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(Research Article)

An insight into the active sites of the catalytic basic protein subunit PB1 of the RNA polymerase of human influenza viruses

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Abstract

RNA polymerase from human influenza viruses is a heterotrimeric enzyme and performs the crucial functions of both transcription and replication for multiplication of the viruses in human cells. The heterotrimeric enzyme is made up of two basic protein subunits (PB1 and PB2) and an acidic protein subunit (PA). All the three subunits perform welldefined function(s) in the transcription and replication processes in the human cells. The basic protein subunit PB1 is shown to possess the polymerization activity, whereas the PB2 and the PA subunits are found to be involved in the capsnatching and proofreading (PR) activities, respectively. The polymerase activity in the catalytic subunit, PB1, is found to be an RNA-dependent RNA polymerase (RdRp). Multiple sequence alignment (MSA) analysis of the PB1 subunits from all the three human influenza viruses, A, B and C shows large number of highly conserved peptides, amino acid motifs and invariant amino acids. Site-directed mutagenesis (SDM) analysis and X-ray crystallographic data have shown that two completely conserved motifs, viz. –GDN- and –SDD-, are involved in binding to the catalytic Mg²⁺ ion. These data are in close agreement with the MSA analysis data of the polymerases from all the three human influenza viruses. Furthermore, two highly conserved polymerase catalytic regions are identified in the PB1 subunits by sequence similarity to other DNA/RNA polymerases and hence, are proposed to function in the nucleotidyl transfer activities. Presence of the two catalytic regions suggest that the polymerase may function in a dual mode, i.e., in phase I, in association with the cap-snatching subunit PB2, it could be involved in the synthesis of mRNAs (transcription mode) and once enough proteins are made from the mRNAs, in the second phase, in association with PR exonuclease subunit PA, it could switch to the replication mode to synthesize error-free, exact copies of the viral genome. For both the activities, it could use the same invariant catalytic Mg²⁺-binding –GDN- and –SDD- motifs.

Keywords: Human Influenza viruses; RNA polymerase; Polymerase Basic Protein subunit PB1; Catalytic Metal-binding motifs; Polymerase active sites; Mechanism of action

1. Introduction

A large number of human and animal viral pathogens belong to RNA viruses. They cause major global health-care crisis and unprecedented economic losses. Attempts have been made to prepare vaccines and synthesize novel antivirals to contain the spread of these viruses. Whereas the vaccines are targeted mainly to the viral surface protein(s), the antivirals are targeted to the crucial enzymes that are involved in the lifecycle of these viruses. As all RNA viruses employ the crucial enzyme, viz. the RdRp for their multiplication in human cells, most of the antiviral drugs are targeted to this enzyme. As the RdRps perform both the transcription and replication processes in these RNA viruses (except retro viruses), the RdRps have been the main target for antiviral drug development to control the spread of RNA viral pathogens, in general. However, these efforts are hindered by limited structural information on the RdRp catalytic core(s) and its catalytic mechanism. In this analysis, attempts are made to understand the catalytic core(s) of this polymerase from all the three human influenza viruses and its possible catalytic mechanism.

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Influenza, commonly known as "the flu", is an infectious disease caused by influenza viruses which also belong to (-) strand RNA viruses. Influenza viral infection is an airborne, highly contagious disease 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 have become a major public health-care concern worldwide. The influenza viruses are enveloped viruses of 150-200 nm diameter and belong to the family, Orthomyxoviridae. Out of the four genera (A-D) only influenza A, B and C viruses infect humans and the D virus infects livestock. Among them, infection by influenza A virus is the most dangerous and is the causative agent for the worldwide flu pandemics. For example, influenza A virus has caused four pandemics so far that have occurred in the last 100 years; in 1918, 1957, 1968 and 2009. Both influenza B and A viruses are also reported to cause seasonal epidemics each year and affect approximately 5–10% of the adult and 20–30% of the pediatric population. According to the World Health Organization, influenza epidemics lead to 3–5 million cases of severe illness and \sim 2,90,000–6,50,000 respiratory deaths each year (This estimate does not take into account of deaths from other diseases such as cardiovascular disease, which can be influenza-related). While influenza A virus shows animal to human transmissions, influenza B and C viruses show very limited host range and appear predominantly in humans [1]. Out of the three human influenza viruses, only the influenza A and B viruses cause substantial morbidity and mortality in humans, whereas the influenza C virus does not cause epidemics/pandemics, but is involved in sporadic outbreaks, causing only mild upper respiratory infections [2]. In contrast to influenza A virus, influenza B and C viruses do not have animal reservoirs, [3] suggesting the pandemic nature of the influenza A virus. Their genomic structure, surface proteins, serotypes, transcription and replication processes are already described by Palanivelu [4].

1.1. Salient Features of the Human Influenza Viral RNA Polymerases

Influenza viruses are (-) strand RNA viruses and replicated by the viral RNA (vRNA) polymerase in the host cell nucleus. Within a viral ribonucleotide particle (vRNP), a single RNA polymerase captures both the 3'- and 5'-termini of the viral RNA (vRNA) and forms a pseudo-circularized structure of the vRNA. The viral RNA polymerase is a heterotrimer and all three subunits are shown to perform well-defined function(s) in viral transcription and replication processes. For example, the PB1 subunit performs the polymerizing function, the PB2 subunit performs the cap-snatching function for priming the mRNA transcriptions [4] and the PA subunit has been suggested to perform the PR exonuclease function [5].

Though the RNA viruses are highly divergent in nature, but their key enzyme, i.e., the RdRp, is structurally and functionally very similar. For example, all the RdRps exhibit a characteristic cupped right-hand structure with the three major domains, viz. fingers, palm and thumb, similar to DNA-dependent DNA polymerases (DdDps) and many DNA-dependent RNA polymerases (DdRps). The X-ray crystallographic structures of the complete heterotrimeric viral polymerase have been reported by many investigators [6-8]. The X-ray structures revealed the PB1 subunits of the flu polymerases also showed the canonical closed right-handed fold, possessing the typical fingers, palm, and thumb domains [6-8]. Furthermore, the polymerase forms a compact structure with PB1 at its centre, capped on one face by PB2 and clamped between the two globular domains of the PA [6-8] (Fig. 1)

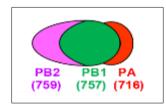


Figure 1 A schematic diagramme showing the various subunits of the influenza viral polymerase. (The number of amino acids are given in brackets and are from influenza A virus)

N	TD	Fingers	Palm	Thump	CTD	
1	35	240	4	98	669 7	57

Adapted from Pflug et al. and Fan et al. [6,8]

Figure 2 Domain Architecture of the PB1 catalytic subunit of the RNA polymerase from human influenza A virus.

NTD, N-terminal domain; CTD, C-terminal domain; (K235, K237 and R239 form the finger priming loop); Palm (K308, K480 and K481, G304, D305, N306, S444, D445, D446; the Mg²⁺⁻ binding -³⁰⁴GDN- and -⁴⁴⁴SDD- motifs are in the palm domain)

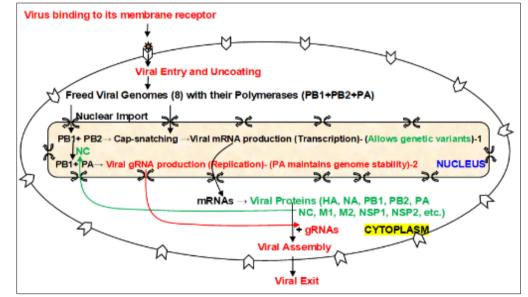
As discussed elsewhere, the influenza viral RNA polymerase (EC 2.7.7.48) performs the crucial steps in the viral multiplication, i.e., it involves both in the transcription and replication processes. As RdRps are not found in mammalian cells, it is suggested that they are an excellent target for designing antiviral compounds.

1.2. Influenza Viral Transcription and Replication

Initiation of transcription is primer-dependent and the primer with the cap is snatched from nascent host mRNAs by the PB2 subunit of the polymerase by a process known as 'cap-snatching'. With the capped primer, the polymerase goes for elongation and at the end of the elongation process, the transcription is terminated at a track of five to seven U residues (a poly-U track) near the 5'-end of the vRNAs, where polyadenylation occurs by a stuttering mechanism [9]. Now the 5'-capped and 3'-tailed viral mRNAs are ready for translation by the host ribosomes in the cytoplasm.

Unlike transcription, the replication is an end-to-end synthesis of the vRNAs. The vRNAs are synthesized in two steps: in the first step, the complementary RNAs (cRNAs; (+) strands) are synthesized using the vRNAs, as templates, and in the second step, the progeny vRNAs, (-) strands, are produced using the cRNAs as templates. In the context of the polymerase, the ten nucleotides at the 5'-termini of both vRNAs and cRNAs fold back into a hook-like structure which is bound tightly in a site formed by the fingers domain of the PB1 subunit and C-terminal of the PA subunit (PA-C) [6]. The initiation of replication starts with the synthesis of a pppApG dinucleotide to the opposite nucleotide positions U_1 - C_2 of the 3'-vRNA terminus. This process requires support from the priming loop, a flexible region of the PB1 subunit that protrudes into the active site of the polymerase and controls the position of the template and initial dinucleotides. It is interesting to note, that for the synthesis of cRNAs and the subsequent synthesis of progeny vRNAs, the polymerase does not follow the transcription signals and thus, the same RdRp acts in different modes during the replication and transcription processes.

Figure 3 shows a schematic diagramme and suggested role(s) of the other two subunits in the transcription, replication processes. The PB2 subunit involves in the cap-snatching for initiation of transcription and the PA subunit is involved in PR and thus, maintaining genome stability. The replication mode is dependent on intracellular nuclear capsid protein (NC) concentrations. In this mode, the polymerase replicates the whole viral genome without recognizing the transcriptional signals, and the replicated genome is not caped or polyadenylated.



gRNA, genomic RNA; NC, Nuclear capsid protein (moves from the cytoplasm to nucleus through the nuclear pores), HA, Hemagglutinin, NA, Neuraminidase, PB1, PB2 & PA, polymerase subunits; M1, Matrix protein, M2; Ion channel; NSP1 & NSP2 (NEP), Non-structural proteins 1 & 2. NEP, Nuclear export protein.

Figure 3 A schematic diagram showing the proposed role(s) of each of the polymerase subunits in the production of viral mRNAs and gRNAs

In this communication, the PB1 subunit of the RNA polymerase from all the three human influenza viruses are analyzed for their active sites and reported. The catalytic metal-binding motifs already confirmed by SDM experiments and X-ray crystallographic techniques are further corroborated by the MSA analysis. Furthermore, the MSA analysis has also shown the possible catalytic amino acids involved in the nucleotide transfer reactions during the polymerization reactions. Based on these results, a catalytic mechanism for the human influenza viral polymerases is proposed.

2. Material and methods

Protein sequence data of the RNA polymerase basic protein subunit, PB1, from all three human 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. The highly conserved motifs identified by the bioinformatics analysis, and along with the data already available from biochemical, SDM and X-ray crystallographic analyses on the PB1 subunits, the possible amino acids that make up the polymerase active sites are proposed. Expasy tool was used for pI calculations of the PB1 subunits of the RNA polymerases.

3. Results and discussion

3.1. MSA Analysis of the Polymerase PB1 subunit of Influenza Virus A

Figure 4 shows the MSA of the PB1 subunits of the polymerase from several subtypes of the human influenza A virus (only the required regions for the discussions are shown here). The H1N1 subtype of the influenza A virus (Puerto Rico, 1934) is used as the standard and it showed a theoretical pI of 9.39. It is clear from Figure 4 that the PB1 subunits of influenza A viral strains from different regions are highly conserved from N- to C-terminals. Strikingly, five highly conserved motifs are identified in all the PB1 subunits of the human influenza A viral subtypes: Motif I (Finger priming loop) -235KLKRR-; Motif II -303TGDN306-; Motif III -403LSPGMMM409GMF412-; Motif IV -438WDGLQSS444DDFALI450- and Motif V (end of the palm domain) -474GINMSKKK481SY483I- (highlighted in yellow, dark and light green). Several mutations in the above 5 conserved motifs from I to V of the PB1 protein were analyzed for their ability to replicate in human and chicken cells [10]. They found that replacement of the invariant amino acids, $S^{444} \rightarrow P$, $D^{445} \rightarrow G$ and $D^{446} \rightarrow N$ in motif IV -(SDD-), and $\mathbf{K}^{481} \rightarrow E/T/N$ mutants in motif V, abolished polymerase activity completely. Furthermore, by minireplicon assays, they confirmed that any mutation altering the -SDD- sequence rendered the polymerase nonfunctional. Moreover, in human cell replication assays, they found that the Y⁴⁸³→H mutation showed only 0.5% of the activity, the $N^{306} \rightarrow T$ of -GDN³⁰⁶- motif mutant showed only 2.4% of the activity and the $M^{409} \rightarrow T$ mutant showed no activity. They suggested that such conserved residues comprising the polymerase modules may serve as potential targets for anti-influenza drugs that can attenuate infection by inhibiting influenza polymerase activity and hence, yiral replication. In contrast, the natural mutation $K^{480} \rightarrow R$ (Motif V) observed in several pandemics causing H1N1 human and swine influenza viruses, slightly increased transcription/replication activity relative to the wild-type. The proposed amino acids in the catalytic regions and the highly conserved fingertip priming loop are highlighted in yellow. A -YAQtriad (highlighted in yellow) was observed and a similar -YAN- triad was found to be involved in NTP selection in Severe acute respiratory syndrome-related Coronaviruses -(SARS-CoVs). The nuclear localization signals (NLSs) are highlighted in orange. The C-terminal ends in the triad -RQK in all.

sp Q07FH7 RDRP 196A3	TGAPQLNPIDGPLPKDNEPSG <mark>YAQ</mark> TDCVLEAMAFLEESHPGIFENSCIETMEVVQQTRVD	120
sp P03431 RDRP_I34A1	TGAPQLNPIDGPLPEDNEPSGYAQTDCVLEAMAFLEESHPGIFENSCIETMEVVQQTRVD	120
sp Q9Q0V0 RDRP_196A0	TGAPQLNPIDGPLPEDNEPSG <mark>YAQ</mark> TDCVLEAMAFLEESHPGIFENSCLETMEVVQQTRVD	120
tr A0A0M3WG62 A0A0M3WG62_9INFA	TGAPQLNPIDGPLPEDNEPSG <mark>YAQ</mark> FDCVLEAMAFLEESHPGIFENSCLETMEVVQQTRVD	120
tr A0A1J0FCD5 A0A1J0FCD5_9INFA	TGAPQLNPIDGPLPEDNEPSG <mark>YAQ</mark> FDCVLEAMAFLEESHPGIFENSCLETMEVVQQTRVD	120
tr A0A023M018 A0A023M018_9INFA	TGAPQLNPIDGPLPEDNEPSG <mark>YAQ</mark> FDCVLEAMAFLEESHPGIFENSCLETMEVVQQTRVD	120
sp Q0A2D9 RDRP_166A0	TGAPQLNPIDGPLPEDNEPSG <mark>YAQ</mark> FDCVLEAMAFLEESHPGIFENSCLETMEVVQQTRVD	120
tr A0A023M258 A0A023M258 9INFA	TGAPQLNPIDGPLPEDNEPSG <mark>YAQ</mark> FDCVLEAMAFLEESHPGIFENSCLETMEVVQQTRVD	120
sp Q2VC92 RDRP I80A2	TGAPQLNPIDGPLPEDNEPSG <mark>YAQ</mark> TDCVLEAVAFLEESHPGIFENSCLETMEVIQQTRVD	120
sp Q30NP3 RDRP I75A0	TGAPQLNPIDGPLPEDNEPSG <mark>YAQ</mark> FDCVLEAMAFLEESHPGIFENSCLETMEVVQQTRVD	120
sp Q910D6 RDRP 168A4	TGAPQLNPIDGPLPEDNEPSG <mark>YAQ</mark> TDCVLEAMAFLEESHPGIFENSCLETMEVVQQTRVD	120
sp P16506 RDRP 168A5	TGAPQLNPIDGPLPEDNEPSG <mark>YAQ</mark> FDCVLEAMAFLEESHPGIFENSCLETMEVIQQTRVD	120
tr A0A1Z1X1S7 A0A1Z1X1S7 9INFA	TGAPQLNPIDGPLPEDNEPSG <mark>YAQ</mark> TDCVLEAMAFLDESHPGIFENSCRETMEVVQQTRVD	120
sp Q20NV3 RDRP I80AD	TGAPQLNPIDGPLPEDNEPSG <mark>YAQ</mark> FDCVLEAMAFLEESHPGIFENSCLETMEVVQQTRVD	120
sp Q0A440 RDRP I49A1	TGAPQLNPIDGPLPEDNEPSG <mark>YAQ</mark> TDCVLEAMAFLEESHPGIFENSCLETMEVVQQTRVD	120
sp Q0A2G8 RDRP I59A0	TGAPQLNPIDGPLPEDNEPSG <mark>YAQ</mark> TDCVLEAMAFLEESHPGIFENSCLETMEVVQQTRVD	120
sp Q0A2H9 RDRP I83A5	TGAPQLNPIDGPLPEDNEPSG <mark>YAQ</mark> TDCVLEAMAFLEESHPGIFENSCLETMEVVQQTRVD	120
sp P16511 RDRP I57A5	TGAPQLNPIDGPLPEDNEPSG <mark>YAQ</mark> TDCVLEAMAFLEESHPGIFENSCLETMEVIQQTRVD	120
sp Q20PL6 RDRP I79A7	TGAPQLNPIDGPLPEDNEPSG <mark>YAQ</mark> TDCVLEAMAFLEESHPGIFENSCLETMEIVQQTRVD	120
sp Q0A2F7 RDRP 183A4	TGA PQLN PIDG PLPE DNE PSG <mark>YAQ</mark> FDCVLEAMA FLEESHPGI FENSCLETMEVVQQTRVD	120
tr A0A1Z1X7E1 A0A1Z1X7E1 9INFA	TGAPQLNPIDGPLPEDNEPSG <mark>YAQ</mark> FDCVLEAMAFLEESHPGIFENSCLETMEIVQQTRVD	120
tr A0A1Z1WYR7 A0A1Z1WYR7 9INFA	TGAPQLNPIDGPLPEDNEPSG <mark>YAQ</mark> TDCVLEAMAFLEESHPGIFENSCLETMEVVQQTRVD	120
tr A0A1U9W475 A0A1U9W475 9INFA	TGAPQLNPIDGPLPEDNEPSG <mark>YAQ</mark> FDCVLEAMAFLEESHPGIFENSCLETMEVVQQTRVD	120
tr A0AlU9W4I3 A0AlU9W4I3 9INFA	TGAPQLNPIDGPLPEDNEPSG <mark>YAQ</mark> TDCVLEAMAFLEESHPGIFENSCLETMEVVQQTRVD	120
sp Q0A451 RDRP I66A1	TGAPQLNPIDGPLPEDNEPSG <mark>YAQ</mark> TDCVLEAMAFLEESHPGIFENSCLETMEVVQQTRVD	120
sp Q0A429 RDRP 156A2	TGAPQLNPIDGPLPEDNEPSG <mark>YAQ</mark> TDCVLEAMAFLEESHPGIFENSCLETMEIVQQTRVD	120
tr A0A0F6ZDR7 A0A0F6ZDR7 9INFA	TGAFQLNFIDGFLFEDNEFSG <mark>YAQ</mark> FDCVLEAMAFLEESHFGIFENSCLETMEVVQQTRVD	120
tr A0A0F6WVQ6 A0A0F6WVQ6 9INFA	TGAPQLNPIDGPLPEDNEPSG <mark>YAQ</mark> TDCVLEAMAFLEESHPGIFENSCLETMEVVQQTRVD	120
sp Q0A2Q6 RDRP 185A3	TGA PQLN PIDG PLPE DNE PSG <mark>YAQ</mark> FDCVLEAMA FLEESH PGI FENSCLETMEVVQQTRVD	120
sp P16503 RDRP_I77AF	TGA PQLN PIDG PLPEDNE PSC <mark>YAQ</mark> IDCVLEAMA FLEESH PGI FENSCLETME VVQQ TRVD	120
sp Q0A3Q1 RDRP I78AC	TGA PQLN PIDG PLPEDNE PSG <mark>YAQ</mark> TDC VLEAMA FLEESH PG I FENSCLETME VVQQ TR VD	120
sp Q08115 RDRP 180A6	TGA PQLN PIDG PLPEDNE PSG <mark>YAQ</mark> IDCVLEAMA FLEESH PGI FENSCLETME VVQQ TRVD	120
sp P16513 RDRP_I80A8	TGA PQLN PIDG PLPE DNE PSG <mark>YAQ</mark> FDCVLEAMA FLEESH PGI FENSCLETMEVVQQTRVD	120
tr A0A023LWC1 A0A023LWC1 9INFA	TGA PQLN PIDG PLPEDNEPSG <mark>YAQ</mark> FDCVLEAMA FLEESH PGI FENSCLETMEVVQQTRVD	120
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3.1.1. CLUSTAL O (1.2.4) MSA of the PB1 catalytic subunits of the RdRp from influenza A viruses

ONVTKKMVTORTIG DNMTKKMITORTIG DNMTKKMVTORTIG				
DNMTKKMVTQRTIG	KKORLNKRSVLTR	CALL DNIMIKDA L	rg <mark>klkrra</mark>	240
	and granting that is	RALTINTMTKDA E	RGKLKRRA	240
	KKKQRLNKR <mark>SYLI</mark> F	RALTLNTMTKDA E	erg <mark>klkrra</mark>	240
PNMTKKMITQRTIG	KKKQRLNKK <mark>SYLI</mark> F	RALTLNTMTKDA E	rg <mark>klkrra</mark>	240
DNMTKKMVTQRTIG	KKKQRLNKK <mark>SYLI</mark> F	RALTLNTMTKDA E	erg <mark>klkrra</mark>	240
DNMTKKMVTQRTIG	KKKQRLNKR <mark>SYLI</mark> F	RALTLNTMTKDA E	rg <mark>klkrra</mark>	240
DNMTKKMVTQRTIG	KKKQKLNKR <mark>SYLI</mark> F	RALTLNTMTKDA E	rg <mark>klkrra</mark>	240
DNMTKKMVTQRTIG	KKKQRLNKRSYLIR	RALTLNTMTKDA E	rg <mark>klkrra</mark>	240
DNMTKKMVTQRTIG	KKKQRLNKR <mark>SYLI</mark> F	RALTLNTMTKDA E	rg <mark>klkrra</mark>	240
DNMTKKMVTQRTIG	KKKQRVNKR <mark>SYLI</mark> F	RALTLNTMTKDA E	erg <mark>klkrra</mark>	240
DNMTKKMVTQRTIG	KKKQRVNKR <mark>SYLI</mark> F	RALTLNTMTKDA E	rg <mark>klkrra</mark>	240
DNMTKKMVTQRTIG	KKKQRLNKRSYLIR	RALTLNTMTKDA E	rg <mark>klkrra</mark>	240
DNMTKKMVTQRTIG	KKKQRLNKR <mark>SYLI</mark> F	RALTLNTMTKDA E	erg <mark>klkrra</mark>	240
DNMTKKMVTQRTIG	KKKQRLNKK <mark></mark> GYLIF	RALTLNTMTKDA E	rg <mark>klkrra</mark>	240
DNMTKKMITORTIG	KKKQRLNKR <mark>SYLIR</mark>	RALTLNTMTKDA E	ERG <mark>KLKRRA</mark>	240
DNITKKMVTQRTIG	KKKQRLNKR <mark>SYLI</mark> F	RALTLNTMTKDA E	erg <mark>klkrra</mark>	240NLS
DNMTKRMVTQRTIG	KKKQRLNKR <mark>SYLI</mark> F	RALTLNTMTKDA E	erg <mark>klkrra</mark>	240
DNMTKKMVTQRTIG	KKKQRLNKR <mark>SYLIR</mark>	RALTLNTMTKDA E	erg <mark>klkrra</mark>	240
DNMTKKMVTQRTIG	KKKQRLNKK <mark>SYLI</mark> F	RALTLNTMTKDA E	erg <mark>klkrra</mark>	240
DNMTKKMVTQRTIG	KKKQRLNKR <mark>SYLI</mark> F	RALTLNTMTKDA E	erg <mark>klkrra</mark>	240
DNMTKKMVTQRTIG	KKKQRLNKR <mark>SYLIR</mark>	RALTLNTMTKDA E	erg <mark>klkrra</mark>	240
DNMTKKMVTQRTIG	KKKQRLNKK <mark>SYLI</mark> R	RALTLNTMTKDA E	erg <mark>klkrra</mark>	240
DNMTKKMVTQRTIG	KKKQRLHKK <mark>SYLI</mark> F	RALTLNTMTKDA E	erg <mark>klkrra</mark>	240
DNMTKKMVTQRTIG	KKKQRLHKK <mark>SYLI</mark> F	RALTLNTMTKDA E	rg <mark>klkrra</mark>	240
DNMTKKMVTORTIG	KKKQRLNKR <mark>SYLIR</mark>	RALTLNTMTKDA E	ERG <mark>KLKRRA</mark>	240
DNMTKKMVTQRTIG	KKKQRLNKR <mark>SYLI</mark> F	RALTLNTMTKDA E	erg <mark>klkrra</mark>	240
DNMTKKMVTQRTIG	KKKQRLNKR <mark>SYLI</mark> F	RALTLNTMTKDA E	rg <mark>klkrra</mark>	240
DNMTKKMVTQRTIG	KKKQRLNKRSYLIR	RALTLNTMTKDA E	ERG <mark>KLKRRA</mark>	240
DNMTKKMVTORTIG	KKKQRLNKRSYLIR	RALTLNTMTKDA E	ERG <mark>KLKRRA</mark>	240
DNMTKKMVTQRTIG	KKKORLNRR SYLIP	RALTLNTMTKDA E	rg <mark>klkrra</mark>	240
DNMTKKMVTQRTIG	KKKQRLNKRSYLIR	RALTLNTMTKDA E	rg <mark>klkrra</mark>	240
DNMTKKMVTORTIG	KKKORLNKR SYLIR	RALTLNTMTKDA E	ERG <mark>KLKRRA</mark>	240
DNMTKKMVTQRTIG	KKKQRLNKRSYLIR	RALTLNTMTKDA E	rg <mark>klkrra</mark>	240
				240 FPLoop
	DNMTKKMVTQRTIG DNMTKKMVTQRTIG DNMTKKMVTQRTIG	DNMTKKMVTORTIG <mark>KKKORLNKR</mark> SYLIF DNMTKKMVTORTIG <mark>KKKORLNKR</mark> SYLIF DNMTKKMVTORTIG <mark>KKKORLNKR</mark> SYLIF	DNMTKKMVTORTIG <mark>KKKORINKR</mark> SYLIRALTLNTMTKDA F DNMTKKMVTORTIG <mark>KKKORINKR</mark> SYLIRALTLNTMTKDA F DNMTKKMVTORTIG <mark>KKKORINKR</mark> SYLIRALTLNTMTKDA F	NMTKKMVTORTIG <mark>KKKORLNKR</mark> SYLIRALTLNTMTKDA ERG <mark>KLKRRA</mark> NMTKKMVTORTIG <mark>KKKORLNKR</mark> SYLIRALTLNTMTKDA ERG <mark>KLKRRA</mark> NMTKKMVTORTIG <mark>KKKORLNKR</mark> SYLIRALTLNTMTKDA ERG <mark>KLKRRA</mark>

sp Q07FH7 RDRP_196A3		MTKWNENQNPRMFLAMITYITKNQPEWFRNILSIAPIMFSNKMARLGKGYMFESK	360
sp P03431 RDRP_I34A1 sp Q9Q0V0 RDRP_I96A0		NTKWNENQNPRMFLAMITYMTRNQPEWFRNVLSIAPIMFSNKMARLGKGYMFESK NTKWNENQNPRMFLAMITYITRNQPEWFRNVLSIAPIMFSNKMARLGKGYMFESK	360 360
r A0A0M3WG62 A0A0M3WG62 9INFA		NTKWNENQN PRMFLAMITIITRNQ PEWFRNVLSIAPIMESNRMARLGRGIMFESR NTKWNENQN PRMFLAMITYITRNO PEWFRNVLSIAPIMFSNRMARLGRGYMFESR	360
r A0A1J0FCD5 A0A1J0FCD5 9INFA		NTRWNENQN PRMFLAMITIITRNQ PEWPRNVLSIAPIMESNRMARLGRGIMEESR NTRWNENQN PRMFLAMITYITRNQ PEWFRNVLSIAPIMESNRMARLGRGYMFESR	360
r A0A023M018 A0A023M018 9INFA			360
· · · –		NTKWNENQNPRMFLAMITYITRNQPEWFRNVLSIAPIMFSNKMARLGKGYMFESK	360
p Q0A2D9 RDRP_166A0		NTKWNENQNPRMFLAMITYITRNQPEWFRNVLSIAPIMFSNKMARLGKGYMFESK	360
r A0A023M258 A0A023M258_9INFA		NTKWNENQNPRMFLAMITYITRNQPEWFRNVLSIAPIMFSNKMARLGKGYMFESK	360
p Q2VC92 RDRP_180A2		NTKWNENQNPRMFLAMITYITRNQPEWFRNVLSIAPIMFSNKMARLGKGYMFESK	
p Q30NP3 RDRP_175A0		NTKWNENQNPRMFLAMITYITKNQPEWFRNILSIAPIMFSNKMARLGKGYMFESK	360
p Q910D6 RDRP_168A4		NTKWNENQNPRMFLAMITYITKNQPEWFRNVLSIAPIMFSNKMARLGKGYMFESK	360
p P16506 RDRP_168A5		NTKWNENQNPRVFLAMITYITRNQPEWFRNVLSIAPIMFSNKMARLGKGYMFESK	360
r A0A1Z1X1S7 A0A1Z1X1S7_9INFA		NTKWNENQNPRMFLAMITYITRNQPEWFRNVLSIAPIMFSNKMARLGKGYMLESK	360
p Q20NV3 RDRP_I80AD		NTKWNENQNPRMFLAMITYITRNQPEWFRNVLSIAPIMFSNKMARLGKGYMFESK	360
p Q0A440 RDRP_I49A1		NTKWNENQNPRMFLAMITYITRNQPEWFRNVLSIAPIMFSNKMARLGKGYMFESK	360
p Q0A2G8 RDRP_I59A0		NTKWNENQNPRMFLAMITYITRNQPEWFRNILSIAPIMFSNKMARLGKGYMFESK	360
p Q0A2H9 RDRP_183A5		NTKWNENQNPRMFLAMITYITRNQPEWFRNVLSIAPIMFSNKMARLGKGYMFESK	360
p P16511 RDRP_I57A5		NTKWNENQNPRMFLAMITYITRNQPEWFRNVLSIAPIMFSNKMARLGKGYMFESK	360
p Q20PL6 RDRP_I79A7		NTKWNENQNPRMFLAMITYITRNQPEWFRNVLSIAPIMFSNKMARLGKGYMFESK	360
p Q0A2F7 RDRP_183A4		NNTKWNENQNPRMFLAMITYITRNQPEWFRNVLSIAPIMFSNKMARLGKGYMFESK	360
r A0A1Z1X7E1 A0A1Z1X7E1_9INFA		M <mark>TKWNENQNPRMFLAMITYITRNQPEWFRNVLSIAPIMFSNKMARLGKGYMFESK</mark>	360
r A0A1Z1WYR7 A0A1Z1WYR7_9INFA	TITGI	M <mark>TKWNENQNPRMFLAMITYITRNQPEWFRNVLSIAPIMFSNKMARLGKGYMFESK</mark>	360
r A0A1U9W475 A0A1U9W475_9INFA	TITGI	M <mark>TKWNENQNPRMFLAMITYITRNQPEWFRNVLSIAPIMFSNKMARLGKGYMFESK</mark>	360
r A0A1U9W4I3 A0A1U9W4I3_9INFA	TITGI	MTKWNENQNPRMFLAMITYITRNQPEWFRNVLSIAPIMFSNKMARLGKGYMFESK	360
p Q0A451 RDRP_166A1	TITGI	NTKWNENQNPRMFLAMITYITRNQPEWFRNVLSIAPIMFSNKMARLGKGYMFESK	360
p Q0A429 RDRP_156A2		N <mark>TKWNENQNPRMFLAMITYITRNQPEWFRNVLSIAPIMFSNKMARLGKGYMFESK</mark>	360
r A0A0F6ZDR7 A0A0F6ZDR7_9INFA	TITGI	MTKWNENQNPRMFLAMITYITRNQPEWFRNVLSIAPIMFSNKMARLGKGYMFESK	360
r A0A0F6WVQ6 A0A0F6WVQ6 9INFA	TITGI	MTKWNENQNPRMFLAMITYITRNQPEWFRNVLSIAPIMFSNKMARLGKGYMFESK	360
p Q0A2Q6 RDRP_185A3	TITGI	MTKWNENQNPRMFLAMITYITRNQPEWFRNVLSIAPIMFSNKMARLGKGYMFESK	360
p P16503 RDRP_177AF	TITGI	MTKWNENQNPRMFLAMITYITRNQPEWFRNVLSIAPIMFSNKMARLGKGYMFESK	360
p Q0A3Q1 RDRP I78AC	TITGI	NTKWNENQNPRMFLAMITYITRNQPEWFRNVLSIAPIMFSNKMARLGKGYMFESK	360
p Q08115 RDRP 180A6	TITGI	NTKWNENQNPRMFLAMITYITRNQPEWFRNVLSIAPIMFSNKMARLGKGYMFESK	360
p P16513 RDRP_180A8	TITG	NTKWNENQNPRMFLAMITYITRNQPEWFRNVLSIAPIMFSNKMARLGKGYMFESK	360
r A0A023LWC1 A0A023LWC1 9INFA	TITG	NTKWNENQNPRMFLAMITYITRNQPEWFRNVLSIAPIMFSNKMARLGKGYMFESK	360
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p Q07FH7 RDRP 196A3	SMKLRTOIPAEMLANIDLKYFNDSTKKKIEKIRPLLIDGTA <mark>SLSPGMMMGMF</mark> NMLSTVLG	420
p P03431 RDRP I34A1	SMKLRTQIPAEMLASIDLKYFNDSTRKKIEKIRPLLIEGTASLSPGMMMGMFNMLSTVLG	420
p Q9Q0V0 RDRP 196A0	SMKLRTQI PAEMLASI DLKYFNE STRKKI EKIR PLLI DGTASLS PGMMMGMFNMLSTVLG	420
r A0A0M3WG62 A0A0M3WG62 9INFA	SMKLRTQI PAEMLASIDLKYFNESTKKKIENIR PLLIDGTA <mark>SLS PGMMMGMF</mark> NMLSTVLG	420
r A0A1J0FCD5 A0A1J0FCD5 9INFA	SMKLRTQI PAEMLAS IDLKYFNE STKKKI EN IR PLLIDGTA <mark>S LS PGMMMGMF</mark> NMLSTVLG	420
r A0A023M018 A0A023M018 9INFA	SMKLRTQIPAEMLASIDLKYFNESTKKKIEKIRPLLIDGTA <mark>SLSPGMMMGMF</mark> NMLSTVLG	420
p Q0A2D9 RDRP I66A0	GMKLRTQIPAEMLASIDLKYFNDSTRKKIEKIRPLLIDGTA <mark>SLSPGMMMGMF</mark> NMLSTVLG	420
r A0A023M258 A0A023M258 _ 9INFA	SMKLRTQIPAEMLASIDLKYFNDSTKKKIEKIRPLLIDGTA <mark>SLSPGMMMGMF</mark> NMLSTVLG	420
p Q2VC92 RDRP 180A2	SMKLRTQIPAEMLANIDLKYFNESTRKKIEKIRPLLIDGTA <mark>SLSPGMMMGMF</mark> NMLSTVLG	420
p Q30NP3 RDRP 175A0	RMKLRTQIPAEMLASIDLKYFNESTRKKIEKIRPLLIDGTA <mark>SLSPGMMMGMF</mark> NMLSTVLG	420
p Q910D6 RDRP 168A4	SMKLRTQIPAEMLASIDLKYFNESTRKKIEKIRPLLIDGTA <mark>SLSPGMMMGMF</mark> NMLSTVLG	420
p P16506 RDRP_168A5	SMKLRTQIPAEMLASIDLKYFNESTRKKIEKIRPLLIDGTV <mark>SLSPGMMMGMF</mark> NMLSTVLG	420
r A0A1Z1X1S7 A0A1Z1X1S7 9INFA	SMKLRTQIPAEMLASIDLKYFNESTRKKIENIRPLLIDGTA <mark>SLSPGMMMGMF</mark> NMLSTVLG	420
p Q20NV3 RDRP 180AD	SMKLRTQIPAEMLANIDLKYFNESTRKKIEKIRPLLIDGTA <mark>SLSPGMMMGMF</mark> NMLSTVLG	420
p Q0A440 RDRP I49A1	SMKLRTQIPAEMLASIDLKYFNESTRKKIEKIRPLLIDGTA <mark>SLSPGMMMGMF</mark> NMLSTVLG	420
p Q0A2G8 RDRP_I59A0	SMKLRTQIPAEMLASIDLKYFNESTRKKIEKIRPLLIDGTA <mark>SLSPGMMMGMF</mark> NMLSTVLG	420
p Q0A2H9 RDRP 183A5	SMKLRTQIPAEMLATIDLKYFNDSTRKKIEKIRPLLIDGTA <mark>SLSPGMMMGMF</mark> NMLSTVLG	420
p P16511 RDRP_I57A5	SMKLRTQIPAEMLASIDLKYFNESTRKKIEKIRPLLIDGTV <mark>SLSPGMMMGMF</mark> MMLSTVLG	420
p Q20PL6 RDRP I79A7	SMKLRTQIPAEMLASIDLKYFNESTRKKIEKIRPLLIDGTA <mark>SLSPGMMMGMF</mark> NMLSTVLG	420
p Q0A2F7 RDRP_183A4	SMKLRTQIPAEMLANIDLKYFNESTRKKIEKIRPLLIDGTA <mark>SLSPGMMMGMF</mark> NMLSTVLG	420
r A0A1Z1X7E1 A0A1Z1X7E1_9INFA	SMKLRTQIPAEMLANIDLKYFNESTRKKIEKIRPLLIDGTA <mark>SLSPGMMMGMF</mark> NMLSTVLG	420
r A0A1Z1WYR7 A0A1Z1WYR7_9INFA	SMKLRTQIPAEILASIDLKYFNESTRKKIENIRPLLIDGTA <mark>SLSPGMMMGMF</mark> NMLSTVLG	420
r A0A1U9W475 A0A1U9W475 9INFA	SMKLRTQVPAEMLASIDLKYFNESTRKKIEKIRPLLIDGTA <mark>SLSPGMMMGMF</mark> NMLSTVLG	420
r A0A1U9W4I3 A0A1U9W4I3_9INFA	SMKLRTQVPAEMLASIDLKYFNESTRKKIEKIRPLLIDGTA <mark>SLSPGMMMGMF</mark> NMLSTVLG	420
p Q0A451 RDRP_166A1	SMKLRTQIPTEMLASIDLKYFNEPTRKKIEKIRPLLIDGTA <mark>SLSPGMMMGMF</mark> NMLSTVLG	420
p Q0A429 RDRP_I56A2	SMKLRTQIPAEMLASIDLKYFNESTRKKIERIRPLLIDGTA <mark>SLSPGMMMGMF</mark> NMLSTVLG	420
r A0A0F6ZDR7 A0A0F6ZDR7_9INFA	SMKLRTQIPAEMLASIDLKYFNESTRKKIERIRPLLIDGTA <mark>SLSPGMMMGMF</mark> NMLSTVLG	420
r A0A0F6WVQ6 A0A0F6WVQ6_9INFA	SMKLRTQIPAEMLASIDLKYFNESTRKKIEKIRPLLIDGTA <mark>SLSPGMMMGMF</mark> NMLSTVLG	420
p Q0A2Q6 RDRP_185A3	SMKLRTQIPAEMLANIDLKYFNESTRKKIEKIRPLLIDGTA <mark>SLSPGMMMGMF</mark> NMLSTVLG	420
p P16503 RDRP_I77AF	SMKLRTQIPAEMLANIDLKYFNESTRKKIEKIRPLLIDGTA <mark>SLSPGMMMGMF</mark> NMLSTVLG	420
p Q0A3Q1 RDRP_I78AC	SMKLRTQIPAEMLANIDLKYFNESTRKKIEKIRPLLIDGTA <mark>SLSPGMMMGMF</mark> NMLSTVLG	420
p Q08II5 RDRP_I80A6	SMKLRTQIPAEMLANIDLKYFNESTRKKIEKIRPLLIDGTA <mark>SLSPGMMMGMF</mark> NMLSTVLG	420
p P16513 RDRP_180A8	SMKLRTQIPAEMLANIDLKYFNESTRKKIEKIRPLLIDGTA <mark>SLSPGMMMGMF</mark> NMLSTVLG	420
r A0A023LWC1 A0A023LWC1_9INFA	SMKLRTQIPAEMLANIDLKYFNESTRKKIEKIRPLLIDGTA <mark>SLSPGMM<mark>M</mark>GMF</mark> NMLSTVLG	420
	******:*:*:**.*******: *:*****.****.***	

