Original Research Article

Eukaryotic Multi-subunit DNA dependent RNA Polymerases: an Insight into their Active Sites and Catalytic Mechanism

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Abstract

Aim: To analyze the most complex multi-subunit (MSU) DNA dependent RNA polymerases (RNAPs) of eukaryotic organisms and find out conserved motifs, metal binding sites and catalytic regions and propose a plausible mechanism of action for these complex eukaryotic MSU RNAPs, using yeast (*Saccharomyces cerevisiae*) RNAP II, as a model enzyme.

Study Design: Bioinformatics, Biochemical, Site-directed mutagenesis and X-ray crystallographic data were analyzed.

Place and Duration of Study: School of Biotechnology, Madurai Kamaraj University, Madurai, India, between 2007- 2013.

Methodology: Bioinformatics, Biochemical, Site-directed mutagenesis (SDM) and X-ray crystallographic data of the enzyme were analyzed. The advanced version of Clustal Omega was used for protein sequence analysis of the MSU DNA dependent RNAPs from various eukaryotic sources. Along with the conserved motifs identified by the bioinformatics analysis, the data already available by biochemical and SDM experiments and X-ray crystallographic analysis of these enzymes were used to confirm the possible amino acids involved in the active sites and catalysis.

Results: Multiple sequence alignment (MSA) of RNAPs from different eukaryotic organisms showed a large number of highly conserved motifs among them. Possible catalytic regions in the catalytic subunits of the yeast Rpb2 (= β in eubacteria) and Rpb1 (= β' in eubacteria) consist of an absolutely conserved amino acid R, in contrast to a K that was reported for DNA polymerases and single subunit (SSU) RNAPs. However, the invariant 'gatekeeper/DNA template binding' YG pair that was reported in all SSU RNAPs, prokaryotic MSU RNAPs and DNA polymerases is also highly conserved in eukaryotic Rpb2 initiation subunits, but unusually a KG pair is found in higher eukaryotes including the human RNAPs. Like the eubacterial initiation subunits of MSU RNAPs, the eukaryotic initiation subunits, viz. Rpb2, exhibit very similar active site and catalytic regions but slightly different distance conservations between the template binding YG/KG pair and the catalytic R. In the eukaryotic initiation subunits, the proposed catalytic R is placed at the -9th position from the YG/KG pair and an invariant R is placed at -5 which are implicated to play a role in nucleoside triphosphate (NTP) selection as reported for SSU RNAPs (viral family) and DNA polymerases.

Similarly, the eukaryotic elongation subunits (Rpb1) are also found to be very much homologous to the elongation subunits (β’) of prokaryotes. Interestingly, the catalytic regions are highly conserved, and the metal binding sites are absolutely conserved as in prokaryotic MSU RNAPs. In eukaryotes, the template binding YG pair is replaced with an FG pair. Another interesting observation is, similar to the prokaryotic β’ subunits, in the eukaryotic Rpb1 elongation subunits also, the proposed catalytic R is placed double the distance, i.e., -18 amino acids downstream from the FG pair unlike in the SSU RNAPs and DNA polymerases where the distance is only -8 amino acids downstream from the YG pair. Thus, the completely conserved FG pair, catalytic R with an invariant R, at -6th position are proposed to play a crucial role in template binding, NTP selection and polymerization reactions in the elongation subunits of eukaryotic MSU RNAPs. Moreover, the Zn binding motif with the three completely conserved Cs is also highly conserved in the eukaryotic elongation subunits. Another important difference is that the catalytic region is placed very close to the N-terminal region in eukaryotes.

Conclusions: Unlike reported for the DNA polymerases and SSU RNA polymerases, the of eukaryotic MSU RNAPs use an R as the catalytic amino acid and exhibit a different distance conservation in the initiation and elongation subunits. An invariant Zn^{2+} binding motif found in the Rpb1 elongation subunits is proposed to participate in proof-reading function. Differences in the active sites of bacterial and human RNA polymerases may pave the way for the design of new and effective drugs for many bacterial infections, including the multidrug resistant strains which are a global crisis at present.

Keywords: *Multi-subunit DNA dependent RNA polymerases, Eukaryotic RNA polymerases, RNA polymerase II, Saccharomyces cerevisiae, Conserved motifs, Polymerase active site, Polymerization mechanism, Transcription slippage diseases, Drug design.*

1. INTRODUCTION

RNAPs (EC 2.7.7.6) are key enzymes which play a vital role in the flow of genetic information from DNA to proteins and the proteins are final players in all cellular processes. Therefore, they are found in all living organisms and play a crucial role in copying DNA sequences into RNA molecules which are subsequently translated into proteins. Thus, transcription forms the first step and a key control point in gene regulation and expression. Errors in the transcription process can potentially lead to aberrant gene products and ultimately lead to various diseases including cancer. One major class of transcription error, known as transcriptional slippages, are implicated in the development of a wide variety of diseases, such as colon cancer, non-familial Alzheimer's, Down's syndrome, etc. (Anikin et al, 2010). Recently the *in vitro* transcribed mRNAs have come into focus as a potential new class of drugs known as 'mRNA therapeutics' to deliver genetic information through mRNAs to correct the malfunction(s) (Sahin et al, 2014) and also potential vaccines against cancer treatment (Conry et al, 1995). In fact, many anti-cancer drugs act by inhibiting the transcription step itself. Therefore, understanding the mechanism and regulation of RNAPs have been a key goal of molecular biologists since its discovery. Interestingly, the sequences, overall 3D framework and functions of these DNA dependent RNAPs are universally conserved in viruses, bacteria, plants and animals with small but significant differences in their active sites and catalytic amino acids. For the discussion about the discovery and dynamics of the polymerization reactions refer to Palanivelu (2018). Instead of a single type of RNAPs in prokaryotes, Robert Roeder and William Rutter discovered in1969 the existence of three different RNAPs in eukaryotic cells that were responsible for transcription of all types of RNAs in the eukaryotic cells (Roeder and Rutter, 1969).

Though RNAPs are found in all organisms, their number and composition vary across taxa, possibly due to evolutionary consequences, changes in the genome structure and the complexity of the transcription process. However, the MSU RNAPs display a conserved core structure across all major domains of life, viz. viruses, bacteria, archaea and eucarya. For example, viruses contain mainly two different RNAPs, viz. DNA dependent RNAPs and RNA dependent RNAPs. Both eubacteria and archaebacteria contain a single type of MSU RNAPs, while eukaryotes contain at least five distinct types of MSU RNAPs (I-V). While the eubacterial enzymes are composed of 5 different subunits, the eukaryotic enzymes are made up of up to 12 -16 different subunits. Despite such differences, there are striking similarities among the transcriptional mechanisms by various types of RNAPs across the three major domains of life [Werner and Grohmann, 2011 and references therein].

Transcription and transcriptional regulation are very important in eukaryotes as it underlies all aspects of cellular metabolism including oncogenesis (cancer) and morphogenesis (development). The major type of RNA polymerase, i.e., the RNA polymerase II, which involves in the transcription of genes, is a large (550 kDa) complex made up of 12 subunits. Unlike in prokaryotes, gene expression, and therefore, RNAP II activity is controlled by several proteins known as general transcription factors. In other words, as there are no Sigma like factors in eukaryotic cells for promoter recognition and to initiate transcription, the eukaryotic RNAPs interact with a variety of protein factors known as general transcription factors. Large volumes of genomic and protein sequence data are available for most of the prokaryotic and eukaryotic MSU RNAPs. Understanding the biological principles buried in these sequencing data is a significant challenge for scientists. Therefore, the purpose of the study is to analyze the available protein sequences of the MSU RNAPs from eukaryotes to find out the highly conserved motifs among them and to understand the structure- function relationships and mechanism of action of these key enzymes, along with the X-ray crystallographic and experimental data available on these enzymes from various sources. A comparative analysis of the bacterial and human RNAPs for their transcription mechanism will the pave way to design new and effective drugs for many bacterial infections, including the antibiotic resistance, especially the multi-drug resistance, which has become a global crisis [Domecq et al., 2008, Ma et al 2016; and references therein]. MSA has been proven to be very useful for assigning a function to a given sequence, by comparing the existing experimental data with the protein sequence data and thus, bridging the gap between the protein sequence and experimental data.

RNAPs catalyze the chemical reactions that synthesize an RNA strand from a DNA template with all the 4 NTPs and a metal ion, usually a Mg^{2+} ion. The RNA synthesis involves three steps, viz. initiation, elongation and termination. RNAPs bind to the promoter region with the help of transcription factors and unwind the double-stranded DNA ahead of them, move forward by adding NTPs one at a time and allow the unwound DNA behind them to rewind. As a result, RNA strand synthesis occurs in a transcription bubble of ~25 unwound DNA bp. Only ~8 nucleotides of newly-synthesized RNA remain base-paired to the template DNA and the rest of the RNA molecules falls-off the template to allow the DNA behind it to rewind. The newly formed RNA copies serve as blueprints for the synthesis of proteins during the next step of translation. The basic transcription unit is the distance between the sites of transcription start site (TSS) and transcription termination site (TTS), and may have one or more genes between them (e.g., mono or poly-cistronic mRNAs, poly-cistronic mRNAs are uncommon in eukaryotes).

2. Types of MSU DNA dependent RNAPs of prokaryotes and eukaryotes

There are at least 4 different types of MSU RNAPs in living cells, viz.

1) MSU DNA dependent RNAPs of eubacteria
2) MSU DNA dependent RNAPs of archaebacteria
3) MSU DNA dependent RNAPs of chloroplasts (Plastid encoded)
4) MSU DNA dependent RNAPs of eukaryotes

2. 1 Types of MSU DNA dependent RNAPs in Eukaryotes

As mentioned elsewhere, bacteria and archaea have only a single RNAP to transcribe all of its genes whereas eukaryotic cells employ different RNAPs to transcribe different types of genes, viz. rRNAs, tRNAs and mRNAs (Table 1).

There are at least 7 major types of RNAPs in eukaryotes. The nuclear genome utilizes three major types of RNAPs which are localized in the nucleus. For example, the RNAP I is localized in the nucleolus and primarily involves in the synthesis of the rRNAs and the other two RNAPs, viz. RNAPs II and III are localized in the nucleoplasm and mainly involved in the synthesis of mRNAs and tRNAs, respectively (Table 1). Plants are unique among eukaryotes in having five nuclear MSU RNAPs. Two plant-specific RNAPs, polymerases IV and V are 12-subunit enzymes that are evolved as specialized forms of Pol II. (Pols IV and V are nonessential for viability but play important roles in RNA-mediated gene silencing pathways that tame transposons and defend against invading viruses (Ream et al., 2014).

Table 1 Types and functions of eukaryotic RNAPs

Type of RNA Polymerase	**Type of RNA(s) synthesized**
1. RNA Polymerase I (Nucleolus)	rRNA genes (5.8S, 18S, 28S rRNAS from 45S pre-rRNA)
2. RNA Polymerase II (Nucleoplasm)	mRNAs, snRNAs, microRNAs
3. RNA Polymerase III (Nucleoplasm)	tRNAs & 5S rRNA, scRNAs, U6 SnRNA
4. RNA Polymerase IV (Plant specific)	siRNAs in plants
5. RNA Polymerase V (Plant specific)	Plant specific RNAs involved in siRNA directed heterochromatin formation in plants.
6. MSU type (Chromosome encoded)	Eubacterial and Chloroplasts
7. SSU type (Plasmid &Nucleus encoded)	Mitochondrial and Chloroplasts

2.2 Basic structure and composition of the eukaryotic RNAPs

All the 5 eukaryotic enzymes (RNAPs I-V) are MSU enzymes. The 12-subunit RNAP II is the enzyme largely responsible for transcription of protein-encoding genes and thus, forms the central component of the eukaryotic transcription machinery. Similarities between the eukaryotic and prokaryotic MSU enzymes, suggest a common lineage in the evolutionary tree. For example, counterparts for all the five core eubacterial RNAP subunits ($\alpha_2\beta\beta'\omega$) are found in the eukaryotic RNAPs I, II and III (Lane and Darst 2010) (Table 2). The 5 orthologs include the two largest catalytic subunits Rpb1 and Rpb2, which correspond to the bacterial β' and β subunits, respectively (Sweetser et al, 1987). Furthermore, Rpb3 and Rpb11 correspond to the two copies of the bacterial α subunit, and the Rpb6 subunit corresponds to the bacterial ω subunit (Minakhin et al, 2001). In addition to, the two large subunits of RNAP II share some sequence homology and antigenic determinants with the corresponding subunits of RNAPs I and III (Nonet et al, 1987) (Refer to also Mix and Match analysis Figs. 5 and 6). Rpb3 is involved in RNAP II assembly. The subunits Rpb4 and Rpb7 form a heterodimer and associate reversibly with the '10-subunit core polymerase' and involves in the initiation process which is otherwise defective in initiation. Rpb5, an evolutionarily highly conserved, universal eukaryotic RNAP subunit, shared by all three enzymes, facilitates communication between the RNAP core with a variety of basal and gene-specific transcription factors (Todone et al., 2000). Rpb7 is essential for the functioning of the RNAP-II as deletion is also found to be lethal. A cleft is formed by jaws; the upper jaw is formed by regions of Rpb1, Rpb2 and Rpb9 whereas the lower jaw is formed by Rpb1 and Rpb5. The jaws are thought to grab the incoming DNA template (Bushnell and Kornberg, 2003) (Fig. 1).

Consistent with the increased complexity of the eukaryotic genome, all three major RNAPs of the eukaryotic transcriptional machinery have several additional subunits that do not have bacterial counterparts. Table 2 shows the subunit compositions of the three major types of nuclear MSU RNAPs. Apart from the 5 orthologs, as discussed above, the nuclear RNAPs share four common subunits, while the remaining subunits are RNAP dependent. Thus, the three major classes of eukaryotic RNAPs: I, II and III, in addition to comprising of two large catalytic subunits also made up of 10-14 smaller subunits (Table 2).

Table 2 Composition of the three major eukaryotic nuclear RNAPs

Features	**Pol I**	**Pol II**	**Poll III**
Subunits unique to each RNAP ($\alpha_2\beta\beta'\omega$- like)	5	5*	5
Common subunits to all 3 RNAPs	4	4	4
Additional unique subunits to each RNAPs	5	3	7
Total No. of subunits	14	12	16
Products	pre-rRNAS (45S RNA → 28S, 5.8S, 18S)	pre-mRNAs 5 snRNAs^ Sno RNAs, microRNAs	pre-tRNAs 5S & 7S RNAs[$], U6-snRNA
Sensitivity to α-Amanitin	Nil	High (1 μg/ml)	Moderate (10 μg /ml)
Sensitivity to Actinomycin-D#	0.05 μg/ml	0.5 μg/ml	5.0 μg/ml

NB:

*The largest subunit, Rpb1, has unique Carboxy Terminal Domain (CTD); #Gnatt et al, 2011

Subunit nomenclatures RNAPs I, II & III: RP A1-A14; RP B1-B12; RP C1-C16

^ U1-U5 of ~200 bases; involves in the formation of spliceosomes

[$] 7S RNA from the signal recognition particle (SRP) which is involved in the transport of proteins into the endoplasmic reticulum.

2.3 Characteristics of the C-terminal domain (CTD) in the largest subunit Rpb1

Though exact functions of all the eukaryotic RNAPs are more or less completely understood, yet much data are not available on the individual subunits except for the larger subunits. An interesting feature of the RNAP II, a 12-subunit complex, is its unique CTD in the largest subunit Rpb1. The Rpb1 elongation subunit consists of a tandem repeat of a conserved heptapeptide repeat sequences (-**YS**^{2}P**TS**^{5}P**S**^{7}**-**). These heptapeptide repeats are completely conserved in sequence and function from yeast to human with varying lengths from 25 to 52. (The CTD domain does not exist in RNAPs I and III suggesting its special importance to mRNA processing). The Ser residues are phosphorylated and dephosphorylated during the active transcription process. Therefore, the RNAP-II exists in two forms, i.e., unphosphorylated and phosphorylated forms (II and II^{P}), respectively (Young, 2003). In fact, the transition between the two forms facilitates different functions during transcription. (The phosphorylation of CTD is catalyzed by TFII-H, one of the six general transcription factors associated with RNAP II. TFII-H plays a dual role: one is to unwind the DNA at the transcription start site and the other is to phosphorylate the heptapeptide repeats. (TFII-H is a large protein complex that contains among others the Cdk7/Cyclin-H kinase complex for phosphorylation of CTD and an ATP dependent DNA helicase to unwind the DNA and open up the transcription bubble at TSS). It also involves in transcription-coupled DNA mismatch repair. (Mutations in the human XPD kinase cause *xeroderma pigmentosum* and *trichothiodystrophy,* Hahn 2004)

The elongation of initiation is accomplished by the phosphorylation of Ser^5 of the heptapeptide, (-**YS^2**P**TS^5**P**S-**) by the TFII-H. The Ser^5 phosphorylation recruits enzymes to cap the 5' end of the newly synthesized mRNA and the 3' processing factors to poly(A) sites. Once the second Ser is phosphorylated, i.e., Ser^2, elongation is activated. West and Cordon (1995) have shown substitution of Ala or Glu for Ser in positions 2 or 5 is lethal. In addition, changing Tyr in position 1 to Phe is also lethal. In order to terminate elongation, dephosphorylation is accomplished by phosphatases. Once the domain is completely dephosphorylated, the RNAP II is "recycled" and catalyzes the same process with another initiation site. Thus, the CTD acts as a platform for various transcription factors as it binds or dissociates them, depending upon their requirements during the transcription process. Thus, the phosphorylation and dephosphorylation of the CTD is an important regulatory mechanism exhibited only by the RNAP II (Sylvain E and Shona, 2008). Ser7 phosphorylation is required for the transcription of SnRNAs and a mutation of Ser7 to Ala causes a specific defect in snRNA expression (Egloff et al, 2007)

The number of heptapeptide repeats in the CTD increases with genomic complexity; for example, 17 in Plasmodium, 26 in yeast, 32 in *Caenorhabditis elegans*, 45 in Drosophila, and 52 in mammals). The CTD deletion experiments have shown the CTD's central role in coupling transcription to all three of the main mRNA processing events (Phatnani and Greenleaf, 2006). For example, deletion of most of the CTD can result in inefficient capping, splicing, and polyadenylation *in vivo*. SDM experiments of the yeast RNAP II has found at least 10 repeats are needed for the viability of the process (McCracken et al. 1997; Fong and Bentley 2001).

2.4 Salient features of the yeast (*S. cerevisiae*) MSU RNAPs

To-date one of the most well-studied eukaryotic RNAPs is from the baker's yeast, *S. cerevisiae*. In fact, our present understanding of the eukaryotic transcription system is mainly based on the yeast system. (For solving the structure and molecular basis of transcription by the yeast RNAP II, Roger Kornberg was awarded Nobel Prize in chemistry in 2006). Like other eukaryotic cells, the yeast cells also contain 3 different polymerases as discussed above. All the three yeast polymerases have five core subunits that exhibit good homology to the β, β', α and ω subunits of *E. coli* RNAP. RNAPs I and III contain the same two non-identical α-like subunits, whereas polymerase II has two copies of a different α-like subunit. All three yeast polymerases share four other common subunits as mentioned elsewhere. In addition, each RNAP contains three to seven unique smaller subunits as shown in Table 3.

The yeast RNAP II, which involves in the production of mRNAs, is extensively characterized and a great deal of information is available. The yeast RNAP II is composed of 12 subunits and the largest subunit (Rpb1) contains the essential CTD, containing 26 heptapeptide repeats (YSPTSPS). Thus, the Rpb1, Rpb2, Rpb3 and Rpb11 subunits are related to the subunits of the eubacterial RNA polymerase core enzyme, whereas the 5 subunits, viz. Rpb5, Rpb6, Rpb8, Rpb10 and Rpb12 are shared among yeast RNA polymerases I, II and III (Kolodziej et al, 1990) (Table 3).

The yeast RNAP II core enzyme is composed of 12 subunits (Fig. 1). The 7 subunits, viz. Rpb1-4, Rpb7, Rpb9 and Rpb11 are unique to RNAP II while the 5 subunits, viz. Rpb5, Rpb6, Rpb8, Rpb10 and Rpb12 are shared between the three RNAPs (Table 3). The Δ*rpb4* phenotypes can be suppressed by overexpression of Rpb7, and the high level of Rpb7 allows its interaction with RNAP II in the absence of Rpb4 (Sheffer et al, 1999), suggesting that Rpb7 is the critical component of the Rpb4–Rpb7 complex and the role of Rpb4 is to stabilize the complex. MSA analysis of the Rpb7 from various eukaryotic sources have shown 3 template binding pairs, possibly decide the right orientation of the template DNA possibly by three-point attachment in addition to two long stretches of conserved motifs (data not shown). Rpb2, a protein of 138,750 Daltons, exists as a single copy in the haploid yeast genome and disruption of the gene is lethal to the yeast cell. (Sweetser et al, 1987).

Table 3. The composition of the yeast RNAP-II

Subunit	Size (~kDa)	Subunit	Size (~kDa)
Rpb1 (β')	192E	Rpb7**	19E
Rpb2 (β)	139E	***Rpb8****	17E/S
Rpb3 (~α)	35E	Rpb9	14NE
Rpb4	25NE	***Rpb10****	8.8E/S
Rpb5*	25E/S	Rpb11	14E
Rpb6* (ω)	18E/S	***Rpb12****	7.7E/S

Adapted from Kolodziej et al (1990); E, Essential; NE, Nonessential; S, Shared.

*The 5 Rpb subunits, viz. 5, 6, 8, 10 and 12 are common for all 3 RNAPs, viz. RNAP I, II & III
The Rpb6 promotes RNAP assembly and contains 9 C2H2 zinc fingers (Woychik and Young, 1992).
** Rpb7 is unique to RNAP II. (Rpbs7 and 4 form a dimer and initiate transcription, not required for elongation)
Rpb3 is not absolutely equivalent to α subunit of *E. coli*.
Subunits Rpb1, Rpb2, Rpb3 and Rpb7 are absolutely required for activity.
Rpb1 is known to bind strongly to Rpb5.
Rpb12 interacts with Rpb3.

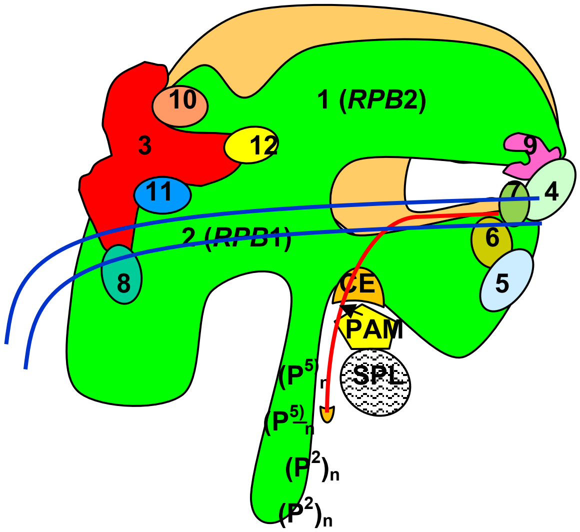

Fig. 1 A schematic diagram of the 12-subunit yeast MSU RNAP-II with the CTD and processing components
CE Capping Enzyme; PAM, Poly-Adenylation Machinery; SPL, Spliceosome;
$(P^{5)}_n$, phosphorylation at Ser5 positions (during initiation); $(P^2)_n$ phosphorylations at Ser2 positions (during elongation).

During the production of the primary transcript by RNAP-II, the phosphorylation state (P) of the CTD changes to allow the transcribing polymerase to associate with the capping, splicing, polyadenylation and mRNA export machinery (Phatnani and Greenleaf, 2006). X-ray crystallographic results also provide evidence for RNA exit in the vicinity of the carboxyl-terminal repeat domain, coupling synthesis to RNA processing by enzymes bound to this domain (Cramer et al 2001). These associations are essential for normal processing of pre-mRNAs to generate mature mRNAs and to export them to the cytoplasm and also for normal termination of transcription by RNAP II. The subunit Rpb1 (*RPO21*) is the largest and catalytic component of RNAP II and similar to the eubacterial β'. Bacterial RNA polymerase subunit ω and eukaryotic RNA polymerase subunit Rpb6 (shared by RNAPs I, II, and III) are the sequence, structural, and functional homologs and promote RNA polymerase assembly (Minakhin, et al, 2001).

In this communication, the yeast RNAP II is used as the model system and the structural studies of yeast RNAP II are directly relevant to RNAP II enzymes in higher organisms, as the yeast RNAP II subunits are very well conserved in sequence and function as discussed elsewhere. These analyses not only bridge the data obtained by protein sequence analysis and the experimental results obtained on the yeast RNAP II but also will pave for more SDM experiments and genetic analysis to dissect the transcription mechanism in eukaryotes in much detail. The following brief discussion on the basic structure of the transcription unit, transcription cycle and the participation of the RNAP II subunits will be useful to further understand the analysis and conclusions.

3. Basic Structure of the Transcription Units in Eukaryotes

The transcription units in eukaryotes are slightly different from the one described in prokaryotes (Palanivelu, 2018) as most of the eukaryotic genes are interrupted with intervening sequences called introns. A typical transcription unit in eukaryotes is shown in Fig. 2.

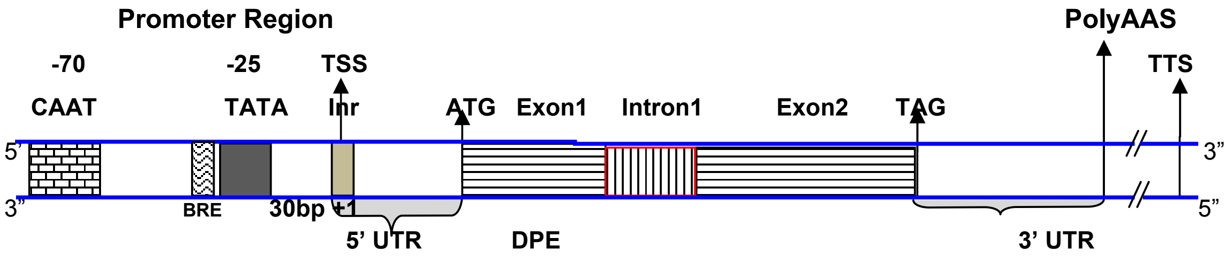

Fig. 2 Schematic diagram of a typical transcription unit in eukaryotes

NB:

Blue lines, DNA strands**; TATA,** TATA box (Hogness box) (some promoters are TATAless), **CAAT**, CAAT box; The starting nucleotide (nt) is always an **A** in eukaryotes; **UTR**, UnTranslated Region); **PolyAAS,** Poly-A Addition Site (AATAAA); **TSS**, Transcription Start Site; **Inr,** Initiation region –pyTC**A**CA-; **DPE**, Downstream Promoter Element (is seen ~ +30 bp in many genes, A**G**ACA); **TTS,** Transcription Termination Site.

[Some transcription units have an InR start site, TATA-like site, Down Stream Promoter Elements (DPE), Upstream activator elements/Enhancer elements, Repressor and even Insulator and Silencer sequences. The poly-A cleavage site is about 30-35 or even 100 nucleotides downstream of the STOP codon (TAG). This sequence at the mRNAs' 3' end is called poly-A signal. The sequence present in the terminal region of the gene is TTATTT (poly-A signal) is usually followed by poly-U of 20 to 35 nts downstream from the poly-A signal.

5' UTR is the portion of an mRNA from the 5' end to the first codon; the 3' UTR is the portion of an mRNA from the last codon to the poly-A site. The UTRs play crucial roles in mRNA stability, transport, translation efficiency, etc].

4. Transcription Processes in Eukaryotes

The basic transcription unit in eukaryotes is the distance between the sites of transcription start site (TSS) and transcription termination site (TTS), and the coding region is usually interrupted by one to many introns (Fig. 2)

The RNA synthesis in eukaryotes involves four steps, viz. formation of pre-initiation complex (PIC), initiation, elongation and termination. It is interesting to note that **t**he eukaryotic RNAPs do not possess any initiator subunits similar to the σ factors, as reported in prokaryotes., However, unlike in prokaryotes where the initiation starts with the specific binding of the single σ subunit, in eukaryotes, at least about half a dozen protein factors involve in the initiation of transcription and are collectively known as General Transcription factors (GTFs). These GTFs assemble at the promoter region to form the PIC. Once the PIC is formed and the RNAP is positioned at TSS, the initiation subunit Rpb2 initiates RNA synthesis by making short RNA primers of ~10 nts, from which the elongation subunit Rpb1 extends and terminates at TTS. In eukaryotes, there is no well-defined transcriptional terminator region as in prokaryotes and therefore, the transcription progresses well beyond 1000 or more nts downstream from the stop codon. Unlike RNAP I and III, RNAP II lacks any specific termination signals.

In my earlier communication, SSU RNAPs and MSU RNAPs (prokaryotic and prokaryotic type, i.e., plastid-encoded) RNAPs were analyzed in detail (Palanivelu 2017, 2018 & 2019). In this communication, the most complex MSU RNAPs of eukaryotic origin are analyzed for their conserved motifs, active sites, metal binding regions and based on these findings, a plausible mechanism of action is proposed for these MSU eukaryotic enzymes using the yeast MSU RNAP II as the model enzyme.

5. MATERIALS AND METHODS

A large number of MSU RNAPs from eubacteria and eukaryotes have been isolated, purified, characterized, cloned and sequenced [Young, 2003; Cramer, 2002; Werner and Grohmann, 2011 and references therein) Complete nucleic acid and protein sequence data are available for these enzymes from different eukaryotic sources. Thus, these data have become valuable tools in analyzing and understanding the structure-function relationships of these most complex enzymes which play a vital role gene expression. This communication presents a consensus model for initiation and elongation processes and also a plausible mechanism of action for these enzymes.

The *S. cerevisiae* DNA-dependent MSU RNAP II is used as the model system for delineating the polymerization mechanism. Biochemically and genetically as this is the most well-studied enzyme, a large amount of data on biochemical, SDM and X-ray analyses of its subunits make this enzyme a convenient model for investigating the physicochemical aspects of transcription in eukaryotes. For MSA of various eukaryotic RNAP II, the sequences were retrieved from SWISS-PROT and PUBMED sites and analyzed using Clustal Omega, an accurate, fast and widely accepted algorithm, available on their website.

6. RESULTS AND DISCUSSION

6.1 MSA of eukaryotic MSU RNA polymerases from different sources

The eukaryotic RNAP II is composed of various subunits as describes elsewhere (Table 2). Only the two catalytic subunits viz. Rpb2 and Rpb1 which involve in the initiation and elongation processes are analyzed to find out the conserved and active site regions among them. Figures 3 and 4 show the MSA of the two catalytic subunits of MSU RNAP II from various eukaryotic sources. To reduce the length of the article, only the relevant and highly conserved regions are shown in the Figures. The possible catalytic, template and substrate binding motifs are highlighted in yellow and the metal binding regions are highlighted in green/orange. The subunit sequences of standard organisms are highlighted in yellow/magenta and used for numbering.

6.1.1 MSA of Rpb2 subunits of eukaryotic MSU RNAPs (RNAP II)

Figure 3 shows the MSA analysis and conserved motifs of the Rpb2 initiation subunits in eukaryotic MSU RNAPs II. There are large numbers of conserved motifs are observed and some are found to be long stretches (highlighted). The yeast *(S. cerevisiae)* Rpb2 subunit (1224 amino acids) is used as the standard for numbering and highlighted in magenta. The catalytic region is found ~400 amino acids from the N-terminal. The invariant template binding YG is replaced by a KG pair in higher eukaryotes including human. The invariant catalytic R is placed at -9 from the template binding pair. This distance conservation is in close agreement with Pal and Luse (2003) findings that the transcription slippage abruptly stopped once the Rpb2 makes about 9 nucleotides. Interestingly, the transition from abortive to productive elongation cycle occurred once the RNAP register +10 nts (Fiedler and Timmers, 2001). The absolutely conserved R, which is implicated in NTP selection in SSU and MSU RNAPs and DNA polymerases, is placed –5 position. In fact, in all the eubacterial β subunits the catalytic R is placed at -7th position from the YG pair and completely conserved R is placed at -8th position downstream from the catalytic R. However, catalytic R is placed at -8th position from the YG pair the completely conserved R was at -4th position in SSU RNAPs and DNA polymerases [Palanivelu 2017 and 2013]. This strongly suggests that the DNA polymerases, SSU and MSU RNAPs use the same set of amino acids for template, substrate binding and catalysis establishing a structure-function relationship among the DNA and RNA polymerases. The immediate upstream amino acid from catalytic K in DNA polymerases is usually a G or A [Palanivelu 2013], but in SSU viral RNA polymerases it is a Q (Palanivelu 2017) and in MSU eubacterial β subunits, it is a D in all (Palanivelu 2018) and in eukaryotic Rpb2 it is S/T, suggesting a possible role in the substrate binding and catalysis. Another catalytic like region is located in ~400 amino acids from the N-terminal but with a YG/FG pair and a catalytic R at -9 and long highly conserved stretches on both the sides. The Zn binding motif with 3 completely conserved Cs is found in the C-terminal region (highlighted in orange) which is followed by a long stretch of conservation till the C-terminal end. There are many highly conserved YG/FG/IG/LG pairs and a WG pair in the Rpb2 subunits.

At least three of them may provide by three-point attachment for stereo specific binding on to the template DNA. However, the DNA polymerases show only one YG pair. Interestingly, the RNA dependent RNAPs do not have the YG pair [Tunitskaya and Kochetkov ,2002]. A long stretch of the C-terminal region is highly conserved in all Rpb2 subunits. Interestingly the higher eukaryotic Rpb2 subunits show a completely conserved motif till the end of the C-terminal whereas the lower eukaryotic Rpb2 subunits also show a completely conserved stretch but not covering all the amino acids till the C- terminal with a consensus sequence “PYAxKLLFQELMxM”. A long stretch of highly conserved end suggests a possible role in the initiation process.

