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(RESEARCH ARTICLE)

Identification of HNH endonuclease domain in the basic protein 2 subunit of the polymerase of human influenza viruses

Peramachi Palanivelu *

Department of Molecular Microbiology, School of Biotechnology, Madurai Kamaraj University, Madurai – 625 021, India.

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Abstract

RNA polymerases of human influenza viruses A, B and C do not have a capping enzyme, as other RNA viruses, to cap their mRNAs for translation in the host cells. So, they employ a unique 'cap-snatching' mechanism, where the mRNA cap structures are snatched from the host cell mRNAs and used as a primer to initiate its own mRNA synthesis. One of the RNA polymerase subunits, the polymerase basic protein subunit 2 (PB2), is shown to involve in the 'cap-snatching' mechanism. The active sites for the 'cap-snatching' and endonuclease by the PB2 were analyzed by multiple sequence alignment (MSA) analysis and corroborated with the results available from biochemical, site-directed mutagenesis (SDM) and X-ray crystallographic techniques. It is found that the PB2 subunit in all three human influenza viruses habours both the cap-binding motif (CBM) and a HNH/N type endonuclease domain. The CBM is aromatic amino acid rich and the HNH/N is a –DH- based endonuclease in influenza viruses A and C and a –DQ- based one in influenza virus B. The invariant H is proposed to act as a general base to initiate catalysis and the invariant first N is implicated in nucleotide binding. In addition, the nuclear localization signals were also identified in all three human influenza viruses. By sequence similarity, similar HNH/N domain are found in the RNA cleaving CRISPR-Cas13a/13b and CRISPR-Cas12a endoribonucleases. The identification of HNH/N domain in all three human influenza viruses suggests that the PB2 subunit itself could cleave the cap structures from the host cell mRNAs, which are subsequently used as primers to initiate viral mRNA synthesis. These results will facilitate the optimization of endonuclease inhibitors as potential new anti-influenza drugs, and could also help in developing new drugs for flu treatments in the future.

Keywords: Human influenza viruses; RNA Polymerase basic protein subunit 2; HNH endonuclease; Cap-snatching; CRISPR-Cas13a endoribonuclease; CRISPR-Cas12a endoribonuclease.

1. Introduction

Influenza is an infectious disease caused by influenza viruses. Influenza viral infection is a highly contagious, airborne that generally causes acute respiratory illness resulting in variable degrees of systemic symptoms from mild fatigue to respiratory failure and death. Therefore, influenza viral infections are a major public health concern worldwide. The A and B viruses cause seasonal influenza every year, which affect approximately 5–10% of the adult and 20–30% of the pediatric population. A report by World Health Organization estimates that seasonal flu may result in 2,90,000-6,50,000 deaths every year due to respiratory diseases alone. (This estimate does not take into account of deaths from other diseases such as cardiovascular disease, which can be influenza-related). The first flu viral pandemic took place in 1918 and was referred to as "Spanish" flu. It was the deadliest, claiming an estimated ~50 million lives worldwide in less than a year [1]. The second flu epidemic was reported in 2019-2020. The Center for Disease Control and Prevention (CDC), USA, estimates, the 2019-2020 had caused 39 million to 56 million flu illnesses and 24,000 to 62,000 deaths and found it was mainly caused by the influenza A virus, H1N1. Only few other pandemics have caused such a devastating effect,

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^{*} Corresponding author: Peramachi Palanivelu

Department of Molecular Microbiology, School of Biotechnology, Madurai Kamaraj University, Madurai - 625 021, India.

like the ones which were caused by the SARS-Coronaviruses (SARS-CoVs) including the current epidemic caused by SARS-CoV-2.

Influenza viruses belong to the family, Orthomyxoviridae. In this family, there are four genera which are named A, B, C and D. Influenza A, B and C viruses infect humans whereas D virus infects animals. Among them, infections by influenza A virus is most common and severe and causes the flu pandemics. Influenza A virus is an avian virus, which is capable of jumping species and infects both humans and other animals. Wild aquatic birds and other animal species like, pigs, ferrets, horses, seals, whales, minks, giant anteaters, cats and dogs are also found to be the reservoir for the influenza A virus. While influenza A virus shows animal to human transmissions, influenza B and C viruses show very limited host range and appear predominantly in humans [2]. Interestingly, influenza viruses, B and C, do not have animal reservoirs like influenza A virus [3]. Out of the three most widely known human influenza viruses, the influenza A and B viral infections peak in winter months, causing substantial morbidity and mortality in humans and a considerable financial burden worldwide, whereas the influenza C virus [4] cause sporadic outbreaks in humans causing only mild upper respiratory infections [5, 6]. Influenza D virus primarily affects cattle and is not known to infect or cause any major illness in humans [3].

1.1. Human Transmission

Influenza viral infections are mediated by viral surface glycoproteins. Types A and B have two surface glycoproteins, viz. haemaggluntinin (H) and neuraminidase (N). (H is a Type I integral membrane glycoprotein that binds to cellsurface receptors and facilitates fusion between the viral envelope and endosomal membrane, whereas N is a Type II integral membrane glycoprotein, which facilitates viral release from cells by removing sialic acid from sialyloligosaccharides on the cell and viral surfaces). The H of the influenza viruses is a trimer (similar to the spike proteins in SARS-CoVs) that recognizes and binds to the host cell-surface receptor, N-acetylneuraminic (sialic) acid. (Sialic acids are nine-carbon acidic monosaccharides commonly found at the termini of many glycoconjugates), which is followed by the release of the virions into the human cells by the sialidase activity of the N. On the other hand, the types C and D have only one surface glycoprotein, known as Hemagglutinin–Esterase Fusion (HEF) protein, which binds to the host cell-surface receptor (9-O-acetylneuraminic acid) and promotes viral membrane and cell membrane fusion. In C and D types, the neuraminate-O-acetyl esterase functions as neuraminidase in viral release from the infected cells. There are at least 18 haemaggluntinins (H1 to H18) and 11 neuraminidases (N1 to N11) reported in influenza A virus, whereas the influenza B and C viruses do not have such subtypes. Although vaccines against influenza A and B viruses are available, the protection that they offer is limited by the antigenic variations mainly in the two glycoproteins, viz. H and N, which are found on the envelope of influenza A viral strains at 4:1 ratio [7].

1.2. Genomes of Human Influenza Viruses

Human influenza A, B and C viruses belong to the Orthomyxoviridae family, which are a group of enveloped, negativesense RNA viruses, characterized by their segmented genome. Influenza viruses A and B are made up of 8 RNA segments and B type showed no antigenic relationship to A type virus. RNA segments are joined by the RNA polymerase subunits (PB1, PB2 and PA) and the nuclearcapsid protein, NP. Influenza A viral genome length is 13,588 nts, and that of B is 14,639 nts. This is due to the 5'- and 3'-UTRs are longer in B viral genome. In influenza viruses A and B, the 8 RNA segments encode at least 10 proteins. Influenza viruses C and D genome consists of only 7 segments and encode only 9 proteins [8]. In all the four genera, the viral RNA (vRNA) genome segments are bound by a heterotrimeric RNAdependent RNA polymerase (RdRp), forming a viral ribonucleoprotein (vRNP) complex [9,10]. In the vRNP, the 5'- and 3'-termini of the vRNA are bound to the RNA polymerase, while the rest of the vRNA associates with oligomeric NPs. Among them, only influenza A virus has many subtypes with different combinations of the two surface glycoproteins.

1.2.1. Transcription and Replication Processes in Influenza Viruses

As they are negative-strand viruses, the viral transcription and replication processes are performed in the host cell nucleus and then transported to the cytoplasm for translation and viral assembly. The crucial enzyme for the multiplication of the viruses in the host cells, is the RNA-dependent RNA polymerases (RdRp), which is a component of the Ribonucleoprotein (RNP) that is imported into the host cell nucleus during the infection process. The viral polymerase is a heterotrimer and made up of three different subunits, viz. two polymerase basic protein subunits (PB1 and PB2) and a polymerase acidic protein subunit (PA) (Fig. 1a). Unlike other RNA viruses, the influenza virus polymerases do not have an inherent capping enzyme to cap its mRNAs for efficient translation in the host cells and therefore, it relies upon the capped pre-mRNAs of the host cells as cap-donors [11]. Thus, during multiplication, the enzyme uses the negative-sense viral RNA (vRNA) as a template to synthesize two positive-sense RNA species, viz. mRNA templates for viral protein synthesis, which are after polyadenylation and capping exported to cytoplasm and translated like other host mRNAs, and complementary RNA (cRNA) intermediates from which the same enzyme

transcribes more copies of negative-sense, genomic vRNAs. In contrast to transcription, the genome replication is capindependent and proceeds via a cRNA replicative intermediate. Thus, genome replication is unprimed and generates exact full-length copies of the template.

The X-ray crystallographic structures of the complete heterotrimeric polymerase ($M_r \sim 255$ kDA) revealed that the polymerase forms a compact particle with PB1 at its centre, capped on one face by PB2 and clamped between the two globular domains of PA. Like other DNA and RNA polymerases, the PB1 had the canonical right-hand-like fold, possessing fingers, palm, and thumb subdomains [12, 13].



Figure 1a. A schematic diagramme showing various subunits of the heterotrimeric influenza viral polymerase. (The number of amino acids of the subunits is given in brackets from influenza A virus)

The influenza viral RNA polymerase (EC 2.7.7.48) is a primer-dependent enzyme. The enzyme cannot copy the (-) strand RNA template without a small piece of RNA that aligns on the template RNA and provides a starting point for mRNA synthesis. They generate the primers by a unique 'cap-snatching' mechanism. As RdRps are not found in mammalian cells, they are an excellent target for designing antiviral compounds.

Figure 1b. A schematic diagram showing various domains of the polymerase PB2 subunit of influenza virus A (CBR, Cap-binding region)

As the virus's initial stages of multiplication are performed in the nucleus, they possess nuclear localization signals (NLSs). The NLSs are generally short peptides rich in basic amino acids that act as a signal to mediate the transport of molecules from the cytoplasm into the nucleus. The NLSs are recognized by the corresponding nuclear transporters, which then interact with nucleoporins to help NLS-containing proteins reach the nucleus through Nuclear Pore Complexes. A K/R rich NLS is found at the C-terminal region and another possible one at the N-terminal region (highlighted in orange). The first NLS to be discovered was the sequence $-^{126}$ PKKKRKV¹³²- in the SV-40 large T-antigen (a monopartite NLS) [14]. Willis et al. [15] identified a slightly different putative NLS (-⁶⁴⁰PKLKRQ⁶⁴⁶-) in vasopressin-activated calcium-mobilizing protein which is similar to the N-terminal one in PB2. In recent years, NLSs are also widely used as targets in cancer treatment and prevention of viral infections [16].

Most of the cellular and eukaryotic viral mRNAs have a cap structure at their 5'-end that is critical for efficient translation. Cap structures also help in mRNA transport from nucleus to cytoplasm and, in addition, protect the mRNAs from degradation by 5'-exonucleases. A common aromatic-rich cap-binding pocket is conserved by convergent evolution. In this pocket the positively charged N(7)-methylated guanine ring of the cap structure is stacked between two aromatic amino acid residues. In the process called 'cap-snatching', the viral polymerase uses its PB2 cap-binding domain to capture the 5'-cap of nascently capped host mRNAs and cleaves and the 5'-cap of ~15 nucleotides which is used as the primer for viral mRNA synthesis. Most attempts to develop anti-influenza drugs against the influenza viruses are for the RdRp and are focused on the highly conserved PB1 polymerase catalytic subunit's active site, the PB2 cap-binding and PA endonuclease domains [17].

Transcription is initiated by adding **GMP**, the nucleotide which is complementary to the second nucleotide at the 3'termini of all eight RNA segments, to the primer. The cap structure (highlighted in blue), snatched from the host mRNAs, is used as the primer for viral mRNA transcription (Fig. 2).



Figure 2 Cap structure of the host mRNAs with the viral polymerase subunits during viral mRNA transcription [11].

There are two different reports on the activities of the polymerase subunits, viz. the PB2 and PA. For example, some reports claim that the cap-binding and endonuclease activities reside on two different subunits, PB2 and PA, respectively [18-21]. Some reports claim that the cap-binding and endonuclease activities reside on the PB2 subunit itself. In this communication, evidences are presented to show that a HNH/N type endonuclease domain is identified in the PB2 subunits of all three human influenza viruses, which not only bind to the cap structure but could also make the endonucleolytic cleavage [21,11].

1.3. HNH Endonucleases

The HNH domains are ubiquitous and reported both in prokaryotes and eukaryotes. All of them invariably harbour an endonuclease site. The HNH domains are small nucleic acid binding motifs (~30 amino acids in length) with an associated DNA cleavage module. Such modules are commonly widespread in α - α - β -metal finger endonucleases. Proteins containing the HNH domain performs variety of functions in the organisms like site-specific group I and group II homing endonucleases, bacterial toxins with non-specific endonuclease activities, restriction enzymes, reverse transcriptase, etc. Their properties and mechanism of action are already discussed in detail by Palanivelu [22].

Based on the active site amino acid analysis, HNH-family of endonucleases are broadly classified into two major subgroups, depending upon the immediate amino acid adjacent to the invariant proton acceptor (His), highlighted in green, i.e., either as –HH- based or –DH- based enzymes (highlighted in red) [22]. (A few exceptions are also observed where the D is replaced by E and the second H is replaced by an N). A typical arrangement of active site amino acids in HNH endonucleases is shown in Fig. 3.



Figure 3 Arrangement and distance conservations active site amino acids in HNH/N endonucleases (Shows the invariant amino acids (green and bold) and the approximate distances between them.

The active site of HNH endonucleases consists of two highly conserved His and Asn, and a variable His (Asn replaces the second H and form another subfamily of HNH endonucleases). The HNH endonucleases can make a nick or a double-stranded break on specific/nonspecific regions on DNA molecules in the presence of a divalent metal ion. The invariant **His** residue in the conserved motif **H**NH/N serves as the general base that activates a metal-bound water molecule for a nucleophilic attack on the sugar-phosphate backbone of nucleic acids [23,24].

2. Material and methods

The protein sequence data of the polymerase basic protein subunit, PB2 of influenza viruses, A, B and C were obtained from PUBMED and SWISS-PROT databases. The advanced version of Clustal Omega was used for protein sequence analysis. Along with the conserved motifs identified by the bioinformatics analysis and from the data already available from biochemical, SDM and X-ray crystallographic analyses on the PB2 subunit and HNH endonucleases were used to arrive at the possible amino acids that make the active site of the enzyme. For pI calculations, the Expasy tool was used.

3. Results and discussion

3.1. MSA analysis of the PB2 subunit of the polymerase

Despite the availability of antivirals for influenza viruses, the emergence of resistant strains calls for antivirals with novel mechanisms of actions. The PB2 subunit of the influenza A viral polymerase is a promising drug target because of its vital role in the unique 'cap-snatching' mechanism. In fact, blocking the influenza virus "cap-snatching" activity was proved to be a new and efficient strategy for the treatment of influenza viral infections. However, all three subunits PB1 [25], PB2 [21] and PA [18, 20] are implicated in endonuclease activity of the polymerase heterotrimer.

Shi et al. [21] have shown that the endonuclease activity resides in the PB2 subunit of the polymerase in influenza A virus. Their results clearly showed that purified virion RNP-complexes cleaved the RNA specifically to generate a capped 14-nt RNA fragment (cap+13 nt) to be further used as primer to initiate viral mRNA synthesis (Fig. 2). Furthermore, they found that the purified anti-PB2 IgG, inhibited the endonuclease activity, but interestingly, anti-PB1 and anti-PA antibodies did not inhibit the cleavage. They have also further found that RNAs containing the 5'-terminal structure, the Gppp------G/A, could not be cleaved to produce these specific fragments in the absence of one or two subunits of the polymerase. The presence of the endonucleolytic domain in the PB2 subunit was further supported by Plotch et al. [11].

They found that the purified trimeric complex, expressed by recombinant baculovirus in insect cells, cleaved the artificial substrate, but if one or two subunits were removed from the complex, the cleavage activity was totally lost. Therefore, they suggested that the viral PB2 is the endonuclease that cleaves the host cell mRNA to produce the primer to initiate viral transcription. Furthermore, they found the uncapped ribopolymer inhibitors of viral mRNA transcription inhibited the cleavage of capped RNAs [11]. UV cross-linking studies and photo-affinity labelling by cap analogues have shown that the PB2 subunit recognizes and binds to the cap structure at the 5'-end of the host cell hnRNAs [26]. By using temperature-sensitive mutants with defects in the PA gene, it was shown that the principal role of the PA subunit is not in the viral mRNA synthesis, but rather in viral RNA replication [27, 28]. However, it was shown that the PA subunit is required for successful assembly of an active polymerase complex with PB1 and PB2 [29].

The present work found that the PB2 subunit not only possesses the cap-binding domain but also an endonuclease domain which possibly involves in cleaving the cap structure. For cleaving the cap structure from the host pre-mRNAs, a HNH type of endonuclease active site is identified in the PB2 subunits itself for the first time, supporting the observations by Plotch et al. [11] and Shi et al. [21].

Figure 4 shows the MSA of PB2 subunits of the polymerase from different strains of influenza A virus. (only the required regions for the discussions are shown here). The influenza A virus strain (1934/ H1N1) is highlighted and it showed a theoretical pl of 9.73. The MSA shows that the entire sequence is highly conserved irrespective of the serotypes. Further analysis of the MSA found, a –DH- based HNH endonuclease domain in the PB2 subunit of polymerase at the N-terminal region. The –DH- dyad is followed by two completely conserved Ns, suggesting it belongs to HNN subfamily (Fig. 4). Two metal-binding –DxD- motifs are identified (data not shown).

Proposed NLSs and cap-binding regions (CBRs) are highlighted in orange and magenta, respectively. Several studies have shown that the CBR is located in the PB2 subunit. Honda et al. [30] identified a ³²P-labelled, V8 protease peptides of PB2 derived by UV cross-linking of the influenza ribonucleoprotein complex to a m7G³²ppp-labelled capped oligonucleotide. They suggested that residues 242–282 and a second region from 538–577, were involved in capbinding. Li et al. [25] extended this approach by UV cross-linking a 4 thioU-containing, ³²P-labelled, capped oligonucleotide. A peptide, -SVLVNTYQWIIRNW- (residues 544–557) was identified after V8 protease digestion. Furthermore, mutation of W⁵⁵²→Ala reduced cap binding to 25 % of wild-type levels. Given the proximity of the 4 thioU residue (at residue 2 of the oligonucleotide) to the labelled cap structure, it was proposed that the isolated peptide must be close to the aromatic sandwich. The authors concluded that one or other of the nearby aromatic residues, i.e., W537, Y550, W557 or W564, form the aromatic sandwich, similar to other cap-binding proteins (such as the eukaryotic initiation factor eIF4E or VP39) in which the 7-methylguanine moiety is sandwiched between two aromatic amino acid residues. Honda et al. [30] reported two regions of PB2 involved in cap binding, whereas Li et al. [25] reported one region only. MSA analysis shows at least two CBRs, one with the likely residues from 445 to 452 (-⁴⁴⁵LFQNWGVE-) and the other one with the residues from 448 to 557 (-⁴⁴⁸NTYQWIIRNW-). The second CBR is proved by SDM and other techniques [30, 25].

CLUSTAL O (1.2.4) MSA of PB2 subunit of polymerase of influenza A viruses

sp P26107 PB2 I56A3	MERIKELRDLMSQSRTREILT <mark>T</mark> TTV	DHMAIIKRYTSGRQEK	PALRMKWMMAMKYPITAD	60
tr D9U0Y7 D9U0Y7 9INFA	MERIKELRNLMSQSRTREILTKTTV	DHMAIIKKYTSGRQEKN	PSLRMKWMMAMKYPITAD	60
tr D2E5N3 D2E5N3 9INFA	MERIKELRNLMSQSRTREILTKTTV	DH <mark>MAIIKKYTSGRQEK</mark> N	PSLRMKWMMAMKYPITAD	60
tr 16s703 16s703 91NFA	MERIKELRNLMSQSRTREILTKTTV	DHMAIIKKYTSGRQEK	PSLRMKWMMAMKYPITAD	60
sp Q1PUC9 PB2_173A5	MERIKELRNLMSQSRTREILTKTTV	DHMAIIKKYTSGRQEKN	PSLRMKWMMAMKYPITAD	60
sp Q6XU90 PB2_I67A0	MERIKELRNLMSQSRTREILTKTTV	DHMAIIKKYTSGRQEK	PSLRMKWMMAMKYPITAD	60
sp Q3YPY5 PB2_I71A1	MERIKELRNLMSQSRTREILTKTTV	DHMAIIKKYTSGRQEKN	PSLRMKWMMAMKYPITAD	60
sp P26105 PB2_186A2	MERIKELRDLMSQSRTREILTKTTV	DHMAIIKKYTSGRQEKN	PALRMKWMMAMKYPITAD	60
sp P0DOG6 PB2S1_I34A1	MERIKELRNLMSQSRTREILTKTTV	DHMAIIKKYTSGRQEKN	PALRMKWMMAMKYPITAD	60
sp P12445 PB2_I34A0	MERIKELRDLMSQSRTREILTKTTV	DHMAIIKKYTSGRQEKN	PALRMKWMMAMKYPITAD	60
sp Q0A2F5 PB2_I83A4	MERIKELRDLMSQSRTREILTKTTV	DHMAIIKKYTSGRQEKN	PALRMKWMMAMKYPITAD	60
sp P26104 PB2_I77AG	MERIK <mark>G</mark> LRDLMSQSRTREILTKTTV	DHMAIIKKYTSGRQEKN	PALRMKWMMAMKYPITAD	60
sp Q20NV1 PB2_I80AD	MERIKELRDLMSQSRTREILTKTTV	DHMAIIKKYTSGRQEKN	PALRMKWMMAMKYPITAD	60
sp P26115 PB2_I77AF	MERIKELRDLMSQSRTREILTKTTV	DHMAIIKKYTSGRQEKN	PALRMKWMMAMKYPITAD	60
sp Q9Q0V1 PB2_196A0	MERIKELRDLMSQSRTREILTKTTV	DHMAIIKKYTSGRQEKN	PALRMKWMMAMKYPITAD	60
sp Q0A449 PB2_I66A1	MERIKELRDLMSQSRTREILTKTTV	DHMAIIKKYTSGRQEKN	PALRMKWMMAMKYPITAD	60
sp Q6DNK1 PB2_I03A1	MERIKELRDLMSQSRTREILTKTTV	DHMAIIKKYTSGRQEKN	PALRMKWMMAMKYPITAD	60
sp P26110 PB2_I82A3	MERIKELRDLMSQSRTREILTKTTV	DHMAIIKKYTSGRQEKN	PALRMKWMMAMKYPITAD	60
sp Q809P5 PB2_I01A3	MERIKELRDLMSQSRTREILTKTTV	DHMAIIKKYTSGRQEKN	PALRMKWMMAMKYPITAD	60
sp P26112 PB2_I80A8	MERIKELRDLMSQSRTREILTKTTV	DHMAIIKKYTSGRQEKN	PALRMKWMMAMKYPITAD	60
sp Q0A438 PB2_I49A1	MERIKELRDLMSQSRTREILTKTTV	DHMAIIKKYTSGRQEKN	PALRMKWMMAMKYPITAD	60
sp Q20P12 PB2_I56A1	MERIKELRDLLSQSRTREILTKTTV	DHMAIIKKYTSGRQEK <mark>N</mark>	PALRMKWMMAMKYPITAD	60
sp Q0A427 PB2_156A2	MERIKELRDLMSQSRTREILTKTTV	DHMAIIKKYTSGRQEK <mark>N</mark>	PALRMKWMMAMKYPITAD	60
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<pre>sp P26107 tr D9U0Y7 tr D2E5N3 tr I6S703 sp Q1FUC9 sp Q2VPY5 sp P26105 sp P0D0G6 sp P12445 sp Q0A2F5 sp Q0A2F5 sp Q0A2F5 sp Q20NV1 sp Q20NV1 sp Q20NV1 sp Q20V1 sp Q20V1 sp Q20V1 sp Q20V1 sp Q20P12 sp P26112 sp Q20P12 sp Q0A427 </pre>	PB2_156A3 D9U0Y7_9INFA D2E5N3_9INFA PB2_173A5 PB2_167A0 PB2_171A1 PB2_186A2 PB251_134A1 PB2_183A4 PB2_183A4 PB2_183A4 PB2_177AF PB2_196A0 PB2_166A1 PB2_166A1 PB2_103A1 PB2_182A3 PB2_180A8 PB2_180A8 PB2_156A1 PB2_156A1 PB2_156A2	KRIMEMI PERNEQGQ' KRITEMVPERNEQGQ' KRITEMVPERNEQGQ' KRITEMVPERNEQGQ' KRITEMVPERNEQGQ' KRITEMVPERNEQGQ' KRIMEMIPERNEQGQ' KRIMEMIPERNEQGQ' KRIMEMIPERNEQGQ' KRIMEMIPERNEQGQ' KRIMEMIPERNEQGQ' KRIMEMIPERNEQGQ' KRIMEMIPERNEQGQ' KRIMEMIPERNEQGQ' KRIMEMIPERNEQGQ' KRIMEMIPERNEQGQ' KRIMEMIPERNEQGQ' KRIMEMIPERNEQGQ' KRIMEMIPERNEQGQ' KRIMEMIPERNEQGQ' KRIMEMIPERNEQGQ' KRIMEMIPERNEQGQ'	TLWSKTNDA(TLWSKMSDA(TLWSKMSDA(TLWSKMSDA(TLWSKMSDA(TLWSKMSDA(TLWSKMSDA(TLWSKMNDA(TLWSKTNDA(SSDRIMVSPLAV SSDRVMVSPLAV	VTWWNRNGPTAVTTHYPKVYKTYFE VTWWNRNGPVTSTVHYPKVYKTYFD VTWWNRNGPVTSTVHYPKVYKTYFD VTWWNRNGPVTSTVHYPKVYKTYFD VTWWNRNGPMTSTVHYPKVYKTYFD VTWWNRNGPMTSTVHYPKVYKTYFE VTWWNRNGPTTSTHYPKVYKTYFE VTWWNRNGPTTSTHYPKVYKTYFE VTWWNRNGPTTSTIHYPKVYKTYFE VTWWNRNGPTTSTHYPKVYKTYFE VTWWNRNGPTTSTHYPKVYKTYFE VTWWNRNGPTTSTVHYPKVYKTYFE VTWWNRNGPTTSTVHYPKVYKTYFE VTWWNRNGPTTSTVHYPKVYKTYFE VTWWNRNGPTTSTVHYPKVYKTYFE VTWWNRNGPTTSTVHYPKVYKTYFE VTWWNRNGPTTSTVHYPKVYKTYFE VTWWNRNGPTTSTVHYPKVYKTYFE VTWWNRNGPTTSTVHYPKVYKTYFE VTWWNRNGPTTSTVHYPKVYKTYFE VTWWNRNGPTTSTVHYPKVYKTYFE VTWWNRNGPTTSTVHYPKVYKTYFE VTWWNRNGPTTSTVHYPKVYKTYFE VTWWNRNGPTTSTVHYPKVYKTYFE VTWWNRNGPTSTVHYPKVYKTYFE	120 120 120 120 120 120 120 120 120 120
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sp P2 6107 tr D9U0Y7 tr D2E5N3 tr I65703 sp Q1FUC9 sp Q6XU90 sp Q3YPY5 sp P2 6105 sp P12445 sp Q0A2F5 sp P2 6104 sp Q20NV1 sp Q20NV1 sp Q0A449 sp Q0Q0V1 sp Q6DNK1 sp Q6DNK1 sp Q6DNK1 sp Q6DNK1 sp P2 6112 sp Q0A438 sp Q2 0P12 sp Q0A427	PB2_I56A3 D9U0Y7_9INFA D2E5N3_9INFA PB2_I73A5 PB2_I67A0 PB2_I71A1 PB2_I86A2 PB251_I34A1 PB2_I34A0 PB2_I83A4 PB2_I77AG PB2_I80AD PB2_I77AF PB2_I96A0 PB2_I66A1 PB2_I66A1 PB2_I03A1 PB2_I80A8 PB2_I80A8 PB2_I49A1 PB2_I56A1 PB2_I56A2	MNRANQRLNPMHQLLI VNRANQRLNPMHQLLI	RHFQKDAKI RHFQKDAKV	CBR LFONWGIEPII LFONWGVEHII LFONWGVEHII LFONWGIEHII LFONWGIEHII LFONWGIEPII	DNIMGMTGILPDMTPSTEMSLRGIRI DSVMGMIGVLPDMTPSTEMSMRGIRV DSVMGMIGVLPDMTPSTEMSMRGIRV DSVMGMIGVLPDMTPSTEMSMRGIRV DNVMGMIGVLPDMTPSTEMSMRGIRV DNVMGMIGVLPDMTPSTEMSMRGIRV DNVMGMIGILPDMTPSTEMSLRGVRV DNVMGMIGILPDMTPSTEMSLRGVRV DNVMGMIGILPDMTPSTEMSLRGVRV DNVMGMIGILPDMTPSTEMSLRGVRV DNVMGMIGILPDMTPSTEMSLRGVRV DNVMGMIGILPDMTPSTEMSLRGVRV DNVMGMIGILPDMTPSTEMSLRGVRV DNVMGMIGILPDMTPSTEMSLRGVRV DNVMGMIGILPDMTPSTEMSLRGVRV DNVMGMIGILPDMTPSAEMSLRGVRV DNVMGMIGILPDMTPSTEMSLRGVRV DNVMGMIGILPDMTPSTEMSLRGVRV DNVMGMIGILPDMTPSTEMSLRGVRV DNVMGMIGILPDMTPSTEMSLRGVRV DNVMGMIGILPDMTPSTEMSLRGVRV DNVMGMIGILPDMTPSTEMSLRGVRV DNVMGMIGILPDMTPSTEMSLRGVRV DNVMGMIGILPDMTPSTEMSLRGVRV DNVMGMIGILPDMTPSTEMSLRGVRV DNVMGMIGILPDMTPSTEMSLRGVRV DNVMGMIGILPDMTPSTEMSLRGVRV	480 480 480 480 480 480 480 480 480 480

sp P26107 PB2_I56A3	GPESIL	VNTYQWIIKNWETVKIQWS	DPTILYNKIEFEPFQSLIPKAARAQYSGFVRTLF	600
tr D9U0Y7 D9U0Y7_9INFA	GPESVL	VNTYQWIIRNWEAVKIQWS	NPAMLYNKMEFEPFQSLVPKAIRSQYSGFVRTLF	600
tr D2E5N3 D2E5N3 9INFA	GPESVL	VNTYQWIIRNWEAVKIQWS	NPAMLYNKMEFEPFQSLVPKAIRSQYSGFVRTLF	600
tr I6S703 I6S703 9INFA	GPESVL	VNTYQWIIRNWEAVKIQWS	NPAMLYNKMEFEPFQSLVPKAIRSQYSGFVRTLF	600
sp Q1PUC9 PB2_173A5	GPESVL	VNTYQWIIRNWETVKIQWS	NPTMLYNKMEFEPFQSLVPKAIRGQYSGFVRTLF	600
sp Q6XU90 PB2_I67A0	GPESVL	VNTYQWIIRNWETVKIQWS	NPTMLYNKMEFEPFQSLVPKAIRGQYSGFVRTLF	600
sp Q3YPY5 PB2_I71A1	GPESVL	VNTYQWIIRNWETVKIQWS	NPTMLYNKMEFEPFQSLVPKAIRGQYSGFVRTLF	600
sp P26105 PB2_I86A2	GPESVL	VNTYQWIIRNWEIVKIQWS	DPTMLYNKIEFEPFQSLVPRATRSQYSGFVRTLF	600
sp P0DOG6 PB2S1_I34A1	GPESVL	VNTYQWIIRNWETVKIQWS(NPTMLYNKMEFEPFQSLVPKAIRGQYSGFVRTLF	600CBR2
sp P12445 PB2_I34A0	GPESVL	VNTYQWIIRNWETVKIQWS	VPATLYNKMEFEPFQSLVPKAARGQYSGFVRTLF	600
sp Q0A2F5 PB2_I83A4	GPESVL	VNTYQWIIRNWETVKIQWS	NPTMLYNKMEFEPFQSLVPKAARGQYSGFVRALF	600
sp P26104 PB2_I77AG	G <mark>S</mark> ESVL	VNTYQWIIRNWETVKIQWS	DPTMLYNKMEFEPFQSLVPKAARGKYSGFVRTLF	600
sp Q20NV1 PB2_I80AD	GPESVL	VNTYQWIIRNWEMIKIQWS	EPTMLYNKMEFEPFQSLVPKAARGQYSGFVRTLF	600
sp P26115 PB2_I77AF	GPESVL	VNTYQWIIRNWEMIKIQWS	NPTMLYNKMEFEPFQSLVPKAARAQYSGFVRTLF	600
sp Q9Q0V1 PB2_I96A0	GPESVL	VNTYQWIIRNWETVKIQWS	DPTMLYNKMEFESFQSLVPKAARSQYSGFVRTLF	600
sp Q0A449 PB2_I66A1	GPESVL	VNTYQWIIRNWEAVKIQWS	DPTMLYNKMEFEPFQSLVPKAARGQYSGFVRTLF	600
sp Q6DNK1 PB2 I03A1	GPESVL	VNTYQWIIRNWETVKIQWS	DPTMLYNKMEFEPFQSLVPKAARGQYSGFVRTLF	600
sp P26110 PB2_I82A3	GPESVL	VNTYQWIIRNWETVKIQWS	DPTMLYNKMEFEPFQSLIPKAARGQYSGFVRTLF	600
sp Q809P5 PB2_I01A3	GPESVL	VNTYQWIIRNWETVKIQWS	DPTMLYNKMEFEPFQSLVPKAARGQYSGFVRTLF	600
sp P26112 PB2_I80A8	GPESVL	VNTYQWIIRNWETVKIQWS	DPTMLYNKMEFEPFQSLVPKAARGQYSGFVRTLF	600
sp Q0A438 PB2_I49A1	GPESVL	VNTYQWIIRNWETVKIQWS	DPTMLYNKMEFEPFQSLVPKAARGQYSGFVRTLF	600
sp Q20P12 PB2_I56A1	GPESVL	VNTYQWIIRNWETVKIQWS	DPTMLYNKMEFEPFQSLVPKAARGQYSGFVRTLF	600
sp Q0A427 PB2_I56A2	GPESVL	VNTYQWIIRNWETVKIQWS(DPTVLYNKMEFEPFQSLVPKAARGQYSGFVRTLF	600
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			V	