sp Q07FH7 RDRP I96A3	VSILNLGQKRYTKTTYWWDGLQS	SDDFALIVNAPNYAGIQAGVDRFYRTCKLL <mark>GINMSKK</mark>	480
sp P03431 RDRP I34A1	VSILNLGQKRYTKTTYWWDGLQS	SDDFALIVNAPNHEGIQAGVDRFYRTCKLLGINMSKK	480
sp Q9Q0V0 RDRP_I96A0	VSILNLGQKRYTKTTYWWDGLQS	SDDFALIVNAPNHEGIEAGVDRFYRTCKLV <mark>GINMTKK</mark>	480
tr A0A0M3WG62 A0A0M3WG62 9INFA	VSILNLGQKRYTKTTYWWDGLQS	SDDFALIVNAPNHEGIQAGVDRFYRTCKLVGINMSKK	480
tr A0A1J0FCD5 A0A1J0FCD5 9INFA	VSILNLGQKRYTKTTYWWDGLQS	SDDFALIVNAPNHEGIQAGVDRFYRTCKLVGINMSKK	480
tr A0A023M018 A0A023M018 91NFA	VSILNLGQKKYTKTTYWWDGLQS	SDDFALIVNAPNHEGIQAGVDRFYRTCKLV <mark>GINMSKK</mark>	480
sp Q0A2D9 RDRP I66A0	VSILNLGQKRYTKTTYWWDGLQS	SDDFALIVNAPNHEGIQAGVDRFYRTCKLV <mark>GINMSKK</mark>	480
tr A0A023M258 A0A023M258 9INFA	VSILNLGQKRYTKTTYWWDGLQS	SDDFALIVNAPNHEGIQAGVDRFYRTCKLV <mark>GINMSKK</mark>	480
sp Q2VC92 RDRP_180A2	VSILNLGQKRYTKTTYWWDGLQS	SDDFALIVNAPNHEGIQAGVDRFYRTCKLV <mark>GINMSKK</mark>	480
sp Q30NP3 RDRP_175A0	VSILNLGQKKYTKTTYWWDGLQS	SDDFALIVNAPNHEGIQAGVDRFYRTCKLV <mark>GINMSKK</mark>	480
sp Q910D6 RDRP_168A4	VSILNLGQKRYTKTTYWWDGLQS	SDDFALIVNAPNHEGIQAGVDRFYRTCKLV <mark>GINMSKK</mark>	480
sp P16506 RDRP_168A5	VSILNLGQKKYTKTTYWWDGLQS	SDDFALIVNAPNHEGIQAGVNRFYRTCKLVGINMSKK	480
tr A0A1Z1X1S7 A0A1Z1X1S7_9INFA	VSILNLGQKRYTKTTYWWDGLQS	SDDFALIVNAPNHEGIQAGVDRFYRTCKLVGINMSKK	480
sp Q20NV3 RDRP_180AD	VSILNLGQKRYTKTTYWWDGLQS	SDDFALIVNAPNHEGIQAGVDRFYRTCKLV <mark>GINMSKK</mark>	480
sp Q0A440 RDRP_I49A1		SDDFALIVNAPNHEGIQAGVDRFYRTCKLVGINMSKK	480
sp Q0A2G8 RDRP_I59A0	VSILNLGQKRYTKTTYWWDGLQS	SDDFALIVNAPNHEGIQAGVDRFYRTCKLV <mark>GINMSKK</mark>	480
sp Q0A2H9 RDRP_183A5	VSILNLGQKRYTKTTYWWDGLQS	SDDFALIVNAPNHEGIQAGVDRFYRTCKLVGINMSKK	480
sp P16511 RDRP_I57A5	VSILNLGQKKYTKTTYWWDGLQS	SDDFALIVNAPNHEGIQAGVDRFYRTCKLVGINMSKK	480
sp Q20PL6 RDRP_179A7	VSILNLGQKRYTKTTYWWDGLQS	SDDFALIVNAPNHEGIQAGVDRFYRTCKLV <mark>GINMSKK</mark>	480
sp Q0A2F7 RDRP_183A4		SDDFALIVNALNHEGIQAGVDRFYRTCKLV <mark>GINMSKK</mark>	480
tr A0A1Z1X7E1 A0A1Z1X7E1_9INFA	~ ~	SDDFALIVNAPNHEGIQAGVDRFYRTCKLV <mark>GINMSKK</mark>	480
tr A0A1Z1WYR7 A0A1Z1WYR7_9INFA	VSILNLGQKRYTKTTYWWDGLQS	SDDFALIVNAPNHEGIQAGVDRFYRTCKLVGINMSKK	480
tr A0A1U9W475 A0A1U9W475_9INFA	VSILNLGQKRYTKTTYWWDGLQS	SDDFALIVNAPNHEGIQAGVDRFYRTCKLVGINMSKK	480
tr A0A1U9W4I3 A0A1U9W4I3_9INFA		SDDFALIVNAPNHEGIQAGVDRFYRTCKLVGINMSKK	480
sp Q0A451 RDRP_I66A1	~ ~	SDDFALIVNAPDHEGIQAGVDRFYRTCKLV <mark>GINMSKK</mark>	480
sp Q0A429 RDRP_I56A2	VSILNLGQKRYTKTTYWWDGLQS	SDDFALIVNAPNHEGIQAGVDRFYRTCKLV <mark>GINMSKK</mark>	480
tr A0A0F6ZDR7 A0A0F6ZDR7_9INFA	VSILNLGQKRYTKTTYWWDGLQS	SDDFALIVNAPNHEGIQAGVDRFYRTCKLV <mark>GINMSKK</mark>	480
tr A0A0F6WVQ6 A0A0F6WVQ6_9INFA	VSILNLGQKRYTKTTYWWDGLQS	SDDFALIVNAPNHEGIQAGVDRFYRTCKLV <mark>GINMSKK</mark>	480
sp Q0A2Q6 RDRP_185A3	~ ~	SDDFALIVNAPNHEGIQAGVDRFYRTCKLV <mark>GINMSKK</mark>	480
sp P16503 RDRP_177AF	VSILNLGQKRYTKTTYWWDGLQS	SDDFALIVNAPNHEGIQAGVDRFYRTCKLV <mark>GINMSKK</mark>	480
sp Q0A3Q1 RDRP_I78AC	~ ~	SDDFALIVNAPNHEGIQAGVDRFYRTCKLV <mark>GINMSKK</mark>	480
sp Q08II5 RDRP_I80A6	~ ~	SDDFALIVNAPNHEGIQAGVDRFYRTCKLV <mark>GINMSKK</mark>	480
sp P16513 RDRP_180A8		SDDFALIVNAPNHEGIQAGVDRFYRTCKLV <mark>GINMSKK</mark>	480
tr A0A023LWC1 A0A023LWC1_9INFA		S <mark>DD</mark> FALIVNAPNHEGIQAGVDRFYRTCKLV <mark>GINMSK</mark> K	480
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	Palm 🧳	- 1	> Thumb			
sp Q07FH7 RDRP_196A3	KS Y	IN	TGTFEFTSFFYF	YG	FVAN FSMELPS FGVSGVNE SADMSIGVTVIKNNMINNDLG FVAN FSMELPS FGVSGINESADMSIGVTVIKNNMINNDLG	540
sp P03431 RDRP_I34A1	KSY	INR	TGTFEFTSFFYF	RYG	FVANFSMELPSFGVSGINESADMSIGVTVIKNNMINNDLG	540
sp Q9Q0V0 RDRP_I96A0	KSY	INR	TGTCEFTSFFYF	YG	FVANFSMELPSFGVSGINESADMSIGVTVIKNNMMDNDLG	540
tr A0A0M3WG62 A0A0M3WG62_9INFA	KS Y	INR	TGTFEFTSFFYF	YG	FVANFSMELPSFGVSGINESADMSIGVTVIKNNMINNDLG	540
tr A0A1J0FCD5 A0A1J0FCD5_9INFA	KSY	INR	TGTFEFTSFFYF	YG	FVANFSMELPSFGVSGINESADMSIGVTVIKNNMINNDLG	540
tr A0A023M018 A0A023M018_9INFA	KS Y	INR	TGTFEFTSFFYF	YG	FVANFSMELPSFGVSGINESADMSIGVTVIKNNMINNDLG	540
sp Q0A2D9 RDRP_I66A0	KS Y	INR	TGTFEFTSFFYF	YG	FVANFSMELPSFGVSGINESADMSIGVTVIKNNMINNDLG	540
tr A0A023M258 A0A023M258_9INFA	KSY	INR	TGTFEFTSFFYF	YG	FVANFSMELPSFGVSGINESADMSIGVTVIKNNMINNDLG	540
sp Q2VC92 RDRP_I80A2	KSY	INR	TGTFEFTSFFYF	YG	FVANFSMELPSFGVSGINESADMSIGVTVIKNNMINNDLG	540
sp Q30NP3 RDRP_I75A0	KS Y	INR	TGTFEFTSFFYF	YG	FVANFSMELPSFGVSGINESADMSIGVTVIKNNMINNDLG	540
sp Q910D6 RDRP_I68A4					FVANFSMELPSFGVSGINESADMSIGVTVIKNNMINNDLG	540
sp P16506 RDRP_I68A5					FVANFSMELPSFGVSGINESADMSIGVTVIKNNMINNDLG	540
tr A0A1Z1X1S7 A0A1Z1X1S7_9INFA					FVANFSMELPSFGVSGINESADMSIGVTVIKNNMINNDLG	540
sp Q20NV3 RDRP_I80AD	KS Y	INR	TGTFEFTSFFYF	YG	FVANFSMELPSFGVSGINESADMSIGVTVIKNNMINNDLG	540
sp Q0A440 RDRP_I49A1	KS Y	INF	TGTFEFTSFFYF	YG	FVANFSMELPSFGVSGINESADMSIGVTVIKNNMINNDLG	540
sp Q0A2G8 RDRP I59A0	KS Y	INR	TGTFEFTSFFYF	YG	FVANFSMELPSFGVSGINESADMSIGVTVIKNNMINNDLG	540
sp Q0A2H9 RDRP_I83A5	KS Y	INF	TGTFEFTSFFYF	YG	FVANFSMELPSFGVSGINESADMSIGVTVIKNNMINNDLG	540
sp P16511 RDRP_I57A5	KS Y	INR	TGTFEFTSFFYF	YG	FVANFSMELPSFGVSGINESADMSIGVTVIKNNMINNDLG	540
sp Q20PL6 RDRP_I79A7	KSY	INR	TGTFEFTSFFYF	YG	FVANFSMELPSFGVSGINESADMSIGVTVIKNNMINNDLG	540
sp Q0A2F7 RDRP_I83A4	KS Y	INR	TGTFEFTSFFYF	YG	FVANFSMELPSFGVSGINESADMSIGVTVIKNNMINNDLG	540
tr A0A1Z1X7E1 A0A1Z1X7E1_9INFA	KS Y	INR	TGTFEFTSFFYF	YG	FVANFSMELPSFGVSGINESADMSIGVTVIKNNMINNDLG	540
tr A0A1Z1WYR7 A0A1Z1WYR7 9INFA	KS Y	INR	TGTFEFTSFFYF	YG	FVANFSMELPSFGVSGINESADMSIGVTVIKNNMINNDLG	540
tr A0A1U9W475 A0A1U9W475_9INFA	KS Y	INR	TGTFEFTSFFYF	YG	FVANFSMELPSFGVSGINESADMSIGVTVIKNNMINNDLG	540
tr A0A1U9W4I3 A0A1U9W4I3_9INFA	KS Y	INR	TGTFEFTSFFYF	YG	FVANFSMELPSFGVSGINESADMSIGVTVIKNNMINNDLG	540
sp Q0A451 RDRP I66A1	KS Y	INR	TGTFEFTSFFYF	YG	FVANFSMELPSFGVSGINESADMSIGVTVIKNNMINNDLG	540
sp Q0A429 RDRP_I56A2	KSY.	INR	TGTFEFTSFFYF	YG	FVANFSMELPSFGVSGINESADMSIGVTVIKNNMINNDLG	540
tr A0A0F6ZDR7 A0A0F6ZDR7_9INFA	KS Y	INR	TGTFEFTSFFYF	YG	FVANFSMELPSFGVSGINESADMSIGVTVIKNNMINNDLG	540
tr A0A0F6WVQ6 A0A0F6WVQ6_9INFA					FVANFSMELPSFGVSGINESADMSIGVTVIKNNMINNDLG	540
sp 00A2Q6 RDRP_185A3 sp P16503 RDRP_177AF sp Q0A3Q1 RDRP_178AC sp Q08115 RDRP_180A6					FVANFSMELPSFGVSGINESADMSIGVTVIKNNMINNDLG	540
sp P16503 RDRP_I77AF					FVANFSMELPSFGVSGINESADMSIGVTVIKNNMINNDLG	540
sp Q0A3Q1 RDRP_I78AC					FVANFSMELPSFGVSGINESADMSIGVTVIKNNMINNDLG	540
sp Q08II5 RDRP_I80A6	KSY	INR	TGTFEFTSFFYF	YG	FVANFSMELPSFGVSGINESADMSIGVTVIKNNMINNDLG	540
sp P16513 RDRP_I80A8	KSY	INR	TGTFEFTSFFYF	YG	FVANFSMELPSFGVSGINESADMSIGVTVIKNNMINNDLG	540
tr A0A023LWC1 A0A023LWC1 9INFA					FVANFSMELPSFGVSGINESADMSIGVTVIKNNMINNDLG	540
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sp Q07FH7 RDRP 196A3	IRNLHIPEVCLKWELMDEDYQGRLCNPLNPFVSHKEIESVNNAVMMPAHGPAKNMEYDAV	660
sp P03431 RDRP I34A1	IRNLHIPEVCLKWELMDEDYQGRLCNPLNPFVSHKEIESMNNAVMMPAHGPAKNMEYDAV	660Ploop
sp Q9Q0V0 RDRP_196A0	IRNLHIPEAGLKWELMDEDYQGRLCNPLNPFVSHKEIESVNNAVVMPAHGPAKSMEYDAV	660
tr A0A0M3WG62 A0A0M3WG62 9INFA	IRNLHIPEVCLKWELMDEDYQGRLCNPLNPFVSHKEIESVNNAVVMPAHGPAKSMEYDAV	660
tr A0A1J0FCD5 A0A1J0FCD5_9INFA	IRNLHIPEVCLKWELMDEDYQGRLCNPLNPFVSHKEIESVNNAVVMPAHGPAKSMEYDAV	660
tr A0A023M018 A0A023M018 91NFA	IRNLHIPEVCLKWELMDEDYQGRLCNPLNPFVSHKEIESVN <mark>S</mark> AVVMPAHGPAK <mark>S</mark> MEYDAV	660
sp Q0A2D9 RDRP I66A0	IRNLHIPEVCLKWELMDEDYQGRLCNPLNPFVSHKEIESVNNAVVMPAHGPAKSMEYDAV	660
tr A0A023M258 A0A023M258 9INFA	IRNLHIPEVCLKWELMDEDYQGRLCNPLNPFVSHKEIESVNNAVVMPAHGPAKSMEYDAV	660
sp Q2VC92 RDRP I80A2	IRNLHIPEVCLKWELMDEDYQGRLCNPLNPFVSHKEIESVNNAVVMPAHGPAKSMEYDAV	660
sp Q30NP3 RDRP I75A0	IRNLHIPEVCLKWELMDEDYQGRLCNPLNPFVSHKEIESVNNAVVMPAHGPAKSMEYDAV	660
sp Q910D6 RDRP_I68A4	IRNLHIPEVCLKWELMDEDYQGRLCNPLNPFVSHKEIESVNNAVVMPAHGPAKSMEYDAV	660
sp P16506 RDRP_168A5	IRNLHIPEVCLKWELMDEDYQGRLCNPLNPFVSHKEIESVNNAVVMPAHGPAKSMEYDAV	660
tr A0A1Z1X1S7 A0A1Z1X1S7 9INFA	IRNLHIPEVCLKWELMDEDYQGRLCNPLNPFVSHKEIESVNNAVVMPAHGPAKSMEYDAV	660
sp Q20NV3 RDRP 180AD	IRNLHIPEVCLKWELMDEDYQGRLCNPLNPFVSHKEIESINNAVVMPAHGPAKSMEYDAV	660
sp Q0A440 RDRP_I49A1	IRNLHIPEVCLKWELMDEEYQGRLCNPLNPFISHKEIESVNNAVVMPAHGPAKSMEYDAF	660
sp Q0A2G8 RDRP_I59A0	IRNLHIPEVCLKWELMDEDYQGRLCNPLNPFVSHKEIESVNNAVVMPAHGPAKSMEYDAV	660
sp Q0A2H9 RDRP 183A5	IRNLHIPEVCLKWELMDEDYQGRLCNPLNPFVSHKEIESVNNAVVMPAHGPAKSMEYDAV	660
sp P16511 RDRP_I57A5	IRNLHIPEVCLKWELMDEDYQGRLCNPLNPFVSHKEIESVNNAVVMPAHGPAKSMEYDAV	660
sp Q20PL6 RDRP I79A7	IRNLHIPEVCLKWELMDEDYOGRLCNPLNPFVSHKEIESVNNAVVMPAHGPAKSMEYDAV	660
sp Q0A2F7 RDRP 183A4	IRNLHIPEVCLKWELMDEDYQGRLCNPLNPFVSHKEIESVNNAVVMPAHGPARSMEYDAV	660
tr A0A1Z1X7E1 A0A1Z1X7E1 9INFA	IRNLHIPEVCLKWELMDEDYQGRLCNPLNPFVSHKEIESVNNAVVMPAHGPAKSMEYDAV	660
tr A0A1Z1WYR7 A0A1Z1WYR7 9INFA	IRNLHIPEVCLKWELMDEDYQGRLCNPLNPFVSHKEIESVNNAVVMPAHGPAKSMEYDAV	660
tr A0A1U9W475 A0A1U9W475 9INFA	IRNLHIPEVCLKWELMDEDYOGRLCNPLNPFVSHKEIESVNNAVVMPAHGPAKSMEYDAV	660
tr A0A1U9W4I3 A0A1U9W4I3 9INFA	IRNLHIPEVCLKWELMDEDYOGRLCNPLNPFVSHKEIESVNNAVVMPAHGPAKSMEYDAV	660
sp Q0A451 RDRP 166A1	IRNLHIPEVCLKWELMDEDYOGRLCNPLNPFVSHKEIESVNNAVVMPAHGPAKSMEYDAV	660
sp Q0A429 RDRP_156A2	IRNLHIPEVCLKWELMDEDYQGRLCNPLNPFVSHKEIESVNNAVVMPAHGPAKSMEYDAV	660
tr A0A0F6ZDR7 A0A0F6ZDR7 9INFA	IRNLHIPEVCLKWELMDEDYQGRLCNPLNPFVSHKEIESVNNAVVMPAHGPAKSMEYDAV	660
tr A0A0F6WVQ6 A0A0F6WVQ6 9INFA	IRNLHIPEVCLKWELMDEDYOGRLCNPLNPFVSHKEIESVNNAVVMPAHGPAKSMEYDAV	660
sp Q0A2Q6 RDRP 185A3	IRNLHIPEVCLKWELMDEDYOGRICNPLNPFVSHKEIESVNNAVVMPAHGPAKSMEYDAV	660
sp P16503 RDRP 177AF	IRNLHIPEVCLKWELMDEDYQGRLCNPLNPFVSHKEIESVNNAVVMPAHGPAK5MEYDAV	660
sp Q0A3Q1 RDRP_I78AC	IRNLHIPEVCLKWELMDEDYQGRLCNPLNPFVSHKEIESVNNAVVMPAHGPAK5MEYDAV	660
sp Q08115 RDRP_180A6	IRNLHIPEVCLKWELMDEDYQGRLCNPLNPFVSHKEIESVNNAVVMPAHGPAK5MEYDAV	660
sp P16513 RDRP_180A8	IRNLHIPEVCLKWELMDEDYÖGRLCNPLNPFVSHKEIESVNNAVVMPAHGPAKNMEYDAV	660
tr A0A023LWC1 A0A023LWC1 9INFA	IRNLHIPEVCLKWELMDEDYOGRLCNPLNPFVSHKEIESVNNAVVMPAHGPAK 5MEYDAV	660
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		C-terminal	
sp Q07FH7 RDRP 196A3	ATTHSWV	PKRNRSILNTSQRGILEDEQMYQRCCNLFEKFFPSSSYRRPVGISSMVEAMVS	720
sp P03431 RDRP_I34A1	ATTHSWI	PKRNRSILNTSQRGVLEDEQMYQRCCNLFEKFFPSSSYRRPVGISSMVEAMVS	720
sp Q9Q0V0 RDRP_I96A0	ATTHSWI	PKRNRSILNTSQRGILEDEQMYQKCCNLFEKFFPSSSYRRPVGISSMVEAMVS	720
r A0A0M3WG62 A0A0M3WG62_9INFA	ATTHSWI	PKRNRSILNTSQRGILEDEQMYQKCCNLFEKFFPSSSYRRPVGISSMVEAMVS	720
r A0A1J0FCD5 A0A1J0FCD5_9INFA	ATTHSWI	PKRNRSILNTSQRGILEDEQMYQKCCNLFEKFFPSSSYRRPVGISSMVEAMVS	720
r A0A023M018 A0A023M018_9INFA	ATTHSWI	PKRNRSILNTSQRGILEDEQMYQKCCNLFEKFFPSSSYRRPVGISSMVEAMVS	720
sp Q0A2D9 RDRP_166A0	ATTHSWI	PKRNRSILNTSQRGILEDEQMYQKCCNLFEKFFPSSSYRRPVGISSMVEAMVS	720
r A0A023M258 A0A023M258_9INFA	ATTHSWI	PKRNRSILNTSQRGILEDEQMYQKCCNLFEKFFPSSSYRRPVGISSMVEAMVS	720
sp Q2VC92 RDRP_I80A2	ATTHSWI	PKRNRSILNTNQRGILEDEQMYQKCCNLFEKFFPSSSYRRPVGISSMVEAMVS	720
sp Q30NP3 RDRP_175A0	ATTHSWI	PKRNRSILNTSQRGILEDEQMYQKCCNLFEKFFPSSSYRRPVGISSMVEAMVS	720
sp Q910D6 RDRP_I68A4		PKRNRSILNTSQRGILEDEQMYQKCCNLFEKFFPSSSYRRPVGISSMVEAMVS	720
sp P16506 RDRP_168A5	ATTHSWT	PKRNRSILNTSQRGILEDEQMYQKCCNLFEKFFPSSSYRRPVGISSMVEAMVS	720
r A0A1Z1X1S7 A0A1Z1X1S7_9INFA		PKRNRSILNTSQRGILEDEQMYQKCCNLFEKFFPSSSYRRPVGISSMVEAMVS	720
sp Q20NV3 RDRP_180AD	ATTHSWI	PKRNRSILNTSQRGILEDEQMYQKCCNLFEKFFPSSSYRRPVGISSMVEAMVS	720
sp Q0A440 RDRP_I49A1	ATTHSWI	PKRNRSILNTSQRGILEDEQMYQKCCNLFEKFFPSSSYRRPVGISSMVEAMVS	720
p Q0A2G8 RDRP_I59A0	ATTHSWI	PKRNRSILNTSQRGILEDEQMYQKCCNLFEKFFPSSSYRRPVGISSMVEAMVS	720
p Q0A2H9 RDRP_I83A5	ATTHSWI	PKRNRSILNTSQRGILEDEQMYQKCCNLFEKFFPSSSYRRPVGISSMVEAMVS	720
p P16511 RDRP_I57A5	ATTHSWI	PKRNRSILNTSQRGILEDEQMYQKCCNLFEKFFPSSSYRRPVGISSMVEAMVS	720
p Q20PL6 RDRP_I79A7	ATTHSWI	PKRNRSILNTSQRGILEDEQMYQKCCNLFEKFFPSSSYRRPVGISSMVEAMVS	720
p Q0A2F7 RDRP_183A4	ATTHSWT	PKRNRSILNTSQRGILEDEQMYQKCCNLFEKFFPSSSYRRPVGISSMVEAMVS	720
r A0A1Z1X7E1 A0A1Z1X7E1_9INFA	ATTHSWI	PKRNRSILNTSQRGILEDEQMYQKCCSLFEKFFPSSSYRRPVGISSMVEAMVS	720
r A0A1Z1WYR7 A0A1Z1WYR7_9INFA	ATTHSWI	PKRNRSILNTSQRGILEDEQMYQKCCNLFEKFFPSSSYRRPVGISSMVEAMVS	720
r A0A1U9W475 A0A1U9W475 9INFA	ATTHSWI	PKRNRSILNTSQRGILEDEQMYQKCCNLFEKFFPSSSYRRPVGISSMVEAMVS	720
r A0A1U9W4I3 A0A1U9W4I3 9INFA	ATTHSWI	PKRNRSILNTSQRGILEDEQMYQKCCNLFEKFFPSSSYRRPVGISSMVEAMVS	720
sp Q0A451 RDRP I66A1	ATTHSWI	PKRNRSILNTSQRGILEDEQMYQKCCNLFEKFFPSSSYRRPVGISSMVEAMVS	720
p Q0A429 RDRP_156A2	ATTHSWI	PKRNRSILNTSQRGILEDEQMYQKCCNLFEKFFPSSSYRRPVGISSMVEAMVS	720
r A0A0F6ZDR7 A0A0F6ZDR7 9INFA	ATTHSWI	PKRNRSILNTSQRGILEDEQMYQKCCNLFEKFFPSSSYRRPVGISSMVEAMVS	720
r A0A0F6WVQ6 A0A0F6WVQ6 9INFA	ATTHSWI	PKRNRSILNTSQRGILEDEQMYQKCCSLFEKFFPSSSYRRPVGISSMVEAMVS	720
sp Q0A2Q6 RDRP 185A3	ATTHSWI	PKRNRSILNTSQRGILEDEQMYQKCCSLFEKFFPSSSYRRPVGISSMVEAMVS	720
p P16503 RDRP_I77AF	ATTHSWI	PKRNRSILNTSQRGILEDEQMYQKCCNLFEKFFPSSSYRRPVGISSMVEAMVS	720
p Q0A3Q1 RDRP I78AC	ATTHSWI	PKRNRSILNTSQRGILEDEQMYQKCCNLFEKFFPSSSYRRPVGISSMVEAMVS	720
p Q08II5 RDRP_I80A6	ATTHSWI	PKRNRSILNTSQRGILEDEQMYQKCCNLFEKFFPSSSYRRPVGISSMVEAMVS	720
p P16513 RDRP 180A8	ATTHSWI	PKRNRSILNTSQRGILEDEQMYQKCCNLFEKFFPSSSYRRPVGISSMVEAMVS	720
r A0A023LWC1 A0A023LWC1_9INFA	ATTHSWI	PKRNRSILNTSQRGILEDEQMYQKCCNLFEKFFPSSSYRRPVGISSMVEAMVS	720
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sp Q07FH7 RDRP_196A3	RARIDARIDFESGRIKKEEFAEIMKTCSTIEDLE <mark>RQK</mark> -	757
sp P03431 RDRP_I34A1	RARIDARIDFESGRIKKEEFTEIMKICSTIEELRRQK-	757
sp Q9Q0V0 RDRP_I96A0	RARIDARIDFESGRIKKEEFAEIMKICSTIEELGROK-	757
tr A0A0M3WG62 A0A0M3WG62_9INFA	RARIDARIDFESGRIKKEEFAEIMKICSTIEELRRQK-	757
tr A0A1J0FCD5 A0A1J0FCD5 9INFA	RARIDARIDFESGRIKKEEFAEIMKICSTIEELFROK-	757
tr A0A023M0I8 A0A023M0I8 9INFA	RARIDARIDFESGRINKEEFAEIMKICSTIEELFROK	757
sp Q0A2D9 RDRP I66A0	RARIDARIDFESGRIKKEEFAEIMKICSTIEELFROK-	757
tr A0A023M258 A0A023M258 9INFA	RARIDARIDFESGRIKKEEFAEIMKICSTIEELFROK-	757
sp Q2VC92 RDRP I80A2	RARIDARIDFESGRIKKEEFAEIMKICSTIEELFRQK-	757
sp Q30NF3 RDRF I75A0	RARIDARIDFESGRIKKEEFSEIMKICSTIEELFROK-	757
sp Q910D6 RDRP_168A4	RARIDARIDFESGRIKKEEFAEIMKICSTIEELFROK-	757
sp P16506 RDRP 168A5	RARIDARIDFESGRIKKEEFAEIMKICSTIEELFROK-	757
tr A0A1Z1X1S7 A0A1Z1X1S7 9INFA	RARIDARIDFESGRIKKEEFAEIVKICSTIEELEROK	757
sp Q20NV3 RDRP I80AD	RARIDARIDFESGRIKKEEFSEIMKICCTIEELFROK	757
sp Q0A440 RDRP I49A1	RARIDARIDFESGRIKKEEFAEIMKICSTIEELFROK-	757
sp Q0A2G8 RDRP I59A0	RARIDARIDFESGRIKKEEFAEIMKICSTIEELEROKO	758
sp Q0A2H9 RDRP I83A5	RARIDARIDFESGRIKKEEFAEIMKICSTIEELFROK	757
sp P16511 RDRP 157A5	RARIDARIDFESGRIKKEEFAEIMKICSTIEELEROK	757
sp Q20PL6 RDRP I79A7	RARIDARIDFESGRIKKEEFAEIMKICSTIEELEROK	757
sp Q0A2F7 RDRP I83A4	RARIDARIDFESGRVKKEEFAEIMKICSTIEELFROK-	757
tr A0A1Z1X7E1 A0A1Z1X7E1 9INFA	RARIDARIDFESGRIKKEEFAEIMKICSTIEEIROK	757
tr A0A1Z1WYR7 A0A1Z1WYR7 9INFA	RARIDARIDFESGRIKKEEFAEIMKICSTIEELEROK	757
tr A0A1U9W475 A0A1U9W475 9INFA	RARIDARIDFESGRIKKEEFAEIMKICSTIEELFROK	757
tr A0A1U9W4I3 A0A1U9W4I3 9INFA	RARIDARIDFESGRIKKEEFAEIMKICSTIEELEROK	757
sp Q0A451 RDRP 166A1	RARIDARIDFESGRIKKEEFAEIMKICSTIEELEROK	757
sp Q0A429 RDRP_I56A2	RARIDARIDFESGRIKKEEFAEIMKICSTIEELEROK	757
tr A0A0F6ZDR7 A0A0F6ZDR7 9INFA	RARIDARIDFESGRIKKEEFAEIMKICSTIEELEROK	757
tr A0A0F6WVO6 A0A0F6WVO6 9INFA	RARIDARIDFESGRIKKEEFAEIMKICSTIEELROK	757
sp Q0A2Q6 RDRP 185A3	RARIDARIDFESGRIKKEEFAEIMKICSTIEELEROK	757
sp P16503 RDRP 177AF	RARIDARIDFESGRIKKEEFAEIMKICSTIEELEROK	757
sp Q0A3Q1 RDRP I78AC	RARIDARIDFESGRIKKEEFAEIMKICSTIEELEROK	757
sp Q08II5 RDRP I80A6	RARIDARIDFESGRIKKEEFAEIMKICSTIEELROK	757
sp P16513 RDRP I80A8	RARIDARIDFESGRIKKEEFAEIMKICSTIEELFROK	757
tr A0A023LWC1 A0A023LWC1 9INFA	RARIDARIDFESGRIKKEEFAEIMKICSTIEELFROK	757
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Q07FH7|RDRP_I96A3 (China/Nanchang/11/1996/ H1N1) P03431|RDRP_I34A1 (Puerto Rico/8/1934/ H1N1) (~pI = 9.39) Q9Q0V0|RDRP_I96A0 (Goose/Guangdong/1/1996/ H5N1) A0A0M3WG62_9INFA (Black-headed gull/Netherlands/26/2009/ H16N3) A0A1J0FCD5_9INFA (Black-headed gull/Netherlands/16/2009/ H16N3) A0A023M0I8_9INFA (Mallard/Wisconsin/503/1976/ H12N6) Q0A2D9|RDRP_I66A0 (Turkey/ Ontario/ 7732/1966/ H5N9) A0A023M258_9INFA (Mallard/Wisconsin/214/1977/ H12N2) Q2VC92|RDRP_I80A2 (Seal/ Massachusetts/ 1/1980/ H7N7) Q30NP3|RDRP_I75A0 (Beijing/39/1975/ H3N2) Q910D6|RDRP_I68A4 (Hong Kong/1/1968/ H3N2) P16506|RDRP_I68A5 (Korea/426/1968/ H2N2) A0A1Z1X1S7_9INFA (Black-headed gull/Netherlands/43/2008/ H16N8) Q20NV3|RDRP_I80AD (Gull/Minnesota/945/1980/ H13N6) Q0A440|RDRP_I49A1 (Duck/Germany/1949/ H10N7) Q0A440|RDRP_I49A1 (Duck/Germany/1949/ H10N7) Q0A2G8|RDRP_I59A0 (Chicken/Scotland/1959/ H5N1) Q0A2H9|RDRP_I83A5 (Chicken/ Pennsylvania/ 1/1983/ H5N2) P16511|RDRP_I57A5 (Singapore/1/1957/ H2N2) Q20PL6|RDRP_I79A7 (Grey teal/ Australia/ 2/1979/ H4N4) Q0A2F7|RDRP_I83A4 (Turkey/ Ireland/ 1378/ 1983/ H5N8) A0A1Z1X7E1_9INFA/ Mallard duck/Sweden/139647/2012/ H15N5) A0A1Z1WYR7_9INFA (Black-headed gull/Netherlands/78/2008/ H16N3) A0A1U9W475_9INFA (Blue-winged teal/Guatemala/CIP049H110-31/2012/ H14N3) A0A1U9W4I3 9INFA (Blue-winged teal/Guatemala/CIP049H113-08/2013/ H14N4) Q0A451|RDRP_I66A1 (Turkey/Wisconsin/1/1966/ H9N2) Q0A429|RDRP_I56A2 (Duck/England/1/1956/ H11N6) A0A0F6ZDR7_9INFA (Environment/Maryland/06OS280/2006/ H7N3) A0A0F6WVQ6_9INFA (Mallard/Maryland/06OS2334/2006/ H12N5) Q0A2Q6|RDRP_I85A3 (Chicken/Victoria/1/1985/ H7N7) P16503|RDRP_I77AF (Gull/Maryland/704/1977/ H13N6) Q0A3Q1|RDRP_I78AC (Turkey/ Minnesota/ 501/1978/ H6N8) Q08II5|RDRP_I80A6 /Duck/Hokkaido/8/1980/ H3N8) P16513]RDRP_I80A8 (Turkey/ Minnesota/ 833/1980/ H4N2) A0A023LWC1_9INFA/ Mallard/Wisconsin/2080/1984(H8N4)

Figure 4 MSA of the PB1 catalytic subunits of the RdRp from human influenza A virus

Figure 5 shows the MSA of the catalytic subunits PB1 of the polymerase in different human influenza B viral strains from different regions. The standard strain, Lee 1948, showed a theoretical pI of 8.78. The subunits from various strains are completely conserved for the entire sequence with only a few amino acid changes (Fig. 5). The metal-binding regions are highlighted in dark green and the proposed amino acids in the catalytic regions and the highly conserved fingertip priming loop are highlighted in yellow. An invariant direct repeat is observed in influenza B viral strains and is marked by arrows. All the five motifs identified in influenza A viral strains are also highly conserved in the B virus: Motif I – KLKRR- Motif II $-^{303}$ TGDN³⁰⁶-; Motif III $-^{403}$ LSPGMMMGMF⁴¹²-; Motif IV $-^{438}$ WDGLQSSDDFAL*F*⁴⁵⁰-; Motif V- 474 GINMSKKKSYC⁴⁸⁴- (highlighted in dark and light green) suggesting their importance in the polymerase function. The NLS region is highlighted in orange. Interestingly, the cold-adapted and wild-type strains differ only in three amino acids and are marked with stars. Among them, two are conservative replacements, whereas only one is a non-conservative type (Y→H), which is found at the C-terminal end. In influenza B virus, also the completely conserved $-^{22}$ YAQ- motif (highlighted in yellow) is found as in influenza A viruses, suggesting its possible importance as in SARS-CoV-2 (YAN). Besides, a zinc-binding domain is also found in the PB1 subunits of the B viral strains in the mRNA catalytic region.