CLUSTAL O (1.2.4) MSA of the **Rpb2, initiation** subunits of eukaryotic MSU RNAP **II** 3

```
sp|P30876|RPB2_HUMAN                MYDAD-EDMQYDE---DDDEITPDLWQEACWIVISSYFDEKGLVRQQLDSFDEFIQMSVQ       56
tr|G3V8Y5|G3V8Y5_RAT                MYDAD-EDMQYDE---DDDEITPDLWQEACWIVISSYFDEKGLVRQQLDSFDEFIQMSVQ       56
tr|A0A250Y753|A0A250Y753_CASCN      MYDAD-EDMQYDE---DDDEITPDLWQEACWIVISSYFDEKGLVRQQLDSFDEFIQMSVQ       56
tr|A0A1U7R4C7|A0A1U7R4C7_MESAU      MYDAD-EDMQYDE---DDDEITPDLWQEACWIVISSYFDEKGLVRQQLDSFDEFIQMSVQ       56
tr|A0A286XIQ9|A0A286XIQ9_CAVPO      MYDAD-EDMQYDE---DDDEITPDLWQEACWIVISSYFDEKGLVRQQLDSFDEFIQMSVQ       56
tr|I3M351|I3M351_ICTTR              MYDAD-EDMQYDE---DDDEITPDLWQEACWIVISSYFDEKGLVRQQLDSFDEFIQMSVQ       56
tr|G7P5R6|G7P5R6_MACFA              MYDAD-EDMQYDE---DDDEITPDLWQEACWIVISSYFDEKGLVRQQLDSFDEFIQMSVQ       56
tr|H2QPI8|H2QPI8_PANTR              MYDAD-EDMQYDE---DDDEITPDLWQEACWIVISSYFDEKGLVRQQLDSFDEFIQMSVQ       56
tr|A0A1U7V0T5|A0A1U7V0T5_TARSY      MYDAD-EDMQYDE---DDDEITPDLWQEACWIVISSYFDEKGLVRQQLDSFDEFIQMSVQ       56
tr|A0A1S2ZSL2|A0A1S2ZSL2_ERIEU      MYDAD-EDMQYDE---DDDEITPDLWQEACWIVISSYFDEKGLVRQQLDSFDEFIQMSVQ       56
tr|A0A0D9QYL1|A0A0D9QYL1_CHLSB      --------MQYDE---DDDEITPDLWQEACWIVISSYFDEKGLVRQQLDSFDEFIQMSVQ       49
tr|A0A2K5ZNR7|A0A2K5ZNR7_MANLE      --------MQYDE---DDDEITPDLWQEACWIVISSYFDEKGLVRQQLDSFDEFIQMSVQ       49
tr|A0A2I2ZIU3|A0A2I2ZIU3_GORGO      MYDAD-EDMQYDE---DDDEITPDLWQEACWIVISSYFDEKGLVRQQLDSFDEFIQMSVQ       56
tr|A0A1D5QGA5|A0A1D5QGA5_MACMU      MYDAD-EDMQYDE---DDDEITPDLWQEACWIVISSYFDEKGLVRQQLDSFDEFIQMSVQ       56
tr|A0A2J8S2N1|A0A2J8S2N1_PONAB      MYDAD-EDMQYDE---DDDEITPDLWQEACWIVISSYFDEKGLVRQQLDSFDEFIQMSVQ       56
tr|A0A2K5K5J5|A0A2K5K5J5_COLAP      MYDAD-EDMQYDE---DDDEITPDLWQEACWIVISSYFDEKGLVRQQLDSFDEFIQMSVQ       56
tr|A0A2J8PEW7|A0A2J8PEW7_PANTR      --------MQYDE---DDDEITPDLWQEACWIVISSYFDEKGLVRQQLDSFDEFIQMSVQ       49
tr|A0A2K5CY83|A0A2K5CY83_AOTNA      MYDAD-EDMQYDE---DDDEITPDLWQEACWIVISSYFDEKGLVRQQLDSFDEFIQMSVQ       56
tr|A0A096NEY4|A0A096NEY4_PAPAN      MYDAD-EDMQYDE---DDDEITPDLWQEACWIVISSYFDEKGLVRQQLDSFDEFIQMSVQ       56
tr|C9J2Y9|C9J2Y9_HUMAN              --------MQYDE---DDDEITPDLWQEACWIVISSYFDEKGLVRQQLDSFDEFIQMSVQ       49
tr|G8BY61|G8BY61_TETPH              --MSQGEEYYADEDPYGFEDENAPISAEDSWTVISSFFREKGLVSQQLDSFNQFVDYTLQ       58
tr|A0A1X7QYA1|A0A1X7QYA1_9SACH      ----MSNDDYYEEDPYGFEDESSPITAEDSWAVISSFFREKGLVSQQLDSFNQFVDYTLQ       56
tr|J7RV95|J7RV95_KAZNA              ----MSNEEYYDEDPYGFEDESAPITAEDSWTVISSFFREKGLVSQQLDSFNQFVDYTLQ       56
tr|H2AVJ8|H2AVJ8_KAZAF              ----MSNEEYYEDDPYGFEDESAPITAEDSWAVISSFFREKGLVSQQLDSFNQFVDYTLQ       56
sp|Q6FLD5|RPB2_CANGA                --MSADNEDYYDEDPYGFEEENAPITAEDTWAVISAFFREKGLVSQQLDSFNQFVDYTLQ       58
sp|P08518|RPB2_YEAST                MSDLANSEKYYDEDPYGFEDESAPITAEDSWAVISAFFREKGLVSQQLDSFNQFVDYTLQ       60
tr|A0A0L8VHA5|A0A0L8VHA5_9SACH      MSDLANSEKYYDEDPYGFEDESAPITAEDSWAVISAFFREKGLVSQQLDSFNQFVDYTLQ       60
tr|A0A0L8RB33|A0A0L8RB33_SACEU      MSDVENSEKYYEEDPYGFEDGSAPITAEDSWAVISAFFREKGLVSQQLDSFNQFVDYTLQ       60
tr|G0VJ71|G0VJ71_NAUCC              MSAPGEEEYYDEDDVYGFEDENAPITAEDAWAVISSFFREKGLVSQQLDSFNQFVDYTLQ       60
tr|G8ZM49|G8ZM49_TORDC              --MSAAEDDYYNEDPYGYEDENSPITAEDSWAVISAFFREKGLVSQQLDSFNQFVDYTLQ       58
tr|A0A1Q3A090|A0A1Q3A090_ZYGRO      MSAAAVDEDYYAEDPYGYEDENFPITAEDSWAVISAFFREKGLVSQQLDSFNQFVDYTLQ       60
tr|A0A0N7IS35|A0A0N7IS35_9SACH      -MSAAVNEEYYAEDPYGYDDETSPITAEDSWAVISAFFREKGLVSQQLDSFNQFVDYTLQ       59
tr|A0A212MG88|A0A212MG88_ZYGBA      -MSAAVNEDYYAEDPYGYEDENSPISAEDSWAVISAFFREKGLVSQQLDSFNQFVDYTLQ       59
tr|A0A1S7HHE1|A0A1S7HHE1_9SACH      -MSAAVNEDYYAEDPYGYEDENSPISAEDSWAVISAFFREKGLVSQQLDSFNQFVDYTLQ       59
tr|S6ESB4|S6ESB4_ZYGB2              -MSAAVNEDYYAEDPYGYEDENSPISAEDSWAVISAFFREKGLVSQQLDSFNQFVDYTLQ       59
tr|B6K5Q5|B6K5Q5_SCHJY              -------------MSYEDYQYNETLTQEDCWTVISSYFEENSLARQQLSSFDEFVQNTMQ       47
sp|Q02061|RPB2_SCHPO                -------------MSYEDYQYNETLTQEDCWTVISSFFEETSLARQQLFSFDEFVQNTMQ       47
tr|S9R8U4|S9R8U4_SCHOY              -------------MSYEDYQYNETLTQEDCWTVISSFFEETSLARQQLFSFDEFVQNTMQ       47
tr|S9W8C6|S9W8C6_SCHCR              -------------MSYEDYQYNETLTQEDCWTVISSFFEETSLARQQLFSFDEFVQNTMQ       47
                                                       : .  :  *  * ***::* *..*. *** **::*:: ::*

sp|P30876|RPB2_HUMAN                RIVEDAPPIDLQAEAQHASGEVEEPPRYLLKFEQIYLSKPTHWERDGAPSPMMPNEARLR       116
tr|G3V8Y5|G3V8Y5_RAT                RIVEDAPPIDLQAEAQHASGEVEEPPRYLLKFEQIYLSKPTHWERDGAPSPMMPNEARLR       116
tr|A0A250Y753|A0A250Y753_CASCN      RIVEDAPPIDLQAEAQHASGEVEEPPRYLLKFEQIYLSKPTHWERDGAPSPMMPNEARLR       116
tr|A0A1U7R4C7|A0A1U7R4C7_MESAU      RIVEDAPPIDLQAEAQHASGEVEEPPRYLLKFEQIYLSKPTHWERDGAPSPMMPNEARLR       116
tr|A0A286XIQ9|A0A286XIQ9_CAVPO      RIVEDAPPIDLQAEAQHASGEVEEPPRYLLKFEQIYLSKPTHWERDGAPSPMMPNEARLR       116
tr|I3M351|I3M351_ICTTR              RIVEDAPPIDLQAEAQHASGEVEEPPRYLLKFEQIYLSKPTHWERDGAPSPMMPNEARLR       116
tr|G7P5R6|G7P5R6_MACFA              RIVEDAPPIDLQAEAQHASGEVEEPPRYLLKFEQIYLSKPTHWERDGAPSPMMPNEARLR       116
tr|H2QPI8|H2QPI8_PANTR              RIVEDAPPIDLQAEAQHASGEVEEPPRYLLKFEQIYLSKPTHWERDGAPSPMMPNEARLR       116
tr|A0A1U7V0T5|A0A1U7V0T5_TARSY      RIVEDAPPIDLQAEAQHASGEVEEPPRYLLKFEQIYLSKPTHWERDGAPSPMMPNEARLR       116
tr|A0A1S2ZSL2|A0A1S2ZSL2_ERIEU      RIVEDAPPIDLQAEAQHASGEVEEPPRYLLKFEQIYLSKPTHWERDGAPSPMMPNEARLR       116
tr|A0A0D9QYL1|A0A0D9QYL1_CHLSB      RIVEDAPPIDLQAEAQHASGEVEEPPRYLLKFEQIYLSKPTHWERDGAPSPMMPNEARLR       109
tr|A0A2K5ZNR7|A0A2K5ZNR7_MANLE      RIVEDAPPIDLQAEAQHASGEVEEPPRYLLKFEQIYLSKPTHWERDGAPSPMMPNEARLR       109
tr|A0A2I2ZIU3|A0A2I2ZIU3_GORGO      RIVEDAPPIDLQAEAQHASGEVEEPPRYLLKFEQIYLSKPTHWERDGAPSPMMPNEARLR       116
tr|A0A1D5QGA5|A0A1D5QGA5_MACMU      RIVEDAPPIDLQAEAQHASGEVEEPPRYLLKFEQIYLSKPTHWERDGAPSPMMPNEARLR       116
tr|A0A2J8S2N1|A0A2J8S2N1_PONAB      RIVEDAPPIDLQAEAQHASGEVEEPPRYLLKFEQIYLSKPTHWERDGAPSPMMPNEARLR       116
tr|A0A2K5K5J5|A0A2K5K5J5_COLAP      RIVEDAPPIDLQAEAQHASGEVEEPPRYLLKFEQIYLSKPTHWERDGAPSPMMPNEARLR       116
tr|A0A2J8PEW7|A0A2J8PEW7_PANTR      RIVEDAPPIDLQAEAQHASGEVEEPPRYLLKFEQIYLSKPTHWERDGAPSPMMPNEARLR       109
tr|A0A2K5CY83|A0A2K5CY83_AOTNA      RIVEDAPPIDLQAEAQHASGEVEEPPRYLLKFEQIYLSKPTHWERDGAPSPMMPNEARLR       116
tr|A0A096NEY4|A0A096NEY4_PAPAN      RIVEDAPPIDLQAEAQHASGEVEEPPRYLLKFEQIYLSKPTHWERDGAPSPMMPNEARLR       116
tr|C9J2Y9|C9J2Y9_HUMAN              RIVEDAPPIDLQAEAQHASGEVEEPPRYLLKFEQIYLSKPTHWERDGAPSPMMPNEARLR       109
tr|G8BY61|G8BY61_TETPH              DIISEDSTLILEQLAQHTTESDNISRKYEISFGKIYVTKPMVNESDGVTHALYPQEARLR       118
tr|A0A1X7QYA1|A0A1X7QYA1_9SACH      DIIFEDSTLILEQIAQHTTEQDNISRKYEISFGKIYVTKPMVNESDGVTHALYPQEARLR       116
tr|J7RV95|J7RV95_KAZNA              DIISEDSRLILEQLAQHTTEADNISRKYEISFGKIYVTKPMVNESDGVTHALYPQESRLR       116
tr|H2AVJ8|H2AVJ8_KAZAF              DIISEDSTLILEQLAQHTTEADNISRKYEISFGKIYVTKPMVNESDGVTHALYPQEARLR       116
sp|Q6FLD5|RPB2_CANGA                DIISEDSTLILEQLAQHTTEQDNISRKYEISFGKIYVTKPMVNESDGVTHALYPQEARLR       118
sp|P08518|RPB2_YEAST                DIICEDSTLILEQLAQHTTESDNISRKYEISFGKIYVTKPMVNESDGVTHALYPQEARLR       120
tr|A0A0L8VHA5|A0A0L8VHA5_9SACH      DIICEDSTLILEQLAQHTTESDNISRKYEISFGKIYVTKPMVNESDGVTHALYPQEARLR       120
tr|A0A0L8RB33|A0A0L8RB33_SACEU      DIICEDSTLILEQLAXHTTESDNISRKYEISFGKIYVTKPMVNESDGVTHALYPQEARLR       120
tr|G0VJ71|G0VJ71_NAUCC              DIISEDSTLILEQLAQHTTETDNVSRKYEIGFGKIYVTKPMVNESDGVTHALYPQEARLR       120
tr|G8ZM49|G8ZM49_TORDC              DIISEDSTLILEQLAQHTTEADNISRKYEISFGKIYVTKPMVNESDGVTHALYPQEARLR       118
tr|A0A1Q3A090|A0A1Q3A090_ZYGRO      DIISEDSTLILEQLAQHTTESDNISRKYEISFGKIYVTKPMVNESDGVTHALYPQEARLR       120
tr|A0A0N7IS35|A0A0N7IS35_9SACH      DIISEDSTLILEQLAQHTTESDNISRKYEIGFGKIYVTKPMVNESDGVTHALYPQEARLR       119
tr|A0A212MG88|A0A212MG88_ZYGBA      DIISEDSTLILEQLAQHTTESDNISRKYEIGFGKIYVTKPMVNESDGVTHALYPQEARLR       119
tr|A0A1S7HHE1|A0A1S7HHE1_9SACH      DIISEDSTLILEQLAQHTTESDNISRKYEIGFGKIYVTKPMVNESDGVTHALYPQEARLR       119
tr|S6ESB4|S6ESB4_ZYGB2              DIISEDSTLILEQLAQHTTESDNISRKYEIGFGKIYVTKPMVNESDGVTHALYPQEARLR       119
tr|B6K5Q5|B6K5Q5_SCHJY              EIVDDDSTLTLDQYAQHTGAQGDYTRRYEINFGQIYLSRPTMTEADGSTTTMFPQEARLR       107
sp|Q02061|RPB2_SCHPO                EIVDDDSTLTLDQYAQHTGAQGDVTRRYEINFGQIYLSRPTMTEADGSTTTMFPQEARLR       107
tr|S9R8U4|S9R8U4_SCHOY              EIVDDDSTLTLDQYAQHTGAQGDVTRRYEINFGQIYLSRPTMTEADGSTTTMFPQEARLR       107
tr|S9W8C6|S9W8C6_SCHCR              EIVDDDSTLTLDQYAQHTGAQGDVTRRYEINFGQIYLSRPTMTEADGSTTTMFPQEARLR       107
                                     *: :   : *:  * *:    :   :* : * :**:::*   * **    : *:*:***
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sp|P30876|RPB2_HUMAN                NLTYSAPLYVDITKTVIKEG--------------EEQLQTQHQKTFIGKIPIMLRSTYCL    162
tr|G3V8Y5|G3V8Y5_RAT                NLTYSAPLYVDITKTVIKEG--------------EEQLQTQHQKTFIGKIPIMLRSTYCL    162
tr|A0A250Y753|A0A250Y753_CASCN      NLTYSAPLYVDITKTVIKEG--------------EEQLQTQHQKTFIGKIPIMLRSTYCL    162
tr|A0A1U7R4C7|A0A1U7R4C7_MESAU      NLTYSAPLYVDITKTVIKEG--------------EEQLQTQHQKTFIGKIPIMLRSTYCL    162
tr|A0A286XIQ9|A0A286XIQ9_CAVPO      NLTYSAPLYVDITKTVIKEG--------------EEQLQTQHQKTFIGKIPIMLRSTYCL    162
tr|I3M351|I3M351_ICTTR              NLTYSAPLYVDITKTVIKEG--------------EEQLQTQHQKTFIGKIPIMLRSTYCL    162
tr|G7P5R6|G7P5R6_MACFA              NLTYSAPLYVDITKTVIKEG--------------EEQLQTQHQKTFIGKIPIMLRSTYCL    162
tr|H2QPI8|H2QPI8_PANTR              NLTYSAPLYVDITKTVIKEG--------------EEQLQTQHQKTFIGKIPIMLRSTYCL    162
tr|A0A1U7V0T5|A0A1U7V0T5_TARSY      NLTYSAPLYVDITKTVIKEG--------------EEQLQTQHQKTFIGKIPIMLRSTYCL    162
tr|A0A1S2ZSL2|A0A1S2ZSL2_ERIEU      NLTYSAPLYVDITKTVIKEG--------------EEQLQTQHQKTFIGKIPIMLRSTYCL    162
tr|A0A0D9QYL1|A0A0D9QYL1_CHLSB      NLTYSAPLYVDITKTVIKEG--------------EEQLQTQHQKTFIGKIPIMLRSTYCL    155
tr|A0A2K5ZNR7|A0A2K5ZNR7_MANLE      NLTYSAPLYVDITKTVIKEG--------------EEQLQTQHQKTFIGKIPIMLRSTYCL    155
tr|A0A2I2ZIU3|A0A2I2ZIU3_GORGO      NLTYSAPLYVDITKTVIKEG--------------EEQLQTQHQKTFIGKIPIMLRSTYCL    162
tr|A0A1D5QGA5|A0A1D5QGA5_MACMU      NLTYSAPLYVDITKTVIKEG--------------EEQLQTQHQKTFIGKIPIMLRSTYCL    162
tr|A0A2J8S2N1|A0A2J8S2N1_PONAB      NLTYSAPLYVDITKTVIKEG--------------EEQLQTQHQKTFIGKIPIMLRSTYCL    162
tr|A0A2K5K5J5|A0A2K5K5J5_COLAP      NLTYSAPLYVDITKTVIKEG--------------EEQLQTQHQKTFIGKIPIMLRSTYCL    162
tr|A0A2J8PEW7|A0A2J8PEW7_PANTR      NLTYSAPLYVDITKTVIKEG--------------EEQLQTQHQKTFIGKIPIMLRSTYCL    155
tr|A0A2K5CY83|A0A2K5CY83_AOTNA      NLTYSAPLYVDITKTVIKEG--------------EEQLQTQHQKTFIGKIPIMLRSTYCL    162
tr|A0A096NEY4|A0A096NEY4_PAPAN      NLTYSAPLYVDITKTVIKEG--------------EEQLQTQHQKTFIGKIPIMLRSTYCL    162
tr|C9J2Y9|C9J2Y9_HUMAN              NLTYSAPLYVDITKTVIKEG--------------EEQLQTQHQKTFIGKIPIMLRSTYCL    155
tr|G8BY61|G8BY61_TETPH              NLTYSSGLFVDVNKRTYEATDVPGRELKYNLIAEESEDSENDKVFIGRLPVMLRSKNCY    178
tr|A0A1X7QYA1|A0A1X7QYA1_9SACH      NLTYSSGLFVDVKKRTYEAVDVPGRELKYELIAEESEDDSESGKVFIGRLPIMLRSKNCY    176
tr|J7RV95|J7RV95_KAZNA              NLTYSSGLFVDVKKRTYEAIDVPGRDLKYELIAEESEDDSERGKVFIGRLPIMLRSKNCY    176
tr|H2AVJ8|H2AVJ8_KAZAF              NLTYSSGLFVDVRKRTYEAVDVPGRDLKYELIAEESEDDSESGKVFIGRLPIMLRSKNCY    176
sp|Q6FLD5|RPB2_CANGA                NLTYSSGLFVDVTKRTYEAVDVPGRDLNYQLIAEESEDDSESGKVFIGRLPIMLRSKNCY    178
sp|P08518|RPB2_YEAST                NLTYSSGLFVDVKKRTYEAIDVPGRELKYELIAEESEDDSESGKVFIGRLPIMLRSKNCY    180
tr|A0A0L8VHA5|A0A0L8VHA5_9SACH      NLTYSSGLFVDVKKRTYEAIDVPGRELKYELIAEESEDDSESGKVFIGRLPIMLRSKNCY    180
tr|A0A0L8RB33|A0A0L8RB33_SACEU      NLTYSSGLFVDVKKRTYEAVDVPGRELKYELIAEESEDDSESGKVFIGRLPIMLRSKNCY    180
tr|G0VJ71|G0VJ71_NAUCC              NLTYSSGLFVDVKKRTYEAVDVPGRELKYELIAEESEEESESGKVFIGRLPIMLRSKNCY    180
tr|G8ZM49|G8ZM49_TORDC              NLTYSSGLFVDVKKRTYEAVDVPGRELKYELIAEESEDDSESGKVFIGRLPIMLRSKNCY    178
tr|A0A1Q3A090|A0A1Q3A090_ZYGRO      NLTYSSGLFVDVKKRTHEAVDIPGRELKYEMIAEESENDSDSGKVFIGRLPIMLRSKNCY    180
tr|A0A0N7IS35|A0A0N7IS35_9SACH      NLTYSSGLFVDVKKRTYEAVDLPGRELKYELIAEESE-EGDSGKVFIGRLPIMLRSKNCY    178
tr|A0A212MG88|A0A212MG88_ZYGBA      NLTYSSGLFVDVKKRTYEAVDLPGRELKYELIAEESEDDSDSGKVFIGRLPIMLRSKNCY    179
tr|A0A1S7HHE1|A0A1S7HHE1_9SACH      NLTYSSGLFVDVKKRTYEAVDLPGRELKYELIAEESEDDSDSGKVFIGRLPIMLRSKNCY    179
tr|S6ESB4|S6ESB4_ZYGB2              NLTYSSGLFVDVKKRTYEAVDLPGRELKYELIAEESEDDSDSGKVFIGRLPIMLRSKNCY    179
tr|B6K5Q5|B6K5Q5_SCHJY              NLTYSSPLYVDMRKKVMRAQDSNVPIGEEIW--LTEEEDDEPSKVFIGKIPIMLRSTFCI    165
sp|Q02061|RPB2_SCHPO                NLTYSSPLYVDMRKKVMVAADSNVPIGEEEW--LVEEEDEEPSKVFIGKIPIMLRSTFCI    165
tr|S9R8U4|S9R8U4_SCHOY              NLTYSSPLYVDMRKKVMVAADSNVPIGEEEW--LVEEEDEDPSKVFIGKIPIMLRSTFCI    165
tr|S9W8C6|S9W8C6_SCHCR              NLTYSSPLYVDMRKKVMVAADSNVPIGEEEW--LVEEEDEDPSKVFIGKIPIMLRSTFCI    165
                                    *****: *:**: * .                   .: : :  *.***::*:****. *

sp|P30876|RPB2_HUMAN                LNGLTDRDLCELNECPLDPGGYFIINGSEKVLIAQEKMATNTVYVFAKKD-SKYAYTGEC    221
tr|G3V8Y5|G3V8Y5_RAT                LNGLTDRDLCELNECPLDPGGYFIINGSEKVLIAQEKMATNTVYVFAKKD-SKYAYTGEC    221
tr|A0A250Y753|A0A250Y753_CASCN      LNGLTDRDLCELNECPLDPGGYFIINGSEKVLIAQEKMATNTVYVFAKKD-SKYAYTGEC    221
tr|A0A1U7R4C7|A0A1U7R4C7_MESAU      LNGLTDRDLCELNECPLDPGGYFIINGSEKVLIAQEKMATNTVYVFAKKD-SKYAYTGEC    221
tr|A0A286XIQ9|A0A286XIQ9_CAVPO      LNGLTDRDLCELNECPLDPGGYFIINGSEKVLIAQEKMATNTVYVFAKKD-SKYAYTGEC    221
tr|I3M351|I3M351_ICTTR              LNGLTDRDLCELNECPLDPGGYFIINGSEKVLIAQEKMATNTVYVFAKKD-SKYAYTGEC    221
tr|G7P5R6|G7P5R6_MACFA              LNGLTDRDLCELNECPLDPGGYFIINGSEKVLIAQEKMATNTVYVFAKKD-SKYAYTGEC    221
tr|H2QPI8|H2QPI8_PANTR              LNGLTDRDLCELNECPLDPGGYFIINGSEKVLIAQEKMATNTVYVFAKKD-SKYAYTGEC    221
tr|A0A1U7V0T5|A0A1U7V0T5_TARSY      LNGLTDRDLCELNECPLDPGGYFIINGSEKVLIAQEKMATNTVYVFAKKD-SKYAYTGEC    221
tr|A0A1S2ZSL2|A0A1S2ZSL2_ERIEU      LNGLTDRDLCELNECPLDPGGYFIINGSEKVLIAQEKMATNTVYVFAKKD-SKYAYTGEC    221
tr|A0A0D9QYL1|A0A0D9QYL1_CHLSB      LNGLTDRDLCELNECPLDPGGYFIINGSEKVLIAQEKMATNTVYVFAKKD-SKYAYTGEC    214
tr|A0A2K5ZNR7|A0A2K5ZNR7_MANLE      LNGLTDRDLCELNECPLDPGGYFIINGSEKVLIAQEKMATNTVYVFAKKD-SKYAYTGEC    214
tr|A0A2I2ZIU3|A0A2I2ZIU3_GORGO      LNGLTDRDLCELNECPLDPGGYFIINGSEKVLIAQEKMATNTVYVFAKKD-SKYAYTGEC    221
tr|A0A1D5QGA5|A0A1D5QGA5_MACMU      LNGLTDRDLCELNECPLDPGGYFIINGSEKVLIAQEKMATNTVYVFAKKD-SKYAYTGEC    221
tr|A0A2J8S2N1|A0A2J8S2N1_PONAB      LNGLTDRDLCELNECPLDPGGYFIINGSEKVLIAQEKMATNTVYVFAKKD-SKYAYTGEC    221
tr|A0A2K5K5J5|A0A2K5K5J5_COLAP      LNGLTDRDLCELNECPLDPGGYFIINGSEKVLIAQEKMATNTVYVFAKKD-SKYAYTGEC    221
tr|A0A2J8PEW7|A0A2J8PEW7_PANTR      LNGLTDRDLCELNECPLDPGGYFIINGSEKVLIAQEKMATNTVYVFAKKD-SKYAYTGEC    214
tr|A0A2K5CY83|A0A2K5CY83_AOTNA      LNGLTDRDLCELNECPLDPGGYFIINGSEKVLIAQEKMATNTVYVFAKKD-SKYAYTGEC    221
tr|A0A096NEY4|A0A096NEY4_PAPAN      LNGLTDRDLCELNECPLDPGGYFIINGSEKVLIAQEKMATNTVYVFAKKD-SKYAYTGEC    221
tr|C9J2Y9|C9J2Y9_HUMAN              LNGLTDRDLCELNECPLDPGGYFIINGSEKVLIAQEKMATNTVYVFAKKD-SKYAYTGEC    214
tr|G8BY61|G8BY61_TETPH              LSDATESDLYKLKECPFDMGGYFIINGSEKVLIAQERSAGNIVQVFKKAAPSPISHVAEI    238
tr|A0A1X7QYA1|A0A1X7QYA1_9SACH      LSDATESDLYKLKECPFDMGGYFIINGSEKVLIAQERSAGNIVQVFKKAAPSPISHIAEI    236
tr|J7RV95|J7RV95_KAZNA              LSDATESDLYKLKECPFDMGGYFIINGSEKVLIAQERSAGNIVQVFKKAAPSPISHVAEI    236
tr|H2AVJ8|H2AVJ8_KAZAF              LSDATESDLYKLKECPFDMGGYFIINGSEKVLIAQERSAGNIVQVFKKAAPSPISHVAEI    236
sp|Q6FLD5|RPB2_CANGA                LSDATESDLYKLKECPFDMGGYFIINGSEKVLIAQERSAGNIVQVFKKAAPSPISHVAEI    238
sp|P08518|RPB2_YEAST                LSEATESDLYKLKECPFDMGGYFIINGSEKVLIAQERSAGNIVQVFKKAAPSPISHVAEI    240
tr|A0A0L8VHA5|A0A0L8VHA5_9SACH      LSEATESDLYKLKECPFDMGGYFIINGSEKVLIAQERSAGNIVQVFKKAAPSPISHVAEI    240
tr|A0A0L8RB33|A0A0L8RB33_SACEU      LSEATESDLYKLKECPFDMGGYFIINGSEKVLIAQERSAGNIVQVFKKAAPSPISHVAEI    240
tr|G0VJ71|G0VJ71_NAUCC              LSDATESDLYKLKECPFDMGGYFIINGSEKVLIAQERSAGNIVQVFKKAAPSPISHVAEI    240
tr|G8ZM49|G8ZM49_TORDC              LSDATELDLYKLKECPFDMGGYFIINGSEKVLIAQERSAGNIVQVFKKAAPSPISHVAEI    238
tr|A0A1Q3A090|A0A1Q3A090_ZYGRO      LSDATESDLYKLKECPFDMGGYFIINGSEKVLIAQERSAGNIVQVFKKAAPSPISHVAEI    240
tr|A0A0N7IS35|A0A0N7IS35_9SACH      LSDATESDLYKLKECPFDMGGYFIINGSEKVLIAQERSAGNIVQVFKKAAPSPISHVAEI    238
tr|A0A212MG88|A0A212MG88_ZYGBA      LSDATESDLYKLKECPFDMGGYFIINGSEKVLIAQERSAGNIVQVFKKAAPSPISHVAEI    239
tr|A0A1S7HHE1|A0A1S7HHE1_9SACH      LSDATESDLYKLKECPFDMGGYFIINGSEKVLIAQERSAGNIVQVFKKAAPSPISHVAEI    239
tr|S6ESB4|S6ESB4_ZYGB2              LSDATESDLYKLKECPFDMGGYFIINGSEKVLIAQERSAGNIVQVFKKAAPSPISHVAEI    239
tr|B6K5Q5|B6K5Q5_SCHJY              LNGVSDSELYDLNECPYDQGGYFIINGSEKVIIAQERSAANIVQVFRKAAPSPIAYVAEI    225
sp|Q02061|RPB2_SCHPO                LNGVSDSELYDLNECPYDQGGYFIINGSEKVIIAQERSAANIVQVFKKAAPSPIAYVAEI    225
tr|S9R8U4|S9R8U4_SCHOY              LNGVSDAELYDLNECPYDQGGYFIINGSEKVIIAQERSAANIVQVFRKAAPSPIALVAEI    225
tr|S9W8C6|S9W8C6_SCHCR              LNGVSDAELYDLNECPYDQGGYFIINGSEKVIIAQERSAANIVQVFRKAAPSPVAYVAEI    225
                                    *.  :: :* .*:*** * ************:****: * * * ** *   *  :  .*
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sp|P30876|RPB2_HUMAN                RSCLENSSRPTSTIWVSMLARGGQGAKKSAIGQRIVATLPYIKQEVPIIIVFRALGFVSD       281
tr|G3V8Y5|G3V8Y5_RAT                RSCLENSSRPTSTIWVSMLARGGQGAKKSAIGQRIVATLPYIKQEVPIIIVFRALGFVSD       281
tr|A0A250Y753|A0A250Y753_CASCN      RSCLENSSRPTSTIWVSMLARGGQGAKKSAIGQRIVATLPYIKQEVPIIIVFRALGFVSD       281
tr|A0A1U7R4C7|A0A1U7R4C7_MESAU      RSCLENSSRPTSTIWVSMLARGGQGAKKSAIGQRIVATLPYIKQEVPIIIVFRALGFVSD       281
tr|A0A286XIQ9|A0A286XIQ9_CAVPO      RSCLENSSRPTSTIWVSMLARGGQGAKKSAIGQRIVATLPYIKQEVPIIIVFRALGFVSD       281
tr|I3M351|I3M351_ICTTR              RSCLENSSRPTSTIWVSMLARGGQGAKKSAIGQRIVATLPYIKQEVPIIIVFRALGFVSD       281
tr|G7P5R6|G7P5R6_MACFA              RSCLENSSRPTSTIWVSMLARGGQGAKKSAIGQRIVATLPYIKQEVPIIIVFRALGFVSD       281
tr|H2QPI8|H2QPI8_PANTR              RSCLENSSRPTSTIWVSMLARGGQGAKKSAIGQRIVATLPYIKQEVPIIIVFRALGFVSD       281
tr|A0A1U7V0T5|A0A1U7V0T5_TARSY      RSCLENSSRPTSTIWVSMLARGGQGAKKSAIGQRIVATLPYIKQEVPIIIVFRALGFVSD       281
tr|A0A1S2ZSL2|A0A1S2ZSL2_ERIEU      RSCLENSSRPTSTIWVSMLARGGQGAKKSAIGQRIVATLPYIKQEVPIIIVFRALGFVSD       281
tr|A0A0D9QYL1|A0A0D9QYL1_CHLSB      RSCLENSSRPTSTIWVSMLARGGQGAKKSAIGQRIVATLPYIKQEVPIIIVFRALGFVSD       274
tr|A0A2K5ZNR7|A0A2K5ZNR7_MANLE      RSCLENSSRPTSTIWVSMLARGGQGAKKSAIGQRIVATLPYIKQEVPIIIVFRALGFVSD       274
tr|A0A2I2ZIU3|A0A2I2ZIU3_GORGO      RSCLENSSRPTSTIWVSMLARGGQGAKKSAIGQRIVATLPYIKQEVPIIIVFRALGFVSD       281
tr|A0A1D5QGA5|A0A1D5QGA5_MACMU      RSCLENSSRPTSTIWVSMLARGGQGAKKSAIGQRIVATLPYIKQEVPIIIVFRALGFVSD       281
tr|A0A2J8S2N1|A0A2J8S2N1_PONAB      RSCLENSSRPTSTIWVSMLARGGQGAKKSAIGQRIVATLPYIKQEVPIIIVFRALGFVSD       281
tr|A0A2K5K5J5|A0A2K5K5J5_COLAP      RSCLENSSRPTSTIWVSMLARGGQGAKKSAIGQRIVATLPYIKQEVPIIIVFRALGFVSD       281
tr|A0A2J8PEW7|A0A2J8PEW7_PANTR      RSCLENSSRPTSTIWVSMLARGGQGAKKSAIGQRIVATLPYIKQEVPIIIVFRALGFVSD       274
tr|A0A2K5CY83|A0A2K5CY83_AOTNA      RSCLENSSRPTSTIWVSMLARGGQGAKKSAIGQRIVATLPYIKQEVPIIIVFRALGFVSD       281
tr|A0A096NEY4|A0A096NEY4_PAPAN      RSCLENSSRPTSTIWVSMLARGGQGAKKSAIGQRIVATLPYIKQEVPIIIVFRALGFVSD       281
tr|C9J2Y9|C9J2Y9_HUMAN              RSCLENSSRPTSTIWVSMLARGGQGAKKSAIGQRIVATLPYIKQEVPIIIVFRALGFVSD       274
tr|G8BY61|G8BY61_TETPH              RSALEKGSRFISTLQVKLYGRES------SSTRTIKATLPYIKQDIPIVIIFRALGIIPD       292
tr|A0A1X7QYA1|A0A1X7QYA1_9SACH      RSALEKGSRFISTLQVKLYGREG------STSRTIKATLPYIKQDIPIVIIFRALGIIPD       290
tr|J7RV95|J7RV95_KAZNA              RSALEKGSRFISTLQVKLYGREG------SSSRTIKATLPYIKQDIPIVIIFRALGVIPD       290
tr|H2AVJ8|H2AVJ8_KAZAF              RSALEKGSRFISTLQVKLYGRES------SSSRTIKATLPYIKQDIPIVIIFRALGIIPD       290
sp|Q6FLD5|RPB2_CANGA                RSALEKGSRFISTLQVKLYGRES------SSARTIKATLPYIKQDIPIVIIFRALGIIPD       292
sp|P08518|RPB2_YEAST                RSALEKGSRFISTLQVKLYGREG------SSARTIKATLPYIKQDIPIVIIFRALGIIPD       294
tr|A0A0L8VHA5|A0A0L8VHA5_9SACH      RSALEKGSRFISTLQVKLYGREG------SSARTIKATLPYIKQDIPIVIIFRALGIIPD       294
tr|A0A0L8RB33|A0A0L8RB33_SACEU      RSALEKGSRFISTLQVKLYGREG------SSARTIKATLPYIKQDIPIVIIFRALGIIPD       294
tr|G0VJ71|G0VJ71_NAUCC              RSALEKGSRFISTLQVKLYGREG------SDARTINATLPYIKQDIPIVIIFRALGIIPD       294
tr|G8ZM49|G8ZM49_TORDC              RSALEKGSRFISTLQVKLYGREG------SSARTIKATLPYIKQDIPIVIIFRALGIIPD       292
tr|A0A1Q3A090|A0A1Q3A090_ZYGRO      RSALEKGSRFISTLQVKLFAREG------NSSRTIKATLPYIKQDIPIVIIFRALGIIPD       294
tr|A0A0N7IS35|A0A0N7IS35_9SACH      RSALEKGSRFISTLQVKLFAREG------NSSRTIKATLPYIKQDIPIVIIFRALGIIPD       292
tr|A0A212MG88|A0A212MG88_ZYGBA      RSALEKGSRFISTLQVKLFAREG------NSSRTIKATLPYIKQDIPIVIIFRALGIIPD       293
tr|A0A1S7HHE1|A0A1S7HHE1_9SACH      RSALEKGSRFISTLQVKLFAREG------NSSRTIKATLPYIKQDIPIVIIFRALGIIPD       293
tr|S6ESB4|S6ESB4_ZYGB2              RSALEKGSRFISTLQVKLFAREG------NSSRTIKATLPYIKQDIPIVIIFRALGIIPD       293
tr|B6K5Q5|B6K5Q5_SCHJY              RSALERGSRLISSMQIKLMARSTE-----NSGQTIKATLPYIRSDIPIVVVFRALGVVPD       280
sp|Q02061|RPB2_SCHPO                RSALERGSRLISSMQIKLMARNTE-----NSGQTIRATLPYIRSDIPIVIVFRALGVVPD       280
tr|S9R8U4|S9R8U4_SCHOY              RSAVERGSRLISSMQIKLMARNAE-----NSGQTIRATLPYIRSDIPIVIVFRALGVVPD       280
tr|S9W8C6|S9W8C6_SCHCR              RSAVERGSRLISSMQIKLMARNAE-----NSGQTIRATLPYIRSDIPIVIVFRALGVVPD       280
                                    **.:*..**  *:: :.: .*           : * ******:.::**:::*****.: *

sp|P30876|RPB2_HUMAN                RDILEHIIYDFEDPEMMEMVKPSLDEAFVIQEQNVALNFIGSRGAKPGVTKEKRIKYAKE       341
tr|G3V8Y5|G3V8Y5_RAT                RDILEHIIYDFEDPEMMEMVKPSLDEAFVIQEQNVALNFIGSRGAKPGVTKEKRIKYAKE       341
tr|A0A250Y753|A0A250Y753_CASCN      RDILEHIIYDFEDPEMMEMVKPSLDEAFVIQEQNVALNFIGSRGAKPGVTKEKRIKYAKE       341
tr|A0A1U7R4C7|A0A1U7R4C7_MESAU      RDILEHIIYDFEDPEMMEMVKPSLDEAFVIQEQNVALNFIGSRGAKPGVTKEKRIKYAKE       341
tr|A0A286XIQ9|A0A286XIQ9_CAVPO      RDILEHIIYDFEDPEMMEMVKPSLDEAFVIQEQNVALNFIGSRGAKPGVTKEKRIKYAKE       341
tr|I3M351|I3M351_ICTTR              RD     IYDFEDPEMMEMVKPSLDEAFVIQEQNVALNFIGSRGAKPGVTKEKRIKYAKE       341
tr|G7P5R6|G7P5R6_MACFA              RDILEHIIYDFEDPEMMEMVKPSLDEAFVIQEQNVALNFIGSRGAKPGVTKEKRIKYAKE       341
tr|H2QPI8|H2QPI8_PANTR              RDILEHIIYDFEDPEMMEMVKPSLDEAFVIQEQNVALNFIGSRGAKPGVTKEKRIKYAKE       341
tr|A0A1U7V0T5|A0A1U7V0T5_TARSY      RDILEHIIYDFEDPEMMEMVKPSLDEAFVIQEQNVALNFIGSRGAKPGVTKEKRIKYAKE       341
tr|A0A1S2ZSL2|A0A1S2ZSL2_ERIEU      RDILEHIIYDFEDPEMMEMVKPSLDEAFVIQEQNVALNFIGSRGAKPGVTKEKRIKYAKE       341
tr|A0A0D9QYL1|A0A0D9QYL1_CHLSB      RDILEHIIYDFEDPEMMEMVKPSLDEAFVIQEQNVALNFIGSRGAKPGVTKEKRIKYAKE       334
tr|A0A2K5ZNR7|A0A2K5ZNR7_MANLE      RDILEHIIYDFEDPEMMEMVKPSLDEAFVIQEQNVALNFIGSRGAKPGVTKEKRIKYAKE       334
tr|A0A2I2ZIU3|A0A2I2ZIU3_GORGO      RDILEHIIYDFEDPEMMEMVKPSLDEAFVIQEQNVALNFIGSRGAKPGVTKEKRIKYAKE       341
tr|A0A1D5QGA5|A0A1D5QGA5_MACMU      RDILEHIIYDFEDPEMMEMVKPSLDEAFVIQEQNVALNFIGSRGAKPGVTKEKRIKYAKE       341
tr|A0A2J8S2N1|A0A2J8S2N1_PONAB      RDILEHIIYDFEDPEMMEMVKPSLDEAFVIQEQNVALNFIGSRGAKPGVTKEKRIKYAKE       341
tr|A0A2K5K5J5|A0A2K5K5J5_COLAP      RDILEHIIYDFEDPEMMEMVKPSLDEAFVIQEQNVALNFIGSRGAKPGVTKEKRIKYAKE       341
tr|A0A2J8PEW7|A0A2J8PEW7_PANTR      RDILEHIIYDFEDPEMMEMVKPSLDEAFVIQEQNVALNFIGSRGAKPGVTKEKRIKYAKE       334
tr|A0A2K5CY83|A0A2K5CY83_AOTNA      RDILEHIIYDFEDPEMMEMVKPSLDEAFVIQEQNVALNFIGSRGAKPGVTKEKRIKYAKE       341
tr|A0A096NEY4|A0A096NEY4_PAPAN      RDILEHIIYDFEDPEMMEMVKPSLDEAFVIQEQNVALNFIGSRGAKPGVTKEKRIKYAKE       341
tr|C9J2Y9|C9J2Y9_HUMAN              RDILEHIIYDFEDPEMMEMVKPSLDEAFVIQEQNVALNFIGSRGAKPGVTKEKRIKYAKE       334
tr|G8BY61|G8BY61_TETPH              GEILEHICYDVNDWQMLEMLKPCVEDGFVIQDRETALDFIGRRGTALGIKKEKRIQYAKD       352
tr|A0A1X7QYA1|A0A1X7QYA1_9SACH      GEILEHICYDVNDWQMLEMLKPCVEDGFVIQDRETALDFIGRRGTALGIKKEKRIQYAKD       350
tr|J7RV95|J7RV95_KAZNA              GEILEHICYDVNDWQMLEMLKPCVEDGFVIQDRETALDFIGRRGTALGIKKEKRIQYAKD       350
tr|H2AVJ8|H2AVJ8_KAZAF              GEILEHICYDVNDWQMLEMLKPCVEDGFVIQDRETALDFIGRRGTALGIKKEKRIQYAKD       350
sp|Q6FLD5|RPB2_CANGA                GEILEHICYDVNDWQMLEMLKPCVEDGFVIQDRETALDFIGRRGTALGIKKEKRIQYAKD       352
sp|P08518|RPB2_YEAST                GEILEHICYDVNDWQMLEMLKPCVEDGFVIQDRETALDFIGRRGTALGIKKEKRIQYAKD       354
tr|A0A0L8VHA5|A0A0L8VHA5_9SACH      GEILEHICYDVNDWQMLEMLKPCVEDGFVIQDRETALDFIGRRGTALGIKKEKRIQYAKD       354
tr|A0A0L8RB33|A0A0L8RB33_SACEU      GEILEHICYDVNDWQMLEMLKPCVEDGFVIQDRETALDFIGRRGTALGIKKEKRIQYAKD       354
tr|G0VJ71|G0VJ71_NAUCC              GEILEHICYDVNDWQMLEMLKPCVEDGFVIQDRETALDFIGRRGTALGIKKEKRIQYAKD       354
tr|G8ZM49|G8ZM49_TORDC              GEILEHICYDVNDWQMLEMLKPCVEDGFVIQDRETALDFIGRRGTALGIKKEKRIQYARD       352
tr|A0A1Q3A090|A0A1Q3A090_ZYGRO      GEILEHICYDVNDWQMLEMLKPCVEDGFVIQDRETALDFIGRRGTALGIKKEKRIQYARD       354
tr|A0A0N7IS35|A0A0N7IS35_9SACH      GEILEHICYDVNDWQMLEMLKPCVEDGFVIQDRETALDFIGRRGTALGIKKEKRIQYARD       352
tr|A0A212MG88|A0A212MG88_ZYGBA      GEILEHICYDVNDWQMLEMLKPCVEDGFVIQDRETALDFIGRRGTALGIKKEKRIQYARD       353
tr|A0A1S7HHE1|A0A1S7HHE1_9SACH      GEILEHICYDVNDWQMLEMLKPCVEDGFVIQDRETALDFIGRRGTALGIKKEKRIQYARD       353
tr|S6ESB4|S6ESB4_ZYGB2              GEILEHICYDVNDWQMLEMLKPCVEDGFVIQDRETALDFIGRRGTALGIKKEKRIQYARD       353
tr|B6K5Q5|B6K5Q5_SCHJY              RDILEHICYDPNDLQMLEMMKPCIEEAFVIQDKDVALDYIGKRGSTTGVTREKRLRYAHD       340
sp|Q02061|RPB2_SCHPO                RDILEHICYDPNDFQMLEMMKPCIEEAFVIQDKDIALDYIGKRGSTTGVTREKRLRYAHD       340
tr|S9R8U4|S9R8U4_SCHOY              RDILEHICYDPNDLQMLEMMKPCIEEAFVIQDKDIALDFIGKRGSTTGVTREKRLRYAHD       340
tr|S9W8C6|S9W8C6_SCHCR              RDILEHICYDPNDLQMLEMMKPCIEEAFVIQDKDIALDFIGKRGSTTGVTREKRLRYAHD       340
                                     :***** ** :* :*:**:**.:::.****::: **::** **:  *:.:***::**::
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sp|P30876|RPB2_HUMAN              VLQKEMLPHVGVSDFGETKKAYFLGYMVHRLLLAALGRRELDDRDHYGNKRLDLAGPLLA     401
tr|G3V8Y5|G3V8Y5_RAT              VLQKEMLPHVGVSDFGETKKAYFLGYMVHRLLLAALGRRELDDRDHYGNKRLDLAGPLLA     401
tr|A0A250Y753|A0A250Y753_CASCN    VLQKEMLPHVGVSDFGETKKAYFLGYMVHRLLLAALGRRELDDRDHYGNKRLDLAGPLLA     401
tr|A0A1U7R4C7|A0A1U7R4C7_MESAU    VLQKEMLPHVGVSDFGETKKAYFLGYMVHRLLLAALGRRELDDRDHYGNKRLDLAGPLLA     401
tr|A0A286XIQ9|A0A286XIQ9_CAVPO    VLQKEMLPHVGVSDFGETKKAYFLGYMVHRLLLAALGRRELDDRDHYGNKRLDLAGPLLA     401
tr|I3M351|I3M351_ICTTR            VLQKEMLPHVGVSDFGETKKAYFLGYMVHRLLLAALGRRELDDRDHYGNKRLDLAGPLLA     401
tr|G7P5R6|G7P5R6_MACFA            VLQKEMLPHVGVSDFGETKKAYFLGYMVHRLLLAALGRRELDDRDHYGNKRLDLAGPLLA     401
tr|H2QPI8|H2QPI8_PANTR            VLQKEMLPHVGVSDFGETKKAYFLGYMVHRLLLAALGRRELDDRDHYGNKRLDLAGPLLA     401
tr|A0A1U7V0T5|A0A1U7V0T5_TARSY    VLQKEMLPHVGVSDFGETKKAYFLGYMVHRLLLAALGRRELDDRDHYGNKRLDLAGPLLA     401
tr|A0A1S2ZSL2|A0A1S2ZSL2_ERIEU    VLQKEMLPHVGVSDFGETKKAYFLGYMVHRLLLAALGRRELDDRDHYGNKRLDLAGPLLA     401
tr|A0A0D9QYL1|A0A0D9QYL1_CHLSB    VLQKEMLPHVGVSDFGETKKAYFLGYMVHRLLLAALGRRELDDRDHYGNKRLDLAGPLLA     394
tr|A0A2K5ZNR7|A0A2K5ZNR7_MANLE    VLQKEMLPHVGVSDFGETKKAYFLGYMVHRLLLAALGRRELDDRDHYGNKRLDLAGPLLA     394
tr|A0A2I2ZIU3|A0A2I2ZIU3_GORGO    VLQKEMLPHVGVSDFGETKKAYFLGYMVHRLLLAALGRRELDDRDHYGNKRLDLAGPLLA     401
tr|A0A1D5QGA5|A0A1D5QGA5_MACMU    VLQKEMLPHVGVSDFGETKKAYFLGYMVHRLLLAALGRRELDDRDHYGNKRLDLAGPLLA     401
tr|A0A2J8S2N1|A0A2J8S2N1_PONAB    VLQKEMLPHVGVSDFGETKKAYFLGYMVHRLLLAALGRRELDDRDHYGNKRLDLAGPLLA     401
tr|A0A2K5K5J5|A0A2K5K5J5_COLAP    VLQKEMLPHVGVSDFGETKKAYFLGYMVHRLLLAALGRRELDDRDHYGNKRLDLAGPLLA     401
tr|A0A2J8PEW7|A0A2J8PEW7_PANTR    VLQKEMLPHVGVSDFGETKKAYFLGYMVHRLLLAALGRRELDDRDHYGNKRLDLAGPLLA     394
tr|A0A2K5CY83|A0A2K5CY83_AOTNA    VLQKEMLPHVGVSDFGETKKAYFLGYMVHRLLLAALGRRELDDRDHYGNKRLDLAGPLLA     401
tr|A0A096NEY4|A0A096NEY4_PAPAN    VLQKEMLPHVGVSDFGETKKAYFLGYMVHRLLLAALGRRELDDRDHYGNKRLDLAGPLLA     401
tr|C9J2Y9|C9J2Y9_HUMAN            VLQKEMLPHVGVSDFGETKKAYFLGYMVHRLLLAALGRRELDDRDHYGNKRLDLAGPLLA     394
tr|G8BY61|G8BY61_TETPH            ILQKEFLPHITQLEGFESRKAFFLGYMINRLLLCALDRKDQDDRDHFGKKRLDLAGPLLG     412
tr|A0A1X7QYA1|A0A1X7QYA1_9SACH    ILQKEFLPHITQLEGFESRKAFFLGYMINRLLLCALDRRDQDDRDHFGKKRLDLAGPLLG     410
tr|J7RV95|J7RV95_KAZNA            ILQKEFLPHITQLEGFESRKAFFLGYMINRLLLCALDRRDQDDRDHFGKKRLDLAGPLLG     410
tr|H2AVJ8|H2AVJ8_KAZAF            ILQKEFLPHITQLEGFESRKAFFLGYMINRLLLCALDRKDQDDRDHFGKKRLDLAGPLLG     410
sp|Q6FLD5|RPB2_CANGA              ILQKEFLPHITQLEGFESRKAFFLGYMINRLLLCALDRKDQDDRDHFGKKRLDLAGPLLA     412
sp|P08518|RPB2_YEAST              ILQKEFLPHITQLEGFESRKAFFLGYMINRLLLCALDRKDQDDRDHFGKKRLDLAGPLLA     414
tr|A0A0L8VHA5|A0A0L8VHA5_9SACH    ILQKEFLPHITQLEGFESRKAFFLGYMINRLLLCALDRKDQDDRDHFGKKRLDLAGPLLA     414
tr|A0A0L8RB33|A0A0L8RB33_SACEU    ILQKEFLPHITQLEGFESRKAFFLGYMINRLLLCALDRKDQDDRDHFGKKRLDLAGPLLA     414
tr|G0VJ71|G0VJ71_NAUCC            ILQKEFLPHITQLEGFESRKAFFLGYMINRLLLCALDRKDQDDRDHFGKKRLDLAGPLLA     414
tr|G8ZM49|G8ZM49_TORDC            ILQKEFLPHITQLEGFESRKAFFLGYMINRLLLCALDRKDQDDRDHFGKKRLDLAGPLLA     412
tr|A0A1Q3A090|A0A1Q3A090_ZYGRO    ILQKEFLPHITQLEGFESRKAFFLGYMINRLLLCALDRRDQDDRDHFGKKRLDLAGPLLA     414
tr|A0A0N7IS35|A0A0N7IS35_9SACH    ILQKEFLPHITQLEGFESRKAFFLGYMINRLLLCALDRRDQDDRDHFGKKRLDLAGPLLA     412
tr|A0A212MG88|A0A212MG88_ZYGBA    ILQKEFLPHITQLEGFESRKAFFLGYMINRLLLCALDRRDQDDRDHFGKKRLDLAGPLLA     413
tr|A0A1S7HHE1|A0A1S7HHE1_9SACH    ILQKEFLPHITQLEGFESRKAFFLGYMINRLLLCALDRRDQDDRDHFGKKRLDLAGPLLA     413
tr|S6ESB4|S6ESB4_ZYGB2            ILQKEFLPHITQLEGFESRKAFFLGYMINRLLLCALDRRDQDDRDHFGKKRLDLAGPLLA     413
tr|B6K5Q5|B6K5Q5_SCHJY            ILQKEMLPHITTLEGFETRKAFFLGYMVHRMLLCALERREPDDRDHFGKKRLDLAGPLLA     400
sp|Q02061|RPB2_SCHPO              ILQKELLPHITTMEGFETRKAFFLGYMIHRMLLCALERREPDDRDHFGKKRLDLAGPLLA     400
tr|S9R8U4|S9R8U4_SCHOY            ILQKELLPHITTMEGFETRKAFFLGYMINRMLLCALERREPDDRDHFGRKRLDLAGPLLA     400
tr|S9W8C6|S9W8C6_SCHCR            ILQKELLPHITTMEGFETRKAFFLGYMINRMLLCALERREPDDRDHFGRKRLDLAGPLLA     4009/9
                                  :****:***:   :  *::**:*****::*:**.** *:: *****:*.**********.


sp|P30876|RPB2_HUMAN              FLFRGMFKNLLKEVRIYAQKFIDRGKDFNLELAIKTRIISDGLKYSLATGNWGDQKKAHQ     461
tr|G3V8Y5|G3V8Y5_RAT              FLFRGMFKNLLKEVRIYAQKFIDRGKDFNLELAIKTRIISDGLKYSLATGNWGDQKKAHQ     461
tr|A0A250Y753|A0A250Y753_CASCN    FLFRGMFKNLLKEVRIYAQKFIDRGKDFNLELAIKTRIISDGLKYSLATGNWGDQKKAHQ     461
tr|A0A1U7R4C7|A0A1U7R4C7_MESAU    FLFRGMFKNLLKEVRIYAQKFIDRGKDFNLELAIKTRIISDGLKYSLATGNWGDQKKAHQ     461
tr|A0A286XIQ9|A0A286XIQ9_CAVPO    FLFRGMFKNLLKEVRIYAQKFIDRGKDFNLELAIKTRIISDGLKYSLATGNWGDQKKAHQ     461
tr|I3M351|I3M351_ICTTR            FLFRGMFKNLLKEVRIYAQKFIDRGKDFNLELAIKTRIISDGLKYSLATGNWGDQKKAHQ     461
tr|G7P5R6|G7P5R6_MACFA            FLFRGMFKNLLKEVRIYAQKFIDRGKDFNLELAIKTRIISDGLKYSLATGNWGDQKKAHQ     461
tr|H2QPI8|H2QPI8_PANTR            FLFRGMFKNLLKEVRIYAQKFIDRGKDFNLELAIKTRIISDGLKYSLATGNWGDQKKAHQ     461
tr|A0A1U7V0T5|A0A1U7V0T5_TARSY    FLFRGMFKNLLKEVRIYAQKFIDRGKDFNLELAIKTRIISDGLKYSLATGNWGDQKKAHQ     461
tr|A0A1S2ZSL2|A0A1S2ZSL2_ERIEU    FLFRGMFKNLLKEVRIYAQKFIDRGKDFNLELAIKTRIISDGLKYSLATGNWGDQKKAHQ     461
tr|A0A0D9QYL1|A0A0D9QYL1_CHLSB    FLFRGMFKNLLKEVRIYAQKFIDRGKDFNLELAIKTRIISDGLKYSLATGNWGDQKKAHQ     454
tr|A0A2K5ZNR7|A0A2K5ZNR7_MANLE    FLFRGMFKNLLKEVRIYAQKFIDRGKDFNLELAIKTRIISDGLKYSLATGNWGDQKKAHQ     454
tr|A0A2I2ZIU3|A0A2I2ZIU3_GORGO    FLFRGMFKNLLKEVRIYAQKFIDRGKDFNLELAIKTRIISDGLKYSLATGNWGDQKKAHQ     461
tr|A0A1D5QGA5|A0A1D5QGA5_MACMU    FLFRGMFKNLLKEVRIYAQKFIDRGKDFNLELAIKTRIISDGLKYSLATGNWGDQKKAHQ     461
tr|A0A2J8S2N1|A0A2J8S2N1_PONAB    FLFRGMFKNLLKEVRIYAQKFIDRGKDFNLELAIKTRIISDGLKYSLATGNWGDQKKAHQ     461
tr|A0A2K5K5J5|A0A2K5K5J5_COLAP    FLFRGMFKNLLKEVRIYAQKFIDRGKDFNLELAIKTRIISDGLKYSLATGNWGDQKKAHQ     461
tr|A0A2J8PEW7|A0A2J8PEW7_PANTR    FLFRGMFKNLLKEVRIYAQKFIDRGKDFNLELAIKTRIISDGLKYSLATGNWGDQKKAHQ     454
tr|A0A2K5CY83|A0A2K5CY83_AOTNA    FLFRGMFKNLLKEVRIYAQKFIDRGKDFNLELAIKTRIISDGLKYSLATGNWGDQKKAHQ     461
tr|A0A096NEY4|A0A096NEY4_PAPAN    FLFRGMFKNLLKEVRIYAQKFIDRGKDFNLELAIKTRIISDGLKYSLATGNWGDQKKAHQ     461
tr|C9J2Y9|C9J2Y9_HUMAN            FLFRGMFKNLLKEVRIYAQKFIDRGKDFNLELAIKTRIISDGLKYSLATGNWGDQKKAHQ     454
tr|G8BY61|G8BY61_TETPH            QLFKTLFRKLTKDIFRYMQRTVEEANDFNMKLAINAKTITSGLKYALATGNWGEQKKAMT     472
tr|A0A1X7QYA1|A0A1X7QYA1_9SACH    QLFKTLFRKLTKDIFRYMQRTVEEANDFNMKLAINAKTITSGLKYALATGNWGEQKKAMS     470
tr|J7RV95|J7RV95_KAZNA            QLFKTLFRKLTKDIFRYMQRTVEEAHDFNMKLAINAKTITSGLKYALATGNWGEQKKAMS     470
tr|H2AVJ8|H2AVJ8_KAZAF            QLFKTLFRKLTKDIFRYMQRTVEEANDFNMKLAINAKTITSGLKYALATGNWGEQKKAMS     470
sp|Q6FLD5|RPB2_CANGA              QLFKTLFRKLTKDIFRYMQRTVEEANDFNMKLAINAKTITSGLKYALATGNWGEQKKAMS     472
sp|P08518|RPB2_YEAST              QLFKTLFKKLTKDIFRYMQRTVEEAHDFNMKLAINAKTITSGLKYALATGNWGEQKKAMS     474
tr|A0A0L8VHA5|A0A0L8VHA5_9SACH    QLFKTLFKKLTKDIFRYMQRTVEEAHDFNMKLAINAKTITSGLKYALATGNWGEQKKAMS     474
tr|A0A0L8RB33|A0A0L8RB33_SACEU    QLFKSLFRKLTKDIFRYMQRTVEEAHDFNMKLAINAKTITSGLKYALATGNWGEQKKAMS     474
tr|G0VJ71|G0VJ71_NAUCC            SLFKTLFRKLTKDIFRYMQRTVEEAHDFNMKLAINAKTITSGLKYALATGNWGEQKKAMS     474