//End of PB2 subunits of influenza A viruses

sp P26107 PB2_I56A3	KANVLIGQGDVVLV	MKRKRD	SSILTDSQTATKRIRMATN	759
tr D9U0Y7 D9U0Y7_9INFA	KANVLIGQGDVVLV	MKRKRD	SSILTDSQTATKRIRMAIN	759
tr D2E5N3 D2E5N3_9INFA	KANVLIGQGDVVLV	MKRKRD	SSILTDSQTATKRIRMAIN	759
tr 165703 165703_91NFA	KANVLIGQGDVVLV	MKRKRD	SSILTDSQTATKRIRMAIN	759
sp Q1PUC9 PB2_173A5	KANVLIGQGDVVLV	MKRKRD	SSILTDSQTATKRIRMAIN	759
sp Q6XU90 PB2_167A0	KANVLIGQGDVVLV	MKRKRD	SSILTDSQTATKRIRMAIN	759
sp Q3YPY5 PB2_171A1	KANVLIGQGDVVLV	MKRKRD	SSILTDSQTATKRIRMAIN	759
sp P26105 PB2_186A2	KANVLIGQGDVVLV	MKRKRD	SSILTDSQTATKRIRMAIN	759
sp P0D0G6 PB2S1_I34A1	KANVLIGQGDVVLV	MKRKRD	SSILTDSQTATKRIRMAIN	759
sp P12445 PB2_I34A0	KANVLIGQGDVVLV	MKRKRD	SSILTDSQTATKRIRMAIN	759
sp Q0A2F5 PB2_183A4	KANVLIGQGDVVLV	MKRKRD	SSILTDSQTATKRIRMAIN	759
sp P26104 PB2_177AG	KANVLIGQGDVVLV	MKRKRD	SSILTDSQTATKRLRMAIN	759
sp Q20NV1 PB2_180AD	KANVLIGQGDVVLV	MKRKRD	SSILTDSQTATKRIRMAIN	759 <mark>NLS2</mark>
sp P26115 PB2_I77AF	KANVLIGQGDVVLV	MKRKRD	SSILTDSQTATKRIRMAIN	759
sp Q9Q0V1 PB2_196A0	KANVLI <mark>M</mark> QGDVVLV	MKRKRD	FSILTDSQTATKRIRMAIN	759
sp Q0A449 PB2_166A1	KANVLIGQGDVVLV	MKRKRD	SSILTDSQTATKRIRMAIN	759
sp Q6DNK1 PB2_103A1	KANVLIGQGDVVLV	MKRKRD	SSILTDSQTATKRIRMAIN	759
sp P26110 PB2_182A3	KANVLIGQGDVVLV	MKRKRD	SSILTDSQTATKRIRMAIN	759
sp Q809P5 PB2_I01A3	KANVLIGQGDVVLV	MKRKRD	SS	742
sp P26112 PB2_I80A8	KANVLIGQGDVVLV	MKRKRD	SSILTDSQTATKRIRMAIN	759
sp Q0A438 PB2_I49A1	KANVLIGQGDVVLV	MKRKRD	SSILTDSQTATKRIRMAIN	759
sp Q20P12 PB2_I56A1	KANVLIGQGDVVLV	MKRKRD	SSILTDSQTATKRIRMAIN	759
sp Q0A427 PB2_156A2	KANVLIGQGDVVLV	MKRKRD	SSILTDSQTATKRIRMAIN	759
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P26107/PB2_I56A3 Influenza A virus (Equine/Prague/1956 H7N7)
D9U0Y7_9INFA Influenza A virus (Peru/2007 H3N2)
D2E5N3_9INFA Influenza A virus (Thailand/2007 H3N2)
I6S703_9INFA Influenza A virus (Nepal/2006 H3N2)
Q1PUC9/PB2_I73A5 Influenza A virus (Port Chalmers/1973 H3N2)
Q6XU90/PB2_I67A0 Influenza A virus (Tokyo/1967 H2N2)
Q3YPY5/PB2_I71A1 Influenza A virus (Tokyo/1967 H2N2)
P26105/PB2_I86A2 Influenza A virus (Equine/Kentucky/1986 H3N8)
P0DOG6/PB2S1_I34A1 Influenza A virus (Puerto Rico/1934 H1N1) (pI = 9.73)
P12445/PB2_I34A0 Influenza A virus (Fowl plague virus/Rostock/1934 H7N1)
Q0A2F5/PB2_I80AD Influenza A virus (Gull/Minnesota/1980 H13N6) (pI = 9.49)
P26115/PB2_I70AF Influenza A virus (Gull/Minnesota/1980 H13N6) (pI = 9.49)
P26115/PB2_I66A1 Influenza A virus (Goose/Guangdong/1996 H5N1 genotype
Q0A449/PB2_I66A1 Influenza A virus (Cuck/Germany/1949 H10N7)
Q6DNK1/PB2_I80A3 Influenza A virus (Seal/Massachusetts/1982 H4N5)
Q809P5/PB2_I01A3 Influenza A virus (Seal/Massachusetts/1982 H4N5)
Q809P5/PB2_I01A3 Influenza A virus (strain A/Turkey/Minnesota/833/1980 H4N2)
Q0A427/PB2_I56A1 Influenza A virus (strain A/Duck/Czechoslovakia/1956 H4N6)

Figure 4 MSA of polymerase basic protein subunits PB2 of different strains of influenza A virus. *NLS, Nuclear localization signal; CBR, Cap-binding region* Figure 5 shows the MSA of the PB2 subunits from various strains of influenza B virus (only the required regions for the discussions are shown here). The Influenza B viral strain (1940) is highlighted and it showed a theoretical pI of 9.24. The PB2 of influenza B viral strains are almost completely conserved from N- to C-terminal than influenza A viral strains. The PB2 subunits of the influenza B viral strains also possess an HNH domain and belong to HNN subfamily. However, in a striking contrast to the influenza A viruses and other HNH endonucleases, in the influenza B viral strains, a –DQ- is identified as the likely first dyad of the HNN domain which is followed by two invariant Ns (highlighted in red). The likely NLSs and CBRs are highlighted in orange and magenta, respectively. DxD/E type of metal binding motifs are found (data not shown). A highly acidic peptide motif is also identified in the C-terminal region (data not shown)

CLUSTAL O (1.2.4) MSA of polymerase PB2 subunit of influenza B viruses

tr A0A4Y5WMY1 A0A4Y5WMY1_9INFB	MTLAKIELLKQLLRDNEAKTVLKQTT	VDC	YNIIRKFNTSRIEK	PSLRMKWAMCS <mark>N</mark> FPLA	60
tr Q4LD02 Q4LD02 9INFB	MTLAKIELLKQLLRDNEAKTVLKQTT	VDC	YNIIRKFNTSRIEK	PSLRMKWAMCS <mark>N</mark> FPLA	60
tr G2U3G6 G2U3G6 9INFB	MTLAKIELLKQLLRDNEAKTVLKQTT	VDC	YNIIRKFNTSRIEK	PSLRMKWAMCS <mark>N</mark> FPLA	60
tr A4D4J2 A4D4J2 9INFB	MTLAKIELLKQLLRDNEAKTVLKQTT	VDC	YNIIRKFNTSRIEK	PSLRMKWAMCS <mark>N</mark> FPLA	60
tr G2U1P7 G2U1P7 9INFB	MTLAKIELLKQLLRDNEAKTVLKQTT	VDC	YNIIRKFNTSRIER	PSLRMKWAMCS <mark>N</mark> FPLA	60
tr A4D5K5 A4D5K5 ⁻ 9INFB	MTLAKIELLKQLLRDNEAKTVLKQTT	VDC	YNIIRKFNTSRIEK	PSLRMKWAMCS <mark>N</mark> FPLA	60
tr U3RKA7 U3RKA7 9INFB	MTLAKIELLKQLLRDNEAKTVLKQTT	VDC	YNIIRKFNTSRIEN	PSLRMKWAMCS <mark>N</mark> FPLA	60
tr U3RTT2 U3RTT2 9INFB	MTLAKIELLKQLLRDNEAKTVLKQTT	VDC	YNIIRKFNTSRIEN	PSLRMKWAMCS <mark>N</mark> FPLA	60
tr U3RWZ8 U3RWZ8 ⁻ 9INFB	MTLAKIELLKQLLRDNEAKTVLKQTT	VDC	YNIIRKFNTSRIER	PSLRMKWAMCS <mark>N</mark> FPLA	60
tr S4SZ00 S4SZ00 9INFB	MTLAKIELLKQLLRDNEAKTVLKQTT	VDC	YNIIRKFNTSRIEK	PSLRMKWAMCS <mark>N</mark> FPLA	60
tr U3RUJ3 U3RUJ3 9INFB	MTLAKIELLKQLLRDNEAKTVLKQTT	VDC	YNIIRKFNTSRIEK	PSLRMKWAMCS <mark>N</mark> FPLA	60
sp Q9QLL6 PB2 INBLE	MTLAKIELLKQLLRDNEAKTVLRQTT	VDC	YNIIRKFNTSRIEKN	NPSLRMKWAMCSNFPLA	60
sp P13875 PB2 INBAC	MTLAKIELLKQLLRDNEAKTVLKQTT	VDC	YNIIRKFNTSRIER	PSLRMKWAMCS <mark>N</mark> FPLA	60
tr U3S2T7 U3S2T7 9INFB	MTLAKIELLKQLLRDNEAKTVLKQTT	VDC	YNIIRKFNTSRIER	PSLRMKWAMCS <mark>N</mark> FPLA	60
tr A0A140EVM2 A0A140EVM2 9INFB	MTLAKIELLKQLLRDNEAKTVLKQTT	VDC	YNIIRKFNTSRIEK	PSLRMKWAMCS <mark>N</mark> FPLA	60
tr A9QXW8 A9QXW8 9INFB	MTLAKIELLKQLLRDNEAKTVLKQTT	VDC	YNIIRKFNTSRIEK	PSLRMKWAMCS <mark>N</mark> FPLA	60
tr 12DDZ0 12DDZ0 9INFB	MTLAKIELLKQLLRDNEAKTVLKQTT	VDC	YNIIRKFNTSRIEK	PSLRMKWAMCS <mark>N</mark> FPLA	60
tr A0A126UI98 A0A126UI98 9INFB	MTLAKIELLKOLLRDNEAKTVLKOTT	VDC	YNIIRKFNTSRIEK	PSLRMKWAMCSNFPLA	60
tr A0A140EUD2 A0A140EUD2 9INFB	MTLAKIELLKOLLRDNEAKTVLKOTT	VDC	YNIIRKFNTSRIEK	PSLRMKWAMCSNFPLA	60
tr A0A140EKH4 A0A140EKH4 9INFB	MTLAKIELLKOLLRDNEAKTVLKOTT	vpc	YNIIRKENTSRIEK	PSIRMKWAMCSNEPLA	60
trlC4L0201C4L020 9TNFB	MTLAKIELIKOLIRDNEAKTVIKOTT	vbc	YNTIRKENTSRIEK	PSIRMKWAMCSNEPLA	60
trla0al40EVH8la0al40EVH8 9TNFB	MTLAKIELIKOLLRDNEAKTVLKOTT	vbc	YNTIRKENTSRIEK	PSTRMKWAMCSNEPTA	60
tr A0A126UDK6 A0A126UDK6 9TNFB	MTLAKIFI.I.KOLIBDNFAKTVI.KOTT	vnc	YNTIRKENTSRIEK	PSTRMKWAMCSNEPLA	60
sn10364311PB2_INBP9	MTLAKIFI.I.KOI.I.BDNFAKTVI.KOTT	vb	VNTIEK FNTSEIF KN	PSI.RMKWAMCSNEPI.A	60
+ x 1 3 200 09 1 3 200 09 01 NFB	MTLARTELLKOLLEDNEARTVERQT		VNTTDEFNTSDIFE	DST.DMKWAMCSMEDTA	60
CT [H3DQF0]H3DQF0_SIMPD	***************************************	***	********	*****	00
	•	-			
tr A0A4Y5WMY1 A0A4Y5WMY1_9INFB	FLRKMRLDNATWGRITFGPVE <mark>RVRKR</mark>	VLI.	LNPLTKEMPPDEASNV	/IMEILFPKEAGIPRES	180
tr Q4LD02 Q4LD02_9INFB	FLRKMRLDNATWGRITFGPVE <mark>RVRKR</mark>	VL1	LNPLTKEMPPDEASNV	/IMEILFPKEAGIPRES	180
tr G2U3G6 G2U3G6_9INFB	FLRKMRLDNATWGRITFGPVE <mark>RVRKR</mark>	VLI.	LNPLTKEMPPDEASNV	/IMEILFPKEAGIPRES	180
tr A4D4J2 A4D4J2_9INFB	FLRKMRLDNATWGRITFGPVE <mark>RVRKR</mark>	VLI.	LNPLTKEMPPDEASNV	/IMEILFPKEAGIPRES	180
tr G2U1P7 G2U1P7_9INFB	FLRKMRLDNATWGRITFGPVE <mark>RVRKR</mark>	VLI.	LNPLTKEMPPDEASNV	/IMEILFPKEAGIPRES	180
tr A4D5K5 A4D5K5_9INFB	FLRKMRLDNATWGRITFGPVE <mark>RVRKR</mark>	VL1	LNPLTKEMPPDEASNV	/IMEILFPKEAGIPRES	180
tr U3RKA7 U3RKA7 9INFB	FLRKMRLDNATWGRITFGPVE <mark>RVRKR</mark>	VLI	LNPLTKEMPPDEASNV	/IMEILFPKEAGIPRES	180
tr U3RTT2 U3RTT2_9INFB	FLRKMRLDNATWGRITFGPVE <mark>RVRKR</mark>	VLI.	LNPLTKEMPPDEASNV	/IMEILFPKEAGIPRES	180
tr U3RWZ8 U3RWZ8_9INFB	FLRKMRLDNATWGRITFGPVE <mark>RVRKR</mark>	VLI.	LNPLTKEMPPDEASNV	/IMEILFPKEAGIPRES	180
tr S4SZ00 S4SZ00 9INFB	FLRKMRLDNATWGRITFGPVE <mark>RVRKR</mark>	VL1	LNPLTKEMPPDEASNV	/IMEILFPKEAGIPRES	180
tr U3RUJ3 U3RUJ3 9INFB	FLRKMRLDNATWGRITFGPVE <mark>RVRKR</mark>	VLI	LNPLTKEMPPDEASNV	/IMEILFPKEAGIPRES	180
sp Q9QLL6 PB2_INBLE	FLRKMRLDNATWGRITFGPVERVRKR	VLI	LNPLTKEMPPDEASNV	/IMEILFPKEAGIPRES	180 NLS1
sp P13875 PB2_INBAC	FLRKMRLDNATWGRITFGPVE <mark>RVRKR</mark>	VLI.	LNPLTKEMPPDEASNV	/IMEILFPKEAGIPRES	180
tr U3S2T7 U3S2T7_9INFB	FLRKMRLDNATWGRITFGPVE <mark>RVRKR</mark>	VL1	JNPLTKEMPPDEASNV	/IMEILFPKEAGIPRES	180
tr A0A140EVM2 A0A140EVM2_9INFB	FLRKMRLDNATWGRITFGPVE <mark>RVRKR</mark>	VLI.	LNPLTKEMPPDEASNV	/IMEILFPKEAGIPRES	180
tr A9QXW8 A9QXW8_9INFB	FLRKMRLDNATWGRITFGPVE <mark>RVRKR</mark>	VLI	INPLTKEMPPDEASNV	/IMEILFPKEAGIPRES	180
tr I2DDZ0 I2DDZ0 9INFB	FLRKMRLDNATWGRITFGPVE <mark>RVRKR</mark>	VLI	LNPLTKEMPPDEASNV	/IMEILFPKEAGIPRES	180
tr A0A126UI98 A0A126UI98 9INFB	FLRKMRLDNATWGRITFGPVERVRKR	VLI	LNPLTKEMPPDEASNV	/IMEILFPKEAGIPRES	180
tr A0A140EUD2 A0A140EUD2 9INFB	FLRKMRLDNATWGRITFGPVERVRKR	VLL		/IMEILFPKEAGIPRES	180
tr A0A140EKH4 A0A140EKH4 9INFB	FLRKMRLDNATWGRITFGPVERVRKR	VLI	LNPLTKEMPPDEASNV	/IMEILFPKEAGIPRES	180
tr C4LQ20 C4LQ20 9INFB			NDT TERMODORASIN	TMETTEDERACTORES	1.9.0
tr A0A140EVH8 A0A140EVH8 9INFB	FLRKMRLDNATWGRITFGPVE <mark>RVRKR</mark>	VLL	DMEDIKEMEEDEASM (IMEILFFREAGIFRES	100
	FLRKMRLDNATWGRITFGPVERVRKR FLRKMRLDNATWGRITFGPVERVRKR	V LI	LNPLTKEMPPDEASN	/IMEILFPKEAGIPRES	180
tr A0A126UDK6 A0A126UDK6 9INFB	FLRKMRLDNATWGRITFGPVERVRKR FLRKMRLDNATWGRITFGPVERVRKR FLRKMRLDNATWGRITFGPVERVRKR	VLI VLI VLT	LNPLTKEMPPDEASN LNPLTKEMPPDEASN LNPLTKEMPPDEASN	VIMEILFPKEAGIPRES	180 180 180
tr A0A126UDK6 A0A126UDK6_9INFB sp 036431 PB2_INBP9	FLRKMRLDNATWGRITFGPVERVRKR FLRKMRLDNATWGRITFGPVERVRKR FLRKMRLDNATWGRITFGPVERVRKR FLRKMRLDNATWGRITFGPVERVRKR	VLI VLI VLI	LNPLTKEMPPDEASN LNPLTKEMPPDEASN LNPLTKEMPPDEASN	VIMEILFPREAGIPRES VIMEILFPREAGIPRES VIMEILFPREAGIPRES	180 180 180 180
tr A0A126UDK6 A0A126UDK6 9INFB sp 036431 FB2_INBF9 tr A3D0P8 A3D0P8_9INFB	FLRKMRLDNATWGRITFGPVERVRKR FLRKMRLDNATWGRITFGPVERVRKR FLRKMRLDNATWGRITFGPVERVRKR FLRKMRLDNATWGRITFGPVERVRKR FLRKMRLDNATWGRITFGPVFRVRKR	VLI VLI VLI	LNPLTKEMPPDEASN LNPLTKEMPPDEASN LNPLTKEMPPDEASN LNPLTKEMPPDEASN	VIMEILFPKEAGIPRES VIMEILFPKEAGIPRES VIMEILFPKEAGIPRES VIMEILFPKEAGIPRES	180 180 180 180

		<u>CBR</u>	
tr A0A4Y5WMY1 A0A4Y5WMY1 9INFB	NFLNRAGQLLSPMYQLQRYFLNRSND	LFDQWGYEESPKASELHGINE <mark>S</mark> MNASDYTLKGVV	480
tr1041D021041D02 9TNFB	NFLNRAGOLLSPMYOLORYFLNRSNI	LEDOWGYEESPKASELHGINESMNASDYTLKGVV	480
+rlc2U3c6lc2U3c6_9INFB	NELNBACOLISPMYOLOBYELNBSNE	LEDOWGYEESDKASELHGINESMNASDYTLKGVV	480
+ x A (D (T2 A (D (T2) G TNEP	NET NDACOT I SDMYOT ODVET NDSNE		100
	NT LNKAGQLLSFMIQLQKIFLNKSNL		400
LIG20IP/G20IP/_9INFB	NFLNRAGQLLSPMIQLQRIFLNRSNL	LFDQWGIEESPKASELHGINESMNASDITLKGVV	480
tr A4D5K5 A4D5K5_9INFB	NFLNRAGQLLSPMYQLQRYFLNRSNI	LFDQWGYEESPKASELHGINESMNASDYTLKGVV	480
tr U3RKA7 U3RKA7_9INFB	NFLNRAGQLLSPMYQLQRYFLNRSNI	LFDQWGYEESPKASELHGINESMNASDYTLKGVV	480
tr U3RTT2 U3RTT2_9INFB	NFLNRAGQLLSPMYQLQRYFLNRSNI	LFDQWGYEESPKASELHGINESMNASDYTLKGVV	480
tr U3RWZ8 U3RWZ8 9INFB	NFLNRAGQLLSPMYQLQRYFLNRSNI	LFDQWGYEESPKASELHGINESMNASDYTLKGVV	480
tr S4SZ00 S4SZ00 9INFB	NFLNRAGQLLSPMYQLQRYFLNRSNI	LFDQWGYEESPKASELHGINESMNASDYTLKGVV	480
tr U3RUJ3 U3RUJ3 9INFB	NFLNRAGOLLSPMYOLORYFLNRSND	LFDOWGYEESPKASELHGINE <mark>S</mark> MNASDYTLKGVV	480
SDI090LL61PB2_INBLE	NFLNRAGOLLSPMYOLORYFLNRSNI	LEDOWGYEESPKASELHGINELMNASDYTLKGVV	480CBR1
splP138751PB2_INBAC	NELNEAGOLLSPMYOLORYFLNESNE	LEDOWGY EEPPKASELHGINELMNASDYTLKGVV	480
+~ U1202m7 U1202m7 OTNED	NELNDACOLI COMVOLODVEL COCNE		100
	NELNRAGULLSPHIQLQRIFLSRSNL		400
LI AUAI4UEVMZ AUAI4UEVMZ_9INFB	NFLNRAGQLLSPMIQLQRIFLSRSNL	LFDQWGIEESPKASELHGINELMINASDITLKGVV	480
tr A9QXW8 A9QXW8_9INFB	NFLNRAGQLLSPMYQLQRYFLSRSNL	LFDQWGYEESPKASELHGINELMNASDYTLKGVV	480
tr I2DDZ0 I2DDZ0_9INFB	NFLNRAGQLLSPMYQLQRYFLSRSNI	LFDQWGYEESPKASELHGINELMNASDYTLKGVV	480
tr A0A126UI98 A0A126UI98_9INFB	NFLNRAGQLLSPMYQLQRYFLSRSND	LFDQWGYEESPKASELHGINELMNASDYTLKGVV	480
tr A0A140EUD2 A0A140EUD2 9INFB	NFLNRAGQLLSPMYQLQRYFLSRSNI	LFDQWGYEESPKASELHGINELMNASDYTLKGVV	480
tr A0A140EKH4 A0A140EKH4 9INFB	NFLNRAGQLLSPMYQLQRYFLSRSND	LFDQWGYEESPKASELHGINELMNASDYTLKGVV	480
tr C4L020 C4L020 9TNFB	NFLNRAGOLLSPMYOLORYFLSRSND	LEDOWGYEESPKASELHGINELMNASDYTLKGVV	480
tr A0A140EVH8 A0A140EVH8 9TNFB	NFLNBAGOLLSPMYOLOBYFLSBSND	LEDOWGYEESPKASELHGINELMNASDYTLKGVV	480
$\pm r a 0 a 1 2 6 UDK 6 a 0 a 1 2 6 UDK 6 9 INFB$	NELNBACOLLSPMYOLOBVELSPSNE	LEDOWGYEESPKASELHGINELMNASDYTLKGVV	480
en LO2CA21 LDD2 INDD0			400
SPI030431 PB2_INBP9	NFLNRAGQLLSPMIQLQRIFLNRSNL		400
LL Y2DOL8 Y3DOL8 - AINER	NFLNRAGQLLSPMYQLQRYFLNRSNL	LFDQWGYEESPKASELHGINELMNASDYTLKGVV	480
	**************************************	******* ** ***************************	
	CBR 🗲		
tr A0A4Y5WMY1 A0A4Y5WMY1 9INFB	MGTTKELVONTYOWVLKN LVTLKAC	FLLGKEDMFOWDAFEAFESIIPOKMAGOYSGFARA	599
tr 04LD02 04LD02 9INFB	MGTTKELVONTYOWVLKN LVTLKAC	FLLGKEDMFOWDAFEAFESIIPOKMAGOYSGFARA	599
tr G2U3G6 G2U3G6 9INFB	MGTTKELVONTYOWVLKN LVTLKAC	FLLGKEDMEONDAFFAFFSTIPOKMAGOYSGFARA	599
trlA4D4.T2 A4D4.T2 GINEB	MGTTKELVONTYOWVLKN LVTLKAC	FLUGKEDMEOWDAFFAFFSTIPOKMAGOVSGFARA	599
tricoulpricoulpr aines	MCTTREDVORTIONVIRM IVTINA	FILCREDMEONDAFEAFESTIDORMACOVSCEADA	500
CI G20IF / G20IF / _ SINEB	MOTINELVONIIOWVERN EVIENA	FLIGKEDME QWDAFEAFESIIFQKHAGQISGFAKA	599
CI AADSKS AADSKS_SINPB	MGTIKELVONIIQWVERN EVIERAC	FLLGKEDMFQWDAFEAFESIIFQKMAGQISGFARA	299
tr U3RKA/ U3RKA/ 91NFB	MGTTKELVQNTYQWVLKN LVTLKAQ	FLLGKEDMFQWDAFEAFESIIFQKMAGQYSGFARA	599
tr U3RTT2 U3RTT2_91NFB	MGTTKELVONTYOWVLKN LVTLKAC	FLLGKEDMFQWDAFEAFESIIPQKMAGQYSGFARA	599
tr U3RWZ8 U3RWZ8_9INFB	MGTTKELVQNTYQWVLKN LVTLKAQ	FLLGKEDMFQWDAFEAFESIIPQKMAGQYSGFARA	599
tr S4SZ00 S4SZ00_9INFB	MGTTKELVQNTYQWVLKN LVTLKAQ	FLLGKEDMFQWDAFEAFESIIPQKMAGQYSGFARA	599
tr U3RUJ3 U3RUJ3_9INFB	MGTTKELVQNTYQWVLKN LVTLKAQ	FLLGKEDMFQWDAFEAFESIIPQKMAGQYSGFARA	599
sp Q9QLL6 PB2_INBLE	MGTTKELVQNTYQWVLKN LVTLKAC	FLLGKEDMFQWDAFEAFESIIPQKMAGQYSGFARA	599CBR2
sp P13875 PB2 INBAC	MGTTKELVQNTYQWVLKN LVTLKAC	FLLGKEDMFQWDAFEAFESIIPQKMAGQYSGFARA	599
tr U3S2T7 U3S2T7 9INFB	MGTTKELVONTYOWVMKN LVTLKAC	FLLGKEDMFQWDAFEAFESIIPQKMAGQYSGFARA	600
tr A0A140EVM2 A0A140EVM2 9INFB	MGTTKELVONTYOWVMKN LVTLKAC	FLLGKEDMFQWDAFEAFESIIPQKMAGQYSGFARA	599
tr A90XW8 A90XW8 9INFB	MGTTKELVONTYOWVMKN LVTLKAC	FLLGKEDMFOWDAFEAFESIIPOKMAGOYSGFARA	599
trII2DDZ01I2DDZ0_9INFB	MGTTKELVONTYOWVMKN LVTLKAC	FLUGKEDMFONDAFEAFESTIPOKMAGOYSGFARA	599
+r1202126019812021260198 91NFB	MGTTKELVONTYOWVMEN LVTLKAC	FLUGKEDMEOWDAFFAFFSTIPOKMAGOVSGFARA	599
+ x A O A 14 O E UD 2 A O A 14 O E UD 2 O A 14 O E UD 2	MGTTKEI VONTVONUMEN I VII BAA	FILCREDMEONDAFEAFESTIDORMACOVSCEADA	599
+ x I A O A 14 O E KH4 I A O A 14 O E KH4 O T MED	MCTTRELY ONTY ONWARD I VTLAA	FILGREDMEONDAFEAFESTIFORMAGQIJGFARA	555
TIMONITUENTIAUNITUENTI_JINTD	MCTTRES VOIT LOWVINN LVT KAC	ELIGREDME QWDATEATEST I FORMAGU 1967 AKA	233
CELCAPOSITOEMOTSOSITOEMO CIMER	MOTINEL VONTIONWIKN LVTLKAC	TLIGKEDHE WUAFLAFESIIPUKMAGUISGFARA	233
TT AUAI4UEVH8 AUAI4UEVH8 91NFB	MGTTKELVQNTYQWVMKN LVTLKAC	FLIGKEDMFQWDAFEAFESIIPQKMAGQYSGFARA	599
tr AUA126UDK6 AOA126UDK6_9INFB	MGTTKELVQNTYQWVLKN LATLKAQ	FLLGKEDMFQWDAFEAFESIIPQKMAGQYSGFARA	599
sp 036431 PB2_INBP9	MGTTKELVQNTYQWVLKN LVTLKAQ	FLLGKEDMFQWDAFEAFESIIPQKMAGQYSGFARA	599
tr A3DQP8 A3DQP8_9INFB	MGTTKELVQNTYQWVLKN LVTLKAC	FLLGKED <mark>MFQW</mark> DAFEAFESIIPQKMAGQYSGFARA	599
	***************************************	************	

