGASHIGWMVKKLAQTAAGISKPLDRIDIANKRVDTTGHIIMFILDGILKQYVKLFLKSAE--CQKN------------LCPYTVLQNSQVITNSIHLCFATGN-WTVKR---IGPPSYVRVGVSQILSNN-NFGA :  400
Frog_virus_3_YP_031641        : KQAEGAKQAKYADRASVEEDRNAKGSKEDYVRHVIAGEIFLH------GGDAAEHIGWMVKRMADAASGIGTCTDRIDLANKRVDATGPIIAFILDGILKQYVKLFVKSAG--CQKN------------LCPYTVLQNSMVMTNSIHMCFATGN-WTVKR---LGPPSYVRVGVSQVLSNN-NYGA :  456
Orpheovirus_IHUMI_LCC2_YP_00  : --AGSLTTN----------------DKMRLTAKTISEQFMSHIP-SSRPQNRLHMIAYMIAISAEYLSGLRKPDDRNSWSIKQAEVAAKIMGDIIRKIYGRITDDIESTVSSDPNAG-----------LPTIIREIGKLENITSDIITSIGKDNKWGYKT----SQNSYYREGVTVTMPRG-SAID :  440
Pithovirus_sibericum@YP_0090  : ------GAK----------------ASDAELAQTILSDELFPQ---MSEPLNKLYMISLMIAQYALYIAGLRGLDDRINVGNKRFESAGPSLQQIFGGIWNKAVNTAEASIASLVSDKKEIEREYSSGHELELFKRYFRANIITDEIVDSFTPGN-WGVR-------GSYTKDNITDTLNRE-SVLS :  446
Cedratvirus_A11_YP_009329295  : -------RE----------------ISDVELAQAITDDLFPQ---TTDVTNKLFMIALMTAQYAMYIAGLRGVDDRISVSNKRFESAGVSLQQIFGSIWNKTITNAEASIEETTKNSKGAIR----GDVLAMVSKFLKFNIITEAIVDTFTPGS-WGIK-------GSYAKNNITDTLNRE-SVLS :  431
                                                                          f                       m                   k            L   6                                                  t             n W
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                               60        *        580        *        600        *        620        *        640        *        660        *        680        *        700        *        720        *        740
gene_54_DhV1                 : FNDHITKISSTVNNIGNKVD--EIRAFDPSSALFICPHNSPDG-RKIGLIKQLNIVTVLS------SYQPLVKG--------------EIYSVI------------LEYFL-MGIDGGEVNLI-INGEVDSTMRCLFDITKSNIYNICIKLKKK-YSHISCFVEN---NNIYIDSSEGRPIVPLVV : 510
gene_25_PaV1                 : YDDHIGKISSSINNVGNKVD--KLRFYDDSSALFICPHNSPDG-RKIGLIKQLSVGTRLS----VAPAEPVSAT--------------FVLDAI----------SSAGMVRGDDVGVGSSSALLIDGTVTCTLKCRRTVYLMDVYRCCMAIKRV-HPHVSVYVRD---NNVYVDSTRGRPMINVRV : 541
gene_35_CmV1                 : YDDHIGKISSSINNVGNKVD--RLRFYDNSSALFVCPHNSPDG-RKIGLIKQLSVGTKLSaaaaaapaapaaaaaaaapaaaaapaaCLIFDII------------ASVgitrgtggggtttllingtVVCELNCSRDVTSVDVYRCCISLKRVYHPHVSMYVHD---NNVYVDSTRGRPMINVRV : 533
Golden_Marseillevirus_YP_009 : AVSNIRKLHAAIGTEGNMTK---PRRVHESSYGFVDPADTPESKERTGLSKVMGIGATLS--------LGCSFV--------------EFFEII-------------SSLDDFLQDFGQGTFIFLNGMIVGST--RNPVGLVSTLSGLK-TSNN-ICWDSCFVYDKYFDEVRINCDAGRLIRPLMV : 584
Tokyovirus_A1_YP_009254756   : SASNIRKVHAAIGTEGNMTK---PRRVHESSYGFICPPDTPESKDKTGLSKVLAISATVS--------LGCTIE--------------ECFEII-------------SALEDFSQDFGLETFVFLNGVIMGST--DSPKALVEALSVLK-RAGN-FFWDCCFVFDEKHNEVRVNCDAGRLVRPLMV : 612
Melbournevirus_YP_009094523  : SCSNIRKVHAAIGTEGNMTK---PRRVHESSYGFICPPDTPESKDKTGLSKVLAISATMS--------LGCTVE--------------ECFEII-------------SALEYFSQDFGLETFVFLNGVIMGST--NSPKELIGELSVLK-RAGD-FFWDCCFVFDEKHNEVRVNCDAGRLIRPLMV : 610
Brazilian_marseillevirus_YP_ : SASNMRKLHAAIGTEGNMTK---PRRVHESSYGFVCPPDTPESKERTGLSKVIAISATVS--------LGCTTE--------------ECMQII-------------GAIPEFSRDFGKGTFVFLNGMIAGST--ETPEELIAVLTDMK-RSNN-FFWDCCFVYDKKFDEVRVNCDSGRLIRPLMV : 588
Lausannevirus_YP_004346997   : A-SNIRKLHAAIGTEGNMTK---PRRVHESSFGFVCPPDTPESKERTGLSKVLAISALVS--------LGCSIE--------------ECFQII-------------DAIPEFSRDFGEGTFVFLNGVIAGST--QNPEFLISVLSELK-RSNN-FFWDCCFVYDKKFDEVRINCDAGRLIRPLML : 590