tr|G8ZM49|G8ZM49_TORDC            QLFKTLFRKLTKDIFRYMQRTVEEAKDFNMKLAINAKTITSGLKYALATGNWGEQKKAMS     472
tr|A0A1Q3A090|A0A1Q3A090_ZYGRO    QLFKTLFRKLTRDIFRYMQRTVEEAKDFNMKLAINAKTITSGLKYALATGNWGEQKKAMS     474
tr|A0A0N7IS35|A0A0N7IS35_9SACH    QLFKTLFRKLTRDIFRYMQRTVEEAKDFNMKLAINAKTITSGLKYALATGNWGEQKKAMS     472
tr|A0A212MG88|A0A212MG88_ZYGBA    QLFKTLFRKLTRDIFRYMQRTVEEAKDFNMKLAINAKTITSGLKYALATGNWGEQKKAMS     473
tr|A0A1S7HHE1|A0A1S7HHE1_9SACH    QLFKTLFRKLTRDIFRYMQRTVEEAKDFNMKLAINAKTITSGLKYALATGNWGEQKKAMS     473
tr|S6ESB4|S6ESB4_ZYGB2            QLFKTLFRKLTRDIFRYMQRTVEEAKDFNMKLAINAKTITSGLKYALATGNWGEQKKAMS     473
tr|B6K5Q5|B6K5Q5_SCHJY            SLFRMLFKKMTRDVYKYMQKCVETNREFNLTLAVKSNTITNGLRYSLATGNWGDQKRGLA     460
sp|Q02061|RPB2_SCHPO              SLFRMLFRKMTRDVYKYMQKCVETNREFNLTLAVKSNIITNGLRYSLATGNWGDQKRSMV     460
tr|S9R8U4|S9R8U4_SCHOY            SLFRMLFRKMTRDVYKYMQKCVETNREFNLTLAVKSNTITNGLRYSLATGNWGDQKRSMM     460
tr|S9W8C6|S9W8C6_SCHCR            SLFRMLFRKMTRDVYKYMQKCVETNREFNLTLAVKSNTITNGLRYSLATGNWGDQKRSMM     460
                                   **: :*::  :::  * *: ::  .:**: **:::. *:.**:*:*******:**:.
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sp|P30876|RPB2_HUMAN                ARAGVSQVLNRLTFASTLSHLRRLNSPIGRDGKLAKPRQLHNTLWGMVCPAETPEGHAVG    521
tr|G3V8Y5|G3V8Y5_RAT                ARAGVSQVLNRLTFASTLSHLRRLNSPIGRDGKLAKPRQLHNTLWGMVCPAETPEGHAVG    521
tr|A0A250Y753|A0A250Y753_CASCN      ARAGVSQVLNRLTFASTLSHLRRLNSPIGRDGKLAKPRQLHNTLWGMVCPAETPEGHAVG    521
tr|A0A1U7R4C7|A0A1U7R4C7_MESAU      ARAGVSQVLNRLTFASTLSHLRRLNSPIGRDGKLAKPRQLHNTLWGMVCPAETPEGHAVG    521
tr|A0A286XIQ9|A0A286XIQ9_CAVPO      ARAGVSQVLNRLTFASTLSHLRRLNSPIGRDGKLAKPRQLHNTLWGMVCPAETPEGHAVG    521
tr|I3M351|I3M351_ICTTR              ARAGVSQVLNRLTFASTLSHLRRLNSPIGRDGKLAKPRQLHNTLWGMVCPAETPEGHAVG    521
tr|G7P5R6|G7P5R6_MACFA              ARAGVSQVLNRLTFASTLSHLRRLNSPIGRDGKLAKPRQLHNTLWGMVCPAETPEGHAVG    521
tr|H2QPI8|H2QPI8_PANTR              ARAGVSQVLNRLTFASTLSHLRRLNSPIGRDGKLAKPRQLHNTLWGMVCPAETPEGHAVG    521
tr|A0A1U7V0T5|A0A1U7V0T5_TARSY      ARAGVSQVLNRLTFASTLSHLRRLNSPIGRDGKLAKPRQLHNTLWGMVCPAETPEGHAVG    521
tr|A0A1S2ZSL2|A0A1S2ZSL2_ERIEU      ARAGVSQVLNRLTFASTLSHLRRLNSPIGRDGKLAKPRQLHNTLWGMVCPAETPEGHAVG    521
tr|A0A0D9QYL1|A0A0D9QYL1_CHLSB      ARAGVSQVLNRLTFASTLSHLRRLNSPIGRDGKLAKPRQLHNTLWGMVCPAETPEGHAVG    514
tr|A0A2K5ZNR7|A0A2K5ZNR7_MANLE      ARAGVSQVLNRLTFASTLSHLRRLNSPIGRDGKLAKPRQLHNTLWGMVCPAETPEGHAVG    514
tr|A0A2I2ZIU3|A0A2I2ZIU3_GORGO      ARAGVSQVLNRLTFASTLSHLRRLNSPIGRDGKLAKPRQLHNTLWGMVCPAETPEGHAVG    521
tr|A0A1D5QGA5|A0A1D5QGA5_MACMU      ARAGVSQVLNRLTFASTLSHLRRLNSPIGRDGKLAKPRQLHNTLWGMVCPAETPEGHAVG    521
tr|A0A2J8S2N1|A0A2J8S2N1_PONAB      ARAGVSQVLNRLTFASTLSHLRRLNSPIGRDGKLAKPRQLHNTLWGMVCPAETPEGHAVG    521
tr|A0A2K5K5J5|A0A2K5K5J5_COLAP      ARAGVSQVLNRLTFASTLSHLRRLNSPIGRDGKLAKPRQLHNTLWGMVCPAETPEGHAVG    521
tr|A0A2J8PEW7|A0A2J8PEW7_PANTR      ARAGVSQVLNRLTFASTLSHLRRLNSPIGRDGKLAKPRQLHNTLWGMVCPAETPEGHAVG    514
tr|A0A2K5CY83|A0A2K5CY83_AOTNA      ARAGVSQVLNRLTFASTLSHLRRLNSPIGRDGKLAKPRQLHNTLWGMVCPAETPEGHAVG    521
tr|A0A096NEY4|A0A096NEY4_PAPAN      ARAGVSQVLNRLTFASTLSHLRRLNSPIGRDGKLAKPRQLHNTLWGMVCPAETPEGHAVG    521
tr|C9J2Y9|C9J2Y9_HUMAN              ARAGVSQVLNRLTFASTLSHLRRLNSPIGRDGKLAKPRQLHNTLWGMVCPAETPEGHAVG    514
tr|G8BY61|G8BY61_TETPH              SRAGVSQVLNRYTYSSTLSHLRRTNTPIGRDGKLAKPRQLHNTHWGLVCPAETPEGQACG    532
tr|A0A1X7QYA1|A0A1X7QYA1_9SACH      SRAGVSQVLNRYTYSSTLSHLRRTNTPIGRDGKLAKPRQLHNTHWGLVCPAETPEGQACG    530
tr|J7RV95|J7RV95_KAZNA              SRAGVSQVLNRYTYSSTLSHLRRTNTPIGRDGKLAKPRQLHNTHWGLVCPAETPEGQACG    530
tr|H2AVJ8|H2AVJ8_KAZAF              SRAGVSQVLNRYTYSSTLSHLRRTNTPIGRDGKLAKPRQLHNTHWGLVCPAETPEGQACG    530
sp|Q6FLD5|RPB2_CANGA                SRAGVSQVLNRYTYSSTLSHLRRTNTPIGRDGKLAKPRQLHNTHWGLVCPAETPEGQACG    532
sp|P08518|RPB2_YEAST                SRAGVSQVLNRYTYSSTLSHLRRTNTPIGRDGKLAKPRQLHNTHWGLVCPAETPEGQACG    534
tr|A0A0L8VHA5|A0A0L8VHA5_9SACH      SRAGVSQVLNRYTYSSTLSHLRRTNTPIGRDGKLAKPRQLHNTHWGLVCPAETPEGQACG    534
tr|A0A0L8RB33|A0A0L8RB33_SACEU      SRAGVSQVLNRYTYSSTLSHLRRTNTPIGRDGKLAKPRQLHNTHWGLVCPAETPEGQACG    534
tr|G0VJ71|G0VJ71_NAUCC              SRAGVSQVLNRYTYSSTLSHLRRTNTPIGRDGKLAKPRQLHNTHWGLVCPAETPEGQACG    534
tr|G8ZM49|G8ZM49_TORDC              SRAGVSQVLNRYTYSSTLSHLRRTNTPIGRDGKLAKPRQLHNTHWGLVCPAETPEGQACG    532
tr|A0A1Q3A090|A0A1Q3A090_ZYGRO      SRAGVSQVLNRYTYSSTLSHLRRTNTPIGRDGKLAKPRQLHNTHWGLVCPAETPEGQACG    534
tr|A0A0N7IS35|A0A0N7IS35_9SACH      SRAGVSQVLNRYTYSSTLSHLRRTNTPIGRDGKLAKPRQLHNTHWGLVCPAETPEGQACG    532
tr|A0A212MG88|A0A212MG88_ZYGBA      SRAGVSQVLNRYTYSSTLSHLRRTNTPIGRDGKLAKPRQLHNTHWGLVCPAETPEGQACG    533
tr|A0A1S7HHE1|A0A1S7HHE1_9SACH      SRAGVSQVLNRYTYSSTLSHLRRTNTPIGRDGKLAKPRQLHNTHWGLVCPAETPEGQACG    533
tr|S6ESB4|S6ESB4_ZYGB2              SRAGVSQVLNRYTYSSTLSHLRRTNTPIGRDGKLAKPRQLHNTHWGLVCPAETPEGQACG    533
tr|B6K5Q5|B6K5Q5_SCHJY              NRVGVSQVLNRYTFASTLSHLRRTNTPIGRDGKLAKPRQLHNTHWGMVCPAETPEGQACG    520
sp|Q02061|RPB2_SCHPO                NRVGVSQVLNRYTFASTLSHLRRTNTPIGRDGKLAKPRQLHNTHWGMVCPAETPEGQACG    520
tr|S9R8U4|S9R8U4_SCHOY              NRVGVSQVLNRYTFASTLSHLRRTNTPIGRDGKLAKPRQLHNTHWGMVCPAETPEGQACG    520
tr|S9W8C6|S9W8C6_SCHCR              NRVGVSQVLNRYTFASTLSHLRRTNTPIGRDGKLAKPRQLHNTHWGMVCPAETPEGQACG    520
                                     *.******** *::******** *:***************** **:*********:* *


sp|P30876|RPB2_HUMAN                LVKNLALMAYISVGSQPSPILEFLEEWSMENLEEISPAAIADATKIFVNGCWVGIHKDPE    581
tr|G3V8Y5|G3V8Y5_RAT                LVKNLALMAYISVGSQPSPILEFLEEWSMENLEEISPAAIADATKIFVNGCWVGIHKDPE    581
tr|A0A250Y753|A0A250Y753_CASCN      LVKNLALMAYISVGSQPSPILEFLEEWSMENLEEISPAAIADATKIFVNGCWVGIHKDPE    581
tr|A0A1U7R4C7|A0A1U7R4C7_MESAU      LVKNLALMAYISVGSQPSPILEFLEEWSMENLEEISPAAIADATKIFVNGCWVGIHKDPE    581
tr|A0A286XIQ9|A0A286XIQ9_CAVPO      LVKNLALMAYISVGSQPSPILEFLEEWSMENLEEISPAAIADATKIFVNGCWVGIHKDPE    581
tr|I3M351|I3M351_ICTTR              LVKNLALMAYISVGSQPSPILEFLEEWSMENLEEISPAAIADATKIFVNGCWVGIHKDPE    581
tr|G7P5R6|G7P5R6_MACFA              LVKNLALMAYISVGSQPSPILEFLEEWSMENLEEISPAAIADATKIFVNGCWVGIHKDPE    581
tr|H2QPI8|H2QPI8_PANTR              LVKNLALMAYISVGSQPSPILEFLEEWSMENLEEISPAAIADATKIFVNGCWVGIHKDPE    581
tr|A0A1U7V0T5|A0A1U7V0T5_TARSY      LVKNLALMAYISVGSQPSPILEFLEEWSMENLEEISPAAIADATKIFVNGCWVGIHKDPE    581
tr|A0A1S2ZSL2|A0A1S2ZSL2_ERIEU      LVKNLALMAYISVGSQPSPILEFLEEWSMENLEEISPAAIADATKIFVNGCWVGIHKDPE    581
tr|A0A0D9QYL1|A0A0D9QYL1_CHLSB      LVKNLALMAYISVGSQPSPILEFLEEWSMENLEEISPAAIADATKIFVNGCWVGIHKDPE    574
tr|A0A2K5ZNR7|A0A2K5ZNR7_MANLE      LVKNLALMAYISVGSQPSPILEFLEEWSMENLEEISPAAIADATKIFVNGCWVGIHKDPE    574
tr|A0A2I2ZIU3|A0A2I2ZIU3_GORGO      LVKNLALMAYISVGSQPSPILEFLEEWSMENLEEISPAAIADATKIFVNGCWVGIHKDPE    581
tr|A0A1D5QGA5|A0A1D5QGA5_MACMU      LVKNLALMAYISVGSQPSPILEFLEEWSMENLEEISPAAIADATKIFVNGCWVGIHKDPE    581
tr|A0A2J8S2N1|A0A2J8S2N1_PONAB      LVKNLALMAYISVGSQPSPILEFLEEWSMENLEEISPAAIADATKIFVNGCWVGIHKDPE    581
tr|A0A2K5K5J5|A0A2K5K5J5_COLAP      LVKNLALMAYISVGSQPSPILEFLEEWSMENLEEISPAAIADATKIFVNGCWVGIHKDPE    581
tr|A0A2J8PEW7|A0A2J8PEW7_PANTR      LVKNLALMAYISVGSQPSPILEFLEEWSMENLEEISPAAIADATKIFVNGCWVGIHKDPE    574
tr|A0A2K5CY83|A0A2K5CY83_AOTNA      LVKNLALMAYISVGSQPSPILEFLEEWSMENLEEISPAAIADATKIFVNGCWVGIHKDPE    581
tr|A0A096NEY4|A0A096NEY4_PAPAN      LVKNLALMAYISVGSQPSPILEFLEEWSMENLEEISPAAIADATKIFVNGCWVGIHKDPE    581
tr|C9J2Y9|C9J2Y9_HUMAN              LVKNLALMAYISVGSQPSPILEFLEEWSMENLEEISPAAIADATKIFVNGCWVGIHKDPE    574
tr|G8BY61|G8BY61_TETPH              LVKNLSLMSCISVGTDPMPIITFLSEWGMEPLEDYVPHQSPDATRVFVNGVWHGVHRNPA    592
tr|A0A1X7QYA1|A0A1X7QYA1_9SACH      LVKNLSLMSCISVGTDPTPIITFLSEWGMEPLEDYVPHQSPDATRVFVNGVWHGVHRNPA    590
tr|J7RV95|J7RV95_KAZNA              LVKNLSLMSSISVGTDPMPIITFLSEWGLEPLEDYVPHQSPDATRVFVNGVWHGVHRNPA    590
tr|H2AVJ8|H2AVJ8_KAZAF              LVKNLSLMSCISVGTDPMPIITFLSEWGMEPLEDYIPHQSPDATRVFVNGVWHGVHRNPA    590
sp|Q6FLD5|RPB2_CANGA                LVKNLSLMSCISVGADPMPIITFLSEWGMEPLEDYVPHQSPDATRVFVNGVWHGVHRNPA    592
sp|P08518|RPB2_YEAST                LVKNLSLMSCISVGTDPMPIITFLSEWGMEPLEDYVPHQSPDATRVFVNGVWHGVHRNPA    594
tr|A0A0L8VHA5|A0A0L8VHA5_9SACH      LVKNLSLMSCISVGTDPMPIITFLSEWGMEPLEDYVPHQSPDATRVFVNGVWHGVHRNPA    594
tr|A0A0L8RB33|A0A0L8RB33_SACEU      LVKNLSLMSCISVGTDPMPIITFLSEWGMEPLEDYVPHQSPDATRVFVNGVWHGVHRNPA    594
tr|G0VJ71|G0VJ71_NAUCC              LVKNLSLMSCISVGTDPMPIITFLSEWGMEPLEDYVPHQSPDATRVFVNGVWHGVHRNPA    594
tr|G8ZM49|G8ZM49_TORDC              LVKNLSLMSCISVGTDPMPIITFLSEWGMEPLEDYVPHQSPDATRVFVNGVWHGVHRNPA    592
tr|A0A1Q3A090|A0A1Q3A090_ZYGRO      LVKNLSLMSCISVGTDPMPIITFLSEWGMEPLEDYIPHQSPEATRVFVNGVWHGVHRNPA    594
tr|A0A0N7IS35|A0A0N7IS35_9SACH      LVKNLSLMSCISVGTDPMPIITFLSEWGMEPLEDYVPHQSPEATRVFVNGVWHGVHRNPA    592
tr|A0A212MG88|A0A212MG88_ZYGBA      LVKNLSLMSCISVGTDPMPIITFLSEWGMEPLEDYVPHQSPEATRVFVNGVWHGVHRNPA    593
tr|A0A1S7HHE1|A0A1S7HHE1_9SACH      LVKNLSLMSCISVGTDPMPIITFLSEWGMEPLEDYVPHQSPEATRVFVNGVWHGVHRNPA    593
tr|S6ESB4|S6ESB4_ZYGB2              LVKNLSLMSCISVGTDAMPIITFLSEWGMEPLEDYVPHQSPEATRVFVNGVWHGVHRNPA    593
tr|B6K5Q5|B6K5Q5_SCHJY              LVKNLSLMSYVSVGSPSAPIIEFLEEWGMESLEDYNPSASPNATKVFVNGIWLGVHRDPV    580
sp|Q02061|RPB2_SCHPO                LVKNLSLMSYVSVGSPSAPIIEFLEEWGLETLEDYNPSASPNATKVFVNGVWLGVHRDPA    580
tr|S9R8U4|S9R8U4_SCHOY              LVKNLALMSYVSVGSPAAPIIEFLEEWGLESLEDFNPSASPNATKVFVNGVWLGVHRDPA    580
tr|S9W8C6|S9W8C6_SCHCR              LVKNLALMSYVSVGSPAAPIIEFLEEWGLESLEDYNPSASPNATKVFVNGVWLGVHRDPA    580
                                    *****:**: :***:   **: **.**.:* **:  *    :**::**** * *:*::*
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sp|P30876|RPB2_HUMAN                QLMNTLRKLRRQMDIIVSEVSMIRDIREREIRIYTDAGRICRPLLIVEKQK-------LL       634
tr|G3V8Y5|G3V8Y5_RAT                QLMNTLRKLRRQMDIIVSEVSMIRDIREREIRIYTDAGRICRPLLIVEKQK-------LL       634
tr|A0A250Y753|A0A250Y753_CASCN      QLMNTLRKLRRQMDIIVSEVSMIRDIREREIRIYTDAGRICRPLLIVEKQK-------LL       634
tr|A0A1U7R4C7|A0A1U7R4C7_MESAU      QLMNTLRKLRRQMDIIVSEVSMIRDIREREIRIYTDAGRICRPLLIVEKQK-------LL       634
tr|A0A286XIQ9|A0A286XIQ9_CAVPO      QLMNTLRKLRRQMDIIVSEVSMIRDIREREIRIYTDAGRICRPLLIVEKQK-------LL       634
tr|I3M351|I3M351_ICTTR              QLMNTLRKLRRQMDIIVSEVSMIRDIREREIRIYTDAGRICRPLLIVEKQK-------LL       634
tr|G7P5R6|G7P5R6_MACFA              QLMNTLRKLRRQMDIIVSEVSMIRDIREREIRIYTDAGRICRPLLIVEKQK-------LL       634
tr|H2QPI8|H2QPI8_PANTR              QLMNTLRKLRRQMDIIVSEVSMIRDIREREIRIYTDAGRICRPLLIVEKQK-------LL       634
tr|A0A1U7V0T5|A0A1U7V0T5_TARSY      QLMNTLRKLRRQMDIIVSEVSMIRDIREREIRIYTDAGRICRPLLIVEKQK-------LL       634
tr|A0A1S2ZSL2|A0A1S2ZSL2_ERIEU      QLMNTLRKLRRQMDIIVSEVSMIRDIREREIRIYTDAGRICRPLLIVEKQK-------LL       634
tr|A0A0D9QYL1|A0A0D9QYL1_CHLSB      QLMNTLRKLRRQMDIIVSEVSMIRDIREREIRIYTDAGRICRPLLIVEKQK-------LL       627
tr|A0A2K5ZNR7|A0A2K5ZNR7_MANLE      QLMNTLRKLRRQMDIIVSEVSMIRDIREREIRIYTDAGRICRPLLIVEKQK-------LL       627
tr|A0A2I2ZIU3|A0A2I2ZIU3_GORGO      QLMNTLRKLRRQMDIIVSEVSMIRDIREREIRIYTDAGRICRPLLIVEKQK-------LL       634
tr|A0A1D5QGA5|A0A1D5QGA5_MACMU      QLMNTLRKLRRQMDIIVSEVSMIRDIREREIRIYTDAGRICRPLLIVEKQK-------LL       634
tr|A0A2J8S2N1|A0A2J8S2N1_PONAB      QLMNTLRKLRRQMDIIVSEVSMIRDIREREIRIYTDAGRICRPLLIVEKQK-------LL       634
tr|A0A2K5K5J5|A0A2K5K5J5_COLAP      QLMNTLRKLRRQMDIIVSEVSMIRDIREREIRIYTDAGRICRPLLIVEKQK-------LL       634
tr|A0A2J8PEW7|A0A2J8PEW7_PANTR      QLMNTLRKLRRQMDIIVSEVSMIRDIREREIRIYTDAGRICRPLLIVEKQK-------LL       627
tr|A0A2K5CY83|A0A2K5CY83_AOTNA      QLMNTLRKLRRQMDIIVSEVSMIRDIREREIRIYTDAGRICRPLLIVEKQK-------LL       634
tr|A0A096NEY4|A0A096NEY4_PAPAN      QLMNTLRKLRRQMDIIVSEVSMIRDIREREIRIYTDAGRICRPLLIVEKQK-------LL       634
tr|C9J2Y9|C9J2Y9_HUMAN              QLMNTLRKLRRQMDIIVSEVSMIRDIREREIRIYTDAGRICRPLLIVEKQK-------LL       627
tr|G8BY61|G8BY61_TETPH              RLMETLRTLRRKGDI-NPEVSMIRDIREQELKIFTDAGRVYRPLFIVDDDDDLG-HKELR       650
tr|A0A1X7QYA1|A0A1X7QYA1_9SACH      RLMETLRTLRRKGDI-NPEVSMVRDIREKELKIFTDAGRVYRPLFIVEDDSELG-HKELK       648
tr|J7RV95|J7RV95_KAZNA              RLMETLRTLRRKGDI-NPEVSMIRDIREKELKIFTDAGRVYRPLFIVEDDEALG-HKELK       648
tr|H2AVJ8|H2AVJ8_KAZAF              RLMETLRTLRRKGDI-NPEVSMIRDIREKELKIFTDAGRVYRPLFIVEDDEALG-HKELK       648
sp|Q6FLD5|RPB2_CANGA                RLMETLRTLRRKGDI-NPEVSMIRDIREQELKIFTDAGRVYRPLFIVEDDEELG-RKELK       650
sp|P08518|RPB2_YEAST                RLMETLRTLRRKGDI-NPEVSMIRDIREKELKIFTDAGRVYRPLFIVEDDESLG-HKELK       652
tr|A0A0L8VHA5|A0A0L8VHA5_9SACH      RLMETLRTLRRKGDI-NPEVSMIRDIREKELKIFTDAGRVYRPLFIVEDDESLG-HKELK       652
tr|A0A0L8RB33|A0A0L8RB33_SACEU      RLMETLRTLRRKGDI-NPEVSMIRDIREKELKIFTDAGRVYRPLFIVEDDETLG-HKELK       652
tr|G0VJ71|G0VJ71_NAUCC              RLMDTLRTLRRKGDI-NPEVSMIRDIREKELKIFTDAGRVYRPLFIVEDDETLG-HKELK       652
tr|G8ZM49|G8ZM49_TORDC              RLMETLRTLRRKGDI-NPEVSMVRDIREKELKIFTDAGRVYRPLFIVEDDETLG-HKELK       650
tr|A0A1Q3A090|A0A1Q3A090_ZYGRO      RLMETLRTLRRKGDI-NPEVSMVRDIREKELKIFTDAGRVYRPLFIVDDDETLN-RKELR       652
tr|A0A0N7IS35|A0A0N7IS35_9SACH      RLMETLRTLRRKGDI-NPEVSMVRDIREKELKIFTDAGRVYRPLFIVDDDETLN-RKELK       650
tr|A0A212MG88|A0A212MG88_ZYGBA      RLMETLRTLRRKGDI-NPEVSMVRDIREKELKIFTDAGRVYRPLFIVDDDESLN-RKELR       651
tr|A0A1S7HHE1|A0A1S7HHE1_9SACH      RLMETLRTLRRKGDI-NPEVSMVRDIREKELKIFTDAGRVYRPLFIVDDDESLN-RKELR       651
tr|S6ESB4|S6ESB4_ZYGB2              RLMETLRTLRRKGDI-NPEVSMVRDIREKELRIFTDAGRVYRPLFIVDDDESLN-RKELR       651
tr|B6K5Q5|B6K5Q5_SCHJY              HLTETLRSLRRRLDI-SAEVSIVRDIREKELRLFTDAGRICRPLFIVDNDSNSDTKGELC       639
sp|Q02061|RPB2_SCHPO                HLTETLRSLRRRLDI-SAEVSIVRDIREKELRLFTDAGRICRPLFIVDNNPNSERRGELC       639
tr|S9R8U4|S9R8U4_SCHOY              HLTDTLRSLRRRLDI-SAEVSIVRDIREKELRLFTDAGRICRPLFIVDNDPNSETRGELA       639
tr|S9W8C6|S9W8C6_SCHCR              HLTDTLRSLRRRLDI-SAEVSIVRDIREKELRLFTDAGRICRPLFIVDNDPNSESRGELC       639
                                    :* :***.***: **   ***::*****:*::::*****: ***:**:.:        *


sp|P30876|RPB2_HUMAN                LKKRHIDQLKEREY----------NNYSWQDLVASGVVEYIDTLEEETVMLAMTPDDLQE       684
tr|G3V8Y5|G3V8Y5_RAT                LKKRHIDQLKEREY----------NNYSWQDLVASGVVEYIDTLEEETVMLAMTPDDLQE       684
tr|A0A250Y753|A0A250Y753_CASCN      LKKRHIDQLKEREY----------NNYSWQDLVASGVVEYIDTLEEETVMLAMTPDDLQE       684
tr|A0A1U7R4C7|A0A1U7R4C7_MESAU      LKKRHIDQLKEREY----------NNYSWQDLVASGVVEYIDTLEEETVMLAMTPDDLQE       684
tr|A0A286XIQ9|A0A286XIQ9_CAVPO      LKKRHIDQLKEREY----------NNYSWQDLVASGVVEYIDTLEEETVMLAMTPDDLQE       684
tr|I3M351|I3M351_ICTTR              LKKRHIDQLKEREY----------NNYSWQDLVASGVVEYIDTLEEETVMLAMTPDDLQE       684
tr|G7P5R6|G7P5R6_MACFA              LKKRHIDQLKEREY----------NNYSWQDLVASGVVEYIDTLEEETVMLAMTPDDLQE       684
tr|H2QPI8|H2QPI8_PANTR              LKKRHIDQLKEREY----------NNYSWQDLVASGVVEYIDTLEEETVMLAMTPDDLQE       684
tr|A0A1U7V0T5|A0A1U7V0T5_TARSY      LKKRHIDQLKEREY----------NNYSWQDLVASGVVEYIDTLEEETVMLAMTPDDLQE       684
tr|A0A1S2ZSL2|A0A1S2ZSL2_ERIEU      LKKRHIDQLKEREY----------NNYSWQDLVASGVVEYIDTLEEETVMLAMTPDDLQE       684
tr|A0A0D9QYL1|A0A0D9QYL1_CHLSB      LKKRHIDQLKEREY----------NNYSWQDLVASGVVEYIDTLEEETVMLAMTPDDLQE       677
tr|A0A2K5ZNR7|A0A2K5ZNR7_MANLE      LKKRHIDQLKEREY----------NNYSWQDLVASGVVEYIDTLEEETVMLAMTPDDLQE       677
tr|A0A2I2ZIU3|A0A2I2ZIU3_GORGO      LKKRHIDQLKEREY----------NNYSWQDLVASGVVEYIDTLEEETVMLAMTPDDLQE       684
tr|A0A1D5QGA5|A0A1D5QGA5_MACMU      LKKRHIDQLKEREY----------NNYSWQDLVASGVVEYIDTLEEETVMLAMTPDDLQE       684
tr|A0A2J8S2N1|A0A2J8S2N1_PONAB      LKKRHIDQLKEREY----------NNYSWQDLVASGVVEYIDTLEEETVMLAMTPDDLQE       684
tr|A0A2K5K5J5|A0A2K5K5J5_COLAP      LKKRHIDQLKEREY----------NNYSWQDLVASGVVEYIDTLEEETVMLAMTPDDLQE       684
tr|A0A2J8PEW7|A0A2J8PEW7_PANTR      LKKRHIDQLKEREY----------NNYSWQDLVASGVVEYIDTLEEETVMLAMTPDDLQE       677
tr|A0A2K5CY83|A0A2K5CY83_AOTNA      LKKRHIDQLKEREY----------NNYSWQDLVASGVVEYIDTLEEETVMLAMTPDDLQE       684
tr|A0A096NEY4|A0A096NEY4_PAPAN      LKKRHIDQLKEREY----------NNYSWQDLVASGVVEYIDTLEEETVMLAMTPDDLQE       684
tr|C9J2Y9|C9J2Y9_HUMAN              LKKRHIDQLKEREY----------NNYSWQDLVASGVVEYIDTLEEETVMLAMTPDDLQE       677
tr|G8BY61|G8BY61_TETPH              VRKGHVARLMATEYQDIEGGFEDVEEYTWTSLLNEGLVEYIDAEEEESILIAMQPEDLDP       710
tr|A0A1X7QYA1|A0A1X7QYA1_9SACH      VRKGHINKLMATEYQDIEGGLDESDEYTWSSLLSEGLVEYIDAEEEETILIAMQPEDLEP       708
tr|J7RV95|J7RV95_KAZNA              VRKGHIAKLMATEYQDIEGGLDEADEYTWTSLLNEGLVEYIDAEEEETILIAMQPEDLEP       708
tr|H2AVJ8|H2AVJ8_KAZAF              VRKGHINKLMATEYQDIEGGFEDSEEYTWTSLLNEGLVEYIDAEEEETILIAMQPEDLEP       708
sp|Q6FLD5|RPB2_CANGA                VRKGHVAKLMATEYQDIEGGFEDAEDYTWSSLLNEGLVEYIDAEEEESILIAMQPEDLEP       710
sp|P08518|RPB2_YEAST                VRKGHIAKLMATEYQDIEGGFEDVEEYTWSSLLNEGLVEYIDAEEEESILIAMQPEDLEP       712
tr|A0A0L8VHA5|A0A0L8VHA5_9SACH      VRKGHIAKLMATEYQDIEGGFEDVEEYTWSSLLNEGLVEYIDAEEEESILIAMQPEDLEP       712
tr|A0A0L8RB33|A0A0L8RB33_SACEU      VRKGHVAKLMTTEYQDIEGGFEDVEEFTWSSLLNEGLVEYIDAEEEESILIAMQPEDLEP       712
tr|G0VJ71|G0VJ71_NAUCC              VRKGHIAKLMATEYQDIEGGFEDAEEYTWTSLLNEGLVEYIDAEEEETILISMQPEDLEP       712
tr|G8ZM49|G8ZM49_TORDC              VRKGHIGKLMATEYQDIEGGFEDSEDYTWSSLLNEGLVEYIDAEEEETILISMQPEDLEP       710
tr|A0A1Q3A090|A0A1Q3A090_ZYGRO      IRKGHISKLMATEYQDIEGGFEDSEEYTWTSLLNDGLVEYIDAEEEETILISMQPEDLEP       712
tr|A0A0N7IS35|A0A0N7IS35_9SACH      IRKGHVGKLMATEYQDIEGGFEDSEEYTWTSLLNEGLVEYIDAEEEETILISMQPEDLEP       710
tr|A0A212MG88|A0A212MG88_ZYGBA      IRKGHVAKLMATEYQDIEGGFEDSEEYTWTSLLNEGLVEYIDAEEEETILISMQPEDLEP       711
tr|A0A1S7HHE1|A0A1S7HHE1_9SACH      IRKGHVAKLMATEYQDIEGGFEDSEEYTWTSLLNEGLVEYIDAEEEETILISMQPEDLEP       711
tr|S6ESB4|S6ESB4_ZYGB2              IRKGHVAKLMATEYQDIEGGFEDSEEYTWTSLLNEGLVEYIDAEEEETILISMQPEDLEP       711
tr|B6K5Q5|B6K5Q5_SCHJY              IRKEHIQQLLEDRD---RFDINAEQRFGWSSLIASGLIEYLDAEEEETVMIAMSPDDLEL       696
sp|Q02061|RPB2_SCHPO                IRKEHIQQLIEDKD---RYDIDPEQRFGWTALVSSGLIEYLDAEEEETVMIAMSPEDLEA       696
tr|S9R8U4|S9R8U4_SCHOY              IRKEHVQQLIEDRD---RFDIDPEQKFGWTALVSSGLIEYLDAEEEETVMIAMTPEDLEA       696
tr|S9W8C6|S9W8C6_SCHCR              IRKEHIQQLIEDRD---RFDIDPEQKFGWTALVSSGLIEYLDAEEEETVMIAMTPEDLEA       696
                                    ::* *: :*   .           : : *  *: .*::**:*: ***:::::* *:**:
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sp|P30876|RPB2_HUMAN                KE----------------------VAYCSTYTHCEIHPSMILGVCASIIPFPDHNQSPRN       722
tr|G3V8Y5|G3V8Y5_RAT                KE----------------------VAYCSTYTHCEIHPSMILGVCASIIPFPDHNQSPRN       722
tr|A0A250Y753|A0A250Y753_CASCN      KE----------------------VAYCSTYTHCEIHPSMILGVCASIIPFPDHNQSPRN       722
tr|A0A1U7R4C7|A0A1U7R4C7_MESAU      KE----------------------VAYCSTYTHCEIHPSMILGVCASIIPFPDHNQSPRN       722
tr|A0A286XIQ9|A0A286XIQ9_CAVPO      KE----------------------VAYCSTYTHCEIHPSMILGVCASIIPFPDHNQSPRN       722
tr|I3M351|I3M351_ICTTR              KE----------------------VAYCSTYTHCEIHPSMILGVCASIIPFPDHNQSPRN       722
tr|G7P5R6|G7P5R6_MACFA              KE----------------------VAYCSTYTHCEIHPSMILGVCASIIPFPDHNQSPRN       722
tr|H2QPI8|H2QPI8_PANTR              KE----------------------VAYCSTYTHCEIHPSMILGVCASIIPFPDHNQSPRN       722
tr|A0A1U7V0T5|A0A1U7V0T5_TARSY      KE----------------------VAYCSTYTHCEIHPSMILGVCASIIPFPDHNQSPRN       722
tr|A0A1S2ZSL2|A0A1S2ZSL2_ERIEU      KE----------------------VAYCSTYTHCEIHPSMILGVCASIIPFPDHNQSPRN       722
tr|A0A0D9QYL1|A0A0D9QYL1_CHLSB      KE----------------------VAYCSTYTHCEIHPSMILGVCASIIPFPDHNQSPRN       715
tr|A0A2K5ZNR7|A0A2K5ZNR7_MANLE      KE----------------------VAYCSTYTHCEIHPSMILGVCASIIPFPDHNQSPRN       715
tr|A0A2I2ZIU3|A0A2I2ZIU3_GORGO      KE----------------------VAYCSTYTHCEIHPSMILGVCASIIPFPDHNQSPRN       722
tr|A0A1D5QGA5|A0A1D5QGA5_MACMU      KE----------------------VAYCSTYTHCEIHPSMILGVCASIIPFPDHNQSPRN       722
tr|A0A2J8S2N1|A0A2J8S2N1_PONAB      KE----------------------VAYCSTYTHCEIHPSMILGVCASIIPFPDHNQSPRN       722
tr|A0A2K5K5J5|A0A2K5K5J5_COLAP      KE----------------------VAYCSTYTHCEIHPSMILGVCASIIPFPDHNQSPRN       722
tr|A0A2J8PEW7|A0A2J8PEW7_PANTR      KE----------------------VAYCSTYTHCEIHPSMILGVCASIIPFPDHNQSPRN       715
tr|A0A2K5CY83|A0A2K5CY83_AOTNA      KE----------------------VAYCSTYTHCEIHPSMILGVCASIIPFPDHNQSPRN       722
tr|A0A096NEY4|A0A096NEY4_PAPAN      KE----------------------VAYCSTYTHCEIHPSMILGVCASIIPFPDHNQSPRN       722
tr|C9J2Y9|C9J2Y9_HUMAN              KE----------------------VAYCSTYTHCEIHPSMILGVCASIIPFPDHNQSPRN       715
tr|G8BY61|G8BY61_TETPH              VSDEPEAI-PDVETDTAKRIR--AVHHATTFTHCEIHPSMILGVAASIIPFPDHNQSPRN       767
tr|A0A1X7QYA1|A0A1X7QYA1_9SACH      ATEEANA--AINEMDPARRIK--AVQHATTFTHCEIHPSMILGVAASIIPFPDHNQSPRN       764
tr|J7RV95|J7RV95_KAZNA              VIEEENPI---DDMDPAKRIK--ASQNATTFTHCEIHPSMILGVAASIIPFPDHNQSPRN       763
tr|H2AVJ8|H2AVJ8_KAZAF              MGEEEETQ-NDTAMDPAKRIK--ATQNATTFTHCEIHPSMILGVAASIIPFPDHNQSPRN       765
sp|Q6FLD5|RPB2_CANGA                TAVEQDI--PKENVDLAKRIK--VTHHATTFTHCEIHPSMILGVAASIIPFPDHNQSPRN       766
sp|P08518|RPB2_YEAST                AEANEE---NDLDVDPAKRIR--VSHHATTFTHCEIHPSMILGVAASIIPFPDHNQSPRN       767
tr|A0A0L8VHA5|A0A0L8VHA5_9SACH      AEANEE---NDLDVDPAKRIR--VSHHATTFTHCEIHPSMILGVAASIIPFPDHNQSPRN       767
tr|A0A0L8RB33|A0A0L8RB33_SACEU      TEGNEE---NGLGVDHAKRIR--VTHHATTFTHCEIHPSMILGVAASIIPFPDHNQSPRN       767
tr|G0VJ71|G0VJ71_NAUCC              PMENEE---VIDDMDPAKRIR--ATQHATTFTHCEIHPSMILGVAASIIPFPDHNQSPRN       767
tr|G8ZM49|G8ZM49_TORDC              VQEAHE---FNEDDDLAKRIR--ATQHATTFTHCEIHPSMILGVAASVIPFPDHNQSPRN       765
tr|A0A1Q3A090|A0A1Q3A090_ZYGRO      VQENTF---NEDDDDLARRIK--ATHHATTFTHCEVHPSMILGVAASIIPFPDHNQSPRN       767
tr|A0A0N7IS35|A0A0N7IS35_9SACH      VQENSY---AEEDDDLAKRIK--ATQHATTFTHCEIHPSMILGVAASIIPFPDHNQSPRN       765
tr|A0A212MG88|A0A212MG88_ZYGBA      VQENPY---SEEEDDLARRIK--ATHHATTFTHCEIHPSMILGVAASVIPFPDHNQSPRN       766
tr|A0A1S7HHE1|A0A1S7HHE1_9SACH      VQENPY---SEEEDDLARRIK--ATHHATTFTHCEIHPSMILGVAASVIPFPDHNQSPRN       766
tr|S6ESB4|S6ESB4_ZYGB2              VQENPY---SEEEDDLARRIK--ATHHATTFTHCEIHPSMILGVAASVIPFPDHNQSPRN       766
tr|B6K5Q5|B6K5Q5_SCHJY              SRQANAGYEMQEELDPAKRVKPAPNPHVHAWTHCEIHPAMILGILASIIPFPDHNQSPRN       756
sp|Q02061|RPB2_SCHPO                SRQMQAGYEVKEELDPAQRVKPAPNPHVHAWTHCEIHPAMILGILASIIPFPDHNQSPRN       756
tr|S9R8U4|S9R8U4_SCHOY              SRQMNAGYEVKEELDPAQRVKPAPNPHVHTYTHCEIHPAMILGILASIIPFPDHNQSPRN       756
tr|S9W8C6|S9W8C6_SCHCR              SRQMNAGYEVKEELDPAQRVKPAPNPHVHAYTHCEIHPAMILGILASIIPFPDHNQSPRN       756
                                                                 ::****:**:****:  **:************

sp|P30876|RPB2_HUMAN                TYQSAMGKQAMGVYITNFHVRMDTLAHVLYYPQKPLVTTRSMEYLRFRELPAGINSIVAI       782
tr|G3V8Y5|G3V8Y5_RAT                TYQSAMGKQAMGVYITNFHVRMDTLAHVLYYPQKPLVTTRSMEYLRFRELPAGINSIVAI       782
tr|A0A250Y753|A0A250Y753_CASCN      TYQSAMGKQAMGVYITNFHVRMDTLAHVLYYPQKPLVTTRSMEYLRFRELPAGINSIVAI       782
tr|A0A1U7R4C7|A0A1U7R4C7_MESAU      TYQSAMGKQAMGVYITNFHVRMDTLAHVLYYPQKPLVTTRSMEYLRFRELPAGINSIVAI       782
tr|A0A286XIQ9|A0A286XIQ9_CAVPO      TYQSAMGKQAMGVYITNFHVRMDTLAHVLYYPQKPLVTTRSMEYLRFRELPAGINSIVAI       782
tr|I3M351|I3M351_ICTTR              TYQSAMGKQAMGVYITNFHVRMDTLAHVLYYPQKPLVTTRSMEYLRFRELPAGINSIVAI       782
tr|G7P5R6|G7P5R6_MACFA              TYQSAMGKQAMGVYITNFHVRMDTLAHVLYYPQKPLVTTRSMEYLRFRELPAGINSIVAI       782
tr|H2QPI8|H2QPI8_PANTR              TYQSAMGKQAMGVYITNFHVRMDTLAHVLYYPQKPLVTTRSMEYLRFRELPAGINSIVAI       782
tr|A0A1U7V0T5|A0A1U7V0T5_TARSY      TYQSAMGKQAMGVYITNFHVRMDTLAHVLYYPQKPLVTTRSMEYLRFRELPAGINSIVAI       782
tr|A0A1S2ZSL2|A0A1S2ZSL2_ERIEU      TYQSAMGKQAMGVYITNFHVRMDTLAHVLYYPQKPLVTTRSMEYLRFRELPAGINSIVAI       782
tr|A0A0D9QYL1|A0A0D9QYL1_CHLSB      TYQSAMGKQAMGVYITNFHVRMDTLAHVLYYPQKPLVTTRSMEYLRFRELPAGINSIVAI       775
tr|A0A2K5ZNR7|A0A2K5ZNR7_MANLE      TYQSAMGKQAMGVYITNFHVRMDTLAHVLYYPQKPLVTTRSMEYLRFRELPAGINSIVAI       775
tr|A0A2I2ZIU3|A0A2I2ZIU3_GORGO      TYQSAMGKQAMGVYITNFHVRMDTLAHVLYYPQKPLVTTRSMEYLRFRELPAGINSIVAI       782
tr|A0A1D5QGA5|A0A1D5QGA5_MACMU      TYQSAMGKQAMGVYITNFHVRMDTLAHVLYYPQKPLVTTRSMEYLRFRELPAGINSIVAI       782
tr|A0A2J8S2N1|A0A2J8S2N1_PONAB      TYQSAMGKQAMGVYITNFHVRMDTLAHVLYYPQKPLVTTRSMEYLRFRELPAGINSIVAI       782
tr|A0A2K5K5J5|A0A2K5K5J5_COLAP      TYQSAMGKQAMGVYITNFHVRMDTLAHVLYYPQKPLVTTRSMEYLRFRELPAGINSIVAI       782
tr|A0A2J8PEW7|A0A2J8PEW7_PANTR      TYQSAMGKQAMGVYITNFHVRMDTLAHVLYYPQKPLVTTRSMEYLRFRELPAGINSIVAI       775
tr|A0A2K5CY83|A0A2K5CY83_AOTNA      TYQSAMGKQAMGVYITNFHVRMDTLAHVLYYPQKPLVTTRSMEYLRFRELPAGINSIVAI       782
tr|A0A096NEY4|A0A096NEY4_PAPAN      TYQSAMGKQAMGVYITNFHVRMDTLAHVLYYPQKPLVTTRSMEYLRFRELPAGINSIVAI       782
tr|C9J2Y9|C9J2Y9_HUMAN              TYQSAMGKQAMGVYITNFHVRMDTLAHVLYYPQKPLVTTRSMEYLRFRELPAGINSIVAI       775
tr|G8BY61|G8BY61_TETPH              TYQSAMGKQAMGVFLTNYNVRMDTMANILYYPQKPLGTTRAMEYLKFRELPAGQNAIVAI       827
tr|A0A1X7QYA1|A0A1X7QYA1_9SACH      TYQSAMGKQAMGVFLTNYNVRMDTMANILYYPQKPLGTTRSMEYLKFRELPAGQNAIVAI       824
tr|J7RV95|J7RV95_KAZNA              TYQSAMGKQAMGVFLTNYNVRMDTMANILYYPQKPLGTTRAMEYLKFRELPAGQNAIVAI       823
tr|H2AVJ8|H2AVJ8_KAZAF              TYQSAMGKQAMGVFLTNFNVRMDTMANILYYPQKPLGTTRAMEYLKFRELPAGQNAIVAI       825
sp|Q6FLD5|RPB2_CANGA                TYQSAMGKQAMGVFLTNYNFRMDTMANILYYPQKPLGTTRAMEYLKFRELPAGQNAIVAI       826
sp|P08518|RPB2_YEAST                TYQSAMGKQAMGVFLTNYNVRMDTMANILYYPQKPLGTTRAMEYLKFRELPAGQNAIVAI       827
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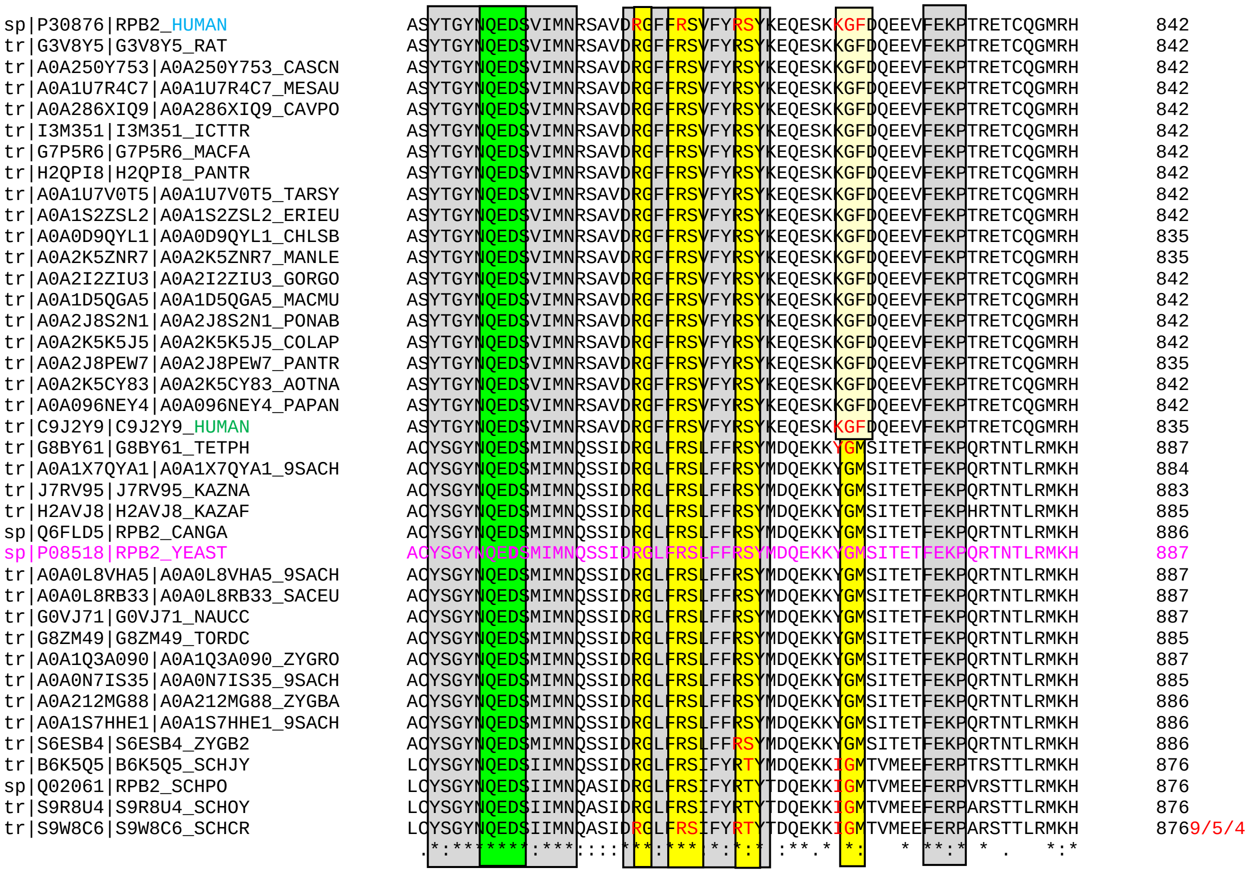

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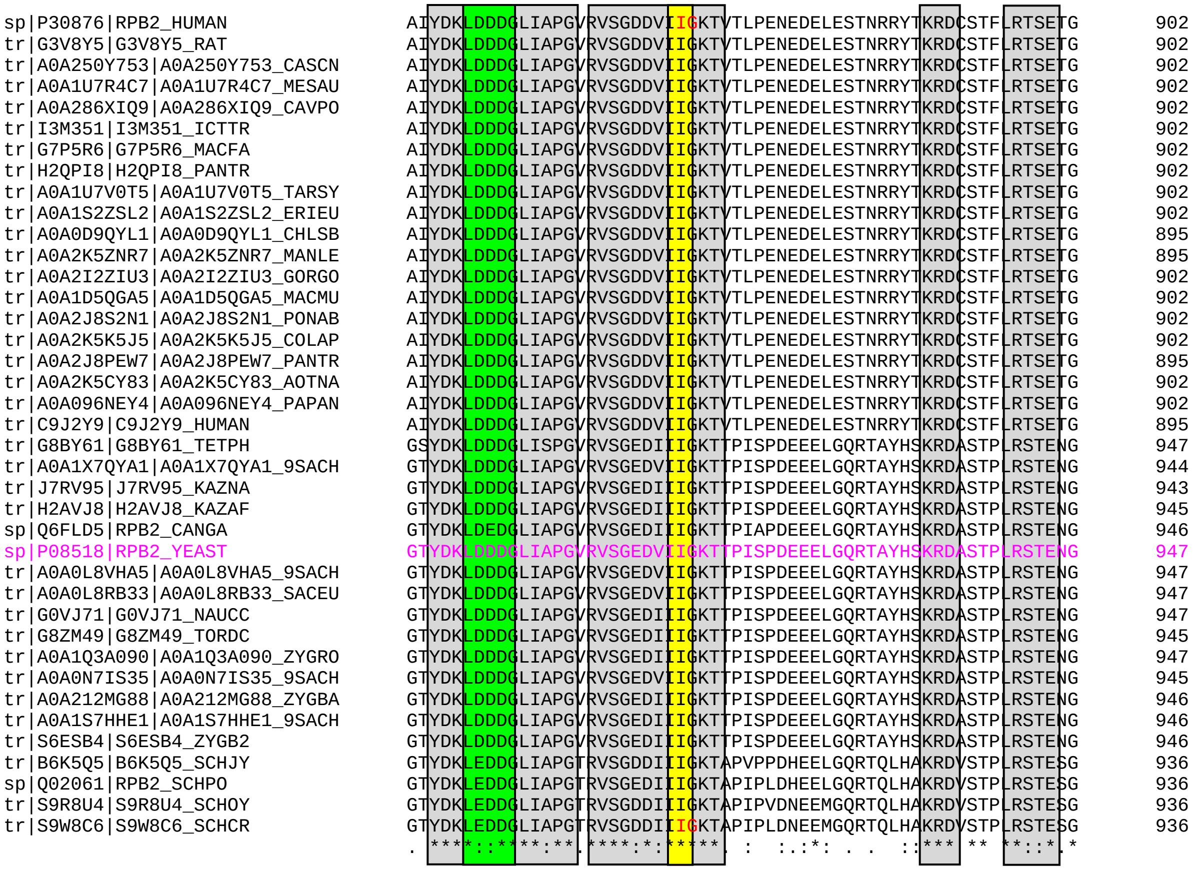

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tr|S6ESB4|S6ESB4_ZYGB2              IVDQILITTNQDGLKFVKVRVRTTKIPQIGDKFASRHGQKGTIGITYSREDMPFTAEGIV       1006
tr|B6K5Q5|B6K5Q5_SCHJY              IVDQVMVTTNQEGLKFVKVRMRSTRIPQIGDKFASRHGQKGTIGMTYRHEDMPFSAQGIV       996
sp|Q02061|RPB2_SCHPO                IVDQVMVTTNQEGLKFVKVRMRSTRIPQIGDKFASRHGQKGTIGMTYRHEDMPFSAQGIV       996
tr|S9R8U4|S9R8U4_SCHOY              IVDQVLVTTNQEGLKFVKVRMRSTRVPQIGDKFASRHGQKGTIGMTYRHEDMPFSAQGVV       996
tr|S9W8C6|S9W8C6_SCHCR              IVDQVLVTTNQEGLKFVKVRMRSTRVPQIGDKFASRHGQKGTIGMTYRHEDMPFSAQGIV       996
                                    *:**:::* **:* ** *:*:*:.:: *************** *: * :*****:.:*:.


sp|P30876|RPB2_HUMAN                PDIIINPHAIPSRMTIGHLIECLQGKVSANKGEIGDATPFNDAVNVQKISNLLSDYGYHL       1022
tr|G3V8Y5|G3V8Y5_RAT                PDIIINPHAIPSRMTIGHLIECLQGKVSANKGEIGDATPFNDAVNVQKISNLLSDYGYHL       1022
tr|A0A250Y753|A0A250Y753_CASCN      PDIIINPHAIPSRMTIGHLIECLQGKVSANKGEIGDATPFNDAVNVQKISNLLSDYGYHL       1022
tr|A0A1U7R4C7|A0A1U7R4C7_MESAU      PDIIINPHAIPSRMTIGHLIECLQGKVSANKGEIGDATPFNDAVNVQKISNLLSDYGYHL       1022
tr|A0A286XIQ9|A0A286XIQ9_CAVPO      PDIIINPHAIPSRMTIGHLIECLQGKVSANKGEIGDATPFNDAVNVQKISNLLSDYGYHL       1022
tr|I3M351|I3M351_ICTTR              PDIIINPHAIPSRMTIGHLIECLQGKVSANKGEIGDATPFNDAVNVQKISNLLSDYGYHL       1022
tr|G7P5R6|G7P5R6_MACFA              PDIIINPHAIPSRMTIGHLIECLQGKVSANKGEIGDATPFNDAVNVQKISNLLSDYGYHL       1022
tr|H2QPI8|H2QPI8_PANTR              PDIIINPHAIPSRMTIGHLIECLQGKVSANKGEIGDATPFNDAVNVQKISNLLSDYGYHL       1022
tr|A0A1U7V0T5|A0A1U7V0T5_TARSY      PDIIINPHAIPSRMTIGHLIECLQGKVSANKGEIGDATPFNDAVNVQKISNLLSDYGYHL       1022
tr|A0A1S2ZSL2|A0A1S2ZSL2_ERIEU      PDIIINPHAIPSRMTIGHLIECLQGKVSANKGEIGDATPFNDAVNVQKISNLLSDYGYHL       1022
tr|A0A0D9QYL1|A0A0D9QYL1_CHLSB      PDIIINPHAIPSRMTIGHLIECLQGKVSANKGEIGDATPFNDAVNVQKISNLLSDYGYHL       1015
tr|A0A2K5ZNR7|A0A2K5ZNR7_MANLE      PDIIINPHAIPSRMTIGHLIECLQGKVSANKGEIGDATPFNDAVNVQKISNLLSDYGYHL       1015
tr|A0A2I2ZIU3|A0A2I2ZIU3_GORGO      PDIIINPHAIPSRMTIGHLIECLQGKVSANKGEIGDATPFNDAVNVQKISNLLSDYGYHL       1022
tr|A0A1D5QGA5|A0A1D5QGA5_MACMU      PDIIINPHAIPSRMTIGHLIECLQGKVSANKGEIGDATPFNDAVNVQKISNLLSDYGYHL       1022
tr|A0A2J8S2N1|A0A2J8S2N1_PONAB      PDIIINPHAIPSRMTIGHLIECLQGKVSANKGEIGDATPFNDAVNVQKISNLLSDYGYHL       1022
tr|A0A2K5K5J5|A0A2K5K5J5_COLAP      PDIIINPHAIPSRMTIGHLIECLQGKVSANKGEIGDATPFNDAVNVQKISNLLSDYGYHL       1022
tr|A0A2J8PEW7|A0A2J8PEW7_PANTR      PDIIINPHAIPSRMTIGHLIECLQGKVSANKGEIGDATPFNDAVNVQKISNLLSDYGYHL       1015
tr|A0A2K5CY83|A0A2K5CY83_AOTNA      PDIIINPHAIPSRMTIGHLIECLQGKVSANKGEIGDATPFNDAVNVQKISNLLSDYGYHL       1022
tr|A0A096NEY4|A0A096NEY4_PAPAN      PDIIINPHAIPSRMTIGHLIECLQGKVSANKGEIGDATPFNDAVNVQKISNLLSDYGYHL       1022
tr|C9J2Y9|C9J2Y9_HUMAN              PDIIINPHAIPSRMTIGHLIECLQGKVSANKGEIGDATPFNDAVNVQKISNLLSDYGYHL       1015
tr|G8BY61|G8BY61_TETPH              PDLIINPHAIPSRMTVAHLIECLLSKVAALSGNEGDASPFTD-ITVEGISKLLREHGYQS       1066
tr|A0A1X7QYA1|A0A1X7QYA1_9SACH      PDLIINPHAIPSRMTVAHLIECLLSKVAALSGNEGDASPFTD-ITVEGISTLLREHGYQS       1063
tr|J7RV95|J7RV95_KAZNA              PDLIINPHAIPSRMTVAHLIECLLSKVAALSGNEGDASPFTD-ITVEGISKLLREHGYHS       1062
tr|H2AVJ8|H2AVJ8_KAZAF              PDLIINPHAIPSRMTVAHLIECLLSKVAALSGNEGDASPFTD-ITVEGISKLLREHGYHS       1064
sp|Q6FLD5|RPB2_CANGA                PDLIINPHAIPSRMTVAHLIECLLSKVAALSGNEGDASPFTD-ITVEGISKLLREHGYQS       1065
sp|P08518|RPB2_YEAST                PDLIINPHAIPSRMTVAHLIECLLSKVAALSGNEGDASPFTD-ITVEGISKLLREHGYQS       1066
tr|A0A0L8VHA5|A0A0L8VHA5_9SACH      PDLIINPHAIPSRMTVAHLIECLLSKVAALSGNEGDASPFTD-ITVEGISKLLREHGYQS       1066
tr|A0A0L8RB33|A0A0L8RB33_SACEU      PDLIINPHAIPSRMTVAHLIECLLSKVAALSGNEGDASPFTD-ITVEGISKLLREHGYQS       1066
tr|G0VJ71|G0VJ71_NAUCC              PDLIINPHAIPSRMTVAHLIECLLSKVAALSGNEGDASPFTD-ITVEGISKLLREHGYQS       1066
tr|G8ZM49|G8ZM49_TORDC              PDLIINPHAIPSRMTVAHLIECLLSKVAALSGNEGDASPFTD-ITVEGISKLLREHGYQS       1064
tr|A0A1Q3A090|A0A1Q3A090_ZYGRO      PDLIINPHAIPSRMTVAHLIECLLSKVAALSGNEGDASPFTD-ITVEGISKLLREHGYQS       1066
tr|A0A0N7IS35|A0A0N7IS35_9SACH      PDLIINPHAIPSRMTVAHLIECLLSKVAALSGNEGDASPFTD-ITVEGISKLLREHGYHS       1064
tr|A0A212MG88|A0A212MG88_ZYGBA      PDLIINPHAIPSRMTVAHLIECLLSKVAALSGNEGDASPFTD-ITVEGISKLLREHGYHS       1065
tr|A0A1S7HHE1|A0A1S7HHE1_9SACH      PDLIINPHAIPSRMTVAHLIECLLSKVAALSGNEGDASPFTD-ITVEGISKLLREHGYHS       1065
tr|S6ESB4|S6ESB4_ZYGB2              PDLIINPHAIPSRMTVAHLIECLLSKVAALSGNEGDASPFTD-ITVEGISKLLREHGYHS       1065
tr|B6K5Q5|B6K5Q5_SCHJY              PDIIINPHAIPSRMTVAHLVECQLSKVSALSGLEGDATPFTE-VTVEAVSKLLRSHGFHS       1055
sp|Q02061|RPB2_SCHPO                PDIIINPHAIPSRMTVAHLVECQLSKVSALSGFEGDATPFTD-VTVEAVSKLLRSHGFQS       1055
tr|S9R8U4|S9R8U4_SCHOY              PDVIINPHAIPSRMTVAHLIECQLSKVSALSGFEGDATPFTD-VTVEAVSKLLRSHGFQS       1055
tr|S9W8C6|S9W8C6_SCHCR              PDVIINPHAIPSRMTVAHLIECQLSKVSALSGFEGDATPFTD-VTVEAISKLLRSHGFQS       1055
                                    **:************:.**:**  .**:* .*  ***:**.: :.*: :*.** .:*: :
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sp|P30876|RPB2_HUMAN                RGNEVLYNGFTGRKITSQIFIGPTYYQRLKHMVDDKIHSRARGPIQILNRQPMEGRSRDG      1082
tr|G3V8Y5|G3V8Y5_RAT                RGNEVLYNGFTGRKITSQIFIGPTYYQRLKHMVDDKIHSRARGPIQILNRQPMEGRSRDG      1082
tr|A0A250Y753|A0A250Y753_CASCN      RGNEVLYNGFTGRKITSQIFIGPTYYQRLKHMVDDKIHSRARGPIQILNRQPMEGRSRDG      1082
tr|A0A1U7R4C7|A0A1U7R4C7_MESAU      RGNEVLYNGFTGRKITSQIFIGPTYYQRLKHMVDDKIHSRARGPIQILNRQPMEGRSRDG      1082
tr|A0A286XIQ9|A0A286XIQ9_CAVPO      RGNEVLYNGFTGRKITSQIFIGPTYYQRLKHMVDDKIHSRARGPIQILNRQPMEGRSRDG      1082
tr|I3M351|I3M351_ICTTR              RGNEVLYNGFTGRKITSQIFIGPTYYQRLKHMVDDKIHSRARGPIQILNRQPMEGRSRDG      1082
tr|G7P5R6|G7P5R6_MACFA              RGNEVLYNGFTGRKITSQIFIGPTYYQRLKHMVDDKIHSRARGPIQILNRQPMEGRSRDG      1082
tr|H2QPI8|H2QPI8_PANTR              RGNEVLYNGFTGRKITSQIFIGPTYYQRLKHMVDDKIHSRARGPIQILNRQPMEGRSRDG      1082
tr|A0A1U7V0T5|A0A1U7V0T5_TARSY      RGNEVLYNGFTGRKITSQIFIGPTYYQRLKHMVDDKIHSRARGPIQILNRQPMEGRSRDG      1082
tr|A0A1S2ZSL2|A0A1S2ZSL2_ERIEU      RGNEVLYNGFTGRKITSQIFIGPTYYQRLKHMVDDKIHSRARGPIQILNRQPMEGRSRDG      1082
tr|A0A0D9QYL1|A0A0D9QYL1_CHLSB      RGNEVLYNGFTGRKITSQIFIGPTYYQRLKHMVDDKIHSRARGPIQILNRQPMEGRSRDG      1075
tr|A0A2K5ZNR7|A0A2K5ZNR7_MANLE      RGNEVLYNGFTGRKITSQIFIGPTYYQRLKHMVDDKIHSRARGPIQILNRQPMEGRSRDG      1075
tr|A0A2I2ZIU3|A0A2I2ZIU3_GORGO      RGNEVLYNGFTGRKITSQIFIGPTYYQRLKHMVDDKIHSRARGPIQILNRQPMEGRSRDG      1082
tr|A0A1D5QGA5|A0A1D5QGA5_MACMU      RGNEVLYNGFTGRKITSQIFIGPTYYQRLKHMVDDKIHSRARGPIQILNRQPMEGRSRDG      1082
tr|A0A2J8S2N1|A0A2J8S2N1_PONAB      RGNEVLYNGFTGRKITSQIFIGPTYYQRLKHMVDDKIHSRARGPIQILNRQPMEGRSRDG      1082
tr|A0A2K5K5J5|A0A2K5K5J5_COLAP      RGNEVLYNGFTGRKITSQIFIGPTYYQRLKHMVDDKIHSRARGPIQILNRQPMEGRSRDG      1082
tr|A0A2J8PEW7|A0A2J8PEW7_PANTR      RGNEVLYNGFTGRKITSQIFIGPTYYQRLKHMVDDKIHSRARGPIQILNRQPMEGRSRDG      1075
tr|A0A2K5CY83|A0A2K5CY83_AOTNA      RGNEVLYNGFTGRKITSQIFIGPTYYQRLKHMVDDKIHSRARGPIQILNRQPMEGRSRDG      1082
tr|A0A096NEY4|A0A096NEY4_PAPAN      RGNEVLYNGFTGRKITSQIFIGPTYYQRLKHMVDDKIHSRARGPIQILNRQPMEGRSRDG      1082
tr|C9J2Y9|C9J2Y9_HUMAN              RGNEVLYNGFTGRKITSQIFIGPTYYQRLKHMVDDKIHSRARGPIQILNRQPMEGRSRDG      1075
tr|G8BY61|G8BY61_TETPH              RGFEVMYNGHTGKKLMAQIFFGPTYYQRLRHMVDDKIHARARGPMQVLTRQPVEGRSRDG      1126
tr|A0A1X7QYA1|A0A1X7QYA1_9SACH      RGFEVMYNGHTGKKLMAQIFFGPTYYQRLRHMVDDKIHARARGPMQVLTRQPVEGRSRDG      1123