//End of PB2 subunits of influenza B viruses

tr A0A4Y5WMY1 A0A4Y5WMY1_9INFB	LKPGEKANILLYQGKPVKV	VKRKR	YSALSNDISQGIKRQRMTVESMGWALS	770
tr Q4LD02 Q4LD02_9INFB	LKPGEKANILLYQGKPVKV	VKRKR	YSALSNDISQGIKRQRMTVESMGWALS	770
tr G2U3G6 G2U3G6_9INFB	LKPGEKANILLYQGKPVKV	VKRKR	YSALSNDISQGIKRQRMTVESMGWALS	770
tr A4D4J2 A4D4J2_9INFB	LKPGEKANILLYQGKPVKV	VKRKR	YSALSNDISQGIKRQRMTVESMGWALS	770
tr G2U1P7 G2U1P7_9INFB	LKPGEKANILLYQGKPVKV	VKRKR	YSALSNDISQGIKRQRMTVESMGWALS	770
tr A4D5K5 A4D5K5_9INFB	LKPGEKANILLYQGKPVKV	VKRKR	YSALSNDISQGIKRQRMTVESMGWALS	770
tr U3RKA7 U3RKA7_9INFB	LKPGEKANILLYQGKPVKV	VKRKR	YSALSNDISQGIKRQRMTVESMGWALS	770
tr U3RTT2 U3RTT2_9INFB	LKPGEKANILLYQGKPVKV	VKRKR	YSALSNDISQGIKRQRMTVESMGWALS	770
tr U3RWZ8 U3RWZ8_9INFB	LKPGEKANILLYQGKPVKV	VKRKR	YSALSNDISQGIKRQRMTVESMGWALS	770
tr S4SZ00 S4SZ00_9INFB	LKPGEKANILLYQGKPVKV	VKRKR	YSALSNDISQGIKRQRMTVESMGWALS	770
tr U3RUJ3 U3RUJ3_9INFB	LKPGEKANILLYQGKPVKV	VKRKR	YSALSNDISQGIKRQRMTVESMGWALS	770
sp Q9QLL6 PB2_INBLE	LKPGEKANILLYQGKPVKV	VKRKR	YSALSNDISQGIKRQRMTVESMGWALS	770 nls2
sp P13875 PB2_INBAC	LKPGEKANILLYQGKPVKV	VKRKR	YSALSNDISQGIKRQRMTVESMGWALS	770
tr U3S2T7 U3S2T7_9INFB	LKPGEKANILLYQGKPVKV	VKRKR	YSALSNDISQGIKRQRMTVESMGWALS	771
tr A0A140EVM2 A0A140EVM2_9INFB	LKPGEKANILLYQGKPVKV	VKRKR	YSALSNDISQGIKRQRMTVESMGWALS	770
tr A9QXW8 A9QXW8_9INFB	LKPGEKANILLYQGKPVKV	VKRKR	YSALSNDISQGIKRQRMTVESMGWALS	770
tr I2DDZ0 I2DDZ0_9INFB	LKPGEKANILLYQGKPVKV	VKRKR	YSALSNDISQGIKRQRMTVESMGWALS	770
tr A0A126UI98 A0A126UI98_9INFB	LKPGEKANILLYQGKPVKV	VKRKR	YSALSNDISQGIKRQRMTVESMGWALS	770
tr A0A140EUD2 A0A140EUD2_9INFB	LKPGEKANILLYQGKPVKV	VKRKR	YSALSNDISQGIKRQRMTVESMGWALS	770
tr A0A140EKH4 A0A140EKH4_9INFB	LKPGEKANILLYQGKPVKV	VKRKR	YSALSNDISQGIKRQRMTVESMGWALS	770
tr C4LQ20 C4LQ20_9INFB	LKPGEKANILLYQGKPVKV	VKRKR	YSALSNDISQGIKRQRMTVESMGWALS	770
tr A0A140EVH8 A0A140EVH8_9INFB	LKPGEKANILLYQGKPVKV	VKRKR	YSALSNDISQGIKRQRMTVESMGWALS	770
tr A0A126UDK6 A0A126UDK6_9INFB	LKPGEKANILLYQGKPVKV	VKRKR	YSALSNDISQGIKRQRMTVESMGWALS	770
sp 036431 PB2_INBP9	LKPGEKANILLYQGKPVKV	VKRKR	YSALSNDISQGIKRQRMTVESMGWALS	770
tr A3DQP8 A3DQP8_9INFB	LKPGEKANILLYQGKPVKV	VKRKR	YSALSNDISQGIKRQRMTVESMGWALS	770
-				

A0A4Y5WMY1_9INFB, Influenza B virus Q4LD02_9INFB, Influenza B virus (Tehran/2002) G2U3G6_9INFB, Influenza B virus (California/2003) A4D4J2_9INFB, Influenza B virus (Taiwan/2007) A4D5K5_9INFB, Influenza B virus (Taiwan/2007) A4D5K5_9INFB, Influenza B virus (Paraguay/2003) U3RKA7_9INFB, Influenza B virus (Waikato/2007) U3RTT2_9INFB, Influenza B virus (Waikato/2007) U3RWZ8_9INFB, Influenza B virus (Sydney/2006) S4SZ00_9INFB, Influenza B virus (Sydney/2006) Q9QLL6/PB2_INBLE, Influenza B virus (Lee/1940) (pI = 9.24) P13875/PB2_INBAC, Influenza B virus (Ann Arbor/1966 [cold-adapted]) (pI = 9.30) U3S2T7_9INFB, Influenza B virus (Sydney/2005) A0A140EVM2_9INFB, Influenza B virus (Guangzhou/2007) I2DDZ0_9INFB, Influenza B virus (Malaysia/2007) A0A126UI98_9INFB, Influenza B virus (Malaysia/2007) A0A140EVM2_9INFB, Influenza B virus (Tasmania/2014) A0A140EUD2_9INFB, Influenza B virus (Tasmania/2013) A0A140EVH4_9INFB, Influenza B virus (Tasmania/2013) A0A140EVH8_9INFB, Influenza B virus (Malaysia/2007) A0A140EUD2_9INFB, Influenza B virus (Tasmania/2014) A0A140EUD2_9INFB, Influenza B virus (Malaysia/2007) A0A140EVH8_9INFB, Influenza B virus (Managua/2008) A0A140EVH8_9INFB, Influenza B virus (Singapore/2014) O36431|PB2_INBP9, Influenza B virus (Johannesburg/2001)

Figure 5 MSA of the polymerases basic protein subunits PB2 of from influenza B viruses

Figure 6 shows the MSA of the PB2 subunits from different strains of influenza C virus (only the required regions for the discussions are shown here). The influenza C virus strain (1947) is highlighted and it showed a theoretical pI of 9.25. But for a small region in the N- and C-terminals, the entire sequence is almost completely conserved in all the strains. The PB2 subunits of the influenza C virus strains are more completely conserved than influenza A viral strains. A –DH- based HNN motif, as in influenza A virus, is indented in a smaller peptide region at the N-terminal, which is followed by two invariant Ns. The likely NLSs, CBRs and metal-binding motifs are highlighted in orange, magenta and green, respectively. The second consecutive basic amino acids which represents the NLS was identified in the N-terminal itself, suggesting a significant divergence in their evolutions.

CLUSTAL O (1.2.4) MSA of the basic protein subunits PB2 of from influenza C viruses.

SDIP217701PB2 INCRE	TTANKEMLEFAOTEKEHNNVALWEDTEDVSKEDHULASASCINVWNECCECVNNSEVIKE	120
trlS4T8F31S4T8F3_90BT0	I I ANKRMI E E AOT PKEHNNVAL WEDTE DVSKROHVLASASCI NYWNFCGPCVNNSEVI KE	120
splP138771PB2_INCJJ	I I ANKRMLEEAOI PKEHNNVALWEDTE DVSKRDHVLASTSCINVWNFCGPCANNSEVI KE	120
trla0a1B0RMT8LA0A1B0RMT8 90RT0	I TANKEMLEEAO I PKEHNNVALWEDTE DVSKEDHVLASASCIN VWNECGPCVNNSEVIKE	120
tr A0A830ZL67 A0A830ZL67_9ORTO	IIANKRMLEEAOIPKEHNNVALWEDTE DVSKRDHVLASASCIN KWNFCGPCVSNSEVIKE	120
tr A0A193PPU8 A0A193PPU8 INCEN	IIANKRMLEEAQIPKEHNNVALWEDTEDVSKRDHVLASASCINYWNFCGPCVNNSEVIKE	120
tr A0A193PPD6 A0A193PPD6 INCP2	IIANKRMLEEAOIPKEHNNVALWEDTEDVSKRDHVLASASCIN (WNFCGPCVNNSEVIKE	120
tr W8CI60 W8CI60 9ORTO	IIANKRMLEEAQIPKEHNNVALWEDTEDVSKRDHVLASASCINYWNFCGPCVNNSEVIKE	103
tr W8CHY7 W8CHY7 9ORTO	IIANKRMLEEAQIPKEHNNVALWE <mark>DTED</mark> VSKR <mark>DH</mark> VLASASCI <mark>NY</mark> WNFCGPCVN <mark>N</mark> SEVIKE	98
sp Q9IMP3 PB2 INCJH	IIANKRMLEEAQIPKEHNNVALWEDTEPVSKRDHVLASASCIN (WNFCGPCVNNSEVIKE	120
tr A0A193PPS9 A0A193PPS9_9ORTO	IIANKRMLEEAQIPKEHNNVALWE <mark>DTED</mark> VSKR <mark>DH</mark> VLASASCI <mark>NY</mark> WNFCGPCVN <mark>N</mark> SEVIKE	120
tr A0A193PPJ9 A0A193PPJ9_9ORTO	IIANKRMLEEAQIPKEHNNVALWE <mark>DTE</mark> DVSKR <mark>DH</mark> VLASASCI <mark>N</mark> YWNFCGPCVN <mark>N</mark> SEVIKE	120
sp Q6I7C4 PB2_INCAA	IIANKRMLEEAQIPKEHNNVALWE <mark>DTE</mark> PVSKR <mark>DH</mark> VLASASCI <mark>N</mark> KWNFCGPCVN <mark>N</mark> SEVIKE	120
tr A0A193PPX7 A0A193PPX7_9ORTO	IIANKRMLEEAQIPKEHNNVALWE <mark>DTED</mark> VSKR <mark>DH</mark> VLASASCI <mark>N</mark> YWNFCGPCVN <mark>N</mark> SEVIKE	120
tr A0A193PQ18 A0A193PQ18_9ORTO	IIANKRMLEEAQIPKEHNNVALWE <mark>DTED</mark> VSKR <mark>DH</mark> VLASASCI <mark>N</mark> YWNFCGPCVN <mark>N</mark> SEVIKE	120
tr A0A193PPR8 A0A193PPR8_9ORTO	IIANKRMLEEAQIPKEHNNVALWE <mark>DTE</mark> DVSKR <mark>DH</mark> VLASASCI <mark>NY</mark> WNFCGPCVN <mark>N</mark> SEVIKE	120
tr A0A193PPB8 A0A193PPB8_INCTA	IIANKRMLEEAQIPKEHNNVALWEDTEDVSKRDHVLASASCINYWNFCGPCVNNSEVIKE	120

sp P21770 PB2 INCBE	VYKSRFG <mark>RLERRKE</mark> IMWKELRFTLVI <mark>RORRRV</mark> DTOPVEQRLRTGEIKDLOMWTLFEDEAP	180
tr S4T8F3 S4T8F3 90RT0	VYKSRFGRLERRKEIMWKELRFTLVIRORRRVDTOPVEORLRTGEIKDLOMWTLFEDEAP	180
sp P13877 PB2 INCJJ	VYKSRFGRLERRKEIMWKELRFTLVIRORRRVDTOPVEORLRTGEIKDLOMWTLFEDEAP	180
tr A0A1B0RMT8 A0A1B0RMT8 90RT0	VYKSRFGRLERRKEIMWKELRFTLVIRORRRVDTOPVEORLRTGEIKDLOMWTLFEDEAP	180
tr A0A830ZL67 A0A830ZL67 90RT0	VYKSREGRLERRKEIMWKELRETLVIRORRRVDTOPVEORLETGEIKDLOMWTLEEDEAP	180
trla0a193PPU8la0a193PPU8 INCEN	VYKSRFGRLERRKEIMWKELRFTLVDRORRRVDTOPVEORLRTGEIKDLOMWTLFEDEAP	180
tria0a193PPD6 a0a193PPD6 TNCP2	VYKSREGRLERRKEIMWKELRETLVIRORRRVDTOPVEORLETGEIKDLOMWTLEEDEAP	180
triw8CI601W8CI60 90BT0	VYKSREGRLERRKEIMWKELRETLVDRORRRVDTOPVEORLETGEIKDLOMWTLEEDEAP	163
trlW8CHY7LW8CHY7 90BT0	VYKSREGRLERRKEIMWKELRETLVIRORRRVDTOPVEORLETGEIKDLOMWTLEEDEAP	158
spl09IMP31PB2_INC.IH	VYKSREGRLERRKEIMWKELRETLVIRORRRVDTOPVEORLETCEIKDLOMWTLEEDEAP	180
+rlana103pps0lana103pps0_00pm0	VIX SECOND FOR METALEMENT IN THE ADDITION OF A DECENTION OF A DECE	180
		190
LI AUAI 95PPO 9 AUAI 95PPO 9 90RIO		100
SP Q61/C4 PB2_INCAA		180
tr AUA193PPX / AUA193PPX / _90RTO	VYKSRFGRLERRKEIMWKELRFTLVURQRRRVDTQPVEQRLRTGEIKDLQMWTLFEDEAP	180
TTIAUA193PQ18 AUA193PQ18_90RTO	VIKSRFGRLERKKELMWKELRFTLVIRQRRRVPTQPVEQRLRTGEIKDLQMWTLFEDEAP	180
tr AUA193PPR8 AUA193PPR8 90RT0	VYKSRFG <mark>RLERRKE</mark> IMWKELRFTLVI <mark>RQRRRV</mark> DTQPVEQRLRTGEIKDLQMWTLFEDEAP	180
tr AUA193PPB8 AOA193PPB8_INCTA	VYKSRFGRLERRKEIMWKELRFTLVDRQRRRVDTQPVEQRLRTGEIKDLQMWTLFEDEAP	180 NL
	****** <mark>******</mark> ************************	