Wiseana_iridescent_virus_YP_ : NYSSIRRVVIPESKDGKEAKTSEIRQIHPSSSFLICPVETPEG-KGVGTVLNMSIFCSVI--------TGISTC--------------EIMDSI-------DHFQDLILCKCRKPNKSNCLTILINGSPFSKLGHANTINNINFMGDK-------SISIVVNKHL---KIIEIFSDPGRLIRPVFD : 596
Infectious_spleen_and_kidney : RISNIRRMTHAVGFKGKNIK---VRQIHNSHNGYICPYETPEG-DRVGNVVQLAISATII--------VPVCPR--------------NIRTLM------------MSALPRFADPQGNQPVL-INGEIVGWVKDRMLCGMAIMHMLWD------YPDVTVVFRHG--YGVHVYSEGGRFMRPLIH : 546
Lymphocystis_disease_virus_Y : RLSHIRRIMHAVGFKGKNFK---IRRLHASHYGFICPYETPEG-ERVGVVLNTAISTAFS--------QGIPKN--------------QIKPLM------------MPYLK----ESGYFRVV-INGEIVGYV--NDPNETVKLLKSVL---PD-GVSVFCFRFTPEIKECHVFSDQGRFLRPVII : 523
Singapore_grouper_iridovirus : KLSHIRRIMHAVSFKGKNIK---MRQLHTSHYGFLCPYETPEG-ERVGIVLNMAESAAVS--------DYTPRE--------------EITAIIDRAGGMPGYEKTAELSHLAWSSSDTFSAVVVDGRLAGFT--TEPREFVKEAKIRLSAQVG-VCWDKIE------DEIHLLGCEGRFMRRMID : 551
Frog_virus_3_YP_031641       : RVSHIRRIMHAVSFRGKNIR---MRQLHSSHYGFLCPYETPEG-EKVGIVLNMAEGAGFS--------LETPRE--------------VVLATVRLGKGLPGFFEGAPARLAWSGAAGSASVD-VDGVLCGVT--GDPVGFVREARLCLPGVSV------VWKKVE--REIHLLGCQGRFVRRVID : 605
Orpheovirus_IHUMI_LCC2_YP_00 : AIGFQMRVSAATNKKSKQPK---VRAVQQSQYGYICPGDTPEG-EPCGIVKVKAITSYFA--------HDRPNS--------------SIVNIA------------NAHVSVDPSLEKPNLFI-INAEPFGWCNSTDLRRIIVEARRQLLL----DFDICIVVDAS--GAIIVSSDAGRPVRPLIV : 581
Pithovirus_sibericum@YP_0090 : SYAQITKINTPTRRQAKQPH---IRMVQMSQLGFVDPVETPEG-RAVGLIKHKAIGAYAS--------LPGDDT--------------VIVEQI------------RPYLAAIRSETATNGCI-VNGRFVGWCAGTELKDFIISLKRSQ-RISH-FTSISIYRD----NVIYVFTDGSRLTRPLIV : 587
Cedratvirus_A11_YP_009329295 : TLSQIIKINTPTRREAKQPH---IRMVQMTQLGFIDAIETPEG-RAVGLIKHKAIGAQST--------PADDDK--------------LIIQQV------------LPFLNVTYSEETPNGVV-CNGKFIGWGLGEKVRKIIIDMRRKR-TVPQ-FTSVALHYD----NVIYISTDSSRLARPLIV : 572
                                     46       g        R    3    6cp  3Pe     G                                                                             1g                                             6    gR  r 6

                                   *        760        *        780        *        800        *        820        *        840        *        860        *        880        *        900        *        920        *
gene_54_DhV1                 : NENEIVYF------------------------------DNAECWYLSLQAIVLTNTSLNET-----------------------------------------------------------------------------------------------------YPRLCCESAPFSSILKH-IPFSTN : 564
gene_25_PaV1                 : NARESFLF------------------------------DSAECWHLDLSRSIM--KNMD-------------------------------------------AGSAH-------------------------------------------------------YPRLCCTAAAFSAIVGKILNYKAY : 597
gene_35_CmV1                 : NEREFFWF------------------------------DNAECWYLELSKSIM--KNMd-------------------------------------ddddaaatttR-------------------------------------------------------EPRLCCAAAAFSAIVSKVLKYKAF : 595
Golden_Marseillevirus_YP_009 : VKDGGLVFTSEDAFRLRMTLAGHEASVSWQEFLTRGIVEFVDAEQQE-HLVIC--PDVEQL-----------------------------------NKSIVAGKSAK-------------------------------------------------------WTHCELHPLLVYGVCSSIISYSNN : 677