tr|J7RV95|J7RV95_KAZNA              RGFEVMYNGHTGKKLMAQIFFGPTYYQRLRHMVDDKIHARARGPMQVLTRQPVEGRSRDG      1122
tr|H2AVJ8|H2AVJ8_KAZAF              RGFEVMYNGHTGKKLMAQIFFGPTYYQRLRHMVDDKIHARARGPMQVLTRQPVEGRSRDG      1124
sp|Q6FLD5|RPB2_CANGA                RGFEVMYNGHTGKKLMAQIFFGPTYYQRLRHMVDDKIHARARGPMQVLTRQPVEGRSRDG      1125
sp|P08518|RPB2_YEAST                RGFEVMYNGHTGKKLMAQIFFGPTYYQRLRHMVDDKIHARARGPMQVLTRQPVEGRSRDG      1126
tr|A0A0L8VHA5|A0A0L8VHA5_9SACH      RGFEVMYNGHTGKKLMAQIFFGPTYYQRLRHMVDDKIHARARGPMQVLTRQPVEGRSRDG      1126
tr|A0A0L8RB33|A0A0L8RB33_SACEU      RGFEVMYNGHTGKKLMAQIFFGPTYYQRLRHMVDDKIHARARGPMQVLTRQPVEGRSRDG      1126
tr|G0VJ71|G0VJ71_NAUCC              RGFEVMYNGHTGKKLMAQIFFGPTYYQRLRHMVDDKIHARARGPMQVLTRQPVEGRSRDG      1126
tr|G8ZM49|G8ZM49_TORDC              RGFEVMYNGHTGKKLMAQIFFGPTYYQRLRHMVDDKIHARARGPMQVLTRQPVEGRSRDG      1124
tr|A0A1Q3A090|A0A1Q3A090_ZYGRO      RGFEVMYNGHTGKKLMSQIFFGPTYYQRLRHMVDDKIHARARGPMQVLTRQPVEGRSRDG      1126
tr|A0A0N7IS35|A0A0N7IS35_9SACH      RGFEVMYNGHTGKKLMSQIFFGPTYYQRLRHMVDDKIHARARGPMQVLTRQPVEGRSRDG      1124
tr|A0A212MG88|A0A212MG88_ZYGBA      RGFEVMYNGHTGKKLMSQIFFGPTYYQRLRHMVDDKIHARARGPMQVLTRQPVEGRSRDG      1125
tr|A0A1S7HHE1|A0A1S7HHE1_9SACH      RGFEVMYNGHTGKKLMSQIFFGPTYYQRLRHMVDDKIHARARGPMQVLTRQPVEGRSRDG      1125
tr|S6ESB4|S6ESB4_ZYGB2              RGFEVMYNGHTGKKLMSQIFFGPTYYQRLRHMVDDKIHARARGPMQVLTRQPVEGRSRDG      1125
tr|B6K5Q5|B6K5Q5_SCHJY              RGFEVMYHGHTGRKLVAQVFLGPTYYQRLKHLVDDKIHARARGPVQILTRQPVEGRSRDG      1115
sp|Q02061|RPB2_SCHPO                RGFEVMYHGHTGRKLVAQVFLGPTYYQRLKHLVDDKIHARARGPVQILTRQPVEGRSRDG      1115
tr|S9R8U4|S9R8U4_SCHOY              RGFEVMYHGHTGRKLVSQVFLGPTYYQRLKHLVDDKIHARARGPVQILTRQPVEGRSRDG      1115
tr|S9W8C6|S9W8C6_SCHCR              RGFEVMYHGHTGRKLVSQVFLGPTYYQRLKHLVDDKIHARARGPVQILTRQPVEGRSRDG      1115
                                    ** **:*:*.**:*: :*:*:********:*:******:*****:*:*.***:*******


sp|P30876|RPB2_HUMAN                GLRFGEMERDCQIAHGAAQFLRERLFEASDPYQVHVCNLCGIMA-IANTRTHTYECRGCR      1141
tr|G3V8Y5|G3V8Y5_RAT                GLRFGEMERDCQIAHGAAQFLRERLFEASDPYQVHVCNLCGIMA-IANTRTHTYECRGCR      1141
tr|A0A250Y753|A0A250Y753_CASCN      GLRFGEMERDCQIAHGAAQFLRERLFEASDPYQVHVCNLCGIMA-IANTRTHTYECRGCR      1141
tr|A0A1U7R4C7|A0A1U7R4C7_MESAU      GLRFGEMERDCQIAHGAAQFLRERLFEASDPYQVHVCNLCGIMA-IANTRTHTYECRGCR      1141
tr|A0A286XIQ9|A0A286XIQ9_CAVPO      GLRFGEMERDCQIAHGAAQFLRERLFEASDPYQVHVCNLCGIMA-IANTRTHTYECRGCR      1141
tr|I3M351|I3M351_ICTTR              GLRFGEMERDCQIAHGAAQFLRERLFEASDPYQVHVCNLCGIMA-IANTRTHTYECRGCR      1141
tr|G7P5R6|G7P5R6_MACFA              GLRFGEMERDCQIAHGAAQFLRERLFEASDPYQVHVCNLCGIMA-IANTRTHTYECRGCR      1141
tr|H2QPI8|H2QPI8_PANTR              GLRFGEMERDCQIAHGAAQFLRERLFEASDPYQVHVCNLCGIMA-IANTRTHTYECRGCR      1141
tr|A0A1U7V0T5|A0A1U7V0T5_TARSY      GLRFGEMERDCQIAHGAAQFLRERLFEASDPYQVHVCNLCGIMA-IANTRTHTYECRGCR      1141
tr|A0A1S2ZSL2|A0A1S2ZSL2_ERIEU      GLRFGEMERDCQIAHGAAQFLRERLFEASDPYQVHVCNLCGIMA-IANTRTHTYECRGCR      1141
tr|A0A0D9QYL1|A0A0D9QYL1_CHLSB      GLRFGEMERDCQIAHGAAQFLRERLFEASDPYQVHVCNLCGIMA-IANTRTHTYECRGCR      1134
tr|A0A2K5ZNR7|A0A2K5ZNR7_MANLE      GLRFGEMERDCQIAHGAAQFLRERLFEASDPYQVHVCNLCGIMA-IANTRTHTYECRGCR      1134
tr|A0A2I2ZIU3|A0A2I2ZIU3_GORGO      GLRFGEMERDCQIAHGAAQFLRERLFEASDPYQVHVCNLCGIMA-IANTRTHTYECRGCR      1141
tr|A0A1D5QGA5|A0A1D5QGA5_MACMU      GLRFGEMERDCQIAHGAAQFLRERLFEASDPYQVHVCNLCGIMA-IANTRTHTYECRGCR      1141
tr|A0A2J8S2N1|A0A2J8S2N1_PONAB      GLRFGEMERDCQIAHGAAQFLRERLFEASDPYQVHVCNLCGIMA-IANTRTHTYECRGCR      1141
tr|A0A2K5K5J5|A0A2K5K5J5_COLAP      GLRFGEMERDCQIAHGAAQFLRERLFEASDPYQVHVCNLCGIMA-IANTRTHTYECRGCR      1141
tr|A0A2J8PEW7|A0A2J8PEW7_PANTR      GLRFGEMERDCQIAHGAAQFLRERLFEASDPYQVHVCNLCGIMA-IANTRTHTYECRGCR      1134
tr|A0A2K5CY83|A0A2K5CY83_AOTNA      GLRFGEMERDCQIAHGAAQFLRERLFEASDPYQVHVCNLCGIMA-IANTRTHTYECRGCR      1141
tr|A0A096NEY4|A0A096NEY4_PAPAN      GLRFGEMERDCQIAHGAAQFLRERLFEASDPYQVHVCNLCGIMA-IANTRTHTYECRGCR      1141
tr|C9J2Y9|C9J2Y9_HUMAN              GLRFGEMERDCQIAHGAAQFLRERLFEASDPYQVHVCNLCGIMA-IANTRTHTYECRGCR      1134
tr|G8BY61|G8BY61_TETPH              GLRFGEMERDCMIAHGAAAFLKERLMEASDAFRVHVCGICGLMTVIAKLNHNQFECKGCD      1186
tr|A0A1X7QYA1|A0A1X7QYA1_9SACH      GLRFGEMERDCMIAHGAAAFLKERLMEASDAFRVHICGNCGLMSVIAKLSHNQFECKGCE      1183
tr|J7RV95|J7RV95_KAZNA              GLRFGEMERDCMIAHGAAAFLKERLMEASDSFRVHICGNCGLMSVIAKLSHNQFECKGCN      1182
tr|H2AVJ8|H2AVJ8_KAZAF              GLRFGEMERDCMIAHGAAAFLKERLMEASDAFRVHICGNCGLMSVIAKLSHNQFECKGCN      1184
sp|Q6FLD5|RPB2_CANGA                GLRFGEMERDCMIAHGAAAFLKERLMEASDAFRVHICGICGLMSVIAKLNHNQFECKGCD      1185
sp|P08518|RPB2_YEAST                GLRFGEMERDCMIAHGAASFLKERLMEASDAFRVHICGICGLMTVIAKLNHNQFECKGCD      1186
tr|A0A0L8VHA5|A0A0L8VHA5_9SACH      GLRFGEMERDCMIAHGAASFLKERLMEASDAFRVHICGICGLMTVIAKLNHNQFECKGCD      1186
tr|A0A0L8RB33|A0A0L8RB33_SACEU      GLRFGEMERDCMIAHGAASFLKERLMEASDAFRVHICGICGLMTVIAKLNHNQFECKGCD      1186
tr|G0VJ71|G0VJ71_NAUCC              GLRFGEMERDCMIAHGAAAFLKERLMEASDAFRVHICGNCGLMSVIAKLNHNQFECKGCD      1186
tr|G8ZM49|G8ZM49_TORDC              GLRFGEMERDCMIAHGAAAFLKERLMEASDAFRVHICGICGLMSVIAKLNHNQFECKGCD      1184
tr|A0A1Q3A090|A0A1Q3A090_ZYGRO      GLRFGEMERDCMIAHGAAAFLKERLMEASDAFRVHICGICGLMSVVAKLNHNQFECRGCD      1186
tr|A0A0N7IS35|A0A0N7IS35_9SACH      GLRFGEMERDCMIAHGAASFLKERLMEASDAFRVHICGICGLMSVVAKLNHNQFECKGCD      1184
tr|A0A212MG88|A0A212MG88_ZYGBA      GLRFGEMERDCMIAHGAAAFLKERLMEASDAFRVHICGICGLMSVVAKLNHNQFECKGCD      1185
tr|A0A1S7HHE1|A0A1S7HHE1_9SACH      GLRFGEMERDCMIAHGAAAFLKERLMEASDAFRVHICGICGLMSVVAKLNHNQFECKGCD      1185
tr|S6ESB4|S6ESB4_ZYGB2              GLRFGEMERDCMIAHGAAAFLKERLMEASDAFRVHICGICGLMSVVAKLNHNQFECKGCD      1185
tr|B6K5Q5|B6K5Q5_SCHJY              GLRFGEMERDCQISHGCSSVLRERLFDCSDAYRVIVCDLCGLIA-IASFKKNSYECRSCQ      1174
sp|Q02061|RPB2_SCHPO                GLRFGEMERDCQISHGCSSVLRERLFDCSDAYRVIVCDICGLIA-IASYKKDSYECRSCQ      1174
tr|S9R8U4|S9R8U4_SCHOY              GLRFGEMERDCQISHGCSSVMRERLFDCSDAYRVVVCDLCGLVA-IASYKKNSYECRSCQ      1174
tr|S9W8C6|S9W8C6_SCHCR              GLRFGEMERDCQISHGCSSVMRERLFDCSDAYRVVVCDLCGLVA-IASYKKNSYECRSCQ      1174
                                    *********** *:**.: .::***::.**.::* :*.:**::  :*.   . :**:.*
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sp|P30876|RPB2_HUMAN                NKTQISLVRMPYACKLLFQELMSMSIAPRMMSV-----   1174
tr|G3V8Y5|G3V8Y5_RAT                NKTQISLVRMPYACKLLFQELMSMSIAPRMMSV-----   1174
tr|A0A250Y753|A0A250Y753_CASCN      NKTQISLVRMPYACKLLFQELMSMSIAPRMMSV-----   1174
tr|A0A1U7R4C7|A0A1U7R4C7_MESAU      NKTQISLVRMPYACKLLFQELMSMSIAPRMMSV-----   1174
tr|A0A286XIQ9|A0A286XIQ9_CAVPO      NKTQISLVRMPYACKLLFQELMSMSIAPRMMSV-----   1174
tr|I3M351|I3M351_ICTTR              NKTQISLVRMPYACKLLFQELMSMSIAPRMMSV-----   1174
tr|G7P5R6|G7P5R6_MACFA              NKTQISLVRMPYACKLLFQELMSMSIAPRMMSV-----   1174
tr|H2QPI8|H2QPI8_PANTR              NKTQISLVRMPYACKLLFQELMSMSIAPRMMSV-----   1174
tr|A0A1U7V0T5|A0A1U7V0T5_TARSY      NKTQISLVRMPYACKLLFQELMSMSIAPRMMSV-----   1174
tr|A0A1S2ZSL2|A0A1S2ZSL2_ERIEU      NKTQISLVRMPYACKLLFQELMSMSIAPRMMSV-----   1174
tr|A0A0D9QYL1|A0A0D9QYL1_CHLSB      NKTQISLVRMPYACKLLFQELMSMSIAPRMMSV-----   1167
tr|A0A2K5ZNR7|A0A2K5ZNR7_MANLE      NKTQISLVRMPYACKLLFQELMSMSIAPRMMSV-----   1167
tr|A0A2I2ZIU3|A0A2I2ZIU3_GORGO      NKTQISLVRMPYACKLLFQELMSMSIAPRMMSV-----   1174
tr|A0A1D5QGA5|A0A1D5QGA5_MACMU      NKTQISLVRMPYACKLLFQELMSMSIAPRMMSV-----   1174
tr|A0A2J8S2N1|A0A2J8S2N1_PONAB      NKTQISLVRMPYACKLLFQELMSMSIAPRMMSV-----   1174
tr|A0A2K5K5J5|A0A2K5K5J5_COLAP      NKTQISLVRMPYACKLLFQELMSMSIAPRMMSV-----   1174
tr|A0A2J8PEW7|A0A2J8PEW7_PANTR      NKTQISLVRMPYACKLLFQELMSMSIAPRMMSV-----   1167
tr|A0A2K5CY83|A0A2K5CY83_AOTNA      NKTQISLVRMPYACKLLFQELMSMSIAPRMMSV-----   1174
tr|A0A096NEY4|A0A096NEY4_PAPAN      NKTQISLVRMPYACKLLFQELMSMSIAPRMMSV-----   1174
tr|C9J2Y9|C9J2Y9_HUMAN              NKTQISLVRMPYACKLLFQELMSMSIAPRMMSV-----   1167

tr|G8BY61|G8BY61_TETPH              NKIDIYQIRIPYAAKLLFQELMAMNITPRLYTDRSKNF   1224
tr|A0A1X7QYA1|A0A1X7QYA1_9SACH      NKIDIYQIQIPYAAKLLFQELMAMNITPRLYTDRSRDF   1221
tr|J7RV95|J7RV95_KAZNA              NKIDIYQIRIPYAAKLLFQELMAMNITPRLYTDRSRDF   1220
tr|H2AVJ8|H2AVJ8_KAZAF              NKIDIYQIHIPYAAKLLFQELMAMNITPRLFTDRSRDF   1222
sp|Q6FLD5|RPB2_CANGA                NKIDIYQIHIPYAAKLLFQELMAMNITPRLYTDRSRDF   1223
sp|P08518|RPB2_YEAST                NKIDIYQIHIPYAAKLLFQELMAMNITPRLYTDRSRDF   1224
tr|A0A0L8VHA5|A0A0L8VHA5_9SACH      NKIDIYQIHIPYAAKLLFQELMAMNITPRLYTDRSRDF   1224
tr|A0A0L8RB33|A0A0L8RB33_SACEU      NKIDIYQIHIPYAAKLLFQELMAMNITPRLYTDRSRDF   1224
tr|G0VJ71|G0VJ71_NAUCC              NKIDIYQIHIPYAAKLLFQELMAMNITPRLYTERSRDF   1224
tr|G8ZM49|G8ZM49_TORDC              NKIDIYQINIPYAAKLLFQELMAMNITPRLYTDRSKDF   1222
tr|A0A1Q3A090|A0A1Q3A090_ZYGRO      NKIDIYQIHIPYAAKLLFQELMAMNITPRLYTDRSKDF   1224
tr|A0A0N7IS35|A0A0N7IS35_9SACH      NKIDIFQIHIPYAAKLLFQELMAMNITPRLYTDRSKDF   1222
tr|A0A212MG88|A0A212MG88_ZYGBA      NKIDIYQIHIPYAAKLLFQELMAMNITPRLYTDRSKDF   1223
tr|A0A1S7HHE1|A0A1S7HHE1_9SACH      NKIDIYQIHIPYAAKLLFQELMAMNITPRLYTDRSKDF   1223
tr|S6ESB4|S6ESB4_ZYGB2              NKIDIYQIHIPYAAKLLFQELMAMNITPRLYTDRSKDF   1223
tr|B6K5Q5|B6K5Q5_SCHJY              NRTRFSQIYLPYAAKLLFQELMSMNIAPRLFTKSHH--   1210
sp|Q02061|RPB2_SCHPO                NRTRFSQVYLPYAAKLLFQELMSMNIAPRLFTKNHK--   1210
tr|S9R8U4|S9R8U4_SCHOY              NRTRFSQIYLPYAAKLLFQELMSMNIAPRLFTKNHKI-   1211
tr|S9W8C6|S9W8C6_SCHCR              NRTRFSQVYLPYAAKLLFQELMSMNIAPRLFTKNHKN-   1211
                                    *:  :  :  :***.********:*.*:**: :
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Fig. 3 MSA of the Rpb2, initiation subunits, of eukaryotic RNAPs II

P30876|RPB2_HUMAN, *Homo sapiens*
A0A250Y753_CASCN, *Castor Canadensis*
A0A286XIQ9_CAVPO, *Caviaporcellus*
I3M351_ICTTR, *Ictidomys tridecemlineatus*
A0A1U7V0T5_TARSY, *Tarsiussyrichta*
A0A0D9QYL1_CHLSB, *Chlorocebussabaeus*
A0A2I2ZIU3_GORGO, *Gorilla gorillagorilla*
A0A2J8PEW7_PANTR, *Pan troglodytes*
A0A2J8S2N1_PONAB, *Pongo abelii*
A0A096NEY4|_PAPAN, *Papio Anubis*
G8BY61_TETPH, *Tetrapisisporaphaffii*
J7RV95_KAZNA, *Kazachstaniana ganishii*
Q6FLD5_CANGA, *Candida glabrata*
A0A0L8VHA5_9SACH,*Saccharomyces boulardii*
G0VJ71_NAUCC, *Naumovozyma castellii*
A0A1Q3A090_ZYGRO,*Zygosaccharomyces rouxii*
A0A0N7IS35_9SACH, *Zygosaccharomyces kombuchaensis*
A0A212MG88_ZYGBA, *Zygosaccharomyces bailii*
A0A1S7HHE1_9SACH, *Zygosaccharomyces parabailii*
S6ESB4_ZYGB2, *Zygosaccharomyces bailii* (strain CLIB 213)
B6K5Q5_SCHJY, *Schizosaccharomyces japonicas*
Q02061_SCHPO, *Schizosaccharomyces pombe*
S9R8U4_SCHOY, Schizosaccharomyces *octosporus*
S9W8C6_SCHCR, *Schizosaccharomyces cryophilus*

G3V8Y5_RAT, *Rattus norvegicus*
A0A1U7R4C7_MESAU, *Mesocricetus auratus*
tr|G7P5R6_MACFA, *Macaca fascicularis*
H2QPI8_PANTR, *Pan troglodytes*
A0A1S2ZSL2_ERIEU, *Erinaceus europaeus*
A0A2K5K5J5_COLAP, *Colobus angolensis palliates*
A0A1D5QGA5_MACMU, *Macaca mulatta*
A0A2K5CY83_AOTNA, *Aotus nancymaae*
A0A2K5ZNR7_MANLE, *Mandrillus leucophaeus*
C9J2Y9_HUMAN, *Homo sapiens*
tr|A0A1X7QYA1_9SACH, *Kazachstania saulgeensis*
H2AVJ8_KAZAF, *Kazachstania africana*
P08518|_Yeast, *Saccharomyces cerevisiae*
A0A0L8RB33_SACEU, *Saccharomyces eubayanus*
G8ZM49|_TORDC, *Torulasporadel brueckii*

Figure 4 shows the MSA analysis and conserved motifs in the Rpb1 elongation subunits in eukaryotic MSU RNAPs II. The yeast subunit with 1733 amino acids is used as standard and highlighted in magenta. Like the Rpb2 subunits, there are large numbers of conserved motifs and some are found to be long stretches (highlighted). However, the Rpb1 subunits are more conserved than the Rpb2 subunits. The 'template binding' pair is invariably an FG rather than a YG pair as reported in other MSU RNAPs. However, the catalytic R is completely conserved, including distance conservation in all the eukaryotic Rpb1 subunits and the upstream neighbour is mostly S/T but in lower eukaryotes like yeasts, it is N. Unlike in prokaryotic elongation subunit, the catalytic region is placed very close to the N-terminal (~ 100 amino acids). It is interesting to note that the distance between the catalytic R and the FG pair is 18 amino acids, i.e., placed exactly double the distance as compared to the Rpb2 initiation subunits. This distance closely agrees with the transcription bubble which extends ~ 20 bp from the TATA box (Pal et al, 2005). The template binding and catalytic conservations strongly suggest that the DNA, SSU and MSU RNA polymerases use the same set of amino acids for template, substrate binding and catalysis establishing a structure-function relationship among the DNA and RNAPs. Interestingly the catalytic region harbouring the Zn binding motif is found very close to the N-terminal region. This is in sharp contrast to the equivalent region in the β' subunit in all eubacteria (Table 1). The Zn binding motif was originally identified by X-ray crystallographic analysis in the equivalent β' subunit of the thermophilic bacterium, *Thermus aquaticus,* [Zhang et al, 1999]. The Zn binding 3 invariant Cs were located in the catalytic region and suggested in possible proof-reading activity during elongation. A completely conserved R found upstream from the catalytic R is located at -6th position which is implicated in NTP selection. It is interesting to note a completely conserved R found upstream from the catalytic R is missing in eubacteria (Table 1) [Palanivelu 2017, Palanivelu 2013]. The immediate downstream amino acid from catalytic K in DNA polymerases is usually a G or A [Palanivelu 2017], but in viral RNA polymerases it is a K or R, in MSU β' subunits, it is a D and in all β' subunits it is an S and it is an S/T in eukaryotes suggesting a possible role in NTP selection. In SSU RNAPs, an invariant hydroxyl amino acid located very close to the YG pair is shown to involve in NTP selection by SDM experiments (Kostyuk et al.1995). In addition to the template binding FG pair, there are 1 YG pair, 4 LG pairs and 3 I/VLG pairs in this subunit. A C- terminal conservation - **SPDDSDE**E**N**- (where the penultimate E is replaced with functionally equivalent D in some species) is seen in all higher forms of life and such sequence was conspicuously absent in the lower eukaryotes like yeasts and also not found in the initiation subunits, Rpb2. The –**D**XD- is a metal binding motif commonly found in glycosyl transferases and interestingly similar motif –**D**XDXT- in metal-dependent phosphatases (**D**xDXE in C-terminals of Rpb1 elongation subunits) where it plays a role for Ser phosphate removal from the CTD at the end of the cycle (Hausmann and Shuman, 2002). Interestingly, this motif invariably ends in N preceded by D/E in all the cases in Rpb1 (Fig 4). As expected the CTD is filled with the "heptapeptide repeats" (YSPTSPS) in all species and its role is discussed elsewhere (Not shown in the Figure). Crammer et al (2001) results provide evidence for RNA exit in the vicinity of the carboxyl-terminal repeat domain, coupling synthesis to RNA processing by enzymes bound to this domain.

CLUSTAL O(1.2.4) MSA of the **Rpb1,** elongation subunits of MSU RNAPs- **II** 4

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tr|A0A1U8DYN0|A0A1U8DYN0_ALLSI      -MHGGAPSGDSACPLRTIKRVQFGILSPDEMKRMSVTEGGIKYPETT--EGGRPKLGGLM       57
tr|A0A1L8H4P4|A0A1L8H4P4_XENLA      --MHGAPSGDSACPLRTIKRVQFGVIGPDELKRMSVTEGGIKYSETT--EGGRPKLGGLM       56
tr|H9GLG5|H9GLG5_ANOCA              -MHGGAPSGDSACPLRTIKRVQFGILSPDEMKRMSVTEGGIKYPETT--EGGRPKLGGLM       57
tr|H2R1J6|H2R1J6_PANTR              MHGGGPPSGDSACPLRTIKRVQFGVLSPDELKRMSVTEGGIKYPETT--EGGRPKLGGLM       58
tr|G1MCZ1|G1MCZ1_AILME              MHGGGPPSGDSACPLRTIKRVQFGVLSPDELKRMSVTEGGIKYPETT--EGGRPKLGGLM       58
tr|O08847|O08847_MOUSE              MHGGGPPSGDSACPLRTIKRVQFGVLSPDELKRMSVTEGGIKYPETT--EGGRPKLGGLM       58
tr|S7PWZ6|S7PWZ6_MYOBR              MHGGGPPSGDSACPLRTIKRVQFGVLSPDELKRMSVTEGGIKYPETT--EGGRPKLGGLM       58
tr|D4A5A6|D4A5A6_RAT                MHGGGPPSGDSACPLRTIKRVQFGVLSPDELKRMSVTEGGIKYPETT--EGGRPKLGGLM       58
sp|P08775|RPB1_MOUSE                MHGGGPPSGDSACPLRTIKRVQFGVLSPDELKRMSVTEGGIKYPETT--EGGRPKLGGLM       58
sp|P24928|RPB1_HUMAN                MHGGGPPSGDSACPLRTIKRVQFGVLSPDELKRMSVTEGGIKYPETT--EGGRPKLGGLM       58
tr|A0A1S3EWL2|A0A1S3EWL2_DIPOR      MHGGGPPSGDSACPLRTIKRVQFGVLSPDELKRMSVTEGGIKYPETT--EGGRPKLGGLM       58
sp|P11414|RPB1_CRIGR                MHGGGPPSGDSACPLRTIKRVQFGVLSPDELKRMSVTEGGIKYPETT--EGGRPKLGGLM       58
tr|O35559|O35559_CRIGR              MHGGGPPSGDSACPLRTIKRVQFGVLSPDELKRMSVTEGGIKYPETT--EGGRPKLGGLM       58
tr|A0A2I3M9H2|A0A2I3M9H2_PAPAN      MHGGGPPSGDSACPLRTIKRVQFGVLSPDELKRMSVTEGGIKYPETT--EGGRPKLGGLM       58
tr|F7HB40|F7HB40_MACMU              MHGGGPPSGDSACPLRTIKRVQFGVLSPDELKRMSVTEGGIKYPETT--EGGRPKLGGLM       58
tr|A0A2K6RYW9|A0A2K6RYW9_SAIBB      MHGGGPPSGDSACPLRTIKRVQFGVLSPDELKRMSVTEGGIKYPETT--EGGRPKLGGLM       58
tr|W5N8Z6|W5N8Z6_LEPOC              --MHGPPSGDSACPLRLIKRVQFGIISPDELKRMSVTEGGIKYPETT--EGGRPKLGGLM       56
tr|I3JRW6|I3JRW6_ORENI              --MHGPPSGDSACPLRTIKRVQFGIISPDELKRMSVTEGGIKYPETT--EGGRPKLGGLM       56
tr|A0A0R4IMS9|A0A0R4IMS9_DANRE      --MHGPPSSDSACPLRLIKRVQFGVLSPDELKRMSVTEGGIKYPETT--EGGRPKLGGLM       56
tr|A0A1A7X327|A0A1A7X327_9TELE      --MHGPPSGDSACPLRTIKRVQFGIISPDELKRMSVTEGGIKYPETT--EGGRPKLGGLM       56
tr|A0A1A8UKD7|A0A1A8UKD7_NOTFU      --MHGPPSGDSACPLRTIKRVQFGIISPDELKRMSVTEGGIKYPETT--EGGRPKLGGLM       56
tr|A0A1A8ER05|A0A1A8ER05_9TELE      --MHGPPSGDSACPLRTIKRVQFGIISPDELKRMSVTEGGIKYPETT--EGGRPKLGGLM       56
tr|A0A1A8DQ60|A0A1A8DQ60_9TELE      --MHGPPSGDSACPLRTIKRVQFGIISPDELKRMSVTEGGIKYPETT--EGGRPKLGGLM       56
tr|A0A1A8NSR8|A0A1A8NSR8_9TELE      --MHGPPSGDSACPLRTIKRVQFGIISPDELKRMSVTEGGIKYPETT--EGGRPKLGGLM       56
tr|A0A1W4YLM7|A0A1W4YLM7_9TELE      --MHGPPSGDSACPLRLIKRVQFGIISPDELKRMSVTEGGIKYPETT--EGGRPKLGGLM       56
tr|A0A1M8A6L7|A0A1M8A6L7_MALS4      MMGH--QFAPSVAPVRPVKEVQFGILSPEEIRALSVCK--IEFPEVKDDATGKYKVGGLS       56
sp|P04050|RPB1_YEAST                --MV--GQQYSSAPLRTVKEVQFGLFSPEEVRAISVAK--IRFPETMDETQTRAKIGGLN       54
tr|A0A1B2J8C6|A0A1B2J8C6_PICPA      --MS--QFPYSSAPLRSVKEVQFGLLSPEEIRAISVVK--IEYPEIMDESRQRPREGGLN       54
tr|F2QW17|F2QW17_KOMPC              --MS--QFPYSSAPLRSVKEVQFGLLSPEEIRAISVVK--IEYPEIMDESRQRPREGGLN       54
tr|A3GID7|A3GID7_PICST              -MSR--QFPYSSAPLRSVKEVQFGLLSPEEVRAISVAK--IEYPETMDQTTKTPREGGLN       55
tr|A0A1D8PUA6|A0A1D8PUA6_CANAL      -MSR--QFPYSSAPLRSVKEVQFGLLSPEEVRAISVAK--IEYPETMDQTTKRPREGGLN       55
tr|G8BEH9|G8BEH9_CANPC              -MSR--TFPFSNAPLRSVKEVQFGLLSPEEVRAISVAK--IEYPETMDQATKRPREGGLN       55
                                              * .*:* :*.****::.*:*:: :** :  *.: *         : ***

tr|A0A1U8DYN0|A0A1U8DYN0_ALLSI      DPRQGVIERTGRCQTCA-GNMTECPGHFGHIELAKPVFHVGFLGKTMKILRCVCFFCSKL       116
tr|A0A1L8H4P4|A0A1L8H4P4_XENLA      DPRQGVIERSGRCQTCA-GNMTECPGHFGHVELAKPVYHVGFLVKTMKVLRCVCFFCSKL       115
tr|H9GLG5|H9GLG5_ANOCA              DPRQGVIERTGRCQTCA-GNMTECPGHFGHIELAKPVFHVGFLGKTMKVLRCVCFFCSKL       116
tr|H2R1J6|H2R1J6_PANTR              DPRQGVIERTGRCQTCA-GNMTECPGHFGHIELAKPVFHVGFLVKTMKVLRCVCFFCSKL       117
tr|G1MCZ1|G1MCZ1_AILME              DPRQGVIERTGRCQTCA-GNMTECPGHFGHIELAKPVFHVGFLVKTMKVLRCVCFFCSKL       117
tr|O08847|O08847_MOUSE              DPRQGVIERTGRCQTCA-GNMTECPGHFGHIELAKPVFHVGFLVKTMKVLRCVCFFCSKL       117
tr|S7PWZ6|S7PWZ6_MYOBR              DPRQGVIERTGRCQTCA-GNMTECPGHFGHIELAKPVFHVGFLVKTMKVLRCVCFFCSKL       117
tr|D4A5A6|D4A5A6_RAT                DPRQGVIERTGRCQTCA-GNMTECPGHFGHIELAKPVFHVGFLVKTMKVLRCVCFFCSKL       117
sp|P08775|RPB1_MOUSE                DPRQGVIERTGRCQTCA-GNMTECPGHFGHIELAKPVFHVGFLVKTMKVLRCVCFFCSKL       117
sp|P24928|RPB1_HUMAN                DPRQGVIERTGRCQTCA-GNMTECPGHFGHIELAKPVFHVGFLVKTMKVLRCVCFFCSKL       117
tr|A0A1S3EWL2|A0A1S3EWL2_DIPOR      DPRQGVIERTGRCQTCA-GNMTECPGHFGHIELAKPVFHVGFLVKTMKVLRCVCFFCSKL       117
sp|P11414|RPB1_CRIGR                DPRQGVIERTGRCQTCA-GNMTECPGHFGHIELAKPVFHVGFLVKTMKVLRCVCFFCSKL       117
tr|O35559|O35559_CRIGR              DPRQGVIERTGRCQTCA-GNMTECPGHFGHIELAKPVFHVGFLVKTMKVLRCVCFFCSKL       117
tr|A0A2I3M9H2|A0A2I3M9H2_PAPAN      DPRQGVIERTGRCQTCA-GNMTECPGHFGHIELAKPVFHVGFLVKTMKVLRCVCFFCSKL       117
tr|F7HB40|F7HB40_MACMU              DPRQGVIERTGRCQTCA-GNMTECPGHFGHIELAKPVFHVGFLVKTMKVLRCVCFFCSKL       117
tr|A0A2K6RYW9|A0A2K6RYW9_SAIBB      DPRQGVIERTGRCQTCA-GNMTECPGHFGHIELAKPVFHVGFLVKTMKVLRCVCFFCSKL       117
tr|W5N8Z6|W5N8Z6_LEPOC              DPRQGVIERSGRCQTCAAGNMTECPGHFGHIELAKPVFHVGFINKIMKVLRCVCFFCSKL       116
tr|I3JRW6|I3JRW6_ORENI              DPRQGVIERTGRCQTCA-GNMTECPGHFGHIELAKPVFHVGFISKIMKVLRCVCFFCSKL       115
tr|A0A0R4IMS9|A0A0R4IMS9_DANRE      DPRQGVIERSGRCQTCA-GNMTECPGHFGHIELAKPVFHVGFITKIMKVLRCVCFFCSKL       115
tr|A0A1A7X327|A0A1A7X327_9TELE      DPRQGVIERSGRCQTCA-GNMTECPGHFGHIELAKPVFHVGFISKIMKILRCVCFFCSKL       115
tr|A0A1A8UKD7|A0A1A8UKD7_NOTFU      DPRQGVIERTGRCQTCA-GNMTECPGHFGHIELAKPVFHVGFISKIMKILRCVCFFCSKL       115
tr|A0A1A8ER05|A0A1A8ER05_9TELE      DPRQGVIERTGRCQTCA-GNMTECPGHFGHIELAKPVFHVGFISKIMKILRCVCFFCSKL       115
tr|A0A1A8DQ60|A0A1A8DQ60_9TELE      DPRQGVIERTGRCQTCA-GNMTECPGHFGHIELAKPVFHVGFISKIMKILRCVCFFCSKL       115
tr|A0A1A8NSR8|A0A1A8NSR8_9TELE      DPRQGVIERTGRCQTCA-GNMTECPGHFGHIELAKPVFHVGFISKIMKILRCVCFFCSKL       115
tr|A0A1W4YLM7|A0A1W4YLM7_9TELE      DPRQGVIERTGRCQTCA-GNMTECPGHFGHIELAKPVFHVGFINKIMKILRCVCFFCSKL       115
tr|A0A1M8A6L7|A0A1M8A6L7_MALS4      DPRLGTIDRNYKCQTCGE-GQAECPGHFGHIDLARPVFHVGFLGKVKKLLECVCVHCGKL       115
sp|P04050|RPB1_YEAST                DPRLGSIDRNLKCQTCQE-GMNECPGHFGHIDLAKPVFHVGFIAKIKKVCECVCMHCGKL       113
tr|A0A1B2J8C6|A0A1B2J8C6_PICPA      DPKLGSIDRNFKCQTCGE-GMAECPGHFGHMELAKPVFHIGFIPKIKKVCECICMNCGKL       113
tr|F2QW17|F2QW17_KOMPC              DPKLGSIDRNFKCQTCGE-GMAECPGHFGHMELAKPVFHIGFIPKIKKVCECICMNCGKL       113
tr|A3GID7|A3GID7_PICST              DPRLGSIDRNFRCQTCGE-DMAECPGHFGHIELAKPVFHIGFIAKIKKVCECVCMHCGKL       114
tr|A0A1D8PUA6|A0A1D8PUA6_CANAL      DPRLGSIDRNFRCQTCGE-DMAECPGHFGHIELAKPVFHIGFIAKIKKACESVCMHCGKL       114
tr|G8BEH9|G8BEH9_CANPC              DPRLGSIDRNFKCQTCGE-DMAECPGHFGHIELAKPVFHIGFIAKIKKVCESICMHCGKL       114
                                    **: * *:*. :****   .  ********::**:**:*:**: *  *  ..:*. *.**
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tr|A0A1U8DYN0|A0A1U8DYN0_ALLSI      LVDSNNPKIKD-ILGKSKGQPKKRLTHVYDLCKGKNICEGGEEMDNKFGVEQTEGDEDLT       175
tr|A0A1L8H4P4|A0A1L8H4P4_XENLA      LVDANNPKIKD-ILIKSKGQPKKRLTHVYELCKGKNICEGGEEMDNKFGVEQTEGDEDIQ       174
tr|H9GLG5|H9GLG5_ANOCA              LVDSNNPKIKD-ILAKSKGQPKKRLTHVYDLCKGKNICEGGEEMDNKFGVEQPEGDEDIT       175
tr|H2R1J6|H2R1J6_PANTR              LVDSNNPKIKD-ILAKSKGQPKKRLTHVYDLCKGKNICEGGEEMDNKFGVEQPEGDEDLT       176
tr|G1MCZ1|G1MCZ1_AILME              LVDSNNPKIKD-ILAKSKGQPKKRLTHVYDLCKGKNICEGGEEMDNKFGVEQPEGDEDLT       176
tr|O08847|O08847_MOUSE              LVDSNNPKIKD-ILAKSKGQPKKRLTHVYDLCKGKNICEGGEEMDNKFGVEQPEGDEDLT       176
tr|S7PWZ6|S7PWZ6_MYOBR              LVDSNNPKIKD-ILAKSKGQPKKRLTHVYDLCKGKNICEGGEEMDNKFGVEQPEGDEDLT       176
tr|D4A5A6|D4A5A6_RAT                LVDSNNPKIKD-ILAKSKGQPKKRLTHVYDLCKGKNICEGGEEMDNKFGVEQPEGDEDLT       176
sp|P08775|RPB1_MOUSE                LVDSNNPKIKD-ILAKSKGQPKKRLTHVYDLCKGKNICEGGEEMDNKFGVEQPEGDEDLT       176
sp|P24928|RPB1_HUMAN                LVDSNNPKIKD-ILAKSKGQPKKRLTHVYDLCKGKNICEGGEEMDNKFGVEQPEGDEDLT       176
tr|A0A1S3EWL2|A0A1S3EWL2_DIPOR      LVDSNNPKIKD-ILAKSKGQPKKRLTHVYDLCKGKNICEGGEEMDNKFGVEQPEGDEDLT       176
sp|P11414|RPB1_CRIGR                LVDSNNPKIKD-ILAKSKGQPKKRLTHVYDLCKGKNICEGGEEMDNKFGVEQPEGDEDLT       176
tr|O35559|O35559_CRIGR              LVDSNNPKIKD-ILAKSKGQPKKRLTHVYDLCKGKNICEGGEEMDNKFGVEQPEGDEDLT       176
tr|A0A2I3M9H2|A0A2I3M9H2_PAPAN      LVDSNNPKIKD-ILSKSKGQPKKRLTHVYDLCKGKNICEGGEEMDNKFGVEQPEGDEDLT       176
tr|F7HB40|F7HB40_MACMU              LVDSNNPKIKD-ILSKSKGQPKKRLTHVYDLCKGKNICEGGEEMDNKFGVEQPEGDEDLT       176
tr|A0A2K6RYW9|A0A2K6RYW9_SAIBB      LVDSNNPKIKD-ILAKSKGQPKKRLTHVYDLCKGKNICEGGEEMDNKFGVEQPEGDEDLT       176
tr|W5N8Z6|W5N8Z6_LEPOC              LVDSNNPKIKD-ILGKSKGQPRKRLTHVYDLCKGKNICEGGEEMDNKFGVEQNETEEDIT       175
tr|I3JRW6|I3JRW6_ORENI              LVDSNNPKIKD-ILAKSKGQPRKRLTHVYELCKGKNICEGGEEMDNKFGMEQQETEEDLT       174
tr|A0A0R4IMS9|A0A0R4IMS9_DANRE      LVDANNPKIKD-ILTKSKGQPRKRLTHVYDLCKGKNICEGGEEMDNKFGVEQPES-EDIT       173
tr|A0A1A7X327|A0A1A7X327_9TELE      LVDANNPKIKE-ILVKSKGQPRKRLTHVYELCKGKNICEGGEEMDNKFGMEQQETEEDIT       174
tr|A0A1A8UKD7|A0A1A8UKD7_NOTFU      LVDANNPKIKE-ILVKSKGQPRKRLTHVYELCKGKNICEGGEEMDNKFGMEQQETEEDIT       174
tr|A0A1A8ER05|A0A1A8ER05_9TELE      LVDANNPKIKE-ILVKSKGQPRKRLTHVYELCKGKNICEGGEEMDNKFGMEQQETEEDIT       174
tr|A0A1A8DQ60|A0A1A8DQ60_9TELE      LVDANNPKIKE-ILVKSKGQPRKRLTHVYELCKGKNICEGGEEMDNKFGMEQQETEEDIT       174
tr|A0A1A8NSR8|A0A1A8NSR8_9TELE      LVDANNPKIKE-ILVKSKGQPRKRLTHVYELCKGKNICEGGEEMDNKFGMEQQETEEDIT       174
tr|A0A1W4YLM7|A0A1W4YLM7_9TELE      LVDSNNPKIKD-ILAKSKGQPRKRLTHVYDLCKGKNICEGGEEMDNKFGMEQAETEEDIT       174
tr|A0A1M8A6L7|A0A1M8A6L7_MALS4      KADPISDPVFKSLLQSTRANRKRRFQRVWEYCSKITICEADEGKDE------DELGDTTQ       169
sp|P04050|RPB1_YEAST                LLDEHNELMRQAL---AIKDSKKRFAAIWTLCKTKMVCETDVPSED----------DPT-       159
tr|A0A1B2J8C6|A0A1B2J8C6_PICPA      LLDETNPTMAQAI---RIRDPKKRFNAVWQLCKTKMVCEADAPVDE----------YSEQ       160
tr|F2QW17|F2QW17_KOMPC              LLDETNPTMAQAI---RIRDPKKRFNAVWQLCKTKMVCEADAPVDE----------YSEQ       160
tr|A3GID7|A3GID7_PICST              LLDENNPAMAQAI---KIRDPKKRFNAVWQLCKAKMVCETDIIEEG----------ATE-       160
tr|A0A1D8PUA6|A0A1D8PUA6_CANAL      LLDETNPAMAQAI---KIRDPKKRFNAVWSLCKTKMVCETDNNEDE----------MTD-       160
tr|G8BEH9|G8BEH9_CANPC              LLDESNPLMAQAI---KIRDPKKRFNAVWSICKSKMVCETATSEEE----------MND-       160
                                      *  .  : . :      : ::*:  ::  *    :**     :


tr|A0A1U8DYN0|A0A1U8DYN0_ALLSI      KEKGHGGCGRYQPRIRRVGLELYAEWKHVNE-------DSQEKKILLSPERVHEIFKRIA       228
tr|A0A1L8H4P4|A0A1L8H4P4_XENLA      KEKGHGGCGRYQPRIRRTGLELYAEWKHVNE-------DSQEKKILLSPERVHEIFKRIT       227
tr|H9GLG5|H9GLG5_ANOCA              KEKGHGGCGRYQPRIRRSGLELYAEWKHVNE-------DSQEKKILLSPERVHEIFKRIS       228
tr|H2R1J6|H2R1J6_PANTR              KEKGHGGCGRYQPRIRRSGLELYAEWKHVNE-------DSQEKKILLSPERVHEIFKRIS       229
tr|G1MCZ1|G1MCZ1_AILME              KEKGHGGCGRYQPRIRRSGLELYAEWKHVNE-------DSQEKKILLSPERVHEIFKRIS       229
tr|O08847|O08847_MOUSE              KEKGHGGCGRYQPRIRRSGLELYAEWKHVNE-------DSQEKKILLSPERVHEIFKRIS       229
tr|S7PWZ6|S7PWZ6_MYOBR              KEKGHGGCGRYQPRIRRSGLELYAEWKHVNE-------DSQEKKILLSPERVHEIFKRIS       229
tr|D4A5A6|D4A5A6_RAT                KEKGHGGCGRYQPRIRRSGLELYAEWKHVNE-------DSQEKKILLSPERVHEIFKRIS       229
sp|P08775|RPB1_MOUSE                KEKGHGGCGRYQPRIRRSGLELYAEWKHVNE-------DSQEKKILLSPERVHEIFKRIS       229
sp|P24928|RPB1_HUMAN                KEKGHGGCGRYQPRIRRSGLELYAEWKHVNE-------DSQEKKILLSPERVHEIFKRIS       229
tr|A0A1S3EWL2|A0A1S3EWL2_DIPOR      KEKGHGGCGRYQPRIRRSGLELYAEWKHVNE-------DSQEKKILLSPERVHEIFKRIS       229
sp|P11414|RPB1_CRIGR                KEKGHGGCGRYQPRIRRSGLELYAEWKHVNE-------DSQEKKILLSPERVHEIFKRIS       229
tr|O35559|O35559_CRIGR              KEKGHGGCGRYQPRIRRSGLELYAEWKHVNE-------DSQEKKILLSPERVHEIFKRIS       229
tr|A0A2I3M9H2|A0A2I3M9H2_PAPAN      KEKGHGGCGRYQPRIRRSGLELYAEWKHVNE-------DSQEKKILLSPERVHEIFKRIS       229
tr|F7HB40|F7HB40_MACMU              KEKGHGGCGRYQPRIRRSGLELYAEWKHVNE-------DSQEKKILLSPERVHEIFKRIS       229
tr|A0A2K6RYW9|A0A2K6RYW9_SAIBB      KEKGHGGCGRYQPRIRRSGLELYAEWKHVNE-------DSQEKKILLSPERVHEIFKRIS       229
tr|W5N8Z6|W5N8Z6_LEPOC              KEKGHGGCGRYQPRIRRSGLELYAEWKHVNE-------DSQEKKILLSPERVHEIFKRIS       228
tr|I3JRW6|I3JRW6_ORENI              KEKGHGGCGRYQPRIKRSGLELYAEWKHVNE-------DSQEKKILLSPERVHEIFKRIS       227
tr|A0A0R4IMS9|A0A0R4IMS9_DANRE      KEKGHGGCGRYQPRIRRSGLELYAEWKHVNE-------DSQEKKILLSPERVHEIFKRIA       226
tr|A0A1A7X327|A0A1A7X327_9TELE      KEKGHGGCGRYQPRIRRSGLELYAEWKHVNE-------DSQEKKILLSPERVHEIFKRIS       227
tr|A0A1A8UKD7|A0A1A8UKD7_NOTFU      KEKGHGGCGRYQPRIRRSGLELYAEWKHVNE-------DSQEKKILLSPERVHEIFKRIS       227
tr|A0A1A8ER05|A0A1A8ER05_9TELE      KEKGHGGCGRYQPRIRRSGLELYAEWKHVNE-------DSQEKKILLSPERVHEIFKRIS       227
tr|A0A1A8DQ60|A0A1A8DQ60_9TELE      KEKGHGGCGRYQPRIRRSGLELYAEWKHVNE-------DSQEKKILLSPERVHEIFKRIS       227
tr|A0A1A8NSR8|A0A1A8NSR8_9TELE      KEKGHGGCGRYQPRIRRSGLELYAEWKHVNE-------DSQEKKILLSPERVHEIFKRIS       227
tr|A0A1W4YLM7|A0A1W4YLM7_9TELE      KEKGHGGCGRYQPLIRRSGLELYAEWKHVNE-------DSQEKKILLSPERVHEIFKRIS       227
tr|A0A1M8A6L7|A0A1M8A6L7_MALS4      QKIGHGGCGRFQPAIRKEALKLFSVWKQSKDEDEDSGGMAQSEKRPLPASEVHTILKKIT       229
sp|P04050|RPB1_YEAST                QLVSRGGCGNTQPTIRKDGLKLVGSWKKDRATGD----ADEPELRVLSTEEILNIFKHIS       215
tr|A0A1B2J8C6|A0A1B2J8C6_PICPA      KVVSRGGCGNTQPVVRKDGMKLWGTWKKSGFSDR----DAQPERKLLTPGEILNVFRHIS       216
tr|F2QW17|F2QW17_KOMPC              KVVSRGGCGNTQPVVRKDGMKLWGTWKKSGFSDR----DAQPERKLLTPGEILNVFKHIS       216
tr|A3GID7|A3GID7_PICST              -TTTRGGCGHTQPTIRRDGLKLWGTWRHNKNFEE----NEQPERRLLTPSEILNVLKHIS       215
tr|A0A1D8PUA6|A0A1D8PUA6_CANAL      -QPSRGGCGHPQPTIRRDGLKLWGTWKQNKNYDD----NDQPERRLLTPSEILNVFKHIS       215
tr|G8BEH9|G8BEH9_CANPC              -HNVRGGCGHTQPTIRRDGLKLWGTWKHNKNFEE----NDQPERRLLTPSEILNVFKHIS       215
                                        :****. ** ::: .::* . *::            : :   *   .:  ::::*:
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tr|A0A1U8DYN0|A0A1U8DYN0_ALLSI      DDECLVLGMDPKFARPEWMVCTVLPVPPLSVRPAVVMQGSARNQDDLTHKLADIVKINNQ      288
tr|A0A1L8H4P4|A0A1L8H4P4_XENLA      DEECFILGMDPRFARPEWLIITVLPVPPLCVRPAVVMQGSARNQDDLTHKLADIVKINNQ      287
tr|H9GLG5|H9GLG5_ANOCA              DEECFILGMDPKFARPEWMICTVLPVPPLSVRPAVVMQGSARNQDDLTHKLADIVKINNQ      288
tr|H2R1J6|H2R1J6_PANTR              DEECFVLGMEPRYARPEWMIVTVLPVPPLSVRPAVVMQGSARNQDDLTHKLADIVKINNQ      289
tr|G1MCZ1|G1MCZ1_AILME              DEECFVLGMEPRYARPEWMIVTVLPVPPLSVRPAVVMQGSARNQDDLTHKLADIVKINNQ      289
tr|O08847|O08847_MOUSE              DEECFVLGMEPRYARPEWMIVTVLPVPPLSVRPAVVMQGSARNQDDLTHKLADIVKINNQ      289
tr|S7PWZ6|S7PWZ6_MYOBR              DEECFVLGMEPRYARPEWMIVTVLPVPPLSVRPAVVMQGSARNQDDLTHKLADIVKINNQ      289
tr|D4A5A6|D4A5A6_RAT                DEECFVLGMEPRYARPEWMIVTVLPVPPLSVRPAVVMQGSARNQDDLTHKLADIVKINNQ      289
sp|P08775|RPB1_MOUSE                DEECFVLGMEPRYARPEWMIVTVLPVPPLSVRPAVVMQGSARNQDDLTHKLADIVKINNQ      289
sp|P24928|RPB1_HUMAN                DEECFVLGMEPRYARPEWMIVTVLPVPPLSVRPAVVMQGSARNQDDLTHKLADIVKINNQ      289
tr|A0A1S3EWL2|A0A1S3EWL2_DIPOR      DEECFVLGMEPRYARPEWMIVTVLPVPPLSVRPAVVMQGSARNQDDLTHKLADIVKINNQ      289
sp|P11414|RPB1_CRIGR                DEECFVLGMEPRYARPEWMIVTVLPVPPLSVRPAVVMQGSARNQDDLTHKLADIVKINNQ      289
tr|O35559|O35559_CRIGR              DEECFVLGMEPRYARPEWMIVTVLPVPPLSVRPAVVMQGSARNQDDLTHKLADIVKINNQ      289
tr|A0A2I3M9H2|A0A2I3M9H2_PAPAN      DEECFVLGMEPRYARPEWMIVTVLPVPPLSVRPAVVMQGSARNQDDLTHKLADIVKINNQ      289
tr|F7HB40|F7HB40_MACMU              DEECFVLGMEPRYARPEWMIVTVLPVPPLSVRPAVVMQGSARNQDDLTHKLADIVKINNQ      289
tr|A0A2K6RYW9|A0A2K6RYW9_SAIBB      DEECFVLGMEPRYARPEWMIVTVLPVPPLSVRPAVVMQGSARNQDDLTHKLADIVKINNQ      289
tr|W5N8Z6|W5N8Z6_LEPOC              DEEDIILGMDPKFARPEWMIVTVLPVPPLAVRPAVVMQGSARNQDDLTHKLADIVKINNQ      288
tr|I3JRW6|I3JRW6_ORENI              DEEDIILGMDPKFARPEWMIVTVLPVPPLAVRPAVVMQGSARNQDDLTHKLADIVKINNQ      287
tr|A0A0R4IMS9|A0A0R4IMS9_DANRE      DEEDIILGMDPKYARPEWMIVTVLPVPPLAVRPAVVMQGSARNQDDLTHKLADIVKINNQ      286
tr|A0A1A7X327|A0A1A7X327_9TELE      DEEDIILGMDPKFARPEWMIVTVLPVPPLAVRPAVVMQGSARNQDDLTHKLADIVKINNQ      287
tr|A0A1A8UKD7|A0A1A8UKD7_NOTFU      DEEDIILGMDPKFARPEWMIVTVLPVPPLAVRPAVVMQGSARNQDDLTHKLADIVKINNQ      287
tr|A0A1A8ER05|A0A1A8ER05_9TELE      DEEDIILGMDPKFARPEWMIVTVLPVPPLAVRPAVVMQGSARNQDDLTHKLADIVKINNQ      287
tr|A0A1A8DQ60|A0A1A8DQ60_9TELE      DEEDIILGMDPKFARPEWMIVTVLPVPPLAVRPAVVMQGSARNQDDLTHKLADIVKINNQ      287
tr|A0A1A8NSR8|A0A1A8NSR8_9TELE      DEEDIILGMDPKFARPEWMIVTVLPVPPLAVRPAVVMQGSARNQDDLTHKLADIVKINNQ      287
tr|A0A1W4YLM7|A0A1W4YLM7_9TELE      DEEDIILGMDPKFARPEWMIVTVLPVPPLAVRPAVVMQGSARNQDDLTHKLADIVKINNQ      287
tr|A0A1M8A6L7|A0A1M8A6L7_MALS4      PEDVVTLGLSEDFAQPDWMVLTVLPVPPPQVRPGVTEFGSGMGQDDLTYKLADIIKASAN      289
sp|P04050|RPB1_YEAST                VKDFTSLGFNEVFSRPEWMILTCLPVPPPPVRPSISFNESQRGEDDLTFKLADILKANIS      275
tr|A0A1B2J8C6|A0A1B2J8C6_PICPA      PEDCFRLGFNEDYARPEWMIITVLPVPPPQVRPSIAMDETTQGQDDLTHKLSDILKANIN      276
tr|F2QW17|F2QW17_KOMPC              PEDCFRLGFNEDYARPEWMIITVLPVPPPQVRPSIAMDETTQGQDDLTHKLSDILKANIN      276
tr|A3GID7|A3GID7_PICST              SLDCLRLGFNEDYARPEWMLITVLPVPPPPVRPSIAFNDTARGEDDLTFKLADVLKANIN      275
tr|A0A1D8PUA6|A0A1D8PUA6_CANAL      PEDCYKMGFNEDYARPEWMLITVLPVPPPPVRPSIAFNETARGEDDLTFKLADIIKANIN      275
tr|G8BEH9|G8BEH9_CANPC              PEDCYRLGFNEDYARPEWMLITVLPVPPPPVRPSIAFNDTARGEDDLTFKLADIIKANIN      275
                                      :   :*:.  :::*:*:: * *****  ***.:    :  .:****.**:*::* . .