3.1.2. CLUSTAL O (1.2.4) MSA of the PB1 catalytic subunits of the RdRp from human influenza B viruses

r A0A126TPY5 A0A126TPY5_9INFB	tgctmvdptngplpednepsa <mark>yaql</mark> dcvlealdrmdeehpglfqaasqnamealmvttvd	12
r I2E0T1 I2E0T1_9INFB	TGCTMVDPTNGPLPEDNEPSA <mark>YAQL</mark> DCVLEALDRMDEEHPGLFQAASQNAMEALMVTTVD	12
r B4UQS5 B4UQS5_9INFB	TGCTMVDPTNGPLPEDNEPSA <mark>YAQL</mark> DCVLEALDRMDEEHPGLFQAASQNAMEALMVTTVD	12
r A3DQQ8 A3DQQ8_9INFB	TGCTMVDPTNGPLPEDNEPSA <mark>YAQL</mark> DCVLEALDRMDEEHPGLFQAASQNAMEALMVTTVD	12
r A0A140ERC2 A0A140ERC2 9INFB	TGCTMVDPTNGPLPEDNEPSA <mark>YAQL</mark> DCVLEALDRMDEEHPGLFQAASQNAMEALMVTTVD	12
r A0A126TR22 A0A126TR22 9INFB	TGCTMVDPTNGPLPEDNEPSA <mark>VAOL</mark> DCVLEALDRMDEEHPGLF0AASONAMEALMVTTVD	12
A0A059TB43 A0A059TB43 9INFB	TGCTMVDPTNGPLPEDNEPSAYAOLDCVLEALDRMDEEHPGLF0AASONAMEALMVTTVD	12
A0A140EMR9 A0A140EMR9 9INFB	T GCTMV DP TN GP L PE DN E P SA YAQL D CV LE AL D RM DE EH PG L FQ AA SQ NAMEA LMVT TV D	12
A0A140EUR3 A0A140EUR3 9INFB	TGCTMVDPTNGPLPEDNEPSAYAQLDCVLEALDRMDEEHPGLFQAA SQNAMEALMVTTVD	12
A0A126TSN3 A0A126TSN3 9INFB	TGCTMVDFTNGFDFEDNEFSATAQLDCVDEALDRMDEENFGDFQAASQNAMEALMVTTVD	12
A0A12613N3 A0A12613N3_91NFB	TGCTMVDFINGFDFEDNEFSATAQIDCVDEALDRMDEENFGDFQAASQNAMEADMVTTVD	12
		12
A0A0D6A5W0 A0A0D6A5W0_9INFB	TGCTMI DPTNGPL PEDNEP SA <mark>YAQL</mark> DCVLEALDRMDE EH PGL FQAA SQNAMEALMVT TVD	
036430 RDRP_INBP9	T GCTMV DP TN GP L PE DN E P SA <mark>YAQ L</mark> DCV LE ALD RM DE EH PG L F Q AA S Q NAMEA LM VT TV D	12
A52216 A52216_91NFB	T GCTMV DP TN GP LPE DN EP SA <mark>YAQ L</mark> D CV LE ALDRM DE EH PGL FQ AA SQNAMEA LMVT TV D	12
A4D528 A4D528_9INFB	TGCTMVDPTNGPLPEDNEPSA <mark>YAQL</mark> DCVLEALDRMDEEHPGLFQAASQNAMEALMVTTVD	12
A4D4U0 A4D4U0_9INFB	TGCTMVDPTNGPLPEDNEPSA <mark>YAQL</mark> DCVLEALDRMDEEHPGLFQAASQNAMEALMVTTVD	1.
A3DRF0 A3DRF0_9INFB	T GC TMV DP TN GP LPE DN EP SA <mark>YAQ L</mark> D CV LEAL DRM DE EH PG LFQAA SQNAMEA LMVT TV D	12
A4D4V1 A4D4V1 9INFB	TGCTMVDPTNGPLPEDNEPSA <mark>YAQL</mark> DCVLEALDRMDEEHPGLFQAASQNAMEALMVTTVD	12
B4UOB0 B4UOB0 9INFB	TGCTMVDPTNGPLPEDNEPSA <mark>YAQ</mark> DCVLEALDRMDEEHPGLFQAASQNAMEALMVTTVD	12
A4D4M4 A4D4M4 9INFB	TGCTMVDPTNGPLPEDNEPSA <mark>YAQ</mark> DCVLEALDRMDEEHPGLFQAASQNAMEALMVTTVD	12
P07832 RDRP INBLE	TGCVMVDPTNGPLPEDNEPSAYAQLDCVLEALDRMDEEHPGLFQAGSQNAMEALMVTTVD	1
G7WTR6 G7WTR6 9INFB	TGCTMVDPTNGPLPEDNEPSA <mark>YAQL</mark> DCVLEALDRMDEEHPGLFQAASQNAMEALMVTTVD	12
A0A2D1W9N9 A0A2D1W9N9 9INFB	TGCTMVDPTNGPLPEDNEPSATAQLDCVLEALDRMDEEHPGLFQAASQNAMEALMVTTVD TGCTMVDPTNGPLPEDNEPSA <mark>YAQL</mark> DCVLEALDRMDEEHPGLFQAASQNAMEALMVTTVD	12
		1
A0A216BBP3 A0A216BBP3_9INFB	TGCTMVDPTNGPLPEDNEPSA <mark>YAQL</mark> DCVLEALDRMDEEHPGLFQAASQNAMEALMVTTVD	
AOA119TNG8 AOA119TNG8 9INFB	TGCTMVDPTNGPLPEDNEPSA <mark>YAQL</mark> DCVLEALDRMDEEHPGLFQAASQNAMEALMVTTVD	1
A0A075CCJ9 A0A075CCJ9_9INFB	T GCTMV DP TN GP L PE DN EP SA <mark>YAQ L</mark> D CV LEALD RM DE EH PG L FQAA SQ NAMEA LMVT TV D	1.
S4SZ61 S4SZ61_9INFB	T GCTMV DP TN GP L PE DN EP SA <mark>YAQL</mark> DCV LEALD RM DE EH PG L FQAA SQNAMEA LM VT TV D	1
A0A0N7GD33 A0A0N7GD33_9INFB	TGCTMVDPTNGPLPEDNEPSA <mark>YAQL</mark> DCVLEALDRMDEEHPGLFQAASQNAMEALMVTTVD	1
A0A248XLR8 A0A248XLR8 9INFB	TGCTMVDPTNGPLPEDNEPSA <mark>YAQL</mark> DCVLEALDRMDEEHPGLFQAASQNAMEALMVTTVD	1.
A0A286NMR2 A0A286NMR2 9 IN FB	TGCTMVDPTNGPLPEDNEPSA <mark>YAQL</mark> DCVLEALDRMDEEHPGLFQAASQNAMEALMVTTVD	1:
A0A2D1W2J9 A0A2D1W2J9 9INFB	TGCTMVDPTNGPLPEDNEPSA <mark>YAQ</mark> DCVLEALDRMDEEHPGLFQAASQNAMEALMVTTVD	1:
A3DR07 A3DR07 INBBK	TGCTMV DP TNGP LPE DNEP SA YAQL DCV LE ALDRMDE EH PG LFQAA SONAMEA LMVT TV D	13
A3DQR9 A3DQR9 9INFB	TGCTMVDPTNGPLPEDNEPSAYAQLDCVLEALDRMDEEHPGLFQAA SQNAMEALMVTTVD	12
A4D4X3 A4D4X3 9INFB	TGCTMVDFINGPLPEDNEPSAYAOLDCVLEALDRMDEEHPGLFOAA SONAMEALMVTTVD	12
ID12071 DDDD TNDAC	MCC3 MUDDENICDI DEDNED C3 VA OLD CULE 3 I DDNDE ENDCI EO 3 3 CONSMES I MUEBUD	
	TGCAMVDPTNGPLPEDNEPSA <mark>YAQL</mark> DCVLEALDRMDEEHPGLFQAASQNAMEALMVTTVD	12
p P13871 RDRP_INBAC p P13872 RDRP_INBAD	TGCAMUDPTNGFLPEDNEPSAYAQLDCVLEALDRMDEEHFGLFQAASQNAMEALMVTTVD TGCAMUDPTNGFLPEDNEPSAYAQLDCVLEALDRMDEEHFGLFQAASQNAMEALMVTTVD ***.*.*******************************	12
	T GCAMV DP TN GP L PE DN E P SA <mark>YAQ L</mark> D CV LE ALD RM DE EH PG L F Q AA S Q NAMEA LM VT TV D	
9 913872 RDRP_INBAD	TGCAMVDPTNGPLPEDNEPSA <mark>YAQL</mark> DCVLEALDRMDEEHPGLFQAASQNAMEALMVTTVD	1:
r A0A126TPY5 A0A126TPY5_9INFB	TGCAMVDPTNGPLPEDNEPSAYAQLDCVLEALDRMDEEHPGLFQAASONAMEALMVTTVD	240
r A0A126TPY5 A0A126TPY5_9INFB r 12E0T1 12E0T1_9INFB	TGCAMVDPTNGPLPEDNEPSA YAQLDCVLEALDRMDEEHPGLFQAASQNAMEALMVTTVD	240 240
<pre>p p13872 RDRP_INBAD r A0A126TPY5 A0A126TPY5_9INFB r I2E0T1 I2E0T1_9INFB r B4UQS5 B4UQS5_9INFB</pre>	TGCAMVDPTNGPLPEDNEPSA YAQLDCVLEALDRMDEEHPGLFQAASONAMEALMVTTVD	1 240 240 240 240
	TGCAMVDPTNGPLPEDNEPSA YAQLDCVLEALDRMDEEHPGLFQAASONAMEALMVTTVD	240 240 240 240 240
<pre>> P13872 RDRP_INBAD c A0A126TPY5 A0A126TPY5_9INFB c I2E0T1 I2E0T1_9INFB c I4UQ55 B4UQ55_9INFB c A3DQ08 A3DQ08_9INFB c A0A140ERC2 A0A140ERC2_9INFB</pre>	TGCAMVDPTNGPLPEDNEPSA YAQLDCVLEALDRMDEEHPGLFQAASQNAMEALMVTTVD *** *********************************	240 240 240 240 240 240
<pre>> P13872 RDRP_INBAD c A0A126TPY5 A0A126TPY5_9INFB c I2E0T1 I2E0T1_9INFB c B4UQS5 B4UQS5_9INFB c A0A140ERC2 A0A140ERC2_9INFB c A0A140ERC2 A0A126TR22_9INFB</pre>	TGCAMVDPTNGPLPEDNEPSA YAQLDCVLEALDRMDEEHPGLFQAASONAMEALMVTTVD	240 240 240 240 240 240 240
<pre>> P13872 RDRP_INBAD </pre> <pre>c A0A126TPY5 A0A126TPY5_9INFB </pre> <pre>c I2E0T1 I2E0T1_9INFB </pre> <pre>c B40Q55 B40Q55_9INFB </pre> <pre>c A0A140ERC2 A0A140ERC2_9INFB </pre> <pre>c A0A126TR22 A0A126TR22_9INFB </pre> <pre>c A0A059TB43 A0A059TB43_9INFB</pre>	TGCAMVDPTNGPLPEDNEPSAYAQLDCVLEALDRMDEEHPGLFQAASONAMEALMVTTVD	240 240 240 240 240 240 240 240
<pre>> P13872 RDRF_INBAD c A0A126TPY5 A0A126TPY5_9INFB c I2E0T1 I2E0T1_9INFB c B4UQ55 B4UQ55_9INFB c A3DQ08 A3DQ08_9INFB c A0A140ERC2 A0A140ERC2_9INFB c A0A140ERC2 A0A126TR22_9INFB c A0A16TR22 A0A140EMR5_9INFB c A0A140EMR9 A0A140EMR5_9INFB</pre>	TGCAMVDPTNGPLPEDNEPSAYAQLDCVLEALDRMDEEHPGLFQAASONAMEALMVTTVD *** *********************************	1. 240 240 240 240 240 240 240 240 240
<pre>> P13872 RDRF_INBAD = A0A126TPY5 A0A126TPY5_9INFB = I2E0T1 I2E0T1_9INFB = B4UQ55 B4UQ55_9INFB = A0A140ERC2 A0A140ERC2_9INFB = A0A146TR22 A0A126TR22_9INFB = A0A140ERR9 A0A140ERR9_9INFB = A0A140ERR9 A0A140ERR9_9INFB</pre>	TGCAMVDPTNGPLPEDNEPSAYAQLDCVLEALDRMDEEHPGLFQAASONAMEALMVTTVD *** *********************************	1. 240 240 240 240 240 240 240 240 240 240
<pre>> P13872 RDRF_INBAD > A0A126TPY5 A0A126TPY5_9INFB > I2E0T1 I2E0T1_9INFB > I2E0T1 I2E0T1_9INFB > A3DQ08 A3DQ08_9INFB > A0A140ERC2 A0A140ERC2_9INFB > A0A126TR22 A0A126TR22_9INFB > A0A140EMR9 A0A140EMR9_9INFB > A0A140EMR3 A0A140EMR9_9INFB > A0A140EMR3 A0A140EMR3_9INFB > A0A126TSN3 A0A126TSN3_9INFB</pre>	TGCAMVDPTNGPLPEDNEPSAYAQLDCVLEALDRMDEEHPGLFQAASONAMEALMVTTVD *** * *******************************	1. 240 240 240 240 240 240 240 240 240 240
<pre>> P13872 RDRP_INBAD > A0A126TPY5 A0A126TPY5_9INFB > I2E0T1 I2E0T1_9INFB > B4UQ55 B4UQ55_9INFB > A3DQ08 A3DQ08_9INFB > A0A140ERC2 A0A140ERC2_9INFB > A0A140ERC2 A0A140ERC2_9INFB > A0A140ERB9 A0A140ERR5_9INFB > A0A140ERB9 A0A140ERR5_9INFB > A0A140ERS1 A0A126TN3_9INFB > A0A126US31 A0A126US3_9INFB > A0A126US31 A0A126US3_9INFB</pre>	TGCAMVDPTNGPLPEDNEPSAYAQLDCVLEALDRMDEEHPGLFQAASONAMEALMVTTVD *** *********************************	1. 240 240 240 240 240 240 240 240 240 240
<pre>(100A126TPY51A0A126TPY5_9INFB (12E0T1)12E0T1_9INFB (12E0T1)12E0T1_9INFB (1A0A126TPY51A0A126TPY5_9INFB (1A0A0051B4UQ55_9INFB (1A0A10ERC21A0A140ERC2_9INFB (1A0A10ERC21A0A140ERC2_9INFB (1A0A140ERC31A0A140ERC3_9INFB (1A0A140ERC31A0A140ERC3_9INFB (1A0A140ERC31A0A140ERC3_9INFB (1A0A140ERC31A0A140ERC3_9INFB (1A0A126TSN31A0A126TSN3_9INFB (1A0A126TSN31A0A126TSN3_9INFB (1A0A126TSN31A0A126TSN3_9INFB (1A0A126TSN31A0A126TSN3_9INFB (1A0A126TSN31A0A126TSN3_9INFB (1A0A06A5%01A0A0D6A5%0_9INFB</pre>	TGCAMVDPTNGPLPEDNEPSA YAQLDCVLEALDRMDEEHPGLFQAASONAMEALMVTTVD *** *********************************	1. 240 240 240 240 240 240 240 240 240 240
P13872 RDRP_INBAD A0A126TPY5 A0A126TPY5_9INFB I2E0T1 I2E0T1_9INFB B4UQ55 B4UQ55_9INFB A0A140ERC2 A0A140ERC2_9INFB A0A140ERC2 A0A140ERC2_9INFB A0A140ERC3 A0A126TR22_9INFB A0A140ERC3 A0A140ERR9_9INFB A0A140ERR9 A0A140ERR9_9INFB A0A126TSN3 A0A126TSN3_9INFB A0A126TSN3 A0A126TSN3_9INFB	T GCAMV DP TN GP LPE DNEP SA YAQ LD CV LEALDRM DE EH PG LFQAA SONAMEALMVTT VD *** ********************************	1. 240 240 240 240 240 240 240 240 240 240
P13872 RDRP_INBAD A0A126TPY5 A0A126TPY5_9INFB I2E0T1 I2E0T1_9INFB B4UQ55 B4UQ55_9INFB A3DQ08 A3DQ08_9INFB A0A140ERC2 A0A140ERC2_9INFB A0A140ERC2 A0A140ERC2_9INFB A0A140ERS]A0A140ERR5_9INFB A0A140ERS]A0A140ERR5_9INFB A0A140ERS]A0A140ERR5_9INFB A0A126TN3 A0A126TN3_9INFB A0A126UA37 A0A126UA37_9INFB A0A126UA37 A0A126UA37_9INFB A0A126UA37 A0A126UA37_9INFB A0A0D6A5W0 A0A0D6A5W0_9INFB A0A2161X200A55W1]BP9 A52216 A52216_9INFB	TGCAMVDPTNGPLPEDNEPSA YAQLDCVLEALDRMDEEHPGLFQAASONAMEALMVTTVD *** *********************************	1. 240 240 240 240 240 240 240 240 240 240
<pre>(100A126TPY51A0A126TPY5_9INFB (12E0T112E0T1_9INFB (12E0T112E0T1_9INFB (1A0A126TPY51A0A126TPY5_9INFB (1A0A10ERC21A0A140ERC2_9INFB (1A0A10ERC21A0A140ERC2_9INFB (1A0A10ERMS1A0A140ERC2_9INFB (1A0A10EMR91A0A140EUR3_9INFB (1A0A140EUR31A0A140EUR3_9INFB (1A0A140EUR31A0A140EUR3_9INFB (1A0A126TSN31A0A126UA37_9INFB (1A0A126TSN31A0A126UA37_9INFB (1A0A126GSN01A0A06A5N0_9INFB (1A0A106A5W01A0A06A5N0_9INFB (1A0216A522I619INFB) (1A522I61A522I6_9INFB (1A522161A522I6_9INFB)</pre>	TGCAMVDPTNGPLPEDNEPSA YAQLDCVLEALDRMDEEHPGLFQAASONAMEALMVTTVD *** *********************************	1. 240 240 240 240 240 240 240 240 240 240
P13872 RDRP_INBAD A0A126TPY5 A0A126TPY5_9INFB I2E0T1 I2E0T1_9INFB B4UQS5 B4UQS5_9INFB A0A140ERC2 A0A140ERC2_9INFB A0A140ERC2 A0A140ERC2_9INFB A0A140ERC3 A0A140ERC3_9INFB A0A140ERC3 A0A140ERC3_9INFB A0A140ERS3 A0A140ERC3_9INFB A0A126TS3 A0A126TS33_9INFB A0A126TS3 A0A126TS33_9INFB A0A126IS3 A0A126TS33_9INFB A0A126IS3 A0A126IS3_9INFB A0A126IS3 A0A126IS3_9INFB A0A126IS3 A0A126IS3_9INFB A0A126IS3 A0A126IS3_9INFB A0A126IS3 A0A126IS3_9INFB A0A26IS3 A0D6A5W0_9INFB A4D528 A4D528_9INFB A4D40 A4D4U0_9INFB	TGCAMVDPTNGPLPEDNEPSA YAQLDCVLEALDRMDEEHPGLFQAASONAMEALMVTTVD *** *********************************	1 240 240 240 240 240 240 240 240 240 240
P13872 RDRP_INBAD A0A126TPY5 A0A126TPY5_9INFB I2E0T1 I2E0T1_9INFB B4UQ55 B4UQ55_9INFB A3DQ08 A3DQ08_9INFB A0A140ERC2 A0A140ERC2_9INFB A0A140ERC2 A0A140ERC2_9INFB A0A140ERS A0A140ERR9_9INFB A0A140ERS A0A140ERR9_9INFB A0A140ERS A0A140ERR9_9INFB A0A126TN3 A0A126UA37_9INFB A0A126UA37 A0A126UA37_9INFB A0A126UA37 A0A126UA37_9INFB A0A126UA37 A0A126UA37_9INFB A0A1528 A4D528_9INFB A4528 A4D528_9INFB A4528 A4D528_9INFB A4528 A4D528_9INFB A4528 A4D528_9INFB A4558 A4D528_9INFB	TGCAMVDPTNGPLPEDNEPSA YAQLDCVLEALDRMDEEHPGLFQAASONAMEALMVTTVD *** *********************************	1. 240 240 240 240 240 240 240 240 240 240
<pre>(A0A126TPY5/A0A126TPY5_9INFB (A0A126TPY5/A0A126TPY5_9INFB (I2E0T1/I2E0T1_9INFB (A3DQ08/A3DQ08_9INFB (A0A140ERC2/A0A140ERC2_9INFB (A0A140ERC2/A0A140ERC2_9INFB (A0A140ERC2/A0A140ERC3_9INFB (A0A140ERC3/A0A140ERC3_9INFB (A0A140ERC3/A0A140ERC3_9INFB (A0A140ERC3/A0A140ERC3_9INFB (A0A140ERC3/A0A140ERC3_9INFB (A0A126TSN3/A0A126TSN3_9INFB (A0A126TSN3/A0A126TSN3_9INFB (A0A126TSN3/A0A126TSN3_9INFB (A0A126TSN3/A0A126TSN3_9INFB (A0A126TSN3/A0A126TSN3_9INFB (A0A126130/A0A056A5W0) (A0A0545W0/A0A056A5W0) (A52216/A52216_9INFB) (A452216/A52216_9INFB (A45218/A5528_9INFB) (A45218/A5528_9INFB) (A45218/A5528_9INFB) (A454400/A44040_9INFB) (A454400/A44040_9INFB)</pre>	TGCAMVDPTNGPLPEDNEPSA YAQLDCVLEALDRMDEEHPGLFQAASONAMEALMVTTVD *** *********************************	1 240 240 240 240 240 240 240 240 240 240
<pre>> P13872 RDRP_INBAD > P13872 RDRP_INBAD > I2071 I2071_91NFB > I2071 I2071_91NFB > I2071 I2071_91NFB > I40025 I40055_91NFB > A00140ERC2 A0A140ERC2_9INFB > A00126TR22 A0A140ERC2_9INFB > A0A140ERC9 A0A140ERC3_9INFB > A0A140ER8 A0A140ERC3_9INFB > A0A140ER8 A0A140ER3_9INFB > A0A126TN3 A0A126TN3]9INFB > A0A126TN3 A0A126UA37_9INFB > A0A126IN3 A0A126UA37_9INFB > A0A126IN3 A0A126UA37_9INFB > A0A126IN3 A0A126UA37_9INFB > A0A126IN3 A0A126UA37_9INFB > A0A126IN5P_INBP9 > A4D528 A4D528_9INFB > A4D40 A4D4U0_9INFB > A4D528 A4D528_9INFB > A4D40 A4D4U0_9INFB > A4D40 A4D4U0_9INFB > A4D40 A4D4U1_9INFB > A4D40 A4D4U1_9INFB > A4D40 A4D4U1_9INFB > A4D40 A4D4U0_9INFB</pre>	TGCAMVDPTNGPLPEDNEPSA YAQLDCVLEALDRMDEEHPGLFQAASONAMEALMVTTVD *** *********************************	1. 240 240 240 240 240 240 240 240 240 240
P13872 RDRP_INBAD A0A126TPY5 A0A126TPY5_9INFB I2E0T1 I2E0T1_9INFB B4UQ55 B4UQ55_9INFB A3DQ08 A3DQ08_9INFB A0A140ERC2 A0A140ERC2_9INFB A0A140ERC2 A0A140ERC2_9INFB A0A140ERS A0A140ERR5_9INFB A0A140ERS A0A140ERR5_9INFB A0A140ERS A0A140ERR5_9INFB A0A126TN3 A0A126UA37_9INFB A0A126UA37 A0A126UA37_9INFB A0A126UA37 A0A126UA37_9INFB A0A1528 A4D528_9INFB A4D528 A4D528_9INFB A4D4V1 A4D4V1_9INFB A4D4V1 A4D4V1_9INFB B4UQ80 B4UQ80_9INFB	TGCAMVDPTNGPLPEDNEPSA YAQLDCVLEALDRMDEEHPGLFQAASONAMEALMVTTVD *** *********************************	1 240 240 240 240 240 240 240 240 240 240
<pre>(A0A126TPY5 A0A126TPY5_9INFB (A0A126TPY5 A0A126TPY5_9INFB (I2E0T1 I2E0T1_9INFB (I2E0T1 I2E0T1_9INFB (A3DQ08 A3DQ08_9INFB (A0A140ERC2 A0A140ERC2_9INFB (A0A140ERC2 A0A140ERC2_9INFB (A0A140ERC2 A0A140ERC3_9INFB (A0A140ERC3 A0A140ERC3_9INFB (A0A140ERC3 A0A140ERC3_9INFB (A0A140ERC3 A0A126TSN3_9INFB (A0A126TSN3 A0A126TSN3_9INFB (A0A126TSN3 A0A126TSN3_9INFB (A0A126A5W0 A0A10A0E6A5W0_9INFB (A0A126A5W0 A0A10A0E6A5W0_9INFB (A0A126A5W0 A0A0E6A5W0_9INFB (A0A0E65W0 A0A0E6A5W0_9INFB (A4D420 A40400_9INFB (A4D420 A40400_9INFB (A4D420)B4UQB0_9INFB (A4D400 B4UQB0_9INFB (A4D400 B4UQB0_9INFB (A4D400 B4UQB0_9INFB (A4D400 B4UQB0_9INFB (A4D400 B4UQB0_9INFB (A4D400 B4UQB0_9INFB (A4D400 B4UQB0_9INFB (A4D400 B4UQB0_9INFB (A4D404 A4D4044_9INFB (A4D404 A4D444_9INFB</pre>	TGCAMVDPTNGPLPEDNEPSA YAQLDCVLEALDRMDEEHPGLFQAASONAMEALMVTTVD	1 240 240 240 240 240 240 240 240 240 240
P13872 RDRP_INBAD A0A126TPY5 A0A126TPY5_9INFB I2E0T1 I2E0T1_9INFB B4UQ55 B4UQ55_9INFB A0A140ERC2 A0A140ERC2_9INFB A0A140ERC2 A0A140ERC2_9INFB A0A126TR22 A0A140ERC3_9INFB A0A126TR22 A0A140ERR9_9INFB A0A126TR22 A0A140ERR9_9INFB A0A126TR31A0A126TR33_9INFB A0A126TS31A0A126TR33_9INFB A0A126UA37 A0A126UA37_9INFB A0A126IS31A0A126UA37_9INFB A0A126IS31A0A126UA37_9INFB A0A126IS31A0A126INF3 A0A126IS31A0A126INF3 A0A126IS31A0A126INFB A0A126IS31A0A126INFB A0A126IS31A0A126INFB A0A126IS31A0A126INFB A0A126IS31A0A126INFB A0A126IS31A0A126INFB A0A126IS31A0A126INFB A0A126IS31A0A126INFB A0A140IA4D4U0_9INFB A4D4U0 A4D4U0_9INFB A4D4U1 A4D4U1_9INFB A4D4M4 A4D4M4_9INFB A0AM4 A4D4M4_9INFB A70M21RDRP_INBLE G7WTR6 G7WTR6_9INFB	TGCAMVDPTNGPLPEDNEPSA YAQLDCVLEALDRMDEEHPGLFQAASQNAMEALMVTTVD *** *********************************	1. 240 240 240 240 240 240 240 240 240 240
P13872 RDRP_INBAD A0A126TPY5 A0A126TPY5_9INFB I2E0T1 I2E0T1_9INFB B4UQ55 B4UQ55_9INFB A3DQ08 A3DQ08_9INFB A0A140ERC2 A0A140ERC2_9INFB A0A140ERC2 A0A140ERC2_9INFB A0A126TR22 A0A140ERR5_9INFB A0A140ERR9 A0A140ERR5_9INFB A0A140ERR9 A0A140ERR5_9INFB A0A126TN3 A0A126TN3_9INFB A0A126UA37 A0A126UA37_9INFB A0A126UA37 A0A126UA37_9INFB A0A126UA37 A0A126UA37_9INFB A0A1528 A4D528_9INFB A4D4V0 A4D4U0_9INFB A4D4V1 A4D4V1_9INFB A4D4V1 A4D4V1_9INFB B4UQB0 B4UQB0_9INFB A4D4V1 A4D4V1_9INFB	TGCAMVDPTNGPLPEDNEPSA YAQLDCVLEALDRMDEEHPGLFQAASONAMEALMVTTVD *** *********************************	1: 240 240 240 240 240 240 240 240 240 240
P13872 RDRP_INBAD A0A126TPY5 A0A126TPY5_9INFB I2E0T1 I2E0T1_9INFB I2E0T1 I2E0T1_9INFB A3DQ08 A3DQ08_9INFB A0A140ERC2 A0A140ERC2_9INFB A0A126TR22 A0A140ERC2_9INFB A0A126TR22 A0A140ERC3_9INFB A0A140ERC3 A0A140ERC3_9INFB A0A140ERC3 A0A140ERC3_9INFB A0A126TSN3 A0A126TSN3_9INFB A0A126TSN3 A0A126TSN3_9INFB A0A126TSN3 A0A126TSN3_9INFB A0A126TSN3 A0A126TSN3_9INFB A0A126IN3 A0A126TSN3_9INFB A0A126IN3 A0A126IN3_9INFB A0A126IN3 A0A126INFB A4D420 A4D4U0_9INFB A4D42V A4D4V1_9INFB A4D4V0 A4D4V1_9INFB A4D4V1 A4D4V1_9INFB A4D4V4 A4D4M4_9INFB B40A016GTWTR6_9INFB A4D421W9N9 A0A2D1W9N9_9INFB A0A216BBB3 A0A216BB3_9INFB	TGCAMVDPTNGPLPEDNEPSA YAQLDCVLEALDRMDEEHPGLFQAASQNAMEALMVTTVD *** *********************************	1: 240 240 240 240 240 240 240 240 240 240
P13872 RDRP_INBAD A0A126TPY5 A0A126TPY5_9INFB I2E0T1 I2E0T1_9INFB B4UQ55 B4UQ55_9INFB A0A140ERC2 A0A140ERC2_9INFB A0A140ERC2 A0A140ERC2_9INFB A0A140ERC2 A0A140ERC3_9INFB A0A126TR22 A0A140ERR3_9INFB A0A140ERR9 A0A140ERR3_9INFB A0A140ERS3 A0A126TN33_9INFB A0A126TN31A0A126UR37_9INFB A0A126IN31A0A126UR37_9INFB A0A126UA37 A0A126UA37_9INFB A0A126INS1A0A126UA37_9INFB A0A126INS1A0A126INFB A0A1528 A4D528_9INFB A4D4V1 A4D4V0_9INFB A4D4V1 A4D4V1_9INFB B4UQ60 B4UQ60_9INFB A4D444 A4D4M4_9INFB B4UQ60 B4UQ60_9INFB A4D444 A4D4M4_9INFB B4UQ60 B4UQ60_9INFB A4D444 A4D4M4_9INFB B4UC67WTR6_9INFB A0A2D1W9N9 A0A2D1W9N9_9INFB A0A216BP3 A0A216BP3_9INFB A0A119TN68 A0A119TN66_9INFB	TGCAMVDPTNGPLPEDNEPSA YAQLDCVLEALDRMDEEHPGLFQAASONAMEALMVTTVD *** *********************************	1: 240 240 240 240 240 240 240 240 240 240
<pre>(I00A126TPY5 A0A126TPY5_9INFB (I20A126TPY5 A0A126TPY5_9INFB (I20T1 I20T1_9INFB (I20T1 I20T1_9INFB (IA0A140ERC2 A0A140ERC2_9INFB (IA0A140ERC2 A0A140ERC2_9INFB (IA0A140ERC2 A0A140ERC2_9INFB (IA0A140ERS A0A140ERR5_9INFB (IA0A140ERS A0A140ERR5_9INFB (IA0A140ERS A0A140ERR5_9INFB (IA0A140ERS A0A140ERR5_9INFB (IA0A126TN3 A0A126TN3_9INFB (IA0A126TN3 A0A126TN3_9INFB (IA0A126TN3 A0A126TN3_9INFB (IA0A126TN3 A0A126TN3_9INFB (IA0A126TN3 A0A126TN3_9INFB (IA0A126TN3 A0A126TN3_9INFB (IA0A126TN3)A0A126TN3_9INFB (IA0A126TN3)A0A126TN3_9INFB (IA0A126TN3)A0A126TN3_9INFB (IA4D4V1 A4D4V0_9INFB (IA4D4V1 A4D4V1_9INFB (IA4D4V1 A4D4V1_9INFB (IA4D4V1 A4D4V1_9INFB (IA4D4V1 A4D4V1_9INFB (IA0A216BP3 A0A216BP3]9INFB (IA0A216BP3 A0A216BP3_9INFB (IA0A216BP3 A0A216BP3_9INFB (IA0A216BP3 A0A216BP3_9INFB (IA0A216BP3 A0A216BP3_9INFB (IA0A216BP3 A0A216BP3_9INFB (IA0A216BP3 A0A216BP3_9INFB (IA0A119TNG8 A0A119TNG8_9INFB</pre>	TGCAMVDPTNGPLPEDNEPSA YAQLDCVLEALDRMDEEHPGLFQAASONAMEALMVTTVD *** *********************************	1: 240 240 240 240 240 240 240 240 240 240
P13872 RDRP_INBAD A0A126TPY5 A0A126TPY5_9INFB 2E0T1 I2E0T1_9INFB B4UQS5 B4UQS5_9INFB A0A140ERC2 A0A140ERC2_9INFB A0A140ERC2 A0A140ERC2_9INFB A0A140ERC2 A0A140ERC2_9INFB A0A126TR22 A0A140ERC3_9INFB A0A140ERC3 A0A140ERC3_9INFB A0A140ERC3 A0A140ERC3_9INFB A0A140ERC3 A0A140ERC3_9INFB A0A126TSN3 A0A126TSN3_9INFB A0A26430 RDRP_INSE9 A52216 A522I6_9INFB A4D243 A4D549_9INFB A4D441 A4D440_9INFB A4D441 A4D444_9INFB A4D441 A4D444_9INFB A0A216BB73 A0A216BB73_9INFB A0A119TNG8 A0A119TNG6_9INFB A0A119TNG8 A0A175CC39_9INFB A0A216 S4526]_9INFB	TGCAMVDPTNGPLPEDNEPSA YAQLDCVLEALDRMDEEHPGLFQAASQNAMEALMVTTVD *** *********************************	1. 240 240 240 240 240 240 240 240
<pre>> P13872 RDRP_INBAD > P13872 RDRP_INBAD > I2071 I2071_91NFB I2071 I2071_91NFB I2071 I2071_91NFB I3008 I30008_91NFB IA0140ERC2 A0A140ERC2_91NFB IA0A140ERC2 A0A140ERC2_91NFB IA0A140ERC2 A0A140ERC3_91NFB IA0A140ERS A0A140ERR3_91NFB IA0A140ERS A0A140ERR3_91NFB IA0A140ERS A0A126TN37_91NFB IA0A140ERS A0A126TN37_91NFB IA0A126TN31A0A126TN37_91NFB IA0A126TN31A0A126TN37_91NFB IA0A126UA37 A0A126UA37_91NFB IA0A126UA37 A0A126UA37_91NFB IA0A165S0 ADA0D6A5W0_91NFB IA0A1601RDP_1NBP9 > IA52216 A52216_91NFB IA40400 A40400_91NFB IA40400 A40400_91NFB IA40400 A40400_91NFB IA40400 B400B0_91NFB IA40401B40P40_91NFB IA0A201W9N9 A0A201W9N9_91NFB IA0A126BB3]A0A216BB3_91NFB IA0A16G7WTR6_91NFB IA0A16G7WTR6_91NFB IA0A216BB3 A0A119TN68_91NFB IA0A176G33 A0A075CJ9_91NFB IA0A075CJ9 A0A075CJ9_91NFB</pre>	TGCAMVDPTNGPLPEDNEPSA YAQLDCVLEALDRMDEEHPGLFQAASONAMEALMVTTVD *** *********************************	1: 240 240 240 240 240 240 240 240 240 240
<pre>(A0A126TPY5 A0A126TPY5_9INFB (A0A126TPY5 A0A126TPY5_9INFB (I2E0T1 I2E0T1_9INFB (I2E0T1 I2E0T1_9INFB (A0A126TPY5 A0A126TPY5_9INFB (A0A140ERC2 A0A140ERC2_9INFB (A0A140ERC2 A0A126TR22_9INFB (A0A140ERC2 A0A126TR22_9INFB (A0A140ERC3 A0A140ERC3_9INFB (A0A140ERC3 A0A140ERC3_9INFB (A0A140ERC3 A0A140ERC3_9INFB (A0A126TSN3 A0A126TSN3_9INFB (A0A126TSN3 A0A126TSN3_9INFB (A0A126TSN3 A0A126TSN3_9INFB (A0A126TSN3 A0A126TSN3_9INFB (A0A126TSN3 A0A126TSN3_9INFB (A0A126TSN3 A0A126TSN3_9INFB (A0A126TSN3 A0A126TSN3_9INFB (A0A126TSN3 A0A126TSN3_9INFB (A0A126TSN3 A0A126TSN3_9INFB (A0A2065W0 A0A056A5W0]9INFB (A3DRF0 A3DRF0_9INFB (A4D4W1 A4D4W1_9INFB (A4D4W1 A4D4W1_9INFB (A4D4W1 A4D4W1_9INFB (A4D4W1 A4D4W1_9INFB (A4D4W1 A4D4W1_9INFB (A0A216BBP3 A0A216BBP3_9INFB (A0A216BBP3 A0A216BBP3_9INFB (A0A1I9TN68 A0A119TN66_9INFB (A0A119TN68 A0A119TN67]9INFB (A0A0119TN63 A0A075CC39_9INFB (A0A0N7GD33 A0A07G33_9INFB (A0A0748SXL88 A0A248SXL88_9INFB</pre>	TGCAMVDPTNGPLPEDNEPS AVAOLDCVLEALDRMDEEHPGLFQAASQNAMEALMVTTVD **********************************	1. 240 240 240 240 240 240 240 240
<pre>> P13872 RDRP_INBAD > P13872 RDRP_INBAD = A0A126TPY5 A0A126TPY5_9 INFB = I2E0T1 I2E0T1_9 INFB = B4UQ55 B4UQ55_9 INFB = A0A140ERC2 A0A126TR22_9 INFB = A0A140ERC2 A0A126TR22_9 INFB = A0A126TR22 A0A126TR22_9 INFB = A0A126TR22 A0A126TR33_9 INFB = A0A140ERG3 A0A126TR33_9 INFB = A0A140ERG3 A0A126TR33_9 INFB = A0A126TR31 A0A126TR33_9 INFB = A0A26130 RDRP_INBE9 = A4D523 A4D528_9 INFB = A4D523 A4D528_9 INFB = A4D414 A4D444_9 INFB = A4D414 A4D444_9 INFB = A4D414 A4D444_9 INFB = A4D421 RDRP_INBE8 = A0A21 BBP3 A0A216BB73_9 INFB = A0A179TNG8 A0A179TNG8_9 INFB = A0A075CC39 A0A075CC39_9 INFB = A0A077GD33 A0A077GD33_9 INFB = A0A248 KL8 A0A248 KLR8_9 INFB = A0A248 KL8 A0A248 KLR8_9 INFB = A0A28 6NMR2 A0A286 NMR2_9 INFB</pre>	TGCAMVDPTNGPLPEDNEPS AVAOLDCVLEALDRMDEEHPGLFQAASONAMEALMVTTVD *** *********************************	1: 240 240 240 240 240 240 240 240 240 240
<pre>> P13872 RDRP_INBAD > P13872 RDRP_INBAD > A0A126TPY5 A0A126TPY5_9INFB > I2E0T1 I2E0T1_9INFB > I2E0T1 I2E0T1_9INFB > A3DQ08 A3DQ08_9INFB > A3DQ08 A3DQ08_9INFB > A0A140ERC2 A0A140ERC2_9INFB > A0A140ERC2 A0A140ERC2_9INFB > A0A140ERC2 A0A140ERC3_9INFB > A0A140ERR9 A0A140ERR3_9INFB > A0A140ERR9 A0A140ERR3_9INFB > A0A140ERR9 A0A140ERR3_9INFB > A0A140ERR9 A0A126TN32]9INFB > A0A126TN31 A0A126TN33_9INFB > A0A126TN31 A0A126TN33_9INFB > A0A126TN31 A0A126TN33_9INFB > A0A126UA37 A0A126UA37_9INFB > A0A126UA37 A0A126UA37_9INFB > A0A126UA37 A0A126UA37_9INFB > A0A126UA37 A0A126UA37_9INFB > A4D400 A4D4407_9INFB > A4D400 A4D4407_9INFB > A4D400 A4D4407_9INFB > A0A210BF0]A3DF0_9INFB > A0A216BF3 A0A216BF3_9INFB > A0A216BF3 A0A119TN68_9INFB > A0A126GJNTR6_9INFB > A0A1216BF3 A0A119TN68_9INFB > A0A126BF3 A0A119TN68_9INFB > A0A216BF3 A0A176J3_9INFB > A0A216JX526]_9INFB > A0A248XLR8 A0A248XLR8_9INFB > A0A248XLR8 A0A248CLR8_9INFB > A0A248XLR8 A0A248CLR8_9INFB > A0A248XLR8 A0A248CLR6_9INFB > A0A248XLR8 A0A248CLR6_9INFB > A0A248XLR8]A0A248CLR6_9INFB > A0A248XLR8]A0A248CLR6_9INFB > A0A248XLR8]A0A248CLR6_9INFB > A0A248XLR8]A0A248CLR6_9INFB A0A248XLR8]A0A248</pre>	TGCAMVDPTNGPLPEDNEPSA YAQLDCVLEALDRMDEEHPGLFQAASONAMEALMVTTVD *** *********************************	1: 240 240 240 240 240 240 240 240 240 240
<pre>> P13872 RDRP_INBAD > P13872 RDRP_INBAD = A0A126TPY5 A0A126TPY5_9 INFB = I2E0T1 I2E0T1_9 INFB = I2E0T1 I2E0T1_9 INFB = A10Q5 B4TQS5_9 INFB = A0A140ERC2 A0A140ERC2_9 INFB = A0A126TR22 A0A126TR22_9 INFB = A0A126TR22 A0A140ERR3_9 INFB = A0A140ERC3 A0A140ERR3_9 INFB = A0A140ER3 A0A140ERR3_9 INFB = A0A140ER3 A0A140ERR3_9 INFB = A0A140ER3 A0A140ERR3_9 INFB = A0A140ER3 A0A140ERR3_9 INFB = A0A126TSN3 A0A126TSN3_9 INFB = A0A126TSN3 A0A126TSN3_9 INFB = A0A126TSN3 A0A126TSN3_9 INFB = A0A216A5W0 A0A0D6A5W0_9 INFB = A0A206A5W0 A0A0D6A5W0_9 INFB = A4D24W1 A4D4V0_9 INFB = A4D4U0 A4D4U0_9 INFB = A4D4W1 A4D4V1_9 INFB = A4D4W1 A4D4V1_9 INFB = A4D4W1 A4D4V1_9 INFB = A4D4W1 A4D4V1_9 INFB = A4D4W4 A4D4M4_9 INFB = A0A216BB73 A0A216BB73_9 INFB = A0A226XLR3 A0A226XMR2_9 INFB = A0A226MR2 A0A226MR2_9 INFB = A0A226MR2 A0A226MR2_9 INFB = A0A2017 A3DR07_IMBEK</pre>	TGCAMVDPTNGPLPEDNEPS AVAOLDCVLEALDRMDEEHPGLFQAASQNAMEALMVTTVD **********************************	1: 240 240 240 240 240 240 240 240 240 240
r A0A126TPY5 A0A126TPY5_9 INFB r A0A126TPY5 A0A126TPY5_9 INFB r I2E0T1 I2E0T1_9INFB r I2E0T1 I2E0T1_9INFB r A0Q5 A3DQ08 9INFB r A0A140ERC2 A0A140ERC2_9INFB r A0A140ERC2 A0A140ERC2_9INFB r A0A126TR22 A0A126TR22_9INFB r A0A126TR22 A0A140ERC3_9INFB r A0A140ERC3 A0A140ERC3_9INFB r A0A126TR3 A0A140ERC3_9INFB r A0A126TSN3 A0A126TSN3_9INFB r A0A16DSN0 A0A006ASW0_9INFB r A0A16BP3 A0A216BP3_9INFB r A0A216BP3 A0A216BP3_9INFB r A0A119TNG8 A0A119TNG8_9INFB r A0A119TNG8 A0A119TNG8_9INFB r A0A075CC3 A0A075CC33_9INFB r A0A26SNR2 A0A226SNR2_9INFB r A0A26SNR2 A0A226SNR2_9INFB r A0A216SNR2 A0A226SNR2_9INFB r A0A26SNR2 A0A226SNR2_9INFB r A0A216SNR2 A0A226SNR2_9INFB r A0A216NR2 A0A226SNR2_9INFB r A0A216NR2 A0A226SNR2_9INFB r A0A216NR2 A0A226SNR2_9INFB r A0A216NR2 A0A226SNR2_9INFB r A0A226SNR2 A0A226SNR2_9INFB r A0A205SNR2 A0A226SNR2 9INFB r A0A25SNR2 A0A226SNR2 9INFB r	TGCAMVDPTNGPLPEDNEPS AND LDCVLEALDRMDEEHPGLFOARSONAMEALMVTTVD *** *********************************	1: 240 240 240 240 240 240 240 240
r A0A126TPY5 A0A126TPY5_9INFB r A0A126TPY5 A0A126TPY5_9INFB r I2E0T1 I2E0T1_9INFB r B4UQS5 B4UQS5_9INFB r A3DQQ8 A3DQQ8_9INFB r A0A126TR22 A0A140ERC2_9INFB r A0A126TR22 A0A140ERC2_9INFB r A0A126TR22 A0A140ERC2_9INFB r A0A15TR23 A0A140EMR9_9INFB r A0A16TSN3 A0A140EMR9_9INFB r A0A16TSN3 A0A126TN329INFB r A0A16TSN3 A0A126UA37_9INFB r A0A16UA37 A0A126UA37_9INFB r A0A16JRDF_INBF9 r A522I6 A522I6_9INFB r A4D401 A4D401_9INFB r A4D401 A4D401_9INFB r A4D404 A4D404_9INFB r A4D404 A4D404_9INFB r A0A22 RDF_INBEF r A0A22 RDF_INBEF r A0A22 RDF_INBEF r A0A22 RDF_INBEF r A0A22 RDF_INBE r A0A216BF3 A0A119TNG8_9INFB r A0A216BF3 A0A119TNG8_9INFB r A0A26MR2 A0A286MR2_9INFB r A0A28KMR2 A0A286MR2_9INFB r A0A286MR2 A0A286MR2_9INFB r A0A20123]A0A07_INBER r A3DQ7 A3DR07_INBER r A4D43 A4D43_9INFB	TGCAMVDPTNGPLPEDNEPS AND LDCVLEALDRMDEEHPGLFQAASQNAMEALMVTTVD **********************************	1: 240 240 240 240 240 240 240 240 240 240
r A0A126TPY5 A0A126TPY5_9 INFB r A0A126TPY5 A0A126TPY5_9 INFB r I2E0T1 I2E0T1_9INFB r I2E0T1 I2E0T1_9INFB r A0Q5 A3DQ08 9INFB r A0A140ERC2 A0A140ERC2_9INFB r A0A140ERC2 A0A140ERC2_9INFB r A0A126TR22 A0A126TR22_9INFB r A0A126TR22 A0A140ERC3_9INFB r A0A140ERC3 A0A140ERC3_9INFB r A0A126TR3 A0A140ERC3_9INFB r A0A126TSN3 A0A126TSN3_9INFB r A0A16DSN0 A0A006ASW0_9INFB r A0A16BP3 A0A216BP3_9INFB r A0A216BP3 A0A216BP3_9INFB r A0A119TNG8 A0A119TNG8_9INFB r A0A119TNG8 A0A119TNG8_9INFB r A0A075CC3 A0A075CC33_9INFB r A0A26SNR2 A0A226SNR2_9INFB r A0A26SNR2 A0A226SNR2_9INFB r A0A216SNR2 A0A226SNR2_9INFB r A0A26SNR2 A0A226SNR2_9INFB r A0A216SNR2 A0A226SNR2_9INFB r A0A216NR2 A0A226SNR2_9INFB r A0A216NR2 A0A226SNR2_9INFB r A0A216NR2 A0A226SNR2_9INFB r A0A216NR2 A0A226SNR2_9INFB r A0A226SNR2 A0A226SNR2_9INFB r A0A205SNR2 A0A226SNR2 9INFB r A0A25SNR2 A0A226SNR2 9INFB r	TGCAMVDPTNGPLPEDNEPS AND LDCVLEALDRMDEEHPGLFOARSONAMEALMVTTVD *** *********************************	1: 240 240 240 240 240 240 240 240 240 240

			_	_		
tr A0A126TPY5 A0A126TPY5_9INFB	~ ~ ·		~ · ·		GNEKKAKLSNAVAKMLSNCPPGGISM	300
tr I2E0T1 I2E0T1_9INFB					GNEKKAKLSNAVAKMLSNCPPGGISM	300
tr B4UQS5 B4UQS5_9INFB	IATAGIQIRGFVLVVENLA	KNICE <mark>N</mark>	<mark>VL</mark> EQSGLI	VG	GNEKKAKLSNAVAKMLSNCPPGGISM	300
tr A3DQQ8 A3DQQ8 9INFB	IATAGIQIRGFVLVVENLA	KNICEN	<mark>VL</mark> EQSGLI	VG	GNEKKAKLSNAVAKMLSNCPPGGISM	300
tr A0A140ERC2 A0A140ERC2 9INFB	IATAGIQIRGFVLVVENLA	KNICEN	<mark>VL</mark> EQSGLI	VG	GNEKKAKLSNAVAKMLSNCPPGGISM	300
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tr A0A140EMR9 A0A140EMR9 9INFB	IATAGIQIRGFVLVVENLA	KNICEN	<mark>VL</mark> EQSGLI	VG	GNEKKAKLSNAVAKMLSNCPPGGISM	300
tr A0A140EUR3 A0A140EUR3 9INFB	IATAGIQIRGFVLVVENLA	KNICEN	<mark>VL</mark> EQSGLI	VG	GNEKKAKLSNAVAKMLSNCPPGGISM	300
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tr A0A126UA37 A0A126UA37 9INFB	IATAGIQIRGFVLVVENLA	KNICEN	VLEQSGLI	VG	CNEKKAKLSNAVAKMLSNCPPGGISM	300
tr A0A0D6A5W0 A0A0D6A5W0 9INFB					GNEKKAKLSNAVAKMLSNCPPGGISM	300
sp 036430 RDRP INBP9	IATAGIQIRGFVLVVENLA	KNICE <mark>N</mark>	<mark>VL</mark> EQSGLI	VG	GNEKKAKLSNAVAKMLSNCPPGGISM	300
tr A5Z2I6 A5Z2I6 9INFB	IATAGIQIRGFVLVVENLA	KNICEN	<mark>VL</mark> EQSGLI	VG	GNEKKAKLSNAVAKMLSNCPPGGISM	300
tr A4D528 A4D528 9INFB	IATAGIQIRGFVLVVENLA	KNICEN	<mark>VL</mark> EQSGLI	VG	GNEKKAKLSNAVAKMLSNCPPGGISM	300
tr A4D4U0 A4D4U0 9INFB	IATAGIQIRGFVLVVENLA	KNICEN	<mark>VL</mark> EQSGLI	VG	GNEKKAKLSNAVAKMLSNCPPGGISM	300
tr A3DRF0 A3DRF0 9INFB	IATAGIQIRGFVLVVENLA	KNICEN	<mark>VL</mark> EQSGLI	VG	GNEKKAKLSNAVAKMLSNCPPGGISM	300
tr A4D4V1 A4D4V1 9INFB	IATAGIQIRGFVLVVENLA	KNICEN	<mark>VL</mark> EQSGLI	VG	GNEKKAKLSNAVAKMLSNCPPGGISM	300
tr B4UQB0 B4UQB0_9INFB					CNEKKAKLSNAVAKMLSNCPPGGISM	300
tr A4D4M4 A4D4M4_9INFB	IATAGIQIRGFVLVVENLA	KNICE <mark>N</mark>	<mark>VL</mark> EQSGLI	VG	GNEKKAKLSNAVAKMLSNCPPGGISM	300
sp P07832 RDRP INBLE	IATAGIQIRGFVLVVENLA	KNICEN	VLEQSGL	PVG	GNEKKAKLSNAVAKMLSNCPPGGISM	300REF
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tr S4SZ61 S4SZ61_9INFB					GNEKKAKLSNAVAKMLSNCPPGGISM	300
tr A0A0N7GD33 A0A0N7GD33_9INFB					CNEKKAKLSNAVAKMLSNCPPGGISM	300
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tr A0A286NMR2 A0A286NMR2_9INFB					GNEKKAKLSNAVAKMLSNCPPGGISM	300
tr A0A2D1W2J9 A0A2D1W2J9_9INFB	IATAGIQIRGFVLVVENLA	KNICE <mark>1</mark>	<mark>VL</mark> EQSGLI	VG	GNEKKAKLSNAVAKMLSNCPPGGISM	300
tr A3DR07 A3DR07 INBBK	IATAGIQIRGFVLVVENLA				GNEKKAKLSNAVAKMLSNCPPGGISM	300
CI ASDRO / ASDRO / _INBBR		UTT OT	TROSCI	VG	NEKKAKLSNAVAKMLSNCPPGGISM	300
tr A3DQR9 A3DQR9_9INFB	IATAGIQIRGFVLVVENLA					
tr A3DQR9 A3DQR9_9INFB tr A4D4X3 A4D4X3_9INFB	IATAGIQIRGFVLVVENLA IATAGIQIRGFVLVVENLA	KNICE <mark>I</mark>	VLEQSGLI	VG	GNEKKAKLSNAVAKMLSNCPPGGISM	300
tr A3DQ7 A3DQ7_INBDR tr A3DQ79 A3DQ79_9INFB tr A4D4X3 A4D4X3_9INFB sp P13871 RDRP_INBAC	IATAGIQIRGFVLVVENLA IATAGIQIRGFVLVVENLA IATAGIQIRGFVLVVENLA	KNICEI KNICEI	NLEQSGLI NLEQSGLI	VG VG	GNEKKAKLSNAVAKMLSNCPPGGISM GNEKKAKLSNAVAKMLSNCPPGGISM	300 300
tr A3DQR9 A3DQR9_9INFB tr A4D4X3 A4D4X3_9INFB	IATAGIQIRGFVLVVENLA IATAGIQIRGFVLVVENLA IATAGIQIRGFVLVVENLA IATAGIQIRGFVLVVENLA	KNICEI KNICEI	NLEQSGLI NLEQSGLI	VG VG	GNEKKAKLSNAVAKMLSNCPPGGISM	