Tokyovirus_A1_YP_009254756   : VKDGKLEFGQEHFERLK------RGDITWQEFVGLGIVEILDAEQQE-HSLIC--PSAEQL----------------------------------------SQSKTK-------------------------------------------------------WTHCEIHPLLVYGVCASIIPYSAN : 694
Melbournevirus_YP_009094523  : VEGGKLRFGPEHYERLM------KGTITWQEFIGLGIVEILDAEQQE-HSLIC--PSAEQL---------------------------------------GQSESKE-------------------------------------------------------WTHCEIHPLLVYGVCASIIPYSAN : 693
Brazilian_marseillevirus_YP_ : VKDGKLVFKREHHEKMM------NGEMTWQDFLGAGILEFVDAEQQE-HSFIC--PSAEEL-----------------------------------------GEGKK-------------------------------------------------------WTHCEMHPLLFYGVCSSIINYSSN : 669
Lausannevirus_YP_004346997   : VQDGKLVFEEEHLRKLR------DGELTWQDFLSLGIVEYIDAEQQE-HMLIC--PSAEEL-----------------------------------------GKHKR-------------------------------------------------------WTHCEIHPILVYGVCSSIIPYSAN : 671
Wiseana_iridescent_virus_YP_ : LNKIIKKSGELIPSFNW--------------FLENQLIKYVDINE---VITNC--VAIEPL-------------------------------------DIVENPKSK-------------------------------------------------------YNLMELHPIGMFGIVAGIIPFSDR : 671
Infectious_spleen_and_kidney : RGQYRMV-----------------------------------CPSLVQELLVRPFPSPTER-----------------------------------VVSMDSMRAD--------------------------------------------------------EMDLP-GIVVLTDAMSAVIPFYNH : 605
Lymphocystis_disease_virus_Y : NDK---------------------------------------------IVRVC----AQEI------------------------------------------HHIA-------------------------------------------------------YKELPAYSI-MTDVMASVIPFYNH : 562
Singapore_grouper_iridovirus : PARIRGEPIEIEPLSLS--------KTRTVTAPSVGRLEEHKTQNLSKYIYIC----IQEI-------------------------------------NCGTVGKD--------------------------------------------------------YLDPPASEI-LTDVMSAVIPFYDH : 631
Frog_virus_3_YP_031641       : PEGIRGSGYDSPPAPEE-------RDIEMDPAPSSSPSDSLPCPP---GVYVC----AQEL-------------------------------------SVCSLGDGE-------------------------------------------------------YADPPASEI-LTDAMSSVIPFYDH : 684
Orpheovirus_IHUMI_LCC2_YP_00 : VGSD--GILEIDKKKMW--------DASFEDLLKNGCVEYLDAWEQEMHSYIA--IGLERVRSRPNEEQEIKRSLGYINTELEAVTMAIERLDEI-ANNINARPGNMWTQ--EETDELKEM-----------------------------------------YTHCELDPTALYGISISLIPGPQY : 711
Pithovirus_sibericum@YP_0090 : VEEGVTVYEKKKLQ-----------GSDFQTLLQEGAVEYVDATEQD-QLYIA--QTLEMLREQRTE-------IANLLMKRNEAQTIVDRLQVPEEQDVKEIRYRLPEQVSSEVDGFEVITNVANLSDEEAYELYRKTLDLALSDLSQANEALERLSKKSSYTHCELNPNALFGISANILPLPEH : 752
Cedratvirus_A11_YP_009329295 : IDDDKPDFTVYETKKLQ--------GADFQTLLEEGAVEFIDAMEQE-HLYIA--QSLDDLRKRRDR-------LDSIMKKVEEARSLVRRLEAS-SSSASSLRQVLPTK--RIIDDMEIAIN---------------------------------------ETHVEMDPNSLLSIAASIVPLPGN : 698
                                                                                                                                                                                                 5                 6

                                      940        *        960        *        980       1000        *       1020        *       1040        *       1060        *       1080        *       1100        *