tr|A0A1U8DYN0|A0A1U8DYN0_ALLSI      LRRNEQNGAAAHVIAEDVKLLQFHVATMVDNELPGLPRAMQKSGRPLKSLKQRLKGKEGR      348
tr|A0A1L8H4P4|A0A1L8H4P4_XENLA      LRRNEQNGAAAHVIAEDVKLLQFHVATMVDNEIPGLPRAMQKSGRPLKSVKQRLKGKEGR      347
tr|H9GLG5|H9GLG5_ANOCA              LRRNEQNGAAAHVIAEDVKLLQFHVATMVDNELPGLPRAMQKSGRPLKSLKQRLKGKEGR      348
tr|H2R1J6|H2R1J6_PANTR              LRRNEQNGAAAHVIAEDVKLLQFHVATMVDNELPGLPRAMQKSGRPLKSLKQRLKGKEGR      349
tr|G1MCZ1|G1MCZ1_AILME              LRRNEQNGAAAHVIAEDVKLLQFHVATMVDNELPGLPRAMQKSGRPLKSLKQRLKGKEGR      349
tr|O08847|O08847_MOUSE              LRRNEQNGAAAHVIAEDVKLLQFHVATMVDNELPGLPRAMQKSGRPLKSLKQRLKGKEGR      349
tr|S7PWZ6|S7PWZ6_MYOBR              LRRNEQNGAAAHVIAEDVKLLQFHVATMVDNELPGLPRAMQKSGRPLKSLKQRLKGKEGR      349
tr|D4A5A6|D4A5A6_RAT                LRRNEQNGAAAHVIAEDVKLLQFHVATMVDNELPGLPRAMQKSGRPLKSLKQRLKGKEGR      349
sp|P08775|RPB1_MOUSE                LRRNEQNGAAAHVIAEDVKLLQFHVATMVDNELPGLPRAMQKSGRPLKSLKQRLKGKEGR      349
sp|P24928|RPB1_HUMAN                LRRNEQNGAAAHVIAEDVKLLQFHVATMVDNELPGLPRAMQKSGRPLKSLKQRLKGKEGR      349
tr|A0A1S3EWL2|A0A1S3EWL2_DIPOR      LRRNEQNGAAAHVIAEDVKLLQFHVATMVDNELPGLPRAMQKSGRPLKSLKQRLKGKEGR      349
sp|P11414|RPB1_CRIGR                LRRNEQNGAAAHVIAEDVKLLQFHVATMVDNELPGLPRAMQKSGRPLKSLKQRLKGKEGR      349
tr|O35559|O35559_CRIGR              LRRNEQNGAAAHVIAEDVKLLQFHVATMVDNELPGLPRAMQKSGRPLKSLKQRLKGKEGR      349
tr|A0A2I3M9H2|A0A2I3M9H2_PAPAN      LRRNEQNGAAAHVIAEDVKLLQFHVATMVDNELPGLPRAMQKSGRPLKSLKQRLKGKEGR      349
tr|F7HB40|F7HB40_MACMU              LRRNEQNGAAAHVIAEDVKLLQFHVATMVDNELPGLPRAMQKSGRPLKSLKQRLKGKEGR      349
tr|A0A2K6RYW9|A0A2K6RYW9_SAIBB      LRRNEQNGAAAHVIAEDVKLLQFHVATMVDNELPGLPRAMQKSGRPLKSLKQRLKGKEGR      349
tr|W5N8Z6|W5N8Z6_LEPOC              LRRNEQSGAAAHVIAEDVKLLQFHVATMVDNELPGLPRAMQKSGRPLKSIKQRLKGKEGR      348
tr|I3JRW6|I3JRW6_ORENI              LRRNEQSGAAAHVIAEDVKLLQFHVATMVDNELPGLPRAMQKSGRPLKSIKQRLKGKEGR      347
tr|A0A0R4IMS9|A0A0R4IMS9_DANRE      LKRNEQSGAAAHVIAEDVKLLQFHVATMVDNELPGLPRAMQKSGRPLKSIKQRLKGKEGR      346
tr|A0A1A7X327|A0A1A7X327_9TELE      LKRNEQSGAAAHVIAEDVKLLQFHVATMVDNELPGLPRAMQKSGRPLKSIKQRLKGKEGR      347
tr|A0A1A8UKD7|A0A1A8UKD7_NOTFU      LKRNEQSGAAAHVIAEDVKLLQFHVATMVDNELPGLPRAMQKSGRPLKSLKQRLKGKEGR      347
tr|A0A1A8ER05|A0A1A8ER05_9TELE      LKRNEQSGAAAHVIAEDVKLLQFHVATMVDNELPGLPRAMQKSGRPLKSIKQRLKGKEGR      347
tr|A0A1A8DQ60|A0A1A8DQ60_9TELE      LKRNEQSGAAAHVIAEDVKLLQFHVATMVDNELPGLPRAMQKSGRPLKSLKQRLKGKEGR      347
tr|A0A1A8NSR8|A0A1A8NSR8_9TELE      LKRNEQSGAAAHVIAEDVKLLQFHVATMVDNELPGLPRAMQKSGRPLKSLKQRLKGKEGR      347
tr|A0A1W4YLM7|A0A1W4YLM7_9TELE      LRRNEQSGAAAHVIAEDVKLLQFHVATMVDNELPGLPRAMQKSGRPLKSIKQRLKGKEGR      347
tr|A0A1M8A6L7|A0A1M8A6L7_MALS4      LRRMEQEGAPAHILNDFADLLQYHTATYMDNDIAGLPQSLQSSGRPVKAIRARLKGKEGR      349
sp|P04050|RPB1_YEAST                LETLEHNGAPHHAIEEAESLLQFHVATYMDNDIAGQPQALQKSGRPVKSIRARLKGKEGR      335
tr|A0A1B2J8C6|A0A1B2J8C6_PICPA      VQKLEMDGSPQHIINEVEQLLQFHVATYMDNDIAGQPQALQKSGRPVKAIRARLKGKEGR      336
tr|F2QW17|F2QW17_KOMPC              VQKLEMDGSPQHIINEVEQLLQFHVATYMDNDIAGQPQALQKSGRPVKAIRARLKGKEGR      336
tr|A3GID7|A3GID7_PICST              VQRLEMDGSPQHVISEFEALLQFHVATYMDNDIAGQPQALQKTGRPIKSIRARLKGKEGR      335
tr|A0A1D8PUA6|A0A1D8PUA6_CANAL      VQRLETDGSPQHVISEFEALLQFHVATYMDNDIAGQPQALQKTGRPIKSIRARLKGKEGR      335
tr|G8BEH9|G8BEH9_CANPC              VQRLEIDGSPQHVISEFEALLQFHVATYMDNDIAGQPQALQKTGRPIKSIRARLKGKEGR      335
                                    :.  * .*:  * : :   ***:*.** :**:: * *:::*.:***:*::: ********
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tr|A0A1U8DYN0|A0A1U8DYN0_ALLSI      VRGNLMGKRVDFSARTVITPDPNLSIDQVGVPRSIAANMTFAEIVTPFNIDRLQELVRRG      408
tr|A0A1L8H4P4|A0A1L8H4P4_XENLA      VRGNLMGKRVDFSARTVITPDPNLSIDQVGVPRSIAANMSFPEIVTPFNIDRLQELVRRG      407
tr|H9GLG5|H9GLG5_ANOCA              VRGNLMGKRVDFSARTVITPDPNLSIDQVGVPRSIAANMTFAEIVTPFNIDRLQELVRRG      408
tr|H2R1J6|H2R1J6_PANTR              VRGNLMGKRVDFSARTVITPDPNLSIDQVGVPRSIAANMTFAEIVTPFNIDRLQELVRRG      409
tr|G1MCZ1|G1MCZ1_AILME              VRGNLMGKRVDFSARTVITPDPNLSIDQVGVPRSIAANMTFAEIVTPFNIDRLQELVRRG      409
tr|O08847|O08847_MOUSE              VRGNLMGKRVDFSARTVITPDPNLSIDQVGVPRSIAANMTFAEIVTPFNIDRLQELVRRG      409
tr|S7PWZ6|S7PWZ6_MYOBR              VRGNLMGKRVDFSARTVITPDPNLSIDQVGVPRSIAANMTFAEIVTPFNIDRLQELVRRG      409
tr|D4A5A6|D4A5A6_RAT                VRGNLMGKRVDFSARTVITPDPNLSIDQVGVPRSIAANMTFAEIVTPFNIDRLQELVRRG      409
sp|P08775|RPB1_MOUSE                VRGNLMGKRVDFSARTVITPDPNLSIDQVGVPRSIAANMTFAEIVTPFNIDRLQELVRRG      409
sp|P24928|RPB1_HUMAN                VRGNLMGKRVDFSARTVITPDPNLSIDQVGVPRSIAANMTFAEIVTPFNIDRLQELVRRG      409
tr|A0A1S3EWL2|A0A1S3EWL2_DIPOR      VRGNLMGKRVDFSARTVITPDPNLSIDQVGVPRSIAANMTFAEIVTPFNIDRLQELVRRG      409
sp|P11414|RPB1_CRIGR                VRGNLMGKRVDFSARTVITPDPNLSIDQVGVPRSIAANMTFAEIVTPFNIDRLQELVRRG      409
tr|O35559|O35559_CRIGR              VRGNLMGKRVDFSARTVITPDPNLSIDQVGVPRSIAANMTFAEIVTPFNIDRLQELVRRG      409
tr|A0A2I3M9H2|A0A2I3M9H2_PAPAN      VRGNLMGKRVDFSARTVITPDPNLSIDQVGVPRSIAANMTFAEIVTPFNIDRLQELVRRG      409
tr|F7HB40|F7HB40_MACMU              VRGNLMGKRVDFSARTVITPDPNLSIDQVGVPRSIAANMTFAEIVTPFNIDRLQELVRRG      409
tr|A0A2K6RYW9|A0A2K6RYW9_SAIBB      VRGNLMGKRVDFSARTVITPDPNLSIDQVGVPRSIAANMTFAEIVTPFNIDRLQELVRRG      409
tr|W5N8Z6|W5N8Z6_LEPOC              VRGNLMGKRVDFSARTVITPDPNLQIDQVGVPRSIAANMTFAEIVTPFNIDRLQELVRRG      408
tr|I3JRW6|I3JRW6_ORENI              VRGNLMGKRVDFSARTVITPDPNLQIDQVGVPRSIAANMTFPEIVTPFNIDRLQELVRRG      407
tr|A0A0R4IMS9|A0A0R4IMS9_DANRE      VRGNLMGKRVDFSARTVITPDPNLQIDQVGVPRSIAANMTFPEIVTPFNIDRLQELVRRG      406
tr|A0A1A7X327|A0A1A7X327_9TELE      VRGNLMGKRVDFSARTVITPDPNLQIDQVGVPRSIAANMTFPEIVTPFNIDRLQELVRRG      407
tr|A0A1A8UKD7|A0A1A8UKD7_NOTFU      VRGNLMGKRVDFSARTVITPDPNLQIDQVGVPRSIAANMTFPEIVTPFNIDRLQELVRRG      407
tr|A0A1A8ER05|A0A1A8ER05_9TELE      VRGNLMGKRVDFSARTVITPDPNLQIDQVGVPRSIAANMTFPEIVTPFNIDRLQELVRRG      407
tr|A0A1A8DQ60|A0A1A8DQ60_9TELE      VRGNLMGKRVDFSARTVITPDPNLQIDQVGVPRSIAANMTFPEIVTPFNIDRLQELVRRG      407
tr|A0A1A8NSR8|A0A1A8NSR8_9TELE      VRGNLMGKRVDFSARTVITPDPNLQIDQVGVPRSIAANMTFPEIVTPFNIDRLQELVRRG      407
tr|A0A1W4YLM7|A0A1W4YLM7_9TELE      VRGNLMGKRVDFSARTVITPDPNLQIDQVGVPRSIAANMTFPEIVTPFNIDRLQELVRRG      407
tr|A0A1M8A6L7|A0A1M8A6L7_MALS4      LRGNLMGKRVDFSARTVITGDPNLELDQVGVPKSIARNLTYPERVTPYNRAYLSDLVRNG      409
sp|P04050|RPB1_YEAST                IRGNLMGKRVDFSARTVISGDPNLELDQVGVPKSIAKTLTYPEVVTPYNIDRLTQLVRNG      395
tr|A0A1B2J8C6|A0A1B2J8C6_PICPA      LRGNLMGKRVDFSARTVISGDPNLELDQVGVPISIAKTLSYPETVTQYNIHRLTEYVRNG      396
tr|F2QW17|F2QW17_KOMPC              LRGNLMGKRVDFSARTVISGDPNLELDQVGVPISIAKTLSYPETVTQYNIHRLTEYVRNG      396
tr|A3GID7|A3GID7_PICST              LRGNLMGKRVDFSARTVISGDPNLDLDQVGVPISIARTLSYPEVVTPYNIHRLTEYVRNG      395
tr|A0A1D8PUA6|A0A1D8PUA6_CANAL      LRGNLMGKRVDFSARTVISGDPNLDLDQVGVPISIAKTLTYPEIVTPYNIHKLTELVRNG      395
tr|G8BEH9|G8BEH9_CANPC              LRGNLMGKRVDFSARTVISGDPNLDLDQVGVPISIAKTLTYPEIVTPYNIHKLTELVRNG      395
                                    :*****************: ****.:****** *** .::: * ** :*   * : **.*

tr|A0A1U8DYN0|A0A1U8DYN0_ALLSI      NSQYPGAKYIIRDNGDRIDLRFHPKPSDLHLQIGYKVERHMCDGDIVIFNRQPTLHKMSM      468
tr|A0A1L8H4P4|A0A1L8H4P4_XENLA      NSQYPGAKYIIRDNGDRIDLRFHPKPSDLHLQIGYKVERHMCDGDIVIFNRQPTLHKMSM      467
tr|H9GLG5|H9GLG5_ANOCA              NSQYPGAKYIIRDNGDRIDLRFHPKPSDLHLQIGYKVERHMCDGDIVIFNRQPTLHKMSM      468
tr|H2R1J6|H2R1J6_PANTR              NSQYPGAKYIIRDNGDRIDLRFHPKPSDLHLQTGYKVERHMCDGDIVIFNRQPTLHKMSM      469
tr|G1MCZ1|G1MCZ1_AILME              NSQYPGAKYIIRDNGDRIDLRFHPKPSDLHLQTGYKVERHMCDGDIVIFNRQPTLHKMSM      469
tr|O08847|O08847_MOUSE              NSQYPGAKYIIRDNGDRIDLRFHPKPSDLHLQTGYKVERHMCDGDIVIFNRQPTLHKMSM      469
tr|S7PWZ6|S7PWZ6_MYOBR              NSQYPGAKYIIRDNGDRIDLRFHPKPSDLHLQTGYKVERHMCDGDIVIFNRQPTLHKMSM      469
tr|D4A5A6|D4A5A6_RAT                NSQYPGAKYIIRDNGDRIDLRFHPKPSDLHLQTGYKVERHMCDGDIVIFNRQPTLHKMSM      469
sp|P08775|RPB1_MOUSE                NSQYPGAKYIIRDNGDRIDLRFHPKPSDLHLQTGYKVERHMCDGDIVIFNRQPTLHKMSM      469
sp|P24928|RPB1_HUMAN                NSQYPGAKYIIRDNGDRIDLRFHPKPSDLHLQTGYKVERHMCDGDIVIFNRQPTLHKMSM      469
tr|A0A1S3EWL2|A0A1S3EWL2_DIPOR      NSQYPGAKYIIRDNGDRIDLRFHPKPSDLHLQTGYKVERHMCDGDIVIFNRQPTLHKMSM      469
sp|P11414|RPB1_CRIGR                NSQYPGAKYIIRDNGDRIDLRFHPKPSDLHLQTGYKVERHMCDGDIVIFNRQPTLHKMSM      469
tr|O35559|O35559_CRIGR              NSQYPGAKYIIRDNGDRIDLRFHPKPSDLHLQTGYKVERHMCDGDIVIFNRQPTLHKMSM      469
tr|A0A2I3M9H2|A0A2I3M9H2_PAPAN      NSQYPGAKYIIRDNGDRIDLRFHPKPSDLHLQTGYKVERHMCDGDIVIFNRQPTLHKMSM      469
tr|F7HB40|F7HB40_MACMU              NSQYPGAKYIIRDNGDRIDLRFHPKPSDLHLQTGYKVERHMCDGDIVIFNRQPTLHKMSM      469
tr|A0A2K6RYW9|A0A2K6RYW9_SAIBB      NSQYPGAKYIIRDNGDRIDLRFHPKPSDLHLQTGYKVERHMCDGDIVIFNRQPTLHKMSM      469
tr|W5N8Z6|W5N8Z6_LEPOC              NSQYPGAKYIIRDNGDRIDLRFHPKPSDLHLQIGYKVERHMCDGDIVIFNRQPTLHKMSM      468
tr|I3JRW6|I3JRW6_ORENI              NSQYPGAKYIIRDNGDRIDLRFHPKPSDLHLQIGYKVERHMCDGDIVIFNRQPTLHKMSM      467
tr|A0A0R4IMS9|A0A0R4IMS9_DANRE      NSQYPGAKYIIRDNGDRIDLRFHPKPSDLHLQIGYKVERHMCDGDIIVFNRQPTLHKMSM      466
tr|A0A1A7X327|A0A1A7X327_9TELE      NSQYPGAKYIIRDNGDRIDLRFHPKPSDLHLQIGYKVERHMCEGDIVIFNRQPTLHKMSM      467
tr|A0A1A8UKD7|A0A1A8UKD7_NOTFU      NSQYPGAKYIIRDNGDRIDLRFHPKPSDLHLQIGYKVERHMCDGDIVIFNRQPTLHKMSM      467
tr|A0A1A8ER05|A0A1A8ER05_9TELE      NSQYPGAKYIIRDNGDRIDLRFHPKPSDLHLQIGYKVERHMCDGDIVIFNRQPTLHKMSM      467
tr|A0A1A8DQ60|A0A1A8DQ60_9TELE      NSQYPGAKYIIRDNGDRIDLRFHPKPSDLHLQIGYKVERHMCDGDIVIFNRQPTLHKMSM      467
tr|A0A1A8NSR8|A0A1A8NSR8_9TELE      NSQYPGAKYIIRDNGDRIDLRFHPKPSDLHLQIGYKVERHMCDGDIVIFNRQPTLHKMSM      467
tr|A0A1W4YLM7|A0A1W4YLM7_9TELE      NSQYPGAKYIIRDNGDRIDLRFHPKPSDLHLQIGYKVERHMCDGDIIIFNRQPTLHKMSM      467
tr|A0A1M8A6L7|A0A1M8A6L7_MALS4      PNEYPGARYVIRDTGERIDLKYNR-RGDIALQAGWIVERHLKDGDYVLFNRQPSLHKMSM      468
sp|P04050|RPB1_YEAST                PNEHPGAKYVIRDSGDRIDLRYSKRAGDIQLQYGWKVERHIMDNDPVLFNRQPSLHKMSM      455
tr|A0A1B2J8C6|A0A1B2J8C6_PICPA      PNEHPGAKYVIRDNGDRIDLRYHKRAGDIVLQYGWKVERHLMDDDPVLFNRQPSLHKMSM      456
tr|F2QW17|F2QW17_KOMPC              PNEHPGAKYVIRDNGDRIDLRYHKRAGDIVLQYGWKVERHLMDDDPVLFNRQPSLHKMSM      456
tr|A3GID7|A3GID7_PICST              PNEHPGAKYVIRDTGDRIDLRYNKRAGDIALQYGWKVERHLMDNDPVLFNRQPSLHKMSM      455
tr|A0A1D8PUA6|A0A1D8PUA6_CANAL      PNEHPGAKYVIRDTGDRIDLRYNKRAGDIALQYGWKVERHLMDDDPVLFNRQPSLHKMSM      455
tr|G8BEH9|G8BEH9_CANPC              PNEHPGAKYVIRDTGDRIDLRYNKRAGDIALQYGWKVERHLMDDDPVLFNRQPSLHKMSM      455
                                     .::***:*:***.*:****::    .*: ** *: ****: :.* ::*****:******
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```
tr|A0A1U8DYN0|A0A1U8DYN0_ALLSI      MGHRVRILPWSTFRLNLSVTTPYNADFDGDEMNLHLPQSLETRAEIQELAMVPRMIVTPQ      528
tr|A0A1L8H4P4|A0A1L8H4P4_XENLA      MGHRVRILPWSTFRLNLSVTTPYNADFDGDEMNLHLPQSLETRAEIQELAMVPRMIVTPQ      527
tr|H9GLG5|H9GLG5_ANOCA              MGHRVRILPWSTFRLNLSVTTPYNADFDGDEMNLHLPQSLETRAEIQELAMVPRMIVTPQ      528
tr|H2R1J6|H2R1J6_PANTR              MGHRVRILPWSTFRLNLSVTTPYNADFDGDEMNLHLPQSLETRAEIQELAMVPRMIVTPQ      529
tr|G1MCZ1|G1MCZ1_AILME              MGHRVRILPWSTFRLNLSVTTPYNADFDGDEMNLHLPQSLETRAEIQELAMVPRMIVTPQ      529
tr|O08847|O08847_MOUSE              MGHRVRILPWSTFRLNLSVTTPYNADFDGDEMNLHLPQSLETRAEIQELAMVPRMIVTPQ      529
tr|S7PWZ6|S7PWZ6_MYOBR              MGHRVRILPWSTFRLNLSVTTPYNADFDGDEMNLHLPQSLETRAEIQELAMVPRMIVTPQ      529
tr|D4A5A6|D4A5A6_RAT                MGHRVRILPWSTFRLNLSVTTPYNADFDGDEMNLHLPQSLETRAEIQELAMVPRMIVTPQ      529
sp|P08775|RPB1_MOUSE                MGHRVRILPWSTFRLNLSVTTPYNADFDGDEMNLHLPQSLETRAEIQELAMVPRMIVTPQ      529
sp|P24928|RPB1_HUMAN                MGHRVRILPWSTFRLNLSVTTPYNADFDGDEMNLHLPQSLETRAEIQELAMVPRMIVTPQ      529
tr|A0A1S3EWL2|A0A1S3EWL2_DIPOR      MGHRVRILPWSTFRLNLSVTTPYNADFDGDEMNLHLPQSLETRAEIQELAMVPRMIVTPQ      529
sp|P11414|RPB1_CRIGR                MGHRVRILPWSTFRLNLSVTTPYNADFDGDEMNLHLPQSLETRAEIQELAMVPRMIVTPQ      529
tr|O35559|O35559_CRIGR              MGHRVRILPWSTFRLNLSVTTPYNADFDGDEMNLHLPQSLETRAEIQELAMVPRMIVTPQ      529
tr|A0A2I3M9H2|A0A2I3M9H2_PAPAN      MGHRVRILPWSTFRLNLSVTTPYNADFDGDEMNLHLPQSLETRAEIQELAMVPRMIVTPQ      529
tr|F7HB40|F7HB40_MACMU              MGHRVRILPWSTFRLNLSVTTPYNADFDGDEMNLHLPQSLETRAEIQELAMVPRMIVTPQ      529
tr|A0A2K6RYW9|A0A2K6RYW9_SAIBB      MGHRVRILPWSTFRLNLSVTTPYNADFDGDEMNLHLPQSLETRAEIQELAMVPRMIVTPQ      529
tr|W5N8Z6|W5N8Z6_LEPOC              MGHRVRILPWSTFRLNLSVTTPYNADFDGDEMNLHLPQSLETRAEIQELAMVPRMIVTPQ      528
tr|I3JRW6|I3JRW6_ORENI              MGHRVRILPWSTFRLNLSVTTPYNADFDGDEMNLHLPQSLETRAEIQELAMVPRMIVTPQ      527
tr|A0A0R4IMS9|A0A0R4IMS9_DANRE      MGHRVRILPWSTFRLNLSVTTPYNADFDGDEMNLHLPQSLETRAEIQELAMVPRMIVTPQ      526
tr|A0A1A7X327|A0A1A7X327_9TELE      MGHRVRILPWSTFRLNLSVTTPYNADFDGDEMNLHLPQSLETRAEIQELAMVPRMIVTPQ      527
tr|A0A1A8UKD7|A0A1A8UKD7_NOTFU      MGHRVRILPWSTFRLNLSVTTPYNADFDGDEMNLHLPQSLETRAEIQELAMVPRMIVTPQ      527
tr|A0A1A8ER05|A0A1A8ER05_9TELE      MGHRVRILPWSTFRLNLSVTTPYNADFDGDEMNLHLPQSLETRAEIQELAMVPRMIVTPQ      527
tr|A0A1A8DQ60|A0A1A8DQ60_9TELE      MGHRVRILPWSTFRLNLSVTTPYNADFDGDEMNLHLPQSLETRAEIQELAMVPRMIVTPQ      527
tr|A0A1A8NSR8|A0A1A8NSR8_9TELE      MGHRVRILPWSTFRLNLSVTTPYNADFDGDEMNLHLPQSLETRAEIQELAMVPRMIVTPQ      527
tr|A0A1W4YLM7|A0A1W4YLM7_9TELE      MGHRVRILPWSTFRLNLSVTTPYNADFDGDEMNLHLPQSLETRAEIQELAMVPRMIVTPQ      527
tr|A0A1M8A6L7|A0A1M8A6L7_MALS4      MAHRVKLMDYSTFRLNLSVTPPYNADFDGDEMNLHVPQSEEARAELAQIAWVPRQIVSPQ      528
sp|P04050|RPB1_YEAST                MAHRVKVIPYSTFRLNLSVTSPYNADFDGDEMNLHVPQSEETRAELSQLCAVPLQIVSPQ      515
tr|A0A1B2J8C6|A0A1B2J8C6_PICPA      MAHRVKVMPYSTFRLNLSVTSPYNADFDGDEMNLHVPQSEETRAELSQLCAVPLQIVSPQ      516
tr|F2QW17|F2QW17_KOMPC              MAHRVKVMPYSTFRLNLSVTSPYNADFDGDEMNLHVPQSEETRAELSQLCAVPLQIVSPQ      516
tr|A3GID7|A3GID7_PICST              MAHRVKVMPYSTFRLNLSVTSPYNADFDGDEMNLHVPQSPETRAELSEICAVPLQIVSPQ      515
tr|A0A1D8PUA6|A0A1D8PUA6_CANAL      MAHRVRVMPYSTFRLNLSVTSPYNADFDGDEMNLHVPQSPETRSELSQICAVPLQIVSPQ      515
tr|G8BEH9|G8BEH9_CANPC              MAHRVKVMPYSTFRLNLSVTSPYNADFDGDEMNLHVPQSPETRSELSQICAVPLQIVSPQ      515
                                    *.***::: :********** **************:*** *:*:*: ::. **  **:**

tr|A0A1U8DYN0|A0A1U8DYN0_ALLSI      SNRPVMGIVQDTLTAVRKFTKRDVFLERGEVMNLLMFLSTWDGKVPQPAILKPRPLWTGK      588
tr|A0A1L8H4P4|A0A1L8H4P4_XENLA      SNRPVMGIVQDTLTAVRKFTKRDVFLERGEVMNLLMFLSTWDGKVPQPAILKPRPLWTGK      587
tr|H9GLG5|H9GLG5_ANOCA              SNRPVMGIVQDTLTAVRKFTKRDVFLERGEVMNLLMFLSTWDGKVPQPAILKPRPLWTGK      588
tr|H2R1J6|H2R1J6_PANTR              SNRPVMGIVQDTLTAVRKFTKRDVFLERGEVMNLLMFLSTWDGKVPQPAILKPRPLWTGK      589
tr|G1MCZ1|G1MCZ1_AILME              SNRPVMGIVQDTLTAVRKFTKRDVFLERGEVMNLLMFLSTWDGKVPQPAVLKPRPLWTGK      589
tr|O08847|O08847_MOUSE              SNRPVMGIVQDTLTAVRKFTKRDVFLERGEVMNLLMFLSTWDGKVPQPAILKPRPLWTGK      589
tr|S7PWZ6|S7PWZ6_MYOBR              SNRPVMGIVQDTLTAVRKFTKRDVFLERGEVMNLLMFLSTWDGKVPQPAILKPRPLWTGK      589
tr|D4A5A6|D4A5A6_RAT                SNRPVMGIVQDTLTAVRKFTKRDVFLERGEVMNLLMFLSTWDGKVPQPAILKPRPLWTGK      589
sp|P08775|RPB1_MOUSE                SNRPVMGIVQDTLTAVRKFTKRDVFLERGEVMNLLMFLSTWDGKVPQPAILKPRPLWTGK      589
sp|P24928|RPB1_HUMAN                SNRPVMGIVQDTLTAVRKFTKRDVFLERGEVMNLLMFLSTWDGKVPQPAILKPRPLWTGK      589
tr|A0A1S3EWL2|A0A1S3EWL2_DIPOR      SNRPVMGIVQDTLTAVRKFTKRDVFLERGEVMNLLMFLSTWDGKVPQPAILKPRPLWTGK      589
sp|P11414|RPB1_CRIGR                SNRPVMGIVQDTLTAVRKFTKRDVFLERGEVMNLLMFLSTWDGKVPQPAILKPRPLWTGK      589
tr|O35559|O35559_CRIGR              SNRPVMGIVQDTLTAVRKFTKRDVFLERGEVMNLLMFLSTWDGKVPQPAILKPRPLWTGK      589
tr|A0A2I3M9H2|A0A2I3M9H2_PAPAN      SNRPVMGIVQDTLTAVRKFTKRDVFLERGEVMNLLMFLSTWDGKVPQPAILKPRPLWTGK      589
tr|F7HB40|F7HB40_MACMU              SNRPVMGIVQDTLTAVRKFTKRDVFLERGEVMNLLMFLSTWDGKVPQPAILKPRPLWTGK      589
tr|A0A2K6RYW9|A0A2K6RYW9_SAIBB      SNRPVMGIVQDTLTAVRKFTKRDVFLERGEVMNLLMFLSTWDGKVPQPAILKPRPLWTGK      589
tr|W5N8Z6|W5N8Z6_LEPOC              SNRPVMGIVQDTLTAVRKFTKRDVFLDRGEVMNLLMFLSTWDGKVPQPAILKPRPLWTGK      588
tr|I3JRW6|I3JRW6_ORENI              SNRPVMGIVQDTLTAVRKFTKRDVFLERGEVMNLLMFLSTWDGKMPQPAILKPRPLWTGK      587
tr|A0A0R4IMS9|A0A0R4IMS9_DANRE      SNRPVMGIVQDTLTAVRKFTKRDVFLERGEVMNLLMFLSTWDGKVPQPAILKPRPLWTGK      586
tr|A0A1A7X327|A0A1A7X327_9TELE      SNRPVMGIVQDTLTAVRKFTKRDVFLERGEVMNLLMFLSTWDGKMPQPAILKPRPLWTGK      587
tr|A0A1A8UKD7|A0A1A8UKD7_NOTFU      SNRPVMGIVQDTLTAVRKFTKRDVFLERGEVMNLLMFLSTWDGKMPQPAILKPRPLWTGK      587
tr|A0A1A8ER05|A0A1A8ER05_9TELE      SNRPVMGIVQDTLTAVRKFTKRDVFLERGEVMNLLMFLSTWDGKMPQPAILKPRPLWTGK      587
tr|A0A1A8DQ60|A0A1A8DQ60_9TELE      SNRPVMGIVQDTLTAVRKFTKRDVFLERGEVMNLLMFLSTWDGKMPQPAILKPRPLWTGK      587
tr|A0A1A8NSR8|A0A1A8NSR8_9TELE      SNRPVMGIVQDTLTAVRKFTKRDVFLERGEVMNLLMFLSTWDGKMPQPAILKPRPLWTGK      587
tr|A0A1W4YLM7|A0A1W4YLM7_9TELE      SNRPVMGIVQDTLTAVRKFTKRDVFLERGEVMNLLMFLSTWDGKVPQPAILKPRPLWSGK      587
tr|A0A1M8A6L7|A0A1M8A6L7_MALS4      ANKPVMGIVQDTLCGIRKFTLRDCLLDFDQVQNVLMWLTDWDGIVPQPCILKPKPYWSGK      588
sp|P04050|RPB1_YEAST                SNKPCMGIVQDTLCGIRKLTLRDTFIELDQVLNMLYWVPDWDGVIPTPAIIKPKPLWSGK      575
tr|A0A1B2J8C6|A0A1B2J8C6_PICPA      SNKPVMGIVQDTLCGVRKMTLRDTFIEYEQVMNMLFWVPSWDGVVPQPAIMKPKPLWTGK      576
tr|F2QW17|F2QW17_KOMPC              SNKPVMGIVQDTLCGVRKMTLRDTFIEYEQVMNMLFWVPSWDGVVPQPAILKPKPLWTGK      576
tr|A3GID7|A3GID7_PICST              SNKPVMGIVQDTLCGIRKMTLRDNFIDYDQVMNMLYWIPNWDGVIPPPAIAKPKPLWTGK      575
tr|A0A1D8PUA6|A0A1D8PUA6_CANAL      SNKPVMGIVQDTLCGIRKMTLRDIFIEYDQVMNMCYWIPNWDGVIPPPAVVKPKQLWTGK      575
tr|G8BEH9|G8BEH9_CANPC              SNKPVMGIVQDTLCGIRKMTLRDIFIEYDQVMNMCYWIPNWDGVIPPPAIIKPKPLWSGK      575
                                    :*:* ******** .:**:* ** :::  :* *:  ::  *** :* *.: **:  *:**
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tr|A0A1U8DYN0|A0A1U8DYN0_ALLSI      QVFSLIIPGHINCVRTHSTHPDDEDSGPYKHISPGDTKVIVENGELIMGILCKKSLGTSA       648
tr|A0A1L8H4P4|A0A1L8H4P4_XENLA      QIFSLIVPGHINCIRTHSTHPDDEDSGPYKHISPGDTKVIVENGELVMGILCKKSLGTSA       647
tr|H9GLG5|H9GLG5_ANOCA              QIFSLIIPGHINCIRTHSTHPDDEDSGPYKHISPGDTKVIVENGELIMGILCKKSLGTSA       648
tr|H2R1J6|H2R1J6_PANTR              QIFSLIIPGHINCIRTHSTHPDDEDSGPYKHISPGDTKVVVENGELIMGILCKKSLGTSA       649
tr|G1MCZ1|G1MCZ1_AILME              QIFSLIVPGHINCIRTHSTHPDDEDSGPYKHISPGDTKVVVENGELIMGILCKKSLGTSA       649
tr|O08847|O08847_MOUSE              QIFSLIIPGHINCIRTHSTHPDDEDSGPYKHISPGDTKVVVENGELIMGILCKKSLGTSA       649
tr|S7PWZ6|S7PWZ6_MYOBR              QIFSLIIPGHINCIRTHSTHPDDEDSGPYKHISPGDTKVVVENGELIMGILCKKSLGTSA       649
tr|D4A5A6|D4A5A6_RAT                QIFSLIIPGHINCIRTHSTHPDDEDSGPYKHISPGDTKVVVENGELIMGILCKKSLGTSA       649
sp|P08775|RPB1_MOUSE                QIFSLIIPGHINCIRTHSTHPDDEDSGPYKHISPGDTKVVVENGELIMGILCKKSLGTSA       649
sp|P24928|RPB1_HUMAN                QIFSLIIPGHINCIRTHSTHPDDEDSGPYKHISPGDTKVVVENGELIMGILCKKSLGTSA       649
tr|A0A1S3EWL2|A0A1S3EWL2_DIPOR      QIFSLIIPGHINCIRTHSTHPDDEDSGPYKHISPGDTKVVVENGELIMGILCKKSLGTSA       649
sp|P11414|RPB1_CRIGR                QIFSLIIPGHINCIRTHSTHPDDEDSGPYKHISPGDTKVVVENGELIMGILCKKSLGTSA       649
tr|O35559|O35559_CRIGR              QIFSLIIPGHINCIRTHSTHPDDEDSGPYKHISPGDTKVVVENGELIMGILCKKSLGTSA       649
tr|A0A2I3M9H2|A0A2I3M9H2_PAPAN      QIFSLIIPGHINCIRTHSTHPDDEDSGPYKHISPGDTKVVVENGELIMGILCKKSLGTSA       649
tr|F7HB40|F7HB40_MACMU              QIFSLIIPGHINCIRTHSTHPDDEDSGPYKHISPGDTKVVVENGELIMGILCKKSLGTSA       649
tr|A0A2K6RYW9|A0A2K6RYW9_SAIBB      QIFSLIIPGHINCIRTHSTHPDDEDSGPYKHISPGDTKVVVENGELIMGILCKKSLGTSA       649
tr|W5N8Z6|W5N8Z6_LEPOC              QVFSLIIPGHINAIRTHSTHPDEEDSGPYKHISPGDTKVIVENGELIMGILCKKSLGTSA       648
tr|I3JRW6|I3JRW6_ORENI              QIFSLIIPGHINVIRTHSTHPDDEDSGPYKHISPGDTKVIVENGELIMGILCKKSLGTSA       647
tr|A0A0R4IMS9|A0A0R4IMS9_DANRE      QIFSLIIPGHINAIRTHSTHPDEEDSGPYKNISPGDTKVIVENGELIMGILCKKSLGTSA       646
tr|A0A1A7X327|A0A1A7X327_9TELE      QVFSLIIPGHINVIRTHSTHPDDEDSGPYKHISPGDTKVIVENGELIMGILCKKSLGTSA       647
tr|A0A1A8UKD7|A0A1A8UKD7_NOTFU      QVFSLIIPGHINVIRTHSTHPDDEDSGPYKHISPGDTKVIVENGELIMGILCKKSLGTSA       647
tr|A0A1A8ER05|A0A1A8ER05_9TELE      QVFSLIIPGHINVIRTHSTHPDDEDSGPYKHISPGDTKVIVENGELIMGILCKKSLGTSA       647
tr|A0A1A8DQ60|A0A1A8DQ60_9TELE      QVFSLIIPGHINVIRTHSTHPDDEDSGPYKHISPGDTKVIVENGELIMGILCKKSLGTSA       647
tr|A0A1A8NSR8|A0A1A8NSR8_9TELE      QVFSLIIPGHINVIRTHSTHPDDEDSGPYKHISPGDTKVIVENGELIMGILCKKSLGTSA       647
tr|A0A1W4YLM7|A0A1W4YLM7_9TELE      QVFSLIIPGHINAIRTHSTHPDDEDSGPYKHISPGDTKVIVENGELIMGILCKKSLGTSA       647
tr|A0A1M8A6L7|A0A1M8A6L7_MALS4      QLLSMCIPKGINVFLG--------DAKAAANNFLKDDGVHIENGEIMYGVINKKVVGSSA       640
sp|P04050|RPB1_YEAST                QILSVAIPNGIHLQRF--------DEGT-TLLSPKDNGMLIIDGQIIFGVVEKKTVGSSN       626
tr|A0A1B2J8C6|A0A1B2J8C6_PICPA      QLLSIAIPSGIHLQRT--------DGGN-SLLSPKDNGMLIVDGNVMFGVVDKKTVGSGG       627
tr|F2QW17|F2QW17_KOMPC              QLLSIAIPSGIHLQRT--------DGGN-SLLSPKDNGMLIVDGKVMFGVVDKKTVGSGG       627
tr|A3GID7|A3GID7_PICST              QLLSMAIPKGIHLQRF--------DGGK-DLLSPKDTGMLIVDGEIMFGVVDKKTVGATG       626
tr|A0A1D8PUA6|A0A1D8PUA6_CANAL      QLLSLAIPKGIHLQRF--------DGGR-DLLSPKDTGMLIVDGEIMFGVVDKKTVGATG       626
tr|G8BEH9|G8BEH9_CANPC              QMLSMAIPKGIHIQRF--------DGGR-DLLSPKDTGMLIVDGEIMFGVVDKKTVGATG       626
                                    *::*: :*  *:            *          *  : : :*::: *:: ** :*:


tr|A0A1U8DYN0|A0A1U8DYN0_ALLSI      GSLVHISYLEMGHDVTRLXXXXXXXXXPQTPLALHFLVXKRGRGHTIGIGDSIADAKTYQ       708
tr|A0A1L8H4P4|A0A1L8H4P4_XENLA      GSLVHISYLEMGHDTTRLFYSNIQTVIN------N---WLLIEGHTIGIGDSIADAKTYQ       698
tr|H9GLG5|H9GLG5_ANOCA              GSLVHISYLEMGHDVTRLFYSNIQTVIN------N---WLLIEGHTIGIGDSIADAKTYQ       699
tr|H2R1J6|H2R1J6_PANTR              GSLVHISYLEMGHDITRLFYSNIQTVIN------N---WLLIEGHTIGIGDSIADSKTYQ       700
tr|G1MCZ1|G1MCZ1_AILME              GSLVHISYLEMGHDVTRLFYSNIQTVIN------N---WLLIEGHTIGIGDSIADSKTYQ       700
tr|O08847|O08847_MOUSE              GSLVHISYLEMGHDITRLFYSNIQTVIN------N---WLLIEGHTIGIGDSIADSKTYQ       700
tr|S7PWZ6|S7PWZ6_MYOBR              GSLVHISYLEMGHDITRLFYSNIQTVIN------N---WLLIEGHTIGIGDSIADSKTYQ       700
tr|D4A5A6|D4A5A6_RAT                GSLVHISYLEMGHDVTRLFYSNIQTVIN------N---WLLIEGHTIGIGDSIADSKTYQ       700
sp|P08775|RPB1_MOUSE                GSLVHISYLEMGHDITRLFYSNIQTVIN------N---WLLIEGHTIGIGDSIADSKTYQ       700
sp|P24928|RPB1_HUMAN                GSLVHISYLEMGHDITRLFYSNIQTVIN------N---WLLIEGHTIGIGDSIADSKTYQ       700
tr|A0A1S3EWL2|A0A1S3EWL2_DIPOR      GSLVHISYLEMGHDITRLFYSNIQTVIN------N---WLLIEGHTIGIGDSIADSKTYQ       700
sp|P11414|RPB1_CRIGR                GSLVHISYLEMGHDITRLFYSNIQTVIN------N---WLLIEGHTIGIGDSIADSKTYQ       700
tr|O35559|O35559_CRIGR              GSLVHISYLEMGHDITRLFYSNIQTVIN------N---WLLIEGHTIGIGDSIADSKTYQ       700
tr|A0A2I3M9H2|A0A2I3M9H2_PAPAN      GSLVHISYLEMGHDITRLFYSNIQTVIN------N---WLLIEGHTIGIGDSIADSKTYQ       700
tr|F7HB40|F7HB40_MACMU              GSLVHISYLEMGHDITRLFYSNIQTVIN------N---WLLIEGHTIGIGDSIADSKTYQ       700
tr|A0A2K6RYW9|A0A2K6RYW9_SAIBB      GSLVHISYLEMGHDITRLFYSNIQTVIN------N---WLLIEGHTIGIGDSIADSKTYQ       700
tr|W5N8Z6|W5N8Z6_LEPOC              GSLVHISYLEMGHDVTRLFYSNIQTVVNN---------WLLIEGHSIGIGDSIADAKTYL       699
tr|I3JRW6|I3JRW6_ORENI              GSLVHISYLEMGHDITRLFYSNIQTVVNN---------WLLIEGHSIGIGDSIADAKTYL       698
tr|A0A0R4IMS9|A0A0R4IMS9_DANRE      GSLVHISYLEMGHDITRLFYSNIQTVVNN---------WLLIEGHSIGIGDSIADKATYQ       697
tr|A0A1A7X327|A0A1A7X327_9TELE      GSLVHISYLEMGHDITRLFYSNIQTVVNN---------WLLIEGHSIGIGDSIADAKTYL       698
tr|A0A1A8UKD7|A0A1A8UKD7_NOTFU      GSLVHISYLEMGHDITRLFYSNIQTVVNN---------WLLIEGHSIGIGDSIADAKTYL       698
tr|A0A1A8ER05|A0A1A8ER05_9TELE      GSLVHISYLEMGHDITRLFYSNIQTVVNN---------WLLIEGHSIGIGDSIADAKTYL       698
tr|A0A1A8DQ60|A0A1A8DQ60_9TELE      GSLVHISYLEMGHDITRLFYSNIQTVVNN---------WLLIEGHSIGIGDSIADAKTYL       698
tr|A0A1A8NSR8|A0A1A8NSR8_9TELE      GSLVHISYLEMGHDITRLFYSNIQTVVNN---------WLLIEGHSIGIGDSIADAKTYL       698
tr|A0A1W4YLM7|A0A1W4YLM7_9TELE      GSLVHISYLEMGHDVTRLFYSNIQTVVNN---------WLLIEGHSIGIGDSIADAKTYL       698
tr|A0A1M8A6L7|A0A1M8A6L7_MALS4      GGLIHIIFRERGPVVCRDFFSGVQRLVNF---------WLLHNGFSIGIGDTVADKATTA       691
sp|P04050|RPB1_YEAST                GGLIHVVTREKGPQVCAKLFGNIQKVVNF---------WLLHNGFSTGIGDTIADGPTMR       677
tr|A0A1B2J8C6|A0A1B2J8C6_PICPA      GGLIHTVMREKGPKICAELFGNIQKVVNY---------WLLHNGFSIGIGDAIADASTMK       678
tr|F2QW17|F2QW17_KOMPC              GGLIHTVMREKGPKICAELFGNIQKVVNY---------WLLHNGFSIGIGDAIADASTMK       678
tr|A3GID7|A3GID7_PICST              GGLIHTVMREKGPRVCAQLFSSIQKVTNY---------WLLHNGFSIGIGDTIADVSTMK       677
tr|A0A1D8PUA6|A0A1D8PUA6_CANAL      GGLIHTVMREKGPKVCAELFSSIQKVVNY---------WLLHNGFSIGIGDTIADAQTMR       677
tr|G8BEH9|G8BEH9_CANPC              GGLIHTVMREKGPQVCAQLFSSIQKVVNF---------WLLHNGFSIGIGDTIADASTMK       677
                                    *.*:*    * *                              .*.: ****::**  *
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tr|A0A1U8DYN0|A0A1U8DYN0_ALLSI      DIQNTIKKAKQDVIEVIEKAHNNELEPTPGNTLRQTFENQVNRILNDARDKTGSSAQKSL     768
tr|A0A1L8H4P4|A0A1L8H4P4_XENLA      DIQNTIKKAKQDVIEVIEKAHNNELEPTPGNTLRQTFENQVNRILNDARDKTGSSAQKSL     758
tr|H9GLG5|H9GLG5_ANOCA              DIQNTIKKAKQDVIEVIEKAHNNELEPTPGNTLRQTFENQVNRILNDARDKTGSSAQKSL     759
tr|H2R1J6|H2R1J6_PANTR              DIQNTIKKAKQDVIEVIEKAHNNELEPTPGNTLRQTFENQVNRILNDARDKTGSSAQKSL     760
tr|G1MCZ1|G1MCZ1_AILME              DIQNTIKKAKQDVIEVIEKAHNNELEPTPGNTLRQTFENQVNRILNDARDKTGSSAQKSL     760
tr|O08847|O08847_MOUSE              DIQNTIKKAKQDVIEVIEKAHNNELEPTPGNTLRQTFENQVNRILNDARDKTGSSAQKSL     760
tr|S7PWZ6|S7PWZ6_MYOBR              DIQNTIKKAKQDVIEVIEKAHNNELEPTPGNTLRQTFENQVNRILNDARDKTGSSAQKSL     760
tr|D4A5A6|D4A5A6_RAT                DIQNTIKKAKQDVIEVIEKAHNNELEPTPGNTLRQTFENQVNRILNDARDKTGSSAQKSL     760
sp|P08775|RPB1_MOUSE                DIQNTIKKAKQDVIEVIEKAHNNELEPTPGNTLRQTFENQVNRILNDARDKTGSSAQKSL     760
sp|P24928|RPB1_HUMAN                DIQNTIKKAKQDVIEVIEKAHNNELEPTPGNTLRQTFENQVNRILNDARDKTGSSAQKSL     760
tr|A0A1S3EWL2|A0A1S3EWL2_DIPOR      DIQNTIKKAKQDVIEVIEKAHNNELEPTPGNTLRQTFENQVNRILNDARDKTGSSAQKSL     760
sp|P11414|RPB1_CRIGR                DIQNTIKKAKQDVIEVIEKAHNNELEPTPGNTLRQTFENQVNRILNDARDKTGSSAQKSL     760
tr|O35559|O35559_CRIGR              DIQNTIKKAKQDVIEVIEKAHNNELEPTPGNTLRQTFENQVNRILNDARDKTGSSAQKSL     760
tr|A0A2I3M9H2|A0A2I3M9H2_PAPAN      DIQNTIKKAKQDVIEVIEKAHNNELEPTPGNTLRQTFENQVNRILNDARDKTGSSAQKSL     760
tr|F7HB40|F7HB40_MACMU              DIQNTIKKAKQDVIEVIEKAHNNELEPTPGNTLRQTFENQVNRILNDARDKTGSSAQKSL     760
tr|A0A2K6RYW9|A0A2K6RYW9_SAIBB      DIQNTIKKAKQDVIEVIEKAHNNELEPTPGNTLRQTFENQVNRILNDARDKTGSSAQKSL     760
tr|W5N8Z6|W5N8Z6_LEPOC              DIQNTIKKAKQDVIEVIEKAHNNELEPTPGNTLRQTFENQVNRILNDARDKTGSSAQKSL     759
tr|I3JRW6|I3JRW6_ORENI              DIQNTIKKAKQDVIEVIEKAHNNELEPTPGNTLRQTFENQVNRILNDARDKTGSSAQKSL     758
tr|A0A0R4IMS9|A0A0R4IMS9_DANRE      DIQNTIKKAKQDVIEVIEKAHNNELEPTPGNTLRQTFENQVNRILNDARDKTGSSAQKSL     757
tr|A0A1A7X327|A0A1A7X327_9TELE      DIQNTIKKAKQDVIEVIEKAHNNELEPTPGNTLRQTFENQVNRILNDARDKTGSSAQKSL     758
tr|A0A1A8UKD7|A0A1A8UKD7_NOTFU      DIQNTIKKAKQDVIEVIEKAHNNELEPTPGNTLRQTFENQVNRILNDARDKTGSSAQKSL     758
tr|A0A1A8ER05|A0A1A8ER05_9TELE      DIQNTIKKAKQDVIEVIEKAHNNELEPTPGNTLRQTFENQVNRILNDARDKTGSSAQKSL     758
tr|A0A1A8DQ60|A0A1A8DQ60_9TELE      DIQNTIKKAKQDVIEVIEKAHNNELEPTPGNTLRQTFENQVNRILNDARDKTGSSAQKSL     758
tr|A0A1A8NSR8|A0A1A8NSR8_9TELE      DIQNTIKKAKQDVIEVIEKAHNNELEPTPGNTLRQTFENQVNRILNDARDKTGSSAQKSL     758
tr|A0A1W4YLM7|A0A1W4YLM7_9TELE      DIQNTIKKAKQDVIEVIEKAHNNELEPTPGNTLRQTFENQVNRILNDARDKTGSSAQKSL     758
tr|A0A1M8A6L7|A0A1M8A6L7_MALS4      NINQTIAKAKAKADVMDLIQAARHDWLKADPGMTLRESFEANVNRILNKARDDVGSHAEQNL     751
sp|P04050|RPB1_YEAST                EITETIAEAKKKVLDVTKEAQANLLTAKHGMTLRESFEDNVVRFLNEARDKAGRLAEVNL     737
tr|A0A1B2J8C6|A0A1B2J8C6_PICPA      EITHAISSAKEQVQEIIYKAQHNELELKPGMTLRESFEGEVSRTLNDARDSAGRSAEMNL     738
tr|F2QW17|F2QW17_KOMPC              EITHAISSAKEQVQEIIYKAQHNELELKPGMTLRESFEGEVSRTLNDARDSAGRSAEMNL     738
tr|A3GID7|A3GID7_PICST              DITSTISEAKIKVQEIILDAQSNKLEPEPGMTLRESFEHNVSRVLNQARDTAGRSAEMNL     737
tr|A0A1D8PUA6|A0A1D8PUA6_CANAL      DVNKTIQEAKQKVQEIIIDAQHNKLEPEPGMTLRESFEHNVSRVLNQARDTAGRSAEMSL     737
tr|G8BEH9|G8BEH9_CANPC              DITKTIQEAKQKVQEIILDAQHNKLDPEPGMTLRESFEHNVSRVLNQARDTAGRSAEMSL     737
                                    ::  :* .** .* ::   *: : *    * ***::** :* * **.*** .*  *: .*

tr|A0A1U8DYN0|A0A1U8DYN0_ALLSI      SEYNNFKSMVVSGAKGSKINISQVIAVVGQQNVEGKRIPFGFKHRTLPHFIKDDYGPESR     828
tr|A0A1L8H4P4|A0A1L8H4P4_XENLA      SEYNNFKSMVVSGAKGSKINISQVIAVVGQQNVEGKRIPFGFKHRTLPHFIKDDYGPESR     818
tr|H9GLG5|H9GLG5_ANOCA              SEYNNFKSMVVSGAKGSKINISQVIAVVGQQNVEGKRIPFGFKHRTLPHFIKDDYGPESR     819
tr|H2R1J6|H2R1J6_PANTR              SEYNNFKSMVVSGAKGSKINISQVIAVVGQQNVEGKRIPFGFKHRTLPHFIKDDYGPESR     820
tr|G1MCZ1|G1MCZ1_AILME              SEYNNFKSMVVSGAKGSKINISQVIAVVGQQNVEGKRIPFGFKHRTLPHFIKDDYGPESR     820
tr|O08847|O08847_MOUSE              SEYNNFKSMVVSGAKGSKINISQVIAVVGQQNVEGKRIPFGFKHRTLPHFIKDDYGPESR     820
tr|S7PWZ6|S7PWZ6_MYOBR              SEYNNFKSMVVSGAKGSKINISQVIAVVGQQNVEGKRIPFGFKHRTLPHFIKDDYGPESR     820
tr|D4A5A6|D4A5A6_RAT                SEYNNFKSMVVSGAKGSKINISQVIAVVGQQNVEGKRIPFGFKHRTLPHFIKDDYGPESR     820
sp|P08775|RPB1_MOUSE                SEYNNFKSMVVSGAKGSKINISQVIAVVGQQNVEGKRIPFGFKHRTLPHFIKDDYGPESR     820
sp|P24928|RPB1_HUMAN                SEYNNFKSMVVSGAKGSKINISQVIAVVGQQNVEGKRIPFGFKHRTLPHFIKDDYGPESR     820
tr|A0A1S3EWL2|A0A1S3EWL2_DIPOR      SEYNNFKSMVVSGAKGSKINISQVIAVVGQQNVEGKRIPFGFKHRTLPHFIKDDYGPESR     820
sp|P11414|RPB1_CRIGR                SEYNNFKSMVVSGAKGSKINISQVIAVVGQQNVEGKRIPFGFKHRTLPHFIKDDYGPESR     820
tr|O35559|O35559_CRIGR              SEYNNFKSMVVSGAKGSKINISQVIAVVGQQNVEGKRIPFGFKHRTLPHFIKDDYGPESR     820
tr|A0A2I3M9H2|A0A2I3M9H2_PAPAN      SEYNNFKSLVFPHT-GKVFVCIRVIAVVGQQNVEGKRIPFGFKHRTLPHFIKDDYGPESR     819
tr|F7HB40|F7HB40_MACMU              SEYNNFKSMVVSGAKGSKINISQVIAVVGQQNVEGKRIPFGFKHRTLPHFIKDDYGPESR     820
tr|A0A2K6RYW9|A0A2K6RYW9_SAIBB      SEYNNFKSMVVSGAKGSKINISQVIAVVGQQNVEGKRIPFGFKHRTLPHFIKDDYGPESR     820
tr|W5N8Z6|W5N8Z6_LEPOC              SEYNNFKSMVVAGSKGSKINISQVIAVVGQQNVEGKRIPFGFKHRTLPHFIKDDYGPESR     819
tr|I3JRW6|I3JRW6_ORENI              SEYNNFKSMVVAGSKGSKINISQVIAVVGQQNVEGKRIPFGFKHRTLPHFIKDDYGPESR     818
tr|A0A0R4IMS9|A0A0R4IMS9_DANRE      SEYNNFKSMVVAGSKGSKINISQVIAVVGQQNVEGKRIPFGFKHRTLPHFIKDDYGPESR     817
tr|A0A1A7X327|A0A1A7X327_9TELE      SEYNNFKSMVVAGSKGSKINISQVIAVVGQQNVEGKRIPFGFKHRTLPHFIKDDYGPESR     818
tr|A0A1A8UKD7|A0A1A8UKD7_NOTFU      SEYNNFKSMVVAGSKGSKINISQVIAVVGQQNVEGKRIPFGFKHRTLPHFIKDDYGPESR     818
tr|A0A1A8ER05|A0A1A8ER05_9TELE      SEYNNFKSMVVAGSKGSKINISQVIAVVGQQNVEGKRIPFGFKHRTLPHFIKDDYGPESR     818
tr|A0A1A8DQ60|A0A1A8DQ60_9TELE      SEYNNFKSMVVAGSKGSKINISQVIAVVGQQNVEGKRIPFGFKHRTLPHFIKDDYGPESR     818
tr|A0A1A8NSR8|A0A1A8NSR8_9TELE      SEYNNFKSMVVAGSKGSKINISQVIAVVGQQNVEGKRIPFGFKHRTLPHFIKDDYGPESR     818
tr|A0A1W4YLM7|A0A1W4YLM7_9TELE      SEYNNFKSMVVAGSKGSKINISQVIAVVGQQNVEGKRIPFGFKHRTLPHFIKDDYGPESR     818
tr|A0A1M8A6L7|A0A1M8A6L7_MALS4      PDWNNVKQMVIAGSKGSFINISQMSACVGQQSVEGKRIPFGFRHRSLPHFTKDDFTPESR     811
sp|P04050|RPB1_YEAST                KDLNNVKQMVMAGSKGSFINIAQMSACVGQQSVEGKRIAFGFVDRTLPHFSKDDYSPESK     797
tr|A0A1B2J8C6|A0A1B2J8C6_PICPA      KDLNNVKQMVSAGSKGSFINIAQMSACVGQQMVEGKRIAFGFADRSLPHFTKDDFSPESK     798
tr|F2QW17|F2QW17_KOMPC              KDLNNVKQMVSAGSKGSFINIAQMSACVGQQMVEGKRIAFGFADRSLPHFTKDDFSPESK     798
tr|A3GID7|A3GID7_PICST              KDLNNVKQMVVSGSKGSFINISQMSACVGQQIVEGKRIPFGFSDRTLPHFTKDDYSPESK     797
tr|A0A1D8PUA6|A0A1D8PUA6_CANAL      KDLNNVKQMVTSGSKGSFINISQMSACVGQQIVEGKRIPFGFGDRSLPHFTKDDYSPESK     797
tr|G8BEH9|G8BEH9_CANPC              KDLNNVKQMVTSGSKGSFINISQMSACVGQQIVEGKRIPFGFADRSLPHFTKDDYSPESK     797
                                     : **.*.:*   : *. :   :: * **** ****** *** .*:**** ***: ***:
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tr|A0A1U8DYN0|A0A1U8DYN0_ALLSI      GFVENSYLAGLTPTEFFFHAMGGREGLIDTAVKTAETGYIQRRLIKSMESVMVKYDATVR       888
tr|A0A1L8H4P4|A0A1L8H4P4_XENLA      GFVENSYLAGLTPTEFFFHAMGGREGLIDTAVKTAETGYIQRRLIKSMESVMVKYDATVR       878
tr|H9GLG5|H9GLG5_ANOCA              GFVENSYLAGLTPTEFFFHAMGGREGLIDTAVKTAETGYIQRRLIKSMESVMVKYDATVR       879
tr|H2R1J6|H2R1J6_PANTR              GFVENSYLAGLTPTEFFFHAMGGREGLIDTAVKTAETGYIQRRLIKSMESVMVKYDATVR       880
tr|G1MCZ1|G1MCZ1_AILME              GFVENSYLAGLTPTEFFFHAMGGREGLIDTAVKTAETGYIQRRLIKSMESVMVKYDATVR       880
tr|O08847|O08847_MOUSE              GFVENSYLAGLTPTEFFFHAMGGREGLIDTAVKTAETGYIQRRLIKSMESVMVKYDATVR       880
tr|S7PWZ6|S7PWZ6_MYOBR              GFVENSYLAGLTPTEFFFHAMGGREGLIDTAVKTAETGYIQRRLIKSMESVMVKYDATVR       880
tr|D4A5A6|D4A5A6_RAT                GFVENSYLAGLTPTEFFFHAMGGREGLIDTAVKTAETGYIQRRLIKSMESVMVKYDATVR       880
sp|P08775|RPB1_MOUSE                GFVENSYLAGLTPTEFFFHAMGGREGLIDTAVKTAETGYIQRRLIKSMESVMVKYDATVR       880
sp|P24928|RPB1_HUMAN                GFVENSYLAGLTPTEFFFHAMGGREGLIDTAVKTAETGYIQRRLIKSMESVMVKYDATVR       880