TVI <mark>GDNT</mark> KWNECLNPRIFLAMTERITRDSPIWFRDFCSIAPVLFSNKIARLGKGFMITSK	360
TVT <mark>GDNT</mark> KWNECLNPRIFLAMTERITRDSPIWFRDFCSIAPVLFSNKIARLGKGFMVTSK	360
TVI <mark>GDNI</mark> KWNECLNPRIFLAMTERITRDSPIWFRDFCSIAPVLFSNKIARLGKGFMVTSK	360
TVI <mark>GDNT</mark> KWNECLNPRIFLAMTERITRDSPIWFRDFCSIAPVLFSNKIARLGKGFMVTSK	360
TVI <mark>GDNT</mark> KWNECLNPRIFLAMTERITRDSPIWFRDFCSIAPVLFSNKIVRLGKGFMITSK	360
TVI <mark>GDNT</mark> KWNECLNPRIFLAMTERITRDSPIWFRDFCSIAPVLFSNKIARLGKGFMITSK	360
TVI <mark>GDNT</mark> KWNECLNPRIFLAMTERITRDSPIWFRDFCSIAPVLFSNKIARLGKGFMVTSK	360
TVI <mark>GDNT</mark> KWNECLNPRIFLAMTERITRDSPIWFRDFCSIAPVLFSNKIARLGKGFMVTSK	360
TVI <mark>GDNI</mark> KWNECLNPRIFLAMTERITRDSPIWFRDFCSIAPVLFSNKIARLGKGFMVTSK	360
TVI <mark>GDNT</mark> KWNECLNPRIFLAMTERITRDSPIWFRDFCSIAPVLFSNKIARLGKGFMITSK	360
TVI <mark>GDNI</mark> KWNECLNPRIFLAMTERITRDSPIWFRDFCSIAPVLFSNKIARLGKGFMITSK	360
TVT <mark>GDNT</mark> KWNECLNPRIFLAMTERITRDSPIWFRDFCSIAPVLFSNKIARLGKGFMITSK	360
TVI <mark>GDNI</mark> KWNECLNPRIFLAMTERITRDSPIWFRDFCSIAPVLFSNKIARLGKGFMITSK	360
TVT <mark>GDNT</mark> KWNECLNPRVFLAMTERITRDSPIWFRDFCSIAPVLFSNKIARLGKGFMITSK	360
TVT <mark>GDNT</mark> KWNECLNPRIFLAMTERITRDSPIWFRDFCSIAPVLFSNKIARLGKGFMITSK	360
TVT <mark>GDNT</mark> KWNECLNPRIFLAMTERITRDSPIWFRDFCSIAPVLFSNKIARLGKGFMITSK	360
TVI <mark>GDN</mark> KWNECLNPRIFLAMTERITRDSPIWFRDFCSIAPVLFSNKIARLGKGFMITSK	360
TVTGDNTKWNECLNPRIFLAMTERITRDSPIWFRDFCSIAPVLFSNKIARLGKGFMITSK	360
TVTGDNTKWNECLNPRIFLAMTERITRDSPIWFRDFCSIAPVLFSNKIARLGKGFMITSK	360
TVT <mark>GDNT</mark> KWNECLNPRIFLAMTERITRDSPIWFRDFCSIAPVLFSNKIARLGKGFMITSK	360
TVTGDNTKWNECLNPRIFLAMTERITRDSPIWFRDFCSIAPVLFSNKIARLGKGFMITSK	360
TVT <mark>GDNT</mark> KWNECLNPRIFLAMTERITRDSPIWFRDFCSIAPVLFSNKIARLGKGFMITSK	360
TVI <mark>GDNT</mark> KWNECLNPRIFLAMTERITRDSPVWFRDFCSIAPVLFSNKVARLGKGFMITSK	360
TVI <mark>GDNT</mark> KWNECLNPRIFLAMTERITRDSPVWFRDFCSIAPVLFSNKIARLGKGFMITSK	360
TVI <mark>GDNT</mark> KWNECLNPRIFLAMTERITRDSPVWFRDFCSIAPVLFSNKIARLGKGFMITSK	360
TVI <mark>GDNI</mark> KWNECLNPRIFLAMTERITRDSPVWFRDFCSIAPVLFSNKIARLGKGFMITSK	360
TVT <mark>GDNT</mark> KWNECLNPRIFLAMTERITRDSPVWFRDFCSIAPVLFSNKIARLGKGFMITSK	360
TVI <mark>GDNI</mark> KWNECLNPRIFLAMTERITRDSPVWFRDFCSIAPVLFSNKIARLGKGFMITSK	360
TVI <mark>GDNT</mark> KWNECLNPRIFLAMTERITRDSPVWFRDFCSIAPVLFSNKIARLGKGFMITSK	360
TVI <mark>GDNT</mark> KWNECLNPRIFLAMTERITRDSPVWFRDFCSIAPVLFSNKIARLGKGFMITSK	360
TVI <mark>GDNI</mark> KWNECLNPRIFLAMTERITRDSPVWFRDFCSIAPVLFSNKIARLGKGFMITSK	360
TVI <mark>GDNI</mark> KWNECLNPRIFLAMTERITRDSPIWFRDFCSIAPVLFSNKIARLGKGFMITSK	360
TVI <mark>GDNT</mark> KWNECLNPRIFLAMTERITRDSPIWFRDFCSIAPVLFSNKIARLGKGFMITSK	360
TVI <mark>GDNT</mark> KWNECLNPRIFLAMTERITRDSPIWFRDFCSIAPVLFSNKIARLGKGFMITSK	360
THE CONTRACT NOT TO A MEED TO DO ADTRODUCT A DUI DONNE ADD CHORMED	360
TVT <mark>GDNT</mark> KWNECLNPRIFLAMTERITRDSPIWFRDFCSIAPVLFSNKIARLGKGFMITSK	200
TVIGDNI KWNECLNPRIFLAMTERITRDSPIWFRDFCSIAPVLFSNKIARLGRGFMITSK TVIGDNI KWNECLNPRIFLAMTERITRDSPIWFRDFCSIAPVLFSNKIARLGRGFMITSK	360
	TVT GDN KWNECLNPRI FLAMTERITRDS PIW FRDFCS IAPVLFSNKIARLGKGFMVTSK TVT GDN KWNECLNPRI FLAMTERITRDS PIW FRDFCS IAPVLFSNKIARLGKGFMITSK TVT GDN KWNECLNPRI FLAMTERITRDS FWFRDFCS IAPVLFSNKIARLGKGFMITSK TVT GDN KW

tr A0A126TPY5 A0A126TPY5_9INFB	TKRLKAQIPCPDLFSIPLERYNEETRA <mark>KLRKLK</mark> PFFNEEGTAS <mark>LSPGMMMGMF</mark> NMLSTVL	420
tr I2E0T1 I2E0T1_9INFB	TKRLKAQIPCPDLFSIPLERYNEETRA <mark>KLRKLK</mark> PFFNEEGTAS <mark>LSPGMMMGMF</mark> NMLSTVL	420
r B4UQS5 B4UQS5_9INFB	TKRLKAQIPCPDLFSIPLERYNEETRA <mark>KLRKLK</mark> PFFNEEGTAS <mark>LSPGMMMGMF</mark> NMLSTVL	420
r A3DQQ8 A3DQQ8 9INFB	TKRLKAQIPCPDLFSIPLERYNEETRAKLRKLKPFFNEEGTAS <mark>LSPGMMMGMF</mark> NMLSTVL	420
r A0A140ERC2 A0A140ERC2 9INFB	TKRLKAQIPCPDLFSIPLERYNEETRA <mark>KLRKLK</mark> PFFNEEGTAS <mark>LSPGMMMGMF</mark> NMLSTVL	420
r A0A126TR22 A0A126TR22 9INFB	TKRLKAQIPCPDLFSIPLERYNEETRA <mark>KLRKLK</mark> PFFNEEGTAS <mark>LSPGMMMGMF</mark> NMLSTVL	420
r A0A059TB43 A0A059TB43 9INFB	TKRLKAQIPCPDLFSIPLERYNEETRAKLRKLKPFFNEEGTAS <mark>LSPGMMMGMF</mark> NMLSTVL	420
r A0A140EMR9 A0A140EMR9 9INFB	TKRLKAQIPCPDLFSIPLERYNEETRAKLRKLKPFFNEEGTAS <mark>LSPGMMMGMF</mark> NMLSTVL	420
r A0A140EUR3 A0A140EUR3 9INFB	TKRLKAQIPCPDLFSIPLERYNEETRAKLRKLKPFFNEEGTAS <mark>LSPGMMMGMF</mark> NMLSTVL	420
r A0A126TSN3 A0A126TSN3 9INFB	TKRLKAOIPCPDLFSIPLERYNEETRAKLRKLKPFFNEEGTASLSPGMMMGMFNMLSTVL	420
r A0A126UA37 A0A126UA37 9INFB	TKRLKAOIPCPDLFSIPLERYNEETRAKLKRLKPFFNEEGTASLSPGMMMGMFNMLSTVL	420
r A0A0D6A5W0 A0A0D6A5W0 9INFB	TKRLKAOIPCPDLFSIPLERYNEETRAKLKRLKPFFNEEGTASLSPGMMMGMFNMLSTVL	420
p 036430 RDRP INBP9	TKRLKAOIPCPDLFSIPLERYNEETRAKLKKLKPFFNEEGTAS <mark>LSPGMMMGMF</mark> NMLSTVL	420
r A52216 A52216 91NFB	TKRLKAOIPCPDLFSIPLERYNEETRAKLKKLKPFFNEEGTASLSPGMMMGMFNMLSTVL	420
r A4D528 A4D528 91NFB	TKRLKAOIPCPDLFSIPLERYNGETRAKLKKLRPFFNEEGTASLSPGMMMGMFNMLSTVL	420
r A4D4U0 A4D4U0 9INFB	TKRLKAOIPCPDLFSIPLERYNEETRAKLKKLKPFFNEEGTASLSPGMMMGMFNMLSTVL	420
r A3DRF0 A3DRF0 9INFB	TKRLKAOIPCPDLFSIPLERYNEETRAKLKKLKPFFNEEGTASLSPGMMMGMFNMLSTVL	420
r A4D4V1 A4D4V1 9INFB	TKRLKAQIPCPDLFSIPLERYNEETRAKLKKLKPFFNEEGTASLSPGMMMGMFNMLSTVL	420
r B4UQB0 B4UQB0 9INFB	TKRLKAOIPCPDLFSIPLERYNEETRAKLKRLKPFFNEEGTASLSPGMMMGMFNMLSTVL	420
r A4D4M4 A4D4M4 9INFB	TKRLKAOIPCPDLFSIPLERYNEETRAKLKRLKPFFNEEGTASLSPGMMMGMFNMLSTVL	420
p P07832 RDRP INBLE	TKRLKAQIPCPDLFNIPLERYNEETRAKLKKLKPFFNEEGTASLSPGMMMGMFNMLSTVL	420
r G7WTR6 G7WTR6 9INFB	TKRLKAQIPCPDLFSIPLERYNEETRAKLKKLKPFFNEEGTASLSPGMMMGMFNMLSTVL	420
r A0A2D1W9N9 A0A2D1W9N9 9INFB	TKRLKAQIPCPDLFSIPLERYNEETRAKLKKLKPFFNEEGTAS <mark>LSPGMMMGMF</mark> NMLSTVL	420
r A0A216BBP3 A0A216BBP3 9INFB	TKRLKAQIPCPDLFSIPLERYNEETRAKLKKLRPFFNEEGTAS <mark>LSPGMMMGMF</mark> NMLSTVL	420
r A0A119TNG8 A0A119TNG8 9INFB	TKRLKAQIPCPDLFSIPLERYNEETRA <mark>KLKKLKP</mark> FFNEEGTAS <mark>LSPGMMMGMF</mark> NMLSTVL	420
r A0A075CCJ9 A0A075CCJ9 9INFB	TKRLKAQIPCPDLFSIPLERYNEETRA <mark>KLKKLKP</mark> FFNEEGTAS <mark>LSPGMMMGMF</mark> NMLSTVL	420
r S4SZ61 S4SZ61 9INFB	TKRLKAQIPCPDLFSIPLERYNEETRAKLKKLKPFFNEEGTAS <mark>LSPGMMMGMF</mark> NMLSTVL	420
r A0A0N7GD33 A0A0N7GD33 9INFB	TKRLKAQIPCPDLFSIPLERYNEETRAKLKKLKPFFNEEGTAS <mark>LSPGMMMGMF</mark> NMLSTVL	420
r A0A248XLR8 A0A248XLR8 9INFB	TKRLKAQIPCPDLFSIPLERYNEETRAKLKKLKPFFNEEGTAS <mark>LSPGMMMGMF</mark> NMLSTVL	420
r A0A286NMR2 A0A286NMR2 9INFB	TKRLKAQIPCPDLFSIPLERYNEETRAKLKKLKPFFNEEGTAS <mark>LSPGMMMGMF</mark> NMLSTVL	420
r A0A2D1W2J9 A0A2D1W2J9 9INFB	TKRLKAQIPCPDLFSIPLERYNEETRAKLKKLKPFFNEEGTAS <mark>LSPGMMMGMF</mark> NMLSTVL	420
r A3DR07 A3DR07 INBBK	TKRLKAQIPCPDLFSIPLERYNEETRA <mark>KLKKLKP</mark> FFNEEGTAS <mark>LSPGMMMGMF</mark> NMLSTVL	420
r A3DQR9 A3DQR9 9INFB	TKRLKAQIPCPDLFSIPLERYNEETRAKLKKLKPFFNEEGTAS <mark>LSPGMMMGMF</mark> NMLSTVL	420
r A4D4X3 A4D4X3 9INFB	TKRLKAQIPCPDLFSIPLERYNEETRAKLKKLKPFFNEEGTAS <mark>LSPGMMMGMF</mark> NMLSTVL	420
p P13871 RDRP INBAC	TKRLKAQI PCPDLFNI PLERYNEETRAKLKKLKPFFNEEGTAS <mark>LSPGMMMGMF</mark> NMLSTVL	420
p P13872 RDRP INBAD	TKRLKAQIPCPDLFNIPLERYNEETRA <mark>KLKKLK</mark> PFFNEEGTAS <mark>LSPGMMMGMF</mark> NMLSTVL	420

r A0A126TPY5 A0A126TPY5_9INFB	GVAALGIKNIGNKEYI <mark>WDGLQS<mark>SDD</mark>FALF<mark>WNAKDEEVCMEGINDFYRTCKLLGINMSKKK</mark></mark>	480
r I2E0T1 I2E0T1 9INFB	GVAALGIKNIGNKEYLWDGLQS <mark>SDDFALF</mark> VNAKDEEKCMEGINDFYRTCKLLGINMSKKK	480

tr A0A126TPY5 A0A126TPY5_9INFB	GVAALGIKNIGNKEYI	WDGLQS <mark>SI</mark>	DFALF	VNAKDEEVCMEGINDFYRTCKLI <mark>GI</mark>	MMSKKK	480
tr I2E0T1 I2E0T1_9INFB	GVAALGIKNIGNKEYI	WDGLQS <mark>SI</mark>	DFALF	VNAKDEEKCMEGINDFYRTCKLI <mark>GI</mark>	MMSKKK	480
tr B4UQS5 B4UQS5_9INFB	GVAALGIKNIGNKEYI	WDGLQS <mark>SI</mark>	DFALF	/NAKDEETCMEGINDFYRTCKLI <mark>GI</mark>	NMSKKK	480
tr A3DQQ8 A3DQQ8_9INFB	GVAALGIKNIGNKEYI	WDGLQS <mark>SI</mark>	DFALF	/NAKDEETCMEGINDFYRTCKLI <mark>GI</mark>	NMSKKK	480
tr A0A140ERC2 A0A140ERC2_9INFB	GVAALGIKNIGNKEYI	WDGLQS <mark>SI</mark>	DFALF	/NAKDEEACMEGINDFYRTCKLI <mark>GI</mark>	NMSKKK	480
tr A0A126TR22 A0A126TR22_9INFB	GVAALGIKNIGNKEYI	WDGLQS <mark>SI</mark>	DFALF	/NAKDEEACMEGINDFYRTCKLI <mark>GI</mark>	MSKKK	480
tr A0A059TB43 A0A059TB43_9INFB	GVAALGIKNIGNKEYI	WDGLQS <mark>SI</mark>	DFALF	VNAKDEEACMEGINDFYRTCKLI <mark>GI</mark>	MSKKK	480
tr A0A140EMR9 A0A140EMR9_9INFB	GVAALGIKNIGNKEYI	WDGLQS <mark>SI</mark>	DFALF	/NAKDEEACMEGINDFYRTCKLI <mark>GI</mark>	NMSKKK	480
tr A0A140EUR3 A0A140EUR3_9INFB	GVAALGIKNIGNKEYI	WDGLQS <mark>SI</mark>	DFALF	/NAKDEEACMEGINDFYRTCKLI <mark>GI</mark>	NMSKKK	480
tr A0A126TSN3 A0A126TSN3_9INFB	GVAALGIKNIGNKEYI	WDGLQS <mark>SI</mark>	DFALF	/NAKDEEACMEGINDFYRTCKLI <mark>GI</mark>	NMSKKK	480
tr A0A126UA37 A0A126UA37_9INFB	GVAALGIKNIGNKEYI	WDGLQS <mark>SI</mark>	DFALF	VNAKDEETCMEGINDFYRTCKLI <mark>GI</mark>	MMSKKK	480
tr A0A0D6A5W0 A0A0D6A5W0_9INFB	GVAALGIKNIGNKEYI	WDGLQS <mark>SI</mark>	DFALF	VNAKDEETCMEGINDFYRTCKLI <mark>GI</mark>	NMSKKK	480
sp 036430 RDRP_INBP9	GVAALGIKNIGNKEYI			VNAKDEETCMEGINDFYRTCKLI <mark>GI</mark>		480
tr A5Z216 A5Z216_9INFB	GVAALGIKNIGNKEYI			VNAKDEETCMEGINDFYRTCKLI <mark>GI</mark>		480
tr A4D528 A4D528_9INFB	GVAALGIKNIGNKEYI	WDGLQS <mark>SI</mark>	DFALF	VNAKDEETCMEGINDFYRTCKLI <mark>GI</mark>	NMSKKK	480
tr A4D4U0 A4D4U0_9INFB	GVAALGIKNIGNKEYI	_		/NAKDEETCMEGINDFYRTCKLI <mark>GI</mark>		480
tr A3DRF0 A3DRF0_9INFB	GVAALGIKNIGNKEYI	WDGLQS <mark>SI</mark>	DFALF	VNAKDEETCMEGINDFYRTCKLI <mark>GI</mark>	NMSKKK	480
tr A4D4V1 A4D4V1_9INFB	GVAALGIKNIGNKEYI	WDGLQS <mark>SI</mark>	DFALF	VNAKDEETCMEGINDFYRTCKLI <mark>GI</mark>	NMSKKK	480
tr B4UQB0 B4UQB0_9INFB	GVAALGIKNIGNKEYI	WDGLQS <mark>SI</mark>	DFALF	VNAKDEETCMEGINDFYRTCKLI <mark>GI</mark>	MMSKKK	480
tr A0ADD6A5W0 A0ADD6A5W0_9INFB sp 036430 RDRP_INBP9 tr A52216 A52216_9INFB tr A4D528 A4D528_9INFB tr A4D4U0 A4D4U0_9INFB tr A4D4U0 A4D4U0_9INFB tr A4D4V1 A4D4V1_9INFB tr A4D4V1 A4D4V1_9INFB tr A4D4W4 A4D4W4_9INFB sp P07832 RDRP_INBLE tr G7WTR6 G7WTR6_9INFB	GVAALGIKNIGNKEYI			/NAKDEETCMEGINDFYRTCKLLGI		480
sp P07832 RDRP_INBLE	GVAALGIKNIGNKEYI			VNAKDEETCMEGINDFYRTCKLLGI		4 80
tr G7WTR6 G7WTR6_9INFB	GVAALGIKNIGNKEYI			/NAKDEETCMEGINDFYRTCKLI <mark>GV</mark>		480
tr A0A2D1W9N9 A0A2D1W9N9_9INFB	GVAALGIKNIGNKEYI			VNAKDEETCMEGINDFYRTCKLI <mark>GI</mark>		480
tr A0A2I6BBP3 A0A2I6BBP3_9INFB				VNAKDEETCMEGINDFYRTCKLI <mark>GI</mark>		480
tr A0A119TNG8 A0A119TNG8_91NFB		-		VNAKDEETCMEGINDFYRTCKLI <mark>GI</mark>		480
tr A0A075CCJ9 A0A075CCJ9_9INFB		_		VNAKDEETCMEGINDFYRTCKLI <mark>G</mark> V		480
tr S4SZ61 S4SZ61_9INFB		-		VNAKDEETCMEGINDFYRTCKLI <mark>GV</mark>		480
tr A0A0N7GD33 A0A0N7GD33_9INFB				VNAKDEETCMKGINDFYRTCKLI <mark>GI</mark>		480
tr A0A248XLR8 A0A248XLR8_9INFB				VNAKDEETCMEGINDFYRTCKLI <mark>GI</mark>		480
tr A0A286NMR2 A0A286NMR2_9INFB				VNAKDEETCMEGINDFYRTCKLI <mark>GI</mark>		480
tr A0A2D1W2J9 A0A2D1W2J9_9INFB	GVAALGIKNIGNKEYI	_		VNAKDEETCMEGINDFYRTCKLI <mark>GI</mark>		480
tr A3DR07 A3DR07_INBBK	GVAALGIKNIGNKEYI			VNAKDEETCMEGINDFYRTCKLI <mark>GI</mark>		480
tr A3DR07 A3DR07_INBBK tr A3DQR9 A3DQR9_9INFB tr A4D4X3 A4D4X3_9INFB sp P13871 RDRP_INBAC sp P13872 RDRP_INBAD	GVAALGIKNIGNKEYI			/NAKDEETCMEGINDFYRTCKLI <mark>GI</mark>		480
tr A4D4X3 A4D4X3_9INFB	GVAALGIKNIGNKEYI			VNAKDEETCMEGINDFYRTCKLI <mark>GI</mark>		480
sp P13871 RDRP_INBAC	GVAALGIKNIGN <mark>K</mark> EYI			/NAKDEETCMEGINDFYRTCKLI <mark>G</mark> I		480*(CA)
sp P13872 RDRP_INBAD	GVAALGIKNIGN <mark>R</mark> EYI			/NAKDEETCMEGINDFYRTCKLI <mark>GI</mark>		480*(WT)
	*********	*****	****	****** **:**************	*****	

tr A0A126TPY5 A0A126TPY5 9INFB		
		E 40
	SYCNETGMFEFTSMFYRDGFVSNFAMEIPSFGVAGVNESADMAIGMTIIKNNMINNGMGP	540
tr I2E0T1 I2E0T1_9INFB	SYCNETGMFEFTSMFYRDGFVSNFAMEIPSFGVAGVNESADMAIGMTIIKNNMINNGMGP	540
tr B4UQS5 B4UQS5_9INFB	SYCNETGMFEFTSMFYRDGFVSNFAMEIPSFGVAGVNESADMAIGMTIIKNNMINNGMGP	540
tr A3DQQ8 A3DQQ8_9INFB	SYCNETGMFEFTSMFYRDGFVSNFAMEIPSFGVAGVNESADMAIGMTIIKNNMINNGMGP	540
tr A0A140ERC2 A0A140ERC2_9INFB	SYCNETGMFEFTSMFYRDGFVSNFAMEIPSFGVAGVNESADMAIGMTIIKNNMINNGMGP	540
tr A0A126TR22 A0A126TR22_9INFB	SYCNETGMFEFTSMFYRDGFVSNFAMEIPSFGVAGVNESADMAIGMTIIKNNMINNGMGP	540
tr A0A059TB43 A0A059TB43 9INFB	SYCNETGMFEFTSMFYRDGFVSNFAMEIPSFGVAGVNESADMAIGMTIIKNNMINNGMGP	540
tr A0A140EMR9 A0A140EMR9 9INFB	SYCNETGMFEFTSMFYRDGFVSNFAMEIPSFGVAGVNESADMAIGMTIIKNNMINNGMGP	540
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tr A0A126UA37 A0A126UA37_9INFB	SYCNETGMFEFTSMFYRDGFVSNFAMEIPSFGVAGVNESADMAIGMTIIKNNMINNGMGP	540
tr A0A0D6A5W0 A0A0D6A5W0_9INFB	SYCNETGMFEFTSMFYRDGFVSNFAMEIPSFGVAGVNESADMAIGMTIIKNNMINNGMGP	540
sp 036430 RDRP_INBP9	SYCNETGMFEFTSMFYRDGFVSNFAMEIPSFGVAGVNESADMAIGMTIIKNNMINNGMGP	540
tr A5Z2I6 A5Z2I6_9INFB	SYCNETGMFEFTSMFYRDGFVSNFAMEIPSFGVAGVNESADMAIGMTIIKNNMINNGMGP	540
tr A4D528 A4D528 9INFB	SYCNETGMFEFTSMFYRDGFVSNFAMEIPSFGVAGVNESADMAIGMTIIKNNMINNGMGP	540
tr A4D4U0 A4D4U0 9INFB	SYCNETGMFEFTSMFYRDGFVSNFAMEIPSFGVAGVNESADMAIGMTIIKNNMINNGMGP	540
tr A3DRF0 A3DRF0 9INFB	SYCNETGMFEFTSMFYRDGFVSNFAMEIPSFGVAGVNESADMAIGMTIIKNNMINNGMGP	540
tr A4D4V1 A4D4V1 9INFB	SYCNETGMFEFTSMFYRDGFVSNFAMEIPSFGVAGVNESADMAIGMTIIKNNMINNGMGP	540
tr B4UQB0 B4UQB0 9INFB	SYCNETGMFEFTSMFYRDGFVSNFAMEIPSFGVAGVNESADMAIGMTIIKNNMINNGMGP	540
tr A4D4M4 A4D4M4_9INFB	SYCNETGMFEFTSMFYRDGFVSNFAMEIPSFGVAGVNESADMAIGMTIIKNNMINNGMGP	540
sp P07832 RDRP_INBLE	SYCNETGMFEFTSMFYRDGFVSNFAMELPSFGVAGVNESADMAIGMTIIKNNMINNGMGP	540
tr G7WTR6 G7WTR6_9INFB	SYCNETGMFEFTSMFYRDGFVSNFAMDLPSFGVAGVNESADMAIGMTIIKNNMINNGMGP	540
tr A0A2D1W9N9 A0A2D1W9N9_9INFB	SYCNETGMFEFTSMFYRDGFVSNFAMELPSFGVAGVNESADMAIGMTIIKNNMINNGMGP	540
tr A0A2I6BBP3 A0A2I6BBP3_9INFB	SYCNETGMFEFTSMFYRDGFVSNFAMELPSFGVAGVNESADMAIGMTIIKNNMINNGMGP	540
tr A0A1I9TNG8 A0A1I9TNG8_9INFB	SY <mark>CNETGMFEFTSMFYRDGFVSNFAMELPSFGVAGVNESADMAIGMTIIKNNMINNGMGP</mark>	540
tr A0A075ccj9 A0A075ccj9_9INFB	SYCNETGMFEFTSMFYRDGFVSNFAMELPSFGVAGVNESADMAIGMTIIKNNMINNGMGP	540
tr \$4\$261 \$4\$261 9INFB	SYCNETGMFEFTSMFYRDGFVSNFAMELPSFGVAGVNESADMAIGMTIIKNNMINNGMGP	540
tr A0A0N7GD33 A0A0N7GD33 9INFB	SYCNETGMFEFTSMFYRDGFVSNFAMELPSFGVAGVNESADMAIGMTIIKNNMINNGMGP	540
tr A0A248XLR8 A0A248XLR8 9INFB	SICNEIGHEEFISMFIRDGFVSNFAMELDFSFGVAGVMESADMAIGHTIIRNMHINNGMGF SYCNEIGMFEFISMFYRDGFVSNFAMELDFSFGVAGVNESADMAIGMTIIRNNHINNGMGF	540
tr A0A286NMR2 A0A286NMR2 9INFB	SICNEIGHFEFISMFIRDGFVSNFAMELFSFGVAGVNESADMAIGMIIIRNNMINNGMGF SYCNEIGMFEFISMFYRDGFVSNFAMELFSFGVAGVNESADMAIGMIIIRNNMINNGMGF	540
tr A0A2D1W2J9 A0A2D1W2J9_9INFB	SY CNETGMFE FT SMFYRDG FV SN FAMELPS FGVAG VNE SADMAI GMTI I KNNM I NNGMGP	540
tr A3DR07 A3DR07_INBBK	SYCNETGMFEFTSMFYRDGFVSNFAMELPSFGVAGVNESADMAIGMTIIKNNMINNGMGP	540
tr A3DQR9 A3DQR9_9INFB	SYCNETGMFEFTSMFYRDGFVSNFAMELPSFGVAGVNESADMAIGMTIIKNNMINNGMGP	540
tr A4D4X3 A4D4X3_9INFB	SYCNETGMFEFTSMFYRDGFVSNFAMELPSFGVAGVNESADMAIGMTIIKNNMINNGMGP	540
sp P13871 RDRP_INBAC	SYCNETGMFEFTSMFYRDGFVSNFAMELPSFGVAGVNESADMAIGMTIIKNNMINNGMGP	540
sp P13872 RDRP INBAD	SYCNETGMFEFTSMFYRDGFVSNFAMELPSFGVAGVNESADMAIGMTIIKNNMINNGMGP	540
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triA0A126TPY5IA0A126TPY5 9TNFR		660
tr A0A126TPY5 A0A126TPY5_9INFB	-	
tr I2E0T1 I2E0T1_9INFB	RNLHIPEIVLKYNLMDPEYKGRLLHPQNPFVGHLSIEGIKEADITPAHGPVKKMDYDAVS	660
	RNLHIPEIVLKYNLMDPEYKGRLLHPQNPFVGHLSIEGIKEADITPAHGPVKKMDYDAVS RNLHIPEIVLKYNLMDPEYKGRLLHPQNPFVGHLSIEGIKEADITPAHGPVKKMDYDAVS	660 660
	RNLHIPEIVLKYNLMDPEYKGRLLHPQNPFVGHLSIEGIKEADITPAHGPVKKMDYDAVS RNLHIPEIVLKYNLMDPEYKGRLLHPQNPFVGHLSIEGIKEADITPAHGPVKKMDYDAVS RNLHIPEIVLKYNLMDPEYKGRLLHPQNPFVGHLSIEGIKEADITPAHGPVKKMDYDAVS	660 660 660
tr I2E0T1 I2E0T1_9INFB tr B4UQS5 B4UQS5_9INFB tr A3DQQ8 A3DQQ8_9INFB tr A0A140ERC2 A0A140ERC2_9INFB	RNLHIPEIVLKYNLMDPEYKGRLLHPQNPFVGHLSIEGIKEADITPAHGPVKKMDYDAVS RNLHIPEIVLKYNLMDPEYKGRLLHPQNPFVGHLSIEGIKEADITPAHGPVKKMDYDAVS RNLHIPEIVLKYNLMDPEYKGRLLHPQNPFVGHLSIEGIKEADITPAHGPVKKMDYDAVS RNLHIPEIVLKYNLMDPEYKGRLLHPQNPFVGHLSIEGIKEADITPAHGPVKKMDYDAVS	660 660 660 660
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tr 12E0T1 12E0T1_9INFB tr B4UQS5 B4UQS5_9INFB tr A0A140ERC2 A0A140ERC2_9INFB tr A0A126TR22 A0A126TR22_9INFB tr A0A126TR22 A0A126TR22_9INFB tr A0A126TR22 A0A140EUR3_9INFB tr A0A140EUR3 A0A140EUR3_9INFB tr A0A140EUR3 A0A140EUR3_9INFB tr A0A126TSN3 A0A140EUR3_9INFB tr A0A126TSN3 A0A126TSN3_9INFB tr A0A006A5W0 A0A006A5W0_9INFB tr A4D400 AA4000_9INFB tr A4D528 A4D528_9INFB tr A4D400 B4UQB0_9INFB tr A4D400 B4UQB0_9INFB tr A4D404 A4D444_9INFB sp F07832 RDRF_INBLE tr A0A019TNG8 A0A119TNG8_9INFB tr A0A119TNG8 A0A119TNG8_9INFB tr A0A075CCJ9 A0A075CCJ9_9INFB tr A0A07GD33 A0A07GD33_9INFB tr A0A266MMR2 A0A248XLR8_9INFB tr A0A266MMR2 A0A261W29_9INFB tr A0A27 A0A21 W399_9INFB tr A0A07GD33 A0A07GD33_9INFB tr A0A266MMR2 A0A248XLR8_9INFB tr A0A266MMR2 A0A248XLR8_9INFB tr A0A201W2J9 A0A201W2J9_9INFB tr A0A207 A3DR07_INBK tr A0A209 A3DQ89_9INFB	RNLHIPEIVLKYNLMDPEYKGRLLHPONPFVGHLSIEGIKEADITPAHGPVKKMDYDAVS RNLHIPEIVLKYNLMDPEYKGRLLHPONPFVGH	660 660 660 660 660 660 660 660 660 660

tr A0A126TPY5 A0A126TPY5_9INFB GTHSWRTKRNRSILNTDORNMILEEC CLARCONLFEAC FNSASYRRPVGQHSMLEAMAHR tr I2E0T1 I2E0T1_9INFB GTHSWRTKRNRSILNTDORNMILEEC CLARCONLFEAC FNSASYRRPVGQHSMLEAMAHR tr B4UQS5 B4UQS5_9INFB GTHSWRTKRNRSILNTDORNMILEEC CLARCONLFEAC FNSASYRRPVGQHSMLEAMAHR tr A3DQQ8 A3DQQ8_9INFB GTHSWRTKRNRSILNTDORNMILEEC CLARCONLFEAC FNSASYRRPVGQHSMLEAMAHR tr A3DQ08 A3DQQ8_9INFB GTHSWRTKRNRSILNTDORNMILEEC CLARCONLFEAC FNSASYRRPVGQHSMLEAMAHR tr A0A140ERC2 A0A140ERC2_9INFB GTHSWRTKRNRSILNTDORNMILEEC CLARCONLFEAC FNSASYRRPVGQHSMLEAMAHR tr A0A126TR22 A0A126TR22 9INFB GTHSWRTKRNRSILNTDORNMILEEC CLARCONLFEAC FNSASYRRPVGQHSMLEAMAHR tr A0A059TB43 A0A059TB43_9INFB GTHSWRTKRNRSILNTDORNMILEEC CLARCONLFEAC FNSASYRRPVGQHSMLEAMAHR tr A0A140EMR9 A0a140EMR9_9INFB GTHSWRTKRNRSILNTDORNMILEEC CLARCONLFEAC FNSASYRRPVGQHSMLEAMAHR	720 720 720 720 720 720 720 720 720 720
tr B4UQS5 B4UQS5 _9INFB GTHSWRTKRNRSILNTDORNMILEECCLARCONLFEACFNSASYRKPVGOHSMLEAMAHR tr A3DQQ8 A3DQQ8 _9INFB GTHSWRTKRNRSILNTDORNMILEECCLARCONLFEACFNSASYRKPVGOHSMLEAMAHR tr A0A140ERC2 A0A140ERC2 _9INFB GTHSWRTKRNRSILNTDORNMILEECCLARCONLFEACFNSASYRKPVGOHSMLEAMAHR tr A0A126TR22 A0A126TR22_9INFB GTHSWRTKRNRSILNTDORNMILEECCLARCONLFEACFNSASYRKPVGOHSMLEAMAHR tr A0A126TR22 A0A126TR22_9INFB GTHSWRTKRNRSILNTDORNMILEECCLARCONLFEACFNSASYRKPVGOHSMLEAMAHR tr A0A059TB43 A0A059TB43_9INFB GTHSWRTKRNRSILNTDORNMILEECCLARCONLFEACFNSASYRKPVGOHSMLEAMAHR tr A0A140EMR9 A0A140EMR9_9INFB GTHSWRTKRNRSILNTDORNMILEECCLARCONLFEACFNSASYRKPVGOHSMLEAMAHR	720 720 720 720 720 720 720 720 720
tr A3DQ08 A3DQ08 9 INFB GTHSWRTKRNRSIINTORNMILEECCARCCNLFERCFNSASYRKPVGOHSMLEAMAHR tr A0A140ERC2 A0A140ERC2 9 INFB GTHSWRTKRNRSIINTOORNMILEECCARCCNLFERCFNSASYRKPVGOHSMLEAMAHR tr A0A126TR22 A0A126TR22 9 INFB GTHSWRTKRNRSIINTOORNMILEECCARCCNLFERCFNSASYRKPVGOHSMLEAMAHR tr A0A126TR22 A0A126TR22 9 INFB GTHSWRTKRNRSIINTOORNMILEECCARCCNLFERCFNSASYRKPVGOHSMLEAMAHR tr A0A059TB43 A0A059TB43 9 INFB GTHSWRTKRNRSIINTOORNMILEECCARCCNLFERCFNSASYRKPVGOHSMLEAMAHR tr A0A140EMR9 A0A140EMR9 _ 9 INFB GTHSWRTKRNRSIINTOORNMILEECCARCCNLFERCFNSASYRKPVGOHSMLEAMAHR	720 720 720 720 720 720 720 720
tr a0a140erc2 a0a140erc2_9infb GTHSWRTKRNRSIINTOGRMILEECCTAKCCNLFEACFNSASYRKPVGOHSMLEAMAHR tr a0a126tr22 a0a126tr22_9infb GTHSWRTKRNRSIINTOGRMILEECCTAKCCNLFEACFNSASYRKPVGOHSMLEAMAHR tr a0a059tB43 a0a059tB43_9infb GTHSWRTKRNRSIINTOGRMILEECCTAKCCNLFEACFNSASYRKPVGOHSMLEAMAHR tr a0a140emr9 a0a140emr9_9infb GTHSWRTKRNRSIINTOGRMILEECCTAKCCNLFEACFNSASYRKPVGOHSMLEAMAHR	720 720 720 720 720 720 720
tr a0a126tr22 a0a126tr22 ⁻ 9INFB GTHSWRTKRNRSIINTDORNMILEECCARCCNLFEACFNSASYRKPVGOHSMLEAMAHR tr a0a059tB43 a0a059tB43 ⁻ 9INFB GTHSWRTKRNRSIINTDORNMILEECCARCCNLFEACFNSASYRKPVGOHSMLEAMAHR tr a0a140emr9 a0a140emr9 ⁻ 9INFB GTHSWRTKRNRSIINTDORNMILEECCARCCNLFEACFNSASYRKPVGOHSMLEAMAHR	720 720 720 720 720
tr a0a059tb43 a0a059tb43 ⁻ 9infb gthswrtknnsii <mark>ntdorn</mark> mileec <mark>ctak</mark> ccnlfeacfnsasyrkpvgghsmleama <mark>h</mark> r tr a0a140emr9 a0a140emr9_9infb gthswrtknnsii <mark>ntdorn</mark> mileec <mark>ctakcc</mark> nlfeacfnsasyrkpvgghsmleama h r	720 720 720 720
tr a0a140emr9 a0a140emr9_9infb gthswrtkrnrsiintdernmileedtarcoulfeacensasyrkpvgghsmleamahr	720 720 720
	720 720
	720
tr A0A140EUR3 A0A140EUR3_9INFB GTHSWRTKRNRSII <mark>NTDØRN</mark> MILEEG <mark>CYAKOC</mark> NLFEA <mark>C</mark> FNSASYRKPVGQHSMLEAMA <mark>H</mark> R	
tr a0a126tsn3 a0a126tsn3_9infb gthswrtkrnrsii <mark>nt</mark> Dqrnmileeq <mark>crak_co</mark> nlfea <mark>c</mark> fnsasyrkpvgqhsmleam2 <mark>h</mark> r	
tr a0a126ua37 a0a126ua37_9infb gthswrtkrnrsii <mark>nt</mark> Dqrnmileeq <mark>crak_co</mark> nlfea <mark>c</mark> fnsasyrkpvgqhsmleam2 <mark>h</mark> r	720
tr A0A0D6A5W0 A0A0D6A5W0_9INFB GTHSWRTKRNRSII <mark>NTDQRN</mark> MILEEQC <mark>YAKOC</mark> NLFEACFNSASYRKPVGQHSMLEAMAHR	720
sp 036430 rdrp_inbp9 gthswrtkrnrsii <mark>nt</mark> DqrnMileeq <mark>ctAkCc</mark> nlfeA <mark>C</mark> rnSasyrkpvgQhsmleam2 <mark>h</mark> r	720
tr a52216 a52216_91nfb gthswrtkrnrs11 <mark>nt</mark> DqrnM1Leeq <mark>crak_cc</mark> nLfeA <mark>cf</mark> nsasyrkpvgQhsmLeam2 <mark>h</mark> r	720
tr a4d528 a4d528_9infb gthswrtkrnrsii <mark>nt</mark> d <mark>qrn</mark> mileeq <mark>ctak_co</mark> nlfea <mark>c</mark> fnsasyrkpvgqhsmleam2 <mark>h</mark> r	720
tr A4D4U0 A4D4U0_9INFB GTHSWRTKRNRSII <mark>NT</mark> D QRN MILEEQ <mark>CYAKCC</mark> NLFEA <mark>CF</mark> NSASYRKPVGQHSMLEAM2 <mark>H</mark> R	720
tr a3drf0 a3drf0_9infb gthswrtkrnrsii <mark>nt</mark> dqrnmileeq <mark>ctak_co</mark> nlfea <mark>c</mark> fnsasyrkpvgqhsmleam2 <mark>h</mark> r	720
tr a4d4v1 a4d4v1_9infb gthswrtkrnrsii <mark>nt</mark> d <mark>qrn</mark> mileeq <mark>ctak_co</mark> nlfea <mark>c</mark> fnsasyrkpvgqhsmleam2 <mark>h</mark> r	720
tr 84uq80 84uq80_91nfb gthswrtkrnrs11 <mark>nt</mark> D qrn M1Leeq <mark>crak_c</mark> nLfea <mark>c</mark> rnsasyrkpvgqhsmLeam2 <mark>h</mark> r	720
tr A4D4M4 A4D4M4_9INFB GTHSWRTKRNRSII <mark>NTDQRN</mark> MILEEQ <mark>CYAKCC</mark> NLFEA <mark>C</mark> FNSASYRKPVGQHSMLEAM2 <mark>H</mark> R	720
sp P07832 RDRP_INBLE GTHSWRTKRNRSILNTDORNMILEEOCYAKCONLFEACFNSASYRKPVGOHSMLEAMAHR	720
tr G7WTR6 G7WTR6_9INFB GTHSWRTKRNRSII <mark>NTDQRN</mark> MILEEdCTARCCRNSASYRRPVGQHSMLEAM2HR	720
tr A0A2D1W9N9 A0A2D1W9N9_9INFB GTHSWRTKRNRSII <mark>NTDQRN</mark> MILEEQ <mark>CYAKCC</mark> NLFEA <mark>CF</mark> NSASYRKPVGQHSMLEAM2 <mark>H</mark> R	720
tr A0A216BBP3 A0A216BBP3_91NFB GTHSWRTKRNRSII <mark>NT</mark> DQRNMILEEQCKAKOCNLFEACENSASYRKPVGQHSMLEAMAHR	720
tr A0A119TNG8 A0A119TNG8_91NFB GTHSWRTKRNRSII <mark>NTDQRN</mark> MILEEQ <mark>CKAKCC</mark> NLFEA <mark>CF</mark> NSASYRKFVGQHSMLEAM2 <mark>H</mark> R	720
tr A0A075ccj9 A0A075ccj9_91NFB GTHSWRTKRNRSI1 <mark>NTDQRN</mark> MILEEQ <mark>CYAK_CC</mark> NLFEA <mark>CF</mark> NSASYRKPVGQHSMLEAM2 <mark>H</mark> R	720
tr S4SZ61 S4SZ61_9INFB GTHSWRTKRNRSIINTDQRMMILEEQCYAKCCNLFEACFNSASYRKPVGQHSMLEAM2HR	720
tr A0A0N7GD33 A0A0N7GD33_91NFB GTHSWRTKRNRSI1 <mark>NTDQRN</mark> MILEEQ <mark>CYAKCC</mark> NLFEA <mark>CF</mark> NSASYRKPVGQHSMLEAM2 <mark>H</mark> R	720
tr a0a248xlr8 a0a248xlr8_9infb gthswrtkrnrsii <mark>nf</mark> d <mark>grn</mark> mileeg <mark>ckakoc</mark> nlfea <mark>c</mark> fnsasyrkpvgqhsmleama <mark>h</mark> r	720
tr a0a286nmr2 a0a286nmr2_9infb gthswrtkrnrsii <mark>nt</mark> Dqrnmileeq <mark>crak_co</mark> nlfea <mark>c</mark> fnsasyrkpvgqhsmleam2 <mark>h</mark> r	720
tr a0a2d1w2j9 a0a2d1w2j9_9infb GTHSwRTKRNRSII <mark>NT</mark> DQRNMILEEQCKAKOCNLFEACFNSASYRKPVGQHSMLEAMAHR	720
tr A3DR07 A3DR07_INBBK GTHSWRTKRNRSII <mark>NT</mark> D ¢RN MILEEC <mark>C*AKOC</mark> NLFEA <mark>C</mark> FNSASYRKFVGQHSMLEAMA <mark>H</mark> R	720
tr A3DQR9 A3DQR9_9INFB GTHSWRTKRNRSII <mark>NTDQRN</mark> MILEEQCKARCCNLFEACFNSASYRKPVGQHSMLEAM2HR	720
tr A4D4X3 A4D4X3_9INFB GTHSWRTKRNRSII <mark>NTDQRN</mark> MILEEdCTAKCCRNSASYRKPVGOHSMLEAM2HR	720
sp P13871 RDRP_INBAC GTHSWRTKRNRSII <mark>NTDQRN</mark> MILEEd <mark>CYAKCC</mark> RNSASYRKPVGOHSMLEAMA <mark>H</mark> R	720
sp P13872 RDRP_INBAD GTHSWRTKRNRSII <mark>NTDQRN</mark> MILEEQ <mark>CKAK_CO</mark> NLFEADFNSASYRKPVGOHSMLEAMA <mark>H</mark> R	720

//End of the PB1 subunits from Flu B viruses

File of the FBT subulits if off File B	VILUSES
tr A0A126TPY5 A0A126TPY5_9INFB	LRMDARLDYESGRMSKDDFEKAMAHLGEIGYT 752
tr 12E0T1 12E0T1_91NFB	LRMDARLDYESGRMSKDDFEKAMAHLGEIGYT 752
tr B4UQS5 B4UQS5_9INFB	LRMDARLDYESGRMSKDDFEKAMAHLGEIGYT 752
tr A3DQQ8 A3DQQ8_9INFB	LRMDARLDYESGRMSKDDFEKAMAHLGEIGYT 752
tr A0A140ERC2 A0A140ERC2_9INFB	LRMDARLDYESGRMSKDDFEKAMAHLGEIGYT 752
tr A0A126TR22 A0A126TR22_9INFB	LRMDARLDYESGRMSKDDFEKAMAHLGEVGYT 752
tr A0A059TB43 A0A059TB43_9INFB	LRMDARLDYESGRMSKDDFEKAMAHLGEIGYT 752
tr A0A140EMR9 A0A140EMR9_9INFB	LRMDARLDYESGRMSKDDFEKAMAHLGEIGYT 752
tr A0A140EUR3 A0A140EUR3_9INFB	LRMDARLDYESGRMSKDDFEKAMAHLGEIGYT 752
tr A0A126TSN3 A0A126TSN3_9INFB	LRMDARLDYESGRMSKDDFEKAMAHLGEIGYT 752
tr A0A126UA37 A0A126UA37_9INFB	LRMDARLDYESGRMSKDDFEKAMAHLGEIGYT 752
tr A0A0D6A5W0 A0A0D6A5W0_9INFB	LRMDARLDYESGRMSKDDFEKAMAHLGEIGYT 752
sp 036430 RDRP_INBP9	LRMDARLDYESGRMSKDDFEKAMAHLGEIGYI 752
tr A5Z2I6 A5Z2I6_9INFB	LRMDARLDYESGRMSKDDFEKAMAHLGEIGYT 752
tr A4D528 A4D528_9INFB	LRMDARLDYESGRMSKDDFEKAMAHLGEIGYT 752
tr A4D4U0 A4D4U0_9INFB	LRMDARLDYESGRMSKDDFEKAMAHLGEIGYT 752
tr A3DRF0 A3DRF0_9INFB	LRMDARLDYESGRMSKDDFEKAMAHLGEIGYT 752
tr A4D4V1 A4D4V1_9INFB	LRMDARLDYESGRMSKDDFEKAMAHLGEIGYT 752
tr B4UQB0 B4UQB0_9INFB	LRMDARLDYESGRMSKDDFEKAMAHLGEIGYT 752
tr A4D4M4 A4D4M4_9INFB	LRMDARLDYESGRMSKDDFEKAMAHLGEIGYT 752
sp P07832 RDRP_INBLE	LRMDARLDYESGRMSKEDFEKAMAHLGEIGYM 752
tr G7WTR6 G7WTR6_9INFB	LRMDARLDYESGRMSKDDFEKAMAHLGEIGYI 752
tr A0A2D1W9N9 A0A2D1W9N9_9INFB	LRMDARLDYESGRMSKDDFEKAMAHLGEIGYI 752
tr A0A2I6BBP3 A0A2I6BBP3_9INFB	LKMDARLDYESGRMSKDDFEKAMAHLGEIGYI 752
tr A0A119TNG8 A0A119TNG8_9INFB	LRMDARLDYESGRMSKDDFEKAMVHLGEIGYI 752
tr A0A075CCJ9 A0A075CCJ9_9INFB	LKMDARLDYESGRMSKDDFEKAMAHLGEIGYI 752
tr S4SZ61 S4SZ61_9INFB	LRMDARLDYESGRMSKDDFEKAMAHLGEIGYI 752
tr A0A0N7GD33 A0A0N7GD33_9INFB	LRMDARLDYESGRMSKDDFEKAMAHLGEIGYI 752
tr A0A248XLR8 A0A248XLR8_9INFB	LRMDARLDYESGRMSKDDFEKAMAHLGEIGYI 752
tr A0A286NMR2 A0A286NMR2_9INFB	LRMDARLDYESGRMSKDDFEKAMAHLGEIGYI 752
tr A0A2D1W2J9 A0A2D1W9N9_9INFB	LRMDARLDYESGRMSKDDFEKAMAHLGEIGYI 752
tr A3DR07 A3DR07_INBBK	LRMDARLDYESGRMSKDDFEKAMAHLGEIGYI 752
tr A3DQR9 A3DQR9_9INFB	LRMDARLDYESGRMSKDDFEKAMAHLGEIGYI 752
tr A4D4X3 A4D4X3_9INFB	LRMDARLDYESGRMSKDDFEKAMAHLGEIGYI 752
sp P13871 RDRP_INBAC	LRMDARLDYESGRMSKDDFEKAMAHLGEIG <mark>Y</mark> I 752*(CA)
sp P13872 RDRP_INBAD	LRMDARLDYESGRMSKDDFEKAMAHLGEIG <mark>H</mark> I 752*(WT)
	* ***************

A0A126TPY5 9INFB (South Australia/12/2013) I2E0T	1_9INFB (Malaysia/1899839/2007)
B4UQS5_9INFB Taiwan/71523/2007) A3DQ	Q8_9INFB (Argentina/132/2001)
A0A140ERC2_9INFB (Darwin/3/2013) A0A12	26TR22_9INFB (Sydney/13/2013)
A0A059TB43_9INFB (Thailand/VIROAF3/2012) A0A14	40EMR9_9INFB (South Auckland/35/2012)
A0A140EUR3_9INFB (Waikato/16/2013) A0A12	26TSN3_9INFB (Tasmania/3/2013)
A0A126UA37_9INFB (Singapore/Tt907/2013) A0A0	D6A5W0_9INFB (Gunma/13G022/2014)
O36430 RDRP_INBP9 (Panama/45/1990) A5Z21	6_9INFB (Vienna/1/1999)
A4D528_9INFB (Paris/549/1999) A4D4	U0_9INFB (Russia/22/1995)
A3DRF0_9INFB (Romania/318/1998) A4D4'	V1_9INFB (Bucharest/311/1998)
B4UQB0_9INFB (Jiangsu/10/2003) A4D4	M4_9INFB (Canada/16188/2000)
P07832 RDRP_INBLE, (Lee/1940) G7WT	R6_9INFB (Managua/5549.04/2010)
	I6BBP3_9INFB (California/66/2017)
	75CCJ9_9INFB (Santa Cruz/761/2012)
S4SZ61_9INFB (Thailand/CU-B4504/2011) A0A0	N7GD33_9INFB (Hawaii/11/2015)
A0A248XLR8_9INFB (Alaska/15/2017) A0A28	86NMR2_9INFB (Nicaragua/6104_08/2016)
	R9_9INFB (Hong Kong/1115/2002)
A4D4X3_9INFB (Osaka/547/1997)	
P13871 RDRP_INBAC (Ann Arbor/1/1966 [cold-adapted])	
P13872 RDRP_INBAD (Ann Arbor/1/1966 [wild-type])	

Figure 5 MSA of the PB1 catalytic subunits from different strains of human influenza B virus CA, cold adapted; WT, wild type

Figure 6 shows the MSA of the catalytic subunits PB1 of the polymerase of different human influenza C viral strains from various regions. The theoretical pI of the standard Yamagata 1964 strain is 8.82 and highlighted in yellow. The PB1 subunits are completely conserved for the entire sequence with only a few changes and these subunits from the C virus are the most conserved among the three human influenza viruses (Fig. 6). The metal-binding regions are highlighted in dark green and the proposed amino acids in the catalytic regions and the highly conserved fingertip priming loop are highlighted in yellow. All the five motifs identified in influenza A and B viral strains are also highly conserved in the C virus: Motif I –KLQRR- (the middle K found in A and B viruses is replaced by Q) Motif II $-^{305}$ TGDN-; Motif III – 405 PGGMLMGMF-; Motif IV $-^{439}$ WTGLQSSDDFVLF-; Motif V $-^{475}$ GINMSLEKSYG– (highlighted in dark and light green). The NLS region is highlighted in orange. In striking contrast, the –YAQ- motif is not observed in the C viral strains.