sp P21770 PB2_INCBE	VRA <mark>VQFEYW</mark> SEQEEFYGEYKSATALFSRKERSLEWITIGGGINEDRKRLLAMCMIFCRDG	420
tr S4T8F3 S4T8F3_90RT0	VRA <mark>VQFEYW</mark> SEQEEFYGEYKSATALFSRKERSLEWITIGGGINEDRQRLLAMCMIFCRDG	420
sp P13877 PB2_INCJJ	VRA <mark>VQFEYM</mark> SEQEEFYGEYKSATALFSRKERSLEWITIGGGINEDRKRLLAMCMIFCRDG	420
tr A0A1B0RMT8 A0A1B0RMT8_90RT0	VRAVQFEYMSEQEEFYGEYKSATALFNRKERSLEWITIGGGINEDRKRLLAMCMIFCRDG	420
tr A0A830ZL67 A0A830ZL67_9ORTO	VRAVQFEYWSEQEEFYGEYKSATALFNRKERSLEWITIGGGINEDRKRLLAMCMIFCRDG	420
tr AUA193PPU8 AUA193PPU8_INCEN	VRAVQFEYWSEQEEFYGEYKSATALFNRKERSLEWITIGGGINEDRKRLLAMCMIFCRDG	420
tr AUAI93PPD6 AUAI93PPD6_INCP2	VRAVQFEINSEQEEFIGEIKSATALFNRKERSLEWITIGGGINEDRKRLLAMCMIFCRDG	420
tr W8C160 W8C160 _ 90RTO	VRAVQFEINSEQEEFIGEIKSATALFNRKERSLEWITIGGGINEDRKRLLAMCMIFCRDG	403
	VRAVUTEIMSEQEEFIGEIRSAIALFSRERSLEWIIIGGGINEDRRELAMOMIFCRUG	420
trla0a193PF39 A0A193FF39 90A10	VRAV QFEINSEQEEFIGEIRSAIALFSREASLEWIIIGGGINEDRRIIAMCMIFCRDG	420
spl0617C4/PB2_INCAA	VRAUTETWISEDEFTGETKSATALESEKERSLEWITIGGGINEDKRLLAMOMIFORDG	420
trla0a193PPX7la0a193PPX7 90RT0	VRAVOFEYMSEOEEFYGEYKSATALESRKERSLEWITIGGGINEDRKRLLAMOMIFORDG	420
tria0a193P018 a0a193P018 908T0	VRAVOFEYMSEOEEFYGEYKSATALESRKERSLEWITIGGGINEDRKRLLAMOMIFORDG	420
trla0a193PPR8la0a193PPR8 90RT0	VRAVOFEYWSEOEEFYGEYKSATALFSRKERSLEWITIGGGINEDRKRLLAMCMIFCRDG	42.0
tr A0A193PPB8 A0A193PPB8 INCTA	VRAVQFEYWSEQEEFYGEYKSATALFSRKERSLEWITIGGGINEDRRRLLAMCMIFCRDG	420
	*** <mark>*****</mark> ****************************	
splP21770/PB2_INCBE		480
tris4T8F31S4T8F3 90RT0	DYFKDAPATITMADLTTKLGREIPYOYVMNWIOKSEDNLEALLYSRGIVETNPGKMGSS	480
sp P13877 PB2 INCJJ	DYFKDAPATITMADLSTKLGREIPYQYVMMNWIOKSEDNLEALLYSRGIVETNPGKMGSS	480
tr A0A1B0RMT8 A0A1B0RMT8 90RT0	DYFKDAPATITMADLTTKLGREIPYQYVMM <mark>NWIQK</mark> SEDNLEALLYSRGIVETNPGKMGSS	480
tr A0A830ZL67 A0A830ZL67 90RT0	DYFKDAPATITMADLTTKLGREIPYQYVMMNWIQKSEDNLEALLYSRGIVETNPGKMGSS	480
tr A0A193PPU8 A0A193PPU8_INCEN	DYFKDAPATITMADLTTKLGREIPYQYVMM <mark>NWIQK</mark> SEDNLEALLYSRGIVE <mark>P</mark> NPGKMGSS	480
tr A0A193PPD6 A0A193PPD6_INCP2	DYFKDAPATITMADLTTKLGREIPYQYVMM <mark>NWIQK</mark> SEDNLEALLYSRGIVETNPGKMGSS	480
tr W8CI60 W8CI60_9ORTO	DYFKDAPATITMADLTTKLGREIPYQYVMM <mark>NWIQK</mark> SEDNLEALLYSRGIVETNPGKMGSS	463
sp Q9IMP3 PB2_INCJH	DYFKDAPATITMADLSTKLGREIPYQYVMM <mark>NWIQK</mark> SEDNLEALLYSRGIVETNPGKMGSS	480
tr A0A193PPS9 A0A193PPS9_9ORTO	DYFKDAPATITMADLSTKLGREIPYQYVMMNWIQKSEDNLEALLYSRGIVETNPGKMGSS	480
tr AUAI93PPJ9 AUAI93PPJ9 90RTO	DYFKDAPATITMADLSTKLGREIPYQYVMMNWIQKSEDNLEALLYSRGIVETNPGKMGSS	480
SP Q61/C4 PB2_INCAA		480
LI AUAIJJEEA/ AUAIJJEEA/ JUNIU	DIFROMENTITIADESTREGRETETQTVMMMUQISEDREADETSRGTVETREGRAGSS	400
+r1202193001812021930018 908TO	DYFKDA PATTTMADI. STKI. CRET PYOVUMNINI OK SEDNI FALLY SRCIVETNPCKMCSS	480
tr A0A193PQ18 A0A193PQ18_90RT0 tr A0A193PPR8 A0A193PPR8_90RT0	DYFKDAPATITMADLSTKLGREIPYQYVMM <mark>NWIQK</mark> SEDNLEALLYSRGIVETNPGKMGSS DYFKDAPATITMADLSTKLGREIPYQYVMMWIQKSEDNLEALLYSRGIVETNPGKMGSS	480 480
tr A0A193PQ18 A0A193PQ18_90RT0 tr A0A193PPR8 A0A193PPR8_90RT0 tr A0A193PPB8 A0A193PPB8_INCTA	DYFKDAPATITMADLSTKLGREIPYQYVMMNUQKSEDNLEALLYSRGIVETNPGKMGSS DYFKDAPATITMADLSTKLGREIPYQYVMMNUQKSEDNLEALLYSRGIVETNPGKMGSS DYFKDAPATITMADLSTKLGREIPYQYVMMNUQKSEDNLEALLYSRGIVETNPGKMGSS	480 480 <mark>480</mark>
tr A0A193PQ18 A0A193PQ18 ⁹ 90RT0 tr A0A193PPR8 A0A193PPR8 ^{90RT0} tr A0A193PPB8 A0A193PPB8_INCTA	DYFKDAPATITMADLSTKLGREIPYQYVMMNWIQKSEDNLEALLYSRGIVETNPGKMGSS DYFKDAPATITMADLSTKLGREIPYQYVMMNWIQKSEDNLEALLYSRGIVETNPGKMGSS DYFKDAPATITMADLSTKLGREIPYQYVMMNWIQKSEDNLEALLYSRGIVETNPGKMGSS ****************	480 480 <mark>480</mark>
tr A0A193PQ18 A0A193PQ18] 90RTO tr A0A193PPR8 A0A193PPR8] 90RTO tr A0A193PPR8 A0A193PPR8] 90RTO tr A0A193PPB8 A0A193PPB8] INCTA	DYFKDAPATITMADLSTKLGREIPYQYVMMNWIQKSEDNLEALLYSRGIVETNPGKMGSS DYFKDAPATITMADLSTKLGREIPYQYVMNWIQKSEDNLEALLYSRGIVETNPGKMGSS DYFKDAPATITMADLSTKLGREIPYQYVMMNWIQKSEDNLEALLYSRGIVETNPGKMGSS	480 480 480
tr A0A193PQ18 A0A193PQ18] 90RT0 tr A0A193PPR8 A0A193PPR8] 90RT0 tr A0A193PPR8 A0A193PPR8] 90RT0 tr A0A193PPB8 A0A193PPB8] INCTA	DYFKDAPATITMADLSTKLGREIPYQYVMMWIQKSEDNLEALLYSRGIVETNPGKMGSS DYFKDAPATITMADLSTKLGREIPYQYVMMWIQKSEDNLEALLYSRGIVETNPGKMGSS DYFKDAPATITMADLSTKLGREIPYQYVMMWIQKSEDNLEALLYSRGIVETNPGKMGSS ***********************************	480 480 480
tr A0A193PQ18 A0A193PQ18 90RT0 tr A0A193PPR8 A0A193PPR8 90RT0 tr A0A193PPR8 A0A193PPR8 90RT0 tr A0A193PPB8 A0A193PPB8 INCTA	DYFKDAPATITMADLSTKLGREIPYQYVMMWIQKSEDNLEALLYSRGIVETNPGKMGSS DYFKDAPATITMADLSTKLGREIPYQYVMMWIQKSEDNLEALLYSRGIVETNPGKMGSS DYFKDAPATITMADLSTKLGREIPYQYVMMWIQKSEDNLEALLYSRGIVETNPGKMGSS ***********************************	480 480 480
tr A0A193PQ18 A0A193PQ18 90RT0 tr A0A193PPR8 A0A193PPR8 90RT0 tr A0A193PPR8 A0A193PPR8 90RT0 tr A0A193PPB8 A0A193PPB8 INCTA //End of PB2 subunits of influenza C virus sp P21770 PB2 INCBE tr S4T8F3 S4T8F3 90RT0 sp P13877 PB2 INCJJ	DYFKDAPATITMADLSTKLGREIPYQYVMMWIQKSEDNLEALLYSRGIVETNPGKMGSS DYFKDAPATITMADLSTKLGREIPYQYVMMWIQKSEDNLEALLYSRGIVETNPGKMGSS DYFKDAPATITMADLSTKLGREIPYQYVMMWIQKSEDNLEALLYSRGIVETNPGKMGSS ***********************************	480 480 480
tr A0A193PQ18 A0A193PQ18 90RT0 tr A0A193PPR8 A0A193PPR8 90RT0 tr A0A193PPR8 A0A193PPR8 90RT0 tr A0A193PPB8 A0A193PPB8 INCTA //End of PB2 subunits of influenza C virus sp P21770 PB2 INCBE tr S478F3 S478F3 90RT0 sp P13877 PB2 INCJJ tr A0A1B0RMT8 A0A1B0RMT8 90RT0	DYFKDAPATITMADLSTKLGREIPYQYVMMWIQKSEDNLEALLYSRGIVETNPGKMGSS DYFKDAPATITMADLSTKLGREIPYQYVMMWIQKSEDNLEALLYSRGIVETNPGKMGSS DYFKDAPATITMADLSTKLGREIPYQYVMMWIQKSEDNLEALLYSRGIVETNPGKMGSS ***********************************	480 480 480
tr A0A193PQ18 A0A193PQ18 90RT0 tr A0A193PPR8 A0A193PPR8 90RT0 tr A0A193PPR8 A0A193PPR8 90RT0 tr A0A193PPB8 A0A193PPB8 _ INCTA //End of PB2 subunits of influenza C virus sp P21770 PB2 _ INCBE tr S478F3 S478F3 _ 90RT0 sp P13877 PB2 _ INCJJ tr A0A1B0RMT8 A0A1B0RMT8 _ 90RT0 tr A0A830ZL67 A0A830ZL67 _ 90RT0	DYFKDAPATITMADLSTKLGREIPYQYVMMWIQKSEDNLEALLYSRGIVETNPGKMGSS DYFKDAPATITMADLSTKLGREIPYQYVMMWIQKSEDNLEALLYSRGIVETNPGKMGSS DYFKDAPATITMADLSTKLGREIPYQYVMMWIQKSEDNLEALLYSRGIVETNPGKMGSS ***********************************	480 480 480
tr A0A193PQ18 A0A193PQ18 90RT0 tr A0A193PPR8 A0A193PPR8 90RT0 tr A0A193PPR8 A0A193PPR8 90RT0 tr A0A193PPB8 A0A193PPB8 INCTA //End of PB2 subunits of influenza C virus sp P21770 PB2 INCBE tr S4T8F3 S4T8F3 90RT0 sp P13877 PB2 INCJJ tr A0A1B0RMT8 A0A1B0RMT8 90RT0 tr A0A830ZL67 A0A830ZL67 90RT0 tr A0A830ZL67 A0A830ZL67 90RT0 tr A0A193PPU8 A0A193PPU8 INCEN	DYFKDAPATITMADLSTKLGREIPYQYVMMIWIQKSEDNLEALLYSRGIVETNPGKMGSS DYFKDAPATITMADLSTKLGREIPYQYVMMIWIQKSEDNLEALLYSRGIVETNPGKMGSS DYFKDAPATITMADLSTKLGREIPYQYVMMIWIQKSEDNLEALLYSRGIVETNPGKMGSS ***********************************	480 480 480
tr A0A193PQ18 A0A193PQ18 90RT0 tr A0A193PPR8 A0A193PPR8 90RT0 tr A0A193PPR8 A0A193PPR8 90RT0 tr A0A193PPB8 A0A193PPB8 INCTA //End of PB2 subunits of influenza C virus sp P21770 PB2_INCBE tr S4T8F3 S4T8F3 90RT0 sp P13877 PB2_INCJJ tr A0A180RMT8 A0A180RMT8 90RT0 tr A0A8302L67 A0A830ZL67 90RT0 tr A0A193PPU8 A0A193PPU8_INCEN tr A0A193PPU8 A0A193PPU8_INCEN tr A0A193PPU6 A0A193PPU6_INCP2	DYFKDAPATITMADLSTKLGREIPYQYVMMIWIQKSEDNLEALLYSRGIVETNPGKMGSS DYFKDAPATITMADLSTKLGREIPYQYVMMWIQKSEDNLEALLYSRGIVETNPGKMGSS DYFKDAPATITMADLSTKLGREIPYQYVMMWIQKSEDNLEALLYSRGIVETNPGKMGSS ***********************************	480 480 480
tr A0A193PQ18 A0A193PQ18 90RT0 tr A0A193PPR8 A0A193PPR8 90RT0 tr A0A193PPR8 A0A193PPR8 90RT0 tr A0A193PPB8 A0A193PPB8 INCTA //End of PB2 subunits of influenza C virus sp P21770 PB2_INCBE tr S4T8F3 S4T8F3 90RT0 sp P13877 PB2_INCJJ tr A0A180RMT8 A0A180RMT8 90RT0 tr A0A830ZL67 A0A830ZL67 90RT0 tr A0A193PPU8 A0A193PPU8_INCEN tr A0A193PPU8 A0A193PPU8_INCEN tr A0A193PPU6 A0A193PPU6_INCP2 tr W8C160 W8C160_90RT0 cr 00RM821BP2_INCM	DYFKDAPATITMADLSTKLGREIPYQYVMMIWIQKSEDNLEALLYSRGIVETNPGKMGSS DYFKDAPATITMADLSTKLGREIPYQYVMMWIQKSEDNLEALLYSRGIVETNPGKMGSS DYFKDAPATITMADLSTKLGREIPYQYVMMWIQKSEDNLEALLYSRGIVETNPGKMGSS ***********************************	480 480 480
tr A0A193PQ18 A0A193PQ18 90RT0 tr A0A193PPR8 A0A193PPR8 90RT0 tr A0A193PPR8 A0A193PPR8 90RT0 tr A0A193PPB8 A0A193PPB8 INCTA //End of PB2 subunits of influenza C virus sp P21770 PB2_INCBE tr S4T8F3 S4T8F3 90RT0 sp P13877 PB2_INCJJ tr A0A180RMT8 A0A180RMT8 90RT0 tr A0A180RMT8 A0A180RMT8 90RT0 tr A0A193PPU8 A0A193PPU8 INCEN tr A0A193PPU6 A0A193PPU6 INCP2 tr W8CI60 W8CI60 90RT0 sp Q9IMP3 PB2_INCJH tr A0A193PPS0 A0A193PPS9 90PT0	DYFKDAPATITMADLSTKLGREIPYQYVMMIWIQKSEDNLEALLYSRGIVETNPGKMGSS DYFKDAPATITMADLSTKLGREIPYQYVMMWIQKSEDNLEALLYSRGIVETNPGKMGSS DYFKDAPATITMADLSTKLGREIPYQYVMMWIQKSEDNLEALLYSRGIVETNPGKMGSS ***********************************	480 480 480
tr A0A193PQ18 A0A193PQ18 90RT0 tr A0A193PPR8 A0A193PPR8 90RT0 tr A0A193PPR8 A0A193PPR8 90RT0 tr A0A193PPB8 A0A193PPB8 INCTA //End of PB2 subunits of influenza C virus sp P21770 PB2 INCBE tr S4T8F3 S4T9F3 90RT0 sp P13877 PB2 INCJJ tr A0A180RMT8 A0A180RMT8 90RT0 tr A0A193PP18 A0A180RMT8 90RT0 tr A0A193PP06 A0A193PP18 INCEN tr A0A193PP06 A0A193PP16 INCP2 tr W8C160 W8C160 90RT0 sp Q91MP3 PB2 INCJH tr A0A193PP59 A0A193PP18 90RT0 tr A0A193PP59 A0A193PP18 90RT0	DYFKDAPATITMADLSTKLGREIPYQYVMMIWIQKSEDNLEALLYSRGIVETNPGKMGSS DYFKDAPATITMADLSTKLGREIPYQYVMMIWIQKSEDNLEALLYSRGIVETNPGKMGSS DYFKDAPATITMADLSTKLGREIPYQYVMMIWIQKSEDNLEALLYSRGIVETNPGKMGSS ***********************************	480 480 480
tr A0A193PQ18 A0A193PQ18 90RT0 tr A0A193PPR8 A0A193PPR8 90RT0 tr A0A193PPR8 A0A193PPR8 90RT0 tr A0A193PPB8 A0A193PPB8 INCTA //End of PB2 subunits of influenza C virus sp P21770 PB2 INCBE tr S4T8F3 S4T9F3 90RT0 sp P13877 PB2 INCJJ tr A0A180RMT8 A0A180RMT8 90RT0 tr A0A180RMT8 A0A180RMT8 90RT0 tr A0A193PPU8 A0A193PPU8 INCEN tr A0A193PPU8 A0A193PPU8 INCEN tr A0A193PPD6 A0A193PPU8 INCEN tr A0A193PPD9 A0A193PPD5 90RT0 tr A0A193PPD9 A0A193PPS9 90RT0 tr A0A193PPJ9 A0A193PPJ9 90RT0 sp 0617C4 IPB2 INCAA	DYFKDAPATITMADLSTKLGREIPYQYVMMIWIQKSEDNLEALLYSRGIVETNPGKMGSS DYFKDAPATITMADLSTKLGREIPYQYVMMIWIQKSEDNLEALLYSRGIVETNPGKMGSS DYFKDAPATITMADLSTKLGREIPYQYVMMIWIQKSEDNLEALLYSRGIVETNPGKMGSS ***********************************	480 480 480
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tr A0A193PQ18 A0A193PQ18 90RT0 tr A0A193PPR8 A0A193PPR8 90RT0 tr A0A193PPR8 A0A193PPR8 90RT0 tr A0A193PPB8 A0A193PPB8 INCTA //End of PB2 subunits of influenza C virus sp P21770 PB2_INCBE tr S478F3 S478F3 90RT0 sp P13877 PB2_INCJJ tr A0A1B0RMT8 A0A1B0RMT8 90RT0 tr A0A8302L67 A0A8302L67 90RT0 tr A0A8302L67 A0A8302L67 90RT0 tr A0A193PPD6 A0A193PPU8_INCEN tr A0A193PPD6 A0A193PP16_INCP2 tr W8C160 W8C160 90RT0 sp Q91MP3 PB2_INCJH tr A0A193PP39 A0A193PP39_90RT0 tr A0A193PP39 A0A193PP39_90RT0 tr A0A193PP37 A0A193PP37_90RT0 tr A0A193P21 A0A193PP38_90RT0 tr A0A193PP8 A0A193PP38_90RT0 tr A0A193PP88 A0A193PP38_90RT0	DYFKDAPATITMADLSTKLGREIPYQYVMMIWIQKSEDNLEALLYSRGIVETNPGKMGSS DYFKDAPATITMADLSTKLGREIPYQYVMMIWIQKSEDNLEALLYSRGIVETNPGKMGSS DYFKDAPATITMADLSTKLGREIPYQYVMMIWIQKSEDNLEALLYSRGIVETNPGKMGSS ***********************************	480 480 480
tr A0A193PQ18 A0A193PQ18 90RT0 tr A0A193PPR8 A0A193PPR8 90RT0 tr A0A193PPR8 A0A193PPR8 90RT0 tr A0A193PPB8 A0A193PPB8 _ INCTA //End of PB2 subunits of influenza C virus sp P21770 PB2 _ INCBE tr S4T8F3 S4T8F3 _ 90RT0 sp P13877 PB2 _ INCJJ tr A0A180RMT8 A0A180RMT8 _ 90RT0 tr A0A180ZL67 A0A830ZL67 _ 90RT0 tr A0A193PPU8 A0A193PPU8 _ INCEN tr A0A193PPU8 A0A193PPU6 _ INCEN tr A0A193PPS9 A0A193PPD6 _ INCE2 tr W8C160 W8C160 _ 90RT0 sp Q9IMP3 PB2 _ INCJH tr A0A193PPS9 A0A193PPS9 _ 90RT0 tr A0A193PPS9 A0A193PPX7 _ 90RT0 sp Q617C4 PB2 _ INCAA tr A0A193PPX8 A0A193PPX7 _ 90RT0 tr A0A193PPX8 A0A193PPX8 _ 90RT0 tr A0A193PPR8 A0A193PP88 _ 90RT0 tr A0A193PP88 A0A193PP88 _ INCTA	DYFKDAPATITMADLSTKLGREIPYQYVMMIWIQKSEDNLEALLYSRGIVETNPGKMGSS DYFKDAPATITMADLSTKLGREIPYQYVMMIWIQKSEDNLEALLYSRGIVETNPGKMGSS DYFKDAPATITMADLSTKLGREIPYQYVMMIWIQKSEDNLEALLYSRGIVETNPGKMGSS ***********************************	480 480 480
tr A0A193PQ18 A0A193PQ18 90RT0 tr A0A193PPR8 A0A193PPR8 90RT0 tr A0A193PPR8 A0A193PPR8 90RT0 tr A0A193PPB8 A0A193PPB8 INCTA //End of PB2 subunits of influenza C virus sp P21770 PB2_INCBE tr S478F3 S478F3 90RT0 sp P13877 FB2_INCJJ tr A0A180RMT8 A0A180RMT8 90RT0 tr A0A8302L67 A0A8302L67 90RT0 tr A0A8302L67 A0A8302L67 90RT0 tr A0A193PPD6 A0A193PPU8_INCEN tr A0A193PPD6 A0A193PPU8_INCEN tr A0A193PPD6 A0A193PPD6_INCP2 tr W8C160 W8C160 90RT0 sp Q91MP3 FB2_INCJH tr A0A193PPJ9 A0A193PPJ9_90RT0 sp Q617C4 FB2_INCAA tr A0A193PP77 A0A193PPX7_90RT0 tr A0A193PP78 A0A193PPR8_90RT0 tr A0A193PP88 A0A193PPR8_90RT0 tr A0A193PP88 A0A193PP88_INCTA	DYFKDAPATITMADLSTKLGREIPYQYVMMIWIQKSEDNLEALLYSRGIVETNPGKMGSS DYFKDAPATITMADLSTKLGREIPYQYVMMWIQKSEDNLEALLYSRGIVETNPGKMGSS DYFKDAPATITMADLSTKLGREIPYQYVMMWIQKSEDNLEALLYSRGIVETNPGKMGSS ***********************************	480 480 480
tr A0A193PQ18 A0A193PQ18 90RT0 tr A0A193PPR8 A0A193PPR8 90RT0 tr A0A193PPR8 A0A193PPR8 90RT0 tr A0A193PPB8 A0A193PPB8 INCTA //End of PB2 subunits of influenza C virus sp P21770 PB2_INCBE tr S478F3 S478F3 90RT0 sp P13877 PB2_INCJJ tr A0A180RMT8 A0A180RMT8 90RT0 tr A0A8302L67 A0A830ZL67 90RT0 tr A0A830ZL67 A0A830ZL67 90RT0 tr A0A193PPD6 A0A193PPU8_INCEN tr A0A193PPD6 A0A193PPD6_INCP2 tr W8C160 W8C160 90RT0 sp Q9IMP3 PB2_INCJH tr A0A193PPJ9 A0A193PPJ9 90RT0 tr A0A193PPJ9 A0A193PPJ9 90RT0 tr A0A193PPJ9 A0A193PPJ7 90RT0 tr A0A193PPT7 A0A193PPJ7 90RT0 tr A0A193PPT8 A0A193PP18 90RT0 tr A0A193PP8 A0A193PP18 90RT0 tr A0A193PP8 A0A193PP18 90RT0 tr A0A193PP8 A0A193PP88 90RT0 tr A0A193PP88 A0A193PP88 90RT0	DYFKDAPATITMADLSTKLGREIPYQYVMMIWIQKSEDNLEALLYSRGIVETNPGKMGSS DYFKDAPATITMADLSTKLGREIPYQYVMMWIQKSEDNLEALLYSRGIVETNPGKMGSS DYFKDAPATITMADLSTKLGREIPYQYVMMWIQKSEDNLEALLYSRGIVETNPGKMGSS ***********************************	480 480 480
tr A0A193PQ18 A0A193PQ18 90RT0 tr A0A193PPR8 A0A193PPR8 90RT0 tr A0A193PPR8 A0A193PPR8 90RT0 tr A0A193PPB8 A0A193PPB8 INCTA //End of PB2 subunits of influenza C virus sp P21770 PB2_INCBE tr S4T8F3 S4T8F3 90RT0 sp P13877 PB2_INCJJ tr A0A180RMT8 A0A180RMT8 90RT0 tr A0A830ZL67 A0A830ZL67 90RT0 tr A0A830ZL67 A0A830ZL67 90RT0 tr A0A193PPU8 A0A193PPU8_INCEN tr A0A193PPU8 A0A193PPU8_INCEN tr A0A193PPU8 A0A193PPU8_INCEN tr A0A193PPU8 A0A193PPU8_INCEN tr A0A193PPU8 A0A193PPU8_90RT0 tr A0A193PPU9 A0A193PPU9_90RT0 sp Q617C4 PB2_INCAA tr A0A193PPU7 A0A193PPU7_90RT0 tr A0A193PPU8 A0A193PPU8_90RT0 tr A0A193PU8 A0A193PPU8_90RT0 tr A0A193PU8 A0A193PU8_90RT0 tr A0A193PU8 A0A193PU8_90RT0 tr A0A193PU8 A0	DYFKDAPATITMADLSTKLGREIPYQYVMMWIQKSEDNLEALLYSRGIVETNPGKMGSS DYFKDAPATITMADLSTKLGREIPYQYVMMWIQKSEDNLEALLYSRGIVETNPGKMGSS DYFKDAPATITMADLSTKLGREIPYQYVMMWIQKSEDNLEALLYSRGIVETNPGKMGSS ***********************************	480 480 480
tr A0A193PQ18 A0A193PQ18 90RT0 tr A0A193PPR8 A0A193PPR8 90RT0 tr A0A193PPR8 A0A193PPR8 90RT0 tr A0A193PPR8 A0A193PPR8 1NCTA //End of PB2 subunits of influenza C virus sp P21770 PB2_INCBE tr S4T8F3 S4T8F3 90RT0 sp P13877 PB2_INCJJ tr A0A180RMT8 A0A180RMT8 90RT0 tr A0A830ZL67 A0A830ZL67 90RT0 tr A0A830ZL67 A0A830ZL67 90RT0 tr A0A193PPU8 A0A193PPU8_INCEN tr A0A193PPD6 A0A193PPU8_INCEN tr A0A193PPD6 A0A193PPU8_INCEN tr A0A193PPD6 A0A193PPU8_90RT0 sp Q91MP3 PB2_INCJH tr A0A193PPS7 A0A193PPJ9 90RT0 sp Q617C4 PB2_INCAA tr A0A193PPX7 A0A193PPX7 90RT0 tr A0A193PPX8 A0A193PP18_90RT0 tr A0A193PP88 A0A193PP88_90RT0 tr A0A193PP88 A0A193PP88_1NCTA P21770 PB2_INCBE, In S4T8F3_90RT0, Influe P13877 PB2_INCJJ, Infl A0A1B0RMT8_90RT0	DYFKDAPATITMADLSTKLGREIPYQYVMMIWIQKSEDNLEALLYSRGIVETNPGKMGSS DYFKDAPATITMADLSTKLGREIPYQYVMMWIQKSEDNLEALLYSRGIVETNPGKMGSS DYFKDAPATITMADLSTKLGREIPYQYVMMWIQKSEDNLEALLYSRGIVETNPGKMGSS THE STANDARD STREAM STRE	480 480 480
tr A0A193PQ18 A0A193PQ18 90RT0 tr A0A193PPR8 A0A193PPR8 90RT0 tr A0A193PPR8 A0A193PPR8 90RT0 tr A0A193PPR8 A0A193PPR8 1NCTA //End of PB2 subunits of influenza C virus sp P21770 PB2_INCBE tr S4T8F3 S4T8F3 90RT0 sp P13877 PB2_INCJJ tr A0A180RMT8 A0A180RMT8 90RT0 tr A0A830ZL67 A0A830ZL67 90RT0 tr A0A830ZL67 A0A830ZL67 90RT0 tr A0A193PPU8 A0A193PPU8_INCEN tr A0A193PPD6 A0A193PPU8_INCEN tr A0A193PPD6 A0A193PPU8_INCEN tr A0A193PPS9 A0A193PPU8_90RT0 sp Q9IMP3 PB2_INCJH tr A0A193PPS9 A0A193PPJ9 90RT0 sp Q6I7C4 PB2_INCAA tr A0A193PPS7 A0A193PPJ7 90RT0 tr A0A193PPS8 A0A193PP18_90RT0 tr A0A193PP88 A0A193PP88_90RT0 tr A0A193PP88 A0A193PP88_INCTA P21770 PB2_INCBE, In S4T8F3_90RT0, Influe P13877 PB2_INCJJ, Infl A0A1B0RMT8_90RT0	DYFKDAPATITMADLSTKLGREIPYQYVMMIWIQKSEDNLEALLYSRGIVETNPGKMGSS DYFKDAPATITMADLSTKLGREIPYQYVMMWIQKSEDNLEALLYSRGIVETNPGKMGSS DYFKDAPATITMADLSTKLGREIPYQYVMMWIQKSEDNLEALLYSRGIVETNPGKMGSS DYFKDAPATITMADLSTKLGREIPYQYVMMWIQKSEDNLEALLYSRGIVETNPGKMGSS TAMPATER STATES STAT	480 480 480

A0A193PPD6 INCP2, Influenza C virus (strain C/Pig/Beijing/1981) (pI = 9.24) W8CI60 9ORTO, Influenza C virus (C/Singapore/2006)

Q9IMP3|PB2_INCJH, Influenza C virus (strain C/Johannesburg/1/1966) (pI = 9.24)

A0A193PPS9_9ORTO, Influenza C virus (C/Paris/1967) (pI = 9.24)

A0A193PPJ9 9ORTO, Influenza C virus (C/Tokyo/2010

Q6I7C4|PB2 INCAA, Influenza C virus (strain C/Ann Arbor/1950)

A0A193PPX7_9ORTO, Influenza C virus (strain C/Aini Aroor/1930) A0A193PQ18_9ORTO, Influenza C virus (C/Yamagata/2008) A0A193PPR8_9ORTO, Influenza C virus (C/Greece/1/1979) A0A193PPB8_INCTA, Influenza C virus (strain C/Taylor/1947) (pI = 9.25)

Figure 6 MSA of BP2 subunit of the polymerase from different strains of Influenza C viruses

Figure 7 shows the mix and match analysis of all the three human influenza viruses (only the required regions for the discussions are shown here). It is interesting to note that the human influenza viruses A and B align in the proposed conserved motifs, suggesting their possible similar origins. The first dyad (-DH/DQ-)- which is shown to involve in Mg²⁺-binding and as the proton acceptor are aligned in the influenza viruses A and B, but not in C. The dipeptide alignment suggests that the B virus could possibly use the Q as the proton acceptor instead of H, as reported in other HNH/N endonucleases. Though one of the proposed NLSs align in all three viruses, the CBRs align only in A and B viruses, further suggesting their similar origins (Fig. 6). From the MSA analysis, it is clear that the A and B influenza viruses are close to each other, whereas the influenza virus C has diverged significantly during evolution or may have a different origin.

CLUSTAL O (1.2.4) Mix and Match Analysis of the PB2 subunits from Influenza A, B & C viruses

<pre>sp P21770 PB2_INCBE sp P13877 PB2_INCJJ sp Q9IMP3 PB2_INCJH sp Q617C4 PB2_INCAA tr A0A193PPX7 A0A193PPX7_9ORTO tr A0A193PQ18 A0A193PQ18_9ORTO tr A0A4Y5WMY1 A0A4Y5WMY1_9INFB tr Q4LD02 Q4LD02_9INFB sp Q9QLL6 PB2_INELE tr U32277 U32277_9INFB sp P13875 PB2_INEAC sp 036431 PB2_INBP9 sp Q1PUC9 PB2_I73A5 sp Q6XU90 PB2_I67A0 sp P0DG6 PB251_I34A1 sp Q0A2F5 PB2_I80AD sp Q0A438 PB2_I49A1</pre>	MSLLLTIAKEYKRLCQDAKAAQMMTVGTVSNYTTFKKWTTSRKEKNPSLRMRWAMSSKFP MSLLLTIAKEYKRLCQDAKAAQMMTVGTVSNYTTFKKWTTSRKEKNPSLRMRWAMSSKFP MSLLLTIAKEYKRLCQDAKAAQMMTVGTVSNYTTFKKWTTSRKEKNPSLRMRWAMSSKFP MSFLLTIAKEYKRLCQDAKAAQMMTVGTVSNYTTFKKWTTSRKEKNPSLRMRWAMSSKFP MSLLLTIAKEYKRLCQDAKAAQMMTVGTVSNYTTFKKWTTSRKEKNPSLRMRWAMSSKFP MSLLLTIAKEYKRLCQDAKAAQMMTVGTVSNYTTFKKWTTSRKEKNPSLRMRWAMSSKFP MTLAKIELLKQLLRDNEAKTVLKQTTVDQYNIIRKFNTSRIEKNPSLRMRWAMSSKFP MTLAKIELLKQLLRDNEAKTVLKQTTVDQYNIIRKFNTSRIEKNPSLRMKWAMCSNFP MTLAKIELLKQLLRDNEAKTVLKQTTVDQYNIIRKFNTSRIEKNPSLRMKWAMCSNFP MTLAKIELLKQLLRDNEAKTVLKQTTVDQYNIIRKFNTSRIEKNPSLRMKWAMCSNFP MTLAKIELLKQLLRDNEAKTVLKQTTVDQYNIIRKFNTSRIEKNPSLRMKWAMCSNFP MTLAKIELLKQLLRDNEAKTVLKQTTVDQYNIIRKFNTSRIEKNPSLRMKWAMCSNFP MTLAKIELLKQLLRDNEAKTVLKQTTVDQYNIIRKFNTSRIEKNPSLRMKWAMCSNFP MTLAKIELLKQLLRDNEAKTVLKQTTVDQYNIIRKFNTSRIEKNPSLRMKWAMCSNFP MTLAKIELLKQLLRDNEAKTVLKQTTVDQYNIIRKFNTSRIEKNPSLRMKWAMCSNFP MTLAKIELLKQLLRDNEAKTVLKQTTVDQYNIIRKFNTSRIEKNPSLRMKWAMCSNFP MTLAKIELLKQLLRDNEAKTVLKQTTVDQYNIIRKFNTSRIEKNPSLRMKWAMCSNFP MERIKELRNLMSQSRTREILTKTTVDHAIIKKYTSGRQEKNPSLRMKWAMKYP MERIKELRNLMSQSRTREILTKTTVDHAIIKKYTSGRQEKNPSLRMKWMAMKYP MERIKELRNLMSQSRTREILTKTTVDHAIIKKYTSGRQEKNPALRMKWMAMKYP MERIKELRDLMSQSRTREILTKTTVDHAIIKKYTSGRQEKNPALRMKWMAMKYP MERIKELRDLMSQSRTREILTKTTVDHAIIKKYTSGRQEKNPALRMKWMAMKYP MERIKELRDLMSQSRTREILTKTTVDHAIIKKYTSGRQEKNPALRMKWMAMKYP MERIKELRDLMSQSRTREILTKTTVDHAIIKKYTSGRQEKNPALRMKWMAMKYP	60 60 60 60 58 58 58 58 58 58 56 56 56 56 56 56 56 56
<pre>sp P21770 PB2_INCBE sp P13877 PB2_INCJJ sp Q9IMP3 PB2_INCJH sp Q617C4 PB2_INCAA tr A0A193PPX7 A0A193PPX7_9ORTO tr A0A193PQ18 A0A193PQ18_9ORTO tr A0A4Y5WMY1 A0A4Y5WMY1_9INFB tr Q4LD02 Q4LD02_9INFB sp Q9QLL6 PB2_INBLE tr U3S2T7 U3S2T7_9INFB sp P13875 PB2_INBAC sp 036431 PB2_INBP9 sp Q1PUC9 PB2_I73A5 sp Q6XU90 PB2_I67A0 sp P0D066 PB251_I34A1 sp Q0A2F5 PB2_I83A4 sp Q0A438 PB2_I49A1</pre>	IIANKRMLEEAQIPKEHNNVALWEDTEDVSKEDHVLASASCINYWNFCGPCVNNSEVIKE IIANKRMLEEAQIPKEHNNVALWEDTEDVSKEDHVLASASCINYWNFCGPCVNNSEVIKE IIANKRMLEEAQIPKEHNNVALWEDTEDVSKEDHVLASASCINYWNFCGPCVNNSEVIKE IIANKRMLEEAQIPKEHNNVALWEDTEDVSKEDHVLASASCINYWNFCGPCVNNSEVIKE IIANKRMLEEAQIPKEHNNVALWEDTEDVSKEDHVLASASCINYWNFCGPCVNNSEVIKE IIANKRMLEEAQIPKEHNNVALWEDTEDVSKEDHVLASASCINYWNFCGPCVNNSEVIKE IIANKRMLEEAQIPKEHNNVALWEDTEDVSKEDHVLASASCINYWNFCGPCVNNSEVIKE IIANKRMLEEAQIPKEHNNVALWEDTEDVSKEDHVLASASCINYWNFCGPCVNNSEVIKE IANKRMLEEAQIPKEHNNVALWEDTEDVSKEDHVLASASCINYWNFCGPCVNNSEVIKE IANKRMLEEAQIPKEHNNVALWEDTEDVSKEDHVLASASCINYWNFCGPCVNNSEVIKE IANKRMLEEAQIPKEHNNVALWEDTEDVSKEDHVLASASCINYWNFCGPCVNNSEVIKE IANKRMLEEAQIPKEHNNVALWEDTEDVSKEDHVLASASCINYWNFCGPCVNNSEVIKE IANKRDMA-NRIPLEYKGIQLKTNAEDIGTK-GQMCSIAAVTWWNTYGPIGD-TEGFER IALTKGDMA-NRIPLEYKGIQLKTNAEDIGTK-GQMCSIAAVTWWNTYGPIGD-TEGFEK IALTKGDMA-NRIPLEYKGIQLKTNAEDIGTK-GQMCSIAAVTWWNTYGPIGD-TEGFEK IALTKGDMA-NRIPLEYKGIQLKTNAEDIGTK-GQMCSIAAVTWWNTYGPIGD-TEGFEK IALTKGDMA-NRIPLEYKGIQLKTNAEDIGTK-GQMCSIAAVTWWNTYGPIGD-TEGFEK IALTKGDMA-NRIPLEYKGIQLKTNAEDIGTK-GQMCSIAAVTWWNTYGPIGD-TEGFEK IALTKGDMA-NRIPLEYKGIQLKTNAEDIGTK-GQMCSIAAVTWWNTYGPIGD-TEGFEK IALTKGDMA-NRIPLEYKGIQLKTNAEDIGTK-GQMCSIAAVTWWNTYGPIGD-TEGFEK ITADKRITE-MVPEREQGQTLWSKMSDAGSD-RVMVSPLAVTWWNRNGPTS-TVHYFK ITADKRITE-MIPEREQGQILWSKMNDAGSD-RVMVSPLAVTWWNRNGPTS-TVHYFK ITADKRITE-MIPEREQGQILWSKTNDAGSD-RVMVSPLAVTWWNRNGPTS-TVHYFK ITADKRITE-MIPEREQGQILWSKTNDAGSD-RVMVSPLAVTWWNRNGPTS-THYFK ITADKRIME-MIPEREQGQILWSKTNDAGSD-RVMVSPLAVTWWNRNGPTS-TVHYFK ITADKRIME-MIPEREQGQILWSKTNDAGSD-RVMVSPLAVTWWNRNGPTS-TVHYFK	120 120 120 120 120 120 120 120
<pre>sp P21770 PB2_INCBE sp P13877 PB2_INCJJ sp Q9IMP3 PB2_INCJJ sp Q617C4 PB2_INCAA tr AOA193PPX7 AOA193PPX7 _ 90RT0 tr AOA193PQ18 AOA193PQ18 _ 90RT0 tr AOA4Y5WMY1 AOA4Y5WMY1 _ 91NFB tr Q4LD02 Q4LD02 _ 91NFB sp Q9QLL6 PB2_INBLE tr U32577 U32577 _ 91NFB sp P138751 PB2_INBAC sp O36431 PB2_INBP9 sp Q1PUC9 PB2_I73A5 sp Q6XU90 PB2_I73A5 sp Q0A2F51 PB2_I83A4 sp Q20NV1 PB2_I80AD sp Q0A438 PB2_I49A1</pre>	VYKSRFGRLERR KEI MWKE LRFTLVIRORR VDT OPVEORLRT GEIKDLOMWT LFE DEAP VYKSRFGRLERR KEI MWKE LRFTLVIRORR VDT OPVEORLRT GEI KDLOMWT LFE DEAP VYKSRFGRLERR KEI MWKE LRFTLVIRORR VDT OPVEORLRT GEI KDLOMWT LFE DEAP VYKSRFGRLERR KEI MWKE LRFTLVIRORR VDT OPVEORLRT GEI KDLOMWT LFE DEAP VYKSRFGRLERR KEI MWKE LRFTLVIRORR VDT OPVEORLRT GEI KDLOMWT LFE DEAP VYKSRFGRLERR KEI MWKE LRFTLVIRORR VDT OPVEORLRT GEI KDLOMWT LFE DEAP VYKSRFGRLERR KEI MWKE LRFTLVIRORR VDT OPVEORLRT GEI KDLOMWT LFE DEAP VYKSRFGRLERR KEI MWKE LRFTLVIRORR VDT OPVEORLRT GEI KDLOMWT LFE DEAP VYESFFLRKMRLDNAT WGR IT FGPVERVRK VLLNPLTKEMPP DEA SNVIMEI LFP KEAG VYESFFLRKMRLDNAT WGR IT FGPVERVRK VLLNPLTKEMPP DEA SNVIMEI LFP KEAG VYESFFLRKMRLDNAT WGR IT FGPVERVRKR VLLNPLTKEMPP DEA SNVIMEI LFP KEAG VYKTYF DKVERLKHGT FGPVHFRNOVKIRR VDINPGHADLSAKEA ODVIMEVVFPNEVG VYKTYF EKVERLKHGT FGPVHFRNOVKIRR VDINPGHADLSAKEAODVIMEVVFPNEVG VYKTYF EKVERLKHGT FGPVHFRNOVKIRR VDINPGHADLSAKEAODVIMEVVFPNEVG VYKTYF EKVERLKHGT FGPVHFRNOVKIRR VDINPGHADLSAKEAODVIMEVVFPNEVG VYKTYFEKVERLKHGT FGPVHFRNOVKIRR VDINPGHADLSAKEAODVIMEVVFPNEVG VYKTYFEKVERLKHGT FGPVHFRNOVKIRR VDINPGHADLSAKEAODVIMEVVFPNEVG VYKTYFEKVERLKHGT FGPVHFRNOVKIRR VDINPGHADLSAKEAODVI	180 180 180 180 180 180 180 175 175 175 175 175 175 175 175