gene_54_DhV1                 : TDGKRLFYATRMFHRAMTNEFLPGKFSLSYPQTPLVPGIPPQEKNPKYL-----------------------------------------------------VANYKKISRIDCPNSPGycpnspsycpnspsycpnspsycpnspI-----------------SGISNSETPVSETLTCSFDVTV : 680
gene_25_PaV1                 : VDGKRLFYMTRLFHHAITNRLLPGKLALVYPQLPTEYVHEKIrrkrrrrksgggdgggvskrrCRFGVGSNggiadagggggddggvggggggaeeeeeeeRSRCYQPLS----PTSSSYDPS--LYTPLSPVYTVEEAsppppppsrrrrssspDAAVPERRqqqqddddAPIDE---------- : 767
gene_35_CmV1                 : VDGKRLFYMTRLFHHAITNCMLPGRLALGYPQLPTEYVYEKIhhhhhhh------------------------------------------------------RRYPpls----ptspsyeps--p-mpsspIYAAVspppppppp--------------------lslspppIDE---------- : 690
Golden_Marseillevirus_YP_009 : NPSPRLSYFASMARSSV------AVPRCDYMYVPFDQ--HVIHY------------------------------------------------------------------------------------PQKPITSTKAGRL-------------------------LGLQDSPISQ---------- : 736
Tokyovirus_A1_YP_009254756   : NPSPRLSYFASMARSSV------AVPRLDFGIAPYDQ--HVIRY------------------------------------------------------------------------------------PQKPISSTKAARL-------------------------LGMNESPICQ---------- : 753
Melbournevirus_YP_009094523  : NPSPRLSYFASMARSSV------AVPRLDFGIAPFDQ--HVIHY------------------------------------------------------------------------------------PQKPITSTKASRL-------------------------LGMNKSPICQ---------- : 752
Brazilian_marseillevirus_YP_ : NPSPRLSYFASMARSSI------AVPRLDYKEALYDQ--HVIHY------------------------------------------------------------------------------------PQAPIASTKAGRL-------------------------LGMNDSPISQ---------- : 728
Lausannevirus_YP_004346997   : NPSPRLSYFASMARSSV------AVPRLDFDEVPYDQ--HVIHY------------------------------------------------------------------------------------PQKSIASTKAARL-------------------------LGLNDSPISQ---------- : 730
Wiseana_iridescent_virus_YP_ : TQSAPNCFYTSMVRQAI------GFVPCHN--LKTETVSHTINY------------------------------------------------------------------------------------PQKPIVTTDIAEF-------------------------NGLNEYPNGI---------- : 730
Infectious_spleen_and_kidney : TQSPRNAYQSNMGRQAV------GLPCLNYM-SRWDVTLDVIMY------------------------------------------------------------------------------------PQVPISRSKAMDA-------------------------LSFDTMPHGA---------- : 665
Lymphocystis_disease_virus_Y : APSPRIAYQSNMGRQAV------GITTLTGGKDRYDPTFYVIDY------------------------------------------------------------------------------------PQKAIARTICYDR-------------------------YKFDIMCHGA---------- : 623
Singapore_grouper_iridovirus : TQSPRNAYQSNMGRQAI------GFPAINCE-DRYDATLHRIDY------------------------------------------------------------------------------------PQSAITESRAIER-------------------------VNFDTMAHGA---------- : 691
Frog_virus_3_YP_031641       : TQSPRNAYQSNMGRQAI------GFPAVNCS-DRYDATLHRIDY------------------------------------------------------------------------------------PQKSIVDSRSVKR-------------------------LGFDEMAHGA---------- : 744
Orpheovirus_IHUMI_LCC2_YP_00 : IQGPRLTYQSSMGRQAL------GLYASNFL-MRYDD-VKMIAN------------------------------------------------------------------------------------PTNPMVATNTYHI-------------------------MGFYKRPAGR---------- : 770
Pithovirus_sibericum@YP_0090 : NMGPRNMYTCGMMRQAL------GAHHSNHP-LRFESVKMMIA-------------------------------------------------------------------------------------PSAPIFATQLNEW-------------------------LGLDELPSGE---------- : 811