3.1.3. CLUSTAL O (1.2.4) MSA of BP1 catalytic subunits of the RdRP from Flu C Viral strains

sp P19703 RDRP_INCJJ	VKFRKVKTMVRREKDKRSGKEIKTKVPVMGIDSIKHDEFLIRALTINTMAKDGER <mark>GKLQR</mark>	240
sp Q9IMP4 RDRP INCJH	IKFKKVKTVVRREKDKRSGKEIKTKVPVMGIDSIKHDEFLIRALTINTMAKDGER <mark>GKLQR</mark>	240
tr A0A193PPL8 A0A193PPL8 90RT0	IKFKKVKTVVRREKDKRSGKEIKTKVPVMGIDSIKHDEFLIRALTINTMAKDGER <mark>GKLQR</mark>	240
r A0A193PPM8 A0A193PPM8 9ORTO	VKFRKVKTMVRREKDKRSGKEIKTKVPVMGIDSIKHDEFLVRALTINTMAKDGER <mark>GKLOR</mark>	240
r A0A193PPP6 A0A193PPP6 90RT0	VKFRKVKTMVRREKDKRSGKEIKTKVPVMGIDSIKHDEFLVRALTINTMAKDGER <mark>GKLQR</mark>	240
r A0A193PPP0 A0A193PPP0 90RT0	VKFRKVKTMVRREKDKRSGKEIKTKVPVMGIDSIKHDEFLIRALTINTMAKDGER <mark>GKLQR</mark>	240
p Q617C3 RDRP INCAA	VKFRKVKTMVRREKDKRSGKEIKTKVPVMGIDSIKHDEFLIRALTINTMAKDGER <mark>GKLOR</mark>	240
r A0A193PPL7 A0A193PPL7 90RT0	VKFRKVKTMVRREKDKRSGKEIKTKVPVMGIDSIKHDEFLIRALTINTMAKDGER <mark>GKLOR</mark>	240
r A0A193PQ43 A0A193PQ43 INCKS	VKFRKVKTMVRREKDKRSGKEIKTKVPVMGIDSIKHDEFLIRALTINTMAKDGER <mark>GKLOR</mark>	240
r A0A193PPP8 A0A193PPP8 ⁻ INCM3	VKFRKVKTMVRREKDKRSGKEIKTKVPVMGIDSIKHDEFLIRALTINTMAKDGER <mark>GKLQR</mark>	240
r A0A193PQ33 A0A193PQ33 INCY6	VKFRKVKTMVRREKDKRSGKEIKTKVPVMGIDSIKHDEFLIRALTINTMAKDGERGKLOR	240
r A0A193PQ35 A0A193PQ35_90RT0	VKFRKVKTMVRREKDKRSGKEIKTKVPVMGIDSIKHDEFLIRALTINTMAKDGER <mark>GKLOR</mark>	240 Floop
	•**•****•*****************************	

sp P19703 RDRP INCJJ	RAIATPGMIVRPFSKIVETVAQKICEKIKESGLEVGGNEKKAKLKTTVTSLNARMNSDQF	300
sp Q9IMP4 RDRP INCJH	RAIATPGMIVRPFSKIVETVAQKICEKIKESGLEVGGNEKKAKIKTTVTSLNARMNSDQF	300
tr A0A193PPL8 A0A193PPL8 90RT0	RAIATPGMIVRPFSKIVETVAQKICE <mark>KI</mark> KESGLE <mark>VG</mark> GNE <mark>KKAKLK</mark> TTVTSLNARMNSDQF	300
tr A0A193PPM8 A0A193PPM8 90RT0	RAIATPGMIVRPFSKIVETVAQKICEKIKESGLEVGGNEKKAKLKTTVTSLNARMNSDQF	300
r A0A193PPP6 A0A193PPP6 90RT0	RAIATPGMIVRPFSKIVETVAQKICE <mark>KI</mark> KESGLE <mark>VG</mark> GNE <mark>KKAKLK</mark> TTVTSLNARMNSDQF	300
r A0A193PPP0 A0A193PPP0 90RT0	RAIATPGMIVRPFSKIVETVAQKICEKIKESGLEVGGNEKKAKLKTTVTSLNARMNSDQF	300 Rep
p Q6I7C3 RDRP INCAA	RAIATPGMIVRPFSKIVETVAQKICEKIKESGLEVGGNEKKAKIKTTVTSLNARMNSDQF	300
r A0A193PPL7 A0A193PPL7 90RT0	RAIATPGMIVRPFSKIVETVAQKICEKIKESGLEVGGNEKKAKLKTTVTSLNARMNSDQF	300
r A0A193PQ43 A0A193PQ43_INCKS	RAIATPGMIVRPFSKIVETVAQKICE <mark>KI</mark> KESGLE <mark>VG</mark> GNE <mark>KKAKLK</mark> TTVTSLNARMNSDQF	300
r A0A193PPP8 A0A193PPP8 INCM3	RAIATPGMIVRPFSKIVETVAQKICE <mark>KI</mark> KESGLE <mark>VG</mark> GNE <mark>KKAKLK</mark> TTVTSLNARMNSDQF	300
tr A0A193PQ33 A0A193PQ33_INCY6	RAIATPGMIVRPFSKIVETVAQKICEKLKESGLPVGGNEKKAKLKTTVTSLNARMNSDQF	300
tr A0A193PQ35 A0A193PQ35 90RT0	RAIATPGMIVRPFSKIVETVA <mark>QK</mark> VCEKIKESGLEVGGNE <mark>KKAKLK</mark> TTVTSLNARMNSDQF	300
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sp P19703 RDRP_INCJJ	NISTLHIPEEVLKFEKMDEQYRNRVFNPKNPFTNFDKTIDIFRAHGPIRVEENEAVVSTH	660
sp Q9IMP4 RDRP_INCJH	NISTLHIPEEVLKFEKMDEQYRNRVFNPKNPFTNFDKTIDIFRAHGPIRVEENEAVVSTH	660
tr A0A193PPL8 A0A193PPL8_9ORTO	NISTLHIPEEVLKFEKMDEQYRNRVFNPKNPFTNFDKTIDIFRAHGPIRVEENEAVVSTH	660
tr A0A193PPM8 A0A193PPM8_9ORTO	NISTLHIPEEVLKFEKMDEQYRNRVFNPKNPFTNFDKTIDIFRAHGPIRVEENEAVVSTH	660
tr A0A193PPP6 A0A193PPP6_9ORTO	NISTLHVPEEVLKFEKMDEQYRNRVFNPKNPFTNFDKTIDIFRAHGPIRVEENEAVVSTH	660
tr A0A193PPP0 A0A193PPP0_9ORTO	NISTLHIPEEVLKFEKMDEQYRNRVFNPKNPFTNFDKTIDIFRAHGPIRVEENEAVVSTH	660
sp Q6I7C3 RDRP_INCAA	NISTLHIPEEVLKFEKMDEQYRNRVFNPKNPFTNFDKTIDIFRAHGPIRVEENEAVVSTH	660
tr A0A193PPL7 A0A193PPL7 9ORTO	NISTLHIPEEVLKFEKMDEQYRNRVFNPKNPFTNFDKTIDIFRAHGPIRVEENEAVVSTH	660
tr A0A193PQ43 A0A193PQ43_INCKS	NISTLHIPEEVLKFEKMDEQYRNRVFNPKNPFTNFDKTIDIFRAHGPIRVEENEAVVSTH	660
tr A0A193PPP8 A0A193PPP8_INCM3	NISTLHIPEEVLKFEKMDEQYRNRVFNPKNPFTNFDKTIDIFRAHGPIRVEENEAVVSTH	660
tr A0A193PQ33 A0A193PQ33_INCY6	NISTLHIPEEVLKFEKMDEQYRNRVFNPKNPFTNFDKTIDIFRAHGPIRVEENEAVVSTH	660
tr A0A193PQ35 A0A193PQ35_90RT0	NISTLHIPEEVLKFEKMDEQYRNRVFNPKNPFTNFDKTIDIFRAHGPIRVEENEAVVSTH	660
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sp P19703 RDRP INCJJ	EKS <mark>YGS</mark> LPELFEFTSMFFDGEFVSNLAMELPAFTTAGVNEGVDFTAAMSIIKTNMINNSL	540
sp Q9IMP4 RDRP INCJH	EKS <mark>YGS</mark> LPELFEFTSMFFDGEFVSNLAMELPAFTTAGVNEGVDFTAAMSIIKTNMINNSL	540
tr A0A193PPL8 A0A193PPL8 90RT0	EKS <mark>YGS</mark> LPELFEFTSMFFDGEFVSNLAMELPAFTTAGVNEGVDFTAAMSIIKTNMINNSL	540
tr A0A193PPM8 A0A193PPM8 90RT0	EKS <mark>YGS</mark> LPELFEFTSMFFDGEFVSNLAMELPAFTTAGVNEGVDFTAAMSIIKTNMINNSL	540
tr A0A193PPP6 A0A193PPP6 90RT0	EKS <mark>YGS</mark> LPELFEFTSMFFDGEFVSNLAMELPAFTTAGVNEGVDFTAAMSIIKTNMINNSL	540
tr A0A193PPP0 A0A193PPP0 90RT0	EKS <mark>YGS</mark> LPELFEFTSMFFDGEFVSNLAMELPAFTTAGVNEGVDFTAAMSIIKTNMINNSL	540
sp Q617C3 RDRP_INCAA	EKS <mark>YGS</mark> LPELFEFTSMFFDGEFVSNLAMELPAFTTAGVNEGVDFTAAMSIIKTNMINNSL	540
tr A0A193PPL7 A0A193PPL7 90RT0	EKS <mark>YGS</mark> LPELFEFTSMFFDGEFVSNLAMELPAFTTAGVNEGVDFTAAMSIIKTNMINNSL	540
tr A0A193PQ43 A0A193PQ43_INCKS	EKS <mark>YGS</mark> LPELFEFTSMFFDGEFVSNLAMELPAFTTAGVNEGVDFTAAMSIIKTNMINNSL	540
tr A0A193PPP8 A0A193PPP8_INCM3	EKS <mark>YGS</mark> LPELFEFTSMFFDGEFVSNLAMELPAFTTAGVNEGVDFTAAMSIIKTNMINNSL	540
tr A0A193PQ33 A0A193PQ33 INCY6	EKSYGSLPELFEFTSMFFDGEFVSNLAMELPAFTTAGVNEGVDFTAAMSIIKTNMINNSL	540
tr A0A193PQ35 A0A193PQ35_9ORTO	EKS <mark>/G</mark> LPELFEFTSMFFDGEFVSNLAMELPAFTTAGVNEGVDFTAAMSIIKTNMINNSL *** <mark>**</mark> **************	540

p P19703 RDRP INCJJ	GVSTLCYMDEELKAKGCFWTGLQSEDDFVLFAVASNWSNIHWTIRRENAVCKLIGINMSL	480
p Q9IMP4 RDRP INCJH	GVSTLCYMDEELKAKGCF <mark>WTGLQS<mark>5DD</mark>FVLF</mark> AVASNWSNIHWTIRRE <mark>N</mark> AVC <mark>KL</mark> IGINMSL	480
r A0A193PPL8 A0A193PPL8 9ORTO	GVSTLCYMDEELKAKGCF <mark>WTGLQS<mark>5DD</mark>FVLF</mark> AVASNWSNIHWTIRRE <mark>N</mark> AVC <mark>KL</mark> IGINMSL	480
r A0A193PPM8 A0A193PPM8_9ORTO	GVSTLCYMDEELKAKGCF <mark>WTGLQS<mark>5DD</mark>FVLF</mark> AVASNWSNIHWTIRRE <mark>N</mark> AVC <mark>KL</mark> IGINMSL	480
r A0A193PPP6 A0A193PPP6 90RT0	GVSTLCYMDEELKAKGCF <mark>WTGLQS<mark>5DD</mark>FVLF</mark> AVASNWSNIHWTIRRE <mark>N</mark> AV <mark>KL</mark> IGINMSL	480
r A0A193PPP0 A0A193PPP0 90RT0	GVSTLCYMDEELKAKGCF <mark>WTGLQS<mark>5DD</mark>FVLF</mark> AVASNWSNIHWTIRRE <mark>N</mark> AVC <mark>KL</mark> IGINMSL	480
p Q617C3 RDRP INCAA -	GVSTLCYMDEELKAKGCF <mark>WTGLQSSDDFVLF</mark> AVASNWSNIHWTIRRE <mark>N</mark> AV <mark>KL</mark> IGINMSL	480
r A0A193PPL7 A0A193PPL7 90RT0	GVSTLCYMDEELKAKGCF <mark>WTGLQS<mark>5DD</mark>FVLF</mark> AVASNWSNIHWTIRRE <mark>N</mark> AVC <mark>KL</mark> IGINMSL	480
r A0A193PQ43 A0A193PQ43 INCKS	GVSTLCYMDEELKAKGCFWTGLQS <mark>SDD</mark> FVLFAVASNWSNIHWTIRRE <mark>N</mark> AV <mark>KL</mark> IGINMSL	480
r A0A193PPP8 A0A193PPP8 INCM3	GVSTLCYMDEELKAKGCF <mark>WTGLQSSDD</mark> FVLFAVASNWSNIHWTIRRE <mark>N</mark> AV <mark>KL</mark> IGINMSL	480
r A0A193PQ33 A0A193PQ33 INCY6	GVSTLCYMDEELKAKGCFWTGLOSSDDFVLFAVASNWSNIHWTIRRFNAVCKLIGINMSL	480
r A0A193PQ35 A0A193PQ35_90RT0	GVSTLCYMDEELKAKGCFWTGLQSSDDFVLFAVASNWSNIHWTIRRENAVOKLIGINMSL	480
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sp P19703 RDRP INCJJ	NKRKTKEVIIKAEKMGKYKNLMREEYKNLFEPLEKYIQKDVCFLPGGMLMGMFNML	420
sp/Q9IMP4/RDRP INCJH	NKRKTKEVIIKAEKMOKTKKEMEREYKNLFEPLEKYIQKDVCFLPGGMLMGMFNMLGTVL	420
tr A0A193PPL8 A0A193PPL8_9ORTO	NKRKTKEVIIKAEKMGKYKNLMREEYKNLFEPLEKYIQKDVCFLPG <mark>GMLMGMFNML</mark> STVL	420
tr A0A193PPM8 A0A193PPM8_9ORTO	NKRKTKEVMIKAEKMGKYKNLMREEYKNLFEPLEKYIQKDVCFLP <mark>GGMLMGMFNML</mark> 5TVL	420
tr A0A193PPP6 A0A193PPP6_9ORTO	NKRKTKEVIIKAEKMGKYKNLMREEYKNLFEPLEKYIQKDVCFLP <mark>GMLMGMFNML</mark> STVL	420
tr A0A193PPP0 A0A193PPP0_9ORTO	NKRKTKEVIIKAEKMGKYKNLMREEYKNLFEPLEKYIQKDVCFLP <mark>GGMLMGMFNML</mark> FTVL	420
sp Q6I7C3 RDRP_INCAA	NKRKTKEVIIKAEKMGKYKNLMREEYKNLFEPLEKYIQKDVCFLPGGMLMGMFNMLFTVL	420
tr A0A193PPL7 A0A193PPL7_9ORTO	NKRKTKEVIIKAEKMGKYKNLMREEYKNLFEPLEKYIQKDVCFLPGGMLMGMFNML5TVL	420
tr A0A193PQ43 A0A193PQ43_INCKS tr A0A193PPP8 A0A193PPP8_INCM3	NKRKTKEVIIKAEKMGKYKNLMREEYKNLFEPLEKYIQKDVCFLPG <mark>GMLMGMFNML</mark> STVL NKRKTKEVIIKAEKMGKYKNLMREEYKNLFEPLEKYIQKDVCFLPG <mark>GMLMGMFNML</mark> STVL	420 420
tr A0A193PPP8 A0A193PPP8_INCM3	NKRKIKEVIIKAEKMGKIKNIMEEIKNIFEPIEKIIQKDVCFIFGGMIMGMFMMIPIVI NKRKKEVIIKAEKMGKYKNIMEEYKNIFEPIEKYIOKDVCFIFGGMIMGMFMMISTVI	420
tr A0A193PQ35 A0A193PQ35_90RT0	NKRKIKEVIIKAEKMOKIKNIMKEEIKNIHEEDEKIIQKDVCFIGOMIMOMENNISIVI NKRKIKEVIIKAEKMOKYKNIMKEEYKNIFEPIEKYIQKDVCFIPOGMIMOMENNISIVI	420

sp P19703 RDRP INCJJ	AVNIT DNSKWNECQQPEAYLALLAYITKDSSDLMKDLCSVAPVLFCNKFVKLGQGIRLS	360
sp Q9IMP4 RDRP INCJH	AVNITGONSKWNECQQPEAYLALLAYITKDSSDLMKDLCSVAPVLFCNKFVKLGQGIRLS	360
tr A0A193PPL8 A0A193PPL8 9ORTO	AVNIT <mark>GDN</mark> SKWNECQQPEAYLALLAYITKDSSDLMKDLCSVAPVLFCNKFVKLGQGIRLS	360
tr A0A193PPM8 A0A193PPM8 90RT0	AVNIT <mark>GDN</mark> SKWNECQQPEAYLALLAYITKDSSDLMKDLCSVAPVLFCNKFVKLGQGIRLS	360
tr A0A193PPP6 A0A193PPP6_9ORTO	AVNIT <mark>GDN</mark> SKWNECQQPEAYLALLAYITKDSSDLMKDLCSVAPVLFCNKFVKLGQGIRLS	360
tr A0A193PPP0 A0A193PPP0_9ORTO	AVNIT <mark>GDN</mark> SKWNECQQPEAYLALLAYITKDSSDLMKDLCSVAPVLFCNKFVKLGQGIRLS	360
sp Q617C3 RDRP INCAA	AVNIT <mark>GDN</mark> SKWNECQQPEAYLALLAYITKDSSDLMKDLCSVAPVLFCNKFVKLGQGIRLS	360
tr A0A193PPL7 A0A193PPL7 90RT0	AVNIT <mark>GDN</mark> SKWNECQQPEAYLALLAYITKDSSDLMKDLCSVAPVLFCNKFVKLGQGIRLS	360
tr A0A193PQ43 A0A193PQ43_INCKS	AVNIT <mark>GDN</mark> SKWNECQQPEAYLALLAYITKDSSDLMKDLCSVAPVLFCNKFVKLGQGIRLS	360
tr A0A193PPP8 A0A193PPP8 INCM3	AVNIT <mark>GDN</mark> SKWNECQQPEAYLALLAYITKDSSDLMKDLCSVAPVLFCNKFVKLGQGIRLS	360
tr A0A193PQ33 A0A193PQ33 INCY6	AVNITGDNSKWNECOOPEAYLALLAYITKDSSDLMKDLCSVAPVLFCNKFVKLGOGIRLS	360
tr A0A193PQ35 A0A193PQ35_90RT0	AVNIT <mark>SON</mark> SKWNECQQPEAYLALLAYITKDSSDLMKDLCSVAPVLFCNKFVKLGQGIRLS	360

//End of the PB1 catalytic subunits of	the RdRp from human influenza C Viral stra	ains
sp P19703 RDRP INCJJ	RAKMKRDIGAIEDSEYEEIKDIIRDAKKARIESR	754
sp Q9IMP4 RDRP INCJH	RAKMKRDIGAIEDSEYEEIKDIIRDAKKARLESR	754
tr A0A193PPL8 A0A193PPL8 9ORTO	RAKMKRDIGAIEDSEYEEIKDIIRDAKKARIESR	754
tr A0A193PPM8 A0A193PPM8 9ORTO	RAKMKRDIGAIEDSEYEEIKDIIRDAKKARIESR	754
tr A0A193PPP6 A0A193PPP6 9ORTO	RAKMKRDIGAIEDSEYEEIKDIIRDAKKARIESR	754
tr A0A193PPP0 A0A193PPP0 90RT0	RAKMKRDIGAIEDSEYEEIKDIIRDAKKARIESR	754
sp Q6I7C3 RDRP_INCAA	RAKMKRDIGAIEDSEYEEIKDIIRDAKKARIESR	754
tr A0A193PPL7 A0A193PPL7 9ORTO	RAKMKRDIGAIEDSEYEEIKDIIRDAKKARIESR	754
tr A0A193PQ43 A0A193PQ43 INCKS	RAKMKRDIGAIEDSEYEEIKDIIRDAKKARIESR	754
tr A0A193PPP8 A0A193PPP8_INCM3	RAKMKRDIGAIEDSEYEEIKDIIRDAKKARIESR	754
tr A0A193PQ33 A0A193PQ33_INCY6	RAKMKRDIGAIEDSEYEEIKDIIRDAKKARIESR	754
tr A0A193PQ35 A0A193PQ35_90RT0	RAKMKRDIGAIEDSEYEEIKDIIRDAKKARIESR	754

	NCJJ (strain C/ JJ/1950) INCJH (strain C/ Johannesburg/1/	1966)
	ORTO (strain C/ Paris/1/1967)	
	ORTO (strain C/ Kyoto/1/1979)	
_	ORTO (strain C/ Miyagi/8/1996)	
	ORTO (strain C/ Yamagata/4/1992	
	INCAA (strain C/ Ann Arbor/1/19	50)
	ORTO (strain C/ Georgia/1/1969)	
A0A193PQ43_11	NCKS (strain C/ Kansas/1/1979)	

Figure 6 MSA of the PB1 catalytic subunits of the polymerase from different human influenza C viral strains

A0A193PPP8_INCM3 (strain C/ Miyagi/5/1991) A0A193PQ33_INCY6 (strain C/ Yamagata/1964) A0A193PQ35_9ORTO (strain C/ Yamagata/9/1988)

Figure 7 shows the 'Mix and Match' MSA of the PB1 catalytic subunits from all the three human influenza viruses. Only a few peptides show complete alignment. Interestingly, all the five motifs, Motif I -²³⁵KLK/QRR- Motif II -³⁰⁵TGDN-; Motif III -⁴⁰⁵PGGMLMGMF-; Motif IV -⁴³⁹WTGLQSSDDFVLF-; Motif V -⁴⁷⁵GINMSLEKSYG- (highlighted in dark and light green) are highly conserved and aligned in all. Furthermore, a striking conservation and alignment is found in the proposed replication catalytic core in all. The proposed replication catalytic pair is highly conserved in all except an – NL- pair is found in B virus instead of a -KL- pair found in A and C viruses. The finger-priming loop in Motif-I is highly conserved in all except a Q replaces the K in C virus. However, the proposed transcription catalytic region is mostly found in the thumb regions. In contrast to the finger-priming loop which is highly conserved in all the three viruses (highlighted in yellow), the suggested priming loop (highlighted in grey) is not conserved in all but for 4 amino acids. It is interesting to note that both the catalytic metal-binding sites are preceded by an invariant hydroxy amino acid, **T/S** in all the three human influenza viruses, suggesting its possible role in metal-binding. Three striking differences among the subunits are, the -YAQ- triad, the -KLKKLK- repeat and a zinc-binding motif (ZBM). The PB1 subunit of the B virus shows a typical ZBM (highlighted in orange) in the mRNA catalytic region and a -KLK- triad repeat (highlighted in grey) preceding the Met cluster at the template entry site and the -YAQ- in the N-terminal region (Fig. 7). The PB1 subunit of the A viruses show two additional metal-binding sites, one in the replication and the other in the mRNA catalytic regions.

The –YAQ- triad is found only in influenza A and B viruses which is similar to the invariant -YAN⁶⁹¹- found in SARS-CoV-1, SARS-CoV-2 and other SARS-related CoVs. It is located in the palm domain and suggested to be involved in the nucleotide selection [11,12]. The N/Q of the triad –YAN/Q- with the dual hydrogen bonding capacity can recognize the 2'-OH group of incoming NTPs and thus, discriminate NTPs and dNTPs during RNA synthesis. It is interesting to note that the YAN/Q type of motif is also found in the RdRps of Dengue, Zika, and Yellow Fever viruses too (data not shown) (11). However, it is intriguing to know that a similar triad is not found in the influenza C virus. The NLSs are found in the N-terminal region in all the three viruses and is highlighted in orange and the metal-binding regions are highlighted in dark green.

Interestingly, a completely conserved peptide with 3 to 4 Met residues, -⁴⁰⁶GMMMGMX₂ML- (MxMxMX₂ML) is found in all the three human influenza viruses. This characteristic methionine-rich loop (-⁴⁰⁶GMMM⁴⁰⁹GMF), is found at the template entry site [Pflug et al. [6]. It is interesting to note that a similar characteristic, highly conserved methionine-rich peptide -⁸⁹⁷GHMLDMYSVML- or (-X₂MX₂MX₃M-) is also found in the RdRps of SARS-CoV-1, SARS-CoV-2 and other SARS-related CoVs. This methionine-rich motif at the template entry site is suggested to be involved in stabilizing the base pair between the template and the incoming NTP [6, 11].

3.1.4. CLUSTAL O (1.2.4) Mix and Match MSA of the PB1 catalytic subunits of the RNA Polymerases all three human influenza viruses