sp P21770 PB2 INCBE	VRAVQFEYW SEQEEFYGEYKSATALFSRKERSLEWITIGGGINEDRKRLLAMCMIFCRDG
splP138771PB2_INCJJ	VRAVOFEYW SECEEFYGEYK SATALFSRKERSLEWITIGGGINEDRKRLLAMCMIFCRDG
aplo0TMD2/DB2_TNCTH	VID NUOPPVWCPOPPPVCPVPCATAL POPPPCI PMT TCCC INPOPVDI LAWCHT PCDC
spigatmesters_incon	VRAV OF EIW DE QEEFIGE IKSATADESKKERSDEWIII GGGINEDKKRDDAMCMIFCKDG
sp Q617C4 PB2 INCAA	VRAVQFEYW5EQEEFYGEYKSATALFSRKERSLEWITIGGGINEDRKRLLAMCMIFCRDG
trla0a193ppx7la0a193ppx7_90pT0	VRAVOFEYM SEOFE FYGEYK SATAL FSRKERSLEWTTIGGGINEDRKRLLAMCMIFCRDG
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tr AUA193PQ18 AUA193PQ18_90RTO	VRAVQFEYW BEQEEFYGEYKSATALFSRKERSLEWITIGGGINEDRKRLLAMCMIFCRDG
tr A0A4Y5WMY1 A0A4Y5WMY1 9INFB	GTIQKIGIWDGEEEFHVRCGECRGILKKSKMKLEKLLINSAKKEDMRDLIILCMVFSQDT
+- 10/1D0210/1D02 01NEP	
CTIGATDOSIGATDOS_ATMED	GIIQKIGIWDGEEEEnvkCGECKGIBKSSKMKBEKBBINSAKKEDMKDBIIBCMvFSQDI
sp Q9QLL6 PB2 INBLE	GTIQKIGIWDGEEEFHVRCGECRGILKKSQMRMEKLLINSAKKEDMKDLIILCMVFSQDT
tr U3S2T7 U3S2T7_9INFB	GT TOKIG IWDGEFFFHVRCGECRGILKKSKMRMFKI, IN SAKKFDMKDI, I LCMVFSODT
sp P13875 PB2_INBAC	GTIQKIGIWDGEEEFHVRCGECRGILKKSKMRMEKLLINSAKKEDMKDLIILCMVFSQDT
sp 036431 PB2 INBP9	GTIQKIGIWDGEEEFHVRCGECRGILKKSKMRMEKLLINSAKKEDMKDLIILCMVFSQDT
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spiQirocsirb2_1/3A3	DUIDKIKVNEGIEETINVGKAIAIDKKAIKEDVQDIV5GKDEQ5IAEAIIVAMVF5QED
sp Q6XU90 PB2 I67A0	LQTLKIRVHEGYEEFTMVGKRATAILRKATRRLVQLIVSGRDEQSIVEAIIVAMVFSQED
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50105000115251_131A1	
splQUA2F5 PB2_183A4	LQTLKIRVHEGYEEFTMVGRRATAILRKATRRLIQLIVSGRDEQSIAEAIIVAMVFSQED
sp Q20NV1 PB2 I80AD	LQTLKIRVHEGYEEFTMVGRRATAILRKATRRLIQLIVSGRDEQSIAEAIIVAMVFSQED
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oblooutooltop_tion	
	DV FEDA DAM TANA DI AMERI CDE I DVOVIDANI VICE CEDNI PALI VCDCIVE MUCCC
spirzi//0/PBZ_INCBE	DIFKDAPATITMADLTTKLGKEIPIQIVMMNNIQASEDNLEALLISKGIVEINPGKMGSS
sp P13877 PB2 INCJJ	DYFKDAPATITMADLSTKLGREIPYQYVMMNWIQKSEDNLEALLYSRGIVETNPGKMGSS
en LOGIMPSIPB2 INC.TH	DY FK DA DAT TTMA DI STKLOPFI DY OV WMNW TO FSF DN LFALLYSDOTVFTN DOKMOSS
SP, WIMIS, IDZ_INCOM	STINSALATTIADUSTRUSKETETQI VIAMMIQASEDNUEAUDISKETVEINPGKM655
sp/Q6I7C4/PB2_INCAA	DYFKDAPATITMADLSTKLGREIPYQYVM <mark>MNWIQK</mark> SEDNLEALLYSRGIVETNPGKMGSS
tr A0A193PPX7 A0A193PPX7 90RT0	DYFKDAPATITMADLSTKLGREIPYOYVMMNWIONSEDNLEALLYSRGIVETNPGKMGSS
+= 1303102D0101303102D010 00DE0	DV FKDA DAM TMAA DI SMKI CDE I DVOVIA (UNITOT SEDNI FALL VSD STUEMNDSKUSSS
CI MONIACEÓIO MONIACEÓIO AORIO	DIFEDREATINADUSTEDERETETOTVARIANTORSEDAUEAUUTSETVETAPGEMGSS
tr A0A4Y5WMY1 A0A4Y5WMY1 9INFB	RMFQGVRGEINFLNRAGQLLSPMYQLQRYFLNRSNDLFDQWGYE-ESPKA
+r104LD02104LD02 9INFB	
CI QIDOZ QIDOZ_JIMED	MICOVROLINI DARAG UNDIMICUQATINASAD DIDOMOTE EJIKA
sp Q9QLL6 PB2_INBLE	RMFQGVRGEINFLNRAGQLLSPMYQLQRYFLNRSNDLFDQWGYE-ESPKA
tr U3S2T7 U3S2T7 9INFB	RMFOGVRGEINFLNRAGOLLSPMYOLORYFLSRSNDLFDOWGYE-ESPKA
SPIPIS0/SIPBZ_INDAC	RMFQGVRGEINFLMRAGQLLSPMIQLQRIFLMRSMDLFDQWGIE-EPPRA
sp 036431 PB2 INBP9	RMFQGVRGEINFLNRAGQLLSPMYQLQRYFLNRSND <mark>LFDQW</mark> GYE-ESPKA
en 0] PUCGI PB2 T 73A5	CMIKAVEGDINEVNEANORINDMHOLLEREOKDAKY
splQ6XU9U PB2_16/AU	CMIKAVRGDLNFVNRANQRLNPMHQLLRHFQKDAKVLFQNWGIE-HIDNV
sp P0D0G6 PB2S1 I34A1	CMIKAVRGDLNFVNRANQRLNPMHQLLRHFQKDAKVLFQNWGVE-PIDNV
ap10072F51PB2 T9274	
SPIQOAZESTEDZ_105A4	CHIRAVEGUNITYWARW QRUMPHIQUURHPQRDARI HPQWWGVE PIDWY
sp Q20NV1 PB2_I80AD	CMIKAVRGDLNFVNRANQRLNPMHQLLRHFQKDAKVLFQNWGIE-PIDNV
sp100A4381PB2_T49A1	CMTKAVEGDINFVNRANORINPMHOLIERFOKDAKVIFONNGTE-PTDNV
-F	
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sp P21770 PB2_INCBE	DLPSDKKVTFQDVSFQHPDLAVLRDEKTAITKGYEALIKRLGTGDNDIPSLIAKKDYLSL
sp P21770 PB2_INCBE sp P13877 PB2_INCJJ	DLP SDK KVT FQDVSFQHPDLAVLRDEKTAIT KGY EAL IKRLGTGDNDIPSLIAKKDYLSL DLP SDK KVT FODVSFOHPDLAVLRDEKTAIT KGY EAL IKRLGTGDNDIPSLIAKKDYLSL
sp P21770 PB2_INCBE sp P13877 PB2_INCJJ	DLP SDKKVT FQDVSFQHPDLAVLRDEKTAIT KGYEALIKRLGTGDDDIPSLIAKKDYLSL DLP SDKKVT FQDVSFQHPDLAVLRDEKTAIT KGYEALIKRLGTGDDDIPSLIAKKDYLSL
sp P21770 PB2_INCBE sp P13877 PB2_INCJJ sp Q9IMP3 PB2_INCJH	DLP SDK KVT FQDVSFQ HPDLAV LRDEKTAIT KGYEAL IKR LGTGDNDIPS LIAKKD YLSL DLP SDK KVT FQDVSFQ HPDLAV LRDEKTAIT KGYEAL IKR LGTGDNDIPS LIAKKD YLSL DLP SDK KVT FQDVSFQ HPDLAV LRDEKTAIT KGYEAL IKR LGTGDNDIPS LIAKKD YLSL
sp P21770 PB2_INCBE sp P13877 PB2_INCJJ sp Q9IMP3 PB2_INCJH sp Q6I7C4 PB2_INCAA	DLP SDK KVT FQDVSFQHPDLAVLRDEKTAIT KGYEALIKRLGTGDNDIPSLIAKKDYLSL DLP SDK KVT FQDVSFQHPDLAVLRDEKTAIT KGYEALIKRLGTGDNDIPSLIAKKDYLSL DLP SDK KVT FQDVSFQHPDLAVLRDEKTAIT KGYEALIKRLGTGDNDIPSLIAKKDYLSL DLP SDK KVT FQDVSFQHPDLAVLRDEKTAIT KGYEALIKRLGTGDNDIPSLIAKKDYLSL
sp P21770 PB2_INCBE sp P13877 PB2_INCJJ sp Q9IMP3 PB2_INCJH sp Q617C4 PB2_INCAA +r a0a193PPX7_B00a193PPX7_90PT0	DLP SDK KVT FQDVSFQHPDLAVLRDEKTAIT KGYEAL IKRLGTGDNDIPSLIAKKDYLSL DLP SDK KVT FQDVSFQHPDLAVLRDEKTAIT KGYEAL IKRLGTGDNDIPSLIAKKDYLSL DLP SDK KVT FQDVSFQHPDLAVLRDEKTAIT KGYEAL IKRLGTGDNDIPSLIAKKDYLSL DLP SDK KVT FQDVSFQHPDLAVLRDEKTAIT KGYEAL IKRLGTGDNDIPSLIAKKDYLSL
sp P21770 PB2_INCBE sp P13877 PB2_INCJJ sp Q9IMP3 PB2_INCJH sp Q6I7C4 PB2_INCAA tr A0A193PPX7 A0A193PPX7_90RT0	DLP SDK KVT FQDVSFQHPDLAVLRDEKTAIT KGYEAL IKRLGTGDNDIPSLIAKKDYLSL DLP SDK KVT FQDVSFQHPDLAVLRDEKTAIT KGYEAL IKRLGTGDNDIPSLIAKKDYLSL
sp P21770 PB2_INCBE sp P13877 PB2_INCJJ sp Q9IMP3 PB2_INCJH sp Q617C4 PB2_INCAA tr A0A193PPX7 A0A193PPX7_90RT0 tr A0A193PQ18 A0A193PQ18_90RT0	DLP SDK KVT FQDVSFQHPDLAVLRDEKTAIT KGYEALIKRLGTGDNDIPSLIAKKDYLSL DLP SDK KVT FQDVSFQHPDLAVLRDEKTAIT KGYEALIKRLGTGDNDIPSLIAKKDYLSL
sp P21770 PB2_INCBE sp P13877 PB2_INCJJ sp Q9IMP3 PB2_INCJH sp Q617C4 PB2_INCAA tr A0A193PPX7 A0A193PPX7_90RT0 tr A0A193PQ18 A0A193PQ18_90RT0 tr A0A475WMY1 A0A475WMY1_91NFB	DLP SDK KVT FQDVSFQHPDLAVLRDEKTAIT KGYEAL IKRLGTGDNDIPSLIAKKDYLSL DLP SDK KVT FQDVSFQHPDLAVLRDEKTAIT KGYEAL IKRLGTGDNDIPSLIAKKDYLSL DVSELE SQAOLMITYDTPKMWEMGTTRE LVDNTY ONVLKN LVTLKAOFLLGKEDM
sp P21770 PB2_INCBE sp P13877 PB2_INCJJ sp Q9IMP3 PB2_INCJJ sp Q6I7C4 PB2_INCJA tr A0A193PPX7 A0A193PPX7_90RT0 tr A0A193PQ18 A0A193PQ18_90RT0 tr A0A495WMY1 A0A495WMY1_91NFB tr A04495WMY1 A0A495WMY1_91NFB	DLP SDK KVT FQDVSFQHPDLAVLRDEKTAIT KGYEAL IKRLGTGDNDIPSLIAKKDYLSL DLP SDK KVT FQDVSFQHPDLAVLRDEKTAIT KGYEAL IKRLGTGDNDIPSLIAKKDYLSL DVSELE SQAQLMITTDTFKMMEMGTTKE LVDNTVOKVLKNLVT KAQFLLGKEDM
sp P21770 PB2_INCBE sp P13877 PB2_INCJJ sp Q9IMP3 PB2_INCJH sp Q617C4 PB2_INCAA tr A0A193PPX7 A0A193PPX7_90RT0 tr A0A193PQ18 A0A193PQ18_90RT0 tr A0A4Y5WMY1 A0A4Y5WMY1_91NFB tr Q4LD02 Q4LD02_91NFB	DLP SDK KVT FQDVSFQHPDLAVLRDEKTAIT KGYEAL IKRLGTGDNDIPSLIAKKDYLSL DLP SDK KVT FQDVSFQHPDLAVLRDEKTAIT KGYEAL IKRLGTGDNDIPSLIAKKDYLSL DVSELE SQAQLMITYDTPKMWEMGTTKELV <mark>DNTYQWVLK</mark> NLVTLKAQFLLGKEDM DVSELE SQAQLMITYDTPKMWEMGTTKELV <mark>DNTYQWVLK</mark> NLVTLKAQFLLGKEDM
sp P21770 PB2_INCBE sp P13877 PB2_INCJJ sp Q9IMP3 PB2_INCJH sp Q6I7C4 PB2_INCAA tr A0A193PPX7 A0A193PPX7_90RT0 tr A0A493PQ18 A0A193PQ18_90RT0 tr A0A4Y5WMY1 A0A4Y5WMY1_9INFB tr Q4LD02 Q4LD02_9INFB sp Q9QLL6 PB2_INBLE	DLP SDK KVT FQDVSFQHPDLAVLRDEKTAIT KGYEAL IKRLGTGDNDIPSLIAKKDYLSL DLP SDK KVT FQDVSFQHPDLAVLRDEKTAIT KGYEAL IKRLGTGDNDIPSLIAKKDYLSL DVSELE SQAQLMITYDTPKMMEMGTTKE LVQNTYQWVLKNLVTLKAQFLLG KEDM DVSELE SQAQLMITYDTPKMMEMGTTKE LVQNTYQWVLKNLVTLKAQFLLG KEDM
sp P21770 PB2_INCBE sp P13877 PB2_INCJJ sp Q9IMP3 PB2_INCJH sp Q6I7C4 PB2_INCAA tr A0A193PPX7]A0A193PPX7_9ORTO tr A0A193PQ18 A0A193PQ18_9ORTO tr A0A4Y5WMY1 A0A4Y5WMY1_9INFB tr Q4LD02 Q4LD02_9INFB sp Q9QLL6 PB2_INBLE tr U3S2T7 U3S277_9INFB	DLP SDKKVT FQDVSFQHPDLAVLRDEKTAIT KGYEAL IKRLGTGDNDIPSLIAKKDYLSL DLP SDKKVT FQDVSFQHPDLAVLRDEKTAIT KGYEAL IKRLGTGDNDIPSLIAKKDYLSL DVSELE SQAQLMITYDTFKMMEMGTTKE LVQNTYQWVLKNLVTLKAQFLLG KEDM DVSELE SQAQLMITYDTFKMMEMGTKE LVQNTYQWVLKNLVTLKAQFLLG KEDM DVSELE SQAQLMITYDTFKMMEMGTKE LVQNTYQWVLKNLVTLKAQFLLG KEDM
sp P21770 PB2_INCBE sp P13877 PB2_INCJJ sp Q9IMP3 PB2_INCJH sp Q617C4 PB2_INCAA tr A0A193PPX7 A0A193PPX7_90RT0 tr A0A193PQ18 A0A193PQ18_90RT0 tr A0A4Y5WMY1 A0A4Y5WMY1_91NFB tr Q4LD02 Q4LD02_91NFB sp Q9QLL6 PB2_INBLE tr U3S2T7 U3S2T7_91NFB	DLP SDKKVT FQDVSFQHPDLAVLRDEKTAIT KGYEAL IKRLGTGDNDIPSLIAKKDYLSL DLP SDKKVT FQDVSFQHPDLAVLRDEKTAIT KGYEAL IKRLGTGDNDIPSLIAKKDYLSL DVSELE SQAQLMITYDTPKMWEMGTTKE LVQNTYQWVLKNLVTLKAQFLLGKEDM DVSELE SQAQLMITYDTPKMWEMGTTKE LVQNTYQWVLKNLVTLKAQFLLGKEDM DVSELE SQAQLMITYDTPKMWEMGTTKE LVQNTYQWVLKNLVTLKAQFLLGKEDM
sp P21770 PB2_INCBE sp P13877 PB2_INCJJ sp Q9IMP3 PB2_INCJH sp Q6I7C4 PB2_INCAA tr A0A193PPX7 A0A193PPX7_90RT0 tr A0A193PQ18 A0A193PQ18_90RT0 tr A0A4Y5WMY1 A0A4Y5WMY1_9INFB tr Q4LD02 Q4LD02_9INFB sp Q9QLL6 PB2_INBLE tr U3S2T7 U3S2T7_9INFB sp P13875 PB2_INBAC	DLP SDK KVT FQDVSFQHPDLAV LRDEKTAIT KGY EAL IKR LGTGDNDIPS LIAKKDYLSL DLP SDK KVT FQDVSFQHPDLAV LRDEKTAIT KGY EAL IKR LGTGDNDIPS LIAKKDYLSL DLP SDK KVT FQDVSFQHPDLAV LRDEKTAIT KGY EAL IKR LGTGDNDIPS LIAKKDYLSL DLP SDK KVT FQDVSFQHPDLAV LRDEKTAIT KGY EAL IKR LGTGDNDIPS LIAKKDYLSL DLP SDK KVT FQDVSFQHPDLAV LRDEKTAIT KGY EAL IKR LGTGDNDIPS LIAKKDYLSL DLP SDK KVT FQDVSFQHPDLAV LRDEKTAIT KGY EAL IKR LGTGDNDIPS LIAKKDYLSL DLP SDK KVT FQDVSFQHPDLAV LRDEKTAIT KGY EAL IKR LGTGDNDIPS LIAKKDYLSL DVSELE SQAQLMITYDTFKMWEMGTKE LVQNTYQWVLKN LVT LKAQFLLG KEDM DVSELE SQAQLMITYDTFKMWEMGTKE LVQNTYQWVLKN LVT LKAQFLLG KEDM DVSELE SQAQLMITYDTFKMWEMGTKE LVQNTYQWVLKN LVT LKAQFLLG KEDM DVSELE SQAQLMITYDTFKMWEMGTKE LVQNTYQWVLKN LVT LKAQFLLG KEDM
sp P21770 PB2_INCBE sp P13877 PB2_INCJJ sp Q9IMP3 PB2_INCJH sp Q617C4 PB2_INCAA tr A0A193PPX7 A0A193PPX7_90RT0 tr A0A193PQ18 A0A193PQ18_90RT0 tr A0A4Y5WMY1 A0A4Y5WMY1_91NFB tr Q4LD02 Q4LD02_91NFB sp Q9QLL6 PB2_INBLE tr U3S2T7 U3S2T7_91NFB sp P13875 PB2_INBAC sp O36431 PB2_INBP9	DLP SDK KVT FQDVSFQHPDLAVLRDEKTAIT KGYEAL IKRLGTGDNDIPSLIAKKDYLSL DLP SDK KVT FQDVSFQHPDLAVLRDEKTAIT KGYEAL IKRLGTGDNDIPSLIAKKDYLSL DVSELE SQAQLMITYDTPKMWEMGTTKE LVQNTYQWVLKNLVTLKAQFLLG KEDM DVSELE SQAQLMITYDTPKMWEMGTTKE LVQNTYQWVLKNLVTLKAQFLLG KEDM DVSELE SQAQLMITYDTPKMWEMGTTKE LVQNTYQWVLKNLVTLKAQFLLG KEDM DVSELE SQAQLMITYDTPKMWEMGTTKE LVQNTYQWVLKNLVTLKAQFLLG KEDM DVSELE SQAQLMITYDTPKMWEMGTTKE LVQNTYQWVLKNLVTLKAQFLLG KEDM
sp P21770 PB2_INCBE sp P13877 PB2_INCJJ sp Q9IMP3 PB2_INCJH sp Q617C4 PB2_INCJH tr A0A193PPX7 A0A193PPX7_90RT0 tr A0A193PQ18 A0A193PQ18_90RT0 tr A0A4Y5WMY1 A0A4Y5WMY1_91NFB tr Q4LD02 Q4LD02_91NFB sp Q9QLL6 PB2_INBLE tr U3S2T7 U3S2T7_91NFB sp P13875 PB2_INBAC sp O36431 PB2_INBP9 sp O36431 PB2_T7355	DLP SDKKVT FQDVSFQHPDLAVLRDEKTAIT KGYEAL IKRLGTGDNDIPSLIAKKDYLSL DLP SDKKVT FQDVSFQHPDLAVLRDEKTAIT KGYEAL IKRLGTGDNDIPSLIAKKDYLSL DVSELE SQAQLMITYDTPKMWEMGTTKE LVQNTYQWVLKNLVTLKAQFLLGKEDM DVSELE SQAQLMITYDTPKMWEMGTTKE LVQNTYQWVLKNLVTLKAQFLLGKEDM DVSELE SQAQLMITYDTPKMWEMGTTKE LVQNTYQWVLKNLVTLKAQFLLGKEDM DVSELE SQAQLMITYDTPKMWEMGTTKE LVQNTYQWVLKNLVTLKAQFLLGKEDM DVSELE SQAQLMITYDTPKMWEMGTTKE LVQNTYQWVLKNLVTLKAQFLLGKEDM DVSELE SQAQLMITYDTPKMWEMGTKE LVQNTYQWVLKNLVTLKAQFLLGKEDM
sp P21770 PB2_INCBE sp P13877 PB2_INCJJ sp Q9IMP3 PB2_INCJH sp Q6I7C4 PB2_INCAA tr A0A193PPX7 A0A193PPX7_9ORTO tr A0A193PQ18 A0A193PQ18_9ORTO tr A0A4Y5WMY1 A0A4Y5WMY1_9INFB tr Q4LD02 Q4LD02 9INFB sp Q9QLL6 PB2_INBLE tr U3S2T7 U3S2T7_9INFB sp P13875 PB2_INBAC sp 036431 PB2_INBP9 sp Q1PUC9 PB2_I73A5	DLP SDKKVT FQDVSFQHPDLAVLRDEKTAIT KGYEAL IKRLGTGDNDIPSLIAKKDYLSL DLP SDKKVT FQDVSFQHPDLAVLRDEKTAIT KGYEAL IKRLGTGDNDIPSLIAKKDYLSL DVSELE SQAQLMITYDTFKMMEMGTTKE LVQNTYQWVLKNLVTLKAQFLLG KEDM DVSELE SQAQLMITYDTFKMMEMGTTKE LVQNTYQWVLKNLVTLKAQFLLG KEDM
<pre>sp P21770 PB2_INCBE sp P13877 PB2_INCJJ sp Q9IMP3 PB2_INCJJ sp Q6I7C4 PB2_INCAA tr A0A193PPX7 A0A193PPX7_90RT0 tr A0A193PQ18 A0A193PQ18_90RT0 tr A0A4Y5WMY1 A0A4Y5WMY1_91NFB tr Q4LD02 Q4LD02_91NFB sp Q9QLL6 PB2_INBLE tr U3S2T7 U3S2T7_91NFB sp P13875 PB2_INBLC sp 036431 PB2_INBP9 sp Q1PUC9 PB2_I73A5 sp Q6XU90 PB2_I67A0</pre>	DLP SDK KVT FQDVSFQHPDLAVLRDEKTAIT KGYEAL IKRLGTGDNDIPSLIAKKDYLSL DLP SDK KVT FQDVSFQHPDLAVLRDEKTAIT KGYEAL IKRLGTGDNDIPSLIAKKDYLSL DVSELE SQAQLMITYDTPKMWEMGTTKE LVQNTYQWVLKNLVTLKAQFLLG KEDM DVSELE SQAQLMITYDTPKMWEMGTTKE LVQNTYQWVLKNLVTLKAQFLLG KEDM DVSELE SQAQLMITYDTPKMWEMGTKE LVQNTYQWVLKNLVTLKAQFLLG KEDM
sp P21770 PB2_INCBE sp P13877 PB2_INCJJ sp Q9IMP3 PB2_INCJH sp Q617C4 PB2_INCJH tr A0A193PPX7 A0A193PPX7_90RT0 tr A0A193PQ18 A0A193PQ18_90RT0 tr A0A4Y5WMY1 A0A4Y5WMY1_91NFB tr Q4LD02 Q4LD02_91NFB sp Q9QLL6 PB2_INBLE tr U3S2T7 U3S2T7_91NFB sp P13875 PB2_INBAC sp O36431 PB2_INBAC sp O36431 PB2_INBAP9 sp Q1PUC9 PB2_I73A5 sp Q6XU90 PB2_I67A0 sp F0DOG6 PB2S1_I34A1	DLP SDK KVT FQDVSFQHPDLAV LRDEKTAIT KGY EAL IKR LGT GDNDIPS LIAKKDYLSL DLP SDK KVT FQDVSFQHPDLAV LRDEKTAIT KGY EAL IKR LGT GDNDIPS LIAKKDYLSL DLP SDK KVT FQDVSFQHPDLAV LRDEKTAIT KGY EAL IKR LGT GDNDIPS LIAKKDYLSL DLP SDK KVT FQDVSFQHPDLAV LRDEKTAIT KGY EAL IKR LGT GDNDIPS LIAKKDYLSL DLP SDK KVT FQDVSFQHPDLAV LRDEKTAIT KGY EAL IKR LGT GDNDIPS LIAKKDYLSL DLP SDK KVT FQDVSFQHPDLAV LRDEKTAIT KGY EAL IKR LGT GDNDIPS LIAKKDYLSL DVSELE SQAQLM ITYDTPKMWEMGT KE LVQNTY QWVLKN LVT LKAQFLLG KEDM DVSELE SQAQLM ITYDTPKMWEMGT TKE LVQNTY QWVLKN LVT LKAQF
sp P21770 PB2_INCBE sp P13877 PB2_INCJJ sp Q9IMP3 PB2_INCJH sp Q6I7C4 PB2_INCAA tr A0A193PPX7]A0A193PPX7_9ORTO tr A0A193PQ18 A0A193PQ18_9ORTO tr A0A4Y5WMY1 A0A4Y5WMY1_9INFB tr Q4LD02 Q4LD02_9INFB sp Q9QLL6 PB2_INBLE tr U32T7 U32T7_9INFB sp P13875 PB2_INBAC sp 036431 PB2_INBP9 sp Q1PUC9 PB2_I73A5 sp Q6XU90 PB2_I67A0 sp P0D066 PB251_I34A1 sp 0032F5 PB2_183A4	DLP SDKKVT FQDVSFQHPDLAVLRDEKTAIT KGYEAL IKRLGTGDNDIPSLIAKKDYLSL DLP SDKKVT FQDVSFQHPDLAVLRDEKTAIT KGYEAL IKRLGTGDNDIPSLIAKKDYLSL DVSELE SQAQLMITYDTFKMMEMGTTKE LVQNTYQWVLKNLVTLKAQFLLGKEDM DVSELE SQAQLMITYDTFKMMEMGTKE LVQNTYQWVLKNLVTLKAQFLLGKEDM DVSELE SQAQLMITYDTFKMMEMGTKE LVQNTYQWVLKNLVTLKAQFLGKEDM DVSELE SQAQLMITYDTFKMMEMGTKE LVQNTYQWVLKNLVTLKAQFLGKEDM DVSELE SQAQLMITYDTFKMMEMGTKE LVQNTYQWVLKNLVTLKAQF
sp P21770 PB2_INCBE sp P13877 PB2_INCJJ sp Q9IMP3 PB2_INCJJ sp Q6I7C4 PB2_INCJA tr A0A193PPX7 A0A193PPX7_90RT0 tr A0A193PP18 A0A193PQ18_90RT0 tr A0A4Y5WMY1 A0A4Y5WMY1_91NFB tr Q4LD02 Q4LD02_91NFB sp Q9QLL6 PB2_INBLE tr U3S2T7 U3S2T7_91NFB sp P13875 PB2_INBAC sp 036431 PB2_INBP9 sp Q1PUC9 PB2_I73A5 sp Q6XU90 PB2_I67A0 sp P0D066 PB251_I34A1 sp 00A2F5 PB2_I83A4	DLP SDK KVT FQDVSFQHPDLAVLRDEKTAIT KGYEAL IKRLGTGDNDIPSLIAKKDYLSL DLP SDK KVT FQDVSFQHPDLAVLRDEKTAIT KGYEAL IKRLGTGDNDIPSLIAKKDYLSL DVSELE SQAQLMITYDTPKMWEMGTTKE LVQNTYQWVLKNLVTLKAQFLLG KEDM DVSELE SQAQLMITYDTPKMWEMGTKE LVQNTYQWVLKNLVTLKAQFLG KEDM DVSELE SQAQLMITYDTPKMWEMGTKE LVQNTYQWVLKNLVTLKAQFLG KEDM DVSELE SQAQLMITYDTPKMWEMGTKE LVQNTYQWVLKNLVTLKAQFSQN PTML EVSETQGTEKLTITYSSSMMWE ING PESVLVNTYQWI IRNWETVKIQWSQN PTML EVSETQGTEKLTITYSSSMMWE ING PESVLVNTYQWI IRNWETVKIQWSQN PTML EVSETQGTEKLTITYSSSMMWE ING PESVLVNTYQWI IRNWETVKIQW
sp P21770 PB2_INCBE sp P13877 PB2_INCJJ sp Q9IMP3 PB2_INCJH sp Q6I7C4 PB2_INCAA tr A0A193PPX7]A0A193PPX7_9ORTO tr A0A193PQ18 A0A193PQ18_9ORTO tr A0A4Y5WMY1 A0A4Y5WMY1_9INFB tr Q4LD02 Q4LD02_9INFB sp Q9QLL6 PB2_INBLE tr U3S2T7 U3S2T7_9INFB sp P13875 PB2_INBAC sp 036431 PB2_INBP9 sp Q1PUC9 PB2_I73A5 sp Q6XU90 PB2_I67A0 sp P0D066 PB251_I34A1 sp Q0A2F5 PB2_I83A4 sp Q20NV1 PB2_I80AD	DLP SDK KVT FQDVSFQHPDLAVLRDEKTAIT KGYEALIKRLGTGDNDIPSLIAKKDYLSL DLP SDK KVT FQDVSFQHPDLAVLRDEKTAIT KGYEALIKRLGTGDNDIPSLIAKKDYLSL DVSELE SQAQLMITYDTFKMMEMGTTKE LVQNTYQWVLKNLVTLKAQFLLG KEDM DVSELE SQAQLMITYDTFKMMEMGTTKE LVQNTYQWVLKNLVTLKAQFSQN FML EVSETQGTERLTITYSSSMMME ING PESVLVNTYQWI IRNWETVKIQWSQN PTML EVSETQGTERLTITYSSSMMME ING PESVLVNTYQWI IRNWETVKIQWSQN PTML EVSETQGTERLTITYSSSMMME ING PESVLVNTYQWI IRNWETVKIQW
sp P21770 PB2_INCBE sp P13877 PB2_INCJJ sp Q9IMP3 PB2_INCJJ sp Q6I7C4 PB2_INCAA tr A0A193PPX7 A0A193PPX7_9ORTO tr A0A193PQ18 A0A193PQ18_9ORTO tr A0A4Y5WMY1 A0A4Y5WMY1_9INFB tr Q4LD02 Q4LD02_9INFB sp Q9QLL6 PB2_INBLE tr U3S2T7 U3S2T7_9INFB sp P13875 PB2_INBAC sp 036431 PB2_INBP9 sp Q1PUC9 PB2_I73A5 sp Q6XU90 PB2_I67A0 sp P0DG6 PB251_I34A1 sp Q0A2F5 PB2_I83A4 sp Q20NV1 PB2_I80AD sp Q0A438 PB2_I49A1	DLP SDK KVT FQDVSFQHPDLAVLRDEKTAIT KGYEAL IKRLGTGDNDIPSLIAKKDYLSL DLP SDK KVT FQDVSFQHPDLAVLRDEKTAIT KGYEAL IKRLGTGDNDIPSLIAKKDYLSL DVSELE SQAQLMITYDTPKMWEMGTTKE LVQNTYQWVLKNLVTLKAQFLLG KEDM DVSELE SQAQLMITYDTPKMWEMGTKE LVQNTYQWVLKNLVTLKAQFSQN PTML EVSETQGTERLTITYSSSMMWE ING PESVLVNTYQWI IRNWETVKIQWSQN PTML EVSETQGTERLTITYSSSMMWE ING PESVLVNTYQWI IRNWETVKIQWSQN PTML EVSETQGTERLTITYSSSMMWE ING PESVLVNTYQWI IRNWETVKIQW
<pre>sp P21770 PB2_INCBE sp P13877 PB2_INCJJ sp Q9IMP3 PB2_INCJJ sp Q6I7C4 PB2_INCAA tr A0A193PPX7 A0A193PPX7_9ORTO tr A0A193PQ18 A0A193PQ18_9ORTO tr A0A4Y5WMY1 A0A4Y5WMY1_9INFB tr Q4LD02 Q4LD02_9INFB sp Q9QLL6 PB2_INBLE tr U3S2T7 U3S2T7_9INFB sp P13875 PB2_INBAC sp 036431 PB2_INBP9 sp Q1PUC9 PB2_I73A5 sp Q6XU90 PB2_I73A5 sp Q0A2F5 PB2_IS3A4 sp Q0A2F5 PB2_IS3A4 sp Q0A438 PB2_I49A1</pre>	DLP SDK KVT FQDVSFQHPDLAV LRDEKTAIT KGYEAL IKRLGTGDNDIPS LIAKKDYLSL DLP SDK KVT FQDVSFQHPDLAV LRDEKTAIT KGYEAL IKRLGTGDNDIPS LIAKKDYLSL DVSELE SQAQLMITYDTPKMWEMGTKE LVQNTY QWVLKNLVT LKAQFLLG KEDM DVSELE SQAQLMITYDTPKMWEMGTKE LVQNTY QWVLKNLVT LKAQF
<pre>sp P21770 PB2_INCBE sp P13877 PB2_INCJJ sp Q9IMP3 PB2_INCJH sp Q6I7C4 PB2_INCAA tr A0A193PPX7 A0A193PPX7_9ORTO tr A0A193PQ18 A0A193PQ18_9ORTO tr A0A4Y5WMY1 A0A4Y5WMY1_9INFB tr Q4LD02 Q4LD02_9INFB sp Q9QLL6 PB2_INBLE tr U3S2T7 U3S2T7_9INFB sp P13875 PB2_INBAC sp 036431 PB2_INBAC sp Q6XU90 PB2_I67A0 sp P0DG6 PB25 I3A41 sp Q0A2F5 PB2_I83A4 sp Q20NV1 PB2_I60AD sp Q0A438 PB2_I49A1</pre>	DLP SDKKVT FQDVSFQHPDLAVLRDEKTAIT KGYEAL IKRLGTGDNDIPSLIAKKDYLSL DLP SDKKVT FQDVSFQHPDLAVLRDEKTAIT KGYEAL IKRLGTGDNDIPSLIAKKDYLSL DVSLLE SQAQLMITYDTFKMMEMGTTKE LVQNTYQWVLKNLVTLKAQFLLGKEDM DVSELE SQAQLMITYDTFKMMEMGTKE LVQNTYQWVLKNLVTLKAQF SQN FTML EVSETQGTERLTITYSSSMMWE ING PESVLVNTYQWI IRNWETVKIQW
<pre>sp P21770 PB2_INCBE sp P13877 PB2_INCJJ sp Q9IMP3 PB2_INCJJ sp Q6I7C4 PB2_INCAA tr A0A193PPX7 A0A193PPX7_9ORTO tr A0A193PP18 A0A193PP18_9ORTO tr A0A4Y5WMY1 A0A4Y5WMY1_9INFB tr Q4LD02 Q4LD02_9INFB sp Q9QLL6 PB2_INBLE tr U3S2T7 U3S2T7_9INFB sp P13875 PB2_INBAC sp 036431 PB2_INBP9 sp Q1PUC9 PB2_I73A5 sp Q6KU90 PB2_I73A5 sp Q6KU90 PB2_I67A0 sp P0D066 PB251_I34A1 sp Q0A2F5 PB2_I83A4 sp Q0A438 PB2_I49A1</pre>	DLP SDKKVT FQDVSFQHPDLAVLRDEKTAIT KGYEAL IKRLGTGDNDIPSLIAKKDYLSL DLP SDKKVT FQDVSFQHPDLAVLRDEKTAIT KGYEAL IKRLGTGDNDIPSLIAKKDYLSL DVSELE SQAQLMITYDTPKMWEMGTTKE LVDNTYQWVLKNLVTLKAQFLLGKEDM DVSELE SQAQLMITYDTPKMWEMGTTKE LVDNTYQWVLKNLVTLKAQFLLGKEDM DVSELE SQAQLMITYDTPKMWEMGTTKE LVDNTYQWVLKNLVTLKAQFLLGKEDM DVSELE SQAQLMITYDTPKMWEMGTTKE LVDNTYQWVLKNLVTLKAQFLLGKEDM DVSELE SQAQLMITYDTPKMWEMGTTKE LVDNTYQWVLKNLVTLKAQFLLGKEDM DVSELE SQAQLMITYDTPKMWEMGTTKE LVDNTYQWVLKNLVTLKAQFLLGKEDM DVSELE SQAQLMITYDTPKMWEMGTKE LVDNTYQWVLKNLVTLKAQFLLGKEDM DVSELE SQAQLMITYDTPKMWEMGTKE LVDNTYQWVLKNLVTLKAQFLGKEDM DVSELE SQAQLMITYDTPKMWEMGTKE LVDNTYQWVLKNLVTLKAQFSQNPTML EVSETQGTERLTITYSSSMMWE ING PESVLVNTYQWI IRNWETVKIQWSQNPTML EVSETQGTERLTITYSSSMMWE ING PESVLVNTYQWI IRNWETVKIQW
sp P21770 PB2_INCBE sp P13877 PB2_INCJJ sp Q9IMP3 PB2_INCJH sp Q6I7C4 PB2_INCAA tr A0A193PPX7]A0A193PPX7_9ORTO tr A0A193PQ18 A0A193PQ18_9ORTO tr A0A4Y5WMY1 A0A4Y5WMY1_9INFB tr Q4LD02 Q4LD02_9INFB sp Q9QLL6 PB2_INBLE tr U3S2T7 U3S2T7_9INFB sp P13875 PB2_INBAC sp 036431 PB2_INBP9 sp Q1PUC9 PB2_I73A5 sp Q6XU90 PB2_I67A0 sp P0D066 PB251_I34A1 sp Q0A2F5 PB2_I83A4 sp Q0A438 PB2_I49A1	DLP SDKKVT FQDVSFQHPDLAVLRDEKTAIT KGYEAL IKRLGTGDNDIPSLIAKKDYLSL DLP SDKKVT FQDVSFQHPDLAVLRDEKTAIT KGYEAL IKRLGTGDNDIPSLIAKKDYLSL DVSELE SQAQLMITYDTFKMWEMGTTKE LVQNTYQWVLKNLVTLKAQFLLG KEDM DVSELE SQAQLMITYDTFKMWEMGTKE LVQNTYQWVLKNLVTLKAQFSQN FTML EVSETQGTERLTITYSSSMMWE ING PESVLVNTYQWI IRNWETVKIQWSQN PTML EVSETQGTERLTITYSSSMMWE ING PESVLVNTYQWI IRNWETVKIQW
<pre>sp P21770 PB2_INCBE sp P13877 PB2_INCJJ sp Q9IMP3 PB2_INCJH sp Q6I7C4 PB2_INCAA tr A0A193PPX7]A0A193PPX7_9ORTO tr A0A193PQ18 A0A193PQ18_9ORTO tr A0A4Y5WMY1 A0A4Y5WMY1_9INFB tr Q4LD02 Q4LD02_9INFB sp Q9QLL6 PB2_INBLE tr U3S2T7 U3S2T7_9INFB sp P13875 PB2_INBAC sp Q6431 PB2_INBP9 sp Q1PUC9 PB2_I73A5 sp Q6XU90 PB2_I67A0 sp P0DG6 PB251_I34A1 sp Q0A2F5 PB2_I83A4 sp Q0A438 PB2_I49A1</pre>	DLP SDKKVT FQDVSFQHPDLAVLRDEKTAIT KGYEAL IKRLGTGDNDIPSLIAKKDYLSL DLP SDKKVT FQDVSFQHPDLAVLRDEKTAIT KGYEAL IKRLGTGDNDIPSLIAKKDYLSL DVSELE SQAQLMITYDTPKMWEMGTKE LVQNTYQWVLKNLVTLKAQFLLGKEDM DVSELE SQAQLMITYDTPKMWEMGTKE LVQNTYQWVLKNLVTLKAQFSQNPTML EVSETQGTERLTITYSSMMWE ING PESVLVNTYQWI IRNWETVKIQWSQNPTML EVSETQGTERLTITYSSMMWE ING PESVLVNTYQWI IRNWETVKIQW
<pre>sp P21770 PB2_INCBE sp P13877 PB2_INCJJ sp Q9IMP3 PB2_INCJJ sp Q6I7C4 PB2_INCAA tr A0A193PPX7]A0A193PPX7_9ORTO tr A0A193PPU8 A0A193PPU8_9ORTO tr A0A4Y5WMY1 A0A4Y5WMY1_9INFB tr Q4LD02 Q4LD02_9INFB sp Q9QLL6 PB2_INBLE tr U3S2T7 U3S2T7_9INFB sp P13875 PB2_INBAC sp 036431 PB2_INBP9 sp Q1PUC9 PB2_I73A5 sp Q6XU90 PB2_I67A0 sp P0D0G6 PB251_I34A1 sp Q0A2F5 PB2_I83A4 sp Q0A438 PB2_I49A1</pre>	DLP SDK KVT FQDVSFQHPDLAVLRDEKTAIT KGYEAL IKRLGTGDNDIPSLIAKKDYLSL DLP SDK KVT FQDVSFQHPDLAVLRDEKTAIT KGYEAL IKRLGTGDNDIPSLIAKKDYLSL DVSELE SQAQLMITYDTPKMWEMGTKELVQNTYQWVLKNLVTLKAQFLLG KEDM DVSELE SQAQLMITYDTPKMWEMGTKELVQNTYQWVLKNLVTLKAQFLLG KEDM DVSELE SQAQLMITYDTPKMWEMGTKELVQNTYQWVLKNLVTLKAQFLLG KEDM DVSELE SQAQLMITYDTPKMWEMGTKELVQNTYQWVLKNLVTLKAQFLLG KEDM DVSELE SQAQLMITYDTPKMWEMGTKELVQNTYQWVLKNLVTLKAQFLLG KEDM DVSELE SQAQLMITYDTPKMWEMGTKELVQNTYQWVLKNLVTLKAQFLLG KEDM DVSELE SQAQLMITYDTPKMWEMGTKELVQNTYQWVLKNLVTLKAQF
<pre>sp P21770 PB2_INCBE sp P13877 PB2_INCJJ sp Q9IMP3 PB2_INCJH sp Q6I7C4 PB2_INCAA tr A0A193PPX7]A0A193PPX7_9ORTO tr A0A193PQ18 A0A193PQ18_9ORTO tr A0A4Y5WMY1 A0A4Y5WMY1_9INFB tr Q4LD02 Q4LD02_9INFB sp Q9QLL6 PB2_INBLE tr U3S2T7 U3S2T7_9INFB sp P13875 PB2_INBAC sp 036431 PB2_INBAC sp 036431 PB2_INBP9 sp Q1PUC9 PB2_I73A5 sp Q6XU90 PB2_I67A0 sp P0DG6 PB251_I34A1 sp Q0A2F5 PB2_I83A4 sp Q0A438 PB2_I49A1</pre>	DLP SDKKVT FQDVSFQHPDLAVLRDEKTAIT KGYEAL IKRLGTGDNDIPSLIAKKDYLSL DLP SDKKVT FQDVSFQHPDLAVLRDEKTAIT KGYEAL IKRLGTGDNDIPSLIAKKDYLSL DVSLLE SQAQLMITYDTFKMMEMGTTKE LVQNTYQWVLKNLVTLKAQFLLGKEDM DVSELE SQAQLMITYDTFKMMEMGTKE LVQNTYQWVLKNLVTLKAQFLLGKEDM DVSELE SQAQLMITYDTFKMMEMGTKE LVQNTYQWVLKNLVTLKAQF
<pre>sp P21770 PB2_INCBE sp P13877 PB2_INCJJ sp Q9IMP3 PB2_INCJJ sp Q6I7C4 PB2_INCAA tr A0A193PPX7]A0A193PPX7_9ORTO tr A0A193PPU8 A0A193PPU8_9ORTO tr A0A4Y5WMY1 A0A4Y5WMY1_9INFB tr Q4LD02 Q4LD02_9INFB sp Q9QLL6 PB2_INBLE tr U3S2T7 U3S2T7_9INFB sp P13875 PB2_INBAC sp 036431 PB2_INBP9 sp Q1PUC9 PB2_I73A5 sp Q6XU90 PB2_I67A0 sp P0D0G6 PB251_I34A1 sp Q0A2F5 PB2_I83A4 sp Q0A438 PB2_I49A1</pre>	DLP SDKKVT FQDVSFQHPDLAVLRDEKTAIT KGYEAL IKRLGTGDNDIPSLIAKKDYLSL DLP SDKKVT FQDVSFQHPDLAVLRDEKTAIT KGYEAL IKRLGTGDNDIPSLIAKKDYLSL DVSELE SQAQLMITYDTPKMWEMGTTKE LVDNTYQWVLKNLVTLKAQFLLGKEDM DVSELE SQAQLMITYDTPKMWEMGTTKE LVDNTYQWVLKNLVTLKAQFLLGKEDM DVSELE SQAQLMITYDTPKMWEMGTTKE LVDNTYQWVLKNLVTLKAQFLLGKEDM DVSELE SQAQLMITYDTPKMWEMGTTKE LVDNTYQWVLKNLVTLKAQFLLGKEDM DVSELE SQAQLMITYDTPKMWEMGTTKE LVDNTYQWVLKNLVTLKAQFLLGKEDM DVSELE SQAQLMITYDTPKMWEMGTTKE LVDNTYQWVLKNLVTLKAQFLLGKEDM DVSELE SQAQLMITYDTPKMWEMGTKE LVDNTYQWVLKNLVTLKAQFLLGKEDM EVSETQGTERLTITYSSSMMWE ING PESVLVNTYQWI IRNWETVKIQWSQN PTML EVSETQGTERLTITYSSSMMWE ING PESVLVNTYQWI IRNWETVKIQWSQN PTML EVSETQGTERLTITYSSSMMWE ING PESVLVNTYQWI IRNWETVKIQW
<pre>sp P21770 PB2_INCBE sp P13877 PB2_INCJJ sp Q9IMP3 PB2_INCJH sp Q6I7C4 PB2_INCAA tr A0A193PPX7 A0A193PPX7_9ORTO tr A0A193PQ18 A0A193PQ18_9ORTO tr A0A4Y5WMY1 A0A4Y5WMY1_9INFB tr Q4LD02 Q4LD02_9INFB sp Q9QLL6 PB2_INBLE tr U3S2T7 U3S2T7_9INFB sp P13875 PB2_INBAC sp 036431 PB2_INBP9 sp Q1PUC9 PB2_I73A5 sp Q6XU90 PB2_I67A0 sp P0D066 PB251_I34A1 sp Q0A2F5 PB2_I83A4 sp Q0A438 PB2_I49A1</pre>	DLP SDKKVT FQDVSFQHPDLAVLRDEKTAIT KGYEAL IKRLGTGDNDIPSLIAKKDYLSL DLP SDKKVT FQDVSFQHPDLAVLRDEKTAIT KGYEAL IKRLGTGDNDIPSLIAKKDYLSL DVSELE SQAQLMITYDTFKMWEMGTTKE LVQNTYQWVLKNLVTLKAQFLLGKEDM DVSELE SQAQLMITYDTFKMWEMGTKEL VQNTYQWVLKNLVTLKAQFLLGKEDM DVSELE SQAQLMITYDTFKMWEMGTKEL VQNTYQWVLKNLVTLKAQFLLGKEDM DVSELE SQAQLMITYDTFKMWEMGTKEL VQNTYQWVLKNLVTLKAQFLLGKEDM DVSELE SQAQLMITYDTFKMWEMGTKEL VQNTYQWVLKNLVTLKAQFLLGKEDM DVSELE SQAQLMITYDTFKMWEMGTKEL VQNTYQWVLKNLVTLKAQFSQNFML EVSETQGTERLTITYSSSMMWE ING PESVLVNTYQWILKNLVTLKAQFSQNFML EVSETQGTERLTITYSSSMMWE ING PESVLVNTYQWI IRNWETVKIQWSQNFML EVSETQGTERLTITYSSSMMWE ING PESVLVNTYQWI IRNWETVKIQWSQNFML EVSETQGTEKLTITYSSSMMWE ING PESVLVNTYQWI IRNWETVKIQW
<pre>sp P21770 PB2_INCBE sp P13877 PB2_INCJJ sp Q9IMP3 PB2_INCJH sp Q6I7C4 PB2_INCAA tr A0A193PPX7]A0A193PPX7_9ORTO tr A0A193PP18 A0A193PQ18_9ORTO tr A0A4Y5WMY1 A0A4Y5WMY1_9INFB tr Q4LD02 Q4LD02_9INFB sp Q9QLL6 PB2_INBLE tr U3S2T7 U3S2T7_9INFB sp P13875 PB2_INBAC sp Q6431 PB2_INBP9 sp Q1PUC9 PB2_I73A5 sp Q6XU90 PB2_I67A0 sp P0DG6 PB251_I34A1 sp Q0A2F5 PB2_I83A4 sp Q0A438 PB2_I49A1 sp P13877 PB2_INCBE sp P13877 PB2_INCBE sp P13877 PB2_INCJJ sp Q9IMP3 PB2_INCJH sp Q6I7C4 PB2_INCAA tr A0A193PPX7 A0A193PPX7_9ORTO</pre>	DLP SDKKVT FQDVSFQHPDLAVLRDEKTAIT KGYEAL IKRLGTGDNDIPSLIAKKDYLSL DLP SDKKVT FQDVSFQHPDLAVLRDEKTAIT KGYEAL IKRLGTGDNDIPSLIAKKDYLSL DVSELE SQAQLMITYDTPKMWEMGTTKE LVQNTYQWVLKNLVTLKAQFLLGKEDM DVSELE SQAQLMITYDTPKMWEMGTTKE LVQNTYQWVLKNLVTLKAQFLLGKEDM DVSELE SQAQLMITYDTPKMWEMGTTKE LVQNTYQWVLKNLVTLKAQFLLGKEDM DVSELE SQAQLMITYDTPKMWEMGTTKE LVQNTYQWVLKNLVTLKAQFLLGKEDM DVSELE SQAQLMITYDTPKMWEMGTTKE LVQNTYQWVLKNLVTLKAQFLLGKEDM DVSELE SQAQLMITYDTPKMWEMGTTKE LVQNTYQWVLKNLVTLKAQFLLGKEDM DVSELE SQAQLMITYDTPKMWEMGTKE LVQNTYQWVLKNLVTLKAQFLLGKEDM DVSELE SQAQLMITYDTPKMWEMGTKE LVQNTYQWVLKNLVTLKAQFSQNPTML EVSETQGTERLTITYSSMMWE INGPESVLVNTYQWI IRNWETVKIQWSQNPTML EVSETQGTERLTITYSSMMWE INGPESVLVNTYQWI IRNWETVKIQWSQNPTML EVSETQGTERLTITYSSMMWE INGPESVLVNTYQWI IRNWETVKIQW
<pre>sp P21770 PB2_INCBE sp P13877 PB2_INCJJ sp Q9IMP3 PB2_INCJJ sp Q6I7C4 PB2_INCAA tr A0A193PPX7]A0A193PPX7_9ORTO tr A0A193PPX7]A0A193PPX7_9ORTO tr A0A193PPX8]A0A193PPX8_9ORTO tr A0A4Y5WMY1 A0A4Y5WMY1_9INFB tr Q4LD02 Q4LD02_9INFB sp Q9QLL6 PB2_INBLE tr U3S2T7 U3S2T7_9INFB sp P13875 PB2_INBAC sp 036431 PB2_INBP9 sp Q1PUC9 PB2_I73A5 sp Q6XU90 PB2_I67A0 sp P0D066 PB251_I34A1 sp Q0A2F5 PB2_I83A4 sp Q0A438 PB2_I49A1 sp P21770 PB2_INCBE sp P13877 PB2_INCJB sp Q9IMP3 PB2_INCJH sp Q6I7C4 PB2_INCAA tr A0A193PPX7 A0A193PPX7_9ORTO tr A0A193PPX7 A0A193PPX7_9ORTO</pre>	DLP SDK KVT FQDVSFQHPDLAVLRDEKTAIT KGYEAL IKRLGTGDNDIPSLIAKKDYLSL DLP SDK KVT FQDVSFQHPDLAVLRDEKTAIT KGYEAL IKRLGTGDNDIPSLIAKKDYLSL DVSELE SQAQLMITYDTPKMWEMGTTKELVQNTYQWVLKNLVTLKAQFLLG KEDM DVSELE SQAQLMITYDTPKMWEMGTTKELVQNTYQWVLKNLVTLKAQFLLG KEDM DVSELE SQAQLMITYDTPKMWEMGTTKELVQNTYQWVLKNLVTLKAQFLLG KEDM DVSELE SQAQLMITYDTPKMWEMGTTKELVQNTYQWVLKNLVTLKAQFLLG KEDM DVSELE SQAQLMITYDTPKMWEMGTTKELVQNTYQWVLKNLVTLKAQFLLG KEDM DVSELE SQAQLMITYDTPKMWEMGTTKELVQNTYQWVLKNLVTLKAQFLLG KEDM DVSELE SQAQLMITYDTPKMWEMGTTKELVQNTYQWVLKNLVTLKAQFSQNPTML EVSETQGTERLTITYSSSMMWE INGPESVLVNTYQWI IRNWETVKIQWSQNPTML EVSETQGTERLTITYSSSMMWE INGPESVLVNTYQWI IRNWETVKIQWSQNPTML EVSETQGTERLTITYSSSMMWE INGPESVLVNTYQWI IRNWETVKIQW
<pre>sp P21770 PB2_INCBE sp P13877 PB2_INCJJ sp Q9IMP3 PB2_INCJH sp Q6I7C4 PB2_INCAA tr A0A193PPX7 A0A193PPX7_9ORTO tr A0A193PQ18 A0A193PQ18_9ORTO tr A0A4Y5WMY1 A0A4Y5WMY1_9INFB tr Q4LD02 Q4LD02_9INFB sp Q9QLL6 PB2_INBLE tr U3S2T7 U3S2T7_9INFB sp P13875 PB2_INBAC sp 036431 PB2_INBAC sp 036431 PB2_INBP9 sp Q1PUC9 PB2_I73A5 sp Q6XU90 PB2_I67A0 sp P0DG6 PB251_I34A1 sp Q0A2F5 PB2_I83A4 sp Q0A438 PB2_I49A1 sp Q0A438 PB2_I49A1 sp Q0A438 PB2_I49A1 sp Q0A438 PB2_INCBE sp P13877 PB2_INCJH sp Q9IMP3 PB2_INCJH sp Q6I7C4 PB2_INCAA tr A0A193PPX7 A0A193PPX7_9ORTO tr A0A193PQ18 A0A193PQ18_9ORTO</pre>	DLP SDKKVT FQDVSFQHPDLAVLRDEKTAIT KGYEAL IKRLGTGDNDIPSLIAKKDYLSL DLP SDKKVT FQDVSFQHPDLAVLRDEKTAIT KGYEAL IKRLGTGDNDIPSLIAKKDYLSL DVSLLE SQAQLMITYDTFKMMEMGTTKE LVQNTYQWVLKNLVTLKAQFLLGKEDM DVSELE SQAQLMITYDTFKMMEMGTKE LVQNTYQWVLKNLVTLKAQFLLGKEDM EVSETQGTERLTITYSSSMMWE ING PESVLVNTYQWI IRNWETVKIQWSQN PTML EVSETQGTERLTITYSSSMMWE ING PESVLVNTYQWI IRNWETVKIQW
<pre>sp P21770 PB2_INCBE sp P13877 PB2_INCJJ sp Q9IMP3 PB2_INCJJ sp Q6I7C4 PB2_INCAA tr A0A193PPX7]A0A193PPX7_9ORTO tr A0A193PPU8 A0A193PPU8_9ORTO tr A0A4Y5WMY1 A0A4Y5WMY1_9INFB tr Q4LD02 Q4LD02_9INFB sp Q9QLL6 PB2_INBLE tr U3S2T7 U3S2T7_9INFB sp P13875 PB2_INBAC sp Q36431 PB2_INBP9 sp Q1PUC9 PB2_I73A5 sp Q6KU90 PB2_I67A0 sp P0DG6 PB2S1_I34A1 sp Q0A2F5 PB2_I83A4 sp Q0A438 PB2_I49A1 sp Q1A38 PB2_I49A1 sp Q1A38 PB2_INCBE sp P13877 PB2_INCBE sp P13877 PB2_INCJJ sp Q9IMP3 PB2_INCJH sp Q6I7C4 PB2_INCJA tr A0A193PPX7 A0A193PPX7_9ORTO tr A0A4455WMY1 A0A4455WMY1_9INFB</pre>	DLP SDKKVT FQDVSFQHPDLAVLRDEKTAIT KGYEAL IKRLGTGDNDIPSLIAKKDYLSL DLP SDKKVT FQDVSFQHPDLAVLRDEKTAIT KGYEAL IKRLGTGDNDIPSLIAKKDYLSL DLS SQAQLMITYDTPKMWEMGTKELVQNTYQWVLKNLVTLKAQFLLGKEDM DVSELE SQAQLMITYDTPKMWEMGTKELVQNTYQWVLKNLVTLKAQFLLGKEDM DVSELE SQAQLMITYDTPKMWEMGTKELVQNTYQWVLKNLVTLKAQFLLGKEDM DVSELE SQAQLMITYDTPKMWEMGTKELVQNTYQWVLKNLVTLKAQFLLGKEDM DVSELE SQAQLMITYDTPKMWEMGTKELVQNTYQWVLKNLVTLKAQFLLGKEDM DVSELE SQAQLMITYDTPKMWEMGTKELVQNTYQWVLKNLVTLKAQFLLGKEDM DVSELE SQAQLMITYDTPKMWEMGTKELVQNTYQWVLKNLVTLKAQFLLGKEDM DVSELE SQAQLMITYDTPKMWEMGTKELVQNTYQWVLKNLVTLKAQFLGKEDM DVSELE SQAQLMITYDTPKMWEMGTKELVQNTYQWVLKNLVTLKAQFSQNPTML EVSETQGTERLTITYSSMMWE ING PESVLVNTYQWI IRNWETVKIQWSQNPTML EVSETQGTERLTITYSSMMWE ING PESVLVNTYQWI IRNWETVKIQWSQNPTML EVSETQGTERLTITYSSMMWE ING PESVLVNTYQWI IRNWETVKIQW
<pre>sp P21770 PB2_INCBE sp P13877 PB2_INCJJ sp Q9IMP3 PB2_INCJH sp Q6I7C4 PB2_INCAA tr A0A193PPX7]A0A193PPX7_9ORTO tr A0A193PQ18 A0A193PQ18_9ORTO tr A0A4Y5WMY1 A0A4Y5WMY1_9INFB tr Q4LD02 Q4LD02_9INFB sp Q9QLL6 PB2_INBLE tr U3S2T7 U3S2T7_9INFB sp 016431 PB2_INBAC sp 036431 PB2_INBP9 sp Q1PUC9 PB2_I73A5 sp Q6XU90 PB2_I67A0 sp P0D066 PB251_I34A1 sp Q0A2F5 PB2_I83A4 sp Q0A438 PB2_I83A4 sp Q0A438 PB2_I49A1</pre> sp 21770 PB2_INCBE sp P13877 PB2_INCJJ sp Q9IMP3 PB2_INCJH sp Q6I7C4 PB2_INCAA tr A0A193PPX7 A0A193PPX7_9ORTO tr A0A4Y5WMY1 A0A4Y5WM1_9INFB tr Q4LD02 Q4LD02_9INFB	DLP SDKKVT FQDVSFQHPDLAVLRDEKTAIT KGYEAL IKRLGTGDNDIPSLIAKKDYLSL DLP SDKKVT FQDVSFQHPDLAVLRDEKTAIT KGYEAL IKRLGTGDNDIPSLIAKKDYLSL DVSELE SQAQLMITYDTFKMWEMGTTKE LVQNTYQWVLKNLVTLKAQFLLGKEDM DVSELE SQAQLMITYDTFKMWEMGTKEL VQNTYQWVLKNLVTLKAQFLLGKEDM DVSELE SQAQLMITYDTFKMWEMGTKEL VQNTYQWVLKNLVTLKAQFLLGKEDM DVSELE SQAQLMITYDTFKMWEMGTKEL VQNTYQWVLKNLVTLKAQFLLGKEDM DVSELE SQAQLMITYDTFKMWEMGTKEL VQNTYQWVLKNLVTLKAQFLLGKEDM DVSELE SQAQLMITYDTFKMWEMGTKEL VQNTYQWVLKNLVTLKAQFLLGKEDM DVSELE SQAQLMITYDTFKMWEMGTKEL VQNTYQWVLKNLVTLKAQFLLGKEDM DVSELE SQAQLMITYDTFKMWEMGTKEL VQNTYQWVLKNLVTLKAQFSQNPTML EVSETQGTERLTITYSSSMMWE ING PESVLVNTYQWI IRNWETVKIQWSQNPTML EVSETQGTERLTITYSSSMMWE ING PESVLVNTYQWI IRNWETVKIQWSQNPTML EVSETQGTERLTITYSSSMMWE ING PESVLVNTYQWI IRNWETVKIQW
<pre>sp P21770 PB2_INCBE sp P13877 PB2_INCJJ sp Q9IMP3 PB2_INCJH sp Q6I7C4 PB2_INCAA tr A0A193PPX7]A0A193PPX7_9ORTO tr A0A193PP18 A0A193PP18_9ORTO tr A0A4Y5WMY1 A0A4Y5WMY1_9INFB tr Q4LD02 Q4LD02_9INFB sp Q9QLL6 PB2_INBLE tr U3S2T7 U3S2T7_9INFB sp P13875 PB2_INBAC sp Q6431 PB2_INBAC sp Q6431 PB2_INBP9 sp Q1PUC9 PB2_I67A0 sp P0DG6 PB251_I34A1 sp Q0A2F5 PB2_I83A4 sp Q0A438 PB2_I49A1 sp P13877 PB2_INCBE sp P13877 PB2_INCBE sp P13877 PB2_INCJJ sp Q9IMP3 PB2_INCJH sp Q6I7C4 PB2_INCAA tr A0A193PP18 A0A193PPX7_9ORTO tr A0A193PQ18 A0A193PP18_9ORT0 tr Q0445WMY1 A0A475WMY1_9INFB tr Q4LD02 Q4LD02_9INFB</pre>	DLP SDKKVT FQDVSFQHPDLAVLRDEKTAIT KGYEAL IKRLGTGDNDIPSLIAKKDYLSL DLP SDKKVT FQDVSFQHPDLAVLRDEKTAIT KGYEAL IKRLGTGDNDIPSLIAKKDYLSL DVSLESQAQLMITYDTFKMMEMGTTKE LVQNTYQWVLKNLVTLKAQFLLGKEDM DVSELE SQAQLMITYDTFKMMEMGTTKE LVQNTYQWVLKNLVTLKAQFLLGKEDM DVSELE SQAQLMITYDTFKMMEMGTTKE LVQNTYQWVLKNLVTLKAQFLLGKEDM DVSELE SQAQLMITYDTFKMMEMGTTKE LVQNTYQWVLKNLVTLKAQFLLGKEDM DVSELE SQAQLMITYDTFKMMEMGTTKE LVQNTYQWVLKNLVTLKAQFLLGKEDM DVSELE SQAQLMITYDTFKMMEMGTTKE LVQNTYQWVLKNLVTLKAQFLLGKEDM DVSELE SQAQLMITYDTFKMMEMGTKE LVQNTYQWVLKNLVTLKAQFSQNPTML EVSETQGTERLTITYSSSMMME ING PESVLVNTYQWI IRNWETVKIQWSQNPTML EVSETQGTERLTITYSSSMMME ING PESVLVNTYQWI IRNWETVKIQWSQNPTML EVSETQGTERLTITYSSSMMME ING PESVLVNTYQWI IRNWETVKIQWSQNPTML EVSETQGTERLTITYSSSMMME ING PESVLVNTYQWI IRNWETVKIQW
<pre>sp P21770 PB2_INCBE sp P13877 PB2_INCJJ sp Q9IMP3 PB2_INCJH sp Q6I7C4 PB2_INCAA tr A0A193PPX7 A0A193PPX7_9ORTO tr A0A193PQ18 A0A193PQ18_9ORTO tr A0A4Y5WMY1 A0A4Y5WMY1_9INFB tr Q4LD02 Q4LD02_9INFB sp Q9QLL6 PB2_INBLE tr U3S2T7 U3S2T7_9INFB sp P13875 PB2_INBAC sp Q36431 PB2_INBP9 sp Q1PUC9 PB2_I73A5 sp Q6XU90 PB2_I67A0 sp P0D066 PB251_I34A1 sp Q0A2F5 PB2_I83A4 sp Q0A438 PB2_I49A1</pre> sp P13877 PB2_INCBE sp P13877 PB2_INCJB sp Q0A438 PB2_IA9A1 sp Q0A438 PB2_INCJJ sp Q9IMP3 PB2_INCJJ sp Q9IMP3 PB2_INCJA tr A0A193PPX7 A0A193PPX7_9ORTO tr A0A475WMY1 A0A475WMY1_9INFB tr Q4LD02 Q4LD02_9INFB sp Q9LL6 PB2_INELE	DLP SDK KVT FQDVSFQHPDLAVLRDEKTAIT KGYEAL IKRLGTGDNDIPSLIAKKDYLSL DLP SDK KVT FQDVSFQHPDLAVLRDEKTAIT KGYEAL IKRLGTGDNDIPSLIAKKDYLSL DVSELE SQAQLMITYDTFKMMEMGTTKE LVQNTYQWVLKNLVTLKAQFLLG KEDM DVSELE SQAQLMITYDTFKMMEMGTTKE LVQNTYQWVLKNLVTLKAQFSQNPTML EVSETQGTERLTITYSSSMMME ING PESVLVNTYQWI IRNWETVKIQWSQNPTML EVSETQGTERLTITYSSSMMME ING PESVLVNTYQWI IRNWETVKIQWSQNPTML EVSETQGTERLTITYSSSMMME ING PESVLVNTYQWI IRNWETVKIQW
<pre>sp P21770 PB2_INCBE sp P13877 PB2_INCJJ sp Q9IMP3 PB2_INCJH sp Q6I7C4 PB2_INCAA tr A0A193PPX7 A0A193PPX7_9ORTO tr A0A193PQ18 A0A193PQ18_9ORTO tr A0A4Y5WMY1 A0A4Y5WMY1_9INFB tr Q4LD02 Q4LD02_9INFB sp Q9QLL6 PB2_INBLE tr U3S2T7 U3S2T7_9INFB sp Q9QLL6 PB2_INBAC sp 036431 PB2_INBAC sp 036431 PB2_INBP9 sp Q1PUC9 PB2_I73A5 sp Q6XU90 PB2_I67A0 sp P0DG6 PB251_I34A1 sp Q0A2F5 PB2_I83A4 sp Q0A438 PB2_I49A1</pre> sp Q1MP3 PB2_INCBE sp P13877 PB2_INCJB sp Q0A438 PB2_INCJH sp Q9IMP3 PB2_INCJH sp Q9IMP3 PB2_INCJH sp Q9IMP3 PB2_INCJH sp Q6I7C4 PB2_INCJH sp Q6I7C4 PB2_INCJH sp Q6I7C4 PB2_INCJH sp Q6I7C4 PB2_INCJH sp Q9IMP3 PB2_INCJH sp Q9UL6 PB2_INFB	DLP SDKKVT FQDVSFQHPDLAVLRDEKTAIT KGYEAL IKRLGTGDNDIPSLIAKKDYLSL DLP SDKKVT FQDVSFQHPDLAVLRDEKTAIT KGYEAL IKRLGTGDNDIPSLIAKKDYLSL DLS SDKKVT FQDVSFQHPDLAVLRDEKTAIT KGYEAL IKRLGTGDNDIPSLIAKKDYLSL DVSELE SQAQLMITYDTFKMMEMGTTKE LVQNTYQWVLKNLVTLKAQFLLGKEDM DVSELE SQAQLMITYDTFKMMEMGTKE LVQNTYQWVLKNLVTLKAQFSQNPTML EVSETQGTERLTITYSSSMMME INGPESVLVNTYQWI IRNWETVKIQWSQNPTML EVSETQGTERLTITYSSSMMME INGPESVLVNTYQWI IRNWETVKIQWSQNPTML EVSETQGTERLTITYSSSMMME INGPESVLVNTYQWI IRNWETVKIQWSQNPTML EVSETQGTERLTITYSSSMMME INGPESVLVNTYQWI IRNWETVKIQW
<pre>sp P21770 PB2_INCBE sp P13877 PB2_INCJJ sp Q9IMP3 PB2_INCJJ sp Q6I7C4 PB2_INCAA tr A0A193PPX7]A0A193PPX7_9ORTO tr A0A193PPU8 A0A193PPU8_9ORTO tr A0A4Y5WMY1 A0A4Y5WMY1_9INFB tr Q4LD02 Q4LD02_9INFB sp Q9QLL6 PB2_INBLE tr U3S2T7 U3S2T7_9INFB sp P13875 PB2_INBAC sp Q6431 PB2_INBP9 sp Q1PUC9 PB2_I73A5 sp Q6434]PB2_IAAA sp Q0A2F5 PB2_I83A4 sp Q0A2F5 PB2_I83A4 sp Q0A438 PB2_I49A1 sp P13877 PB2_INCJB sp P13877 PB2_INCJB sp P13877 PB2_INCJB sp Q1FC4 PB2_INCJA tr A0A193PPX7 A0A193PPX7_9ORTO tr A0A4Y5WMY1 A0A4Y5WMY1_9INFB tr Q4LD02 Q4LD02_9INFB sp Q9LL6 PB2_INBLE tr U3S2T7 U3S2T7_9INFB sp Q9LL6 PB2_INB2_ sp Q9LL6 PB2_INB2</pre>	DLP SDKKVT FQDVSFQHPDLAVLRDEKTAIT KGYEAL IKRLGTGDNDIPSLIAKKDYLSL DLP SDKKVT FQDVSFQHPDLAVLRDEKTAIT KGYEAL IKRLGTGDNDIPSLIAKKDYLSL DVSELE SQAQLMITYDTPKMWEMGTKE LV <mark>NTYQWVLKNLVTLKAQFLLGKEDM DVSELE SQAQLMITYDTPKMWEMGTKE LVNTYQWVLKNLVTLKAQFLLGKEDM DVSELE SQAQLMITYDTPKMWEMGTKE LVNTYQWVLKNLVTLKAQFLLGKEDM DVSELE SQAQLMITYDTPKMWEMGTKE LVNTYQWVLKNLVTLKAQFLLGKEDM DVSELE SQAQLMITYDTPKMWEMGTKE LVNTYQWVLKNLVTLKAQFLLGKEDM DVSELE SQAQLMITYDTPKMWEMGTKE LVNTYQWVLKNLVTLKAQFLLGKEDM DVSELE SQAQLMITYDTPKMWEMGTKE LVNTYQWVLKNLVTLKAQFLLGKEDM DVSELE SQAQLMITYDTPKMWEMGTKE LVNTYQWVLKNLVTLKAQFSQNPTML EVSETQGTERLTITYSSSMMWE ING PESVLVNTYQWI IRNWETVKIQWSQNPTML EVSETQGTERLTITYSSSMMWE ING PESVLVNTYQWI IRNWETVKIQWSQNPTML EVSETQGTERLTITYSSSMMWE ING PESVLVNTYQWI IRNWETVKIQWSQNPTML EVSETQGTERLTITYSSSMMWE ING PESVLVNTYQWI IRNWETVKIQW</mark>
<pre>sp P21770 PB2_INCBE sp P13877 PB2_INCJJ sp Q9IMP3 PB2_INCJH sp Q6I7C4 PB2_INCAA tr A0A193PPX7 A0A193PPX7_9ORTO tr A0A193PQ18 A0A193PQ18_9ORTO tr A0A4Y5WMY1 A0A4Y5WMY1_9INFB tr Q4LD02 Q4LD02_9INFB sp Q9QLL6 PB2_INBLE tr U3S2T7 U3S2T7_9INFB sp Q16000000000000000000000000000000000000</pre>	DLP SDKKVT FQDVSFQHPDLAVLRDEKTAIT KGYEAL IKRLGTGDNDIPSLIAKKDYLSL DLP SDKKVT FQDVSFQHPDLAVLRDEKTAIT KGYEAL IKRLGTGDNDIPSLIAKKDYLSL DVSELE SQAQLMITYDTFKMWEMGTTKE LVQNTYQWVLKNLVTLKAQFLLGKEDM DVSELE SQAQLMITYDTFKMWEMGTKE LVQNTYQWVLKNLVTLKAQFSQNPTML EVSETQGTERLTITYSSSMMWE ING PESVLVNTYQWI IRNWETVKIQWSQNPTML EVSETQGTERLTITYSSSMMWE ING PESVLVNTYQWI IRNWETVKIQWSQNPTML EVSETQGTERLTITYSSMMWE ING PESVLVNTYQWI IRNWETVKIQWSQNPTML EVSETQGTERLTITYSSMMWE ING PESVLVNTYQWI IRNWETVKIQW
<pre>sp P21770 PB2_INCBE sp P13877 PB2_INCJJ sp Q9IMP3 PB2_INCJJ sp Q6I7C4 PB2_INCAA tr A0A193PPX7 A0A193PPX7_9ORTO tr A0A193PP18 A0A193PP18_9ORTO tr A0A4Y5WMY1 A0A4Y5WMY1_9INFB tr Q4LD02 Q4LD02_9INFB sp Q9QLL6 PB2_INBLE tr U3S2T7 U3S2T7_9INFB sp P13875 PB2_INBAC sp 036431 PB2_INBAC sp 036431 PB2_INBP9 sp Q1PUC9 PB2_I73A5 sp Q6XU90 PB2_I67A0 sp P0DOG6 PB251_I34A1 sp Q0A2F5 PB2_I83A4 sp Q20NV1 PB2_I80AD sp Q0A438 PB2_I49A1 sp P13877 PB2_INCBE sp P13877 PB2_INCBE sp P13877 PB2_INCJA sp Q6 ITC4 PB2_INCAA tr A0A193PPX7 A0A193PPX7_9ORTO tr A0A193PQ18 A0A193PQ18_9ORTO tr A0A4Y5WMY1 A0A4Y5WMY1_9INFB tr Q4LD02 Q4LD02_9INFB sp Q9LL6 PB2_INBAC sp 036431 PB2_INBAC sp 036431 PB2_INBP9</pre>	DLP SDK KVT FQDVSFQ HPDLAVLRDEKTAIT KGYEAL IKRLGTGDNDIPSLIAKKDYLSL DLP SDK KVT FQDVSFQ HPDLAVLRDEKTAIT KGYEAL IKRLGTGDNDIPSLIAKKDYLSL DVSELE SQAQLMITYDTPKMWEMGTTKE LVDNTYQWVLKNLVTLKAQFLLGKEDM DVSELE SQAQLMITYDTPKMWEMGTTKE LVDNTYQWVLKNLVTLKAQFLLGKEDM DVSELE SQAQLMITYDTPKMWEMGTTKE LVDNTYQWVLKNLVTLKAQFLLGKEDM DVSELE SQAQLMITYDTPKMWEMGTTKE LVDNTYQWVLKNLVTLKAQFLLGKEDM DVSELE SQAQLMITYDTPKMWEMGTTKE LVDNTYQWVLKNLVTLKAQFLLGKEDM DVSELE SQAQLMITYDTPKMWEMGTTKE LVDNTYQWVLKNLVTLKAQFLLGKEDM DVSELE SQAQLMITYDTPKMWEMGTTKE LVDNTYQWVLKNLVTLKAQFLLGKEDM EVSETQGTEKLTITYSSSMMWE INGPESVLVNTYQWI IRNWETVKIQW
<pre>sp P21770 PB2_INCBE sp P13877 PB2_INCJJ sp Q9IMP3 PB2_INCJH sp Q6I7C4 PB2_INCAA tr A0A193PPX7 A0A193PPX7_9ORTO tr A0A193PQ18 A0A193PQ18_9ORTO tr A0A4Y5WMY1 A0A4Y5WMY1_9INFB tr Q4LD02 Q4LD02_9INFB sp Q9QLL6 PB2_INBLE tr U3S2T7 U3S2T7_9INFB sp P13875 PB2_INBAC sp Q36431 PB2_INBP9 sp Q1PUC9 PB2_I73A5 sp Q6XU90 PB2_I67A0 sp P0D066 PB251_I34A1 sp Q0A2F5 PB2_I83A4 sp Q0A438 PB2_I49A1</pre> sp P13877 PB2_INCBE sp P13877 PB2_INCJB sp Q6I7C4 PB2_INCJA tr A0A193PPX7 A0A193PPX7_9ORTO tr A0A475WMY1 A0A475WMY1_9INFB tr Q4LD02 Q4LD02_9INFB sp Q9LL6 PB2_INBLE tr U3S2T7 U3S2T7_9INFB sp Q3C451 PB2_INBAC sp Q0L6 PB2_INBLE tr U3S2T7 U3S2T7_9INFB sp Q3C451 PB2_INBAC sp Q3C451 PB2_INBAC	DLP SDK KVT FQD VSFQ HPD LAV LRDEKTAIT KGYEAL IKR LGT GDN DI PS LIA KKD YLSL DLP SDK KVT FQD VSFQ HPD LAV LRDEKTAIT KGYEAL IKR LGT GDN DI PS LIA KKD YLSL DLP SDK KVT FQD VSFQ HPD LAV LRDEKTAIT KGYEAL IKR LGT GDN DI PS LIA KKD YLSL DLP SDK KVT FQD VSFQ HPD LAV LRDEKTAIT KGYEAL IKR LGT GDN DI PS LIA KKD YLSL DLP SDK KVT FQD VSFQ HPD LAV LRDEKTAIT KGYEAL IKR LGT GDN DI PS LIA KKD YLSL DLP SDK KVT FQD VSFQ HPD LAV LRDEKTAIT KGYEAL IKR LGT GDN DI PS LIA KKD YLSL DVSELE SQA QLM ITYD TP KMWEMGT KE LVQ NTY QWV LKN LVT LKAQFLLG KEDM DVSELE SQA QLM ITYD TP KMWEMGT KE LVQ NTY QWV LKN LVT LKAQFLLG KEDM DVSELE SQA QLM ITYD TP KMWEMGT KE LVQ NTY QWV LKN LVT LKAQF
<pre>sp P21770 PB2_INCBE sp P13877 PB2_INCJJ sp Q9IMP3 PB2_INCJH sp Q6I7C4 PB2_INCAA tr A0A193PPX7 A0A193PPX7_9ORTO tr A0A193PQ18 A0A193PQ18_9ORTO tr A0A4Y5WMY1 A0A4Y5WMY1_9INFB tr Q4LD02 Q4LD02_9INFB sp Q9QLL6 PB2_INBLE tr U3S2T7 U3S2T7_9INFB sp Q9QLL6 PB2_INBAC sp 036431 PB2_INBP9 sp Q1PUC9 PB2_I73A5 sp Q6XU90 PB2_I67A0 sp P0DO66 PB251_I34A1 sp Q0A2F5 PB2_I83A4 sp Q0A438 PB2_I49A1</pre> sp Q1A438 PB2_I49A1 sp Q0A438 PB2_INCJH sp Q6I7C4 PB2_INCJH sp Q6I7C4 PB2_INCJH sp Q6I7C4 PB2_INCJH sp Q6I7C4 PB2_INCJH sp Q6I7C4 PB2_INCJH sp Q9IMP3 PB2_INCJH sp Q9IMP3 PB2_INCJH sp Q9IMP3 PB2_INCJH sp Q9IMP3 PB2_INCJH sp Q9IMP3 PB2_INCJH sp Q9IL6 PB2_INBLE tr Q4LD02 Q4LD02_9INFB sp Q9QL6 PB2_INBLE tr U3S2T7 U3S2T7_9INFB sp Q36431 PB2_INBP9 sp Q1PUC9 PB2_I73A5 sp Q36431 PB2_INBP9 sp Q1PUC9 PB2_I73A5	DLP SDK KVT FQDVSFQ HPDLAVLRDEKTAIT KGYEAL IKRLGTGDNDIPSLIAKKDYLSL DLP SDK KVT FQDVSFQ HPDLAVLRDEKTAIT KGYEAL IKRLGTGDNDIPSLIAKKDYLSL DVSELE SQAQLMITYDTPKMWEMGTTKE LVQNTYQWVLKNLVTLKAQFLLGKEDM DVSELE SQAQLMITYDTPKMWEMGTTKE LVQNTYQWVLKNLVTLKAQFLLGKEDM DVSELE SQAQLMITYDTPKMWEMGTTKE LVQNTYQWVLKNLVTLKAQFLLGKEDM DVSELE SQAQLMITYDTPKMWEMGTTKE LVQNTYQWVLKNLVTLKAQFLLGKEDM DVSELE SQAQLMITYDTPKMWEMGTTKE LVQNTYQWVLKNLVTLKAQFLLGKEDM DVSELE SQAQLMITYDTPKMWEMGTTKE LVQNTYQWVLKNLVTLKAQF
<pre>sp P21770 PB2_INCBE sp P13877 PB2_INCJJ sp Q9IMP3 PB2_INCJJ sp Q6I7C4 PB2_INCAA tr A0A193PP180A193PP18_90RT0 tr A0A193PP18 A0A193PP18_90RT0 tr A0A4Y5WMY1 A0A4Y5WMY1_91NFB tr Q4LD02 Q4LD02_91NFB sp Q9QLL6 PB2_INBLE tr U3S2T7 U3S2T7_91NFB sp P13875 PB2_INBAC sp Q36431 PB2_INBP9 sp Q1PUC9 PB2_I73A5 sp Q6XU90 PB2_I67A0 sp P0D0G6 PB2S1_I34A1 sp Q0A2F5 PB2_I83A4 sp Q0A438 PB2_I49A1 sp P13877 PB2_INCJJ sp Q0A438 PB2_I49A1 sp Q1F4 PB2_INCJH sp Q617C4 PB2_INCJH sp Q617C4 PB2_INCJH sp Q9IMP3 PB2_INCJH sp Q9L6 PB2_INBLE tr U3S2T7 U3S2T7_9INFB sp P13875 PB2_INBLC sp Q36431 PB2_INBP9 sp Q1PUC9 PB2_I73A5 sp Q6U90 PB2_I67A0</pre>	DLP SDK KVT FQDVSFQ HPDLAVLRDEKTAIT KGYEAL IKRLGTGDNDIPSLIAKKDYLSL DLP SDK KVT FQDVSFQ HPDLAVLRDEKTAIT KGYEAL IKRLGTGDNDIPSLIAKKDYLSL DVSELE SQAQLMITYDTPKMWEMGTKE LVQNTYQWVLKNLVTLKAQFLLGKEDM DVSELE SQAQLMITYDTPKMWEMGTTKE LVQNTYQWVLKNLVTLKAQFLLGKEDM DVSELE SQAQLMITYDTPKMWEMGTTKE LVQNTYQWVLKNLVTLKAQFLLGKEDM DVSELE SQAQLMITYDTPKMWEMGTTKE LVQNTYQWVLKNLVTLKAQFLLGKEDM DVSELE SQAQLMITYDTPKMWEMGTTKE LVQNTYQWVLKNLVTLKAQFLLGKEDM DVSELE SQAQLMITYDTPKMWEMGTTKE LVQNTYQWVLKNLVTLKAQFLLGKEDM DVSELE SQAQLMITYDTPKMWEMGTTKE LVQNTYQWVLKNLVTLKAQF
<pre>sp P21770 PB2_INCBE sp P13877 PB2_INCJJ sp Q9IMP3 PB2_INCJH sp Q6I7C4 PB2_INCAA tr A0A193PPX7 A0A193PPX7_9ORTO tr A0A193PQ18 A0A193PQ18_9ORTO tr A0A4Y5WMY1 A0A4Y5WMY1_9INFB tr Q4LD02 Q4LD02_9INFB sp Q9QLL6 PB2_INBLE tr U3S2T7 U3S2T7_9INFB sp Q13875 PB2_INBAC sp Q36431 PB2_INBP9 sp Q1PUC9 PB2_I73A5 sp Q6XU90 PB2_I67A0 sp P0D066 PB251_I34A1 sp Q0A2F5 PB2_I83A4 sp Q0A438 PB2_I49A1 sp Q1770 PB2_INCBE sp P13877 PB2_INCJJ sp Q9IMP3 PB2_INCJH sp Q6I7C4 PB2_INCBE tr Q4LD02 Q4LD02_9INFB tr Q4LD02 Q4LD02_9INFB sp P13875 PB2_INBLE tr U3S2T7 U3S2T7_9INFB sp P13875 PB2_INBAC sp Q3C431 PB2_INBP9 sp Q1PUC9 PB2_I73A5 sp Q6XU90 PB2_I67A0 sp P0D066 PB25 I34A1</pre>	DLP SDK KVT FQDVSFQHPDLAVLRDEKTAIT KGYEAL IKRLGTGDNDIPSLIAKKDYLSL DLP SDK KVT FQDVSFQHPDLAVLRDEKTAIT KGYEAL IKRLGTGDNDIPSLIAKKDYLSL DVSELE SQAQLM ITYDTPKMWEMGT KE LV <mark>DNTYQWVLKNLVT LKAQFLLGKEDM DVSELE SQAQLM ITYDTPKMWEMGT KE LVDNTYQWVLKNLVT LKAQFLGKEDM DVSELE SQAQLM ITYDTPKMWEMGT KE LVDNTYQWVLKNLVT LKAQFLGKEDM EVSETQGTERLT ITYS SSMMWE ING PESVLVNTYQWI IRNWETVKI QWSQN PTML EVSETQGTE KLT ITYS SSMMWE ING PESVLVNTYQWI IRNWETVKI QWSQN PTML ILLLEG FSVCENDPRAPMVT RQDLIDVGFGQKVRL FVGQGSVRTF KRTASQRAASSDV LALLEG FSVCENDPRAPMVT RQDLIDVGFGQKVRL FVGQGSVRTF KRTASQRAASSDV LALLEG FSVCENDPRAPMVT RQDLIDVGFGQKVRL FVGQGSVRTF KRTASQRAASSDV LALLEG FSVCENDPRAPMVT RQDLIDVGFGQKVRL FVGQGSVRTF KRTASQRAASSDV NAVLAG FLV SGK YDPDLGD FKT IEE LERLKPGEKANI LLY QG FVKVVV RKRY SALSNDI NAVLAG FLV SGK YDPDLGD FKT IEE L</mark>
<pre>sp P21770 PB2_INCBE sp P13877 PB2_INCJJ sp Q9IMP3 PB2_INCJH sp Q6I7C4 PB2_INCAA tr A0A193PPX7 A0A193PPX7_9ORTO tr A0A193PP18 A0A193PQ18_9ORTO tr A0A4Y5WMY1 A0A4Y5WMY1_9INFB tr Q4LD02 Q4LD02_9INFB sp Q9LL6 PB2_INBLE tr U3S2T7 U3S2T7_9INFB sp P13875 PB2_INBAC sp Q6431 PB2_INBAC sp Q6431 PB2_INBP9 sp Q1PUC9 PB2_I73A5 sp Q6431 PB2_I83A4 sp Q0A2F5 PB2_I83A4 sp Q0A438 PB2_I49A1 sp P1770 PB2_INCBE sp P13877 PB2_INCJJ sp Q0A438 PB2_I49A1 sp Q0A438 PB2_INCJH sp Q617C4 PB2_INCAA tr A0A193PP18_INCJH sp Q9IMP3 PB2_INCJH sp Q9L6 PB2_INBAC tr A0A193PP18_INBAC sp Q3431 PB2_INBAC sp Q3431 PB2_INBAC sp Q3431 PB2_INBAC sp Q3431 PB2_INBAC sp Q3431 PB2_INBP9 sp Q1PUC9 PB2_I73A5 sp Q6KU90 PB2_I67A0 sp P0D0G6 PB25_IB32_I34A1 sp Q0A2F5 BB2_I34A1</pre>	DLP SDK KVT FQDVSFQHPDLAVLRDEKTAIT KGYEAL IKRLGTGDNDIPSLIAKKDYLSL DLP SDK KVT FQDVSFQHPDLAVLRDEKTAIT KGYEAL IKRLGTGDNDIPSLIAKKDYLSL DVSELE SQAQLMITYDTPKMWEMGTKELVQNTYQWVLKNLVTLKAQFLGKEDM DVSELE SQAQLMITYDTPKMWEMGTTKELVQNTYQWVLKNLVTLKAQFLGKEDM DVSELE SQAQLMITYDTPKMWEMGTTKELVQNTYQWVLKNLVTLKAQFLGKEDM DVSELE SQAQLMITYDTPKMWEMGTTKELVQNTYQWVLKNLVTLKAQFLGKEDM DVSELE SQAQLMITYDTPKMWEMGTKELVQNTYQWVLKNLVTLKAQFLGKEDM DVSELE SQAQLMITYDTPKMWEMGTTKELVQNTYQWVLKNLVTLKAQFLGKEDM DVSELE SQAQLMITYDTPKMWEMGTKELVQNTYQWILKNLVTLKAQFLGKEDM EVSETQGTERLTITYS SSMMWE ING PESVLVNTYQWI IRNWETVKI QWSQN PTML EVSETQGTEKLTITYS SSMMWE ING PESVLVNTYQWI IRNWETVKI QWSQN PTML EVSETQGTEKLTITYS SSMMWE ING PESVLVNTYQWI IRNWETVKI QW
<pre>sp P21770 PB2_INCBE sp P13877 PB2_INCJJ sp Q9IMP3 PB2_INCJH sp Q6I7C4 PB2_INCAA tr A0A193PPX7 A0A193PPX7_9ORTO tr A0A193PQ18 A0A193PQ18_9ORTO tr A0A4Y5WMY1 A0A4Y5WMY1_9INFB tr Q4LD02 Q4LD02_9INFB sp Q9QLL6 PB2_INBLE tr U3S2T7 U3S2T7_9INFB sp 036431 PB2_INBP9 sp Q1PUC9 PB2_I73A5 sp Q6XU90 PB2_I67A0 sp P0D066 PB251_I34A1 sp Q0A2F5 PB2_I83A4 sp Q0A438 PB2_I49A1</pre> sp 21770 PB2_INCBE sp P13877 PB2_INCJJ sp Q0IMP3 PB2_INCJH sp Q6I7C4 PB2_INCAA tr A0A193PPX7 A0A193PPX7_9ORTO tr A0A495WMY1 A0A4Y5WMY1_9INFB tr Q4LD02 Q4LD02_9INFB sp Q1617E4]PB2_INBLE tr U3S2T7 U3S2T7_9INFB sp P13875 PB2_INBAC sp Q3C431 PB	DLP SDK KVT FQDVSFQHPDLAVLRDEKTAIT KGYEAL IKRLGTGDNDIPSLIAKKDYLSL DLP SDK KVT FQDVSFQHPDLAVLRDEKTAIT KGYEAL IKRLGTGDNDIPSLIAKKDYLSL DVSELE SQAQLMITYDTPKMWEMGT KE LVDNTYQWVLKNLVTLKAQFLLGKEDM DVSELE SQAQLMITYDTPKMWEMGT KE LVDNTYQWVLKNLVTLKAQFLLGKEDM DVSELE SQAQLMITYDTPKMWEMGT KE LVDNTYQWVLKNLVTLKAQFLLGKEDM DVSELE SQAQLMITYDTPKMWEMGT KE LVDNTYQWVLKNLVTLKAQFLGKEDM DVSELE SQAQLMITYDTPKMWEMGT KE LVDNTYQWVLKNLVTLKAQFLGKEDM EVSELGGTERLTITYS SSMMWE ING PESVLVNTYQWI IRNWETVKI QWSQN PTML EVSETQGTERLTITYS SSMMWE ING PESVLVNTYQWI IRNWETVKI QW
<pre>sp P21770 PB2_INCBE sp P13877 PB2_INCJJ sp Q9IMP3 PB2_INCJH sp Q6I7C4 PB2_INCAA tr A0A193PPX7 A0A193PPX7_9ORTO tr A0A193PP18 A0A193PP18_9ORTO tr A0A4Y5WMY1 A0A4Y5WMY1_9INFB tr Q4LD02 Q4LD02_9INFB sp Q9QLL6 PB2_INBLE tr U3S2T7 U3S2T7_9INFB sp Q9QL16 PB2_INBAC sp 036431 PB2_INBP9 sp Q1PUC9 PB2_I73A5 sp Q6XU90 PB2_I67A0 sp P0DG6 PB251_I34A1 sp Q0A2F5 PB2_I83A4 sp Q20NV1 PB2_I80AD sp Q0A438 PB2_I49A1</pre> sp Q1MP3 PB2_INCJH sp Q6I7C4 PB2_INCJH sp Q6I7C4 PB2_INCJH sp Q9IMP3 PB2_INCJH sp Q9QL6 PB2_INFB sp Q9QL6 PB2_INFB sp Q36431 PB2_INBLE tr U3S2T7 U3S2T7_9INFB sp Q36431 PB2_INBP9 sp Q1PUC9 PB2_I73A5 sp Q6XU90 PB2_I67A0 sp P0DG6 PB251_I34A1 sp Q0A2F5 PB2_I83A4 sp Q20NV1 PB2_I80AD	DLP SDK KVT FQDVSFQHPDLAVLRDEKTAIT KGYEAL IKRLGTGDNDIPSLIAKKDYLSL DLP SDK KVT FQDVSFQHPDLAVLRDEKTAIT KGYEAL IKRLGTGDNDIPSLIAKKDYLSL DVSELE SQAQLM ITYD TPKMWEMGTTKE LVQNTYQWVLKNLVTLKAQFLGKEDM DVSELE SQAQLM ITYD TPKMWEMGTTKE LVQNTYQWVLKNLVTLKAQFSQN PTML EVSETQGTEKLT ITYS SSMMWE ING PESVLVNTYQWI IRNWETVKI QWSQN PTML EVSETQGTEKLT ITYS SSMMWE ING PESVLVNTYQWI IRNWETVKI QW
<pre>sp P21770 PB2_INCBE sp P13877 PB2_INCJJ sp Q9IMP3 PB2_INCJH sp Q6I7C4 PB2_INCAA tr A0A193PP18 A0A193PP18_90RT0 tr A0A193PP18 A0A193PP18_90RT0 tr A0A4Y5WMY1 A0A4Y5WMY1_91NFB tr Q4LD02 Q4LD02_91NFB sp Q9QLL6 PB2_INBLE tr U3S2T7 U3S2T7_91NFB sp P13875 PB2_INBAC sp Q36431 PB2_INBP9 sp Q1PUC9 PB2_I73A5 sp Q6XU90 PB2_I67A0 sp P0D0G6 PB2S1_I34A1 sp Q0A2F5 PB2_I83A4 sp Q0A438 PB2_I49A1 sp Q1A438 PB2_INCJH sp Q1MP3 PB2_INCJH sp Q1MP3 PB2_INCJH sp Q617C4 PB2_INCJA tr A0A193PP18A_INCJH sp Q9LL6 PB2_INCJH sp Q9LL6 PB2_INCJH sp Q9LL6 PB2_INCJH sp Q9LL6 PB2_INCJA tr A0A193PP18A_INCJH sp Q9LL6 PB2_INBLE tr U3S2T7 U3S2T7_91NFB sp Q9LL6 PB2_INBLE tr U3S2T7 U3S2T7_91NFB sp Q36431 PB2_INBAC sp Q36431 PB2_INBAC sp Q36431 PB2_INBAC sp Q36431 PB2_INBAC sp Q36431 PB2_IT3A5 sp Q6U90 PB2_I67A0 sp P0D0G6 PB2S1_I34A1 sp Q0A2F5 PB2_I83A4 sp Q0A2F5 PB2_I83A4</pre>	DLP SDKKVT PQDVSFQHPDLAV LRDEKTAITKGYEAL IKR LGTGDNDIPSLIAKKDYLSL DLP SDKKVT PQDVSFQHPDLAV LRDEKTAITKGYEAL IKR LGTGDNDIPSLIAKKDYLSL DLS SDAQLM ITYDTPKMWEMGT TKE LVQNTYGWVLKN LVT LKAQFLLGKEDM DVSELE SQAQLM ITYDTPKMWEMGT TKE LVQNTYGWVLKN LVT LKAQFLLGKEDM EVSETQGTERLT ITYS SSMMWE ING PESVLVNTYGWI IRNWETVKI QWSQN PTML EVSETQGTE KLT ITYS SSMMWE ING PESVLVNTYGWI IRNWETVKI QWSQN PTML EVSETQGTE KLT ITYS SSMMWE ING PESVLVNTYGWI IRNWETVKI QWSQN PTML EVSETQGTE KLT ITYS SSMMWE ING PESVLVNTYGWI IRNWETVKI QW
<pre>sp P21770 PB2_INCBE sp P13877 PB2_INCJJ sp Q9IMP3 PB2_INCJH sp Q6I7C4 PB2_INCAA tr A0A193PPX7 A0A193PPX7_9ORTO tr A0A193PQ18 A0A193PQ18_9ORTO tr A0A4Y5WMY1 A0A4Y5WMY1_9INFB tr Q4LD02 Q4LD02_9INFB sp Q9QLL6 PB2_INBLE tr U3S2T7 U3S2T7_9INFB sp Q13875 PB2_INBAC sp Q36431 PB2_INBP9 sp Q1PUC9 PB2_I73A5 sp Q6XU90 PB2_I67A0 sp P0D066 PB251_I34A1 sp Q0A2F5 PB2_I83A4 sp Q0A438 PB2_I49A1 sp Q1770 PB2_INCBE sp P13877 PB2_INCJH sp Q617C4 PB2_INCBE tr Q4LD02 Q4LD02_9INFB tr Q4LD02 Q4LD02_9INFB sp P13875 PB2_INBLE tr U3S2T7 U3S2T7_9INFB sp P13875 PB2_INBAC sp Q3C431 PB2_INBP9 sp Q1PUC9 PB2_I73A5 sp Q6XU90 PB2_I67A0 sp Q0A2F5 PB2_I83A4 sp Q0A2F5 PB2_I83A4 sp Q0A2F5 PB2_I83A4 sp Q0A2F5 PB2_I83A4 sp Q0A438 PB2_I49A1</pre>	DLP SDKKVT PODVSFQHPDLAV LRDEKTAIT KGYEAL IKR LGT GDNDIPSLIAKKDYLSL DLP SDKKVT PODVSFQHPDLAV LRDEKTAIT KGYEAL IKR LGT GDNDIPSLIAKKDYLSL DLS SDAQLMITYDTPKMWEMGTTKE LVONTY QWVLKN LVT LKAQFLIGKEDM DVS ELE SQAQLMITYDTPKMWEMGTTKE LVONTY QWVLKN LVT LKAQFLIGKEDM EVS ETQ GTE RLT ITYS SSMMWE ING PES VLVNTY QWI IRNWETVKI QWSQN PTML EVS ETQ GTE RLT ITYS SSMMWE ING PES VLVNTY QWI IRNWETVKI QWSQN PTML EVS ETQ GTE RLT ITYS SSMMWE ING PES VLVNTY QWI IRNWETVKI QWSQN PTML EVS ETQ GTE RLT ITYS SSMMWE ING PES VLVNTY QWI IRNWETVKI QWSQN PTML EVS ETQ GTE RLT ITYS SSMMWE ING PES VLVNTY QWI IRNWETVKI QWSQN PTML EVS ETQ GTE RLT ITYS SSMMWE ING PES VLVNTY QWI IRNWETVKI QWSQN PTML EVS ETQ GTE RLT ITYS SSMMWE ING PES VLVNTY QWI IRNWETVKI QWSQN PTML EVS ETQ GTE RLT ITYS SSMMWE ING PES VLVNTY QWI IRNWETVKI QWSQN PTML EVS ETQ GTE RLT ITYS SSMMWE ING PES VLVNTY QWI IRNWETVKI QWSQN PTML EVS ETQ GTE RLT ITYS SSMMWE ING PES VLVNTY QWI IRNWETVKI QWSQN PTML ILL LEG FSV CENDPRAPWTR QD LID VGF GQK VRLF VG GGS VRTF KRT ASQRAA SSDV LAL LEG FSV CENDPRAPWTR QD LID VGF GQK VRLF VG GGS VRTF KRT ASQRAA SSDV LAL LEG FSV CENDPRAPWTR QD LID VGF GQK VRLF VG GGS VRTF KRT ASQRAA SSDV LAL LEG