tr|A0A1S3EWL2|A0A1S3EWL2_DIPOR      GFVENSYLAGLTPTEFFFHAMGGREGLIDTAVKTAETGYIQRRLIKSMESVMVKYDATVR       880
sp|P11414|RPB1_CRIGR                GFVENSYLAGLTPTEFFFHAMGGREGLIDTAVKTAETGYIQRRLIKSMESVMVKYDATVR       880
tr|O35559|O35559_CRIGR              GFVENSYLAGLTPTEFFFHAMGGREGLIDTAVKTAETGYIQRRLIKSMESVMVKYDATVR       880
tr|A0A2I3M9H2|A0A2I3M9H2_PAPAN      GFVENSYLAGLTPTEFFFHAMGGREGLIDTAVKTAETGYIQRRLIKSMESVMVKYDATVR       879
tr|F7HB40|F7HB40_MACMU              GFVENSYLAGLTPTEFFFHAMGGREGLIDTAVKTAETGYIQRRLIKSMESVMVKYDATVR       880
tr|A0A2K6RYW9|A0A2K6RYW9_SAIBB      GFVENSYLAGLTPTEFFFHAMGGREGLIDTAVKTAETGYIQRRLIKSMESVMVKYDATVR       880
tr|W5N8Z6|W5N8Z6_LEPOC              GFVENSYLAGLTPTEFFFHAMGGREGLIDTAVKTAETGYIQRRLIKSMESVMVKYDATVR       879
tr|I3JRW6|I3JRW6_ORENI              GFVENSYLAGLTPTEFFFHAMGGREGLIDTAVKTAETGYIQRRLIKSMESVMVKYDGTVR       878
tr|A0A0R4IMS9|A0A0R4IMS9_DANRE      GFVENSYLAGLTPTEFFFHAMGGREGLIDTAVKTAETGYIQRRLIKSMESVMVKYDATVR       877
tr|A0A1A7X327|A0A1A7X327_9TELE      GFVENSYLAGLTPTEFFFHAMGGREGLIDTAVKTAETGYIQRRLIKSMESVMVKYDATVR       878
tr|A0A1A8UKD7|A0A1A8UKD7_NOTFU      GFVENSYLAGLTPTEFFFHAMGGREGLIDTAVKTAETGYIQRRLIKSMESVMVKYDATVR       878
tr|A0A1A8ER05|A0A1A8ER05_9TELE      GFVENSYLAGLTPTEFFFHAMGGREGLIDTAVKTAETGYIQRRLIKSMESVMVKYDATVR       878
tr|A0A1A8DQ60|A0A1A8DQ60_9TELE      GFVENSYLAGLTPTEFFFHAMGGREGLIDTAVKTAETGYIQRRLIKSMESVMVKYDATVR       878
tr|A0A1A8NSR8|A0A1A8NSR8_9TELE      GFVENSYLAGLTPTEFFFHAMGGREGLIDTAVKTAETGYIQRRLIKSMESVMVKYDATVR       878
tr|A0A1W4YLM7|A0A1W4YLM7_9TELE      GFVENSYLAGLTPTEFFFHAMGGREGLIDTAVKTAETGYIQRRLIKSMESVMVKYDATVR       878
tr|A0A1M8A6L7|A0A1M8A6L7_MALS4      GFVENSYLRGLTAHEFFFHAMAGREGLIDTAVKTAETGYIQRRLVKALEDVTICYDGTVR       871
sp|P04050|RPB1_YEAST                GFVENSYLRGLTPQEFFFHAMGGREGLIDTAVKTAETGYIQRRLVKALEDIMVHYDNTTR       857
tr|A0A1B2J8C6|A0A1B2J8C6_PICPA      GFVENSYLRGLTPQEFFFHAMAGREGLIDTAVKTAETGYIQRRLVKALEDIMVHYDGTTR       858
tr|F2QW17|F2QW17_KOMPC              GFVENSYLRGLTPQEFFFHAMAGREGLIDTAVKTAETGYIQRRLVKALEDIMVHYDGTTR       858
tr|A3GID7|A3GID7_PICST              GFVENSYLRGLTPQEFFFHAMAGREGLIDTAVKTAETGYIQRRLVKALEDIMVHYDGTTR       857
tr|A0A1D8PUA6|A0A1D8PUA6_CANAL      GFVENSYLRGLTPQEFFFHAMAGREGLIDTAVKTAETGYIQRRLVKALEDIMVHYDGTTR       857
tr|G8BEH9|G8BEH9_CANPC              GFVENSYLRGLTPQEFFFHAMAGREGLIDTAVKTAETGYIQRRLVKALEDIMVHYDGTTR       857
                                    ******** ***  *******.**********************:*::*.: : ** *.*

tr|A0A1U8DYN0|A0A1U8DYN0_ALLSI      NSINQVVQLRYGEDGLAGESVEFQNLATLKPSNKAFEKKFKFDYANERALRRTLQEEMVK       948
tr|A0A1L8H4P4|A0A1L8H4P4_XENLA      NSINQVVQLRYGEDGLAGEGVEFQNLATLKPSNKAFEKKFKFDYANERALRRTLQEDVVK       938
tr|H9GLG5|H9GLG5_ANOCA              NSINQVVQLRYGEDGLAGESVEFQNLATLKPSNKAFEKKFKFDYTNERALRRTLQEEMVK       939
tr|H2R1J6|H2R1J6_PANTR              NSINQVVQLRYGEDGLAGESVEFQNLATLKPSNKAFEKKFRFDYTNERALRRTLQEDLVK       940
tr|G1MCZ1|G1MCZ1_AILME              NSINQVVQLRYGEDGLAGESVEFQNLATLKPSNKAFEKKFRFDYTNERALRRTLQEDLVK       940
tr|O08847|O08847_MOUSE              NSINQVVQLRYGEDGLAGESVEFQNLATLKPSNKAFEKKFRFDYTNERALRRTLQEDLVK       940
tr|S7PWZ6|S7PWZ6_MYOBR              NSINQVVQLRYGEDGLAGESVEFQNLATLKPSNKAFEKKFRFDYTNERALRRTLQEDLVK       940
tr|D4A5A6|D4A5A6_RAT                NSINQVVQLRYGEDGLAGESVEFQNLATLKPSNKAFEKKFRFDYTNERALRRTLQEDLVK       940
sp|P08775|RPB1_MOUSE                NSINQVVQLRYGEDGLAGESVEFQNLATLKPSNKAFEKKFRFDYTNERALRRTLQEDLVK       940
sp|P24928|RPB1_HUMAN                NSINQVVQLRYGEDGLAGESVEFQNLATLKPSNKAFEKKFRFDYTNERALRRTLQEDLVK       940
tr|A0A1S3EWL2|A0A1S3EWL2_DIPOR      NSINQVVQLRYGEDGLAGESVEFQNLATLKPSNKAFEKKFRFDYTNERALRRTLQEDLVK       940
sp|P11414|RPB1_CRIGR                NSINQVVQLRYGEDGLAGESVEFQNLATLKPSNKAFEKKFRFDYTNERALRRTLQEDLVK       940
tr|O35559|O35559_CRIGR              NSINQVVQLRYGEDGLAGESVEFQNLATLKPSNKAFEKKFRFDYTNERALRRTLQEDLVK       940
tr|A0A2I3M9H2|A0A2I3M9H2_PAPAN      NSINQVVQLRYGEDGLAGESVEFQNLATLKPSNKAFEKKFRFDYTNERALRRTLQEDLVK       939
tr|F7HB40|F7HB40_MACMU              NSINQVVQLRYGEDGLAGESVEFQNLATLKPSNKAFEKKFRFDYTNERALRRTLQEDLVK       940
tr|A0A2K6RYW9|A0A2K6RYW9_SAIBB      NSINQVVQLRYGEDGLAGESVEFQNLATLKPSNKAFEKKFRFDYTNERALRRTLQEDLVK       940
tr|W5N8Z6|W5N8Z6_LEPOC              NSINQVVQLRYGEDGLAGEAVEFQNMATLKPSNKAFEKKFKFDYTNERALRRTLQEDVVK       939
tr|I3JRW6|I3JRW6_ORENI              NSINQVVQLRYGEDGLAGENVEFQNLATVKPSHKAFEKKFKFDCTNERALRRTLQEDVVK       938
tr|A0A0R4IMS9|A0A0R4IMS9_DANRE      NSINQVVQLRYGEDGLAGEAVEFQNMATLKPSHKAFEKKFKFDYANERALRRTLQEDVVK       937
tr|A0A1A7X327|A0A1A7X327_9TELE      NSINQVVQLRYGEDGLAGENVEFQNLATLKPSHKAFEKKFKFDCTNERALRRILQEDVVK       938
tr|A0A1A8UKD7|A0A1A8UKD7_NOTFU      NSINQVVQLRYGEDGLAGENVEFQNLATLKPSHKAFEKKFKFDCTNERALRRILQEDVVK       938
tr|A0A1A8ER05|A0A1A8ER05_9TELE      NSINQVVQLRYGEDGLAGENVEFQNLATLKPSHKAFEKKFKFDCTNERALRRILQEDVVK       938
tr|A0A1A8DQ60|A0A1A8DQ60_9TELE      NSINQVVQLRYGEDGLAGENVEFQNLATLKPSHKAFEKKFKFDCTNERALRRILQEDVVK       938
tr|A0A1A8NSR8|A0A1A8NSR8_9TELE      NSINQVVQLRYGEDGLAGENVEFQNLATLKPSHKAFEKKFKFDCTNERALRRILQEDVVK       938
tr|A0A1W4YLM7|A0A1W4YLM7_9TELE      NSINQVVQLRYGEDGLAGEAVEFQNMATLKPSNKAFEKKFKFDYTNERALRRTLQEDVVK       938
tr|A0A1M8A6L7|A0A1M8A6L7_MALS4      NSTNNVIEFAYGEDGIDGAMVERQKLITHGLNDKEFRRRFKVDLSHGGF--KKGTLRAGL       929
sp|P04050|RPB1_YEAST                NSLGNVIQFIYGEDGMDAAHIEKQSLDTIGGSDAAFEKRYRVDLLNTDHTLDPSLLESGS       917
tr|A0A1B2J8C6|A0A1B2J8C6_PICPA      NSLGDIIQFLYGEDGLDGTQVERQTIDTIPGSDKAFHKRYYVDLMDEKNSIKADVIEYAA       918
tr|F2QW17|F2QW17_KOMPC              NSLGDIIQFLYGEDGLDGTQVERQTIDTIPGSDKAFHKRYYVDLMDEKNSIKPDVIEYAA       918
tr|A3GID7|A3GID7_PICST              NSLGDIIQFVYGEDGIDGTQVEKQSVDTIPGSNDSFERRFRIDVLDSSKSIPESLLESGK       917
tr|A0A1D8PUA6|A0A1D8PUA6_CANAL      NSLGDIIQFIYGEDGIDGTQVEKQSVDTIPGSDESFERRYKIDVLDTENVISESLLESGK       917
tr|G8BEH9|G8BEH9_CANPC              NSLGDIIQFIYGEDGIDATQVEKQSVDTIPGSDASFERRYRIDLLEKNGSISESLLESGK       917
                                    ** .::::: *****: .  :* *.: *   ..  *.::: .*
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tr|A0A1U8DYN0|A0A1U8DYN0_ALLSI      DILSNAHIQNELEREFEKMREDREVLRV-IFPTGDSKVVLPCNLLRMIWNAQKIFHVNAR       1007
tr|A0A1L8H4P4|A0A1L8H4P4_XENLA      EILSDAHVQNELEKEFEKMKEDREVLRV-IFPTGDSKVVLPCNLQRMIWNAQKIFHINTR       997
tr|H9GLG5|H9GLG5_ANOCA              DILSNAHIQNELEREFEKMKEDREVLRV-IFPTGDSKVVLPCNLLRMIWNAQKIFHINTR       998
tr|H2R1J6|H2R1J6_PANTR              DVLSNAHIQNELEREFERMREDREVLRV-IFPTGDSKVVLPCNLLRMIWNAQKIFHINPR       999
tr|G1MCZ1|G1MCZ1_AILME              DVLSNAHIQNELEREFERMREDREVLRV-IFPTGDSKVVLPCNLLRMIWNAQKIFHINPR       999
tr|O08847|O08847_MOUSE              DVLSNAHIQNELEREFERMREDREVLRV-IFPTGDSKVVLPCNLLRMIWNAQKIFHINPR       999
tr|S7PWZ6|S7PWZ6_MYOBR              DVLSNAHIQNELEREFERMREDREVLRV-IFPTGDSKVVLPCNLLRMIWNAQKIFHINPR       999
tr|D4A5A6|D4A5A6_RAT                DVLSNAHIQNELEREFERMREDREVLRV-IFPTGDSKVVLPCNLLRMIWNAQKIFHINPR       999
sp|P08775|RPB1_MOUSE                DVLSNAHIQNELEREFERMREDREVLRV-IFPTGDSKVVLPCNLLRMIWNAQKIFHINPR       999
sp|P24928|RPB1_HUMAN                DVLSNAHIQNELEREFERMREDREVLRV-IFPTGDSKVVLPCNLLRMIWNAQKIFHINPR       999
tr|A0A1S3EWL2|A0A1S3EWL2_DIPOR      DVLSNAHIQNELEREFERMREDREVLRV-IFPTGDSKVVLPCNLLRMIWNAQKIFHINPR       999
sp|P11414|RPB1_CRIGR                DVLSNAHIQNELEREFERMREDREVLRV-IFPTGDSKVVLPCNLLRMIWNAQKIFHINPR       999
tr|O35559|O35559_CRIGR              DVLSNAHIQNELEREFERMREDREVLRV-IFPTGDSKVVLPCNLLRMIWNAQKIFHINPR       999
tr|A0A2I3M9H2|A0A2I3M9H2_PAPAN      DVLSNAHIQNELEREFERMREDREVLRV-IFPTGDSKVVLPCNLLRMIWNAQKIFHINPR       998
tr|F7HB40|F7HB40_MACMU              DVLSNAHIQNELEREFERMREDREVLRV-IFPTGDSKVVLPCNLLRMIWNAQKIFHINPR       999
tr|A0A2K6RYW9|A0A2K6RYW9_SAIBB      DVLSNAHIQNELEREFERMREDREVLRV-IFPTGDSKVVLPCNLLRMIWNAQKIFHINPR       999
tr|W5N8Z6|W5N8Z6_LEPOC              EVLTNAHVQGELEREFEKMREDREILRA-IFPTGDSKVVLPCNLARMIWNAQKIFRINTR       998
tr|I3JRW6|I3JRW6_ORENI              DVMTNAHVQGTLEREFDKMKEDREILRA-IFPTGDSKVVLPCNLARMIWNAQKIFRINPR       997
tr|A0A0R4IMS9|A0A0R4IMS9_DANRE      DVMTNAHVQSSLEREFEKMREDREILRA-IFPTGDSKVVLPCNLARMIWNAQKIFRINPR       996
tr|A0A1A7X327|A0A1A7X327_9TELE      DVQTNALVQSTLEREFEKMKEDREILRA-IFPTGDSKVVLPCNLARMIWNAQKIFRINPR       997
tr|A0A1A8UKD7|A0A1A8UKD7_NOTFU      DVQTNAHVQSVLEREFEKMKEDREILRA-IFPTGDSKVVLPCNLARMIWNAQKIFRINPR       997
tr|A0A1A8ER05|A0A1A8ER05_9TELE      DVQTNAHVQSVLEREFEKMKEDREILRA-IFPTGDSKVVLPCNLARMIWNAQKIFRINPR       997
tr|A0A1A8DQ60|A0A1A8DQ60_9TELE      DVQTNAHVQSVLEREFEKMKEDREILRA-IFPTGDSKVVLPCNLARMIWNAQKIFRINPR       997
tr|A0A1A8NSR8|A0A1A8NSR8_9TELE      DVQTNAHVQSVLEREFEKMKEDREILRA-IFPTGDSKVVLPCNLARMIWNAQKIFRINPR       997
tr|A0A1W4YLM7|A0A1W4YLM7_9TELE      DVMTNAHVQSALEHEFEKMREDREILRA-IFPTGDSKVVLPCNLARMIWNAQKIFRINPR       997
tr|A0A1M8A6L7|A0A1M8A6L7_MALS4      G-DWSPELEQLLDEEFEQLERDRMLLRTEIFRTDRVDTYLPLNIARLVLNAQQIFHIDPR       988
sp|P04050|RPB1_YEAST                EILGDLKLQVLLDEEYKQLVKDRKFLREV-FVDGEANWPLPVNIRRIIQNAQQTFHIDHT       976
tr|A0A1B2J8C6|A0A1B2J8C6_PICPA      DIIGDVELQKELNSEYEQLVNDRKFLREIVFVNGDHNWPLPVNLRRIIQNAQQIFHLDRA       978
tr|F2QW17|F2QW17_KOMPC              DILGDVELQKELNSEYEQLVSDRKFLREIVFVNGDHNWPLPVNLRRIIQNAQQIFHLDRA       978
tr|A3GID7|A3GID7_PICST              EIKGDVKLQKVLDEEYKQLLDDRKYLREVCFPNGDFSWPLPVNLRRIIQNAQQIFHNGRY       977
tr|A0A1D8PUA6|A0A1D8PUA6_CANAL      EIRGDVQLQKILDEEYNQLLKDRKYLREVCFPNGDFSWPLPVNLRRIIQNAQQIFHNGRY       977
tr|G8BEH9|G8BEH9_CANPC              EIQGDVKLQKLLDEEYNQLLKDRRYLRDVCFPNGDFSWPLPVNLRRIIQNAQQIFHNGRY       977
                                        .  ::  *: *:.::  **  **   *  .  .  ** *: *:: ***: *: .


tr|A0A1U8DYN0|A0A1U8DYN0_ALLSI      LSAQAFDWLLGEIESKFNQAIAHPGEMGGALAAQSLGEPATQMTLNTFHYAGVSAKNVTL       1127
tr|A0A1L8H4P4|A0A1L8H4P4_XENLA      LSGEAFDWLLGEIESKFNQAIAHPGEMVGALAAQSLGEPATQMTLNTFHYAGVSAKNVTL       1117
tr|H9GLG5|H9GLG5_ANOCA              LSGEAFDWLLGEIESKFNQAIAHPGEMVGALAAQSLGEPATQMTLNTFHYAGVSAKNVTL       1118
tr|H2R1J6|H2R1J6_PANTR              LSGEAFDWLLGEIESKFNQAIAHPGEMVGALAAQSLGEPATQMTLNTFHYAGVSAKNVTL       1119
tr|G1MCZ1|G1MCZ1_AILME              LSGEAFDWLLGEIESKFNQAIAHPGEMVGALAAQSLGEPATQMTLNTFHYAGVSAKNVTL       1119
tr|O08847|O08847_MOUSE              LSGEAFDWLLGEIESKFNQAIAHPGEMVGALAAQSLGEPATQMTLNTFHYAGVSAKNVTL       1119
tr|S7PWZ6|S7PWZ6_MYOBR              LSGEAFDWLLGEIESKFNQAIAHPGEMVGALAAQSLGEPATQMTLNTFHYAGVSAKNVTL       1119
tr|D4A5A6|D4A5A6_RAT                LSGEAFDWLLGEIESKFNQAIAHPGEMVGALAAQSLGEPATQMTLNTFHYAGVSAKNVTL       1119
sp|P08775|RPB1_MOUSE                LSGEAFDWLLGEIESKFNQAIAHPGEMVGALAAQSLGEPATQMTLNTFHYAGVSAKNVTL       1119
sp|P24928|RPB1_HUMAN                LSGEAFDWLLGEIESKFNQAIAHPGEMVGALAAQSLGEPATQMTLNTFHYAGVSAKNVTL       1119
tr|A0A1S3EWL2|A0A1S3EWL2_DIPOR      LSGEAFDWLLGEIESKFNQAIAHPGEMVGALAAQSLGEPATQMTLNTFHYAGVSAKNVTL       1119
sp|P11414|RPB1_CRIGR                LSGEAFDWLLGEIESKFNQAIAHPGEMVGALAAQSLGEPATQMTLNTFHYAGVSAKNVTL       1119
tr|O35559|O35559_CRIGR              LSGEAFDWLLGEIESKFNQAIAHPGEMVGALAAQSLGEPATQMTLNTFHYAGVSAKNVTL       1119
tr|A0A2I3M9H2|A0A2I3M9H2_PAPAN      LSGEAFDWLLGEIESKFNQAIAHPGEMVGALAAQSLGEPATQMTLNTFHYAGVSAKNVTL       1118
tr|F7HB40|F7HB40_MACMU              LSGEAFDWLLGEIESKFNQAIAHPGEMVGALAAQSLGEPATQMTLNTFHYAGVSAKNVTL       1119
tr|A0A2K6RYW9|A0A2K6RYW9_SAIBB      LSGEAFDWLLGEIESKFNQAIAHPGEMVGALAAQSLGEPATQMTLNTFHYAGVSAKNVTL       1119
tr|W5N8Z6|W5N8Z6_LEPOC              LSTEAYEWLLGEIETKFNQSIAHPGEMVGALAAQSLGEPATQMTLNTFHYAGVSAKNVTL       1118
tr|I3JRW6|I3JRW6_ORENI              LSTEAFDWLLGEIETKFNQSIAHPGEMVGALAAQSLGEPATQMTLNTFHYAGVSAKNVTL       1117
tr|A0A0R4IMS9|A0A0R4IMS9_DANRE      LSTEAFDWLLGEIETKFNQSIAHPGEMVGALAAQSLGEPATQMTLNTFHYAGVSAKNVTL       1116
tr|A0A1A7X327|A0A1A7X327_9TELE      LSTEAFDWLLGEIETKFNQSIVHPGEMVGALAAQSLGEPATQMTLNTFHYAGVSAKNVTL       1117
tr|A0A1A8UKD7|A0A1A8UKD7_NOTFU      LSMEAFDWLLGEIETKFNQSIVHPGEMVGALAAQSLGEPATQMTLNTFHYAGVSAKNVTL       1117
tr|A0A1A8ER05|A0A1A8ER05_9TELE      LSMEAFDWLLGEIETKFNQSIVHPGEMVGALAAQSLGEPATQMTLNTFHYAGVSAKNVTL       1117
tr|A0A1A8DQ60|A0A1A8DQ60_9TELE      LSMEAFDWLLGEIETKFNQSIVHPGEMVGALAAQSLGEPATQMTLNTFHYAGVSAKNVTL       1117
tr|A0A1A8NSR8|A0A1A8NSR8_9TELE      LSMEAFDWLLGEIETKFNQSIVHPGEMVGALAAQSLGEPATQMTLNTFHYAGVSAKNVTL       1117
tr|A0A1W4YLM7|A0A1W4YLM7_9TELE      LSTEAFEWLLGEIETKFNQAIVHPGEMVGALAAQSLGEPATQMTLNTFHYAGVSAKNVTL       1117
tr|A0A1M8A6L7|A0A1M8A6L7_MALS4      LSREAWEWILGEIEGQFARSVAQPGEMCGTLAAQSIGEPATQMTLNTFHYAGVSSKNVTL       1108
sp|P04050|RPB1_YEAST                LTKQAFDWVLSNIEAQFLRSVVHPGEMVGVLAAQSIGEPATQMTLNTFHFAGVASKKVTS       1096
tr|A0A1B2J8C6|A0A1B2J8C6_PICPA      LNRDAFEWVLGTIEAQFQRSLVHPGEMVGVIAAQSIGEPATQMTLNTFHYAGVSSKNVTL       1098
tr|F2QW17|F2QW17_KOMPC              LNRDAFEWVLGTIEAQFQRSLVHPGEMVGVIAAQSIGEPATQMTLNTFHYAGVSSKNVTL       1098
tr|A3GID7|A3GID7_PICST              LNRSSFEWVVGEIETQFQKSIVHPGEMVGVIAAQSIGEPATQMTLNTFHYAGVSSKNVTL       1097
tr|A0A1D8PUA6|A0A1D8PUA6_CANAL      LNRASFEWVMGEIETQFQKSIVHPGEMVGVVAAQSIGEPATQMTLNTFHYAGVSSKNVTL       1097
tr|G8BEH9|G8BEH9_CANPC              LNRSSFDWVLGEIETQFQKSIVHPGEMVGVVAAQSIGEPATQMTLNTFHYAGVSSKNVTL       1097
                                    *.  :::*::. ** :* :::.:**** *.:****:*************:***::*:**
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tr|A0A1U8DYN0|A0A1U8DYN0_ALLSI      GVPRLKELINISKKPKTPSLTVFLLGQSARDAERAKDILCRLEHTTLRKVTANTAIYYDP      1187
tr|A0A1L8H4P4|A0A1L8H4P4_XENLA      GVPRLKELINISKKPKTPSLTVFLLGQSARDAERAKDILCRLEHTTLRKVTANTAIYYDP      1177
tr|H9GLG5|H9GLG5_ANOCA              GVPRLKELINISKKPKTPSLTVFLLGQSARDAERAKDILCRLEHTTLRKVTANTAIYYDP      1178
tr|H2R1J6|H2R1J6_PANTR              GVPRLKELINISKKPKTPSLTVFLLGQSARDAERAKDILCRLEHTTLRKVTANTAIYYDP      1179
tr|G1MCZ1|G1MCZ1_AILME              GVPRLKELINISKKPKTPSLTVFLLGQSARDAERAKDILCRLEHTTLRKVTANTAIYYDP      1179
tr|O08847|O08847_MOUSE              GVPRLKELINISKKPKTPSLTVFLLGQSARDAERAKDILCRLEHTTLRKVTANTAIYYDP      1179
tr|S7PWZ6|S7PWZ6_MYOBR              GVPRLKELINISKKPKTPSLTVFLLGQSARDAERAKDILCRLEHTTLRKVTANTAIYYDP      1179
tr|D4A5A6|D4A5A6_RAT                GVPRLKELINISKKPKTPSLTVFLLGQSARDAERAKDILCRLEHTTLRKVTANTAIYYDP      1179
sp|P08775|RPB1_MOUSE                GVPRLKELINISKKPKTPSLTVFLLGQSARDAERAKDILCRLEHTTLRKVTANTAIYYDP      1179
sp|P24928|RPB1_HUMAN                GVPRLKELINISKKPKTPSLTVFLLGQSARDAERAKDILCRLEHTTLRKVTANTAIYYDP      1179
tr|A0A1S3EWL2|A0A1S3EWL2_DIPOR      GVPRLKELINISKKPKTPSLTVFLLGQSARDAERAKDILCRLEHTTLRKVTANTAIYYDP      1179
sp|P11414|RPB1_CRIGR                GVPRLKELINISKKPKTPSLTVFLLGQSARDAERAKDILCRLEHTTLRKVTANTAIYYDP      1179
tr|O35559|O35559_CRIGR              GVPRLKELINISKKPKTPSLTVFLLGQSARDAERAKDILCRLEHTTLRKVTANTAIYYDP      1179
tr|A0A2I3M9H2|A0A2I3M9H2_PAPAN      GVPRLKELINISKKPKTPSLTVFLLGQSARDAERAKDILCRLEHTTLRKVTANTAIYYDP      1178
tr|F7HB40|F7HB40_MACMU              GVPRLKELINISKKPKTPSLTVFLLGQSARDAERAKDILCRLEHTTLRKVTANTAIYYDP      1179
tr|A0A2K6RYW9|A0A2K6RYW9_SAIBB      GVPRLKELINISKKPKTPSLTVFLLGQSARDAERAKDILCRLEHTTLRKVTANTAIYYDP      1179
tr|W5N8Z6|W5N8Z6_LEPOC              GVPRLKELINISKKPKTPSLTVFLLGQAARDAERAKDILCRLEHTTLRKVTANTAIYYDP      1178
tr|I3JRW6|I3JRW6_ORENI              GVPRLKELINISKRPKTPSLTVFLLGQAARDAERAKDILCRLEHTTLRKVTANTAIYYDP      1177
tr|A0A0R4IMS9|A0A0R4IMS9_DANRE      GVPRLKELINISKRPKTPSLTVFLLGQAARDAERAKDILCRLEHTTLRKVTANTAIYYDP      1176
tr|A0A1A7X327|A0A1A7X327_9TELE      GVPRLKELINISKRPKTPSLTVFLLGQAARDAERAKDILCRLEHTTLRKVTANTAIYYDP      1177
tr|A0A1A8UKD7|A0A1A8UKD7_NOTFU      GVPRLKELINISKRPKTPSLTVFLLGQAARDAERAKDILCRLEHTTLRKVTANTAIYYDP      1177
tr|A0A1A8ER05|A0A1A8ER05_9TELE      GVPRLKELINISKRPKTPSLTVFLLGQAARDAERAKDILCRLEHTTLRKVTANTAIYYDP      1177
tr|A0A1A8DQ60|A0A1A8DQ60_9TELE      GVPRLKELINISKRPKTPSLTVFLLGQAARDAERAKDILCRLEHTTLRKVTANTAIYYDP      1177
tr|A0A1A8NSR8|A0A1A8NSR8_9TELE      GVPRLKELINISKRPKTPSLTVFLLGQAARDAERAKDILCRLEHTTLRKVTANTAIYYDP      1177
tr|A0A1W4YLM7|A0A1W4YLM7_9TELE      GVPRLKELINISKRPKTPSLTVFLLGQAARDAERAKDILCRLEHTTLRKVTANTAIYYDP      1177
tr|A0A1M8A6L7|A0A1M8A6L7_MALS4      GVPRLKEIINCAENIKTPSVTVYLHPKYSASSESAKVIQTALAYTTLQTVTSAVEVFYDP      1168
sp|P04050|RPB1_YEAST                GVPRLKEILNVAKNMKTPSLTVYLEPGHAADQEQAKLIRSAIEHTTLKSVTIASEIYYDP      1156
tr|A0A1B2J8C6|A0A1B2J8C6_PICPA      GVPRLKEILNVAKNIKTPALTVYLDREIALDIEKAKVIQSSIEYTTLKNVTSATEIYYDP      1158
tr|F2QW17|F2QW17_KOMPC              GVPRLKEILNVAKNIKTPALTVYLDREIALDIEKAKVIQSSIEYTTLKNVTSATEIYYDP      1158
tr|A3GID7|A3GID7_PICST              GVPRLKEILNVAKNIKTPALTVYLDPALSDDIEKAKVVQSAIEHTSLKNVTSSTEIYYDP      1157
tr|A0A1D8PUA6|A0A1D8PUA6_CANAL      GVPRLKEILNVAKNIKTPAMTVFLDPEVASDIEKAKIVQSAIEHTTLKNVTSSTEIYYDP      1157
tr|G8BEH9|G8BEH9_CANPC              GVPRLKEILNVAKNIKTPALTVYLDPEVASDIELAKIVQSSIEHTTLKNVTSSTEIYYDP      1157
                                    *******::* ::. ***::**:*    : . * ** :   : :*:*:.**    ::***

tr|A0A1U8DYN0|A0A1U8DYN0_ALLSI      SPQSTVVAEDQEWVNVYYEMPDFDV----SRISPWLLRVELDRKHMTDRKLTMEQIAEKI      1243
tr|A0A1L8H4P4|A0A1L8H4P4_XENLA      NPQNTVVAEDQEWVNVYYEMPDFDV----TRISPWLLRVELDRKHMTDRKLTMEQIAEKI      1233
tr|H9GLG5|H9GLG5_ANOCA              NPQNTVVAEDQEWVNVYYEMPDFDV----TRISPWLLRVELDRKHMTDRKLTMEQIAEKI      1234
tr|H2R1J6|H2R1J6_PANTR              NPQSTVVAEDQEWVNVYYEMPDFDV----ARISPWLLRVELDRKHMTDRKLTMEQIAEKI      1235
tr|G1MCZ1|G1MCZ1_AILME              NPQSTVVAEDQEWVNVYYEMPDFDV----ARISPWLLRVELDRKHMTDRKLTMEQIAEKI      1235
tr|O08847|O08847_MOUSE              NPQSTVVAEDQEWVNVYYEMPDFDV----ARISPWLLRVELDRKHMTDRKLTMEQIAEKI      1235
tr|S7PWZ6|S7PWZ6_MYOBR              NPQSTVVAEDQEWVNVYYEMPDFDV----ARISPWLLRVELDRKHMTDRKLTMEQIAEKI      1235
tr|D4A5A6|D4A5A6_RAT                NPQSTVVAEDQEWVNVYYEMPDFDV----ARISPWLLRVELDRKHMTDRKLTMEQIAEKI      1235
sp|P08775|RPB1_MOUSE                NPQSTVVAEDQEWVNVYYEMPDFDV----ARISPWLLRVELDRKHMTDRKLTMEQIAEKI      1235
sp|P24928|RPB1_HUMAN                NPQSTVVAEDQEWVNVYYEMPDFDV----ARISPWLLRVELDRKHMTDRKLTMEQIAEKI      1235
tr|A0A1S3EWL2|A0A1S3EWL2_DIPOR      NPQSTVVAEDQEWVNVYYEMPDFDV----ARISPWLLRVELDRKHMTDRKLTMEQIAEKI      1235
sp|P11414|RPB1_CRIGR                NPQSTVVAEDQEWVNVYYEMPDFDV----ARISPWLLRVELDRKHMTDRKLTMEQIAEKI      1235
tr|O35559|O35559_CRIGR              NPQSTVVAEDQEWVNVYYEMPDFDV----ARISPWLLRVELDRKHMTDRKLTMEQIAEKI      1235
tr|A0A2I3M9H2|A0A2I3M9H2_PAPAN      NPQSTVVAEDQEWVNVYYEMPDFDV----ARISPWLLRVELDRKHMTDRKLTMEQIAEKI      1234
tr|F7HB40|F7HB40_MACMU              NPQSTVVAEDQEWVNVYYEMPDFDV----ARISPWLLRVELDRKHMTDRKLTMEQIAEKI      1235
tr|A0A2K6RYW9|A0A2K6RYW9_SAIBB      NPQSTVVAEDQEWVNVYYEMPDFDV----ARISPWLLRVELDRKHMTDRKLTMEQIAEKI      1235
tr|W5N8Z6|W5N8Z6_LEPOC              NPQNTVVAEDQEWVNVYYEMPDFDV----TRISPWLLRIELDRKHMTDRKLTMEQIAEKI      1234
tr|I3JRW6|I3JRW6_ORENI              NPQNTVVAEDQEWVNVYYEMPDFDV----TRISPWLLRIELDRKHMTDRKLTMEQIAEKI      1233
tr|A0A0R4IMS9|A0A0R4IMS9_DANRE      NPQNTVVTEDQEWVNVYYEMPDFDV----TRISPWLLRIELDRKHMTDRKLTMEQIAEKI      1232
tr|A0A1A7X327|A0A1A7X327_9TELE      NPQNTVVAEDQEWVNVYYEMPDFDV----TRISPWLLRIELDRKHMTDRKLTMEQIAEKI      1233
tr|A0A1A8UKD7|A0A1A8UKD7_NOTFU      NPQNTVVAEDQEWVNVYYEMPDFDV----TRISPWLLRIELDRKHMTDRKLTMEQIAEKI      1233
tr|A0A1A8ER05|A0A1A8ER05_9TELE      NPQNTVVAEDQEWVNVYYEMPDFDV----TRISPWLLRIELDRKHMTDRKLTMEQIAEKI      1233
tr|A0A1A8DQ60|A0A1A8DQ60_9TELE      NPQNTVVAEDQEWVNVYYEMPDFDV----TRISPWLLRIELDRKHMTDRKLTMEQIAEKI      1233
tr|A0A1A8NSR8|A0A1A8NSR8_9TELE      NPQNTVVAEDQEWVNVYYEMPDFDV----TRISPWLLRIELDRKHMTDRKLTMEQIAEKI      1233
tr|A0A1W4YLM7|A0A1W4YLM7_9TELE      NPQNTVVTEDQEWVNVYYEMPDFDV----TRISPWLLRIELDRKHMTDRKLTMEQIAEKI      1233
tr|A0A1M8A6L7|A0A1M8A6L7_MALS4      DPSSTVIPEDRDFVDAFFAIPDEEVEASLERQSPWLLRLVLDRAQMLDKNLTMAEVASKI      1228
sp|P04050|RPB1_YEAST                DPRSTVIPEDEEIIQLHFSLLDEEAEQSFDQQSPWLLRLELDRAAMNDKDLTMGQVGERI      1216
tr|A0A1B2J8C6|A0A1B2J8C6_PICPA      DPTSTVIEEDFDTVEAYFSIPDEKVEETIDKQSPWLLRLELDRARMLDKQLTMNQVADKI      1218
tr|F2QW17|F2QW17_KOMPC              DPTSTVIEEDFDTVEAYFSIPDEKVEETIDKQSPWLLRLELDRARMLDKQLTMNQVADKI      1218
tr|A3GID7|A3GID7_PICST              DPRTTVIEEDYDTVEAYFSIPDEKVEESIEKQSPWLLRLELDRAKMLDKQLTMAQVAEKI      1217
tr|A0A1D8PUA6|A0A1D8PUA6_CANAL      DPRTTVIEDDYDTVEAYFAIPDQKVEESIDKQSPWLLRLELDRAKMLDKQLTMAQVAEKI      1217
tr|G8BEH9|G8BEH9_CANPC              DPRTTVIEEDYDTVEAYFAIPDQKVEESIEKQSPWLLRLELDRAKMLDKQLTMAQVAEKI      1217
                                    .* .**: :* : :: .: : * ..     : ******: ***  * *:.*** ::..:*
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tr|A0A1U8DYN0|A0A1U8DYN0_ALLSI      MTLQGIEQISKVYMHLPQTDNKKKIIITEDGEFKALQEWILETDGVSLMRVLSEKDVDPV        1363
tr|A0A1L8H4P4|A0A1L8H4P4_XENLA      MTLQGIEQISKVYMHLPQTDNKKKIIITEDGEFKALQEWILETDGVSLMRVLSEKDVDPV        1353
tr|H9GLG5|H9GLG5_ANOCA              MTLQGIEQISKVYMHLPQTDNKKKIIITEDGEFKALQEWILETDGVSLMRVLSEKDVDPV        1354
tr|H2R1J6|H2R1J6_PANTR              MTLQGIEQISKVYMHLPQTDNKKKIIITEDGEFKALQEWILETDGVSLMRVLSEKDVDPV        1355
tr|G1MCZ1|G1MCZ1_AILME              MTLQGIEQISKVYMHLPQTDNKKKIIITEDGEFKALQEWILETDGVSLMRVLSEKDVDPV        1355
tr|O08847|O08847_MOUSE              MTLQGIEQISKVYMHLPQTDNKKKIIITEDGEFKALQEWILETDGVSLMRVLSEKDVDPV        1355
tr|S7PWZ6|S7PWZ6_MYOBR              MTLQGIEQISKVYMHLPQTDNKKKIIITEDGEFKALQEWILETDGVSLMRVLSEKDVDPV        1355
tr|D4A5A6|D4A5A6_RAT                MTLQGIEQISKVYMHLPQTDNKKKIIITEDGEFKALQEWILETDGVSLMRVLSEKDVDPV        1355
sp|P08775|RPB1_MOUSE                MTLQGIEQISKVYMHLPQTDNKKKIIITEDGEFKALQEWILETDGVSLMRVLSEKDVDPV        1355
sp|P24928|RPB1_HUMAN                MTLQGIEQISKVYMHLPQTDNKKKIIITEDGEFKALQEWILETDGVSLMRVLSEKDVDPV        1355
tr|A0A1S3EWL2|A0A1S3EWL2_DIPOR      MTLQGIEQISKVYMHLPQTDNKKKIIITEDGEFKALQEWILETDGVSLMRVLSEKDVDPV        1355
sp|P11414|RPB1_CRIGR                MTLQGIEQISKVYMHLPQTDNKKKIIITEDGEFKALQEWILETDGVSLMRVLSEKDVDPV        1355
tr|O35559|O35559_CRIGR              MTLQGIEQISKVYMHLPQTDNKKKIIITEDGEFKALQEWILETDGVSLMRVLSEKDVDPV        1355
tr|A0A2I3M9H2|A0A2I3M9H2_PAPAN      MTLQGIEQISKVYMHLPQTDNKKKIIITEDGEFKALQEWILETDGVSLMRVLSEKDVDPV        1354
tr|F7HB40|F7HB40_MACMU              MTLQGIEQISKVYMHLPQTDNKKKIIITEDGEFKALQEWILETDGVSLMRVLSEKDVDPV        1355
tr|A0A2K6RYW9|A0A2K6RYW9_SAIBB      MTLQGIEQISKVYMHLPQTDNKKKIIITEDGEFKALQEWILETDGVSLMRVLSEKDVDPV        1355
tr|W5N8Z6|W5N8Z6_LEPOC              MTLQGIEQISKVYMHLPQTDNKKKIIITEDGEFKALQEWILETDGVGLMRVLSEKDVDPV        1354
tr|I3JRW6|I3JRW6_ORENI              MTLQGIEQISKVYMHLPQTDNKKKIIITEDGEFKALQEWILETDGVSLMRVLSEKDVDPV        1353
tr|A0A0R4IMS9|A0A0R4IMS9_DANRE      MTLQGIEQISKVYMHLPQTDNKKKIIITEDGEFKALQEWILETDGVSLMRVLSEKDVDPV        1352
tr|A0A1A7X327|A0A1A7X327_9TELE      MTLQGIEQISKVYMHLPQTDNKKKIIITEDGEFKALQEWILETDGVSLMRVLSEKDVDPV        1353
tr|A0A1A8UKD7|A0A1A8UKD7_NOTFU      MTLQGIEQISKVYMHLPQTDNKKKIIITEDGEFKALQEWILETDGVSLMRVLSEKDVDPV        1353
tr|A0A1A8ER05|A0A1A8ER05_9TELE      MTLQGIEQISKVYMHLPQTDNKKKIIITEDGEFKALQEWILETDGVSLMRVLSEKDVDPV        1353
tr|A0A1A8DQ60|A0A1A8DQ60_9TELE      MTLQGIEQISKVYMHLPQTDNKKKIIITEDGEFKALQEWILETDGVSLMRVLSEKDVDPV        1353
tr|A0A1A8NSR8|A0A1A8NSR8_9TELE      MTLQGIEQISKVYMHLPQTDNKKKIIITEDGEFKALQEWILETDGVSLMRVLSEKDVDPV        1353
tr|A0A1W4YLM7|A0A1W4YLM7_9TELE      MTLQGIEQISKVYMHLPQTDNKKKIIITEDGEFKALQEWILETDGVGLMRVLSEKDVDPV        1353
tr|A0A1M8A6L7|A0A1M8A6L7_MALS4      IALKGVPGISKVFIVKQD--KSSRRFDPQTGEWDTIKEYVLETDGTNLKDVLAVDGVDVS        1339
sp|P04050|RPB1_YEAST                ITLRGVENIERVVMMKYD--RK---VPSPTGEYVKEPEWVLETDGVNLSEVMTVPGIDPT        1325
tr|A0A1B2J8C6|A0A1B2J8C6_PICPA      IALRGIPGISKVYMVKHK--VS---VPDESGEYKNEELWALETDGINLAEVMAVPGVDSS        1328
tr|F2QW17|F2QW17_KOMPC              IALRGIPGISKVYMVKHK--VS---VPDESGEYKNEELWALETDGINLAEVMAVPGVDSS        1328
tr|A3GID7|A3GID7_PICST              ISLRGIPGITRVFMMQHK--VN---TPDATGEFKQGKEWVLETDGVNLADVMAVPGVDSS        1327
tr|A0A1D8PUA6|A0A1D8PUA6_CANAL      ISLRGIPGITRVFMMQHK--VS---HPDETGEFKQGKEWVLETDGVNLADVMAVPGVDST        1327
tr|G8BEH9|G8BEH9_CANPC              ISLRGIPGITRVFMMQHK--VS---KPDETGEFKQGKEWVLETDGVNLADVMAVPGVDSA        1327
                                    ::*:*:  * :* :   .   .        **:     : ***** .*  *::  .:*

tr|A0A1U8DYN0|A0A1U8DYN0_ALLSI      RTTSNDIVEIFTVLGIEAVRKALERELYHVISFDGSYVNYRHLALLCDTMTSRGHLMAIT        1423
tr|A0A1L8H4P4|A0A1L8H4P4_XENLA      RTTSNDIVEIFTVLGIEAVRKALERELYHVISFDGSYVNYRHLALLCDTMTCRGHLMAIT        1413
tr|H9GLG5|H9GLG5_ANOCA              RTTSNDIVEIFTVLGIEAVRKALERELYHVISFDGSYVNYRHLALLCDTMTCRGHLMAIT        1414
tr|H2R1J6|H2R1J6_PANTR              RTTSNDIVEIFTVLGIEAVRKALERELYHVISFDGSYVNYRHLALLCDTMTCRGHLMAIT        1415
tr|G1MCZ1|G1MCZ1_AILME              RTTSNDIVEIFTVLGIEAVRKALERELYHVISFDGSYVNYRHLALLCDTMTCRGHLMAIT        1415
tr|O08847|O08847_MOUSE              RTTSNDIVEIFTVLGIEAVRKALERELYHVISFDGSYVNYRHLALLCDTMTCRGHLMAIT        1415
tr|S7PWZ6|S7PWZ6_MYOBR              RTTSNDIVEIFTVLGIEAVRKALERELYHVISFDGSYVNYRHLALLCDTMTCRGHLMAIT        1415
tr|D4A5A6|D4A5A6_RAT                RTTSNDIVEIFTVLGIEAVRKALERELYHVISFDGSYVNYRHLALLCDTMTCRGHLMAIT        1415
sp|P08775|RPB1_MOUSE                RTTSNDIVEIFTVLGIEAVRKALERELYHVISFDGSYVNYRHLALLCDTMTCRGHLMAIT        1415
sp|P24928|RPB1_HUMAN                RTTSNDIVEIFTVLGIEAVRKALERELYHVISFDGSYVNYRHLALLCDTMTCRGHLMAIT        1415
tr|A0A1S3EWL2|A0A1S3EWL2_DIPOR      RTTSNDIVEIFTVLGIEAVRKALERELYHVISFDGSYVNYRHLALLCDTMTCRGHLMAIT        1415
sp|P11414|RPB1_CRIGR                RTTSNDIVEIFTVLGIEAVRKALERELYHVISFDGSYVNYRHLALLCDTMTCRGHLMAIT        1415
tr|O35559|O35559_CRIGR              RTTSNDIVEIFTVLGIEAVRKALERELYHVISFDGSYVNYRHLALLCDTMTCRGHLMAIT        1415
tr|A0A2I3M9H2|A0A2I3M9H2_PAPAN      RTTSNDIVEIFTVLGIEAVRKALERELYHVISFDGSYVNYRHLALLCDTMTCRGHLMAIT        1414
tr|F7HB40|F7HB40_MACMU              RTTSNDIVEIFTVLGIEAVRKALERELYHVISFDGSYVNYRHLALLCDTMTCRGHLMAIT        1415
tr|A0A2K6RYW9|A0A2K6RYW9_SAIBB      RTTSNDIVEIFTVLGIEAVRKALERELYHVISFDGSYVNYRHLALLCDTMTCRGHLMAIT        1415
tr|W5N8Z6|W5N8Z6_LEPOC              RTTSNDIVEIFTVLGIEAVRKALERELYHVISFDGSYVNYRHLALLCDTMTCRGHLMAIT        1414
tr|I3JRW6|I3JRW6_ORENI              RTTSNDIVEIFTVLGIEAVRKALERELYHVISFDGSYVNYRHLALLCDTMTCRGHLMAIT        1413
tr|A0A0R4IMS9|A0A0R4IMS9_DANRE      RTTSNDIVEIFTVLGIEAVRKALERELYHVISFDGSYVNYRHLALLCDTMTCRGHLMAIT        1412
tr|A0A1A7X327|A0A1A7X327_9TELE      RTTSNDIVEIFTVLGIEAVRKALERELYHVISFDGSYVNYRHLALLCDTMTCRGHLMAIT        1413
tr|A0A1A8UKD7|A0A1A8UKD7_NOTFU      RTTSNDIVEIFTVLGIEAVRKALERELYHVISFDGSYVNYRHLALLCDTMTCRGHLMAIT        1413
tr|A0A1A8ER05|A0A1A8ER05_9TELE      RTTSNDIVEIFTVLGIEAVRKALERELYHVISFDGSYVNYRHLALLCDTMTCRGHLMAIT        1413
tr|A0A1A8DQ60|A0A1A8DQ60_9TELE      RTTSNDIVEIFTVLGIEAVRKALERELYHVISFDGSYVNYRHLALLCDTMTCRGHLMAIT        1413
tr|A0A1A8NSR8|A0A1A8NSR8_9TELE      RTTSNDIVEIFTVLGIEAVRKALERELYHVISFDGSYVNYRHLALLCDTMTCRGHLMAIT        1413
tr|A0A1W4YLM7|A0A1W4YLM7_9TELE      RTTSNDIVEIFTVLGIEAVRKALERELYHVISFDGSYVNYRHLALLCDTMTCRGHLMAIT        1413
tr|A0A1M8A6L7|A0A1M8A6L7_MALS4      RTISNNCVEVFRVFGIEAARGSLLKEVRNVIEFDGSYVNYRHLALLVDIMTSQGTLMAIT        1399
sp|P04050|RPB1_YEAST                RIYTNSFIDIMEVLGIEAGRAALYKEVYNVIASDGSYVNYRHMALLVDVMTTQGGLTSVT        1385
tr|A0A1B2J8C6|A0A1B2J8C6_PICPA      RTYSNSFVEILSVLGIEATRSSLYKEILNVIAFDGSYVNYRHMALLVDVMTSRGYLMAIT        1388
tr|F2QW17|F2QW17_KOMPC              RTYSNSFVEILSVLGIEATRSSLYKEILNVIAFDGSYVNYRHMALLVDVMTSRGYLMAIT        1388
tr|A3GID7|A3GID7_PICST              RTYSNNFIEILSVLGIEATRAALFKEILNVLSFDGSYVNYRHMALLVDVMTSRGHLMAIT        1387
tr|A0A1D8PUA6|A0A1D8PUA6_CANAL      RTYSNDFIEVLSVLGIEATRSSLYKEILNVIAFDGSYVNYRHMALLVDVMTSRGHLMAIT        1387
tr|G8BEH9|G8BEH9_CANPC              RIYSNDFIEILSVLGIEATRSALYKEILNVIAFDGSYVNYRHMALLVDVMTSRGHLMAIT        1387
                                    *  :*. :::: *:**** * :* :*: :*:  *********:*** * ** :* * ::*
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tr|A0A1U8DYN0|A0A1U8DYN0_ALLSI      RHGVNRQDTGPLMKCSFEETVDVLMEAAAHGESDPMKGVSENIMLGQLAPAGTGCFDLLL       1483
tr|A0A1L8H4P4|A0A1L8H4P4_XENLA      RHGVNRQDTGPLMKCSFEETVDVLMEAAAHGESDPMKGVSENIMLGQLAPAGTGCFDLLL       1473
tr|H9GLG5|H9GLG5_ANOCA              RHGVNRQDTGPLMKCSFEETVDVLMEAAAHGESDPMKGVSENIMLGQLAPAGTGCFDLLL       1474
tr|H2R1J6|H2R1J6_PANTR              RHGVNRQDTGPLMKCSFEETVDVLMEAAAHGESDPMKGVSENIMLGQLAPAGTGCFDLLL       1475
tr|G1MCZ1|G1MCZ1_AILME              RHGVNRQDTGPLMKCSFEETVDVLMEAAAHGESDPMKGVSENIMLGQLAPAGTGCFDLLL       1475
tr|O08847|O08847_MOUSE              RHGVNRQDTGPLMKCSFEETVDVLMEAAAHGESDPMKGVSENIMLGQLAPAGTGCFDLLL       1475
tr|S7PWZ6|S7PWZ6_MYOBR              RHGVNRQDTGPLMKCSFEETVDVLMEAAAHGESDPMKGVSENIMLGQLAPAGTGCFDLLL       1475
tr|D4A5A6|D4A5A6_RAT                RHGVNRQDTGPLMKCSFEETVDVLMEAAAHGESDPMKGVSENIMLGQLAPAGTGCFDLLL       1475
sp|P08775|RPB1_MOUSE                RHGVNRQDTGPLMKCSFEETVDVLMEAAAHGESDPMKGVSENIMLGQLAPAGTGCFDLLL       1475
sp|P24928|RPB1_HUMAN                RHGVNRQDTGPLMKCSFEETVDVLMEAAAHGESDPMKGVSENIMLGQLAPAGTGCFDLLL       1475
tr|A0A1S3EWL2|A0A1S3EWL2_DIPOR      RHGVNRQDTGPLMKCSFEETVDVLMEAAAHGESDPMKGVSENIMLGQLAPAGTGCFDLLL       1475
sp|P11414|RPB1_CRIGR                RHGVNRQDTGPLMKCSFEETVDVLMEAAAHGESDPMKGVSENIMLGQLAPAGTGCFDLLL       1475
tr|O35559|O35559_CRIGR              RHGVNRQDTGPLMKCSFEETVDVLMEAAAHGESDPMKGVSENIMLGQLAPAGTGCFDLLL       1475
tr|A0A2I3M9H2|A0A2I3M9H2_PAPAN      RHGVNRQDTGPLMKCSFEETVDVLMEAAAHGESDPMKGVSENIMLGQLAPAGTGCFDLLL       1474
tr|F7HB40|F7HB40_MACMU              RHGVNRQDTGPLMKCSFEETVDVLMEAAAHGESDPMKGVSENIMLGQLAPAGTGCFDLLL       1475
tr|A0A2K6RYW9|A0A2K6RYW9_SAIBB      RHGVNRQDTGPLMKCSFEETVDVLMEAAAHGESDPMKGVSENIMLGQLAPAGTGCFDLLL       1475
tr|W5N8Z6|W5N8Z6_LEPOC              RHGVNRQDTGPLMKCSFEETVDVLMEAAAHGESDPMKGVSENIMLGQLAPAGTGCFDLLL       1474
tr|I3JRW6|I3JRW6_ORENI              RHGINRQDTGPLMKCSFEETVDVLMEASSHGECDPMKGVSENIMLGQLAPAGTGCFDLLL       1473
tr|A0A0R4IMS9|A0A0R4IMS9_DANRE      RHGINRQDTGPLMKCSFEETVDVLMEASSHGESDPMKGVSENIMLGQLAPAGTGCFDLLL       1472
tr|A0A1A7X327|A0A1A7X327_9TELE      RHGINRQDTGPLMKCSFEETVDVLMEASSHGECDPMKGVSENIMLGQLAPAGTGCFDLLL       1473
tr|A0A1A8UKD7|A0A1A8UKD7_NOTFU      RHGINRQDTGPLMKCSFEETVDVLMEASSHGECDPMKGVSENIMLGQLAPAGTGCFDLLL       1473
tr|A0A1A8ER05|A0A1A8ER05_9TELE      RHGINRQDTGPLMKCSFEETVDVLMEASSHGECDPMKGVSENIMLGQLAPAGTGCFDLLL       1473
tr|A0A1A8DQ60|A0A1A8DQ60_9TELE      RHGINRQDTGPLMKCSFEETVDVLMEASSHGECDPMKGVSENIMLGQLAPAGTGCFDLLL       1473
tr|A0A1A8NSR8|A0A1A8NSR8_9TELE      RHGINRQDTGPLMKCSFEETVDVLMEASSHGECDPMKGVSENIMLGQLAPAGTGCFDLLL       1473
tr|A0A1W4YLM7|A0A1W4YLM7_9TELE      RHGINRQDTGPLMKCSFEETVDVLMEAASHGECDPMKGVSENIMLGQLAPAGTGCFDLLL       1473
tr|A0A1M8A6L7|A0A1M8A6L7_MALS4      RHGINRTSQGALMRCTFEETVEILMEAASMGDMDDCKGVGQNILLGQMAPMGTGAFDLNL       1459
sp|P04050|RPB1_YEAST                RHGFNRSNTGALMRCSFEETVEILFEAGASAELDDCRGVSENVILGQMAPIGTGAFDVMI       1445
tr|A0A1B2J8C6|A0A1B2J8C6_PICPA      RHGINRADTGALMRCSFEETVEILFEAGAAAELDDCRGVSENVMLGQLAPMGTGAFDVMI       1448
tr|F2QW17|F2QW17_KOMPC              RHGINRADTGALMRCSFEETVEILFEAGAAAELDDCRGVSENVMLGQLAPMGTGAFDVMI       1448
tr|A3GID7|A3GID7_PICST              RHGINRSDTGALMRCSFEETVEILLEAGASAELDDCRGISENVMLGQMAPLGTGAFDVML       1447
tr|A0A1D8PUA6|A0A1D8PUA6_CANAL      RHGINRSDTGALMRCSFEETVEILLDAAAAAELDDCKGISENVMLGQMAPLGTGSFDLMV       1447
tr|G8BEH9|G8BEH9_CANPC              RHGINRSDTGALMRCSFEETVEILLDAAAAAELDDCKGISENVMLGQMAPLGTGAFDVMV       1447
                                    ***.** . * **:*:*****::*::*.: .: *  :*:.:*::***:** ***.**: :

tr|A0A1U8DYN0|A0A1U8DYN0_ALLSI      SPNYSPTSPSYS---PTSPSYSPTTPSY--SPTSPSYSPTTPSYSPTT------------       1676
tr|A0A1L8H4P4|A0A1L8H4P4_XENLA      SPSYSPTSPNYS---PTSPSYSPTSPSY--SPTSPSYSPTSPSYSPTSPS----------       1668
tr|H9GLG5|H9GLG5_ANOCA              SPSYSPTSPNYS---PTSPSYSPTSPSY--SPTSPSYSPTSPSYSPTSPS----------       1669
tr|H2R1J6|H2R1J6_PANTR              SPSYSPTSPNYS---PTSPSYSPTSPSY--SPTSPSYSPTSPSYSPTSPS----------       1660
tr|G1MCZ1|G1MCZ1_AILME              SPSYSPTSPNYS---PTSPSYSPTSPSY--SPTSPSYSPTSPSYSPTSPS----------       1673
tr|O08847|O08847_MOUSE              SPSYSPTSPNYS---PTSPSYSPTSPSY--SPTSPSYSPTSPSYSPTSPS----------       1670
tr|S7PWZ6|S7PWZ6_MYOBR              SPSYSPTSPNYS---PTSPSYSPTSPSY--SPTSPSYSPTSPSYSPTSPS----------       1670
tr|D4A5A6|D4A5A6_RAT                SPSYSPTSPNYS---PTSPSYSPTSPSY--SPTSPSYSPTSPSYSPTSPS----------       1670
sp|P08775|RPB1_MOUSE                SPSYSPTSPNYS---PTSPSYSPTSPSY--SPTSPSYSPTSPSYSPTSPS----------       1670
sp|P24928|RPB1_HUMAN                SPSYSPTSPNYS---PTSPSYSPTSPSY--SPTSPSYSPTSPSYSPTSPS----------       1670
tr|A0A1S3EWL2|A0A1S3EWL2_DIPOR      SPSYSPTSPNYS---PTSPSYSPTSPSY--SPTSPSYSPTSPSYSPTSPS----------       1670
sp|P11414|RPB1_CRIGR                SPSYSPTSPNYS---PTSPSYSPTSPSY--SPTSPSYSPTSPSYSPTSPS----------       1670
tr|O35559|O35559_CRIGR              SPSYSPTSPNYS---PTSPSYSPTSPSY--SPTSPSYSPTSPSYSPTSPS----------       1670
tr|A0A2I3M9H2|A0A2I3M9H2_PAPAN      SPSYSPTSPNYS---PTSPSYSPTSPSY--SPTSPSYSPTSPSYSPTSPS----------       1631
tr|F7HB40|F7HB40_MACMU              SPSYSPTSPNYS---PTSPSYSPTSPSY--SPTSPSYSPTSPSYSPTSPS----------       1632
tr|A0A2K6RYW9|A0A2K6RYW9_SAIBB      SPSYSPTSPNYS---PTSPSYSPTSPSY--SPTSPSYSPTSPSYSPTSPS----------       1632