sp P19703 RDRP INCJJ	FNIPRRKFCNCLEDKDDLVKPTGNVDISSLLGLAEMMEKRMGEGFFKHCVMEAETEILKM	120
sp Q9IMP4 RDRP INCJH	FNIPRRKFCNCLEDKDELVKPTGNVDISSLLGLAEMMEKRMGEGFFKHCVMEAETEILKM	120
r A0A193PPL8 A0A193PPL8 9ORTO	FNIPRRKFCNCLEDKDELVKPTGNVDISSLLGLAEMMEKRMGEGFFKHCVMEAETEILKM	120
r A0A193PPM8 A0A193PPM8 9ORTO	FNIPRRKFCNCLEDKDELVKPTGNVDISSLLGLAEMMEKRMGEGFFKHCVMEAETEILKM	120
r A0A193PPP6 A0A193PPP6 90RT0	FNIPRKFCNCLEDKDELVKPTGNVDISSLLGLAEMMEKRMGEGFFKHCVMEAETEILKM	120 C
		120
p Q617C3 RDRP_INCAA	FNIPRRKFCNCLEDKDELVKPTGNVDISSLLGLAEMMEKRMGEGFFKHCVMEAETEILKM	
r A0A193PQ43 A0A193PQ43_INCKS	FNIPRRKFCNCLEDKDELVKPTGNVDISSLLGLAEMMEKRMGEGFFKHCVMEAETEILKM	120
r A0A193PPP8 A0A193PPP8_INCM3	FNIPRRKFCNCLEDKDELVKPTGNVDISSLLGLAEMMEKRMGEGFFKHCVMEAETEILKM	120
r A0A193PQ33 A0A193PQ33_INCY6	FNIPRRKFCNCLEDKDELVKPTGNVDISSLLGLAEMMEKRMGEGFFKHCVMEAETEILKM	120
r A0A193PPP0 A0A193PPP0_90RTO	FNIPRRKFCNCLEDKNELVKPTGNVDISSLLGLAEMMEKRMGEGFFKHCVMEAETEILKM	120
p P07832 RDRP INBLE	TGCVMVDPINGPLPEDNEPSAYAOLDCVLEALDRMDE-EHPGLFOAGSONAMEALMVT	1177
r A0A0D6A5W0 A0A0D6A5W0 9INFB	TGCTMIDPTNGPLPEDNEPSAYAQLDCVLEALDRMDE-EHPGLFQAASQNAMEALMVT	117
r A0A059TB43 A0A059TB43 9INFB	TGCTMVDPTNGPLPEDNEPSAYAQLDCVLEALDRMDE-EHPGLFOAASONAMEALMVT	117
r A0A075CCJ9 A0A075CCJ9 9INFB	TGCTMVDFINGFL-PEDNEPSAYACLDCVLEALDRMDE-EHPGLFOAASONAMEALMVT	117
r A0A024CND8 A0A024CND8_9INFB	TGCTMVDPTNGPLPEDNEPSA <mark>YAQ</mark> LDCVLEALDRMDE-EHPGLFQAASQNAMEALMVT	117 <mark>B</mark>
r A0A0N7GD33 A0A0N7GD33_9INFB	TGCTMVDPTNGPLPEDNEPSA <mark>YAQ</mark> LDCVLEALDRMDE-EHPGLFQAASQNAMEALMVT	117
p O36430 RDRP_INBP9	TGCTMVDPTNGPLPEDNEPSA <mark>YAQ</mark> LDCVLEALDRMDE-EHPGLFQAASQNAMEALMVT	117
r A3DR07 A3DR07_INBBK	TGCTMVDPTNGPLPEDNEPSA <mark>YAQ</mark> LDCVLEALDRMDE-EHPGLFQAASQNAMEALMVT	117
p P13871 RDRP INBAC	TGCAMVDPTNGPLPEDNEPSA <mark>YAQ</mark> LDCVLEALDRMDE-EHPGLFQAASQNAMEALMVT	117
p P13872 RDRP_INBAD	TGCAMVDPTNGPLPEDNEPSAYAQLDCVLEALDRMDE-EHPGLFQAASQNAMEALMVT	117
p P03431 RDRP_I34A1	TGAPQLNPIDGPLPEDNEPSG <mark>YAQ</mark> TDCVLEAMAFLEE-SHPGIFENSCIETMEVVQQT	117
p Q9Q0V0 RDRP 196A0	TGAPQLNPIDGPLPEDNEPSG <mark>YAQ</mark> TDCVLEAMAFLEE-SHPGIFENSCLETMEVVQQT	117
p Q30NP3 RDRP_175A0	TGAPOLNPIDGPLPEDNEPSG <mark>YAQ</mark> TDCVLEAMAFLEE-SHPGIFENSCLETMEVVQQT	117
p P16511 RDRP_I57A5	TGAPOLNPIDGPLPEDNEPSCYAOTDCVLEAMAFLEE-SHPGIFENSCLETMEVIOOT	117
p Q0A2F7 RDRP 183A4	TGAPQLNPIDGPL-PEDNEPSG <mark>YAQ</mark> TDCVLEAMAFLEE-SHPGIFENSCLETMEVVQQT	117 A
	TGAPQLNPIDGPLPEDNEPSG <mark>YAQ</mark> TDCVLEAMAFLEE-SHPGIFENSCLETMEVVQQT	117
· · <u> </u>	TGAPQLNPIDGPLPEDNEPSG <mark>YAQ</mark> TDCVLEAMAFLEE-SHPGIFENSCLETMEVVQQT	117
p P16513 RDRP_180A8		
p P16513 RDRP_180A8 p Q08115 RDRP_180A6	TGAPQLNPIDGPLPEDNEPSG <mark>YAQ</mark> TDCVLEAMAFLEE-SHPGIFENSCLETMEVVQQT	117
p P16513 RDRP_180A8 p Q08115 RDRP_180A6	TGAPQLNPIDGPLPEDNEPSG <mark>YAQ</mark> TDCVLEAMAFLEE-SHPGIFENSCLETMEVVQQT TGAPQLNPIDGPLPEDNEPSG <mark>YAQ</mark> TDCVLEAMAFLEE-SHPGIFENSCLETMEVVQQT	117
sp P16503 RDRP_I77AF sp P16513 RDRP_I80A8 sp Q08II5 RDRP_I80A6 sp Q0A3Q1 RDRP_I78AC sp Q0A451 RDRP_I66A1	TGAPQLNPIDGPLPEDNEPSG <mark>YAQ</mark> TDCVLEAMAFLEE-SHPGIFENSCLETMEVVQQT TGAPQLNPIDGPLPEDNEPSG <mark>YAQ</mark> TDCVLEAMAFLEE-SHPGIFENSCLETMEVVQQT	
p P16513 RDRP_180A8 p Q08115 RDRP_180A6 p Q0A3Q1 RDRP_178AC	TGAPQLNPIDGPLPEDNEPSG <mark>YAQ</mark> TDCVLEAMAFLEE-SHPGIFENSCLETMEVVQQT	117
sp P16513 RDRP_180A8 sp Q08115 RDRP_180A6 sp Q0A3Q1 RDRP_178AC	TGAPQLNPIDGPLPEDNEPSG <mark>YAQ</mark> TDCVLEAMAFLEE-SHPGIFENSCLETMEVVQQT TGAPQLNPIDGPLPEDNEPSG <mark>YAQ</mark> TDCVLEAMAFLEE-SHPGIFENSCLETMEVVQQT	117
p P16513 RDRP_180A8 p Q08115 RDRP_180A6 p Q0A3Q1 RDRP_178AC p Q0A451 RDRP_166A1	TGAPQLNPIDGPLPEDNEPSG <mark>YAQ</mark> TDCVLEAMAFLEE-SHPGIFENSCLETMEVVQQT TGAPQLNPIDGPLPEDNEPSG <mark>YAQ</mark> TDCVLEAMAFLEE-SHPGIFENSCLETMEVVQQT	117
p P16513 RDRP_180A8 p Q08115 RDRP_180A6 p Q0A3Q1 RDRP_178AC p Q0A451 RDRP_166A1 p P19703 RDRP_INCJJ	TGAPOLNFIDGPLPEDNEPSGYAQTDCVLEAMAFLEE-SHPGIFENSCLETMEVVQQT TGAPOLNFIDGPLPEDNEPSGYAQTDCVLEAMAFLEE-SHPGIFENSCLETMEVVQQT : : :*: :*: *:*: :: : :* ::: *:*: :: EVKFRKVKTMVREKEKE	117 117 239 Flo
p P16513 RDRP_180A8 p Q08115 RDRP_180A6 p Q0A3Q1 RDRP_178AC p Q0A451 RDRP_166A1 p P19703 RDRP_INCJJ p Q9IMP4 RDRP_INCJH	TGAPOLNPIDGPLPEDNEPSGYACTDCVLFAMAFLEE-SHPGIFENSCLETMEVVQQT TGAPOLNPIDGPLPEDNEPSGYACTDCVLFAMAFLEE-SHPGIFENSCLETMEVVQQT : : :::: ::: ::: ::: :::::::::::::	117 117 239 239 239
p P16513 RDRP_I80A8 p Q08II5 RDRP_I80A6 p Q0A3Q1 RDRP_I78AC p Q0A451 RDRP_I66A1 p P19703 RDRP_INCJJ p Q9IMP4 RDRP_INCJH r A0A193PPL8 A0A193PPL8_90RT0	TGAPOLNPIDGPLPEDNEPSGYACTDCVLEAMAFLEE-SHPGIFENSCLETMEVVQQT TGAPOLNPIDGPLPEDNEPSGYACTDCVLEAMAFLEE-SHPGIFENSCLETMEVVQQT : : ::::::::::::::::::::::::::::::	117 117 239 239 239 239
p P16513 RDRP_I80A8 p Q08II5 RDRP_I80A6 p Q0A3Q1 RDRP_I78AC p Q0A451 RDRP_I66A1 p P19703 RDRP_INCJJ p Q9IMP4 RDRP_INCJH r A0A193PPL8 A0A193PPL8_90RT0 r A0A193PPM8 A0A193PPM8_90RT0	TGAPOLNPIDGPLPEDNEPSGYACTDCVLEAMAFLEE-SHPGIFENSCLETMEVVQQT TGAPOLNPIDGPLPEDNEPSGYACTDCVLEAMAFLEE-SHPGIFENSCLETMEVVQQT : : ::: ::: ::: ::: ::: ::: ::: :::	117 117 239 239 239 239 239 239
p P16513 RDRP_I80A8 p Q08II5 RDRP_I80A6 p Q0A3Q1 RDRP_I78AC p Q0A451 RDRP_I66A1 p P19703 RDRP_INCJJ p Q9IMP4 RDRP_INCJH r A0A193PPL8 A0A193PPL8_90RT0 r A0A193PPM8 A0A193PPM8_90RT0 r A0A193PPP6 A0A193PPP6_90RT0	TGAPOLNPIDGPLPEDNEPSGYACTDCVLEAMAFLEE-SHPGIFENSCLETMEVVQQT TGAPOLNPIDGPLPEDNEPSGYACTDCVLEAMAFLEE-SHPGIFENSCLETMEVVQQT : : ::::::::::::::::::::::::::::::	117 117 239 239 239 239 239 239
p P16513 RDRP_I80A8 p Q08II5 RDRP_I80A6 p Q0A3Q1 RDRP_I78AC p Q0A451 RDRP_I66A1 p P19703 RDRP_INCJJ p Q9IMP4 RDRP_INCJH r A0A193PPL8 A0A193PPL8_90RT0 r A0A193PPL8 A0A193PPM8_90RT0 r A0A193PPP6 A0A193PPP6_90RT0 p Q6I7C3 RDRP_INCAA	TGAPOLNFIDGPLPEDNEPSGYACTDCVLFAMAFLEE-SHPGIFENSCLETMEVVQQT TGAPOLNFIDGPLPEDNEPSGYACTDCVLFAMAFLEE-SHPGIFENSCLETMEVVQQT : : ::::::::::::::::::::::::::::::	117 117 239 239 239 239 239 239 239 239 C
<pre>p P16513 RDRP_I80A8 p Q08II5 RDRP_I80A6 p Q0A3Q1 RDRP_I78AC p Q0A3Q1 RDRP_I78AC p Q0A451 RDRP_I66A1 p P19703 RDRP_ICJJ p Q0MP4 RDRP_INCJH r A0A193PPL8 A0A193PPL8_90RT0 r A0A193PPP6 A0A193PPM8_90RT0 r A0A193PPP6 A0A193PPP6_90RT0 p Q617C3 RDRP_INCAA r A0A193PQ43 A0A193PQ43_INCKS</pre>	TGAPOLNFIDGPLPEDNEPSGYACTDCVLFAMAFLEE-SHPGIFENSCLETMEVVQQT TGAPOLNFIDGPLPEDNEPSGYACTDCVLFAMAFLEE-SHPGIFENSCLETMEVVQQT : : ::::::::::::::::::::::::::::::	117 117 239 239 239 239 239 239 239 239 239 239
<pre>p [p16513]RDRP_I80A8 p [Q08II5]RDRP_I80A6 p [Q0A3Q1]RDRP_I78AC p [Q0A451]RDRP_I78AC p [Q0A451]RDRP_I66A1 </pre>	TGAPOLNPIDGPLPEDNEPSGYACTDCVLEAMAFLEE-SHPGIFENSCLETMEVVQQT TGAPOLNPIDGPLPEDNEPSGYACTDCVLEAMAFLEE-SHPGIFENSCLETMEVVQQT : : ::::::::::::::::::::::::::::::	117 117 239 239 239 239 239 239 239 239 239 239
<pre>p [p16513]RDRP_I80A8 p [Q08II5]RDRP_I80A6 p [Q0A3Q1]RDRP_I78AC p [Q0A451]RDRP_I78AC p [Q0A451]RDRP_I66A1 </pre>	TGAPOLNPIDGPLPEDNEPSGYACTDCVLEAMAFLEE-SHPGIFENSCLETMEVVQQT TGAPOLNPIDGPLPEDNEPSGYACTDCVLEAMAFLEE-SHPGIFENSCLETMEVVQQT : : ::::::::::::::::::::::::::::::	117 117 239 239 239 239 239 239 239 239 239 239
<pre>p [p16513]RDRP_I80A8 p [Q08II5]RDRP_I80A6 p [Q0A3Q1]RDRP_I78AC p [Q0A451]RDRP_I78AC p [Q0A451]RDRP_I66A1 </pre>	TGAPOLNPIDGPLPEDNEPSGYACTDCVLEAMAFLEE-SHPGIFENSCLETMEVVQQT TGAPOLNPIDGPLPEDNEPSGYACTDCVLEAMAFLEE-SHPGIFENSCLETMEVVQQT : : ::::::::::::::::::::::::::::::	117 117 239 239 239 239 239 239 239 239 239 239
<pre>p [p16513]RDRP_I80A8 p [Q08II5]RDRP_I80A6 p [Q0A3Q1]RDRP_I78AC p [Q0A451]RDRP_I78AC p [Q0A451]RDRP_I66A1 </pre>	TGAPOLNPIDGPLPEDNEPSGYACTDCVLEAMAFLEE-SHPGIFENSCLETMEVVQQT TGAPOLNPIDGPLPEDNEPSGYACTDCVLEAMAFLEE-SHPGIFENSCLETMEVVQQT : : ::::::::::::::::::::::::::::::	117 117 239 239 239 239 239 239 239 239 239 239
D P16513 RDRP_180A8 D Q08115 RDRP_180A6 D Q08301 RDRP_178AC D Q0A301 RDRP_178AC D Q0A451 RDRP_166A1 D Q0A451 RDRP_166A1 D Q0A451 RDRP_10CJH C Q01MP4 RDRP_INCJH C Q01MP4 RDRP_INCJH C Q01MP4 RDRP_1NCJH C Q01MP4	TGAPOLNFIDGPLPEDNEPSGYAC TDCVLEAMAFLEE-SHPGIFENSCLETMEVVQQT TGAPOLNFIDGPLPEDNEPSGYAC TDCVLEAMAFLEE-SHPGIFENSCLETMEVVQQT : : ::::::::::::::::::::::::::::::	117 117 239 239 239 239 239 239 239 239 239 239
D P16513 RDRP_I80A8 D Q08II5 RDRP_I80A6 D Q0A3Q1 RDRP_I78AC D Q0A451 RDRP_I78AC D Q0A451 RDRP_I66A1 D Q0A451 RDRP_I66A1 D Q0IMP4 RDRP_INCJH : A0A193PP18 A0A193PP18_90RT0 : A0A193PP48 A0A193PP48_90RT0 : A0A193PP48 A0A193PP46_90RT0 : A0A193PP48 A0A193PP43_INCKS : A0A193PP48 A0A193PP43_INCKS : A0A193PP48 A0A193PP43_INCKS : A0A193PP48 A0A193PP43_INCKS : A0A193PP48 A0A193PP43_INCK5 : A0A193PP48 A0A193PP43_INCK5 : A0A193PP48 A0A193PP43_INCK5 : A0A193PP48 A0A193PP43_INCK5 : A0A193PP48 A0A193PP43_INCK5 : A0A193PP48 A0A193PP43_INCK5 : A0A193PP48 A0A193PP43_INC56 : A0A193PP48 A0A193PP43_INC56 : A0A193PP48 A0A193PP43_INC56 : A0A193PP48 A0A193PP43_INC56 : A0A193PP58 A0A193P43_INC56 : A0A193P43 RD84_IN566 : A0A193P43 R084_IN566 : A0A193P43 R084 : A0A193P43 R084_IN566 : A0A193P43 R084 : A0A193P43 R084	TGAPOLNPIDGPLPEDNEPSGYAC TDCVLEAMAFLEE-SHPGIFENSCLETMEVVQQT TGAPOLNPIDGPLPEDNEPSGYAC TDCVLEAMAFLEE-SHPGIFENSCLETMEVVQQT : : ::::::::::::::::::::::::::::::	117 117 239 239 239 239 239 239 239 239 239 239
<pre>> P16513 RDRP_I80A8 > Q081I5 RDRP_I80A6 > Q0A301 RDRP_I78AC > Q0A451 RDRP_I78AC > Q0A451 RDRP_I66A1 > Q09IM94 RDRP_INCJH : A0A193PPL8 A0A193PPL8 _90RT0 : A0A193PPM8 A0A193PPM8_90RT0 : A0A193PPM8 A0A193PPM8_90RT0 : A0A193PP48 A0A193PPM8_90RT0 : A0A193PP48 A0A193PP43_INCKS : A0A193PP48 A0A193PP43_INCKS : A0A193PP88 A0A193PP43_INCKS : A0A193PP78 A0A193PP43_INCKS : A0A193PP70 A0A193PP70_90RT0 > P07832 RDRP_INELE : A0A0D6A5W0 A0A0D6A5W0_9INFB : A0A059TB43 A0A059TB43_9INFB</pre>	TGAPOLNFIDGPLPEDNEPSGYACTDCVLEAMAFLEE-SHPGIFENSCLETMEVVQQT TGAPOLNFIDGPLPEDNEPSGYACTDCVLEAMAFLEE-SHPGIFENSCLETMEVVQQT : : : :: :: :: :: :: :: :: :: :: ::	117 117 239 239 239 239 239 239 239 239 239 239
D P16513 RDRP_180A8 D Q08115 RDRP_180A6 D Q0A3Q1 RDRP_178AC D Q0A3Q1 RDRP_178AC D Q0A451 RDRP_166A1 D Q0A451 RDRP_166A1 D Q0A451 RDRP_10CJH C Q0A455 RDP_10CJH C Q0A455 R	TGAPOLNFIDGPLPEDNEPSGYAC TDCVLFAMAFLEE-SHPGIFENSCLETMEVVQQT TGAPOLNFIDGPLPEDNEPSGYAC TDCVLFAMAFLEE-SHPGIFENSCLETMEVVQQT : : : ::::::::::::::::::::::::::::	117 117 239 239 239 239 239 239 239 239 239 239
<pre>p1f16513 RDRP_180A8 p208115 RDRP_180A6 p208115 RDRP_180A6 p200301 RDRP_178Ac p200451 RDRP_178Ac p200451 RDRP_166A1 p200451 RDRP_166A1 p200451 RDRP_166A1 p200451 RDRP_1054 p200451 RDRP_1054 p2005555 p2005555 RDRP_10555 p2005555 RDRP_105555 p2005555 RDRP_105555 p2005555 RDRP_105555 p2005555 RDRP_105555 p2005555 RDRP_1055555 p2005555 RDRP_1055555 p20055555 RDRP_1055555 p20055555 RDRP_1055555 p20055555 RDRP_1055555 p20055555 RDRP_1055555 p20055555 RDRP_1055555 p20055555 RDRP_1055555 p200555555 p200555555 p200555555 p200555555 p200555555 p200555555 p200555555 p20055555 p200555555 p20055555 p20055555 p20055555 p20055555 p20055555 p20055555 p20055555 p20055555 p20055555 p20055555 p20055555 p20055555 p200555555 p200555555 p200555555 p20055555555 p20055555555 p20055555555 p2005555555555</pre>	TGAPOLNFIDGPLPEDNEPSGYACTDCVLEAMAFLEE-SHPGIFENSCLETMEVVQQT TGAPOLNFIDGPLPEDNEPSGYACTDCVLEAMAFLEE-SHPGIFENSCLETMEVVQQT 	117 117 239 239 239 239 239 239 239 239 239 239
<pre>> P16513 RDRP_180A8 > Q08115 RDRP_180A6 > Q00A301 RDRP_178Ac > Q0A301 RDRP_178Ac > Q0A451 RDRP_166A1 > Q0A451 RDRP_166A1 > Q00A451 RDRP_166A1 > Q00A451 RDRP_10CJH : A0A193PPL8 A0A193PPL8_90RT0 : A0A193PPB8 A0A193PPM8_90RT0 : A0A193PPB6 A0A193PPP6_90RT0 > Q617C3 RDRP_INCAA : A0A193PQ43 A0A193PQ43_INCKS : A0A193PQ43 A0A193PQ43_INCKS : A0A193PP88 A0A193PP8_INCM3 : A0A193PP28 A0A193PP8_INCM3 : A0A193PP70 A0A193PP70_90RT0 > P07832 RDRP_INELE : A0A06A5W0 A0A006A5W0_9INFB : A0A075CJ9 A0A075CJ9_9INFB : A0A075CJ9 A0A075CJ9_9INFB : A0A075CJ9 A0A074CNB_9INFB : A0A075CJ9 A0A074CNB_9INFB</pre>	TGAPOLNFIDGPLPEDNEPSGYACTDCVLEAMAFLEE-SHPGIFENSCLETMEVVQQT TGAPOLNFIDGPLPEDNEPSGYACTDCVLEAMAFLEE-SHPGIFENSCLETMEVVQQT 	117 117 239 239 239 239 239 239 239 239 239 239
<pre>p[P16513]RDRP_I80A8 p[Q08I15]RDRP_I80A6 p[Q0A301]RDRP_I78AC p[Q0A451]RDRP_I78AC p[Q0A451]RDRP_I78AC p[Q0A451]RDRP_I66A1 p[Q9IMP4]RDRP_INCJH c]A0A193PP18]A0A193PP18_90RT0 c]A0A193PP48]A0A193PP18_90RT0 c]A0A193PP48]A0A193PP48_90RT0 c]A0A193PP48]A0A193PP48_90RT0 c]A0A193PP48]A0A193PP48_90RT0 c]A0A193PP48]A0A193PP43_INCKS c]A0A193PP78]A0A193PP43_INCKS c]A0A193PP78]A0A193PP78_INCM3 c]A0A193PP78]A0A193PP78_INCM3 c]A0A193PP78]A0A193PP70_90RT0 p]P07832[RDRP_INBLE c]A0A059TB43]A0A059TB43_9INFB c]A0A075CCJ9]A0A075CCJ9_9INFB c]A0A024CNB8]A0A059TB43_9INFB c]A0A07GD33]A0A0N7GD33_9INFB c]A0A07GD33]A0A0N7GD33_9INFB</pre>	TGAPOLNFIDGPLPEDNEPSGYAC TDCVLEAMAFLEE-SHPGIFENSCLETMEVVQQT TGAPOLNFIDGPLPEDNEPSGYAC TDCVLEAMAFLEE-SHPGIFENSCLETMEVVQQT 	117 117 239 239 239 239 239 239 239 239 239 239
<pre>> P16513 RDRP_I80A8 > Q08115 RDRP_I80A6 > Q0A3Q1 RDRP_I78AC > Q0A3Q1 RDRP_I78AC > Q0A451 RDRP_I66A1 > Q0A451 RDRP_I66A1 > Q0A451 RDRP_I66A1 > Q0A451 RDRP_I66A1 > Q0A451 RDRP_ICCH > A0A193PP08 A0A193PP18_90RT0 > A0A193PP08 A0A193PP18_90RT0 > A0A193PP08 A0A193PP18_90RT0 > Q617C3 RDRP_INCAA > A0A193PQ43 A0A193PQ43_INCKS > A0A193PP03 A0A193PP28_INCM3 > A0A193PP03 A0A193PP28_INCM3 > A0A193PP03 A0A193PP28_INCM3 > A0A193PP03 A0A193PP20_90RT0 > P07832 RDRP_INBLE > A0A06A5W0 A0A006A5W0_9INFB > A0A075CCJ9 A0A075CCJ9_9INFB > A0A075CCJ9 A0A075CCJ9_9INFB > A0A07CD3 ADA07CD33_9INFB > A0A07CJ3 ADA07_INBEK</pre>	TGAPOLNFIDGPLPEDNEPSGYAC TDCVLFAMAFLEE-SHPGIFENSCLETMEVVQQT TGAPOLNFIDGPLPEDNEPSGYAC TDCVLFAMAFLEE-SHPGIFENSCLETMEVVQQT : : : :: :: :: :: :: :: :: :: :: ::	117 117 239 239 239 239 239 239 239 239 239 239
D P16513 RDRP_180A8 D Q0A3Q1 RDRP_180A6 D Q0A3Q1 RDRP_178AC D Q0A451 RDRP_178AC D Q0A451 RDRP_166A1 D Q0A451 RDRP_166A1 D Q0A451 RDRP_10CJH D Q91MF4 RDRP_INCJH D Q91MF4	TGAPOLNFIDGPLPEDNEPSGYAC TDCVLEAMAFLEE-SHPGIFENSCLETMEVVQQT TGAPOLNFIDGPLPEDNEPSGYAC TDCVLEAMAFLEE-SHPGIFENSCLETMEVVQQT 	117 117 239 239 239 239 239 239 239 239 239 239
D P16513 RDRP_180A8 D Q08115 RDRP_180A6 D Q0A3Q1 RDRP_178AC D Q0A451 RDRP_178AC D Q0A451 RDRP_178AC D Q0A451 RDRP_166A1 D Q19703 RDRP_166A1 D Q19703 RDRP_10CJH C A0A193PP18 A0A193PP18_90RT0 C A0A193PP18 A0A193PP18_90RT0 C A0A193PP18 A0A193PP18_90RT0 C A0A193PP18 A0A193PP18_90RT0 C A0A193PP18 A0A193PP18_90RT0 C A0A193PP18 A0A193PP18_90RT0 C A0A193PP28 A0A193PP18_10CM3 C A0A193PP28 A0A193PP23_10CKS C A0A193PP18 A0A193PP18_10CM3 C A0A193PP18 A0A193PP19_90RT0 D P07832 RDRP_1NBLE C A0A059TB43 A0A05TB43_91NFB C A0A075CCJ9 A0A075CCJ9_91NFB C A0A075CCJ9 A0A075CCJ9_91NFB C A0A07GD33 A0A07TGB3_91NFB D 036430 RDRP_1NBP9 C A3DR07 A3DR07_1NBBK D P13872 RDRP_1NBAD	TGAPOLNFIDGPLPEDNEPSGYAC TDCVLEAMAFLEE-SHPGIFENSCLETMEVVQQT TGAPOLNFIDGPLPEDNEPSGYAC TDCVLEAMAFLEE-SHPGIFENSCLETMEVVQQT 	117 117 239 239 239 239 239 239 239 239 239 239
<pre>pp16513 RDRP_I80A8 p)Q08II5 RDRP_I80A6 p)Q0A3Q1 RDRP_I78AC p)Q0A3Q1 RDRP_I78AC p)Q0A451 RDRP_I66A1 p)Q0A451 RDRP_I66A1 p)Q0A451 RDRP_ICJH c)A0A193PP18 A0A193PP18_90RT0 c)A0A193PP18 A0A193PP18_90RT0 c)A0A193PP48 A0A193PP18_90RT0 c)A0A193PP48 A0A193PP46_90RT0 c)Q617C3 RDRP_INCAA c)A0A193PP43 A0A193PP43_INCKS c)A0A193PP43 A0A193PP43_INCKS c)A0A193PP43 A0A193PP43_INCKS c)A0A193PP43 A0A193PP43_INCKS c)A0A193PP43 A0A193PP43_INCKS c)A0A193PP43 A0A193PP43_INCKS c)A0A193PP43 A0A193PP43_INCY6 c)A0A059TB43 A0A059TB43_9INFB c)A0A059TB43 A0A059TB43_9INFB c)A0A075CCJ9 A0A075CCJ9_9INFB c)A0A07ACJ3 A0A075CCJ9_9INFB c)A0A07ACJ3 A0A07TCJ3_9INFB c)A0A07 A3DR07_INBBK c)P13871 RDRP_INBAC c)P13872 RDRP_INBAD c)P03431 RDRP_I3A1</pre>	TGAPOLNFIDGPLPEDNEPSGYAC TDCVLEAMAFLEE-SHPGIFENSCLETMEVVQQT TGAPOLNFIDGPLPEDNEPSGYAC TDCVLEAMAFLEE-SHPGIFENSCLETMEVVQQT 	117 117 239 239 239 239 239 239 239 239 239 239
<pre>pip16513 RDRP_I80A8 plQ08II5 RDRP_I80A6 plQ0A3Q1 RDRP_I78AC plQ0A451 RDRP_I78AC plQ0A451 RDRP_I66A1 plQ0A451 RDRP_I66A1 plQ0A451 RDRP_ICJH respectively and the second sec</pre>	TGAPOLNFIDGPLPEDNEPSGYAC TDCVLEAMAFLEE-SHPGIFENSCLETMEVVQQT TGAPOLNFIDGPLPEDNEPSGYAC TDCVLEAMAFLEE-SHPGIFENSCLETMEVVQQT 	117 117 239 239 239 239 239 239 239 239 239 239
D P16513 RDRP_I80A8 D Q08II5 RDRP_I80A6 D Q08II5 RDRP_I80A6 D Q0A301 RDRP_I78AC D Q0A451 RDRP_I78AC D Q0A451 RDRP_I66A1 D Q0A451 RDRP_I66A1 D Q0A451 RDRP_ICJH C Q0A451 RDRP_INCJH C Q0A451 RDRP_INCJH C Q0A451 RDRP_INCJH C Q0A451 RDRP_INCAA C Q0A193PP48 A0A193PP48_90RTO C Q0A193PP48 A0A193PP48_90RTO C Q0A193PP48 A0A193PP48_90RTO D Q0F7C3 RDRP_INCAA C A0A193PP48 A0A193PP43_INCKS C A0A193PP48 A0A193PP43_INCKS C A0A193PP48 A0A193PP43_INCKS C A0A193PP58 A0A193PP43_INCKS C A0A193PP58 A0A193PP43_INCKS C A0A193PP58 A0A193PP43_INCKS C A0A193PP58 A0A193PP43_INCKS C A0A0193PP48 A0A193PP43_INCKS C A0A059TB43 A0A0193PP43_INCKS C A0A059TB43 A0A059TB43_9INFB C A0A075CJ9 A0A075CJ9_9INFB C A0A075CJ9 A0A075CJ9_9INFB C A0A075CJ3 A0A077GD33_9INFB C A0A077GD33 A0A077GD33_7GD7_1NBBK D A077GD37 A077GD33 A0A077GD33_7GD7_1NBBK D A077GD37 A077GD37 A077GD37 C A077GD37 A077GD37 C A0	TGAPOLNPIDGPLPEDNEPSGYAC TDCVLEAMAFLEE-SHPGIFENSCLETMEVVQQT TGAPOLNPIDGPLPEDNEPSGYAC TDCVLEAMAFLEE-SHPGIFENSCLETMEVVQQT 	117 117 239 239 239 239 239 239 239 239 239 239
D P16513 RDRP_180A8 D Q08115 RDRP_180A6 D Q08115 RDRP_180A6 D Q0A301 RDRP_178AC D Q0A451 RDRP_178AC D Q0A451 RDRP_166A1 D Q0A451 RDRP_166A1 D Q0A451 RDRP_10CJH C A0A193PP18 A0A193PP18_90RT0 C A0A193PP18 A0A193PP18_90RT0 C A0A193PP18 A0A193PP18_90RT0 C A0A193PP18 A0A193PP18_90RT0 D Q617C3 RDRP_INCAA C A0A193PP243 A0A193PP23_INCKS C A0A193PP243 A0A193PP23_INCKS C A0A193PP28 A0A193PP23_INCKS C A0A193PP28 A0A193PP23_INCKS C A0A193PP28 A0A193PP23_INCKS C A0A193PP28 A0A193PP29_SINCM3 C A0A059TB43 A0A193PP3_INCKS C A0A059TB43 A0A193PP3_INCF8 C A0A059TB43 A0A0575CCJ9_9INF8 C A0A075CCJ9 A0A075CCJ9_9INF8 C A0A075CJ9 A0A075CCJ9_9INF8 C A0A075CJ9 A0A075CCJ9_9INF8 C A0A075CJ9 A0A075CCJ9_9INF8 C A0A075CJ9 RDRP_INBL8 D A0A075CJ9 RDRP_INBEK D P13871 RDRP_INBEK D P13872 RDRP_ISAC D P03431 RDRP_I3A1 D Q20VV RDRP_I57A5 D P16511 RDRP_I57A5	TGAPOLNPIDGPLPEDNEPSGYAC TDCVLEAMAFLEE-SHPGIFENSCLETMEVVQQT TGAPOLNPIDGPLPEDNEPSGYAC TDCVLEAMAFLEE-SHPGIFENSCLETMEVVQQT 	117 117 117 239 239 239 239 239 239 239 239
<pre>pp16513 RDRP_I80A8 p)Q08II5 RDRP_I80A6 p)Q08II5 RDRP_I80A6 p)Q0A3Q1 RDRP_I78AC p)Q0A4S1 RDRP_I78AC p)Q0A4S1 RDRP_I66A1 p)Q0A4S1 RDRP_I66A1 p)Q0A4S1 RDRP_ICCH c)A0A193PP18 A0A193PP18_9ORTO c)A0A193PP18 A0A193PP18_9ORTO c)A0A193PP26 A0A193PP16_9ORTO c)A0A193PP26 A0A193PP26_9ORTO c)Q6I7C3 RDRP_INCAA c)A0A193PP23 A0A193PP23_INCKS c)A0A193PP23 A0A193PP23_INCKS c)A0A193PP23 A0A193PP23_INCKS c)A0A193PP23 A0A193PP23_INCY6 c)A0A059TB43 A0A059TB43_9INFB c)A0A059TB43 A0A059TB43_9INFB c)A0A024CND8 A0A024CND8_9INFB c)A0A075CCJ9 A0A075CCJ9_9INFB c)A0A024CND8 A0A024CND8_9INFB c)A0A024CND8 A0A024CND8_9INFB c)A0A024CND8 A0A024CND8_9INFB c)A0A024CND8 A0A024CND8_9INFB c)A0A024CND8 A0A024CND8_9INFB c)A0A07 A3DR07_INBBK c)P13871 RDRP_INBAC c)P13872 RDRP_INBAD c)P03431 RDRP_I34A1 c)Q9Q0V0 RDRP_I57A5 c)Q0A2F7 RDRP_I83A4</pre>	TGAPOLNPIDGPLPEDNEPSGYAC TDCVLEAMAFLEE-SHPGIFENSCLETMEVVQQT TGAPOLNPIDGPLPEDNEPSGYAC TDCVLEAMAFLEE-SHPGIFENSCLETMEVVQQT : : : : : : : : : : : : : : : : :	117 117 117 239 239 239 239 239 239 239 239
<pre>p p16513 RDRP_I80A8 p Q08II5 RDRP_I80A6 p Q08II5 RDRP_I80A6 p Q0A3Q1 RDRP_I78AC p Q0A451 RDRP_I78AC p Q0A451 RDRP_I66A1</pre>	TGAPQLNPIDGPLPEDNEPSG YAGTDCVLEAMAFLEE-SHPGIFENSCLETMEVVQQT TGAPQLNPIDGPLPEDNEPSG YAGTDCVLEAMAFLEE-SHPGIFENSCLETMEVVQQT : : : :: :: :: :: :: :: :: :: :: :	117 117 117 239 239 239 239 239 239 239 239
<pre>p[p16513]RDRP_I80A8 p[Q08II5]RDRP_I80A6 p[Q0A3Q1]RDRP_I80A6 p[Q0A3Q1]RDRP_I78AC p]Q0A451]RDRP_I78AC p]Q0A451]RDRP_I66A1</pre>	TGAPQLNPIDGPLPEDNEPSG YAGTDCVLEAMAFLEE-SHPGIFENSCLETMEVVQQT TGAPQLNPIDGPLPEDNEPSG YAGTDCVLEAMAFLEE-SHPGIFENSCLETMEVVQQT : : : :: :: :: :: :: :: :: :: :: :	117 117 239 239 239 239 239 239 239 239 239 239
<pre>p p16513 RDRP_I80A8 p Q08II5 RDRP_I80A6 p Q0A3Q1 RDRP_I80A6 p Q0A3Q1 RDRP_I78AC p Q0A451 RDRP_I78AC p Q0A451 RDRP_I66A1</pre>	TGAPQLNPIDGPLPEDNEPSG YAGTDCVLEAMAFLEE-SHPGIFENSCLETMEVVQQT TGAPQLNPIDGPLPEDNEPSG YAGTDCVLEAMAFLEE-SHPGIFENSCLETMEVVQQT : : : :: :: :: :: :: :: :: :: :: :	117 117 239 239 239 239 239 239 239 239 239 239
<pre>p p16513 RDRP_I80A8 p Q08II5 RDRP_I80A6 p Q0A3Q1 RDRP_I78AC p Q0A451 RDRP_I78AC p Q0A451 RDRP_I66A1</pre>	TGAPQLNPIDGPLPEDNEPSG YAGTDCVLEAMAFLEE-SHPGIFENSCLETMEVVQQT TGAPQLNPIDGPLPEDNEPSG YAGTDCVLEAMAFLEE-SHPGIFENSCLETMEVVQQT : : : :: :: :: :: :: :: :: :: :: :	117 117 117 239 239 239 239 239 239 239 239 239 239
p P16513 RDRP_I80A8 p Q08II5 RDRP_I80A6 p Q0A3Q1 RDRP_I78AC p Q0A451 RDRP_I66A1 p P19703 RDRP_ICJJ p Q9IMP4 RDRP_INCJH r A0A193PPL8 A0A193PPL8_90RTO r A0A193PPL8 A0A193PPM8_90RTO r A0A193PPP6 A0A193PPP6_90RTO p Q617C3 RDRP_INCAA	TGAPQLNPIDGPLPEDNEPSG YAGTDCVLEAMAFLEE-SHPGIFENSCLETMEVVQQT TGAPQLNPIDGPLPEDNEPSG YAGTDCVLEAMAFLEE-SHPGIFENSCLETMEVVQQT : : ::::::::::::::::::::::::::::	117 117 117 239 239 239 239 239 239 239 239 239 239