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GEEEFN YKCGECKGIDKAS MMMEKDDIN SAKKEDMKDDIIDCMYFSOFD GEEEFN YKCGECKGIDKAS MMEMEKDDIN SAKKEDMKDDIIDCMYFSOFD	410
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GYEEFTMVGRRATAILRKATRRLIQLIVSGRDEQSIAEAIIVAMVFSQED	408
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TMADLTTKLGREIPYQYVM <mark>MNWIQK</mark> SEDNLEALLYSRGIVETNPGKMGSS	480
TMADLSTKLGREIPYQYVM <mark>MNWIQK</mark> SEDNLEALLYSRGIVETNPGKMGSS	480 CBR1
TMADLSTKLGREIPYQYVM <mark>MNWIQK</mark> SEDNLEALLYSRGIVETNPGKMGSS	480
TMADLSTKLGREIPYQYVMMNWIQKSEDNLEALLYSRGIVETNPGKMGSS	480 C
TMADLSTKLGREIPYQYVMMNWIQKSEDNLEALLYSRGIVETNPGKMGSS	480
TMADLSTKLGREIPYQYVM <mark>MNWIQK</mark> SEDNLEALLYSRGIVETNPGKMGSS	480
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	459 45 CBD1
NFLNRAG QUUSEMIQUQAIFUNASNO DEDQUISIE EFERA	450
NEVNDANOPI.NDMHOLI.PHEOKDAKVI.FONMGIE-HIDNV	457
NFVNRANORLNPMHOLLRHFOKDAKVIFONWGIE-HIDNV	457 B&A
NFVNRANORLNPMHOLLRHFOKDAKVLFONWGVE-PIDNV	457
NFVNRANQRLNPMHQLLRHFQKDAKILFQNWGVE-PIDNV	457
NFVNRANQRLNPMHQLLRHFQKDAKV <mark>LFQNW</mark> GIE-PIDNV	457
NFVNRANQRLNPMHQLLRHFQKDAKV <mark>LFQNW</mark> GIE-PIDNV	457)
<mark>*:.</mark> *	-
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QDVSFQHPDLAVLRDEKTAITKGYEALIKRLGTGDNDIPSLIAKKDYLSL	594
LMITIDTPRMWEMGTTRELV <mark>UNTIQWVLRNLVTLRAQFLLCREDM</mark>	572
IMITIDIPRMWEMGIIRELV <mark>UNIYOWULK</mark> ULWILKAQELLCKEDM	572
IMITIDIFREMEMOTIKELVONTVONUMENLUTIKAOF – DIGREDM	573
LMITIDIFRAWEMGTIKELVONTYOWVIKNIVIKAOFLIGKEDM	572 CBR2
LMITYDTPKMWEMGTTKELVONTYOWVLKNLVTLKAOFLLGKEDM	572
LTITYSSSMMWEINGPESVLVNTYOWIIRNWETVKIOWSONPTML	571
LTITYSSSMMWEINGPESVLVNTYOWIIRNWETVKIOWSONPTML	571 B&A
LTITYSSSMMWEINGPESVL <mark>VNTYQWIIR</mark> NWETVKIQWSQNPTML	571
LTITYSSSMMWEINGPESVL <mark>VNTYQWIIR</mark> NWETVKIQWSQNPTML	571
LTITYSSSMMWEINGPESVL <mark>VNTYQWIIR</mark> NWEMIKIQWSQEPTML	571
LTITYSSSMMWEINGPESVL <mark>VNTYQWIIR</mark> NWETVKIQWSQDPTML	571)
	-
ENDPRAPMVTGQDLIDVGFGQKVRLFVGQGSVRTFKRTASQRAASSDV	763
ENDPRAPMVTRQDLIDVGFGQKVRLFIGQGSVRTFKRTASQRAASSDV	763
ENDPRAPMVTRQDLIDVGFGQKVRLFVGQGSVRTFKRTASQRAASSDV	763
END-PRAPMVTRUDLIDVGFGUKVRLFVGUGSVRTFKKTASURAASSDV	763
ENDPRAPMVIRQULIDVGFGQKVRLFVGQG3VRIFKRIASQRAASSUV	763
GK ADBDI'GD EKL LEET'EK I'K DUEK VILLITA OGROAKTE VETEVET VOGROAV VANDA FILD – EVELMA FILDA OFLOOK ANTELAGAO AKTE VETEVET VANDA	751
GKYDPDLGDFKTTEELEKLKPGFKANTLLYGGKPVKVVKDKDVSALSNDT	751
GKYDPDLGDFKTTEELERLKPGEKANTLLYOGKPVKVVKRKPYSLISNDT	751
GKYDPDLGDFKTIEELEKLKPGEKANILLYQGKPVKVVKRKRYSALSNDI	752 NLS2
GKYDPDLGDFKTIEELEKLKPGEKANILLYQGKPVKVV <mark>KRKRYSA</mark> LSNDI	751
GKYDPDLGDFKTIEELEKLKPGEKANILLYOGKPVKVV <mark>KRKRYS</mark> ALSNDI	751 (B&A
GKEERRYGPALSINELSNLAKGEKANVLIGQGDVVLVM <mark>KRKRDS</mark> 5ILTDS	747 /
GKEDRRYGPALSINELSNLAKGEKANVLIGQGDVVLVM <mark>KRKRDS</mark> FILTDS	747
GKEDKRYGPALSINELSNLAKGEKANVLIGQGDVVLVM <mark>KRKRDS</mark> FILTDS	
	/4/
GKEDKRYGPALSINELSNLAKGEKANVLIGQGDVVLVM <mark>KRKRDS</mark> FILTDS	747
GKEDKRYGPALSINELSNLAKGEKANVLIGQGDVVLMKRKRDSILTDS GKEDKRYGPALSINELSNLAKGEKANVLIGQGDVVLM <mark>KRKRDS</mark> ILTDS	747 747 747
GKEDKRYGPALSINELSNLARGEKANVLIGQGDVVLVMKRKDSILTDS GKEDKRYGPALSINELSNLARGEKANVLIGQGDVVLVMKRKDSILTDS GKEDKRYGPALSINELSNLARGEKANVLIGQGDVVLVM <mark>KRKDS</mark> ILTDS	747 747 747 747