Cedratvirus_A11_YP_009329295 : NMGPRNMYTCSMMRQAL------GIYHSGHN-LRFDSTIKMIAT------------------------------------------------------------------------------------PTPPIFQTQTNEW-------------------------LGLNDLPAGD---------- : 758
                                   R  5   6 k  6                        1                                                                                      P                                           p
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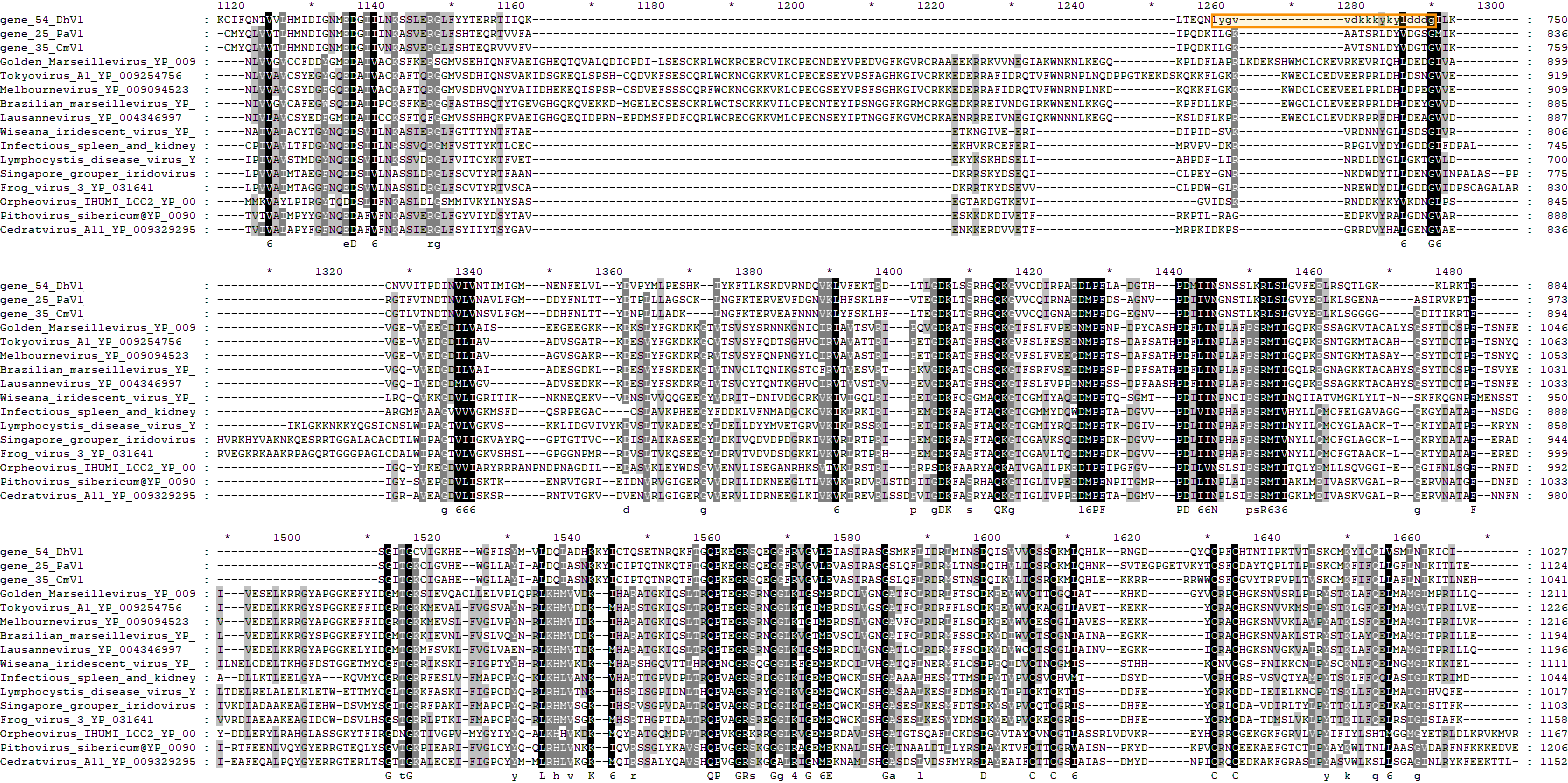

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                               1120         *      1140         *      1160         *      1180         *      1200         *      1220         *      1240         *      1260         *      1280         *      1300
gene_54_DhV1                 : KCIFQNTVVLHMIDIGNMEDGIILNKSSLERGLFYYTERRTIIQK--------------------------------------------------------------------------------------------LTEQNlygv---------------vdkkkykyldddgIIK--------- :  750
gene_25_PaV1                 : -CMYCLVVTLHMNDIGNMEDGIIINKASVERGLFSHTEQRTVVFA--------------------------------------------------------------------------------------------IPQDKILGE---------------AATSRLDYVDGSGMIK--------- :  836
gene_35_CmV1                 : -CMYCLVVTLHMNDIGNMEDGIIVNKASVERGLFSHTEQRVVVFV--------------------------------------------------------------------------------------------IPQDKILGE---------------AVTSNLDYVDGTGVIK--------- :  759
Golden_Marseillevirus_YP_009 : ----NLVVGVCCFDDYGMEDAIVACKSFKERSGMVSEHIQNFVAEIGHEQTQVALQDICPDI-LSESCKRLWCKRCERCVIKCPECNDEYVPEDVGFKGVRCRAAEEKRRKVVNEGIAKWNKNLKEGQ---------KPLDFLAPELKDEKSHWMCLCKEVRKEVRIQHLDEDGIVA--------- :  899
Tokyovirus_A1_YP_009254756   : ----NLVVAVCSYEGYGQEDAIVACKAFTQRGGMVSDHIQNSVAKIDSGKEQLSPSH-CQDVKFSESCQRLWCKNCGKKVKLCPECESEYVPSFAGHKGIVCRKKEDERRAFIDRQTVFWNRNPLNQDPPGTKEKDSKQKKFLGKE------KWECLCEDVEERPRLDHIDSNGVVE--------- :  919
Melbournevirus_YP_009094523  : ----NLVVAVCSYDGFGQEDAIVACKAFTQRGGMVSDHVQNYVAIIDHEKEQISPSR-CSDVEFSSSCQRFWCKNCGKKVKLCPECGSEYVPSFSGHKGIVCRKKEDERRAFIDRQTVFWNRNPLNKD---------KQKKFLGKE------KWDCLCEEVEELPRLDHIDPEGVVE--------- :  909
Brazilian_marseillevirus_YP_ : ----NIVVGVCAFEGYSQEDAIIPCKSFKERGGFASTHSQTYTGEVGHGQKQVEKKD-MGELECSESCKRLWCTSCKKKVILCPECNTEYIPSNGGFKGRMCRKGEDKRREIVNDGIRKWNENLKKGQ---------KPFDLLKPE------EWGCLCLEVEERPRLDHIDEYGVVD--------- :  885
Lausannevirus_YP_004346997   : ----NIVLAVCSYEDFGMEDAIICCKSFTQFGGMVSSHHQKPVAEIGHGQEQIDPRN-EPDMSFPDFCQRLWCRECGKKVMLCPECNSEYIPTNGGFKGVMCRKAENRRREIVNEGIQKWNNNLKEGQ---------KSLDFLKPE------EWECLCLEVDKRPRFDHIDEAGVVD--------- :  887
Wiseana_iridescent_virus_YP_ : ----NAIVAIACYTGYNQEDSVILNKASIERGLFGTTTYNTFTAE------------------------------------------------------------ETKNGIVE-ERI--------------------DIPID-SVE---------------VRDNNYGLISDSGIVR--------- :  806
Infectious_spleen_and_kidney : ----CPIVAVLTFDGYNQEDSIILNKSSVQRGMFVSTTYKTLCEC------------------------------------------------------------EKHVKRCEFERI--------------------MRVPV-DKE---------------RPGLVYDYIGDDGIFDPAL------ :  745