sp P19703 RDRP INCJJ	RI	AIATPGMIVRPFSKIVET	AOK		BKL	KESGLF	<mark>vg</mark> gnekkakl	KTTVTSLNARMNSDO	299	٦
sp Q9IMP4 RDRP INCJH	RF	AIATPGMIVRPFSKIVET	AOK		KL	KESGLF	vggnekkakl	KTTVTSLNARMNSD	299	
tr A0A193PPL8 A0A193PPL8 9ORTO	RE	AIATPGMIVRPFSKIVET	AOK		KL	KESGLF	<mark>vg</mark> gnekkakl	KTTVTSLNARMNSD	299	
tr A0A193PPM8 A0A193PPM8 9ORTO		AIATPGMIVRPFSKIVET								
tr A0A193PPP6 A0A193PPP6 9ORTO		AIATPGMIVRPFSKIVET								
sp Q617C3 RDRP INCAA	RF	AIATPGMIVRPFSKIVET	AOR		RKL	KESGLF	VGGNEKKAKL	KTTVTSLNARMNSDO	299	Rep
tr A0A193PQ43 A0A193PQ43 INCKS	PE	ATATOCMINPOFSKINET		TC	KT.	KESCLE	VCCNEKKAKI.	KTTVTST NA PMNSD	200	1.
tr A0A193PPP8 A0A193PPP8 INCM3	RF	AIATPGMIVRPFSKIVET	A <mark>Q</mark> K		K L	KESGLF	<mark>vg</mark> gnekkakl	KTTVTSLNARMNSD	2 299	
tr A0A193PQ33 A0A193PQ33 INCY6	RF	AIATPGMIVRPFSKIVET	A <mark>Q</mark> K	:I <mark>C</mark>	BKL	KESGLF	<mark>vg</mark> gnekkakl	KTTVTSLNARMNSD	2 299	
tr A0A193PPP0 A0A193PPP0 9ORTO		AIATPGMIVRPFSKIVET								J
—										
sp P07832 RDRP INBLE	RF	AIATAGIQIRGFVLVVENI	A <mark>KN</mark>		BNL	EQSGLF	<mark>VG</mark> GNEKKAKL	SNAVAKMLSNCPPG	G 297	1
tr A0A0D6A5W0 A0A0D6A5W0_9INFB	RF	AIATAGIQIRGFVLVVENI	A <mark>KI</mark>	I I C	BNL	EQSGLF	<mark>VG</mark> GNEKKAKL	SNAVAKMLSNCPPG	G 297	
tr A0A059TB43 A0A059TB43_9INFB		AIATAGIQIRGFVLVVENI								
tr A0A075CCJ9 A0A075CCJ9_9INFB	RF	AIATAGIQIRGFVLVVENI	AKN	I I C	BNL	EQSGLF	<mark>VG</mark> GNEKKAKL	SNAVAKMLSNCPPG	G 297	
tr A0A024CND8 A0A024CND8_9INFB	RF	AIATAGIQIRGFVLVVENI	A <mark>KI</mark>	I I C	BNL	EQSGLF	<mark>VG</mark> GNEKKAKL	SNAVAKMLSNCPPG	G 297	В
tr A0A0N7GD33 A0A0N7GD33 9INFB	RF	AIATAGIQIRGFVLVVENI	AKN		ENL	EQSGLF	<mark>VG</mark> GNEKKAKL	SNAVAKMLSNCPPG	G 297	Re
sp 036430 RDRP INBP9	RF	AIATAGIQIRGFVLVVENI	A <mark>KN</mark>		BNL	EQSGLF	<mark>vg</mark> gnekkakl	SNAVAKMLSNCPPG	G 297	
tr A3DR07 A3DR07 INBBK	RF	AIATAGIQIRGFVLVVENI	AKN		INL	EQSGLF	<mark>VG</mark> GNEKKAKL	SNAVAKMLSNCPPG	G 297	
sp P13871 RDRP INBAC	RF	AIATAGIQIRGFVLVVENI	A <mark>KN</mark>	I I C	ENL	EQSGLF	<mark>VG</mark> GNEKKAKL	SNAVAKMLSNCPPG	G 297	
sp P13872 RDRP_INBAD		AIATAGIQIRGFVLVVENI								J
									-	
sp P03431 RDRP_I34A1		AIATPGMQIRGFVYFVETI]
sp Q9Q0V0 RDRP_I96A0	RF	AIATPGMQIRGFVYFVETI	A <mark>RS</mark>	IC	<u> K</u> L	EQSGLF	<mark>VG</mark> GNEKKAKL	ANVVRKMMTNSQ <mark>DTI</mark>	E 297	
sp Q30NP3 RDRP_I75A0	RF	AIATPGMQIRGFVYFVETI AIATPGMQIRGFVYFVETI	A <mark>R\$</mark>	IC	<u> K</u> L	EQSGLF	<mark>VG</mark> GNEKKAKL	ANVVRKMMTNSQ <mark>DTI</mark>	z 297	
sp P16511 RDRP_I57A5	RF	AIATPGMQIRGFVYFVETI	A <mark>RS</mark>	IC	<u> K</u> L	EQSGLF	<mark>VG</mark> GNEKKAKL	ANVVRKMMTNSQ <mark>DTI</mark>	E 297	
sp Q0A2F7 RDRP_I83A4	RF	AIATPGMQIRGFVYFVETI	A <mark>R\$</mark>	IC	BKL	EQSGLF	<mark>VG</mark> GNEKKAKL	ANVVRKMMTNSQ <mark>DTH</mark>	297	Α
sp P16503 RDRP I77AF	RF	AIATPGMQIRGFVYFVETI	A <mark>RS</mark>	IC	BKL	EQSGLF	<mark>VG</mark> GNEKKAKL	ANVVRKMMTNSQ <mark>DTI</mark>	E 297	Rep
sp P16513 RDRP_I80A8		AIATPGMQIRGFVYFVETI								
sp Q08II5 RDRP_I80A6	RF	AIATPGMQIRGFVYFVETI	A <mark>R\$</mark>		8KL	EQSGLF	<mark>VG</mark> GNEKKAKL	ANVVRKMMTNSQDTI	297	
sp Q0A3Q1 RDRP_I78AC	RF	AIATPGMQIRGFVYFVETI	A <mark>R</mark> S	IC	EKL	EQSGLF	<mark>VG</mark> GNEKKAKL	ANVVRKMMTNSQDT	297	
sp Q0A451 RDRP 166A1 FPloop	RE	AIATPGMQIRGFVYFVETI	A <mark>R</mark> S		KL	EQSGLE	<mark>vg</mark> gnekkakl	ANVVRKMMTNSODTI	297	J
	**	**** *: :* * .**.:	* : .	**	: *	****	<mark>**</mark> ******	* .: :. 1		
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sp P19703 RDRP_INCJJ	FAVNIT		KWNECQQPEAYLALLAYITKDSSDLMKDLCSVAPVLFCNKFVKLGQGIRL	359
sp Q9IMP4 RDRP_INCJH	FAVNIT	GDNS	KWNECQQPEAYLALLAYITKDSSDLMKDLCSVAPVLFCNKFVKLGQGIRL	359
tr A0A193PPL8 A0A193PPL8_9ORTO	FAVNIT	GDNS	KWNECQQPEAYLALLAYITKDSSDLMKDLCSVAPVLFCNKFVKLGQGIRL	359
tr A0A193PPM8 A0A193PPM8_9ORTO	FAVNIT	GDNS	KWNECQQPEAYLALLAYITKDSSDLMKDLCSVAPVLFCNKFVKLGQGIRL	359
tr A0A193PPP6 A0A193PPP6_9ORTO	FAVNIT	GDNS	K <mark>WNECQQPEAYLALLAYITKDSSDLMKDLCSVAPVLFCNKFVKLGQGIRL</mark>	359
sp Q617C3 RDRP_INCAA	FAVNIT	GDNS	KWNECQQPEAYLALLAYITKDSSDLMKDLCSVAPVLFCNKFVKLGQGIRL	359
tr A0A193PQ43 A0A193PQ43_INCKS	FAVNIT	GDNS	K <mark>WNECQQPEAYLALLAYITKDSSDLMKDLCSVAPVLFCNKFVKLGQGIRL</mark>	359
tr A0A193PPP8 A0A193PPP8_INCM3	FAVNIT	GDNS	K <mark>WNECQQPEAYLALLAYITKDSSDLMKDLCSVAPVLFCNKFVKLGQGIRL</mark>	359
tr A0A193PQ33 A0A193PQ33_INCY6	FAVNIT	GDNS	K <mark>WNECQQPEAYLALLAYITKDSSDLMKDLCSVAPVLFCNKFVKLGQGIRL</mark>	359
tr A0A193PPP0 A0A193PPP0_9ORTO	FAVNIT	GDNS	K <mark>WNECQQPEAYLALLAYITKDSSDLMKDLCSVAPVLFCNKFVKLGQGIRL</mark>	359
sp P07832 RDRP_INBLE	ISMTVI	GDNT	K <mark>WNECLNPRIFLAMTERITRDSPIWFRDFCSIAPVLFSNKIARLGKGFMI</mark>	357
tr A0A0D6A5W0 A0A0D6A5W0_9INFB	ISMTVI	GDNT	K <mark>WNECLNPRIFLAMTERITRDSPIWFRDFCSIAPVLFSNKIARLGKGFMI</mark>	357
tr A0A059TB43 A0A059TB43_9INFB	ISMTVI	GDNT	K <mark>WNECLNPRIFLAMTERITRDSPIWFRDFCSIAPVLFSNKIARLGKGFMV</mark>	357
tr A0A075CCJ9 A0A075CCJ9_9INFB	ISMTVI	GDNT	K <mark>WNECLNPRIFLAMTERITRDSPVWFRDFCSIAPVLFSNKIARLGKGFMI</mark>	357
tr A0A024CND8 A0A024CND8_9INFB	ISMTVI	GDNT	K <mark>WNECLNPRIFLAMTERITRDSPVWFRDFCSIAPVLFSNKIARLGKGFMI</mark>	357
tr A0A0N7GD33 A0A0N7GD33_9INFB	ISMTVI	GDNT	K <mark>WNECLNPRIFLAMTERITRDSPVWFRDFCSIAPVLFSNKIARLGKGFMI</mark>	357
sp 036430 RDRP_INBP9	ISMTVI	GDNT	K <mark>WNECLNPRIFLAMTERITRDSPIWFRDFCSIAPVLFSNKIARLGKGFMI</mark>	357
tr A3DR07 A3DR07_INBBK	ISMTVI	GDNT	K <mark>WNECLNPRIFLAMTERITRDSPIWFRDFCSIAPVLFSNKIARLGKGFMI</mark>	357
sp P13871 RDRP_INBAC	ISMTVI	GDNT	K <mark>WNECLNPRIFLAMTERITRDSPIWFRDFCSIAPVLFSNKIARLGKGFMI</mark>	357
sp P13872 RDRP_INBAD	ISMTVI	GDNT	K <mark>WNECLNPRIFLAMTERITRDSPIWFRDFCSIAPVLFSNKIARLGKGFMI</mark>	357
sp P03431 RDRP_I34A1	LSFTIT	GDNT	K <mark>WNENQNPRMFLAMITYMTRNQPEWFRNVLSIAPIMFSNKMARLGKGYMF</mark>	357
sp Q9Q0V0 RDRP_196A0	LSFTIT	GDNT	K <mark>WNENQNPRMFLAMITYITRNQPEWFRNVLSIAPIMFSNKMARLGKGYMF</mark>	357
sp Q30NP3 RDRP_175A0	LSFTII	GDNT	K <mark>WNENQNPRMFLAMITYITKNQPEWFRNILSIAPIMFSNKMARLGKGYMF</mark>	357
sp P16511 RDRP_157A5	LSFTIT	GDNT	K <mark>WNENQNPRMFLAMITYITRNQPEWFRNVLSIAPIMFSNKMARLGKGYMF</mark>	357
sp Q0A2F7 RDRP_183A4	LSFTIT	GDNT	K <mark>WNENQNPRMFLAMITYITRNQPEWFRNVLSIAPIMFSNKMARLGKGYMF</mark>	357
sp P16503 RDRP_177AF	LSFTII	GDNT	K <mark>WNENQNPRMFLAMITYITRNQPEWFRNVLSIAPIMFSNKMARLGKGYMF</mark>	357
sp P16513 RDRP_180A8	LSFTII	GDNT	K <mark>WNENQNPRMFLAMITYITRNQPEWFRNVLSIAPIMFSNKMARLGKGYMF</mark>	357
sp Q08II5 RDRP_I80A6	LSFTIT	GDNT	K <mark>WNENQNPRMFLAMITYITRNQPEWFRNVLSIAPIMFSNKMARLGKGYMF</mark>	357
sp Q0A3Q1 RDRP_I78AC	LSFTII	GDNT	K <mark>WNENQNPRMFLAMITYITRNQPEWFRNVLSIAPIMFSNKMARLGKGYMF</mark>	357
sp Q0A451 RDRP_I66A1	LSFTII	GDNT	K <mark>WNENQNPRMFLAMITYITRNQPEWFRNVLSIAPIMFSNKMARLGKGYMF</mark>	357
	:::*	***:	<mark>*</mark> *** :*. :**: :*::. :::. *:**::*.**:.:**:*	
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p P19703 RDRP_INCJJ	FAVNIT <mark>GDNSK</mark> NNECQQPEAYLALLAYITKDSSDLMKDLCSVAPVLFCNKFVKLGQGIRL	359
p Q9IMP4 RDRP INCJH	FAVNIT <mark>GDNSK</mark> NNECQQPEAYLALLAYITKDSSDLMKDLCSVAPVLFCNKFVKLGQGIRL	359
A0A193PPL8 A0A193PPL8 90RT0	FAVNITGONSKWNECQQPEAYLALLAYITKDSSDLMKDLCSVAPVLFCNKFVKLGQGIRL	359
A0A193PPM8 A0A193PPM8 9ORTO	FAVNITGONSKWNECQQPEAYLALLAYITKDSSDLMKDLCSVAPVLFCNKFVKLGQGIRL	359
A0A193PPP6 A0A193PPP6 9ORTO	FAVNIT GDNSKNNECOOPEAYLALLAYITKDSSDLMKDLCSVAPVLFCNKFVKLGOGIRL	359
Q6I7C3 RDRP INCAA	FAVNITGDNSKNNECQQPEAYLALLAYITKDSSDLMKDLCSVAPVLFCNKFVKLGQGIRL	359
A0A193PQ43 A0A193PQ43 INCKS	FAVNIT GDNSK WNECQQPEAYLALLAYITKDSSDLMKDLCSVAPVLFCNKFVKLGQGIRL	359
A0A193PPP8 A0A193PPP8 INCM3	FAVNITGONSKVNECQQPEAYLALLAYITKDSSDLMKDLCSVAPVLFCNKFVKLGQGIRL	359
A0A193PQ33 A0A193PQ33 INCY6	FAVNIIGONSKUNECQOPEAYLALLAYITKDSSDLMKDLCSVAPVLFCNKFVKLGQGIRL	359
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A0A193PPP0 A0A193PPP0 90RT0	FAVNIT <mark>GDNSK</mark> WNECQQPEAYLALLAYITKDSSDLMKDLCSVAPVLFCNKFVKLGQGIRL	359
P07832 RDRP_INBLE	ISMTVT <mark>GDNTKN</mark> NECLNPRIFLAMTERITRDSPIWFRDFCSIAPVLFSNKIARLGKGFMI	357
A0A0D6A5W0 A0A0D6A5W0_9INFB	ISMTVT <mark>GDNT</mark> KNNECLNPRIFLAMTERITRDSPIWFRDFCSIAPVLFSNKIARLGKGFMI	357
A0A059TB43 A0A059TB43_9INFB	ISMTVI <mark>GDNIK</mark> WNECLNPRIFLAMTERITRDSPIWFRDFCSIAPVLFSNKIARLGKGFMV	357
A0A075CCJ9 A0A075CCJ9_9INFB	ISMTVT <mark>GDNTK</mark> NNECLNPRIFLAMTERITRDSPVWFRDFCSIAPVLFSNKIARLGKGFMI	357
A0A024CND8 A0A024CND8_9INFB	ISMTVT <mark>GDNTK</mark> WNECLNPRIFLAMTERITRDSPVWFRDFCSIAPVLFSNKIARLGKGFMI	357 L
A0A0N7GD33 A0A0N7GD33 9INFB	ISMTVT <mark>GDNT</mark> KNNECLNPRIFLAMTERITRDSPVWFRDFCSIAPVLFSNKIARLGKGFMI	357
O36430 RDRP INBP9	ISMTVT <mark>GDNT</mark> KWNECLNPRIFLAMTERITRDSPIWFRDFCSIAPVLFSNKIARLGKGFMI	357
A3DR07 A3DR07 INBBK	ISMTVT <mark>GDNTK</mark> WNECLNPRIFLAMTERITRDSPIWFRDFCSIAPVLFSNKIARLGKGFMI	357
P13871 RDRP INBAC	ISMTVTGDNTKNNECLNPRIFLAMTERITRDSPIWFRDFCSIAPVLFSNKIARLGKGFMI	357
P13872 RDRP INBAD	ISMTVIGDNIKWNECLNPRIFLAMTERITRDSPIWFRDFCSIAPVLFSNKIARLGKGFMI	357
P03431 RDRP I34A1	LSFTIIGDNIKWNENONPRMFLAMITYMTRNOPEWFRNVLSIAPIMFSNKMARLGKGYMF	357
203431 RDRP_134A1 Q9Q0V0 RDRP_196A0	LSFTITGDNIKNNENQNFRMELAMITIMTRNQFEWFRNVLSIAFIMFSNKMARLGRGIMF LSFTIT <mark>GDNIK</mark> NNENQNPRMFLAMITYITRNQFEWFRNVLSIAFIMFSNKMARLGRGYMF	357
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Q30NP3 RDRP_175A0	LSFTIT <mark>GDNTK</mark> NNENQNPRMFLAMITYITKNQPEWFRNILSIAPIMFSNKMARLGKGYMF	357
P16511 RDRP_I57A5	LSFTIT <mark>GDNT</mark> KNNENQNPRMFLAMITYITRNQPEWFRNVLSIAPIMFSNKMARLGKGYMF	357
QOA2F7 RDRP_183A4	LSFTIT <mark>GDNTKN</mark> NNENQNPRMFLAMITYITRNQPEWFRNVLSIAPIMFSNKMARLGKGYMF	357
P16503 RDRP_177AF	LSFTIT <mark>GDNTK</mark> NNENQNPRMFLAMITYITRNQPEWFRNVLSIAPIMFSNKMARLGKGYMF	357
P16513 RDRP_180A8	LSFTIT <mark>GDNT</mark> K <mark>NNENQNPRMFLAMITYITRNQPEWFRNVLSIAPIMFSNKMARLGKGYMF</mark>	357
Q08115 RDRP_180A6	LSFTIT <mark>GDNT</mark> KNNENQNPRMFLAMITYITRNQPEWFRNVLSIAPIMFSNKMARLGKGYMF	357
Q0A3Q1 RDRP I78AC	LSFTIT <mark>GDNTK</mark> WNENQNPRMFLAMITYITRNQPEWFRNVLSIAPIMFSNKMARLGKGYMF	357
	LSFTIT <mark>GDNT</mark> KNNENQNPRMFLAMITYITRNQPEWFRNVLSIAPIMFSNKMARLGKGYMF	357
p QUA451 RDRP I66A1	LSETIT GENTIN N EN ON FRME LAMITIITRN OF EWERNYLSIAFIMESN KMARLGRGIME	337
p QUA451 RDRP_166A1	LSETIIduudin nu hvyner mei LAMIIIIIR ny etwern v LSIAFIMES NAMAR LGAGIME :: ****::****:*********************	
p Q0A451 RDRP_I66A1	:::****::***::*:*:::*::*::*::*::*::*::	
p P19703 RDRP_INCJJ	:::****:**** :*. :**: :*::. :::. *:**:*.**:**:**:***:*	417
p P19703 RDRP_INCJJ p Q9IMP4 RDRP_INCJH	:::****:*** :*. :**: :*::. :::. *:**:*.**:**:**:**:**:***:*	417 417
- p P19703 RDRP_INCJJ p Q9IMP4 RDRP_INCJH r A0A193PPL8 A0A193PPL8_90RT0	:::****:*** :*. :**: :*::. :::. *:**:*.**:**:**:**:**:**:**:**:**:**:**:	417 417 417
- p P19703 RDRP_INCJJ p Q9IMP4 RDRP_INCJH r A0A193PPL8 A0A193PPL8_90RT0 r A0A193PPM8 A0A193PPM8_90RT0	:::****:*** :*. :**: :*:: ::: *::**:********	417 417 417 417 417
p P19703 RDRP_INCJJ p Q9IMP4 RDRP_INCJH r A0A193PPL8 A0A193PPL8_90RT0 r A0A193PPM8 A0A193PPM8_90RT0 r A0A193PPP6 A0A193PPP6_90RT0	:::****:***:***: :*::: :::: *::*:*:*:*	417 417 417 417 417 417 417
- p P19703 RDRP_INCJJ p Q9IMP4 RDRP_INCJH c A0A193PPL8 A0A193PPL8_90RT0 c A0A193PPM8 A0A193PPM8_90RT0 c A0A193PPP6 A0A193PPP6_90RT0 p Q6I7C3 RDRP_INCAA	SNKRKTKEVIIKAEKMGKYK-NLMREEYKNLFEPL-EKYIQKDVCFLPG SNKRKTKEVIIKAEKMGKYK-NLMREEYKNLFEPL-EKYIQKDVCFLPG SNKRKTKEVIIKAEKMGKYK-NLMREEYKNLFEPL-EKYIQKDVCFLPG SNKRKTKEVIIKAEKMGKYK-NLMREEYKNLFEPL-EKYIQKDVCFLPG SNKRKTKEVIIKAEKMGKYK-NLMREEYKNLFEPL-EKYIQKDVCFLPG SNKRTKEVIIKAEKMGKYK-NLMREEYKNLFEPL-EKYIQKDVCFLPG SNKRTKEVIIKAEKMGKYK-NLMREEYKNLFEPL-EKYIQKDVCFLPG SNKRTKEVIIKAEKMGKYK-NLMREEYKNLFEPL-EKYIQKDVCFLPG SNKRTKEVIIKAEKMGKYK-NLMREEYKNLFEPL-EKYIQKDVCFLPG SNKRTKEVIIKAEKMGKYK-NLMREEYKNLFEPL-EKYIQKDVCFLPG	417 417 417 417 417 417 417 417
- p P19703 RDRP_INCJJ p Q9IMP4 RDRP_INCJH r A0A193PPL8 A0A193PPL8_90RT0 r A0A193PPM8 A0A193PPM8_90RT0 r A0A193PPP6 A0A193PPP6_90RT0 p Q6I7C3 RDRP_INCAA r A0A193PQ43 A0A193PQ43_INCKS	SNKRKTKEVI I KAEKMGKYK-NLMREEYKNLFEPL-EKY IQKDVCFLPG GMLMGMFNMLS SNKRKTKEVI I KAEKMGKYK-NLMREEYKNLFEPL-EKY IQKDVCFLPG GMLMGMFNMLS	417 417 417 417 417 417 417 417 417
- p P19703 RDRP_INCJJ p Q9IMP4 RDRP_INCJH r A0A193PPL8 A0A193PPL8_90RTO r A0A193PPM8 A0A193PPM8_90RTO r A0A193PPP6 A0A193PPP6_90RTO p Q617C3 RDRP_INCAA r A0A193PQ43 A0A193PQ43_INCKS r A0A193PPP8 A0A193PPP8_INCM3	SNKRKTKEVI I KAEKMGKYK-NLMREEYKNLFEPL-EKYIQKDVCFLPG GMLMGMFNMLS SNKRKTKEVI I KAEKMGKYK-NLMREEYKNLFEPL-EKYIQKDVCFLPG GMLMGMFNMLS	417 417 417 417 417 417 417 417 417 417
- p P19703 RDRP_INCJJ p Q9IMP4 RDRP_INCJH r A0A193PPL8 A0A193PPL8_90RT0 r A0A193PPM8 A0A193PPM8_90RT0 r A0A193PPP6 A0A193PP6_90RT0 p Q6I7C3 RDRP_INCAA r A0A193PQ43 A0A193PQ43_INCKS r A0A193PP8 A0A193PP8_INCM3 r A0A193PQ33 A0A193PQ33_INCY6	SNKRKTKEVI I KAEKMGKYK-NLMREEYKNLFEPL-EKYIQKDVCFLPG GMLMGMFNMLS SNKRKTKEVI I KAEKMGKYK-NLMREEYKNLFEPL-EKYIQKDVCFLPG GMLMGMFNMLS	417 417 417 417 417 417 417 417 417 417
- p P19703 RDRP_INCJJ p Q9IMP4 RDRP_INCJH r A0A193PPL8 A0A193PPL8_90RTO r A0A193PPM8 A0A193PPM8_90RTO r A0A193PPP6 A0A193PPP6_90RTO p Q6I7C3 RDRP_INCAA r A0A193PQ43 A0A193PQ43_INCKS r A0A193PPP8 A0A193PPP8_INCM3 r A0A193PP80 A0A193PP03_INCY6 r A0A193PPP0 A0A193PPP0_90RTO	SNKRKTKEVI I KAEKMGKYK-NLMREEYKNLFEPL-EKYIQKDVCFLPG GMLMGMFNMLS SNKRKTKEVI I KAEKMGKYK-NLMREEYKNLFEPL-EKYIQKDVCFLPG GMLMGMFNMLS	417 417 417 417 417 417 417 417 417 417
- p P19703 RDRP_INCJJ p Q9IMP4 RDRP_INCJH r A0A193PP18 A0A193PP18_90RT0 r A0A193PP06 A0A193PP06_90RT0 p Q6I7C3 RDRP_INCAA r A0A193PP243 A0A193PQ43_INCKS r A0A193PP28 A0A193PP28_INCM3 r A0A193PP28 A0A193PP28_INCM3 r A0A193PP20 A0A193PP70_90RT0 p P07832 RDRP_INBLE	SNKRKTKEVI I KAEKMGKYK-NLMREEYKNLFEPL-EKY IQKDVCFLPG GMLMGMFNMLS SNKRKTKEVI I KAEKMGKYK-NLMREEYKNLFEPL-EKY IQKDVCFLPG GMLMGMFNMLS	417 417 417 417 417 417 417 417 417 417
D P19703 RDRP_INCJJ D Q9IMP4 RDRP_INCJH r A0A193PPL8 A0A193PPL8_9ORTO r A0A193PPM8 A0A193PPM8_9ORTO r A0A193PPP6 A0A193PPP6_9ORTO D Q6I7C3 RDRP_INCAA r A0A193PQ43 A0A193PQ43_INCKS r A0A193PP8 A0A193PP88_INCM3 r A0A193PP83 A0A193PP83_INCY6 r A0A193PPP0 A0A193PPP0_9ORTO D P07832 RDRP_INBLE r A0A0D6A5W0 A0A0D6A5W0_9INFB	SNKRKTKEVI I KAEKMGKYK-NLMREEYKNLFEPL-EKY IQKDVCFLPG GMLMGMFNMLS SNKRKTKEVI I KAEKMGKYK-NLMREEYKNLFEPL-EKY IQKDVCFLPG GMLMGMFNMLS	417 417 417 417 417 417 417 417 417 417
<pre></pre>	SNKRKTKEVI I KAEKMGKYK-NLMREEYKNLFEPL-EKY IQKDVCFLPG GMLMGMFNMLS SNKRKTKEVI I KAEKMGKYK-NLMREEYKNLFEPL-SKY IQKDVCFLPG GMLMGMFNMLS	417 417 417 417 417 417 417 417 417 417
- p P19703 RDRP_INCJJ p Q9IMP4 RDRP_INCJH r A0A193PPL8 A0A193PPL8_9ORTO r A0A193PPM8 A0A193PPM8_9ORTO r A0A193PPP6 A0A193PPP6_9ORTO p Q6I7C3 RDRP_INCAA r A0A193PQ43 A0A193PQ43_INCKS r A0A193PPP8 A0A193PPP8_INCM3 r A0A193PPP8 A0A193PPP8_INCM3 r A0A193PPP0 A0A193PPP0_9ORTO p P07832 RDRP_INBLE r A0A0D6A5W0 A0A0D6A5W0_9INFB r A0A059TB43 A0A059TB43_9INFB r A0A075CCJ9 A0A075CCJ9_9INFB	SNKRKTKEVI I KAEKMGKYK-NLMREEYKNLFEPL-EKY IQKDVCFLPG GMLMGMFNMLS SNKRKTKEVI I KAEKMGKYK-NLMREEYKNLFEPL-SKY IQKDVCFLPG GMLMGMFNMLS SNKRKTKEVI I KAEKMGYK-NLMREYNEETRAKLKK FFNEEGTASLSP GMMMGMFNMLS SNKRKTKEVI I PCPLFSI PLERYNEETRAKLKKK FFNEEGTASLSP GMMMGMFNMLS SNKRKTKEVA AQ I PCPLFSI PLERYNEETRAKLKKK FFNEEGTASLSP GMMMGMFNMLS	417 417 417 417 417 417 417 417 417 417
- 	SNKRKTKEVI I KAEKMGKYK-NLMREEYKNLFEPL-EKY IQKDVCFLPG GMLMGMFNMLS SNKRKTKEVI I KAEKMGKYK-NLMREEYKNLFEPL-SKY IQKDVCFLPG GMLMGMFNMLS SNKKKTKLKAQI PCPLFSI PLERYNEETRAKLKKLKFFFNEEGTASLSP GMMMGMFNMLS TSKTKRLKAQI PCPLFSI PLERYNEETRAKLKKLKFFFNEEGTASLSP GMMMGMFNMLS TSKTKRLKAQI PCPLFSI PLERYNEETRAKLKKKLKFFFNEEGTASLSP GMMMGMFNMLS TSKTKRLKAQI PCPLFSI PLERYNEETRAKLKKKKFFFNEEGTASLSP GMMMGMFNMLS	417 417 417 417 417 417 417 417 417 417
p P19703 RDRP_INCJJ p Q9IMP4 RDRP_INCJH c A0A193PP18 A0A193PP18_9ORTO c A0A193PP48 A0A193PP18_9ORTO c A0A193PP96 A0A193PP76_9ORTO p Q6I7C3 RDRP_INCAA c A0A193PP28 A0A193PP243_INCKS c A0A193PP23 A0A193PP23_INCM3 c A0A193PP20 A0A193PP20_9ORTO p P07832 RDRP_INBLE c A0A059TB43 A0A059TB43_9INFB c A0A059TB43 A0A059TB43_9INFB c A0A075CCJ9 A0A075CCJ9_9INFB c A0A024CND8 A0A024CND8_9INFB c A0A07GD33 A0A07GD33_9INFB	SNKRKTKEVI I KAEKMGKYK-NLMREEYKNLFEPL-EKYIQKDVCFLPG GMLMGMFNMLS SNKRKTKEVI I KAEKMGKYK-NLMREYKNLFEPL-EKYIQKDVCFLPG GMLMGMFNMLS SNKRKTKEVI I KAEKMGYK-NLMREYKNLFEPL-EKYIQKDVCFLPG GMLMGMFNMLS SNKRKTKEVI I FOPLFSI FLERYNEETRAKLKKLKFFFNEGTASLSF GMMMGMFNMLS SNKKRLKAQI FCPDLFSI FLERYNEETRAKLKKLKFFFNEGTASLSF GMMMGMFNMLS SNKKRLKAQI FCPDLFSI FLERYNEETRAKLKKLKFFFNEGTASLSF GMMMGMFNMLS SNKKRLKAQI FCPDLFSI FLERYNEETRAKLKKLKFFFNEGTASLSF GMMMGMFNMLS SNKRKRLKAQI FCPDLFSI FLERYNEETRAKLKKLKFFFNEGTASLSF GMMMGMFNMLS	417 417 417 417 417 417 417 417 417 417
- 	SNKRKTKEVI I KAEKMGKYK-NLMREEYKNLFEPL-EKYIQKDVCFLPG GMLMGMFNMLS SNKRKTKEVI I KAEKMGKYK-NLMREYKNLFEPL-EKYIQKDVCFLPG GMLMGMFNMLS SNKRKTKLKAQI PCPLFSI PLERYNEETRAKLKKLKF FFNEEGTASLSF GMMMGMFNMLS SNKRKTKLKAQI PCPLFSI PLERYNEETRAKLKKLKF FFNEEGTASLSF GMMMGMFNMLS SNKTRKLKAQI PCPLFSI PLERYNEETRAKLKKLKF FFNEEGTASLSF GMMMGMFNMLS SNKTRKLKAQI PCPLFSI PLERYNEETRAKLKKLKF FFNEEGTASLSF GMMMGMFNMLS SNKTKRLKAQI PCPLFSI PLERYNEETRAKLKKLKF FFNEEGTASLSF GMMMGMFNMLS SNKTRKLKAQI PCPLFSI PLERYNEETRAKLKKLKF FFNEEGTASLSF GMMMGMFNMLS SNKTRKLKAQI PCPLFSI PLERYNEETRAKLKKLKF FFNEEGTASLSF GMMMGMFNMLS SNKTRKLKAQI PCPLFSI PLERYNEETRAKLKKLKFFNEEGTASLSF GMMMGMFNMLS SNKTRKLKAQI PCPLFSI PLERYNEETRAKLKKKKLKFFNEEGTASLSF GMMMGMFNMLS	417 417 417 417 417 417 417 417 417 417
D P19703 RDRP_INCJJ D Q9IMP4 RDRP_INCJH AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	SNKRKTKEVI I KAEKMGKYK-NLMREEYKNLFEPL-EKYIQKDVCFLPG GMLMGMFNMLS SNKRKTKEVI I KAEKMGKYK-NLMREEYKNLFEPL-EKYIQKDVCFLPG GMLMGMFNMLS SNKRKTREVI I KAEKMGKYK-NLMREEYKNLFEPL-EKYIQKDVCFLPG GMLMGMFNMLS SNKRKTREVI I KAEKMGKYK-NLMREEYKNLFEPL-EKYIQKDVCFLPG GMLMGMFNMLS TSKTKRLKAQI PCPDLFSI PLERYNEETRAKLKKLKF FFNEEGTASLSF GMMMGMFNMLS TSKTKRLKAQI PCPDLFSI PLERYNEETRAKLKKLKF FFNEEGTASLSF GMMMGMFNMLS	417 417 417 417 417 417 417 417 417 417
D P19703 RDRP_INCJJ D Q9IMP4 RDRP_INCJH C A0A193PPL8 A0A193PPL8_90RTO C A0A193PPM8 A0A193PPM8_90RTO C A0A193PPP6 A0A193PPP6_90RTO D Q6I7C3 RDRP_INCAA C A0A193PQ43 A0A193PQ43_INCKS C A0A193PP8 A0A193PP8_INCM3 C A0A193PP0 A0A193PP70_90RTO D P07832 RDRP_INBLE C A0A0D6A5W0 A0A0D6A5W0_9INFB C A0A059TB43 A0A059TB43_9INFB C A0A059TB43 A0A075CCJ9_9INFB C A0A024CND8 A0A024CND8_9INFB C A0A07GD33 A0A07_INBBK D D36430 RDRP_INBAC	SNKRKTKEVI I KAEKMGKYK-NLMREEYKNLFEPL-EKYIQKDVCFLPG GMLMGMFNMLS SNKRKTKEVI I KAEKMGKYK-NLMREEYKNLFEPL-EKYIQKDVCFLPG GMLMGMFNMLS TSKTKRLKAQI PCPDLFSI PLERYNEETRAKLKKLKF FFNEEGTASLSF GMMMGMFNMLS TSKTKRLKAQI PCPDLFSI PLERYNEETRAKLKKLKF FFNEEGTASLSF GMMMGMFNMLS	417 417 417 417 417 417 417 417 417 417
- 	SNKRKTKEVI I KAEKMGKYK-NLMREEYKNLFEPL-EKYIQKDVCFLPG GMLMGMFNMLS SNKRKTKEVI I KAEKMGKYK-NLMREEYKNLFEPL-EKYIQKDVCFLPG GMLMGMFNMLS TSKTKRLKAQI PCPDLFSI PLERYNEETRAKLKKLKF FFNEEGTASLSF GMMMGMFNMLS TSKTKRLKAQI PCPDLFNI PLERYNEETRAKLKKLKFFFNEEGTASLSF GMMMGMFNMLS TSKTKRLKAQI PCPDLFNI PLERYNEETRAKLKKLKFFFNEEGTASLSF GMMMGMFNMLS	417 417 417 417 417 417 417 417 417 417
- 	SNKRKTKEVI I KAEKMGKYK-NLMREEYKNLFEPL-EKYIQKDVCFLPG GMLMGMFNMLS SNKRKTKEVI I KAEKMGKYK-NLMREEYKNLFEPL-EKYIQKDVCFLPG GMLMGMFNMLS TSKTKRLKAQI PCPLFSI PLERYNEETRAKLKKLKF FFNEEGTASLSP GMMMGMFNMLS TSKTKRLKAQI PCPLFNI PLERYNEETRAKLKKLKF FFNEEGTASLSP GMMMGMFNMLS TSKTKRLKAQI PCPLFNI PLERYNEETRAKLKKLKF FFNEEGTASLSP GMMMGMFNML	417 417 417 417 417 417 417 417 417 417
- 	SNKRKTKEVI I KAEKMGKYK-NLMREEYKNLFEPL-EKYIQKDVCFLPG GMLMGMFNMLS SNKRKTKEVI I KAEKMGKYK-NLMREEYKNLFEPL-EKYIQKDVCFLPG GMLMGMFNMLS TSKTKRLKAQI PCPDLFSI PLERYNEETRAKLKKLKF FFNEEGTASLSF GMMMGMFNMLS TSKTKRLKAQI PCPDLFNI PLERYNEETRAKLKKLKF FFNEEGTASLS	417 417 417 417 417 417 417 417 417 417
- 	SNKRKTKEVI I KAEKMGKYK-NLMREEYKNLFEPL-EKYIQKDVCFLPG GMLMGMFNMLS SNKRKTKEVI I KAEKMGKYK-NLMREEYKNLFEPL-EKYIQKDVCFLPG GMLMGMFNMLS TSKTKRLKAQI PCPLFSI PLERYNEETRAKLKKLKF FFNEEGTASLSP GMMMGMFNMLS TSKTKRLKAQI PCPLFSI PLERYNEETRAKLKKLKF FFNEEGTASLSP GMMMGMFNML	417 417 417 417 417 417 417 417 417 417
- 	SNKRKTKEVI I KAEKMGKYK-NLMREEYKNLFEPL-EKY IQKDVCFLPG SMLMGMFNMLS SNKRKTKEVI I KAEKMGYK-NLMREEYKNLFEPL-EKY IQKDVCFLPG SMLMGMFNMLS SNKRKTKEVI I KAEKMGYK-NLMREEYKNLFEPL-EKY IQKDVCFLPG SMLMGMFNMLS SNKRKTKEVI I KAEKMGYK-NLMREEYKNLFEPL-EKY IQKDVCFLPG SMLMGMFNMLS SNKRKTKELKAQ IPCDLFSI PLERYNEETRA KLKKLKP FFNEEGTASLSP SMMMGMFNMLS TSKTKRLKAQ IPCDLFSI PLERYNEETRA KLKKLKP FFNEEGTASLSP SMMMGMFNMLS TSKTKRLKAQ IPCPDLFSI PLERYNEETRA KLKKLKP FFNEEGTASLSP SMMMGMFNMLS TSKTKRLKAQ IPCPDLFSI PLERYNEETRA KLKKLKP FFNEEGTASLSP SMMMGMFNMLS TSKTKRLKAQ IPCPDLFSI PLERYNEETRA KLKKLKP FFNEEGTASLSP SMMMGMFNMLS TSKTKRLKAQ IPCPDLFSI PLERYNEETRA KLKKLKP FFNEEGTASLSP SMMMGMFNMLS TSKTKRLKAQ IPCPLFNI PLERYNEETRA KLKKLKP FFNEEGTASLSP SMMMGMFNMLS SKSMKLRTQ IPAEMLASI DLKYFNESTRKKIEKIRPLLI-GTASLSP SMMMGMFNMLS ESKSMKLRTQ IPAEMLASI DLKYFNESTRKKIEKIRPLLI-DGTASLSP SMMMGMFNMLS ESKSMKLRTQ IPAEMLASI DLKYFNESTRKKIEKIRPLLI-DGTASLSP SMMMGMFNMLS	417 417 417 417 417 417 417 417 417 417
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- 	SNKRKTKEVI I KAEKMGKYK-NLMREEYKNLFEPL-EKY IQKDVCFLPG SMLMGMFNMLS SNKRKTKEVI I KAEKMGYK-NLMREEYKNLFEPL-EKY IQKDVCFLPG SMLMGMFNMLS SNKRKTKEVI I KAEKMGYK-NLMREEYKNLFEPL-EKY IQKDVCFLPG SMLMGMFNMLS SNKRKTKEVI I KAEKMGYK-NLMREEYKNLFEPL-EKY IQKDVCFLPG SMLMGMFNMLS SNKRKTKELKAQ IPCDLFSI PLERYNEETRA KLKKLKP FFNEEGTASLSP SMMMGMFNMLS TSKTKRLKAQ IPCDLFSI PLERYNEETRA KLKKLKP FFNEEGTASLSP SMMMGMFNMLS TSKTKRLKAQ IPCPDLFSI PLERYNEETRA KLKKLKP FFNEEGTASLSP SMMMGMFNMLS TSKTKRLKAQ IPCPDLFSI PLERYNEETRA KLKKLKP FFNEEGTASLSP SMMMGMFNMLS TSKTKRLKAQ IPCPDLFSI PLERYNEETRA KLKKLKP FFNEEGTASLSP SMMMGMFNMLS TSKTKRLKAQ IPCPDLFSI PLERYNEETRA KLKKLKP FFNEEGTASLSP SMMMGMFNMLS TSKTKRLKAQ IPCPLFNI PLERYNEETRA KLKKLKP FFNEEGTASLSP SMMMGMFNMLS SKSMKLRTQ IPAEMLASI DLKYFNESTRKKIEKIRPLLI-GTASLSP SMMMGMFNMLS ESKSMKLRTQ IPAEMLASI DLKYFNESTRKKIEKIRPLLI-DGTASLSP SMMMGMFNMLS ESKSMKLRTQ IPAEMLASI DLKYFNESTRKKIEKIRPLLI-DGTASLSP SMMMGMFNMLS	417 417 417 417 417 417 417 417 417 417
<pre></pre>	SNKRKTKEVI I KAEKMGKYK-NLMREEYKNLFEPL-EKYIQKDVCFLPG SMLMGMFNMLS SNKRKTKEVI I KAEKMGYK-NLMREEYKNLFEPL-EKYIQKDVCFLPG SMMGMFNMLS SNKRKTKEVI I KAEKMGYK-NLMREEYKNLFFTAKKKKKFFFNEEGTASLSP SMMMGMFNMLS SNKRKRLKQIPCDLFSIPLERYNEETRAKKKKKFFFNEEGTASLSP SMMMGMFNMLS SSKTKRLKQIPCDLFSIPLERYNEETRAKKKKKFFFNEEGTASLSP SMMMGMFNMLS SSKTKRLKQIPCDLFSIPLERYNEETRAKKKKKFFFNEEGTASLSP SMMMGMFNMLS SSKMKLRQIPAEMLASIDLKYFNDSTRKKIEKIRPLLI-DGTASLSP SMMMGMFNMLS ESKSMKLRQIPAEMLASIDLKYFNESTRKKIEKIRPLLI-DGTASLSP SMMMGMFNMLS ESKSMKLRQIPAEMLASIDLKYFNESTRKKIEKIRPLLI-DGTASLSP SMMMGMFNMLS ESKSMKLRQIPAEMLASIDLKYFNESTRKKIEKIRPLLI-DGTASLSP SMMMGMFNMLS ESKSMKLRQIPAEMLASIDLKYFNESTRKKIEKIRPLLI-DGTASLSP SMMMGMFNMLS	417 417 417 417 417 417 417 417 417 417
- p P19703 RDRP_INCJJ p Q9IMP4 RDRP_INCJH r A0A193PPL8 A0A193PPL8_9ORTO r A0A193PPM8 A0A193PPM8_9ORTO r A0A193PPP6 A0A193PP43_INCKS r A0A193PQ43 A0A193PQ43_INCKS r A0A193PQ43 A0A193PQ43_INCKS r A0A193PP28 A0A193PQ43_INCKS r A0A193PP28 A0A193PP28_INCM3 r A0A193PP28 A0A193PP28_INCM3 r A0A193PP28 A0A193PP20_9ORTO p P07832 RDRP_INBLE r A0A006A5W0 A0A006A5W0_9INFB r A0A059TB43 A0A059TB43_9INFB r A0A059TB43 A0A059TB43_9INFB r A0A075CCJ9 A0A075CCJ9_9INFB r A0A075CCJ9 A0A075CCJ9_9INFB r A0A07GD33 A0A075CCJ9_9INFB r A0A07GD33 A0A07GD33_9INFB p 036430 RDRP_INBE4 p P13872 RDRP_INBAC p P13872 RDRP_INBAC p P13872 RDRP_ISAA1 p 0230NP3 RDRP_I57A5 p Q0A2F7 RDRP_I7AF p P16513 RDRP_I80A8	SNKRKTKEVI I KAEKMGKYK-NLMREEYKNLFEPL-EKYIQKDVCFLPG MLMGMFNMLS SNKRKTKEVI I KAEKMGKYK-NLMREEYKNLFEPL-SKYQKDVCFLPG MLMGMFNMLS SNKRKTKEVI I KAEKMGYK-NLMREEYKNLFEPL-SKYQKDVCFLPG MLMGMFNMLS SNKRKTKEVI I KAEKMGKYK-NLMREEYKNLFEPL-SKYQKDVCFLPG MLMGMFNMLS TSKTKRLKAQI PCPDLFSI PLERYNEETRAKLKKLKFFFNEEGTASLSP MMMGMFNMLS TSKTKRLKAQI PCPDLFNI PLERYNEETRAKLKKLKFFFNEEGTASLSP MMMGMFNMLS TSKTKRLKAQI PCPDLFNI PLERYNEETRAKLKKLKFFFNEEGTASLSP MMMGMFNMLS SKSMKLRQI PAEMLASI DLKYFNDSTRKKIEKIRPLLI-DGTASLSP MMMGMFNMLS ESKSMKLRQI PAEMLASI DLKYFNESTRKKIEKIRPLLI-DGTASLSP MMMGMFNMLS ESKSMKLRQI PAEMLASI DLKYFNESTRKKIEKIRPLLI-DGTASLSP MMMGMFNMLS ESKSMKLRQI PAEMLANI DLKYFNESTRKKIEKIRPLLI-DGTASLSP MMMGMFNMLS ESKSMKLRQI PAEMLANI DLKYFNESTRKKIEKIRPLLI-DGTASLSP MMMGMFNMLS	417 417 417 417 417 417 417 417 417 417
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p P19703 RDRP_INCJJ p Q9IMP4 RDRP_INCJH r A0A193PPL8 A0A193PPL8_90RT0	SNKRKTKEVI I KAEKMGKYK-NLMREEYKNLFEPL-EKYIQKDVCFLPG SMLMGMFNMIS SNKRKTKEVI I KAEKMGKYK-NLMREEYKNLFEPL-EKYIQKDVCFLPG SMLMGMFNMIS SNKRKTKLKAQI PCPDLFSI PLERYNEETRAKLKKKKF FFNEEGTASLSP SMMMGMFNMIS SNKRKLKAQI PCPDLFSI PLERYNEETRAKLKKKKF FFNEEGTASLSP SMMMGMFNMIS SNKTRLKAQI PCPDLFSI PLERYNEETRAKLKKKKF FFNEEGTASLSP SMMMGMFNMIS SNKRKLKQI PCPDLFNI PLERYNEETRAKLKKKKF FFNEEGTASLSP SMMMGMFNMIS SNKRKLKQI PCPDLFNI PLERYNEETRAKLKKKKF FFNEEGTASLSP SMMMGMFNMIS SNKRKLKQI PAEMLASIDLKYFNESTRKKIEKIRPLLI-DGTASLSP SMMMGMFNMIS SNSMKLRQI PAEMLASIDLKYFNESTRKKIEKIRPLLI-DGTASLSP SMMMGMFNMIS SNSMKLRQI PAEMLANIDLKYFNESTRKKIEKIRPLLI-DGTASLSP SMMMGMFNMIS SNSMKLRQI PAEMLANIDLKYFNESTRKKIEKIRPLLI-DGTASLSP SMMMGMFNMIS SNSMKLRQI PAEMLANIDLKYFNESTRKKIEKIRPLLI-DGTASLSP SMMMGMFNMIS SNSMKLRQI PAE	417 417 417 417 417 417 417 417 417 417

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sp P19703 RDRP_INCJJ	TVLGV <mark>5TLCYMDEELKAKGCFWT</mark> GLQ <mark>5SDDE</mark> VLFAVASNWSNIHWTIRRE <mark>N</mark> AVC <mark>KLIGIN</mark>	477
sp Q9IMP4 RDRP_INCJH	TVLGV5TLCYMDEELKAKGCFWIGLQS <mark>SDD5</mark> VLFAVASNWSNIHWTIRRE <mark>N</mark> AVC <mark>KL</mark> GIN	477
tr A0A193PPL8 A0A193PPL8_9ORTO	TVLGV5TLCYMDEELKAKGCFWTGLQS <mark>SDD5</mark> VLFAVASNWSNIHWTIRRE <mark>N</mark> AVC <mark>KL</mark> GIN	477
tr A0A193PPM8 A0A193PPM8_9ORTO	TVLGV5TLCYMDEELKAKGCFWTGLQS <mark>SDDE</mark> VLFAVASNWSNIHWTIRRE <mark>N</mark> AVC <mark>KL</mark> IGIN	477
tr A0A193PPP6 A0A193PPP6 9ORTO	TVLGV5TLCYMDEELKAKGCFWTGLQS <mark>SDDE</mark> VLFAVASNWSNIHWTIRRE <mark>N</mark> AVCKLIGIN	47 🖵
sp Q617C3 RDRP INCAA	TVLGV5TLCYMDEELKAKGCFWTGLQS <mark>SDDE</mark> VLFAVASNWSNIHWTIRRE <mark>N</mark> AVCKLIGIN	477 [
tr A0A193PQ43 A0A193PQ43 INCKS	TVLGV5TLCYMDEELKAKGCFWIGLQS <mark>SDDE</mark> VLFAVASNWSNIHWTIRRE <mark>N</mark> AVCKLIGIN	477
tr A0A193PPP8 A0A193PPP8 INCM3	TVLGV5TLCYMDEELKAKGCFWTGLQS <mark>SDDE</mark> VLFAVASNWSNIHWTIRRE <mark>N</mark> AVCKLIGIN	477
tr A0A193PQ33 A0A193PQ33_INCY6	TVLGV5TLCYMDEELKAKGCFWIGLQS <mark>SDDE</mark> VLFAVASNWSNIHWTIRRE <mark>N</mark> AVC <mark>KL</mark> GIN	477
tr A0A193PPP0 A0A193PPP0_9ORTO	TVLGV5TLCYMDEELKAKGCFWIGLQS <mark>SDD5</mark> VLFAVASNWSNIHWTIRRE <mark>N</mark> AVO <mark>KL</mark> IGIN	477
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sp P07832 RDRP_INBLE	TVLGVAALGIKNIGNKEYLWIGLQS <mark>SDDB</mark> ALFVNAKDEETCMEGINDFYRTCKLI <mark>GIN</mark>	475
tr A0A0D6A5W0 A0A0D6A5W0_9INFB	TVLGVAALGIKNIGNKEYLWOGLQS <mark>SDDE</mark> ALFVNAKDEETCMEGINDFYRTCKLI <mark>GIN</mark>	475
tr A0A059TB43 A0A059TB43_9INFB	TVLGVAALGIKNIGNKEYLWIGLQS <mark>SDDF</mark> ALFVNAKDEEACMEGINDFYRTCKLI <mark>GIN</mark>	475
tr A0A075CCJ9 A0A075CCJ9_9INFB	TVLGVAALGIKNIGNKEYLWIGLQS <mark>SDDE</mark> ALFVNAKDEETCMEGINDFYRTCKLI <mark>GVN</mark>	475
tr A0A024CND8 A0A024CND8 9INFB	TVLGVAALGIKNIGNKEYLWIGLQS <mark>SDDE</mark> ALFVNAKDEETCMEGINDFYRTCKLI <mark>GIN</mark>	475 🕒
tr A0A0N7GD33 A0A0N7GD33_9INFB	TVLGVAALGIKNIGNKEYLWIGLQS <mark>SDDF</mark> ALFVNAKDEETCMKGINDFYRTCKLI <mark>GIN</mark>	475
sp 036430 RDRP INBP9	TVLGVAALGIKNIGNKEYLWIGLQS <mark>SDDE</mark> ALFVNAKDEETCMEGINDFYRTCKLI <mark>GIN</mark>	475
tr A3DR07 A3DR07_INBBK	TVLGVAALGIKNIGNKEYLWIGLQS <mark>SDDF</mark> ALFVNAKDEETCMEGINDFYRTCKLI <mark>GIN</mark>	475
sp P13871 RDRP_INBAC	TVLGVAALGIKNIGNKEYLWIGLQS <mark>SDDF</mark> ALFVNAKDEETCMEGINDFYRTCKLI <mark>GIN</mark>	475
sp P13872 RDRP_INBAD	TVLGVAALGIKNIGNREYLWIGLQS <mark>SDOB</mark> ALFVNAKDEETCMEGINDFYRTCKLI <mark>GIN</mark>	475
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sp P03431 RDRP_I34A1	TVLGVBILNLGQKRYTKTTYWWIGLQS <mark>SDDB</mark> ALIVNAPNHEGIQAGVDRFYRTCKLI <mark>GIN</mark>	476
sp Q9Q0V0 RDRP_I96A0	TVLGV <mark>5ILNLGQKRYTKTTYWWD</mark> GLQS <mark>SDDE</mark> ALIVNAPNHEGIEAGVDRFYRTCKLV <mark>GIN</mark>	476
sp Q30NP3 RDRP_175A0	TVLGV5ILNLGQKKYTKTTYWWDGLQS <mark>SDDE</mark> ALIVNAPNHEGIQAGVDRFYRTCKLV <mark>GIN</mark>	476
sp P16511 RDRP_157A5	TVLGVBILNLGQKKYTKTTYWWDGLQS <mark>SDDE</mark> ALIVNAPNHEGIQAGVDRFYRTCKLV <mark>GIN</mark>	476
sp Q0A2F7 RDRP 183A4	TVLGV <mark>5ILNLGQKRYTKTTYWWD</mark> GLQS <mark>SDDB</mark> ALIVNALNHEGIQAGVDRFYRTCKLV <mark>GIN</mark>	476 📥
sp P16503 RDRP_I77AF	TVLGV <mark>5ILNLGQKRYTKTTYWWD</mark> GLQS <mark>SDDB</mark> ALIVNAPNHEGIQAGVDRFYRTCKLV <mark>GIN</mark>	476
sp P16513 RDRP_I80A8	TVLGV <mark>5ILNLGQKRYTKTTYWWD</mark> GLQS <mark>SDDB</mark> ALIVNAPNHEGIQAGVDRFYRTCKLV <mark>GIN</mark>	476
sp Q08II5 RDRP_I80A6	TVLGV <mark>BILNLGQKRYTKTTYWWIGLQS<mark>SDDB</mark>ALIVNAPNHEGIQAGVDRFYRTCKLV<mark>GIN</mark></mark>	476
sp Q0A3Q1 RDRP_I78AC	TVLGV <mark>BILNLGQKRYTKTTYWWI</mark> GLQS <mark>SDDE</mark> ALIVNAPNHEGIQAGVDRFYRTCKLV <mark>GIN</mark>	476
sp Q0A451 RDRP_I66A1	TVLGV <mark>BILNLGQKRYTKTTYWWLGLQS<mark>SDDB</mark>ALIVNAPDHEGIQAGVDRFYRTCKLV<mark>GIN</mark></mark>	476
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sp P19703 RDRP INCJJ	MSLEKSY	GSLPELFEFTSMFFDGEFVSNLAMELPAFTTAGVNEGVDFTAAMSIIKTNMIN	5371
sp/Q9IMP4/RDRP_INCJH	MSLEKSY	CSLPELFEFTSMFFDGEFVSNLAMELPAFTTAGVNEGVDFTAAMSIIKTNMIN	537
tr A0A193PPL8 A0A193PPL8 9ORTO	MSLERSY	CSLPELFEFTSMFFDGEFVSNLAMELPAFTTAGVNEGVDFTAAMSIIKTNMIN	537
tr A0A193PPM8 A0A193PPM8_9ORTO	MSLEKSY	CSLPELFEFTSMFFDGEFVSNLAMELPAFTTAGVNEGVDFTAAMSIIKTNMIN	537
tr A0A193PPP6 A0A193PPP6 90RT0	MSLERSY	CSLPELFEFTSMFFDGEFVSNLAMELPAFTTAGVNEGVDFTAAMSIIKTNMIN	537 C
sp Q617C3 RDRP_INCAA	MSLEKSY	CSLPELFEFTSMFFDGEFVSNLAMELPAFTTAGVNEGVDFTAAMSIIKTNMIN	537
tr A0A193PQ43 A0A193PQ43 INCKS	MSLEKSY	GSLPELFEFTSMFFDGEFVSNLAMELPAFTTAGVNEGVDFTAAMSIIKTNMIN	537 mRNA
tr A0A193PPP8 A0A193PPP8 INCM3	MSLERSY	CSLPELFEFTSMFFDGEFVSNLAMELPAFTTAGVNEGVDFTAAMSIIKTNMIN	537
tr A0A193Pg33 A0A193Pg33 INCY6	MSLEKSY	CSLPELFEFTSMFFDGEFVSNLAMELPAFTTAGVNEGVDFTAAMSIIKTNMIN	537
tr A0A193PPP0 A0A193PPP0_9ORTO	MSLEKSY	CSLPELFEFTSMFFDGEFVSNLAMELPAFTTAGVNEGVDFTAAMSIIKTNMIN	537
			-
sp P07832 RDRP_INBLE	MSKKKSY	CNETGMFEFTSMFYRDGFVSNFAMELPSFGVAGVNESADMAIGMTIIKNNMIN	535
tr A0A0D6A5W0 A0A0D6A5W0_9INFB	MSK <mark>K</mark> SY	CNETGMFEFTSMFYRDGFVSNFAMEIPSFGVAGVNESADMAIGMTIIKNNMIN	535
tr A0A059TB43 A0A059TB43_9INFB		CNETGMFEFTSMFYRDGFVSNFAMEIPSFGVAGVNESADMAIGMTIIKNNMIN	535
tr A0A075CCJ9 A0A075CCJ9_9INFB	MSK <mark>K</mark> KSY	CNETGMFEFTSMFYRDGFVSNFAMELPSFGVAGVNESADMAIGMTIIKNNMIN	535
tr A0A024CND8 A0A024CND8_9INFB	MSK <mark>K</mark> SY	CNETGMFEFTSMFYRDGFVSNFAMELPSFGVAGVNESADMAIGMTIIKNNMIN	535 B
tr A0A0N7GD33 A0A0N7GD33_9INFB	MSKKKSY	CNETGMFEFTSMFYRDGFVSNFAMELPSFGVAGVNESADMAIGMTIIKNNMIN	535
sp 036430 RDRP_INBP9	MSK <mark>K</mark> KSY	CNETGMFEFTSMFYRDGFVSNFAMEIPSFGVAGVNESADMAIGMTIIKNNMIN	535
tr A3DR07 A3DR07_INBBK	MSKKKSY	CNETGMFEFTSMFYRDGFVSNFAMELPSFGVAGVNESADMAIGMTIIKNNMIN	535
sp P13871 RDRP_INBAC	MSREESY	CNETGMFEFTSMFYRDGFVSNFAMELPSFGVAGVNESADMAIGMTIIKNNMIN	535
sp P13872 RDRP_INBAD	MSKKRSY	CNETGMFEFTSMFYRDGFVSNFAMELPSFGVAGVNESADMAIGMTIIKNNMIN	535
cm/D02421/DDDD_72431	MSKKKSY	IN <mark>RT</mark> STFEFTSFFYR <mark>YG</mark> FVANFSMELPSFGVSGINESADMSIGVTVIKNNMIN	536]
sp P03431 RDRP_I34A1 sp Q9Q0V0 RDRP_I96A0		INRTSTCEPTSFFFFFGVSAR SALLPSFGVSGINESALMSTGVFVFRAMMIN	536
sp[Q30NP3]RDRP_175A0		INRTSTCEPTSFYRYGEVANPSMELPSPOVSGINESADMSTGVTVINNMAD	536
sp[P16511]RDRP_157A5		INRTSTFEFTSFFTNGFVANFSMELPSFGVSGINESADMSIGVTVIKNNMIN	536
50/20A2F7/RDRP_183A4		INRTSTFEFTSFFTNGFVANFSMELPSFGVSGINESADMSIGVTVIKNNMIN	536 A
sp[P16503]RDRP_177AF			536 mRNA
sp[P16503]RDRP_177AF sp[P16513]RDRP_180A8		IN RTSTFEFTSFFYRYGFVANFSMELPSFGVSGINESADMSIGVTVIKNNMIN IN RTSTFEFTSFFYRYGFVANFSMELPSPGVSGINESADMSIGVTVIKNNMIN	536 mRNA
sp[008115]RDRP_180A6		INRTSTFEFTSFFTRYGFVANFSMELPSFGVSGINESADMSIGVTVI INNMIN	536
5p[Q0A3Q1]RDRP_178AC		INRTSTFEFTSFFINGEVANESMELPSPGVSGINESADMSTGVTVIKNNMIN	536
sp[00A451]RDRP_166A1		IN RTSTFEFTSFFTRIGFVANFSMELPSF0V3GINESADMSIGVTVINNMIN	536
shi Koura i krute Toour	** ***	****:*: **:*:*:*:*:*:*:*:*:*:*:	100

sp P19703 RDRP INCJJ	NSLSPSTALMALRICLQEFRAT <mark>Y</mark> RVHPWDSKVKGGRMKIINEFIKTIESKDGLLIADGGK	597
sp Q9IMP4 RDRP_INCJH	NSLSPSTALMALRICLQEFRATYRVHPWDSRVKGGRMKIINEFIKTIENKDGLLIADGGK	597
tr A0A193PPL8 A0A193PPL8 9ORTO	NSLSPSTALMALRICLQEFRATYRVHPWDSRVKGGRMKIINEFIKTIENKDGLLIADGGK	597
tr A0A193PPM8 A0A193PPM8 90RT0	NSLSPSTALMALRICLQEFRATYRVHPWDSRVKGGRMKIINEFIKTIENKDGLLIADGGK	597
tr A0A193PPP6 A0A193PPP6 90RT0	NSLSPSTALMALRICLQEFRATYRVHPWDSRVKGGRMKIINEFIKTIENKDGLLIADGGK	597
sp Q617C3 RDRP INCAA	NSLSPSTALMALRICLQEFRATYRVHPWDSRVKGGRMKIINEFIKTIENKDGLLIADGGK	597
tr A0A193PQ43 A0A193PQ43 INCKS	NSLSPSTALMALRICLQEFRATYRVHPWDSRVKGGRMKIINEFIKTIENKDGLLIADGGK	597
tr A0A193PPP8 A0A193PPP8 INCM3	NSLSPSTALMALRICLQEFRATYRVHPWDSRVKGGRMKIINEFIKTIENKDGLLIADGGK	597
tr A0A193PQ33 A0A193PQ33 INCY6	NSLSPSTALMALRICLQEFRATYRVHPWDSRVKGGRMKIINEFIKTIENKDGLLIADGGK	597
tr A0A193PPP0 A0A193PPP0 9ORTO	NSLSPSTALMALRICLQEFRATYRVHPWDSRVKGGRMKIINEFIKTIENKDGLLIADGGK	597
sp P07832 RDRP INBLE	NGMGPATAQTAIQLFIADYRYTYKCHRGDSKVEGKRMKIIKELWENTKGRDGLLVADGGP	595
tr A0A0D6A5W0 A0A0D6A5W0 9INFB	NGMGPATAQTAIQLFIADYRYTYKCHRGDSKVEGKRMKIIKELWENTKGRDGLLVADGGP	595
tr A0A059TB43 A0A059TB43 9INFB	NGMGPATAQTAIQLFIADYRYTYKCHRGDSKVEGKRMKIIKELWENTKGRDGLLVADGGP	595
r A0A075CCJ9 A0A075CCJ9 9INFB	NGMGPATAQTAIQLFIADYRYTYKCHRGDSKVEGKRMKIIKELWENTKGRDGLLVADGGP	595
tr A0A024CND8 A0A024CND8 9INFB	NGMGPATAQTAIQLFIADYRYTYKCHRGDSKVEGKRMKIIKELWENTKGRDGLLVADGGP	595
tr A0A0N7GD33 A0A0N7GD33 9INFB	NGMGPATAQTAIQLFIADYRYTYKCHRGDSKVEGKRMKIIKELWENTKGRDGLLVADGGP	595
sp 036430 RDRP INBP9	NGMGPATAQTAIQLFIADYRYTYKCHRGDSKVEGKRMKIIKELWENTKGRDGLLVADGGP	595
r A3DR07 A3DR07 INBBK	NGMGPATAQTAIQLFIADYRYTYKCHRGDSKVEGKRMKIIKELWENTKGRDGLLVADGGP	595
sp P13871 RDRP INBAC	NGMGPATAQTAIQLFIADYRYTYKCHRGDSKVEGKRMKIIKELWENTKGRDGLLVADGGP	595
sp P13872 RDRP_INBAD	NGMGPATAQTAIQLFIADYRYTYKCHRGDSKVEGKRMKIIKELWENTKGRDGLLVADGGP	595
sp P03431 RDRP_I34A1	NDLGPATAQMALQLFIKDYRYTYRCHRGDTQIQTRRSFEIKKLWEQTRSKAGLLVSDGGP	596
5p Q9Q0V0 RDRP 196A0	NDLGPATAQMALQLFIKDYRYPYRCHRGDTQIQTRRSFELKKLWEQTRSKAGLLVSDGGP	596
sp Q30NP3 RDRP I75A0	NDLGPATAQMALQLFIKDYRYTYRCHRGDTQIQTRRSFELKKLWEQTRSKAGLLVSDGGP	596
sp P16511 RDRP_I57A5	NDLGPATAQMALQLFIKDYRYTYRCHRGDTQIQTRRSFELKKLWEQTRSKAGLLVSDGGP	596
sp Q0A2F7 RDRP_183A4	NDLGPATAQMALQLFIKDYRYTYRCHRGDTQIQTRRSFELKKLWEQTRSKAGLLVSDGGP	596
sp P16503 RDRP_177AF	NDLGPATAQMALQLFIKDYRYTYRCHRGDTQIQTRRSFELKKLWEQTRSKAGLLVSDGGP	596
sp P16513 RDRP_I80A8	NDLGPATAQMALQLFIKDYRYTYRCHRGDTQIQTRRSFELKKLWEQTRSKAGLLVSDGGP	596
sp Q08II5 RDRP_I80A6	NDLGPATAQMALQLFIKDYRYTYRCHRGDTQIQTRRSFELKKLWEQTRSKAGLLVSDGGP	596
sp Q0A3Q1 RDRP_I78AC	NDLGPATAQMALQLFIKDYRYTYRCHRGDTQIQTRRSFELKKLWEQTRSKAGLLVSDGGP	596
sp Q0A451 RDRP_166A1	NDLGPATAQMALQLFIKDYRYTYRCHRGDTQIQTRRSFELKKLWEQTRSKAGLLVSDGGP **:** *::::::::* *: * *:::: * ::::: * :::::	596