//End of PB2 subunits of influenza A, B	and C viruses	
sp P21770 PB2 INCBE	NKNVKKIKMSN	774
sp P13877 PB2_INCJJ	NKNVKKIKMSN	774
sp Q9IMP3 PB2_INCJH	NKNVKKIKMSN	774
sp Q6I7C4 PB2_INCAA	NKNVKKIKMSN	774
tr A0A193PPX7 A0A193PPX7_9ORTO	NKNVKKIKMSN	774
tr A0A193PQ18 A0A193PQ18_90RT0	NKNVKKIKMSN	774
tr A0A4Y5WMY1 A0A4Y5WMY1_9INFB	SQGIKRQRMTVESMGWALS	770
tr Q4LD02 Q4LD02_9INFB	SQGIKRQRMTVESMGWALS	770
sp Q9QLL6 PB2_INBLE	SQGIKRORMTVESMGWALS	770
tr U3S2T7 U3S2T7_9INFB	SQGIKRORMTVESMGWALS	771
sp P13875 PB2_INBAC	SQGIKRQRMTVESMGWALS	770
sp 036431 PB2_INBP9	SQGIKRQRMTVESMGWALS	770
sp Q1PUC9 PB2 I73A5	QTATKRIRMAIN	759
sp Q6XU90 PB2_I67A0	QTATKRIRMAIN	759
sp P0DOG6 PB2S1_I34A1	QTATKRIRMAIN	759
sp Q0A2F5 PB2_I83A4	QTATKRIRMAIN	759
sp Q20NV1 PB2_I80AD	QTATKRIRMAIN	759
sp Q0A438 PB2_I49A1	QTATKRIRMAIN	759
	. *: :*:	