tr|W5N8Z6|W5N8Z6_LEPOC              LSLGG----------AMSPSYSPTSPAY--EPRSPG------------G----------       1662
tr|I3JRW6|I3JRW6_ORENI              SPSYSPTSPNYS---PTSPSYSPTSPSY--SPTSPSYSPTSPSYSPTSPS----------       1668
tr|A0A0R4IMS9|A0A0R4IMS9_DANRE      SPSYSPTSPNYS---PTSPSYSPTSPSY--SPTSPSYSPTSPSYSPTSPS----------       1667
tr|A0A1A7X327|A0A1A7X327_9TELE      SPSYSPTSPNYS---PTSPSYSPTSPSY--SPTSPSYSPTSPSYSPTSPS----------       1668
tr|A0A1A8UKD7|A0A1A8UKD7_NOTFU      SPSYSPTSPNYS---PTSPSYSPTSPSY--SPTSPSYSPTSPSYSPTSPS----------       1668
tr|A0A1A8ER05|A0A1A8ER05_9TELE      SPSYSPTSPNYS---PTSPSYSPTSPSY--SPTSPSYSPTSPSYSPTSPS----------       1668
tr|A0A1A8DQ60|A0A1A8DQ60_9TELE      SPSYSPTSPNYS---PTSPSYSPTSPSY--SPTSPSYSPTSPSYSPTSPS----------       1668
tr|A0A1A8NSR8|A0A1A8NSR8_9TELE      SPSYSPTSPNYS---PTSPSYSPTSPSY--SPTSPSYSPTSPSYSPTSPS----------       1668
tr|A0A1W4YLM7|A0A1W4YLM7_9TELE      SPSYSPTSPNYS---PTSPSYSPTSPSY--SPTSPSYSPTSPSYSPTSPS----------       1668
tr|A0A1M8A6L7|A0A1M8A6L7_MALS4      SPAMGAMSPWVGAAGATSPAYSPTSPRIFAEATSPAYSPTSPSYSPSSPMIGATHVRSAY       1633
sp|P04050|RPB1_YEAST                SPTYSP----------TSPAYSPTSPSY--SPTSPSYSPTSPSYSPTSPS----------       1583
tr|A0A1B2J8C6|A0A1B2J8C6_PICPA      SPGYSP----------TSPSYSPTSPSY--SPTSPSYSPTSPSYSPTSPS----------       1594
tr|F2QW17|F2QW17_KOMPC              SPGYSP----------TSPSYSPTSPSY--SPTSPSYSPTSPSYSPTSPS----------       1594
tr|A3GID7|A3GID7_PICST              SPSYSP----------TSPSYSPTSPAY--SPTSPSYSPTSPSYSPTSPS----------       1598
tr|A0A1D8PUA6|A0A1D8PUA6_CANAL      SPAYSP----------TSPSYAPTSPAY--SPTSPSYAPTSPAYSPTSPA----------       1598
tr|G8BEH9|G8BEH9_CANPC              SPSYSP----------TSPSYSPTSPSY--SPTSPSYSPTSPSYSPTSPS----------       1602
                                        .            **:*:**:*    .  **.
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tr|A0A1U8DYN0|A0A1U8DYN0_ALLSI      PTSPSYSPTSPSYSPTSPSYSPTSPNYSPTSPNYTPTSPSYSPTSPSYSPTSPNYTPTSP       1754
tr|A0A1L8H4P4|A0A1L8H4P4_XENLA      PTSPSYSPTSPSYSPTSPSYSPTSPSYSPTSPNYSPSSPNYTPTSPSYSPTSPSYSPTSP       1779
tr|H9GLG5|H9GLG5_ANOCA              PTSPSYSPTSPSYSPTSPSYSPTSPNYSPTSPNYTPTSPSYSPTSPSYSPTSPNYTPTSP       1780
tr|H2R1J6|H2R1J6_PANTR              PTSPSYSPTSPSYSPTSPSYSPTSPNYSPTSPNYTPTSPSYSPTSPSYSPTSPNYTPTSP       1771
tr|G1MCZ1|G1MCZ1_AILME              PTSPSYSPTSPSYSPTSPSYSPTSPNYSPTSPNYTPTSPSYSPTSPSYSPTSPNYTPTSP       1784
tr|O08847|O08847_MOUSE              PTSPSYSPTSPSYSPTSPSYSPTSPNYSPTSPNYTPTSPSYSPTSPSYSPTSPNYTPTSP       1781
tr|S7PWZ6|S7PWZ6_MYOBR              PTSPSYSPTSPSYSPTSPSYSPTSPNYSPTSPNYTPTSPSYSPTSPSYSPTSPNYTPTSP       1781
tr|D4A5A6|D4A5A6_RAT                PTSPSYSPTSPSYSPTSPSYSPTSPNYSPTSPNYTPTSPSYSPTSPSYSPTSPNYTPTSP       1781
sp|P08775|RPB1_MOUSE                PTSPSYSPTSPSYSPTSPSYSPTSPNYSPTSPNYTPTSPSYSPTSPSYSPTSPNYTPTSP       1781
sp|P24928|RPB1_HUMAN                PTSPSYSPTSPSYSPTSPSYSPTSPNYSPTSPNYTPTSPSYSPTSPSYSPTSPNYTPTSP       1781
tr|A0A1S3EWL2|A0A1S3EWL2_DIPOR      PTSPSYSPTSPSYSPTSPSYSPTSPNYSPTSPNYTPTSPSYSPTSPSYSPTSPNYTPTSP       1781
sp|P11414|RPB1_CRIGR                PTSPSYSPTSPSYSPTSPSYSPTSPNYSPTSPNYTPTSPSYSPTSPSYSPTSPNYTPTSP       1781
tr|O35559|O35559_CRIGR              PTSPSYSPTSPSYSPTSPSYSPTSPNYSPTSPNYTPTSPSYSPTSPSYSPTSPNYTPTSP       1781
tr|A0A2I3M9H2|A0A2I3M9H2_PAPAN      PTSPSYSPTSPSYSPTSPSYSPTSPNYSPTSPNYTPTSPSYSPTSPSYSPTSPNYTPTSP       1742
tr|F7HB40|F7HB40_MACMU              PTSPSYSPTSPSYSPTSPSYSPTSPNYSPTSPNYTPTSPSYSPTSPSYSPTSPNYTPTSP       1743
tr|A0A2K6RYW9|A0A2K6RYW9_SAIBB      PTSPSYSPTSPSYSPTSPSYSPTSPNYSPTSPNYTPTSPSYSPTSPSYSPTSPNYTPTSP       1743
tr|W5N8Z6|W5N8Z6_LEPOC              PTSPSYSPTSPSYSPTSPSYSPTSPSYSPTSPNYTPTSPSYSPTSPSYSPTSPNYTPTSP       1770
tr|I3JRW6|I3JRW6_ORENI              PTSPSYSPTSPSYSPTSPSYSPTSPSYSPTSPNYTPTSPSYSPTSPSYSPTSPSYSPTSP       1779
tr|A0A0R4IMS9|A0A0R4IMS9_DANRE      PTSPSYSPTSPSYSPTSPSYSPTSPSYSPTSPNYTPTSPSYSPTSPSYSPTSPSYSPTSP       1778
tr|A0A1A7X327|A0A1A7X327_9TELE      PTSPSYSPTSPSYSPTSPSYSPTSPSYSPTSPNYTPTSPSYSPTSPSYSPTSPSYSPTSP       1779
tr|A0A1A8UKD7|A0A1A8UKD7_NOTFU      PTSPSYSXTSPSYSPTSPSYSPTSPSYSPTSPNYTPTSPSYSPTSPSYSPTSPSYSPTSP       1779
tr|A0A1A8ER05|A0A1A8ER05_9TELE      PTSPSYSPTSPXXXXTSPSYSPTSPSYSPTSPNYTPTSPSYSPTSPSYSPTSPSYSPTSP       1779
tr|A0A1A8DQ60|A0A1A8DQ60_9TELE      PTSPSYSPTSPSYSPTSPSYSPTSPSYSPTSPNYTPTSPSYSPTSPSYSPTSPSYSPTSP       1772
tr|A0A1A8NSR8|A0A1A8NSR8_9TELE      PTSPSYSPTSPSYSPTSPSYSPTSPSYSPTSPNYTPTSPSYSPTSPSYSPTSPSYSPTSP       1772
tr|A0A1W4YLM7|A0A1W4YLM7_9TELE      PTSPSYSPTSPSYSPTSPSYSPTSPSYSPTSPNYTPTSPSYSPTSPSYSPTSPSYSPTSP       1779
tr|A0A1M8A6L7|A0A1M8A6L7_MALS4      PTSPQYSPTSPQYSPTSPQYSPTSPQYSPTSPQYSPTSPQYSPTSPQYSPTSPQYSPTSP       1753
sp|P04050|RPB1_YEAST                PTSPSYSPTSPSYSPTSPSYSPTSPSYSPTSPAYSPTSPSYSPTSPSYSPTSPSYSPTSP       1687
tr|A0A1B2J8C6|A0A1B2J8C6_PICPA      PTSPQYSPTSPQYSPTSPQYSPTSPQYSPTSPQYSPTSPQYSPTSPQYSPTSPQYSPTSP       1698
tr|F2QW17|F2QW17_KOMPC              PTSPQYSPTSPQYSPTSPQYSPTSPQYSPTSPQYSPTSPQYSPTSPQYSPTSPQYSPTSP       1698
tr|A3GID7|A3GID7_PICST              ----SYSPTSPSYSPTSPSYSPTSPSYSPTSPSYSPTSPSYSPTSPSYSPTSPQYSPTSP       1695
tr|A0A1D8PUA6|A0A1D8PUA6_CANAL      PTSPSYSPTSPAYSPTSPSYSPTSPSYSPTSPQYSPTSPSYSPTSPQYSPTSPSYSPTSP       1688
tr|G8BEH9|G8BEH9_CANPC              PTSPSYSPTSPSYSPTSPSYSPTSPSYSPTSPSYSPTSPSYSPTSPSYSPTSPSYSPTSP       1706
                                        .** ***    ***.******.****** *:*:**.*:****.******.*:****

tr|A0A1U8DYN0|A0A1U8DYN0_ALLSI      NYSPTSPSYSPTSPSYSPTSPSYSPSSPRYTPQSPTYTPSSPSYSPSSPSYSPTSPKYTP       1814
tr|A0A1L8H4P4|A0A1L8H4P4_XENLA      SYSPTSPNYSPTSPSYSPTSPSYSPSSPRYTPQSPSYTPSSPSYSPSSPSYSPTSPKYTP       1839
tr|H9GLG5|H9GLG5_ANOCA              NYSPTSPSYSPTSPSYSPTSPSYSPSSPRYTPQSPTYTPSSPSYSPSSPSYSPTSPKYTP       1840
tr|H2R1J6|H2R1J6_PANTR              NYSPTSPSYSPTSPSYSPTSPSYSPSSPRYTPQSPTYTPSSPSYSPSSPSYSPTSPKYTP       1831
tr|G1MCZ1|G1MCZ1_AILME              NYSPTSPSYSPTSPSYSPTSPSYSPSSPRYTPQSPTYTPSSPSYSPSSPSYSPTSPKYTP       1844
tr|O08847|O08847_MOUSE              NYSPTSPSYSPTSPSYSPTSPSYSPSSPRYTPQSPTYTPSSPSYSPSSPSYSPTSPKYTP       1841
tr|S7PWZ6|S7PWZ6_MYOBR              NYSPTSPSYSPTSPSYSPTSPSYSPSSPRYTPQSPTYTPSSPSYSPSSPSYSPTSPKYTP       1841
tr|D4A5A6|D4A5A6_RAT                NYSPTSPSYSPTSPSYSPTSPSYSPSSPRYTPQSPTYTPSSPSYSPSSPSYSPTSPKYTP       1841
sp|P08775|RPB1_MOUSE                NYSPTSPSYSPTSPSYSPTSPSYSPSSPRYTPQSPTYTPSSPSYSPSSPSYSPTSPKYTP       1841
sp|P24928|RPB1_HUMAN                NYSPTSPSYSPTSPSYSPTSPSYSPSSPRYTPQSPTYTPSSPSYSPSSPSYSPASPKYTP       1841
tr|A0A1S3EWL2|A0A1S3EWL2_DIPOR      NYSPTSPSYSPTSPSYSPTSPSYSPSSPRYTPQSPTYTPSSPSYSPSSPSYSPTSPKYTP       1841
sp|P11414|RPB1_CRIGR                NYSPTSPSYSPTSPSYSPTSPSYSPSSPRYTPQSPTYTPSSPSYSPSSPSYSPTSPKYTP       1841
tr|O35559|O35559_CRIGR              NYSPTSPSYSPTSPSYSPTSPSYSPSSPRYTPQSPTYTPSSPSYSPSSPSYSPTSPKYTP       1841
tr|A0A2I3M9H2|A0A2I3M9H2_PAPAN      NYSPTSPSYSPTSPSYSPTSPSYSPSSPRYTPQSPTYTPSSPSYSPSSPSYSPTSPKYTP       1802
tr|F7HB40|F7HB40_MACMU              NYSPTSPSYSPTSPSYSPTSPSYSPSSPRYTPQSPTYTPSSPSYSPSSPSYSPTSPKYTP       1803
tr|A0A2K6RYW9|A0A2K6RYW9_SAIBB      NYSPTSPSYSPTSPSYSPTSPSYSPSSPRYTPQSPTYTPSSPSYSPSSPSYSPTSPKYTP       1803
tr|W5N8Z6|W5N8Z6_LEPOC              NYSPTSPSYSPTSPSYSPTSPSYSSTSPRYTPQSPTYTPSSPSYSPSSPSYSPTSPKYTP       1830
tr|I3JRW6|I3JRW6_ORENI              NYTPTSPNYSPTSPSYSPTSPSYSPSSPRYTPQSPTYTPSSPSYSPSSPSYSPTSPKYTP       1839
tr|A0A0R4IMS9|A0A0R4IMS9_DANRE      NYTPTSPNYSPTSPSYSPTSPSYSPSSPRYTPQSPTYTPSSPSYSPSSPSYSPTSPKYTP       1838
tr|A0A1A7X327|A0A1A7X327_9TELE      NYTPTSPNYSPTSPSYSPTSPSYSPSSPRYTPQSPTYTPSSPSYSPSSPSYSPTSPKYTP       1839
tr|A0A1A8UKD7|A0A1A8UKD7_NOTFU      NYTPTSPNYSPTSPSYSPTSPSYSPSSPRYTPQSPTYTPSSPSYSPSSPSYSPTSPKYTP       1839
tr|A0A1A8ER05|A0A1A8ER05_9TELE      NYTPTSPNYSPTSPSYSPTSPSYSPSSPRYTPQSPTYTPSSPSYSPSSPSYSPTSPKYTP       1839
tr|A0A1A8DQ60|A0A1A8DQ60_9TELE      NYTPTSPNYSPTSPSYSPTSPSYSPSSPRYTPQSPTYTPSSPSYSPSSPSYSPTSPKYTP       1832
tr|A0A1A8NSR8|A0A1A8NSR8_9TELE      NYTPTSPNYSPTSPSYSPTSPSYSPSSPRYTPQSPTYTPSSPSYSPSSPSYSPTSPKYTP       1832
tr|A0A1W4YLM7|A0A1W4YLM7_9TELE      NYTPTSPNYSPTSPSYSPTSPSYSPSSPRYTPQSPTYTPSSPSYSPSSPSYSPTSPKYTP       1839
tr|A0A1M8A6L7|A0A1M8A6L7_MALS4      QYSPTSPQYSPTSPQYSPTSPQYSPGGAGGAAGAASPRRSRMT---SKPTWQR-------       1803
sp|P04050|RPB1_YEAST                SYSPTSPNYSPTSPSYSPTSPGYSPGSPAYSPKQDEQKHNENE---NSR-----------       1733
tr|A0A1B2J8C6|A0A1B2J8C6_PICPA      QYSPTSPQYSPTSPQYSPTSPQYSPASPQYSPSRHSPNGESKE---GE------------       1743
tr|F2QW17|F2QW17_KOMPC              QYSPTSPQYSPTSPQYSPTSPQYSPASPQYSPSRHSPNGESKE---GE------------       1743
tr|A3GID7|A3GID7_PICST              QYSPTSPSYSPTSPQYSPTSPQYSPGSPEYSPNSPKTEDKKNE---D-------------       1739
tr|A0A1D8PUA6|A0A1D8PUA6_CANAL      QYSPTSPQYSPTSPQYSPTSPQYSPGSPGYEPEPPKKDEN--------------------       1728
tr|G8BEH9|G8BEH9_CANPC              TYSPTSPQYSPTSPQYSPTSPSYSPGSPGYNPESPKKEEK--------------------       1746
                                     *:****.******.****** **  .            .
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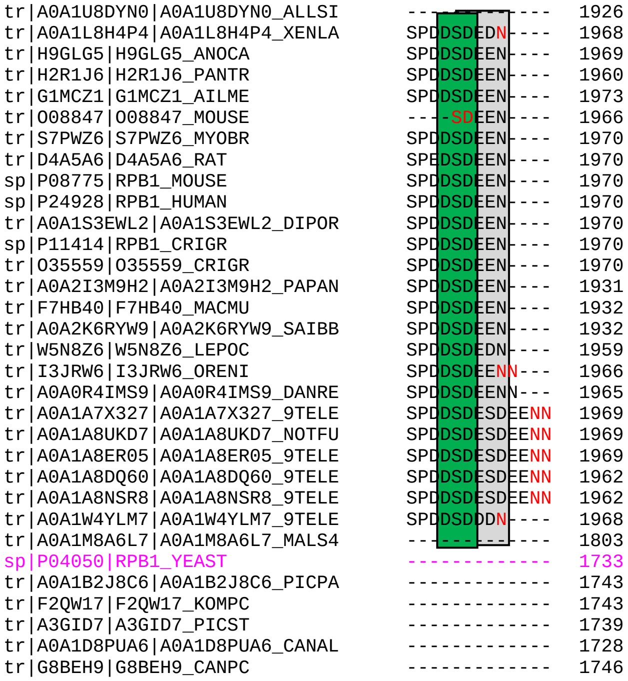

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tr|A0A1U8DYN0|A0A1U8DYN0_ALLSI      -------------  1926
tr|A0A1L8H4P4|A0A1L8H4P4_XENLA      SPDDSDEDN----  1968
tr|H9GLG5|H9GLG5_ANOCA              SPDDSDEEN----  1969
tr|H2R1J6|H2R1J6_PANTR              SPDDSDEEN----  1960
tr|G1MCZ1|G1MCZ1_AILME              SPDDSDEEN----  1973
tr|O08847|O08847_MOUSE              ----SDEEN----  1966
tr|S7PWZ6|S7PWZ6_MYOBR              SPDDSDEEN----  1970
tr|D4A5A6|D4A5A6_RAT                SPEDSDEEN----  1970
sp|P08775|RPB1_MOUSE                SPDDSDEEN----  1970
sp|P24928|RPB1_HUMAN                SPDDSDEEN----  1970
tr|A0A1S3EWL2|A0A1S3EWL2_DIPOR      SPDDSDEEN----  1970
sp|P11414|RPB1_CRIGR                SPDDSDEEN----  1970
tr|O35559|O35559_CRIGR              SPDDSDEEN----  1970
tr|A0A2I3M9H2|A0A2I3M9H2_PAPAN      SPDDSDEEN----  1931
tr|F7HB40|F7HB40_MACMU              SPDDSDEEN----  1932
tr|A0A2K6RYW9|A0A2K6RYW9_SAIBB      SPDDSDEEN----  1932
tr|W5N8Z6|W5N8Z6_LEPOC              SPDDSDEDN----  1959
tr|I3JRW6|I3JRW6_ORENI              SPDDSDEENN---  1966
tr|A0A0R4IMS9|A0A0R4IMS9_DANRE      SPDDSDEENN---  1965
tr|A0A1A7X327|A0A1A7X327_9TELE      SPDDSDESDEENN  1969
tr|A0A1A8UKD7|A0A1A8UKD7_NOTFU      SPDDSDESDEENN  1969
tr|A0A1A8ER05|A0A1A8ER05_9TELE      SPDDSDESDEENN  1969
tr|A0A1A8DQ60|A0A1A8DQ60_9TELE      SPDDSDESDEENN  1962
tr|A0A1A8NSR8|A0A1A8NSR8_9TELE      SPDDSDESDEENN  1962
tr|A0A1W4YLM7|A0A1W4YLM7_9TELE      SPDDSDDDN----  1968
tr|A0A1M8A6L7|A0A1M8A6L7_MALS4      -------------  1803
sp|P04050|RPB1_YEAST                -------------  1733
tr|A0A1B2J8C6|A0A1B2J8C6_PICPA      -------------  1743
tr|F2QW17|F2QW17_KOMPC              -------------  1743
tr|A3GID7|A3GID7_PICST              -------------  1739
tr|A0A1D8PUA6|A0A1D8PUA6_CANAL      -------------  1728
tr|G8BEH9|G8BEH9_CANPC              -------------  1746
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Fig. 4 MSA of the Rpb1 the elongation subunits of eukaryotic RNAP II

A0A1U8DYN0 _ALLSI *Alligator sinensis*
H9GLG5 _ANOCA *Anolis carolinensis*
G1MCZ1 _AILME *Ailuropoda melanoleuca*
S7PWZ6 _MYOBR *Myotis brandtii*
P08775 _MOUSE *Mus musculus*
A0A1S3EWL2 _DIPOR *Dipodomys ordii*
O35559 _CRIGR *Cricetulus griseus*
F7HB40| _MACMU *Macaca mulatta*
W5N8Z6 _LEPOC *Lepisosteus oculatus*
A0A0R4IMS9 _DANRE *Danio rerio*
A0A1A8UKD7 _NOTFU *Nothobranchius furzeri*
A0A1A8DQ60 _9TELE *Nothobranchius kadleci*
A0A1W4YLM7 _9TELE *Scleropages formosus*
P04050|RPB1_YEAST *Saccharomyces cerevisiae*
F2QW17 _KOMPC *Komagataella phaffii*
A0A1D8PUA6 _CANAL *Candida albicans*
A0A1L8H4P4 _XENLA *Xenopus laevis*
H2R1J6 _PANTR *Pan troglodytes*
O08847 _MOUSE *Mus musculus*
D4A5A6 _RAT *Rattus norvegicus*
P24928|RPB1_HUMAN *Homo sapiens*
P11414 _CRIGR *Cricetulus griseus*
A0A2I3M9H2 _PAPAN *Papio Anubis*
A0A2K6RYW9 _SAIBB *Saimiri boliviensis*
I3JRW6 _ORENI *Oreochromis niloticus*
A0A1A7X327 _9TELE *Aphyosemion striatum*
A0A1A8ER05 _9TELE *Nothobranchius korthausae*
A0A1A8NSR8 _9TELE *Nothobranchius rachovii*
A0A1M8A6L7 _MALS4 *Malassezia sympodialis*
A0A1B2J8C6 _PICPA *Komagataella pastoris*
A3GID7 _PICST *Scheffersomyces stipitis*
G8BEH9 _CANPC *Candida parapsilosis*

7. Mix and Match analysis of eubacterial and eukaryotic initiation and elongation subunits

For this analysis a small number of initiation and elongation subunits of eubacterial and eukaryotic MSU RNAPs were subjected to MSA with ClustalW Omega programme and presented in Figs. 5 and 6. For eubacteria, *E. coli* MSU RNAP and for eukaryote, *S. cerevisiae* MSU RNAP II sequences were used as standards. Only highly conserved regions are shown in the figures.

7.1 Mix and Match analysis of the *E. coli* (β) and *S. cerevisiae* (Rpb2) initiation subunits

Figure 5 shows the mix and match analysis of the initiation subunits from pro- and eukaryotic MSU RNAPs. The eukaryotic sequences are shown in red. The active site regions are highlighted in yellow the representative sequences are highlighted in yellow. There are a good number of sequences aligning in both. Significant among them are -FI/VINGS/TEK/RVL/II/VA/SQ- (~200), IETPE (~500) preceding this sequence a WG in eukaryotic and YG in prokaryotic sequences, -ASI/LIPF-, the metal ion binding regions -GYNQ/FEDS- (~800), -LDD/ED/SGL/I- (~850); -GDKF/MAS/GRHGXKG- (~1000), HLVDDKI/MHAR (~1050), RFGEME (~1100). The catalytic regions are matching but among themselves only and there is no complete consensus among them, i.e., they are located at different regions. However, the metal binding motifs are aligning in both the initiation subunits suggesting the metal binding regions are preserved as a domain and did not diverge much during evolution. The prokaryotic active site region is placed around 540-555/1342 amino acids whereas eukaryotic active site region is placed around 851-866/1224 amino acids. The notable difference in the eukaryotic template binding pair sis KG in lower eukaryotes like human and in lower eukaryotes it uses YG like yeasts. The eukaryotes follow two very similar ending sequences at the C-terminal end as –ACKLLFQELMSMSIAPRMMSV- (~1150) and –AAKLLFQELMAMNITPRLYT- (~1200) (deviating amino acids are shown in red) and the prokaryotes follow an altogether different consensus end sequence as –SFNVLLKEIRSL- (~1280). Thus, the eukaryotic and prokaryotic ending sequences are different and their significance is not clear now.

CLUSTAL O(1.2.4): Mix and Match analysis of eukaryotic Rpb2 and eubacterial β initiation subunits 5

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sp|P30876|RPB2_HUMAN                LLNGLTDRDLCELNECPLDPGGYFIINGSEKVLIAQEKMATNTVYVF-AKKD-SKYAYTG       219
tr|G3V8Y5|G3V8Y5_RAT                LLNGLTDRDLCELNECPLDPGGYFIINGSEKVLIAQEKMATNTVYVF-AKKD-SKYAYTG       219
tr|A0A250Y753|A0A250Y753_CASCN      LLNGLTDRDLCELNECPLDPGGYFIINGSEKVLIAQEKMATNTVYVF-AKKD-SKYAYTG       219
tr|A0A1U7R4C7|A0A1U7R4C7_MESAU      LLNGLTDRDLCELNECPLDPGGYFIINGSEKVLIAQEKMATNTVYVF-AKKD-SKYAYTG       219
tr|A0A286XIQ9|A0A286XIQ9_CAVPO      LLNGLTDRDLCELNECPLDPGGYFIINGSEKVLIAQEKMATNTVYVF-AKKD-SKYAYTG       219
tr|I3M351|I3M351_ICTTR              LLNGLTDRDLCELNECPLDPGGYFIINGSEKVLIAQEKMATNTVYVF-AKKD-SKYAYTG       219
tr|G7P5R6|G7P5R6_MACFA              LLNGLTDRDLCELNECPLDPGGYFIINGSEKVLIAQEKMATNTVYVF-AKKD-SKYAYTG       219
tr|H2QPI8|H2QPI8_PANTR              LLNGLTDRDLCELNECPLDPGGYFIINGSEKVLIAQEKMATNTVYVF-AKKD-SKYAYTG       219
tr|A0A1U7V0T5|A0A1U7V0T5_TARSY      LLNGLTDRDLCELNECPLDPGGYFIINGSEKVLIAQEKMATNTVYVF-AKKD-SKYAYTG       219
tr|A0A1S2ZSL2|A0A1S2ZSL2_ERIEU      LLNGLTDRDLCELNECPLDPGGYFIINGSEKVLIAQEKMATNTVYVF-AKKD-SKYAYTG       219
tr|A0A0D9QYL1|A0A0D9QYL1_CHLSB      LLNGLTDRDLCELNECPLDPGGYFIINGSEKVLIAQEKMATNTVYVF-AKKD-SKYAYTG       212
tr|A0A2K5ZNR7|A0A2K5ZNR7_MANLE      LLNGLTDRDLCELNECPLDPGGYFIINGSEKVLIAQEKMATNTVYVF-AKKD-SKYAYTG       212
tr|A0A2I2ZIU3|A0A2I2ZIU3_GORGO      LLNGLTDRDLCELNECPLDPGGYFIINGSEKVLIAQEKMATNTVYVF-AKKD-SKYAYTG       219
tr|A0A1D5QGA5|A0A1D5QGA5_MACMU      LLNGLTDRDLCELNECPLDPGGYFIINGSEKVLIAQEKMATNTVYVF-AKKD-SKYAYTG       219
tr|A0A2J8S2N1|A0A2J8S2N1_PONAB      LLNGLTDRDLCELNECPLDPGGYFIINGSEKVLIAQEKMATNTVYVF-AKKD-SKYAYTG       219
tr|A0A2K5K5J5|A0A2K5K5J5_COLAP      LLNGLTDRDLCELNECPLDPGGYFIINGSEKVLIAQEKMATNTVYVF-AKKD-SKYAYTG       219
tr|A0A2J8PEW7|A0A2J8PEW7_PANTR      LLNGLTDRDLCELNECPLDPGGYFIINGSEKVLIAQEKMATNTVYVF-AKKD-SKYAYTG       212
tr|A0A2K5CY83|A0A2K5CY83_AOTNA      LLNGLTDRDLCELNECPLDPGGYFIINGSEKVLIAQEKMATNTVYVF-AKKD-SKYAYTG       219
tr|A0A096NEY4|A0A096NEY4_PAPAN      LLNGLTDRDLCELNECPLDPGGYFIINGSEKVLIAQEKMATNTVYVF-AKKD-SKYAYTG       219
tr|C9J2Y9|C9J2Y9_HUMAN              LLNGLTDRDLCELNECPLDPGGYFIINGSEKVLIAQEKMATNTVYVF-AKKD-SKYAYTG       212
tr|G8BY61|G8BY61_TETPH              YLSDATESDLYKLKECPFDMGGYFIINGSEKVLIAQERSAGNIVQVF-KKAAPSPISHVA       236
tr|A0A1X7QYA1|A0A1X7QYA1_9SACH      YLSDATESDLYKLKECPFDMGGYFIINGSEKVLIAQERSAGNIVQVF-KKAAPSPISHIA       234
tr|J7RV95|J7RV95_KAZNA              YLSDATESDLYKLKECPFDMGGYFIINGSEKVLIAQERSAGNIVQVF-KKAAPSPISHVA       234
tr|H2AVJ8|H2AVJ8_KAZAF              YLSDATESDLYKLKECPFDMGGYFIINGSEKVLIAQERSAGNIVQVF-KKAAPSPISHVA       234
sp|Q6FLD5|RPB2_CANGA                YLSDATESDLYKLKECPFDMGGYFIINGSEKVLIAQERSAGNIVQVF-KKAAPSPISHVA       236
sp|P08518|RPB2_YEAST                YLSEATESDLYKLKECPFDMGGYFIINGSEKVLIAQERSAGNIVQVF-KKAAPSPISHVA       238
tr|A0A0L8VHA5|A0A0L8VHA5_9SACH      YLSEATESDLYKLKECPFDMGGYFIINGSEKVLIAQERSAGNIVQVF-KKAAPSPISHVA       238
tr|A0A0L8RB33|A0A0L8RB33_SACEU      YLSEATESDLYKLKECPFDMGGYFIINGSEKVLIAQERSAGNIVQVF-KKAAPSPISHVA       238
tr|G0VJ71|G0VJ71_NAUCC              YLSDATESDLYKLKECPFDMGGYFIINGSEKVLIAQERSAGNIVQVF-KKAAPSPISHVA       238
tr|G8ZM49|G8ZM49_TORDC              YLSDATELDLYKLKECPFDMGGYFIINGSEKVLIAQERSAGNIVQVF-KKAAPSPISHVA       236
tr|A0A1Q3A090|A0A1Q3A090_ZYGRO      YLSDATESDLYKLKECPFDMGGYFIINGSEKVLIAQERSAGNIVQVF-KKAAPSPISHVA       238
tr|A0A0N7IS35|A0A0N7IS35_9SACH      YLSDATESDLYKLKECPFDMGGYFIINGSEKVLIAQERSAGNIVQVF-KKAAPSPISHVA       236
tr|A0A212MG88|A0A212MG88_ZYGBA      YLSDATESDLYKLKECPFDMGGYFIINGSEKVLIAQERSAGNIVQVF-KKAAPSPISHVA       237
tr|A0A1S7HHE1|A0A1S7HHE1_9SACH      YLSDATESDLYKLKECPFDMGGYFIINGSEKVLIAQERSAGNIVQVF-KKAAPSPISHVA       237
tr|S6ESB4|S6ESB4_ZYGB2              YLSDATESDLYKLKECPFDMGGYFIINGSEKVLIAQERSAGNIVQVF-KKAAPSPISHVA       237
tr|B6K5Q5|B6K5Q5_SCHJY              ILNGVSDSELYDLNECPYDQGGYFIINGSEKVIIAQERSAANIVQVF-RKAAPSPIAYVA       223
sp|Q02061|RPB2_SCHPO                ILNGVSDSELYDLNECPYDQGGYFIINGSEKVIIAQERSAANIVQVF-KKAAPSPIAYVA       223
tr|S9R8U4|S9R8U4_SCHOY              ILNGVSDAELYDLNECPYDQGGYFIINGSEKVIIAQERSAANIVQVF-RKAAPSPIALVA       223
tr|S9W8C6|S9W8C6_SCHCR              ILNGVSDAELYDLNECPYDQGGYFIINGSEKVIIAQERSAANIVQVF-RKAAPSPVAYVA       223
sp|Q8RQE9|RPOB_THET8                --------------------DGSFIINGADRVIVSQIHRSPGVYFTPDPAR---PGRYIA       160
ASR51304.1                          --------------------NGTFVINGTERVIVSQMHRSPGVLFDHDRGKTHSSGKYLF       184
OXR47929.1                          --------------------TGSFVINGTERVIVSQLHRSPGVFFEHDRGKTHSSGKLLF       176
WP_093971860.1                      --------------------TGSFVINGTERVIVSQLHRSPGVFFEHDRGKTHSSGKLLF       176
sp|Q2NWR6|RPOB_SODGM                --------------------NGTFVINGTERVIVSQLHRSPGVFFDSDKGKTHSSGKVLY       172
sp|B4EYU9|RPOB_PROMH                --------------------NGTFVINGTERVIVSQLHRSPGVFFDSDKGKTHSSGKVLY       172
sp|A7FNI3|RPOB_YERP3                --------------------NGTFVINGTERVIVSQLHRSPGVFFDSDKGKTHSSGKVLY       172
sp|Q1C1U1|RPOB_YERPA                --------------------NGTFVINGTERVIVSQLHRSPGVFFDSDKGKTHSSGKVLY       172
sp|B2K113|RPOB_YERPB                --------------------NGTFVINGTERVIVSQLHRSPGVFFDSDKGKTHSSGKVLY       172
sp|A8G8E7|RPOB_SERP5                --------------------NGTFVINGTERVIVSQLHRSPGVFFDSDKGKTHSSGKVLY       172
sp|Q6DAN0|RPOB_PECAS                --------------------NGTFVINGTERVIVSQLHRSPGVFFDSDKGKTHSSGKVLY       172
sp|C6DHR5|RPOB_PECCP                --------------------NGTFVINGTERVIVSQLHRSPGVFFDSDKGKTHSSGKVLY       172
sp|Q7N9A4|RPOB_PHOLL                --------------------NGTFVINGTERVIVSQLHRSPGVFFDSDKGKTHSSGKVLY       172
sp|C5BHE3|RPOB_EDWI9                --------------------NGTFVINGTERVIVSQLHRSPGVFFDSDKGKTHSSGKVLY       172
sp|A7MQQ9|RPOB_CROS8                --------------------NGTFVINGTERVIVSQLHRSPGVFFDSDKGKTHSSGKVLY       172
sp|B5XYF5|RPOB_KLEP3                --------------------NGTFVINGTERVIVSQLHRSPGVFFDSDKGKTHSSGKVLY       172
sp|P0A8V2|RPOB_ECOLI                --------------------NGTFVINGTERVIVSQLHRSPGVFFDSDKGKTHSSGKVLY       172
sp|C5A0S7|RPOB_ECOBW                --------------------NGTFVINGTERVIVSQLHRSPGVFFDSDKGKTHSSGKVLY       172
sp|Q31U10|RPOB_SHIBS                --------------------NGTFVINGTERVIVSQLHRSPGVFFDSDKGKTHSSGKVLY       172
sp|Q32AF9|RPOB_SHIDS                --------------------NGTFVINGTERVIVSQLHRSPGVFFDSDKGKTHSSGKVLY       172
sp|A8AKT9|RPOB_CITK8                --------------------NGTFVINGTERVIVSQLHRSPGVFFDSDKGKTHSSGKVLY       172
sp|B5RFK1|RPOB_SALG2                --------------------NGTFVINGTERVIVSQLHRSPGVFFDSDKGKTHSSGKVLY       172
sp|B5BJQ3|RPOB_SALPK                --------------------NGTFVINGTERVIVSQLHRSPGVFFDSDKGKTHSSGKVLY       172
sp|B4T0Y9|RPOB_SALNS                --------------------NGTFVINGTERVIVSQLHRSPGVFFDSDKGKTHSSGKVLY       172
sp|P06173|RPOB_SALTY                --------------------NGTFVINGTERVIVSQLHRSPGVFFDSDKGKTHSSGKVLY       172
                                                         * *:***:::*:::* : : .

sp|P30876|RPB2_HUMAN                YSLATGNWGDQKKAHQARAGVSQVLNRLTFASTLSHLRRLNSP----IGRDGKLAKPRQL       501
tr|G3V8Y5|G3V8Y5_RAT                YSLATGNWGDQKKAHQARAGVSQVLNRLTFASTLSHLRRLNSP----IGRDGKLAKPRQL       501
tr|A0A250Y753|A0A250Y753_CASCN      YSLATGNWGDQKKAHQARAGVSQVLNRLTFASTLSHLRRLNSP----IGRDGKLAKPRQL       501
tr|A0A1U7R4C7|A0A1U7R4C7_MESAU      YSLATGNWGDQKKAHQARAGVSQVLNRLTFASTLSHLRRLNSP----IGRDGKLAKPRQL       501
tr|A0A286XIQ9|A0A286XIQ9_CAVPO      YSLATGNWGDQKKAHQARAGVSQVLNRLTFASTLSHLRRLNSP----IGRDGKLAKPRQL       501
tr|I3M351|I3M351_ICTTR              YSLATGNWGDQKKAHQARAGVSQVLNRLTFASTLSHLRRLNSP----IGRDGKLAKPRQL       501
tr|G7P5R6|G7P5R6_MACFA              YSLATGNWGDQKKAHQARAGVSQVLNRLTFASTLSHLRRLNSP----IGRDGKLAKPRQL       501
tr|H2QPI8|H2QPI8_PANTR              YSLATGNWGDQKKAHQARAGVSQVLNRLTFASTLSHLRRLNSP----IGRDGKLAKPRQL       501
tr|A0A1U7V0T5|A0A1U7V0T5_TARSY      YSLATGNWGDQKKAHQARAGVSQVLNRLTFASTLSHLRRLNSP----IGRDGKLAKPRQL       501
tr|A0A1S2ZSL2|A0A1S2ZSL2_ERIEU      YSLATGNWGDQKKAHQARAGVSQVLNRLTFASTLSHLRRLNSP----IGRDGKLAKPRQL       501
tr|A0A0D9QYL1|A0A0D9QYL1_CHLSB      YSLATGNWGDQKKAHQARAGVSQVLNRLTFASTLSHLRRLNSP----IGRDGKLAKPRQL       494
tr|A0A2K5ZNR7|A0A2K5ZNR7_MANLE      YSLATGNWGDQKKAHQARAGVSQVLNRLTFASTLSHLRRLNSP----IGRDGKLAKPRQL       494
tr|A0A2I2ZIU3|A0A2I2ZIU3_GORGO      YSLATGNWGDQKKAHQARAGVSQVLNRLTFASTLSHLRRLNSP----IGRDGKLAKPRQL       501
tr|A0A1D5QGA5|A0A1D5QGA5_MACMU      YSLATGNWGDQKKAHQARAGVSQVLNRLTFASTLSHLRRLNSP----IGRDGKLAKPRQL       501
tr|A0A2J8S2N1|A0A2J8S2N1_PONAB      YSLATGNWGDQKKAHQARAGVSQVLNRLTFASTLSHLRRLNSP----IGRDGKLAKPRQL       501
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tr|A0A2K5K5J5|A0A2K5K5J5_COLAP      YSLATGNWGDQKKAHQARAGVSQVLNRLTFASTLSHLRRLNSP----IGRDGKLAKPRQL       501
tr|A0A2J8PEW7|A0A2J8PEW7_PANTR      YSLATGNWGDQKKAHQARAGVSQVLNRLTFASTLSHLRRLNSP----IGRDGKLAKPRQL       494
tr|A0A2K5CY83|A0A2K5CY83_AOTNA      YSLATGNWGDQKKAHQARAGVSQVLNRLTFASTLSHLRRLNSP----IGRDGKLAKPRQL       501
tr|A0A096NEY4|A0A096NEY4_PAPAN      YSLATGNWGDQKKAHQARAGVSQVLNRLTFASTLSHLRRLNSP----IGRDGKLAKPRQL       501
tr|C9J2Y9|C9J2Y9_HUMAN              YSLATGNWGDQKKAHQARAGVSQVLNRLTFASTLSHLRRLNSP----IGRDGKLAKPRQL       494
tr|G8BY61|G8BY61_TETPH              YALATGNWGEQKKAMTSRAGVSQVLNRYTYSSTLSHLRRTNTP----IGRDGKLAKPRQL       512
tr|A0A1X7QYA1|A0A1X7QYA1_9SACH      YALATGNWGEQKKAMSSRAGVSQVLNRYTYSSTLSHLRRTNTP----IGRDGKLAKPRQL       510
tr|J7RV95|J7RV95_KAZNA              YALATGNWGEQKKAMSSRAGVSQVLNRYTYSSTLSHLRRTNTP----IGRDGKLAKPRQL       510
tr|H2AVJ8|H2AVJ8_KAZAF              YALATGNWGEQKKAMSSRAGVSQVLNRYTYSSTLSHLRRTNTP----IGRDGKLAKPRQL       510
sp|Q6FLD5|RPB2_CANGA                YALATGNWGEQKKAMSSRAGVSQVLNRYTYSSTLSHLRRTNTP----IGRDGKLAKPRQL       512
sp|P08518|RPB2_YEAST                YALATGNWGEQKKAMSSRAGVSQVLNRYTYSSTLSHLRRTNTP----IGRDGKLAKPRQL       514
tr|A0A0L8VHA5|A0A0L8VHA5_9SACH      YALATGNWGEQKKAMSSRAGVSQVLNRYTYSSTLSHLRRTNTP----IGRDGKLAKPRQL       514
tr|A0A0L8RB33|A0A0L8RB33_SACEU      YALATGNWGEQKKAMSSRAGVSQVLNRYTYSSTLSHLRRTNTP----IGRDGKLAKPRQL       514
tr|G0VJ71|G0VJ71_NAUCC              YALATGNWGEQKKAMSSRAGVSQVLNRYTYSSTLSHLRRTNTP----IGRDGKLAKPRQL       514
tr|G8ZM49|G8ZM49_TORDC              YALATGNWGEQKKAMSSRAGVSQVLNRYTYSSTLSHLRRTNTP----IGRDGKLAKPRQL       512
tr|A0A1Q3A090|A0A1Q3A090_ZYGRO      YALATGNWGEQKKAMSSRAGVSQVLNRYTYSSTLSHLRRTNTP----IGRDGKLAKPRQL       514
tr|A0A0N7IS35|A0A0N7IS35_9SACH      YALATGNWGEQKKAMSSRAGVSQVLNRYTYSSTLSHLRRTNTP----IGRDGKLAKPRQL       512
tr|A0A212MG88|A0A212MG88_ZYGBA      YALATGNWGEQKKAMSSRAGVSQVLNRYTYSSTLSHLRRTNTP----IGRDGKLAKPRQL       513
tr|A0A1S7HHE1|A0A1S7HHE1_9SACH      YALATGNWGEQKKAMSSRAGVSQVLNRYTYSSTLSHLRRTNTP----IGRDGKLAKPRQL       513
tr|S6ESB4|S6ESB4_ZYGB2              YALATGNWGEQKKAMSSRAGVSQVLNRYTYSSTLSHLRRTNTP----IGRDGKLAKPRQL       513
tr|B6K5Q5|B6K5Q5_SCHJY              YSLATGNWGDQKRGLANRVGVSQVLNRYTFASTLSHLRRTNTP----IGRDGKLAKPRQL       500
sp|Q02061|RPB2_SCHPO                YSLATGNWGDQKRSMVNRVGVSQVLNRYTFASTLSHLRRTNTP----IGRDGKLAKPRQL       500
tr|S9R8U4|S9R8U4_SCHOY              YSLATGNWGDQKRSMMNRVGVSQVLNRYTFASTLSHLRRTNTP----IGRDGKLAKPRQL       500
tr|S9W8C6|S9W8C6_SCHCR              YSLATGNWGDQKRSMMNRVGVSQVLNRYTFASTLSHLRRTNTP----IGRDGKLAKPRQL       500x8
sp|Q8RQE9|RPOB_THET8                -------------EFFSRSQLSQFKDETNPLSSLRHKRRISALGPGGLTRERAGFDVRDV       430x8
ASR51304.1                          -------------EFFGSSQLSQFMDQTNPLAEVTHKRRVSALGPGGLTRERAGFEVRDV       564
OXR47929.1                          -------------EFFGSSQLSQFMDQTNPLSEITHKRRVSALGPGGLTRERAGFEVRDV       556
WP_093971860.1                      -------------EFFGSSQLSQFMDQTNPLSEITHKRRVSALGPGGLTRERAGFEVRDV       556
sp|Q2NWR6|RPOB_SODGM                -------------EFFGSSQLSQFMDQNNPLSEITHKRRISALGPGGLTRERAGFEVRDV       550
sp|B4EYU9|RPOB_PROMH                -------------EFFGSSQLSQFMDQNNPLSEITHKRRISALGPGGLTRERAGFEVRDV       550
sp|A7FNI3|RPOB_YERP3                -------------EFFGSSQLSQFMDQNNPLSEITHKRRISALGPGGLTRERAGFEVRDV       550
sp|Q1C1U1|RPOB_YERPA                -------------EFFGSSQLSQFMDQNNPLSEITHKRRISALGPGGLTRERAGFEVRDV       550
sp|B2K113|RPOB_YERPB                -------------EFFGSSQLSQFMDQNNPLSEITHKRRISALGPGGLTRERAGFEVRDV       550
sp|A8G8E7|RPOB_SERP5                -------------EFFGSSQLSQFMDQNNPLSEITHKRRISALGPGGLTRERAGFEVRDV       550
sp|Q6DAN0|RPOB_PECAS                -------------EFFGSSQLSQFMDQNNPLSEITHKRRISALGPGGLTRERAGFEVRDV       550
sp|C6DHR5|RPOB_PECCP                -------------EFFGSSQLSQFMDQNNPLSEITHKRRISALGPGGLTRERAGFEVRDV       550
sp|Q7N9A4|RPOB_PHOLL                -------------EFFGSSQLSQFMDQNNPLSEITHKRRISALGPGGLTRERAGFEVRDV       550
sp|C5BHE3|RPOB_EDWI9                -------------EFFGSSQLSQFMDQNNPLSEITHKRRISALGPGGLTRERAGFEVRDV       550
sp|A7MQQ9|RPOB_CROS8                -------------EFFGSSQLSQFMDQNNPLSEITHKRRISALGPGGLTRERAGFEVRDV       550
sp|B5XYF5|RPOB_KLEP3                -------------EFFGSSQLSQFMDQNNPLSEITHKRRISALGPGGLTRERAGFEVRDV       550
sp|P0A8V2|RPOB_ECOLI                -------------EFFGSSQLSQFMDQNNPLSEITHKRRISALGPGGLTRERAGFEVRDV       550
sp|C5A0S7|RPOB_ECOBW                -------------EFFGSSQLSQFMDQNNPLSEITHKRRISALGPGGLTRERAGFEVRDV       550
sp|Q31U10|RPOB_SHIBS                -------------EFFGSSQLSQFMDQNNPLSEITHKRRISALGPGGLTRERAGFEVRDV       550
sp|Q32AF9|RPOB_SHIDS                -------------EFFGSSQLSQFMDQNNPLSEITHKRRISALGPGGLTRERAGFEVRDV       550
sp|A8AKT9|RPOB_CITK8                -------------EFFGSSQLSQFMDQNNPLSEITHKRRISALGPGGLTRERAGFEVRDV       550
sp|B5RFK1|RPOB_SALG2                -------------EFFGSSQLSQFMDQNNPLSEITHKRRISALGPGGLTRERAGFEVRDV       550
sp|B5BJQ3|RPOB_SALPK                -------------EFFGSSQLSQFMDQNNPLSEITHKRRISALGPGGLTRERAGFEVRDV       550
sp|B4T0Y9|RPOB_SALNS                -------------EFFGSSQLSQFMDQNNPLSEITHKRRISALGPGGLTRERAGFEVRDV       550
sp|P06173|RPOB_SALTY                -------------EFFGSSQLSQFMDQNNPLSEITHKRRISALGPGGLTRERAGFEVRDV       550
                                                        :**. :. .  : : * ** .:     : *:    . *::

sp|P30876|RPB2_HUMAN                HNTLWGMVCPAETPEGHAVGLVKNLALMAYISVGSQPSPILEFLEEWSMENLEEISPAAI       561
tr|G3V8Y5|G3V8Y5_RAT                HNTLWGMVCPAETPEGHAVGLVKNLALMAYISVGSQPSPILEFLEEWSMENLEEISPAAI       561
tr|A0A250Y753|A0A250Y753_CASCN      HNTLWGMVCPAETPEGHAVGLVKNLALMAYISVGSQPSPILEFLEEWSMENLEEISPAAI       561
tr|A0A1U7R4C7|A0A1U7R4C7_MESAU      HNTLWGMVCPAETPEGHAVGLVKNLALMAYISVGSQPSPILEFLEEWSMENLEEISPAAI       561
tr|A0A286XIQ9|A0A286XIQ9_CAVPO      HNTLWGMVCPAETPEGHAVGLVKNLALMAYISVGSQPSPILEFLEEWSMENLEEISPAAI       561
tr|I3M351|I3M351_ICTTR              HNTLWGMVCPAETPEGHAVGLVKNLALMAYISVGSQPSPILEFLEEWSMENLEEISPAAI       561
tr|G7P5R6|G7P5R6_MACFA              HNTLWGMVCPAETPEGHAVGLVKNLALMAYISVGSQPSPILEFLEEWSMENLEEISPAAI       561
tr|H2QPI8|H2QPI8_PANTR              HNTLWGMVCPAETPEGHAVGLVKNLALMAYISVGSQPSPILEFLEEWSMENLEEISPAAI       561
tr|A0A1U7V0T5|A0A1U7V0T5_TARSY      HNTLWGMVCPAETPEGHAVGLVKNLALMAYISVGSQPSPILEFLEEWSMENLEEISPAAI       561
tr|A0A1S2ZSL2|A0A1S2ZSL2_ERIEU      HNTLWGMVCPAETPEGHAVGLVKNLALMAYISVGSQPSPILEFLEEWSMENLEEISPAAI       561
tr|A0A0D9QYL1|A0A0D9QYL1_CHLSB      HNTLWGMVCPAETPEGHAVGLVKNLALMAYISVGSQPSPILEFLEEWSMENLEEISPAAI       554
tr|A0A2K5ZNR7|A0A2K5ZNR7_MANLE      HNTLWGMVCPAETPEGHAVGLVKNLALMAYISVGSQPSPILEFLEEWSMENLEEISPAAI       554
tr|A0A2I2ZIU3|A0A2I2ZIU3_GORGO      HNTLWGMVCPAETPEGHAVGLVKNLALMAYISVGSQPSPILEFLEEWSMENLEEISPAAI       561
tr|A0A1D5QGA5|A0A1D5QGA5_MACMU      HNTLWGMVCPAETPEGHAVGLVKNLALMAYISVGSQPSPILEFLEEWSMENLEEISPAAI       561
tr|A0A2J8S2N1|A0A2J8S2N1_PONAB      HNTLWGMVCPAETPEGHAVGLVKNLALMAYISVGSQPSPILEFLEEWSMENLEEISPAAI       561
tr|A0A2K5K5J5|A0A2K5K5J5_COLAP      HNTLWGMVCPAETPEGHAVGLVKNLALMAYISVGSQPSPILEFLEEWSMENLEEISPAAI       561
tr|A0A2J8PEW7|A0A2J8PEW7_PANTR      HNTLWGMVCPAETPEGHAVGLVKNLALMAYISVGSQPSPILEFLEEWSMENLEEISPAAI       554
tr|A0A2K5CY83|A0A2K5CY83_AOTNA      HNTLWGMVCPAETPEGHAVGLVKNLALMAYISVGSQPSPILEFLEEWSMENLEEISPAAI       561
tr|A0A096NEY4|A0A096NEY4_PAPAN      HNTLWGMVCPAETPEGHAVGLVKNLALMAYISVGSQPSPILEFLEEWSMENLEEISPAAI       561
tr|C9J2Y9|C9J2Y9_HUMAN              HNTLWGMVCPAETPEGHAVGLVKNLALMAYISVGSQPSPILEFLEEWSMENLEEISPAAI       554
tr|G8BY61|G8BY61_TETPH              HNTHWGLVCPAETPEGQACGLVKNLSLMSCISVGTDPMPIITFLSEWGMEPLEDYVPHQS       572
tr|A0A1X7QYA1|A0A1X7QYA1_9SACH      HNTHWGLVCPAETPEGQACGLVKNLSLMSCISVGTDPTPIITFLSEWGMEPLEDYVPHQS       570
tr|J7RV95|J7RV95_KAZNA              HNTHWGLVCPAETPEGQACGLVKNLSLMSSISVGTDPMPIITFLSEWGLEPLEDYVPHQS       570
tr|H2AVJ8|H2AVJ8_KAZAF              HNTHWGLVCPAETPEGQACGLVKNLSLMSCISVGTDPMPIITFLSEWGMEPLEDYIPHQS       570
sp|Q6FLD5|RPB2_CANGA                HNTHWGLVCPAETPEGQACGLVKNLSLMSCISVGADPMPIITFLSEWGMEPLEDYVPHQS       572
sp|P08518|RPB2_YEAST                HNTHWGLVCPAETPEGQACGLVKNLSLMSCISVGTDPMPIITFLSEWGMEPLEDYVPHQS       574
tr|A0A0L8VHA5|A0A0L8VHA5_9SACH      HNTHWGLVCPAETPEGQACGLVKNLSLMSCISVGTDPMPIITFLSEWGMEPLEDYVPHQS       574
tr|A0A0L8RB33|A0A0L8RB33_SACEU      HNTHWGLVCPAETPEGQACGLVKNLSLMSCISVGTDPMPIITFLSEWGMEPLEDYVPHQS       574
tr|G0VJ71|G0VJ71_NAUCC              HNTHWGLVCPAETPEGQACGLVKNLSLMSCISVGTDPMPIITFLSEWGMEPLEDYVPHQS       574
tr|G8ZM49|G8ZM49_TORDC              HNTHWGLVCPAETPEGQACGLVKNLSLMSCISVGTDPMPIITFLSEWGMEPLEDYVPHQS       572
tr|A0A1Q3A090|A0A1Q3A090_ZYGRO      HNTHWGLVCPAETPEGQACGLVKNLSLMSCISVGTDPMPIITFLSEWGMEPLEDYIPHQS       574
tr|A0A0N7IS35|A0A0N7IS35_9SACH      HNTHWGLVCPAETPEGQACGLVKNLSLMSCISVGTDPMPIITFLSEWGMEPLEDYVPHQS       572
tr|A0A212MG88|A0A212MG88_ZYGBA      HNTHWGLVCPAETPEGQACGLVKNLSLMSCISVGTDPMPIITFLSEWGMEPLEDYVPHQS       573
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tr|A0A1S7HHE1|A0A1S7HHE1_9SACH      HNTHWGLVCPAETPEGQACGLVKNLSLMSCISVGTDPMPIITFLSEWGMEPLEDYVPHQS       573
tr|S6ESB4|S6ESB4_ZYGB2              HNTHWGLVCPAETPEGQACGLVKNLSLMSCISVGTDAMPIITFLSEWGMEPLEDYVPHQS       573
tr|B6K5Q5|B6K5Q5_SCHJY              HNTHWGMVCPAETPEGQACGLVKNLSLMSYVSVGSPSAPIIEFLEEWGMESLEDYNPSAS       560
sp|Q02061|RPB2_SCHPO                HNTHWGMVCPAETPEGQACGLVKNLSLMSYVSVGSPSAPIIEFLEEWGLETLEDYNPSAS       560
tr|S9R8U4|S9R8U4_SCHOY              HNTHWGMVCPAETPEGQACGLVKNLALMSYVSVGSPAAPIIEFLEEWGLESLEDFNPSAS       560
tr|S9W8C6|S9W8C6_SCHCR              HNTHWGMVCPAETPEGQACGLVKNLALMSYVSVGSPAAPIIEFLEEWGLESLEDYNPSAS       560