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		(F)
P19703 RDRP_INCJJ	LMNNISTLHIPEEVLKFEKMDEQYRNRVFNPKNPFTNFDKTIDIFFAHGFIRVEE	652 652
Q9IMP4 RDRP_INCJH	LMNNISTLHIPEEVLKFEKMDEQYRNRVFNPKNPFTNFDKTIDIFRAHGPIRVEE	
AOA193PPL8 AOA193PPL8 9ORTO	LMNNISTLHIPEEVLKFEKMDEQYRNRVFNPKNPFTNFDKTIDIFFAHGFIRVEE	652 652
AOA193PPM8 AOA193PPM8 9ORTO	LMNNISTLHIPEEVLKFEKMDEQYRNRVFNPKNPFTNFDKTIDIFFAHGFIRVEE	I
A0A193PPP6 A0A193PPP6_9ORTO	LMNNISTLHVPEEVLKFEKMDEQYRNRVFNPKNPFTNFDKTIDIFFAHGFIRVEE	652
Q617C3 RDRP_INCAA	LMNNISTLHIPEEVLKFEKMDEQYRNRVFNPKNPFTNFDKTIDIFFAHGFIRVEE	652
A0A193PQ43 A0A193PQ43_INCKS	LMNNISTLHIPEEVLKFEKMDEQYRNRVFNPKNPFTNFDKTIDIFFAHGFIRVEE	652
A0A193PPP8 A0A193PPP8_INCM3	LMNNISTLHIPEEVLKFEKMDEQYRNRVFNPKNPFTNFDKTIDIFFAHGFIRVEE	652
A0A193PQ33 A0A193PQ33 INCY6	LMNNISTLHIPEEVLKFEKMDEQYRNRVFNPKNPFTNFDKTIDIFFAHGFIRVEE	652
A0A193PPP0 A0A193PPP0_9ORTO	LMNNISTLHIPEEVLKFEKMDEQYRNRVFNPKNPFTNFDKTIDIFFAHGFIRVEE	652
P07832 RDRP INBLE	NLYNLRNLHI PEIILKYNIMD PEYKGRLLHP ON PFVGHLSIEGIKEADIT HAHG FIKKMD	655
AOAOD6A5W0 AOAOD6A5W0 9INFB	NIYNLRNLHIPEIVLKYNLMDPEYKGRLLHPONPFVGHLSIEGIKEADITHAHGPVRKMD	655
A0A059TB43 A0A059TB43 9INFB	NIYNLRNLHI PE IVLKYNLMD PEYKGRLLHP ON PFVGHLS IE GIKEADI THAHG FVKKMD	655
A0A075CCJ9 A0A075CCJ9 9INFB	NIYNLRNLHIPEIVLKYNLMDPEYKGRLLHPONPFVGHLSIEGIKEADITHAHGPVKKMD	655
A0A024CND8 A0A024CND8 9INFB	NIYNLRNLHIPEIVLKYNLMDPEYKGRLLHPONPFVGHLSIEGIKEADITHAHGPVKKMD	655 L
A0A0N7GD33 A0A0N7GD33 9INFB	NIYNLRNLHIPEIVLKYNLMDPEYKGRLLHPONPFVGHLSIEGIKEADITHAHGPVKKMD	655
036430 RDRP INBP9	NIYNLRNLHIPEIVLKYNLMDPEYKGRLLHPONPFVGHLSIEGIKEADITHAHGPVKKMD	655
A3DR07 A3DR07 INBBK	NIYNLRNLHIPEIVLKYNLMDPEYKGRLLHPONPFVGHLSIEGIKEADITHAHGPVKKMD	655
P13871 RDRP INBAC	NIYNLRNLHIPEIVLKYNLMDPEYKGRLLHPONPFVGHLSIEGIKEADITHAHGFVKKMD	655
P13872 RDRP_INBAD	NIYNLRNLHIPEIVLKYNLMDPEYKGRLLHPQNPFVGHLSIEGIKEADITHAHGHIKKMD	655
P03431 RDRP I34A1	NLYNIRNLHIPEVCLKWELMDEDYOGRLCNPLNPFVSHKEIESMNNAVMMHAHGFAKNME	656
Q9Q0V0 RDRP 196A0	NPYNIRNLHIPEAGLKWELMDEDY OGRLCNPLNPFVSHKEIE SVNNAVVMHAHG FAKSME	656
Q30NP3 RDRP 175A0	NLYNIRNLHIPEVCLKWELMDEDYQGRLCNPLNPFVSHKEIESVNNAVVMHAHGHAKSME	656
P16511 RDRP 157A5	NLYNIRNLHIPEVCLKWELMDEDYOGRLCNPLNPFVSHKEIESVNNAVVMHAHGFAKSME	656
00A2F7 RDRP 183A4	NLYNI RNLHI PEVCLKWELMDEDY OGRLCNPLN PFVSHKE IE SVNNA VVMBAHG FARSME	656
P16503 RDRP 177AF	NLYNI RNLHI PEVCLKWELMDEDY OGRLCNPLN PFVSHKE IE SVNNAVVMAHG FAKSME	656
P16513 RDRP 180A8	NLYNI RNLHI PEVCLKWELMDEDY OGRLCNPLN PFVSHKE IE SVNNA VYMRAHG FASME	656
008115 RDRP 180A6	NLYNIRNLHI PEVCLKWELMDEDY OGRLCNPLN PFVSHKE IE SVNNAVVMEAHGFAKME	656
Q0A3Q1 RDRP 178AC	NLYNIRNLHI PEVCLKWELMDEDY OGRLCNPLNPFVSHKE IE SVNNAVVMEAHGFAKSME	656
Q0A451 RDRP 166A1	NLYNIRNLHI PEVCLKWELMDEDY OGRLCNPLNPFVSHKE IE SVNNAVVMEAHGFAISME NLYNIRNLHI PEVCLKWELMDEDY OGRLCNPLNPFVSHKE IE SVNNAVVMEAHGFAISME	656
TYONG THE TOTAL	*: .**:** **:: ** :*: :* **** : *****	0.00

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sp P19703 RDRP_INCJJ	NEAVVSTHSFRTRANRTLLNTDMRAMMAEEKRYQMVCDIFKSVFESADINPPIGAMSIGE	712
sp Q9IMP4 RDRP_INCJH	NEAVVSTHSFRTRANRTLLNTDMRAMMAEEKRYQMVCDMFKSVFESADINPPIGAMSIGE	712
tr A0A193PPL8 A0A193PPL8_90RT0	NEAVVSTHSFRTRANRTLLNTDMRAMMAEEKRYQMVCDMFKSVFESADINPPIGAMSIGE	712
tr A0A193PPM8 A0A193PPM8_90RT0	NEAVVSTHSFRTRANRTLLNTDMRAMMAEEKRYQMVCDMFKSVFESADINPPIGAMSIGE	712
tr A0A193PPP6 A0A193PPP6_9ORTO	NEAVVSTHSFRTRANRTLLNTDMRAMMAEEKRYQMVCDMFKSVFESADINPPIGAMSIGE	712 <u>C</u>
sp Q617C3 RDRP_INCAA	NEAVVSTHSFRTRANRTLLNTDMRAMMAEEKRYQMVCDMFKSVFESADINPPIGAMSIGE	712
r A0A193PQ43 A0A193PQ43_INCKS	NEAVVSTHSFRTRANRTLLNTDMRAMMAEEKRYQMVCDMFKSVFESADINPPIGAMSIGE	712
r A0A193PPP8 A0A193PPP8_INCM3	NEAVVSTHSFRTRANRTLLNTDMRAMMAEEKRYQMVCDMFKSVFESADINPPIGAMSIGE	712
r A0A193PQ33 A0A193PQ33_INCY6	NEAVVSTHSFRTRANRTLLNTDMRAMMAEEKRYQMVCDMFKSVFESADINPPIGAMSIGE	712
r A0A193PPP0 A0A193PPP0_9ORTO	NEAVVSTHSFRTRANRTLLNTDMRAMMAEEKRYQMVCDMFKSVFESADINPPIGAMSIGE	712
p P07832 RDRP INBLE	YDAVSGTHSWRTKENRSIINTDORNMILEEC <mark>ZYAK CO</mark> NLFEACENSASYRKPVGCHEMLE	715
r A0A0D6A5W0 A0A0D6A5W0 9INFB	YDAVSGTHSWRTKENRSII <mark>NT D</mark> ORNMILEE OCYAKCCNLFEACENSASYRKPVGOHEMLE	715
r A0A059TB43 A0A059TB43 9INFB	YDAVSGTHSWRTKE <mark>N</mark> RSII <mark>NT</mark> DORNMILEEO <mark>CYAKCC</mark> NLFEACFNSASYRKPVGOHSMLE	715
r A0A075CCJ9 A0A075CCJ9_9INFB	ydavsgthswrtk <mark>en</mark> rsii <mark>nt</mark> ogrnmileeg <mark>ckak</mark> cculfeacfnsasyrkpugg <mark>h</mark> emle	715
r A0A024CND8 A0A024CND8_9INFB	YDAVSGTHSWRTKE <mark>N</mark> RSII <mark>NT</mark> DORNMILEEO <mark>CKAKCC</mark> NLFEA <mark>C</mark> FNSASYRKPVGO <mark>H</mark> FMLE	715 🕒
r A0A0N7GD33 A0A0N7GD33_9INFB	YDAVSGTHSWRTKE <mark>N</mark> RSII <mark>NT</mark> DORNMILEEO <mark>CYAKCC</mark> NLFEA <mark>C</mark> FNSASYRKPVGO <mark>H</mark> FMLE	715 mRNA
p 036430 RDRP_INBP9	YDAVSGTHSWRTKE <mark>N</mark> RSII <mark>NT</mark> DORNMILEEO <mark>CYAKCC</mark> NLFEA <mark>C</mark> FNSASYRKPVGO <mark>H</mark> FMLE	715
r A3DR07 A3DR07_INBBK	YDAVSGTHSWRTKE <mark>NR</mark> SII <mark>NTD</mark> QRNMILEEQ <mark>CYA</mark> KCCNLFEA <mark>C</mark> FNSASYRKPVGC <mark>H</mark> FMLE	715
p P13871 RDRP_INBAC	YDAVSGTHSWRTKE <mark>N</mark> RSII <mark>NT</mark> DORNMILEEO <mark>CKAKCC</mark> NLFEA <mark>CF</mark> NSASYRKPVGO <mark>H</mark> BMLE	715
p P13872 RDRP_INBAD	Y DAVSGTHSWRTKE <mark>N</mark> RSII <mark>NT</mark> DQRNMILEEQ <mark>CKA</mark> K <mark>CC</mark> NLFEA <mark>C</mark> FNSASYRKPVGC <mark>H</mark> EMLE	715
p P03431 RDRP I34A1	YDAVATTHSWIPKRNRSILNTSQRGVI <mark>EDE</mark> QMYQRCCNLFEKFFPSSSYRRPVGISSMVE	716
p Q9Q0V0 RDRP 196A0	Y DA VATTHSWI PKRNRSILNT SORGII <mark>E DE</mark> OMYOKCCNLFEK FFPSSSYRRPVGISSMVE	716
p Q30NP3 RDRP I75A0	YDAVATTHSWIPKRNRSILNTSQRGII <mark>EDE</mark> OMYQKCCNLFEKFFPSSSYRRPVGISSMVE	716
p P16511 RDRP_I57A5	YDAVATTHSWIPKRNRSILNTSORGII <mark>EDE</mark> OMYOKCCNLFEKFFPSSSYRRPVGISSMVE	716
p Q0A2F7 RDRP_I83A4	Y DA VATTHSWT PKRNRS ILNT SORG II <mark>E DE</mark> OM YOKCCNLFEK FFPS SS YR PVG I SSMVE	716 🗛
p P16503 RDRP_I77AF	YDAVATTHSWIPKRNRSILNTSQRGII <mark>EDE</mark> OMYQKCCNLFEKFFPSSSYRRPVGISSMVE	716
p P16513 RDRP_180A8	YDAVATTHSWIPKRNRSILNTSQRGII <mark>EDE</mark> OMYQKCCNLFEKFFPSSSYRRPVGISSMVE	716
p Q08115 RDRP 180A6	YDAVATTHSWIPKRNRSILNTSQRGII <mark>EDE</mark> OMYQKCCNLFEKFFPSSSYRRPVGISSMVE	716
p Q0A3Q1 RDRP_I78AC	YDAVATTHSWIPKRNRSILNTSQRGII <mark>EDE</mark> QMYQKCCNLFEKFFPSSSYRRPVGISSMVE	716
p Q0A451 RDRP 166A1	YDAVATTHSWIPKRNRSILNTSQRGII <mark>EDE</mark> OMYQKCCNLFEKFFPSSSYRRPVGISSMVE	716
	:** ***: : **::***. * : <mark>: :*</mark> : * *::*: * *: *:* *: *	

p P19703 RDRP INCJJ	s of the all three human influenza viruses A, B & C	754
p Q9IMP4 RDRP INCJH	AIEEKLLERAKMKRDIGAIEDSEYEEIKDIIRDAKKARLESR	754
r A0A193PPL8 A0A193PPL8 9ORTO	AIEEKLLERAKMKRDIGAIEDSEYEEIKDIIRDAKKARIESR	754
r A0A193PPM8 A0A193PPM8 9ORTO	AIEEKLLERAKMKRDIGAIEDSEYEEIKDIIRDAKKARIESR	754
r A0A193PPP6 A0A193PPP6 90RT0	AIEEKLLERAKMKRDIGAIEDSEYEEIKDIIRDAKKARIESR	754 LC
p Q617C3 RDRP INCAA	AIEEKLLERAKMKRDIGAIEDSEYEEIKDIIRDAKKARIESR	754
r A0A193PQ43 A0A193PQ43 INCKS	AIEEKLLERAKMKRDIGAIEDSEYEEIKDIIRDAKKARIESR	754
r A0A193PPP8 A0A193PPP8 INCM3	AIEEKLLERAKMKRDIGAIEDSEYEEIKDIIRDAKKARIESR	754
r A0A193PQ33 A0A193PQ33 INCY6	AIEEKLLERAKMKRDIGAIEDSEYEEIKDIIRDAKKARIESR	754
r A0A193PPP0 A0A193PPP0 90RT0	AIEEKLLERAKMKRDIGAIEDSEYEEIKDIIRDAKKARIESR	754
-		
p P07832 RDRP_INBLE	AMAHRLRMDARLDYESGRMSKEDFEKAMAHLGEIGYM	752
r A0A0D6A5W0 A0A0D6A5W0_9INFB	AMAHRLRMDARLDYESGRMSKDDFEKAMAHLGEIGYT	752
r A0A059TB43 A0A059TB43_9INFB	AMAHRLRMDARLDYESGRMSKDDFEKAMAHLGEIGYT	752
r A0A075CCJ9 A0A075CCJ9_9INFB	AMAHRLKMDARLDYESGRMSKDDFEKAMAHLGEIGYI	752
r A0A024CND8 A0A024CND8_9INFB	AMAHRLRMDARLDYESGRMSKDDFEKAMAHLGEIGYI	752 🕒
r A0A0N7GD33 A0A0N7GD33 9INFB	AMAHRLRMDARLDYESGRMSKDDFEKAMAHLGEIGYI	752
p 036430 RDRP_INBP9	AMAHRLRMDARLDYESGRMSKDDFEKAMAHLGEIGYI	752
r A3DR07 A3DR07_INBBK	AMAHRLRMDARLDYESGRMSKDDFEKAMAHLGEIGYI	752
p P13871 RDRP_INBAC	AMAHRLRMDARLDYESGRMSKDDFEKAMAHLGEIGYI	752
p P13872 RDRP_INBAD	AMAHRLRMDARLDYESGRMSKDDFEKAMAHLGEIGHI	752
p P03431 RDRP_I34A1	AMVSRARIDARIDFESGRIKKEEFTEIMKICSTIEELRRQK-	757
p Q9Q0V0 RDRP_196A0	AMVSRARIDARIDFESGRIKKEEFAEIMKICSTIEELGRQK-	757
p Q30NP3 RDRP_175A0	AMVSRARIDARIDFESGRIKKEEFSEIMKICSTIEELRRQK-	757
p P16511 RDRP_157A5	AMVSRARIDARIDFESGRIKKEEFAEIMKICSTIEELRRQK-	757
p Q0A2F7 RDRP 183A4	AMVSRARIDARIDFESGRVKKEEFAEIMKICSTIEELRRQK-	757 🔔
p P16503 RDRP_177AF	AMVSRARIDARIDFESGRIKKEEFAEIMKICSTIEELRRQK-	757
p P16513 RDRP_180A8	AMVSRARIDARIDFESGRIKKEEFAEIMKICSTIEELRRQK-	757
p Q08115 RDRP_180A6	AMVSRARIDARIDFESGRIKKEEFAEIMKICSTIEELRRQK-	757
p Q0A3Q1 RDRP_I78AC	AMVSRARIDARIDFESGRIKKEEFAEIMKICSTIEELRRQK-	757
p Q0A451 RDRP_I66A1	AMVSRARIDARIDFESGRIKKEEFAEIMKICSTIEELRROK-	757

Human Influenza C Viral Strains P19703|RDRP_INCJJ (strain C/JJ/1950) O9IMP4|RDRP_INCJH (strain C/ Johannesburg/1/1966) A0A193PPL8_9ORTO (strain C/ Paris/1/67) A0A193PPM8_9ORTO (strain C/ Kyoto/1/1979) A0A193PPP6_9ORTO (strain C/ Miyagi/8/1996) Q6I7C3|RDRP_INCAA (strain C/ Ann Arbor/1/1950) A0A193PQ43_INCKS (strain C/ Kansas/1/1979) A0A193PPP8_INCM3 (strain C/ Miyagi/5/1991) A193PQ33_INCY6 (strain C/ Yamagata/1964) A0A193PPP0 9ORTO (strain C/ Yamagata/4/92) Human Influenza B Viral Strains P07832|RDRP_INBLE, (strain B/ Lee/1940) A0A0D6A5W0 9INFB (strain B/ Gunma/13G022/2014) A0A059TB43_9INFB (strain B/ Thailand/VIROAF3/2012) A0A075CCJ9_9INFB (strain B/ Santa Cruz/761/2012) A0A024CND8 9INFB (strain B/ Nicaragua/AGB2-12/2012 A0A0N7GD33_9INFB, (strain B/ Hawaii/11/2015) O36430|RDRP_INBP9 (strain B/ Panama/45/1990) A3DR07 INBBK, (strain B/ Bangkok/163/1990) P13871 RDRP INBAC, (strain B/ Ann Arbor/1/1966 [cold-adapted]) P13872 RDRP_INBAD, (strain B/ Ann Arbor/1/1966 [wild-type]) Human Influenza A Viral Subtypes P03431|RDRP_I34A1 (strain A/ Puerto Rico/8/1934/ H1N1) Q9Q0V0|RDRP_I96A0 (strain A/ Goose/Guangdong/1/1996/H5N1) Q30NP3|RDRP_I75A0 (strain A/ Beijing/39/1975/ H3N2) P16511|RDRP_I57A5 (strain A/ Singapore/1/1957/H2N2) Q0A2F7|RDRP I83A4 (strain A/ Turkey/ Ireland/ 1378/ 1983/ H5N8) P16503|RDRP_I77AF (strain A/ Gull/Maryland/704/1977/ H13N6) P16513|RDRP_I80A8 (strain A/ Turkey/ Minnesota/ 833/1980/ H4N2) Q08II5|RDRP_I80A6 (strain A/ Duck/Hokkaido/8/1980/ H3N8) Q0A3Q1|RDRP_I78AC (strain A/ Turkey/ Minnesota/ 501/1978/ H6N8 Q0A451|RDRP_I66A1 (strain A/ Turkey/Wisconsin/1/1966/H9N2)

Figure 7 Mix and Match MSA of the PB1 subunits of the RNA polymerases of all the three human influenza viruses

3.2. Active site Analyses of the Catalytic Subunit PB1 of Human Influenza Polymerases

3.2.1. Analyses of Metal-Binding Sites in RdRps of RNA Viral Human Pathogens

Human RNA pathogens mostly possess either (+) strand or (-) strand RNA genomes. The (+) RNA strand viruses, including the pandemic causing SARS-CoVs, are known to use two invariant Ds, one from the –A/SDD- and the other from the –GDD- motifs for catalytic metal-binding and are confirmed by SDM experiments and X-ray crystallographic techniques. For example, Sankar and Porter [13] have shown that the point mutations generated by SDM experiments in the metal-binding motif -G $D^{332}D$ - drastically affected the polymerization activity of RdRp of encephalomyocarditis virus, a small non-enveloped, (+) strand RNA virus (the causative agent of not only myocarditis and encephalitis, but also neurological diseases, reproductive disorders and diabetes in many mammalian species). Their results showed that all three amino acids of the –GDD- motif are important in maintaining the structure and function of the catalytic metal (Mg²⁺)-binding (the G in the –GDD- motif is known to generate tight bends in the structure) (Table 1).

Similar experiments have also shown that a slightly different –GDN- catalytic metal-binding motif is essential for catalysis in the (-) strand RNA viral pathogens. The (-) strand human RNA viral pathogens such as influenza, measles, mumps and respiratory syncytial viruses and Ebola virus (EBOV) also use Mg^{2+} as a co-factor for RdRp reaction. By MSA analysis, SDM experiments and minigenome assays [14] Schmidt and Hoenen, [14] have shown that -GDN- is the invariant motif in all the (-) strand RNA viral RdRps like Ebola, influenza, rabies, measles and mumps (Table 1). Furthermore, by SDM experiments, Schmidt and Hoenen [14] have confirmed that the triple mutation, $-^{741}$ GDNQ- $\rightarrow -^{741}$ GAAA- in Ebola viral RdRp abolished both the replication as well as transcription activities. In addition to the above findings, present MSA analysis has shown that all the (-) strand RNA viral pathogens possess the invariant –GDN- in their RdRps, indicating that this motif is absolutely essential for genome replication, transcription, or both. Tchesnokov et al. [15] found that the $D^{742} \rightarrow A$ mutant in the $-GD^{742}N$ - motif of Ebola viral RdRp lacked the ability to extend the primer in the presence of Mg^{2+} and hence, the Ebola viral RdRp mutant $D^{742} \rightarrow A$ abolished the catalytic Mg^{2+} -binding activity which resulted in the absence of polymerase activity. Similar observations were made by Schnell and Conzelmann [16] on another human pathogenic (-) strand RNA virus, viz. the rabies virus. They found by SDM experiments that any modification of the $-^{728}$ GDN- motif by conservative and non-conservative amino acids resulted in complete loss of the

RNA polymerase activity. In addition to this motif, the (-) strand RNA viral pathogens also possess a regular -G/SDDmotif as found in (+) strand RNA viral RdRps (Table 1) which provides the second D for the catalytic Mg²⁺-binding.

Metal-Binding Sites in Human Influenza Viruses

Human influenza viruses, as typical (-) strand RNA viruses, possess both the invariant catalytic Mg²⁺-binding –GDN- and -SDD- motifs in their RdRps (Table 1). These two metal-binding motifs were extensively analyzed by Biswas and Navak [17] in human influenza A virus. They found that the -DD- in the $-^{444}SDD$ - motif was absolutely critical for influenza A viral polymerase activity. When either of these –DD- residues were mutated, $D^{445} \rightarrow H/E$, or $D^{446} \rightarrow Y/N/E$, the mutated PB1 polymerase subunit became nonfunctional. Furthermore, the polymerase containing an active-site mutation D445→A/D446→A (also known as PB1a) of the -444SDD- motif in influenza A virus has been used as a polymerasenegative strain in experiments [18]. When the -S⁴⁴⁴ of the above -⁴⁴⁴SDD- motif was mutated to G, modifying the sequence to -444GDD- as is found in (+) strand RNA viral RdRps, the polymerase activity was drastically reduced (1.9%), suggesting that the influenza A viral PB1 polymerase subunit cannot accommodate G in this position (Table 1). The second invariant metal-binding motif is the –GDN- motif in all (–) strand RNA viruses. When the - D^{305} in the – GD^{305} Nmotif was mutated to a conservative amino acid 0, it showed only feeble polymerase activity, suggesting its involvement in the metal-binding. These findings were further corroborated by the SDM analysis of the -GDN- motif of Ebola virus RdRp, again a (-) strand RNA virus like influenza viruses as discussed elsewhere. Further insights were provided by the X-ray crystallographic analysis of the influenza A viral polymerase PB1 subunit by Pflug et al. [6]. They found that the conserved active site -D³⁰⁵ of -GD³⁰⁵N- motif, together with -D⁴⁴⁵ and -D⁴⁴⁶ of the -⁴⁴⁴SDD- motif coordinate binding to metal ions and promote catalysis [6, 15]. Thus, it is clear from the above SDM experiments, X-ray crystallographic and MSA analyses that the invariant -GDN- and -SDD- are the signature metal-binding motifs in all three human influenza viral RdRps (Table 1) [19].

3.2.2. Analyses of the Catalytic Core Regions of the Polymerase Subunit PB1

In addition to the two invariant catalytic Mg²⁺-binding motifs, viz. –GDN- and -SDD-, (Fig. 7 and Table 1), all the three influenza viruses also possess two highly conserved catalytic cores. The catalytic cores consist essentially three components, viz. a template–binding pair and a catalytic amino acid for initiating catalysis by proton abstraction from 3'-OH and usually a basic amino acid at -4 to -5 position from the catalytic amino acid which has been proposed in nucleotide selection. Interestingly, two different catalytic cores are identified in human influenza viruses, suggesting one for the viral gRNA and the other for mRNA syntheses. An invariant -VG- pair is identified as the template–binding pair for the replication in all three human influenza viruses. However, the catalytic pair for the replication is found to be a –KL- in influenza A and C viruses and an -NL- for the influenza B virus. The nucleotide selection amino acid at -5 position is R/K/Q, respectively. It is interesting to note that the replication catalytic core of human influenza viruses are very similar to the other viral, prokaryotic and eukaryotic replicase enzymes (Table 2). The additional catalytic core identified in the PB1 subunits comprises of an –YG/A pair for the template-binding, a RT/NT/KL catalytic pair for initiating the catalysis and the nucleotide selection amino acid at -5 position is found to be K/N/N, respectively. The second catalytic core is similar to mRNA synthesis (Table 2), and hence could be involved in transcription.

The next conserved motif is a –KK- dyad (K⁴⁸⁰ and K⁴⁸¹), at the end of the palm domain in influenza A and B viruses. These two residues are found in the NTP entry site and are suggested to be involved in NTP binding [6]. This putative NTP tunnel directly leads to the tip of the putative priming loop which is composed of highly conserved basic residues R⁴⁵, K²³⁵, K²³⁷ and R²³⁹ (the last three amino acids form the finger-tip subdomain), -K³⁰⁸ (of the –GDNTK³⁰⁸-motif), and K⁴⁸⁰ and K⁴⁸¹ (of the palm domain) [6]. The catalytic core encompasses the polymerase active site, which is connected to the exterior by several channels, including channels for the template entry and NTPs as well as for the exit of the template and product. Near the active site, the priming loop is a feature that is essential for primer-independent initiation on the vRNA templates, but that is not required for primer-dependent transcription and, surprisingly, also not for primer-independent initiation on the cRNA templates [20] as also proposed here.

Table 1 Catalytic metal-binding sites in viral RNA-dependent RNA polymerases

Organism	Metal-biding site(s)	Method and Reference
RdRps (EC 2.7.7.48) of (+) Strand RNA Viruses	
SARS-CoV-2	-LSDD ⁷⁶¹ A- & -QGDD ⁸²⁵ Y-	X-ray [21]
SARS-CoV-1	-LSD ⁷⁶⁰ DA- & -QGDD ⁸²⁵ Y-	SDM [22]
MERS-CoV	-LSDD ⁷⁶² A- & -QGDD ⁸²⁶ Y-	By seq. similarity
Polio		X-ray [21]
Hepatitis-C		X-ray [21]
Dengue	-YADD ⁵³³ TA- &-SGDD ⁶⁶⁴ CV-	X-ray [23]
Zika	-YADD ⁵³⁵ TA- &-SGDD ⁶⁶⁶ CV-	By seq. similarity
Yellow Fever	-YADD ²⁸⁴ TA- &-SGDD ⁴¹⁷ CV-	By seq. similarity
Rubella	-LGDD ²⁶ A- & -QGDD ⁶⁶⁷ M-	By seq. similarity
Encephalomyocarditis		SDM [13]
RdRps (EC 2.7.7.48) of (-) Strand RNA Viruses	
Ebola	-MG ⁷⁴¹ DNQC- & -HTSDD ⁶¹⁷ FG-	SDM [14]
Ebola	-MGD ⁷⁴² NQC- & "	SDM [15]
Rabies	-QGD ⁷²⁹ NQV- & -LESDD ¹⁵⁸⁹ NI-	By seq. similarity
Nipah	-QGD ⁸³² NES- & -IDSDD ¹⁵²⁵ NI-	By seq. similarity
Mumps	-QGD ⁷⁷⁹ NQA- & -SSGDD ¹¹⁹⁵ KF-	By seq. similarity
Measles	-QGD ⁷⁷³ NQT- & -AYGDD ¹²⁵⁶ DS- &	By seq. similarity
	-LIGDD ¹⁴⁷⁰ D- & -ESDE	D ¹⁵⁹⁸ V-
RdRps (EC 2.7.7.48) of (-) Strand Segmented RNA Viruses	
Influenza A	-TGD ³⁰⁵ NTK- & -QS <mark>SDD</mark> ⁴⁴⁶ FA-	SDM [17]
Influenza B	-TGD ³⁰⁵ NTK- & -QSSDD ⁴⁴⁵ FA-	By seq. similarity
Influenza C	-TGD ³⁰⁷ NSK- & -QSSDD ⁴⁵¹ FV-	By seq. similarity

Adapted from Palanivelu [11]

Table 2 Catalytic region(s) in the viral, prokaryotic and eukaryotic (nuclear and organellar) polymerases

Polymerase Type	Catalytic Region(s)	
SSU RNA and DNA Polymer	ases	
Viral T7 SSU RNA pol Viral SP6 SSU RNA Pol Mitochondrial SSU RNA pol (\ Chloroplast SSU pol (ARATH) <i>E. coli</i> DNA pol I (SSU)	-	
Initiation Subunits of Proka	ryotic and Eukaryotic MSU DdRps (mRNAs)	
E. <i>coli</i> MSU RNAP β subunit S. <i>cerevisia</i> e MSU RNAP II R Human MSU RNAP II Rpb2 si		
Elongation Subunits of Pro-	aryotic and Eukaryotic MSU DdRps (mRNAs)	
<i>E. coli</i> MSU RNAP β' subunit <i>S. cerevisiae</i> MSU RNAP II R Human MSU RNAP II Rpb1 si	-833NSV ⁻⁶ DAVKV <mark>RS¹</mark> VVSC ⁵ DTDFGVC ¹² AHC ¹⁵ Y ¹⁶ G ¹⁷ RDL ₈₆₁ - pb1 subunit -55DPR ⁻⁶ LGSIDRN ¹ LKC ⁴ QTC ⁷ QEGMNEC ¹⁴ PGHF ¹⁸ G ¹⁹ HI ₈₄ - ubunit -59DPR ⁶ QGVIERT ¹ GRC ⁴ QTC ⁷ AGNMTEC ¹⁴ PGHF ¹⁸ G ¹⁹ HI ₈₈ .	
Active Site Regions in Prok	aryotic and Eukaryotic DNA Polymerases#	
T7 DNA polymerase (Rep) <i>P. furiosus</i> DNA polymerase	- ⁶²² AYGVT R - ⁴ SVT <mark>R</mark> ⁶³¹ R ¹ SVMTLA <mark>R</mark> ⁶³⁹ G ⁹ SKEFG [26] - ₄₇₈ ILLDY <mark>R</mark> - ⁵ QKAI KL¹LANSFY ⁷ GYYGYAK-	
Yeast DNA polymerase α (Re Human DNA polymerase α (R		
Human DNA polymerase δ (R (Catalytic subunit) Human DNA polymerase ε (R		
(Catalytic subunit) Yeast DNA polymerase ε (Re (Catalytic subunit)	b) - ⁸¹⁶ YDSLQ ⁻⁴ LAHKV ¹ ILNSF ²⁸³¹ G ⁸ YVMR- [27]	
Human DNA polymerase γ (R	ep) - ₈₁₇ TTVGISR ⁻⁴ EHAKI ¹ FNYGRIY ⁸ GAGQPFAER-	
(+) Strand RNA Viruses- (SA	RS-Coronaviruses)	
RdRps (NSP12)		
SARS-CoV-1 SARS-CoV-2 MERS-CoV	-STMTNR ^{-\$} QFHQKL ¹ LKSIAATRGATVVIGTSKF <mark>Y²¹G</mark> G ₅₉₇ - -STMTNR ^{-\$} QFHQKL ¹ LKSIAATRGATVVIGTSKF <mark>TT</mark> GG ₅₉₇ - [13] -STMTNR ^{\$} QYHQKM ¹ LKSMAATRGATCVIGTTKFY ²¹ GG ₅₉₈ -	
(-) Strand RNA Viruses- (Hu	man Influenza Viruses)	
PB1 Catalytic Subunits of th	e RdRps	
Human influenza A virus		
Human influenza B virus	- ²⁵⁶ ENLA <mark>K ⁵NICENL¹EQSGLPV⁸GGN- gRNA</mark> - ⁵⁵⁶ RTKR <mark>N -⁵RSILN T'</mark> DQRNMILEEQCY ¹³ AKCCX ₅ CF- mRNA#	
Human influenza C virus	- ²⁵⁸ ETVAQK ⁻⁴ ICEKL ¹ KESGLPV ⁸ GGN- gRNA - ⁴⁶⁴ IRRFN ⁻⁴ AVCKL ¹ IGINMSLEKSY ¹² GSL- mRNA#	
	Adapted from Palanivelu [11.27].	

Adapted from Palanivelu [11,27]. gRNA, genomic RNA; Rep, Replicase. *P. furiosus, Pyrococcus furiosus*; The amino acids confirmed by SDM and by other techniques in the active sites are highlighted in dark blue; *The catalytic region of the human influenza viruses is arrived at by sequence similarity with other DNA/RNA polymerases. In the human influenza viruses, two such possible catalytic regions are found: one similar to RNA polymerases may involve in transcriptions and the other one similar to SSU DNA/RNA polymerases and eukaryotic replicases may involve in viral genome replications.

Table 3 shows the effect of mutations in SDM and natural mutations in the conserved motifs of the PB1 catalytic subunit of the human influenza A virus and their effects on polymerase activity/ replicative ability in human cells.

Metal-binding site	Polymerase activity (%)	Reference
Metal-Binding Site-1	(- ⁴⁴⁴ SDD-)	
⁴⁴⁵ D/ ⁴⁴⁶ D→A	0	[18]
⁴⁴⁴ S→G	1.9	[17]
⁴⁴⁵ D→H/E	0	[17]
⁴⁴⁶ D→Y/N/E	0	[17]
⁴⁴⁴ S→P	0	[10]
⁴⁴⁵ D→G	0	[10]
⁴⁴⁶ D→N	0	[10]
Metal-Binding Site-2	(- ³⁰⁴ GDN-)	
- ³⁰⁵ D→ Q	Feeble	[17]
- ³⁰⁶ N→ T	2.4	[10]
Metal-Binding Site-2	(- ⁷⁴¹ GDNQ-), Ebola virus- a (-) Strand RNA virus
- ⁷⁴¹ GDNQ→ ⁷⁴¹ GAAA	0	[14]
- ⁷⁴² D→A	0	[15]
Polymerase Active S	ite	
⁴⁷⁶ N→L/ ⁴⁷⁷ M→T (DM)	0	[10]
⁴⁷⁶ N→ T / ⁴⁷⁸ S→ T (DM)		[10]
⁴⁷⁸ S→ T/R	0	[10]
⁴⁸⁰ K→ R	117.2	[10]
⁴⁸¹ K→ E/T/N	0	[10]
⁴⁸³ Y→ H	0.5	[10]

Table 3 Effect of mutations by SDM and natural mutations in the conserved motifs of the polymerase subunit PB1

4. Proposed Mechanism of Action of the Polymerase Catalytic Subunit PB1 of Human Influenza Viruses

It is interesting to note that all DNA and RNA polymerases, irrespective of their sources, possess not highly conserved active sites but also very similar 3D structures, suggesting a similar catalytic mechanism [4, 28,29]. The finding that the PB1 subunit alone could transcribe RNA templates *in vitro*, suggested it possessed all the required active sites to synthesize a new strand of RNA from vRNA templates and possesses similar active sites and 3D structure [6, 30, 31].

A minimal number of steps involved in the catalytic cycle of the DNA/RNA polymerases are i) NTP selection and Watson-Crick base pairing with the complementary nucleotide to the template, ii) Addition of the nucleotide to the growing primer, iii) Inorganic pyrophosphate formation and iv) Restoration of the active site and translocation.

The catalysis is initiated by the proton abstraction by the catalytic amino acid from the 3'-OH of the primer, which is followed by an electrophilic-nucleophilic attack between the α -phosphate of the Watson-Crick base-paired NTP at the active site and the 3'-Oxyanion of the growing primer, resulting in the phosphodiester bond formation with the subsequent release of pyrophosphate. The proton abstracted in the first step is transferred to the pyrophosphate resulting in the formation of inorganic pyrophosphate (ppi). The active site is restored and translocated for the next addition.

Based on the data available, Figs. 8 and 9 describe plausible mechanisms of action of the PB1 polymerase subunits of the human influenza viruses.

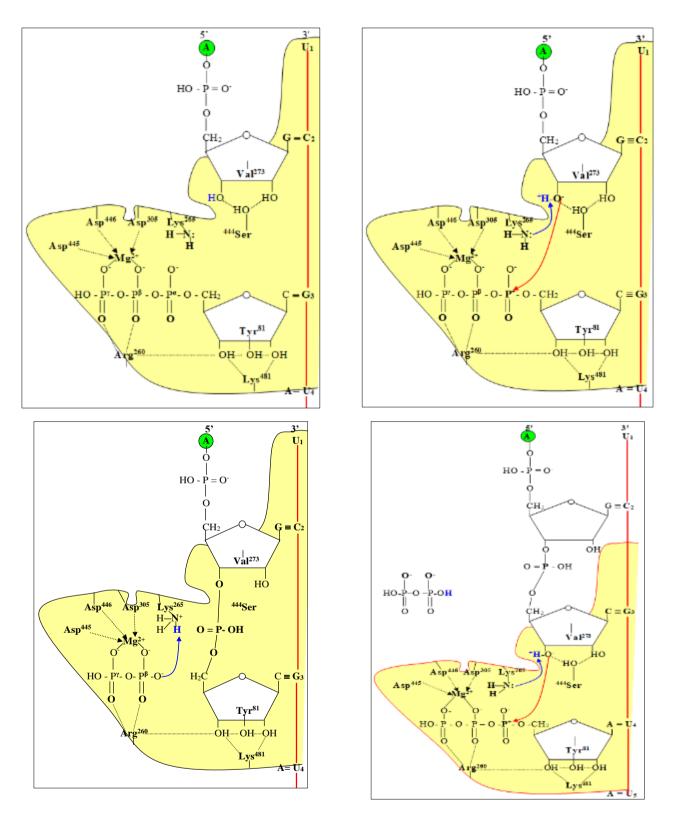


Figure 8 Proposed steps in the replication of viral genomic RNAs

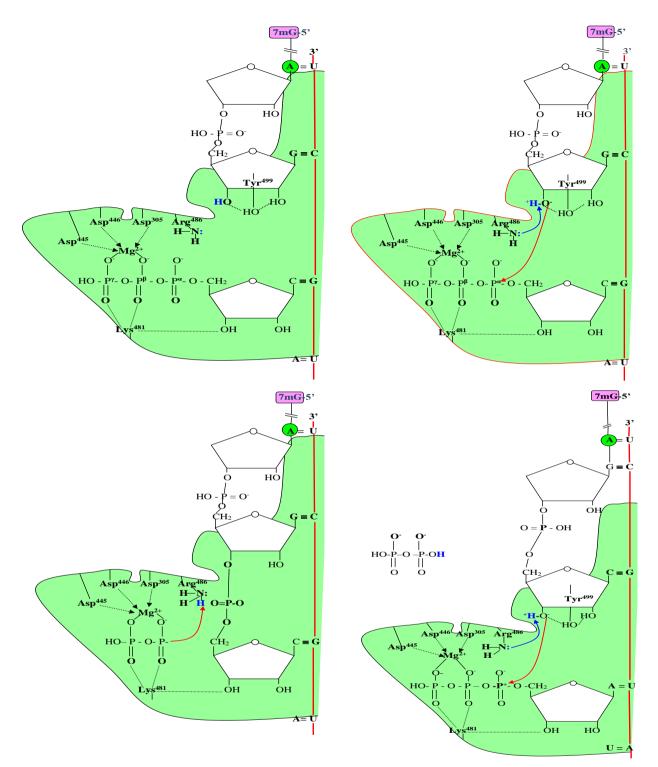


Figure 9 Proposed steps in the transcription of viral mRNAs

• **Step 1.** Enzyme with the Watson-Crick base-paired NTP at the Entry Site: In replication, the initiation step of RNA synthesis begins at the 3'- end of the vRNA template by means of a *primer-independent* mechanism. The primer-independent initiation consists in the addition of a GTP to the 3'-OH of the first initiating ATP and is followed by the next base (Fig. 8). Viral mRNA synthesis is *primer-dependent* and the primer is obtained from the host mRNAs by the cap-snatching method using the PB2 subunit. The primer is base-paired with the U at the 3' end of the viral RNA. The Y residue in the YG template-binding pair is suggested to be involved in base stacking as well as hydrogen bonding to the ribose moiety at the 3'- growing end and the G provides the necessary kink for the effective positioning with the template. The catalytic site amino acid R⁴⁸⁶ is positioned near the 3'- growing end for proton abstraction. The invariant K⁴⁸¹ is shown to be involved in the NTP selection.

(The epsilon group of K⁴⁸¹ could form the necessary hydrogen bonds with the substrate in the ternary complex). The catalytic Mg²⁺ is shown coordinating with the catalytic D⁴⁴⁵ and D⁴⁴⁶, D³⁰⁵ shielding the β - and γ - phosphates of the incoming NTP and exposing the α -phosphate to the electrophilic- nucleophilic attack at the polymerizing site (Figs. 8 and 9).

- **Step 2.** Proton abstraction by the active site amino acid K²⁶⁵ (R⁴⁸⁶ in transcription site) with the simultaneous electrophilic-nucleophilic attack at the polymerase site. Formation of phosphodiester bond between the 3'-Oxyanion and the α-phosphate of the NTP.
- **Step 3.** Proton transfer from the active site amino acid K²⁶⁵ (R⁴⁸⁶ in transcription site) to the pyrophosphate and formation of inorganic pyrophosphate.
- Step 4. Restoration of the active site and translocation of the enzyme to the next nucleotide (Figs. 8 and 9).

5. Conclusions

The human influenza viral RNA polymerase is a heterotrimeric enzyme and made up of three different subunits, viz. two basic protein subunits (PB1 and PB2) and an acidic protein subunit (PA). The PB1 polymerase subunits of the viruses contain the active sites for nucleotide polymerization and perform the synthesis of both the mRNAs and gRNAs. The two typical invariant catalytic metal-binding motifs, viz. –GDN and –SDD- reported in (-) strand RNA viruses are also found in the PB1 polymerase subunits. Furthermore, MSA analysis shows two possible catalytic regions in the polymerase PB1 catalytic subunits from all the three human influenza viruses. The two possible catalytic regions suggest that the polymerase may follow a dual mode, i.e., it could use one for mRNA synthesis (transcription) and the other for viral gRNA synthesis (replication) depending upon its association to the cap-snatching PB2 (for mRNA synthesis, transcription) or its association with the proofreading PA subunit for gRNA synthesis (replication). It could use the same metal-binding motifs for both the mRNA and gRNA syntheses. Thus, all the three human influenza viruses exhibit common and distinct features among them. These data throw more light on the functioning of the key enzyme and may help in designing structure-based antiviral drugs targeting the PB1 subunit's active sites for the treatment of flu in the future.

Compliance with ethical standards

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