Lymphocystis_disease_virus_Y : ----IPIVAVSTMDGYNQEDSVILNKSSVDRGLFVITCYKTFVET------------------------------------------------------------EKYKSKHDSELI--------------------AHPDF-LIE---------------NRDLDYGLIGKTGVLD--------- :  700
Singapore_grouper_iridovirus : ----LPVVAIMTAEGFNQEDSIVLNASSLDRGLFSCVTYRTFAAN------------------------------------------------------------DKRRSKYDSEQI--------------------CLPEY-GNE---------------NKDWDYTLIDENGVINPALAS--PP :  775
Frog_virus_3_YP_031641       : ----LPVVAIMTAGGFNQEDSVVLNASSLDRGLFSCVTYRTVSCA------------------------------------------------------------DKRRTKYDSEVV--------------------CLPDW-GLE---------------NREWDYDLIGDDGVIDPSCAGALAR :  830
Orpheovirus_IHUMI_LCC2_YP_00 : ----MMKVAYLPIRGYTQDDSLIFNKASLDLGSMMIVKYLNYSAS------------------------------------------------------------EGTAKDGTKEVI-----------------------GVIDSE---------------RNDDKYKYVKDNGIPS--------- :  845
Pithovirus_sibericum@YP_0090 : ----TVTVAIMPYYGYNQEDAFVFNKASVERGLFGYVIYDSYTAV------------------------------------------------------------ESKKDKDIVETF--------------------RKPTL-RAG---------------EDPKVYRAIGDNGVAR--------- :  888
Cedratvirus_A11_YP_009329295 : ----TVIVALAPYFGFNQEDAFVFNKASIERGLFSYIIYTSYGAV------------------------------------------------------------ENKKERDVVETF--------------------MRPKIDKPS---------------GRRDVYHAIGENGVAE--------- :  836
                                      6          eD  6       rg                                                                                                                                         6   G6

                                      *      1320         *      1340         *      1360         *      1380         *      1400         *      1420         *      1440         *      1460         *      1480
gene_54_DhV1                 : ------------------------CNVVITPDINVIVNTIMIGM---NENFELVL--YIVPYMLPESHK--IYKFTLKSKDVRNDQVKLVFEKTRD---LTIGDKLSSRHGQKGVVCDIRPAEDLPELA-DGTH---PDMIINSNSSLKRLSLGVFEELRSQTLGK--------KLRKTE------ :  884
gene_25_PaV1                 : ------------------------RGTFVTNDTNVLVNAVLFGM---DDYFNLTT--YITPLLLAGSCK--INGFKTERVEVFDGNVKLHFSKLHF---VTEGDKLTSRHGQKGVVCQIRNAEDMPEDS-AGNV---PDIIVNGNSTLKRLSLGVYEELKLSGENA-----ASIRVKPTE------ :  973
gene_35_CmV1                 : ------------------------CGTLVTNDTNVLVNSVLFGM---DDHFNLTT--YINPLLLADK----INGFKTERVEAFNNNVKLYFSKLHF---LTEGDKLTSRHGQKGVVCQIGNAEDMPEDG-EGNV---PDIIINGNSTLKRLSLGVYEELKLSGGGG-----GDITIKRTE------ :  894
Golden_Marseillevirus_YP_009 : ------------------------VGE-VVEEGDILVAIS-------EEGEEGKK--KIKSLYFGKDKKGTVTSVSYSRNNKGNICIRIAVTSVRI---PQVGDKATSFHSQKGTFSLFVPEENMPENP-DPYCASHPDFLINPLAFPSRMTIGQPKESSAGKVTACALYSGSFTDCSPE-TSNFE : 1046
Tokyovirus_A1_YP_009254756   : ------------------------VGE-VVEDGDILIAV--------ADVSGATR--KIESVYFGKDKKGCVTSVSYFQDTSGHVCIRVAVATTRI---PETGDKATSFHSQKGVFSLFESEENMPETS-DAFSATHPDFLINPLAFPSRMTIGQPKESNTGKMTACAH--GSYTDCTPE-TSNYQ : 1063
Melbournevirus_YP_009094523  : ------------------------VGE-VVEDGDILIAV--------AGVSGAKR--KIESIYFGKDKRGRVTSVSYFQNPNGYLCIRVAVASTRI---PETGDKATSFHSQKGVFSLFVEEQDMPETS-DAFSATHPDFLINPLAFPSRMTIGQPKESNTGKMTASAY--GSYTDCTPE-TSNYQ : 1053
Brazilian_marseillevirus_YP_ : ------------------------VGQ-VVEDGDILVAI--------ADESGDKL--RIESVYFSKDEKGIVTNVCLTQNIKGSTCFRVTVESVRT---PKVGDKATSCHSQKGTFSRFVSEEDMPESP-DPFSATHPDFLINPLAFPSRMTIGQLREGNAGKKTACAHYSGSYTDCSPE-TSVYE : 1031