Figure 7 A mix and match analysis of human influenza viruses A, B and C (For legends, see Figs. 4, 5 and 6)

Table 1 shows the active site regions of different HNH/N endonucleases which makes both double-stranded breaks or nicks on DNAs and single-stranded cleavage on RNAs (CRIPSR-Cas13a and CRIPSR-Cas12a) suggesting the proposed regions on the influenza viral polymerase PB2 subunits could also make a cleavage on the host cell mRNAs in the cap-snatching process. Proposed HNH/N endonuclease domains, by sequence similarity, are highlighted in yellow and needs further experimental validation.

Table 1 Active site regions in different HNH/N family of endonucleases

HNH/N Type (Organism)	Active Site Region	
HH-Homing endonuclease domain (Bacteriophage Bp7 I-Tev II) -YEIHHKDGNRENNDLDNLMCLSIQEHY49-		
HH-based (HNH/N) group II introns (S. cerevisiae)	-LEVHHVRTLNNAANKIKDDYLLGRMIKMNRKQITICKTCHF842-	
HH-based mcr A (HNH) restriction endonuclease (E. coli)	-LEVHHVIPLSSGGADTTDNCVALCPNCHRELHYS ²⁵⁸ -	
DH-based HNN endonucleases (E. coli plasmids)	-WYADHVQAV// PEADCPENLVPACAPCNLLK85-	
DH-based HNN endonucleases (E. proavitum)	-MEADHITPWHEGGKTTSVNCQMLCKDCNRRK355-	
DH-based HNH Endonuclease VII (Resolvase) (T4 Phage)	-LDHDHELNGPKAGKVRGLLCNLCNAAEGQMKHKFNR ⁷⁴ -	
HH based HNH Colicin endonuclease (Type 9*) (E. coli)	-YELHHDKPISQGGEVYDMDNIRVTTPKRHIDIHRGK ⁵⁹² -	
HH- HNH Pyocins endonuclease (Type-S1) (P. aeruginosa)	-IEIHHKVRVADGGGVYNMGNLVAVTPKRHIEIHKGGK ⁶¹⁸ -	
HH- HNH Pyocins endonuclease (Type-S2) (P. aeruginosa)	-IEIHHKVRIADGGGVYNMGNLVAVTPKRHIEIHKGGK689-	
DH- based Influenza virus A (HNN endonuclease domain)*	-TTVDH ²⁷ MAIIKKYTSGRQEKN ⁴² PALRMKWM//PITADKRITEMIPERN ⁷¹ E-	
DQ-based Influenza virus B (HNN endonuclease domain)*	-TTVDQ ²⁹ YNIIRKFNTSRIEKN44PSLRMKWAMCSN ⁵⁶ F-	
DH -based Influenza virus C (HNN endonuclease domain) *	-SKRDH94VLASASCIN183YWNFCGPCVN113NS-	
HH-based CRISPR-Cas13a (HNH endonucleases domains)* >sp P0DPB8 CS13A), Listeria seeligeri	-TLIHH ¹¹ LGVLFFCDYMYN ² °RRE//DRKKVLISRDKNG ⁶⁸ . -QIMH ¹¹ Y ⁴ KKSSFYKSVVN ⁴⁴ KTICRPEQKQMKKLVHG ¹⁰² -	
HH-based CRISPR-Cas13b (HNN endonuclease domain) >tr E6K398 Prevotella buccae	-DYMHH ¹¹⁹⁹ ENIDMQRDFTHLN ²¹² RKKQVGRTKN ²²² II-	
DH-based CRISPR-Cas12a (HNN endonuclease domain)* >sp U2UMQ6 CS12A, Acidaminococcus sp.	-AKGHH ^{7/35} GKPNLHTLYWTGLFSPEN773*LAKTSIKLNG783-	
DH-based CRISPR-Cas9 (HNN endonuclease domain)* >sp[J3F2B0 CRISPR-CAS9, Actinomyces naeslundii	-CQLDH ⁹⁸¹ IVPQAGPGSNN ⁵⁹³ RRGNLVAVCERCN ⁸⁰⁶ RSKS ⁶¹⁰ -	
DH-based CRISPR-Cas9 (HNN endonuclease domain) >sp/Q99ZW2/CRIPRS-Cas9, Streptococcus pyogene	-YDVD <mark>H</mark> 840IVPQSFLKDDSID <mark>N</mark> 854KVLTRSDK <mark>N</mark> 863RGKS867- S	
SOM & X-ray data		
Type II restriction endonuclease R.KpnI	-LTP <mark>D</mark> 148 <mark>H</mark> 149//DVND//RH <mark>D</mark> 175VMKK- <mark>Mg²⁺</mark> [31]	
ColE7 HNH endonuclease (E. coli) (Colicin)	-FELH <mark>H</mark> ⁵⁴⁵ EKPISQNGGVYDMD <mark>N</mark> ⁵⁶⁰ ISVVTPKRHIDI <mark>H</mark> ⁵⁷³ RGK- <mark>Zn^{2*}</mark> [32]	
Pyocin S8 (P. aeruginosa)	-Y <mark>EIHH</mark> ⁷⁸⁹ VVQISQGGAVYDIDN ⁸⁰⁴ LRVMTPKMHIQVHSN ⁸¹⁹ KGK- <mark>Zn²⁺ [33]</mark>	
Vvn (Vibrio vulnicus HNN nuclease)	-EWE <mark>1</mark> 80VVHN ¹¹⁸ LTPAIGEV <mark>N</mark> ¹²⁷ GDR- <mark>Mg²⁺ [34]</mark>	

Adapted from Palanivelu (22) *By sequence similarity. Experimentally validated active site amino acids of the HNH/N domains are highlighted in dark blue (SDM) and light blue (X-ray crystallography).

CRISPR-Cas13a is a single-molecule effector of the Class II, Type VI family of CRISPR-Cas systems that is part of the bacterial and archaeal defense systems. All so far characterized Cas13-family members possess two distinct active sites: one for precrRNA processing and the other for target ssRNA cleavage. Recently, Kick et al. [35] found that the Cas13a from the purple bacteria, Rhodobacter capsulatus, possessed two HEPN (higher eukaryotes and prokaryotes nucleotide binding) domains which exhibited nuclease activity. Interestingly, they found that RcCas13a did not rely on the catalytic HEPN-domains for pre-crRNA processing since RcCas13a mutants, where the active-site residues in one or both of the HEPN1 or HEPN2 domains were mutated to Ala, were not affected in their pre-crRNA processing activity, suggesting the active site is elsewhere and possibly in the HNH domain.

The CRISPR-associated protein Cas12a (Cpf1) possesses two distinct nuclease activities: endoribonuclease activity for processing its own guide RNAs and RNA-guided DNase activity for target DNA cleavage. Like CRISPR-Cas9, CRISPR-Cas12a has a conserved RuvC nuclease domain at its C-terminal region.

In CRISPR-Cas9 enzymes, the HNH domain binds to the target DNA and cleaves it.

3.2. HNH/N Active Site Analyses of Human Influenza Viruses A, B and C

Saravanan et al. [31] have analyzed the HNH motif in the Type II restriction endonuclease R.KpnI, a member of the HNH nuclease superfamily, which possess the HNH domain with the conserved amino acids D148, H149 and Q175. By SDM analysis they have shown that the D148 \rightarrow G/A and H149 \rightarrow L/A led to complete loss of activity and the mutant Q175 \rightarrow E, failed to bind DNA at the standard conditions, although the DNA binding and cleavage was rescued at pH 6.0.

Furthermore, the nuclease domain of ColE7 (nuclease-ColE7) purified from *Escherichia coli* contained a one-to-one stoichiometry of zinc ion and that this zinc-containing enzyme hydrolyzed DNA without externally added divalent metal ions. The apo-enzyme, in which the indigenous zinc ion was removed from the nuclease-ColE7, had no detectable DNase activity [36]. SDM experiments followed by fluorescence resonance energy transfer (FRET) assays, by Huang and Yuan [32] to decipher the role of conserved Asn and His residues in the H545, N560, H573 motif of the Colicin, ColE7, found that in the H545 mutants, the activity was completely abolished while activities of N560 and H573 mutants varied from 6.9% to 83.2% of the wild-type activity. Both N560 \rightarrow A and N560 \rightarrow D mutants contained a disordered loop in the HNH motif due to the disruption of the hydrogen bond network surrounding the side-chain of residue of N560 [32].

The active site amino acids of Vvn HNH endonuclease were analyzed by both SDM and X-ray crystallography by Li et al. [34]. They found that the mutation of the invariant His80 \rightarrow Ala abolished the endonuclease activity of Vvn, demonstrating the critical importance of this residue in DNA hydrolysis. The X-ray crystallographic study has further suggested that the Vvn HNH endonuclease hydrolyzed DNA by a general single-metal ion mechanism. The metal ion located in the $\beta\beta\alpha$ -metal motif was assigned as a magnesium ion in Vvn [34]. The X-ray crystallographic data have further shown that the magnesium ion was bound to Glu79, Asn127 and four water molecules. A water molecule, W1, bridges the invariant His80 and a Mg²⁺-bound water (Table 1).

3.3. Proposed Mechanism of Action of HNN of Human Influenza Viruses A, B and C

The invariant D/H is always found to be engaged with a metal ion and the first invariant **His** of D/H**H**NH/N domain acts as a general base to activate a metal-bound water molecule for the nucleophilic attack on the scissile phosphate bond of nucleic acids, and the first Asn interacts with base to be cleaved and thus, generating 3'-OH for subsequent viral mRNA synthesis (in the nucleus) by the PB1 subunit of the polymerase in influenza viruses. The second His/Asn stabilizes the leaving group (Fig. 7) [22, 23].





4. Conclusions

The endonuclease is suggested to be present in the PB1 and PA subunits of the heterotrimeric human influenza polymerases. However, by sequence similarity, a typical HNH/N motif is identified in the cap-snatching PB2 subunit itself, suggesting that it could not only bind the cap structures of the host mRNAs but also could cleave it. The PB2 subunits of the human influenza viruses A and B are very close to each other, whereas the C has significantly diverged from them. MSA analyses have also shown that even though these viruses are genetically diverged, but share a common genetic ancestry. These results will facilitate the optimization of endonuclease inhibitors as potential new anti-influenza drugs, and could also help in developing new antiviral drugs for the treatments of flu in the future.

Compliance with ethical standards

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Disclosure of conflict of interest

The author has declared that no competing interests exist.

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