Lausannevirus_YP_004346997   : ------------------------VGQ-IVEDGDMLVGV--------ADVSEDKK--KIESLYFSKDKRGIVTSVCYTQNTKGHVCIRVTVVSTRV---PEVGDKATSFHSQKGTFSLFVPPENMPESS-DPFAASHPDFIINPLAFPSRMTIGQPKESSAGKKTACAHYSGSYTDCTPE-TSNFE : 1033
Wiseana_iridescent_virus_YP_ : ------------------------LRQ-QVKKGDVLIGRITIK----NKNEQEKV--VINSIVVQQGEEGYVDRIT-DNIVDGCRKVKIVIGQLRI---PEIGDKFCSGMAQKGTCGMIYAQEDMPETQ-SGMT---PDIIINPNCIPSRMTINQIIATVMGKLYLT-N--SKFKQGNPEMENSST :  950
Infectious_spleen_and_kidney : ------------------------ARGMFVAAGVVVVGKMSFD----QSRPEGAC----CSLAVKPHEEGYFDDKLVFNMADGCKCVKIKLRKIRI---PEMGDKFASFTAQKGTCGMMYDQWDMPETA-DGVV---PDIVINPHAFPSRMTVHYLLQMCFELGAVAGG--GKGYDATAE--NSDG :  888
Lymphocystis_disease_virus_Y : ----------IKLGKKNKKYQGSICNSLWIPAGTVLVGKVS------KKLIDGVIVYKIVSLTVKADEEGYLDELLDYYMVETGRVVKIKLRSSKI---PEIGDKFASFTAQKGTCGMIYRQEDMPETK-DGIV---PDLIINPHAFPSRMTINYILQMCYGLAACK-T--GKIYDATPE--KRYN :  858
Singapore_grouper_iridovirus : HVRKHYVAKNKQESRRTGGALACACDTLWIPAGTVIIGKVAYRQ---GPTGTTVC--KIISLAIKASEEGYIDKIVQDVDPDGRKIVKVRLRTPRI---PEMGDKFASFTAQKGTCGAVKSQEDMPEDK-DGVV---PDLIINPHAFPSRMTVNYLLQMCFGLAGCK-L--GKRYDATAE--ERAD :  944
Frog_virus_3_YP_031641       : RVEGKRKAAKRPAGQRTGGGPAGLCDALWIPAGTVLVGKVSHSL---GPGGNPMR--RIVSLTVKQSEEGYIDRVTVDVDSDGKKLVKVRLRTPRH---PEMGDKFASFTAQKGTCGAVLTQEDMPEDK-DGVV---PDLIINPHAFPSRMTVNYLLQMCFGTAACK-L--GKTYDATAE--ERED :  999
Orpheovirus_IHUMI_LCC2_YP_00 : ------------------------IGQ-YIKEGDVVIARYRRRANPNDPNAGDIL--EIASVKLEYWDSGVVENVLISEGANRHKSVTVKLRSTRI---PRPSDKFAARYAQKATVGAILPKEDIPEIPGFGV----PDILVNSLSIPSRMTITQLYEMLLSQVGGI-E--GGIFNLSGE--RNFD :  992
Pithovirus_sibericum@YP_0090 : ------------------------IGY-SVEPGDVLISKTK------ENRVTGRI--EIDNVRVGIGERGVVDRILIDKNEEGLTLVKVKIRDVRILSTDPIIGDKFASRHAQKGTIGLIVPEEDMPENPITGMR---PDILINPLAIPSRMTIAKLMEIVASKVGAL-R--GERVNATGE--DNFD : 1033
Cedratvirus_A11_YP_009329295 : ------------------------IGR-AVEAGDVLISKSR------RNTVTGKV--DVENVRLGIGERGVVERVLIDRNEEGLKIVKVKIREVRISSDPVIGDKFASRYAQKGTIGLIVPPEDMPETA-DGMV---PDIIINPLSIPSRMTIGKLMEIVASKVGAL-R--GERVNATAE--NNFN :  980
                                                               g 666                     d          g                  6          p  gDK  s   QKg         16PF          PD 66N    psR636                  g       F

                                *      1500         *      1520         *      1540         *      1560         *      1580         *      1600         *      1620         *      1640         *      1660         *
gene_54_DhV1                 : -----------------------SGITGCVIGKHE--WGFISYM-VLDQLADHKKYICTQSETNRQKFTGQPKEGRSQEGGFRVGVLEIASIRASGSMKFLIDRIMINSDQISVVVCSSCKMLQHLK--RNGD------QYQCPFCHTNTIPKTVTISKCMRYICQLVSMINIKICI--------- : 1027
gene_25_PaV1                 : -----------------------SGITGRCLGVHE--WGLLAYI-ALDQIASNKKYICIPTQTNKQTFTGQPKEGRSQEGGFRVGVLEVASIRASGSLQFIRDRMLTNSDQIHVLICSRCKMLQHNK--SVTEGPGETVKYTCSFCDAYTQPLTLPISKCMRFIFCLLGFLNIKITLTE------- : 1124
gene_35_CmV1                 : -----------------------SGITGRCIGAHE--WGLLAYI-ALDQIASNKKYICIPTQTNRQTFTGQPKEGRSQEGGFRVGVLEVASIRASGSLQFIRDRMSTNSDQIKVLICSRCKMLQHLE--KKRR-----RRWWCSFCGVYTRPVPLTVSKCMRFIFCLLAFLNIKITLNEH------ : 1041
Golden_Marseillevirus_YP_009 : I---VESELKRRGYAPGGKEFYIDGMIGRSIEVQACLLELVPLQPRLKHMVVDK--IHARATGKIQSLTRQPTEGRSRNGGLKIGSMERDCIVGNGATFCIRDRIFTSCDKHEVWVCTTCGQIAT----KHKD------GYVCRPCHGKSNVSRLPIRYSTRLAFQELMAMGIMPRILLQ------ : 1211
Tokyovirus_A1_YP_009254756   : I---VEDELKKRGYSPGGKEFFIDGRIGRKMEVAL-FVGSVAYN-RLKHMVDDK--MHARSTGKIQSLTRQPTEGRSRNGGLKTGIMERDSLVGSGATFCIRDRFFLSCDKHEVWVCKACGLLAVET--KEKK--------YCRACHGKSNVVKMSIPYSTRLGFQELMAMGVTPRILVE------ : 1226
Melbournevirus_YP_009094523  : V---VEDELKRRGYAPGGKEFFIDGRIGRKMEVSL-FVGLVPYN-RLKHMVIDK--IHARATGKIQSLTRQPTEGRSRNGGLKTGIMERDSLVGNGAVFCIRDRIFLSCDKHEVWVCESCGLIAVES--KEKK--------YCRACHGKSNVVKLAVPYATRLSFQELMAMGITPRILVK------ : 1216
Brazilian_marseillevirus_YP_ : L---VEDELKKRGYSPGGKEFYIDGMIGRKIEVNL-FVSLVQYN-RLKHMVDDK--IHARATGKIQSLTRQPTEGRSRNGGLKVGTMEVSCLVGNGAIFCIRDRMFSSCDKYDIWVCTSCGNIAINA--EGKK--------ICRACHGKSNVAKLSTRYSTRLAYQELMAMGITPRILLE------ : 1194
Lausannevirus_YP_004346997   : I---VEDELKKRGYAPGGKELYIDGMIGRMFSVKL-FVGLVAEN-RLKHMVTDK--MHARATGKIQSLTRQPTEGRSRNGGLKIGSMERDCLVGNGATLCIRDRMFFSCDKYDVWCCTSCGLIAINV--EGKK--------ICRACHGKSNVGKVAIRYSTRLAFQELMAMGITPRILLQ------ : 1196
Wiseana_iridescent_virus_YP_ : ILNELCDELTKHGFDSTGGETMYCGFIGRRIKSKI-FIGPTYYH-RLKHMVKDK--MHARSHGCVTTIHRQPNCGRSQGGGIRFGEMEKDCIIVHGATQFINERMFLCSDPFQIDVCTNCGMIS-----STHH--------KCNVCGS-FNIKKCNIPYSCRNLFQELNGMGIKIKIEL------- : 1111
Infectious_spleen_and_kidney : A--DLIKTLEELGYA---KQVMYCGRTGRRFESLV-FMAPCPYQ-KLKHLVANK--VHARTTGPVDPLTRQPVAGRSRDGGIKIGEMEQWCKISHGAAAAIHESMTTMSDPYTVPVCSVCHVMT-----DSYD--------VCRHCRS-VSVQTYAMPYTSRLFFQQLASIGIKTRIMD------- : 1044
Lymphocystis_disease_virus_Y : LTDELRELALELKLETW-ETTMYCGLTGRKFASKI-FIGPCDYQ-RLRHLVTNK--IHSRISGPIDNLTHQPVAGRSRYGGIKVGEMEQWCKISHGASAAIKESIFDMSDKYTIPICKTCKTIS-----DDFE--------YCRKCDD-IEIELKNCPYTSRLLFQELMAIGIHVQFE-------- : 1017
Singapore_grouper_iridovirus : IVKDIADAAKEAGIEHW-DSVMYSGITGRRFPAKI-FMAPCPYQ-RLRHMVSGK--IHSRVSGPVDALTRQPVAGRSRDGGIKIGEMEQWCKISHGASESIKESMFDTSDKYSVPVCQTCGRIS-----DHFE--------YCRLCDA-VDIRLTYIPYTTRLLFQELKAIGISITFK-------- : 1103
Frog_virus_3_YP_031641       : VVRDIAEAAKEAGIDCW-DSVLHSGSTGRRLPTKI-FMAPCPYQ-RLKHMVSGK--MHSRTHGPTDALTRQPVAGRSREGGIKIGEMEQWCKISHGASESIKESVYDMSDKYEVPVCKECGRIS-----DHFE--------YCRMCDA-TDMSLVKIPYTTRILFQELRSIGISIAFK-------- : 1158
Orpheovirus_IHUMI_LCC2_YP_00 : Y-DDLERYLRAHGLASSGKYTFIRGDNGRTIVGPV-MYGYIYYQ-ALKHHVKDK--KQYRATGQMDPVTRQPVKGRKRRGGIRVGEMERDAVISHGATGTSQAFICKDSDGYVTAYCVNCGTLASSRLVDVKR------EYHCRRCGEKGKFGRVLVPYIFIYLSHTMGGMGYETRLDLKRVKMVR : 1167
Pithovirus_sibericum@YP_0090 : I-RTFEENLVQYGYERRGTEQLYSGVIGRPIEARI-FVGLCYYQ-QLRHLVNKK--IQVRSSGLYKAVSHQPVGGRSKGGGIRAGEMEKNALISHGATNAALDTILYRSDAYKTVFCTTCGRVAISN--PKYD------KPVCRNCEEKAEFGTCTIPYAYRWLTNLLAASGVDARFNFKKKEDVE : 1206
Cedratvirus_A11_YP_009329295 : I-EAFEQALPQYGYERRGTERLTSGTIGRALECEI-FIGPCYYM-MLRHLVKGK--MQIRSSALYQAVSHQPVGGRSKGGAIRIGNMEKNAMISHGASDSIVDSFMYRSDAYEAIFCTTCGSIAIAS--DMYD------NPICRQCEDKAKFGRASIPYASVWLKSLLSGAGINLRYKFEEKTTL- : 1152
                                                       G tG              y   L h v  K  6  r          QP  GRs  Gg 4 G 6E       Ga   l        D      C  C  6                   C  C            y  k   q 6   g
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