sp|Q8RQE9|RPOB_THET8                HRTHYGRICPVETPEGANIGLITSLAAYARVD-------------ELGFI----------       4677
ASR51304.1                          HPTHYGRICPIETPEGPNIGLINSLASFSRVN-------------KYGFI----------       601
OXR47929.1                          HPTHYGRVCPIETPEGPNIGLINSMALYARLN-------------EYGFL----------       593
WP_093971860.1                      HPTHYGRVCPIETPEGPNIGLINSMALYARLN-------------EYGFL----------       593
sp|Q2NWR6|RPOB_SODGM                HPTHYGRVCPIETPEGPNIGLINSLSVYAQTN-------------EYGFL----------       587
sp|B4EYU9|RPOB_PROMH                HPTHYGRVCPIETPEGPNIGLINSLSVYAQTN-------------EYGFL----------       587
sp|A7FNI3|RPOB_YERP3                HPTHYGRVCPIETPEGPNIGLINSLSVYAQTN-------------EYGFL----------       587
sp|Q1C1U1|RPOB_YERPA                HPTHYGRVCPIETPEGPNIGLINSLSVYAQTN-------------EYGFL----------       587
sp|B2K113|RPOB_YERPB                HPTHYGRVCPIETPEGPNIGLINSLSVYAQTN-------------EYGFL----------       587
sp|A8G8E7|RPOB_SERP5                HPTHYGRVCPIETPEGPNIGLINSLSVYAQTN-------------EYGFL----------       587
sp|Q6DAN0|RPOB_PECAS                HPTHYGRVCPIETPEGPNIGLINSLSVYAQTN-------------EYGFL----------       587
sp|C6DHR5|RPOB_PECCP                HPTHYGRVCPIETPEGPNIGLINSLSVYAQTN-------------EYGFL----------       587
sp|Q7N9A4|RPOB_PHOLL                HPTHYGRVCPIETPEGPNIGLINSLSVYAQTN-------------EYGFL----------       587
sp|C5BHE3|RPOB_EDWI9                HPTHYGRVCPIETPEGPNIGLINSLSVYAQTN-------------EYGFL----------       587
sp|A7MQQ9|RPOB_CROS8                HPTHYGRVCPIETPEGPNIGLINSLSVYAQTN-------------EYGFL----------       587
sp|B5XYF5|RPOB_KLEP3                HPTHYGRVCPIETPEGPNIGLINSLSVYAQTN-------------EYGFL----------       587
sp|P0A8V2|RPOB_ECOLI                HPTHYGRVCPIETPEGPNIGLINSLSVYAQTN-------------EYGFL----------       587
sp|C5A0S7|RPOB_ECOBW                HPTHYGRVCPIETPEGPNIGLINSLSVYAQTN-------------EYGFL----------       587
sp|Q31U10|RPOB_SHIBS                HPTHYGRVCPIETPEGPNIGLINSLSVYAQTN-------------EYGFL----------       587
sp|Q32AF9|RPOB_SHIDS                HPTHYGRVCPIETPEGPNIGLINSLSVYAQTN-------------EYGFL----------       587
sp|A8AKT9|RPOB_CITK8                HPTHYGRVCPIETPEGPNIGLINSLSVYAQTN-------------EYGFL----------       587
sp|B5RFK1|RPOB_SALG2                HPTHYGRVCPIETPEGPNIGLINSLSVYAQTN-------------EYGFL----------       587
sp|B5BJQ3|RPOB_SALPK                HPTHYGRVCPIETPEGPNIGLINSLSVYAQTN-------------EYGFL----------       587
sp|B4T0Y9|RPOB_SALNS                HPTHYGRVCPIETPEGPNIGLINSLSVYAQTN-------------EYGFL----------       587
sp|P06173|RPOB_SALTY                HPTHYGRVCPIETPEGPNIGLINSLSVYAQTN-------------EYGFL----------       587
                                    * * .* :** *****   **:..::  :  .             : .:

sp|P30876|RPB2_HUMAN                ILGVCASIIPFPDHNQSPRNTYQSAMGKQAMGVYITNFHVRMDTLAH-------------       749
tr|G3V8Y5|G3V8Y5_RAT                ILGVCASIIPFPDHNQSPRNTYQSAMGKQAMGVYITNFHVRMDTLAH-------------       749
tr|A0A250Y753|A0A250Y753_CASCN      ILGVCASIIPFPDHNQSPRNTYQSAMGKQAMGVYITNFHVRMDTLAH-------------       749
tr|A0A1U7R4C7|A0A1U7R4C7_MESAU      ILGVCASIIPFPDHNQSPRNTYQSAMGKQAMGVYITNFHVRMDTLAH-------------       749
tr|A0A286XIQ9|A0A286XIQ9_CAVPO      ILGVCASIIPFPDHNQSPRNTYQSAMGKQAMGVYITNFHVRMDTLAH-------------       749
tr|I3M351|I3M351_ICTTR              ILGVCASIIPFPDHNQSPRNTYQSAMGKQAMGVYITNFHVRMDTLAH-------------       749
tr|G7P5R6|G7P5R6_MACFA              ILGVCASIIPFPDHNQSPRNTYQSAMGKQAMGVYITNFHVRMDTLAH-------------       749
tr|H2QPI8|H2QPI8_PANTR              ILGVCASIIPFPDHNQSPRNTYQSAMGKQAMGVYITNFHVRMDTLAH-------------       749
tr|A0A1U7V0T5|A0A1U7V0T5_TARSY      ILGVCASIIPFPDHNQSPRNTYQSAMGKQAMGVYITNFHVRMDTLAH-------------       749
tr|A0A1S2ZSL2|A0A1S2ZSL2_ERIEU      ILGVCASIIPFPDHNQSPRNTYQSAMGKQAMGVYITNFHVRMDTLAH-------------       749
tr|A0A0D9QYL1|A0A0D9QYL1_CHLSB      ILGVCASIIPFPDHNQSPRNTYQSAMGKQAMGVYITNFHVRMDTLAH-------------       742
tr|A0A2K5ZNR7|A0A2K5ZNR7_MANLE      ILGVCASIIPFPDHNQSPRNTYQSAMGKQAMGVYITNFHVRMDTLAH-------------       742
tr|A0A2I2ZIU3|A0A2I2ZIU3_GORGO      ILGVCASIIPFPDHNQSPRNTYQSAMGKQAMGVYITNFHVRMDTLAH-------------       749
tr|A0A1D5QGA5|A0A1D5QGA5_MACMU      ILGVCASIIPFPDHNQSPRNTYQSAMGKQAMGVYITNFHVRMDTLAH-------------       749
tr|A0A2J8S2N1|A0A2J8S2N1_PONAB      ILGVCASIIPFPDHNQSPRNTYQSAMGKQAMGVYITNFHVRMDTLAH-------------       749
tr|A0A2K5K5J5|A0A2K5K5J5_COLAP      ILGVCASIIPFPDHNQSPRNTYQSAMGKQAMGVYITNFHVRMDTLAH-------------       749
tr|A0A2J8PEW7|A0A2J8PEW7_PANTR      ILGVCASIIPFPDHNQSPRNTYQSAMGKQAMGVYITNFHVRMDTLAH-------------       742
tr|A0A2K5CY83|A0A2K5CY83_AOTNA      ILGVCASIIPFPDHNQSPRNTYQSAMGKQAMGVYITNFHVRMDTLAH-------------       749
tr|A0A096NEY4|A0A096NEY4_PAPAN      ILGVCASIIPFPDHNQSPRNTYQSAMGKQAMGVYITNFHVRMDTLAH-------------       749
tr|C9J2Y9|C9J2Y9_HUMAN              ILGVCASIIPFPDHNQSPRNTYQSAMGKQAMGVYITNFHVRMDTLAH-------------       742
tr|G8BY61|G8BY61_TETPH              ILGVAASIIPFPDHNQSPRNTYQSAMGKQAMGVFLTNYNVRMDTMAN-------------       794
tr|A0A1X7QYA1|A0A1X7QYA1_9SACH      ILGVAASIIPFPDHNQSPRNTYQSAMGKQAMGVFLTNYNVRMDTMAN-------------       791
tr|J7RV95|J7RV95_KAZNA              ILGVAASIIPFPDHNQSPRNTYQSAMGKQAMGVFLTNYNVRMDTMAN-------------       790
tr|H2AVJ8|H2AVJ8_KAZAF              ILGVAASIIPFPDHNQSPRNTYQSAMGKQAMGVFLTNFNVRMDTMAN-------------       792
sp|Q6FLD5|RPB2_CANGA                ILGVAASIIPFPDHNQSPRNTYQSAMGKQAMGVFLTNYNFRMDTMAN-------------       793
sp|P08518|RPB2_YEAST                ILGVAASIIPFPDHNQSPRNTYQSAMGKQAMGVFLTNYNVRMDTMAN-------------       794
tr|A0A0L8VHA5|A0A0L8VHA5_9SACH      ILGVAASIIPFPDHNQSPRNTYQSAMGKQAMGVFLTNYNVRMDTMAN-------------       794
tr|A0A0L8RB33|A0A0L8RB33_SACEU      ILGVAASIIPFPDHNQSPRNTYQSAMGKQAMGVFLTNYNVRMDTMAN-------------       794
tr|G0VJ71|G0VJ71_NAUCC              ILGVAASIIPFPDHNQSPRNTYQSAMGKQAMGVFLTNYNVRMDTMAN-------------       794
tr|G8ZM49|G8ZM49_TORDC              ILGVAASVIPFPDHNQSPRNTYQSAMGKQAMGVFLTNYNVRMDTMAN-------------       792
tr|A0A1Q3A090|A0A1Q3A090_ZYGRO      ILGVAASIIPFPDHNQSPRNTYQAAMGKQAMGVFLTNYNVRMDTMAN-------------       794
tr|A0A0N7IS35|A0A0N7IS35_9SACH      ILGVAASIIPFPDHNQSPRNTYQSAMGKQAMGVFLTNYNVRMDTMAN-------------       792
tr|A0A212MG88|A0A212MG88_ZYGBA      ILGVAASVIPFPDHNQSPRNTYQSAMGKQAMGVFLTNYNVRMDTMAN-------------       793
tr|A0A1S7HHE1|A0A1S7HHE1_9SACH      ILGVAASVIPFPDHNQSPRNTYQSAMGKQAMGVFLTNYNVRMDTMAN-------------       793
tr|S6ESB4|S6ESB4_ZYGB2              ILGVAASVIPFPDHNQSPRNTYQSAMGKQAMGVFLTNYNVRMDTMAN-------------       793
tr|B6K5Q5|B6K5Q5_SCHJY              ILGILASIIPFPDHNQSPRNTYQSAMGKQAMGIYLTNYQVRMDTMAN-------------       783
sp|Q02061|RPB2_SCHPO                ILGILASIIPFPDHNQSPRNTYQSAMGKQAMGVYLTNYQVRMDTMAN-------------       783
tr|S9R8U4|S9R8U4_SCHOY              ILGILASIIPFPDHNQSPRNTYQSAMGKQAMGVYLTNYQVRMDTMAN-------------       783
tr|S9W8C6|S9W8C6_SCHCR              ILGILASIIPFPDHNQSPRNTYQSAMGKQAMGVYLTNYQVRMDTMAN-------------       783
sp|Q8RQE9|RPOB_THET8                VFSVNTNLIPFLEHDDANRALMGSNMQTQAVPLIRAQAPVVMTGLEERVVRDSLAALYAE       598
ASR51304.1                          LVSVAASLIPFLENDDANRALMGSNMQRQAVPLVQAEAPFVGTGMEETVARDSGAAIAAK       733
OXR47929.1                          IVSVAASLIPFLEHDDANRALMGANMQRQAVPCLRPEKTLVGTGIERTVAVDSGTTVQAL       725
WP_093971860.1                      IVSVAASLIPFLEHDDANRALMGANMQRQAVPCLRPEKTLVGTGIERTVAVDSGTTVQAL       725
sp|Q2NWR6|RPOB_SODGM                VVSVGASLIPFLEHDDANRALMGANMQRQAVPTLCTDKPLVGTGMERAVAVDSGVTAVAK       719
sp|B4EYU9|RPOB_PROMH                VVSVGASLIPFLEHDDANRALMGANMQRQAVPTLRGDKPLVGTGMERAVAVDSGVTAVAK       719
sp|A7FNI3|RPOB_YERP3                IVSVGASLIPFLEHDDANRALMGANMQRQAVPTLRADKPLVGTGMERAVAVDSGVTSVAK       719
sp|Q1C1U1|RPOB_YERPA                IVSVGASLIPFLEHDDANRALMGANMQRQAVPTLRADKPLVGTGMERAVAVDSGVTSVAK       719
sp|B2K113|RPOB_YERPB                IVSVGASLIPFLEHDDANRALMGANMQRQAVPTLRADKPLVGTGMERAVAVDSGVTSVAK       719
sp|A8G8E7|RPOB_SERP5                VVSVGASLIPFLEHDDANRALMGANMQRQAVPTLRADKPLVGTGMERAVAVDSGVTAVAR       719
sp|Q6DAN0|RPOB_PECAS                IVSVGASLIPFLEHDDANRALMGANMQRQAVPTLRADKPLVGTGMERAVAVDSGVTAVAK       719
sp|C6DHR5|RPOB_PECCP                VVSVGASLIPFLEHDDANRALMGANMQRQAVPTLRADKPLVGTGMERAVAVDSGVTAVAK       719
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sp|Q7N9A4|RPOB_PHOLL                VVSVGASLIPFLEHDDANRALMGANMQRQAVPTLRADKPLVGTGMERAVAVDSGVTSVAK       719
sp|C5BHE3|RPOB_EDWI9                VVSVGASLIPFLEHDDANRALMGANMQRQAVPTLRADKPLVGTGMERAVAVDSGVTSVAK       719
sp|A7MQQ9|RPOB_CROS8                VVSVGASLIPFLEHDDANRALMGANMQRQAVPTLRADKPLVGTGMERAVAVDSGVTAVAK       719
sp|B5XYF5|RPOB_KLEP3                VVSVGASLIPFLEHDDANRALMGANMQRQAVPTLRADKPLVGTGMERAVAVDSGVTAVAK       719
sp|P0A8V2|RPOB_ECOLI                VVSVGASLIPFLEHDDANRALMGANMQRQAVPTLRADKPLVGTGMERAVAVDSGVTAVAK       719
sp|C5A0S7|RPOB_ECOBW                VVSVGASLIPFLEHDDANRALMGANMQRQAVPTLRADKPLVGTGMERAVAVDSGVTAVAK       719
sp|Q31U10|RPOB_SHIBS                VVSVGASLIPFLEHDDANRALMGANMQRQAVPTLRADKPLVGTGMERAVAVDSGVTAVAK       719
sp|Q32AF9|RPOB_SHIDS                VVSVGASLIPFLEHDDANRALMGANMQRQAVPTLRADKPLVGTGMERAVAVDSGVTAVAK       719
sp|A8AKT9|RPOB_CITK8                VVSVGASLIPFLEHDDANRALMGANMQRQAVPTLRADKPLVGTGMERAVAVDSGVTAVAK       719
sp|B5RFK1|RPOB_SALG2                VVSVGASLIPFLEHDDANRALMGANMQRQAVPTLRADKPLVGTGMERAVAVDSGVTAVAK       719
sp|B5BJQ3|RPOB_SALPK                VVSVGASLIPFLEHDDANRALMGANMQRQAVPTLRADKPLVGTGMERAVAVDSGVTAVAK       719
sp|B4T0Y9|RPOB_SALNS                VVSVGASLIPFLEHDDANRALMGANMQRQAVPTLRADKPLVGTGMERAVAVDSGVTAVAK       719
sp|P06173|RPOB_SALTY                VVSVGASLIPFLEHDDANRALMGANMQRQAVPTLRADKPLVGTGMERAVAVDSGVTAVAK       719
                                    :..: :.:*** ::::: *    : *  **:     :  .    : .

sp|P30876|RPB2_HUMAN                -----SMEYLRFRELPAGINSIVAIASYTGYNQEDSVIMNRSAVDRGFFRSVFYRSYKEQ       817
tr|G3V8Y5|G3V8Y5_RAT                -----SMEYLRFRELPAGINSIVAIASYTGYNQEDSVIMNRSAVDRGFFRSVFYRSYKEQ       817
tr|A0A250Y753|A0A250Y753_CASCN      -----SMEYLRFRELPAGINSIVAIASYTGYNQEDSVIMNRSAVDRGFFRSVFYRSYKEQ       817
tr|A0A1U7R4C7|A0A1U7R4C7_MESAU      -----SMEYLRFRELPAGINSIVAIASYTGYNQEDSVIMNRSAVDRGFFRSVFYRSYKEQ       817
tr|A0A286XIQ9|A0A286XIQ9_CAVPO      -----SMEYLRFRELPAGINSIVAIASYTGYNQEDSVIMNRSAVDRGFFRSVFYRSYKEQ       817
tr|I3M351|I3M351_ICTTR              -----SMEYLRFRELPAGINSIVAIASYTGYNQEDSVIMNRSAVDRGFFRSVFYRSYKEQ       817
tr|G7P5R6|G7P5R6_MACFA              -----SMEYLRFRELPAGINSIVAIASYTGYNQEDSVIMNRSAVDRGFFRSVFYRSYKEQ       817
tr|H2QPI8|H2QPI8_PANTR              -----SMEYLRFRELPAGINSIVAIASYTGYNQEDSVIMNRSAVDRGFFRSVFYRSYKEQ       817
tr|A0A1U7V0T5|A0A1U7V0T5_TARSY      -----SMEYLRFRELPAGINSIVAIASYTGYNQEDSVIMNRSAVDRGFFRSVFYRSYKEQ       817
tr|A0A1S2ZSL2|A0A1S2ZSL2_ERIEU      -----SMEYLRFRELPAGINSIVAIASYTGYNQEDSVIMNRSAVDRGFFRSVFYRSYKEQ       817
tr|A0A0D9QYL1|A0A0D9QYL1_CHLSB      -----SMEYLRFRELPAGINSIVAIASYTGYNQEDSVIMNRSAVDRGFFRSVFYRSYKEQ       810
tr|A0A2K5ZNR7|A0A2K5ZNR7_MANLE      -----SMEYLRFRELPAGINSIVAIASYTGYNQEDSVIMNRSAVDRGFFRSVFYRSYKEQ       810
tr|A0A2I2ZIU3|A0A2I2ZIU3_GORGO      -----SMEYLRFRELPAGINSIVAIASYTGYNQEDSVIMNRSAVDRGFFRSVFYRSYKEQ       817
tr|A0A1D5QGA5|A0A1D5QGA5_MACMU      -----SMEYLRFRELPAGINSIVAIASYTGYNQEDSVIMNRSAVDRGFFRSVFYRSYKEQ       817
tr|A0A2J8S2N1|A0A2J8S2N1_PONAB      -----SMEYLRFRELPAGINSIVAIASYTGYNQEDSVIMNRSAVDRGFFRSVFYRSYKEQ       817
tr|A0A2K5K5J5|A0A2K5K5J5_COLAP      -----SMEYLRFRELPAGINSIVAIASYTGYNQEDSVIMNRSAVDRGFFRSVFYRSYKEQ       817
tr|A0A2J8PEW7|A0A2J8PEW7_PANTR      -----SMEYLRFRELPAGINSIVAIASYTGYNQEDSVIMNRSAVDRGFFRSVFYRSYKEQ       810
tr|A0A2K5CY83|A0A2K5CY83_AOTNA      -----SMEYLRFRELPAGINSIVAIASYTGYNQEDSVIMNRSAVDRGFFRSVFYRSYKEQ       817
tr|A0A096NEY4|A0A096NEY4_PAPAN      -----SMEYLRFRELPAGINSIVAIASYTGYNQEDSVIMNRSAVDRGFFRSVFYRSYKEQ       817
tr|C9J2Y9|C9J2Y9_HUMAN              -----SMEYLRFRELPAGINSIVAIASYTGYNQEDSVIMNRSAVDRGFFRSVFYRSYKEQ       810
tr|G8BY61|G8BY61_TETPH              -----AMEYLKFRELPAGQNAIVAIACYSGYNQEDSMIMNQSSIDRGLFRSLFFRSYMDQ       862
tr|A0A1X7QYA1|A0A1X7QYA1_9SACH      -----SMEYLKFRELPAGQNAIVAIACYSGYNQEDSMIMNQSSIDRGLFRSLFFRSYMDQ       859
tr|J7RV95|J7RV95_KAZNA              -----AMEYLKFRELPAGQNAIVAIACYSGYNQEDSMIMNQSSIDRGLFRSLFFRSYMDQ       858
tr|H2AVJ8|H2AVJ8_KAZAF              -----AMEYLKFRELPAGQNAIVAIACYSGYNQEDSMIMNQSSIDRGLFRSLFFRSYMDQ       860
sp|Q6FLD5|RPB2_CANGA                -----AMEYLKFRELPAGQNAIVAIACYSGYNQEDSMIMNQSSIDRGLFRSLFFRSYMDQ       861
sp|P08518|RPB2_YEAST                -----AMEYLKFRELPAGQNAIVAIACYSGYNQEDSMIMNQSSIDRGLFRSLFFRSYMDQ       862
tr|A0A0L8VHA5|A0A0L8VHA5_9SACH      -----AMEYLKFRELPAGQNAIVAIACYSGYNQEDSMIMNQSSIDRGLFRSLFFRSYMDQ       862
tr|A0A0L8RB33|A0A0L8RB33_SACEU      -----AMEYLKFRELPAGQNAIVAIACYSGYNQEDSMIMNQSSIDRGLFRSLFFRSYMDQ       862
tr|G0VJ71|G0VJ71_NAUCC              -----SMEYLKFRELPAGQNAIVAIACYSGYNQEDSMIMNQSSIDRGLFRSLFFRSYMDQ       862
tr|G8ZM49|G8ZM49_TORDC              -----AMEYLKFRELPAGQNAIVAIACYSGYNQEDSMIMNQSSIDRGLFRSLFFRSYMDQ       860
tr|A0A1Q3A090|A0A1Q3A090_ZYGRO      -----AMEYLKFRELPAGQNAIVAIACYSGYNQEDSMIMNQSSIDRGLFRSLFFRSYMDQ       862
tr|A0A0N7IS35|A0A0N7IS35_9SACH      -----AMEYLKFRELPAGQNAIVAIACYSGYNQEDSMIMNQSSIDRGLFRSLFFRSYMDQ       860
tr|A0A212MG88|A0A212MG88_ZYGBA      -----AMEYLKFRELPAGQNAIVAIACYSGYNQEDSMIMNQSSIDRGLFRSLFFRSYMDQ       861
tr|A0A1S7HHE1|A0A1S7HHE1_9SACH      -----AMEYLKFRELPAGQNAIVAIACYSGYNQEDSMIMNQSSIDRGLFRSLFFRSYMDQ       861
tr|S6ESB4|S6ESB4_ZYGB2              -----AMEYLKFRELPAGQNAIVAIACYSGYNQEDSMIMNQSSIDRGLFRSLFFRSYMDQ       861
tr|B6K5Q5|B6K5Q5_SCHJY              -----SMEYLKFRELPAGQNAIVAILCYSGYNQEDSIIMNQSSIDRGLFRSIFYRTYMDQ       851
sp|Q02061|RPB2_SCHPO                -----SMEYLKFRELPAGQNAIVAILCYSGYNQEDSIIMNQASIDRGLFRSIFYRTYTDQ       851
tr|S9R8U4|S9R8U4_SCHOY              -----SMEYLKFRELPAGQNAIVAILCYSGYNQEDSIIMNQASIDRGLFRSIFYRTYTDQ       851
tr|S9W8C6|S9W8C6_SCHCR              -----SMEYLKFRELPAGQNAIVAILCYSGYNQEDSIIMNQASIDRGLFRSIFYRTYTDQ       851x6
sp|Q8RQE9|RPOB_THET8                GDLLADGPASENGFLALGQNVLVAIMPFDGYNFEDAIVISEELLKRDFYTSIHIERYEIE       711
ASR51304.1                          GDIIADGPSTDLGELALGRNALVAFMPWNGYNYEDSILISERIVKDDVFTSIHIEEFEVM       852
OXR47929.1                          GDVLADGASTDLGELALGQNMLIAFMPWNGYNFEDSILISEKVVADDRYTSIHIEELTVV       845
WP_093971860.1                      GDVLADGASTDLGELALGQNMLIAFMPWNGYNFEDSILISEKVVADDRYTSIHIEELTVV       845
sp|Q2NWR6|RPOB_SODGM                GDVLADGPSTDLGELALGQNMRIAFMPWNGYNFEDSMLVSERVVQEDRFTTIHIQELACV       839
sp|B4EYU9|RPOB_PROMH                GDVLADGPSTDLGELALGQNMRVAFMPWNGYNYEDSILVSERVVQEDRFTTIHIQELACV       839
sp|A7FNI3|RPOB_YERP3                GDVLADGPSTDLGELALGQNMRVAFMPWNGYNFEDSILVSERVVQEDRFTTIHIQELACV       839
sp|Q1C1U1|RPOB_YERPA                GDVLADGPSTDLGELALGQNMRVAFMPWNGYNFEDSILVSERVVQEDRFTTIHIQELACV       839
sp|B2K113|RPOB_YERPB                GDVLADGPSTDLGELALGQNMRVAFMPWNGYNFEDSILVSERVVQEDRFTTIHIQELACV       839
sp|A8G8E7|RPOB_SERP5                GDVLADGPSTDLGELALGQNMRVAFMPWNGYNFEDSILVSERVVQEDRFTTIHIQELACV       839
sp|Q6DAN0|RPOB_PECAS                GDVLADGPSTDLGELALGQNMRVAFMPWNGYNFEDSILVSERVVQEDRFTTIHIQELACV       839
sp|C6DHR5|RPOB_PECCP                GDVLADGPSTDLGELALGQNMRVAFMPWNGYNFEDSILVSERVVQEDRFTTIHIQELACV       839
sp|Q7N9A4|RPOB_PHOLL                GDVLADGPSTDLGELALGQNMRVAFMPWNGYNFEDSILVSERVVQEDRFTTIHIQELACV       839
sp|C5BHE3|RPOB_EDWI9                GDVLADGPSTDLGELALGQNMRVAFMPWNGYNFEDSILVSERVVQEDRFTSIHIQELACV       839
sp|A7MQQ9|RPOB_CROS8                GDVLADGPSTDLGELALGQNMRVAFMPWNGYNFEDSILVSERVVQEDRFTTIHIQELACV       839
sp|B5XYF5|RPOB_KLEP3                GDVLADGPSTDLGELALGQNMRVAFMPWNGYNFEDSILVSERVVQEDRFTTIHIQELACV       839
sp|P0A8V2|RPOB_ECOLI                GDVLADGPSTDLGELALGQNMRVAFMPWNGYNFEDSILVSERVVQEDRFTTIHIQELACV       839
sp|C5A0S7|RPOB_ECOBW                GDVLADGPSTDLGELALGQNMRVAFMPWNGYNFEDSILVSERVVQEDRFTTIHIQELACV       839
sp|Q31U10|RPOB_SHIBS                GDVLADGPSTDLGELALGQNMRVAFMPWNGYNFEDSILVSERVVQEDRFTTIHIQELACV       839
sp|Q32AF9|RPOB_SHIDS                GDVLADGPSTDLGELALGQNMRVAFMPWNGYNFEDSILVSERVVQEDRFTTIHIQELACV       839
sp|A8AKT9|RPOB_CITK8                GDVLADGPSTDLGELALGQNMRVAFMPWNGYNFEDSILVSERVVQEDRFTTIHIQELACV       839
sp|B5RFK1|RPOB_SALG2                GDVLADGPSTDLGELALGQNMRVAFMPWNGYNFEDSILVSERVVQEDRFTTIHIQELACV       839
sp|B5BJQ3|RPOB_SALPK                GDVLADGPSTDLGELALGQNMRVAFMPWNGYNFEDSILVSERVVQEDRFTTIHIQELACV       839
sp|B4T0Y9|RPOB_SALNS                GDVLADGPSTDLGELALGQNMRVAFMPWNGYNFEDSILVSERVVQEDRFTTIHIQELACV       839
sp|P06173|RPOB_SALTY                GDVLADGPSTDLGELALGQNMRVAFMPWNGYNFEDSILVSERVVQEDRFTTIHIQELACV       839
                                                  *  * *  :*:  : *** **:::..   :  . : ::. .
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sp|P30876|RPB2_HUMAN                ESKKGFDQEEVFEKPTRETCQGMRHAIYDKLDDDGLIAPGVRVSGDDVIIGKTVTLPENE       877x9
tr|G3V8Y5|G3V8Y5_RAT                ESKKGFDQEEVFEKPTRETCQGMRHAIYDKLDDDGLIAPGVRVSGDDVIIGKTVTLPENE       877
tr|A0A250Y753|A0A250Y753_CASCN      ESKKGFDQEEVFEKPTRETCQGMRHAIYDKLDDDGLIAPGVRVSGDDVIIGKTVTLPENE       877
tr|A0A1U7R4C7|A0A1U7R4C7_MESAU      ESKKGFDQEEVFEKPTRETCQGMRHAIYDKLDDDGLIAPGVRVSGDDVIIGKTVTLPENE       877
tr|A0A286XIQ9|A0A286XIQ9_CAVPO      ESKKGFDQEEVFEKPTRETCQGMRHAIYDKLDDDGLIAPGVRVSGDDVIIGKTVTLPENE       877
tr|I3M351|I3M351_ICTTR              ESKKGFDQEEVFEKPTRETCQGMRHAIYDKLDDDGLIAPGVRVSGDDVIIGKTVTLPENE       877
tr|G7P5R6|G7P5R6_MACFA              ESKKGFDQEEVFEKPTRETCQGMRHAIYDKLDDDGLIAPGVRVSGDDVIIGKTVTLPENE       877
tr|H2QPI8|H2QPI8_PANTR              ESKKGFDQEEVFEKPTRETCQGMRHAIYDKLDDDGLIAPGVRVSGDDVIIGKTVTLPENE       877
tr|A0A1U7V0T5|A0A1U7V0T5_TARSY      ESKKGFDQEEVFEKPTRETCQGMRHAIYDKLDDDGLIAPGVRVSGDDVIIGKTVTLPENE       877
tr|A0A1S2ZSL2|A0A1S2ZSL2_ERIEU      ESKKGFDQEEVFEKPTRETCQGMRHAIYDKLDDDGLIAPGVRVSGDDVIIGKTVTLPENE       877
tr|A0A0D9QYL1|A0A0D9QYL1_CHLSB      ESKKGFDQEEVFEKPTRETCQGMRHAIYDKLDDDGLIAPGVRVSGDDVIIGKTVTLPENE       870
tr|A0A2K5ZNR7|A0A2K5ZNR7_MANLE      ESKKGFDQEEVFEKPTRETCQGMRHAIYDKLDDDGLIAPGVRVSGDDVIIGKTVTLPENE       870
tr|A0A2I2ZIU3|A0A2I2ZIU3_GORGO      ESKKGFDQEEVFEKPTRETCQGMRHAIYDKLDDDGLIAPGVRVSGDDVIIGKTVTLPENE       877
tr|A0A1D5QGA5|A0A1D5QGA5_MACMU      ESKKGFDQEEVFEKPTRETCQGMRHAIYDKLDDDGLIAPGVRVSGDDVIIGKTVTLPENE       877
tr|A0A2J8S2N1|A0A2J8S2N1_PONAB      ESKKGFDQEEVFEKPTRETCQGMRHAIYDKLDDDGLIAPGVRVSGDDVIIGKTVTLPENE       877
tr|A0A2K5K5J5|A0A2K5K5J5_COLAP      ESKKGFDQEEVFEKPTRETCQGMRHAIYDKLDDDGLIAPGVRVSGDDVIIGKTVTLPENE       877
tr|A0A2J8PEW7|A0A2J8PEW7_PANTR      ESKKGFDQEEVFEKPTRETCQGMRHAIYDKLDDDGLIAPGVRVSGDDVIIGKTVTLPENE       870
tr|A0A2K5CY83|A0A2K5CY83_AOTNA      ESKKGFDQEEVFEKPTRETCQGMRHAIYDKLDDDGLIAPGVRVSGDDVIIGKTVTLPENE       877
tr|A0A096NEY4|A0A096NEY4_PAPAN      ESKKGFDQEEVFEKPTRETCQGMRHAIYDKLDDDGLIAPGVRVSGDDVIIGKTVTLPENE       877
tr|C9J2Y9|C9J2Y9_HUMAN              ESKKGFDQEEVFEKPTRETCQGMRHAIYDKLDDDGLIAPGVRVSGDDVIIGKTVTLPENE       870
tr|G8BY61|G8BY61_TETPH              EKKYGMSITETFEKPQRTNTLRMKHGSYDKLDDDGLISPGVRVSGEDIIIGKTTPISPDE       922
tr|A0A1X7QYA1|A0A1X7QYA1_9SACH      EKKYGMSITETFEKPQRTNTLRMKHGTYDKLDDDGLIAPGVRVSGEDVIIGKTTPISPDE       919
tr|J7RV95|J7RV95_KAZNA              EKKYGMSITETFEKPQRTNTLRMKHGTYDKLDDDGLIAPGVRVSGEDIIIGKTTPISPDE       918
tr|H2AVJ8|H2AVJ8_KAZAF              EKKYGMSITETFEKPHRTNTLRMKHGTYDKLDDDGLIAPGVRVSGEDIIIGKTTPISPDE       920
sp|Q6FLD5|RPB2_CANGA                EKKYGMSITETFEKPQRTNTLRMKHGTYDKLDEDGLIAPGVRVSGEDIIIGKTTPIAPDE       921
sp|P08518|RPB2_YEAST                EKKYGMSITETFEKPQRTNTLRMKHGTYDKLDDDGLIAPGVRVSGEDVIIGKTTPISPDE       922
tr|A0A0L8VHA5|A0A0L8VHA5_9SACH      EKKYGMSITETFEKPQRTNTLRMKHGTYDKLDDDGLIAPGVRVSGEDVIIGKTTPISPDE       922
tr|A0A0L8RB33|A0A0L8RB33_SACEU      EKKYGMSITETFEKPQRTNTLRMKHGTYDKLDDDGLIAPGVRVSGEDVIIGKTTPISPDE       922
tr|G0VJ71|G0VJ71_NAUCC              EKKYGMSITETFEKPQRTNTLRMKHGTYDKLDDDGLIAPGVRVSGEDIIIGKTTPISPDE       922
tr|G8ZM49|G8ZM49_TORDC              EKKYGMSITETFEKPQRTNTLRMKHGTYDKLDDDGLIAPGVRVSGEDIIIGKTTPISPDE       920
tr|A0A1Q3A090|A0A1Q3A090_ZYGRO      EKKYGMSITETFEKPQRTNTLRMKHGTYDKLDDDGLIAPGVRVSGEDIIIGKTTPISPDE       922
tr|A0A0N7IS35|A0A0N7IS35_9SACH      EKKYGMSITETFEKPQRTNTLRMKHGTYDKLDDDGLIAPGVRVSGEDVIIGKTTPISPDE       920
tr|A0A212MG88|A0A212MG88_ZYGBA      EKKYGMSITETFEKPQRTNTLRMKHGTYDKLDDDGLIAPGVRVSGEDIIIGKTTPISPDE       921
tr|A0A1S7HHE1|A0A1S7HHE1_9SACH      EKKYGMSITETFEKPQRTNTLRMKHGTYDKLDDDGLIAPGVRVSGEDIIIGKTTPISPDE       921
tr|S6ESB4|S6ESB4_ZYGB2              EKKYGMSITETFEKPQRTNTLRMKHGTYDKLDDDGLIAPGVRVSGEDIIIGKTTPISPDE       921
tr|B6K5Q5|B6K5Q5_SCHJY              EKKIGMTVMEEFERPTRSTTLRMKHGTYDKLEDDGLIAPGTRVSGDDIIIGKTAPVPPDH       911
sp|Q02061|RPB2_SCHPO                EKKIGMTVMEEFERPVRSTTLRMKHGTYDKLEDDGLIAPGTRVSGEDIIIGKTAPIPLDH       911
tr|S9R8U4|S9R8U4_SCHOY              EKKIGMTVMEEFERPARSTTLRMKHGTYDKLEDDGLIAPGTRVSGDDIIIGKTAPIPVDN       911
tr|S9W8C6|S9W8C6_SCHCR              EKKIGMTVMEEFERPARSTTLRMKHGTYDKLEDDGLIAPGTRVSGDDIIIGKTAPIPLDN       911x9
sp|Q8RQE9|RPOB_THET8                ARDTKLGPERI-----TRDIPHLSEAALRDLDEEGVVRIGAEVKPGDILVGRTSFKGESE       766
ASR51304.1                          ARDTKLGPEDI-----TRDIPNVGEEALRNLDEAGIVYIGAEVHPGDILVGKITPKGESP       907
OXR47929.1                          ARDTKLGAEEI-----TRDISNLPEIQLNRLDDSGIVHIGAEVRADDVLVGKVTPKGETQ       900
WP_093971860.1                      ARDTKLGAEEI-----TRDISNLPEIQLNRLDDSGIVHIGAEVRADDVLVGKVTPKGETQ       900
sp|Q2NWR6|RPOB_SODGM                SRDTKLGPEEI-----TADIPNVGEAALSKLDESGIVYIGAEVTGGDILVGKVTPKGETQ       894
sp|B4EYU9|RPOB_PROMH                SRDTKLGPEEI-----TADIPNVGEAALSKLDESGIVYIGAEVKGGDILVGKVTPKGETQ       894
sp|A7FNI3|RPOB_YERP3                SRDTKLGPEEI-----TADIPNVGEAALSKLDESGIVYIGAEVTGGDILVGKVTPKGETQ       894
sp|Q1C1U1|RPOB_YERPA                SRDTKLGPEEI-----TADIPNVGEAALSKLDESGIVYIGAEVTGGDILVGKVTPKGETQ       894
sp|B2K113|RPOB_YERPB                SRDTKLGPEEI-----TADIPNVGEAALSKLDESGIVYIGAEVTGGDILVGKVTPKGETQ       894
sp|A8G8E7|RPOB_SERP5                SRDTKLGPEEI-----TADIPNVGEAALSKLDESGIVYIGAEVTGGDILVGKVTPKGETQ       894
sp|Q6DAN0|RPOB_PECAS                SRDTKLGPEEI-----TADIPNVGEAALSKLDESGIVYIGAEVTGGDILVGKVTPKGETQ       894
sp|C6DHR5|RPOB_PECCP                SRDTKLGPEEI-----TADIPNVGEAALSKLDESGIVYIGAEVTGGDILVGKVTPKGETQ       894
sp|Q7N9A4|RPOB_PHOLL                SRDTKLGPEEI-----TADIPNVGEAALSKLDESGIVYIGAEVTGGDILVGKVTPKGETQ       894
sp|C5BHE3|RPOB_EDWI9                SRDTKLGPEEI-----TADIPNVGEAALSKLDESGIVYIGAEVKGGDILVGKVTPKGETQ       894
sp|A7MQQ9|RPOB_CROS8                SRDTKLGPEEI-----TADIPNVGEAALSKLDESGIVYIGAEVTGGDILVGKVTPKGETQ       894
sp|B5XYF5|RPOB_KLEP3                SRDTKLGPEEI-----TADIPNVGEAALSKLDESGIVYIGAEVTGGDILVGKVTPKGETQ       894
sp|P0A8V2|RPOB_ECOLI                SRDTKLGPEEI-----TADIPNVGEAALSKLDESGIVYIGAEVTGGDILVGKVTPKGETQ       894
sp|C5A0S7|RPOB_ECOBW                SRDTKLGPEEI-----TADIPNVGEAALSKLDESGIVYIGAEVTGGDILVGKVTPKGETQ       894
sp|Q31U10|RPOB_SHIBS                SRDTKLGPEEI-----TADIPNVGEAALSKLDESGIVYIGAEVTGGDILVGKVTPKGETQ       894
sp|Q32AF9|RPOB_SHIDS                SRDTKLGPEEI-----TADIPNVGEAALSKLDESGIVYIGAEVTGGDILVGKVTPKGETQ       894
sp|A8AKT9|RPOB_CITK8                SRDTKLGPEEI-----TADIPNVGEAALSKLDESGIVYIGAEVTGGDILVGKVTPKGETQ       894
sp|B5RFK1|RPOB_SALG2                SRDTKLGPEEI-----TADIPNVGEAALSKLDESGIVYIGAEVTGGDILVGKVTPKGETQ       894
sp|B5BJQ3|RPOB_SALPK                SRDTKLGPEEI-----TADIPNVGEAALSKLDESGIVYIGAEVTGGDILVGKVTPKGETQ       894
sp|B4T0Y9|RPOB_SALNS                SRDTKLGPEEI-----TADIPNVGEAALSKLDESGIVYIGAEVTGGDILVGKVTPKGETQ       894
sp|P06173|RPOB_SALTY                SRDTKLGPEEI-----TADIPNVGEAALSKLDESGIVYIGAEVTGGDILVGKVTPKGETQ       894
                                      .  :                :  .     *:: *::  *..*   *:::*:

sp|P30876|RPB2_HUMAN                IGDKFASRHGQKGTCGIQYRQEDMPFTCEGITPDIIINPHAIPSRMTIGHLIECLQGKVS       990
tr|G3V8Y5|G3V8Y5_RAT                IGDKFASRHGQKGTCGIQYRQEDMPFTCEGITPDIIINPHAIPSRMTIGHLIECLQGKVS       990
tr|A0A250Y753|A0A250Y753_CASCN      IGDKFASRHGQKGTCGIQYRQEDMPFTCEGITPDIIINPHAIPSRMTIGHLIECLQGKVS       990
tr|A0A1U7R4C7|A0A1U7R4C7_MESAU      IGDKFASRHGQKGTCGIQYRQEDMPFTCEGITPDIIINPHAIPSRMTIGHLIECLQGKVS       990
tr|A0A286XIQ9|A0A286XIQ9_CAVPO      IGDKFASRHGQKGTCGIQYRQEDMPFTCEGITPDIIINPHAIPSRMTIGHLIECLQGKVS       990
tr|I3M351|I3M351_ICTTR              IGDKFASRHGQKGTCGIQYRQEDMPFTCEGITPDIIINPHAIPSRMTIGHLIECLQGKVS       990
tr|G7P5R6|G7P5R6_MACFA              IGDKFASRHGQKGTCGIQYRQEDMPFTCEGITPDIIINPHAIPSRMTIGHLIECLQGKVS       990
tr|H2QPI8|H2QPI8_PANTR              IGDKFASRHGQKGTCGIQYRQEDMPFTCEGITPDIIINPHAIPSRMTIGHLIECLQGKVS       990
tr|A0A1U7V0T5|A0A1U7V0T5_TARSY      IGDKFASRHGQKGTCGIQYRQEDMPFTCEGITPDIIINPHAIPSRMTIGHLIECLQGKVS       990
tr|A0A1S2ZSL2|A0A1S2ZSL2_ERIEU      IGDKFASRHGQKGTCGIQYRQEDMPFTCEGITPDIIINPHAIPSRMTIGHLIECLQGKVS       990
tr|A0A0D9QYL1|A0A0D9QYL1_CHLSB      IGDKFASRHGQKGTCGIQYRQEDMPFTCEGITPDIIINPHAIPSRMTIGHLIECLQGKVS       983
tr|A0A2K5ZNR7|A0A2K5ZNR7_MANLE      IGDKFASRHGQKGTCGIQYRQEDMPFTCEGITPDIIINPHAIPSRMTIGHLIECLQGKVS       983
tr|A0A2I2ZIU3|A0A2I2ZIU3_GORGO      IGDKFASRHGQKGTCGIQYRQEDMPFTCEGITPDIIINPHAIPSRMTIGHLIECLQGKVS       990
tr|A0A1D5QGA5|A0A1D5QGA5_MACMU      IGDKFASRHGQKGTCGIQYRQEDMPFTCEGITPDIIINPHAIPSRMTIGHLIECLQGKVS       990
tr|A0A2J8S2N1|A0A2J8S2N1_PONAB      IGDKFASRHGQKGTCGIQYRQEDMPFTCEGITPDIIINPHAIPSRMTIGHLIECLQGKVS       990
tr|A0A2K5K5J5|A0A2K5K5J5_COLAP      IGDKFASRHGQKGTCGIQYRQEDMPFTCEGITPDIIINPHAIPSRMTIGHLIECLQGKVS       990
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tr|A0A2J8PEW7|A0A2J8PEW7_PANTR      IGDKFASRHGQKGTCGIQYRQEDMPFTCEGITPDIIINPHAIPSRMTIGHLIECLQGKVS       983
tr|A0A2K5CY83|A0A2K5CY83_AOTNA      IGDKFASRHGQKGTCGIQYRQEDMPFTCEGITPDIIINPHAIPSRMTIGHLIECLQGKVS       990
tr|A0A096NEY4|A0A096NEY4_PAPAN      IGDKFASRHGQKGTCGIQYRQEDMPFTCEGITPDIIINPHAIPSRMTIGHLIECLQGKVS       990
tr|C9J2Y9|C9J2Y9_HUMAN              IGDKFASRHGQKGTCGIQYRQEDMPFTCEGITPDIIINPHAIPSRMTIGHLIECLQGKVS       983
tr|G8BY61|G8BY61_TETPH              IGDKFASRHGQKGTIGITYGREDMPFTAEGIVPDLIINPHAIPSRMTVAHLIECLLSKVA       1035
tr|A0A1X7QYA1|A0A1X7QYA1_9SACH      IGDKFASRHGQKGTIGITYRREDMPFTAEGIVPDLIINPHAIPSRMTVAHLIECLLSKVA       1032
tr|J7RV95|J7RV95_KAZNA              IGDKFASRHGQKGTIGITYSREDMPFTAEGIVPDLIINPHAIPSRMTVAHLIECLLSKVA       1031
tr|H2AVJ8|H2AVJ8_KAZAF              IGDKFASRHGQKGTIGITYRREDMPFTADGIVPDLIINPHAIPSRMTVAHLIECLLSKVA       1033
sp|Q6FLD5|RPB2_CANGA                IGDKFASRHGQKGTIGITYRREDMPFTAEGIVPDLIINPHAIPSRMTVAHLIECLLSKVA       1034
sp|P08518|RPB2_YEAST                IGDKFASRHGQKGTIGITYRREDMPFTAEGIVPDLIINPHAIPSRMTVAHLIECLLSKVA       1035
tr|A0A0L8VHA5|A0A0L8VHA5_9SACH      IGDKFASRHGQKGTIGITYRREDMPFTAEGIVPDLIINPHAIPSRMTVAHLIECLLSKVA       1035
tr|A0A0L8RB33|A0A0L8RB33_SACEU      IGDKFASRHGQKGTIGITYRREDMPFTAEGIVPDLIINPHAIPSRMTVAHLIECLLSKVA       1035
tr|G0VJ71|G0VJ71_NAUCC              IGDKFASRHGQKGTIGITYRREDMPFTAEGIVPDLIINPHAIPSRMTVAHLIECLLSKVA       1035
tr|G8ZM49|G8ZM49_TORDC              IGDKFASRHGQKGTIGITYGREDMPFTAEGIVPDLIINPHAIPSRMTVAHLIECLLSKVA       1033
tr|A0A1Q3A090|A0A1Q3A090_ZYGRO      IGDKFASRHGQKGTIGITYGREDMPFTAEGIVPDLIINPHAIPSRMTVAHLIECLLSKVA       1035
tr|A0A0N7IS35|A0A0N7IS35_9SACH      IGDKFASRHGQKGTIGITYGREDMPFTSEGIVPDLIINPHAIPSRMTVAHLIECLLSKVA       1033
tr|A0A212MG88|A0A212MG88_ZYGBA      IGDKFASRHGQKGTIGITYSREDMPFTAEGIVPDLIINPHAIPSRMTVAHLIECLLSKVA       1034
tr|A0A1S7HHE1|A0A1S7HHE1_9SACH      IGDKFASRHGQKGTIGITYSREDMPFTAEGIVPDLIINPHAIPSRMTVAHLIECLLSKVA       1034
tr|S6ESB4|S6ESB4_ZYGB2              IGDKFASRHGQKGTIGITYSREDMPFTAEGIVPDLIINPHAIPSRMTVAHLIECLLSKVA       1034
tr|B6K5Q5|B6K5Q5_SCHJY              IGDKFASRHGQKGTIGMTYRHEDMPFSAQGIVPDIIINPHAIPSRMTVAHLVECQLSKVS       1024
sp|Q02061|RPB2_SCHPO                IGDKFASRHGQKGTIGMTYRHEDMPFSAQGIVPDIIINPHAIPSRMTVAHLVECQLSKVS       1024
tr|S9R8U4|S9R8U4_SCHOY              IGDKFASRHGQKGTIGMTYRHEDMPFSAQGVVPDVIINPHAIPSRMTVAHLIECQLSKVS       1024
tr|S9W8C6|S9W8C6_SCHCR              IGDKFASRHGQKGTIGMTYRHEDMPFSAQGIVPDVIINPHAIPSRMTVAHLIECQLSKVS       1024
sp|Q8RQE9|RPOB_THET8                VGDKLANRHGNKGVVAKILPVEDMPHLPDGTPVDVILNPLGVPSRMNLGQILETHLGLAG       894
ASR51304.1                          PGDKMAGRHGNKGIISRILPIEDMPFLEDGTHVDFVLNPLGVPSRMNVGQIFETHLGWAA       1147
OXR47929.1                          PGDKMAGRHGNKGVVSRITPVEDMPHMADGTPADIVLNPLGVPSRMNVGQVLEVHLGWAA       1140
WP_093971860.1                      PGDKMAGRHGNKGVVSRITPVEDMPHMADGTPADIVLNPLGVPSRMNVGQVLEVHLGWAA       1140
sp|Q2NWR6|RPOB_SODGM                PGDKMAGRHGNKGVISKINPIEDMPYDENGVPVDIVLNPLGVPSRMNIGQILETHLGMAA       1121
sp|B4EYU9|RPOB_PROMH                PGDKMAGRHGNKGVISKINPIEDMPYDENGNPVDLVLNPLGVPSRMNIGQILETHLGMAA       1121
sp|A7FNI3|RPOB_YERP3                PGDKMAGRHGNKGVISKINPIEDMPYDENGTPVDIVLNPLGVPSRMNIGQILETHLGMAA       1121
sp|Q1C1U1|RPOB_YERPA                PGDKMAGRHGNKGVISKINPIEDMPYDENGTPVDIVLNPLGVPSRMNIGQILETHLGMAA       1121
sp|B2K113|RPOB_YERPB                PGDKMAGRHGNKGVISKINPIEDMPYDENGTPVDIVLNPLGVPSRMNIGQILETHLGMAA       1121
sp|A8G8E7|RPOB_SERP5                PGDKMAGRHGNKGVISKINPIEDMPYDENGTPVDIVLNPLGVPSRMNIGQILETHLGMAA       1121
sp|Q6DAN0|RPOB_PECAS                PGDKMAGRHGNKGVISKINPIEDMPYDENGTPVDIVLNPLGVPSRMNIGQILETHLGMAA       1121
sp|C6DHR5|RPOB_PECCP                PGDKMAGRHGNKGVISKINPIEDMPYDENGTPVDIVLNPLGVPSRMNIGQILETHLGMAA       1121
sp|Q7N9A4|RPOB_PHOLL                PGDKMAGRHGNKGVISKINPIEDMPYDENGTPVDIVLNPLGVPSRMNIGQILETHLGMAA       1121
sp|C5BHE3|RPOB_EDWI9                PGDKMAGRHGNKGVISKINPIEDMPYDENGTPVDIVLNPLGVPSRMNIGQILETHLGMAA       1121
sp|A7MQQ9|RPOB_CROS8                PGDKMAGRHGNKGVISKINPIEDMPYDENGTPVDIVLNPLGVPSRMNIGQILETHLGMAA       1121
sp|B5XYF5|RPOB_KLEP3                PGDKMAGRHGNKGVISKINPIEDMPHDANGTPVDIVLNPLGVPSRMNIGQILETHLGMAA       1121
sp|P0A8V2|RPOB_ECOLI                PGDKMAGRHGNKGVISKINPIEDMPYDENGTPVDIVLNPLGVPSRMNIGQILETHLGMAA       1121
sp|C5A0S7|RPOB_ECOBW                PGDKMAGRHGNKGVISKINPIEDMPYDENGTPVDIVLNPLGVPSRMNIGQILETHLGMAA       1121
sp|Q31U10|RPOB_SHIBS                PGDKMAGRHGNKGVISKINPIEDMPYDENGTPVDIVLNPLGVPSRMNIGQILETHLGMAA       1121
sp|Q32AF9|RPOB_SHIDS                PGDKMAGRHGNKGVISKINPIEDMPYDENGTPVDIVLNPLGVPSRMNIGQILETHLGMAA       1121
sp|A8AKT9|RPOB_CITK8                PGDKMAGRHGNKGVISKINPIEDMPYDENGTPVDIVLNPLGVPSRMNIGQILETHLGMAA       1121
sp|B5RFK1|RPOB_SALG2                PGDKMAGRHGNKGVISKINPIEDMPYDENGTPVDIVLNPLGVPSRMNIGQILETHLGMAA       1121
sp|B5BJQ3|RPOB_SALPK                PGDKMAGRHGNKGVISKINPIEDMPYDENGTPVDIVLNPLGVPSRMNIGQILETHLGMAA       1121
sp|B4T0Y9|RPOB_SALNS                PGDKMAGRHGNKGVISKINPIEDMPYDENGTPVDIVLNPLGVPSRMNIGQILETHLGMAA       1121
sp|P06173|RPOB_SALTY                PGDKMAGRHGNKGVISKINPIEDMPYDENGTPVDIVLNPLGVPSRMNIGQILETHLGMAA       1121
                                     ***:*.***:**  .     ****.  :*   *.::** .:****.:.::.*   . ..


sp|P30876|RPB2_HUMAN                RKITSQIFIGPTYYQRLKHMVDDKIHSRARGPIQILNRQPMEGRSRDGGLRFGEMERDCQ       1094
tr|G3V8Y5|G3V8Y5_RAT                RKITSQIFIGPTYYQRLKHMVDDKIHSRARGPIQILNRQPMEGRSRDGGLRFGEMERDCQ       1094
tr|A0A250Y753|A0A250Y753_CASCN      RKITSQIFIGPTYYQRLKHMVDDKIHSRARGPIQILNRQPMEGRSRDGGLRFGEMERDCQ       1094
tr|A0A1U7R4C7|A0A1U7R4C7_MESAU      RKITSQIFIGPTYYQRLKHMVDDKIHSRARGPIQILNRQPMEGRSRDGGLRFGEMERDCQ       1094
tr|A0A286XIQ9|A0A286XIQ9_CAVPO      RKITSQIFIGPTYYQRLKHMVDDKIHSRARGPIQILNRQPMEGRSRDGGLRFGEMERDCQ       1094
tr|I3M351|I3M351_ICTTR              RKITSQIFIGPTYYQRLKHMVDDKIHSRARGPIQILNRQPMEGRSRDGGLRFGEMERDCQ       1094
tr|G7P5R6|G7P5R6_MACFA              RKITSQIFIGPTYYQRLKHMVDDKIHSRARGPIQILNRQPMEGRSRDGGLRFGEMERDCQ       1094
tr|H2QPI8|H2QPI8_PANTR              RKITSQIFIGPTYYQRLKHMVDDKIHSRARGPIQILNRQPMEGRSRDGGLRFGEMERDCQ       1094
tr|A0A1U7V0T5|A0A1U7V0T5_TARSY      RKITSQIFIGPTYYQRLKHMVDDKIHSRARGPIQILNRQPMEGRSRDGGLRFGEMERDCQ       1094
tr|A0A1S2ZSL2|A0A1S2ZSL2_ERIEU      RKITSQIFIGPTYYQRLKHMVDDKIHSRARGPIQILNRQPMEGRSRDGGLRFGEMERDCQ       1094
tr|A0A0D9QYL1|A0A0D9QYL1_CHLSB      RKITSQIFIGPTYYQRLKHMVDDKIHSRARGPIQILNRQPMEGRSRDGGLRFGEMERDCQ       1087
tr|A0A2K5ZNR7|A0A2K5ZNR7_MANLE      RKITSQIFIGPTYYQRLKHMVDDKIHSRARGPIQILNRQPMEGRSRDGGLRFGEMERDCQ       1087
tr|A0A2I2ZIU3|A0A2I2ZIU3_GORGO      RKITSQIFIGPTYYQRLKHMVDDKIHSRARGPIQILNRQPMEGRSRDGGLRFGEMERDCQ       1094
tr|A0A1D5QGA5|A0A1D5QGA5_MACMU      RKITSQIFIGPTYYQRLKHMVDDKIHSRARGPIQILNRQPMEGRSRDGGLRFGEMERDCQ       1094
tr|A0A2J8S2N1|A0A2J8S2N1_PONAB      RKITSQIFIGPTYYQRLKHMVDDKIHSRARGPIQILNRQPMEGRSRDGGLRFGEMERDCQ       1094
tr|A0A2K5K5J5|A0A2K5K5J5_COLAP      RKITSQIFIGPTYYQRLKHMVDDKIHSRARGPIQILNRQPMEGRSRDGGLRFGEMERDCQ       1094
tr|A0A2J8PEW7|A0A2J8PEW7_PANTR      RKITSQIFIGPTYYQRLKHMVDDKIHSRARGPIQILNRQPMEGRSRDGGLRFGEMERDCQ       1087
tr|A0A2K5CY83|A0A2K5CY83_AOTNA      RKITSQIFIGPTYYQRLKHMVDDKIHSRARGPIQILNRQPMEGRSRDGGLRFGEMERDCQ       1094
tr|A0A096NEY4|A0A096NEY4_PAPAN      RKITSQIFIGPTYYQRLKHMVDDKIHSRARGPIQILNRQPMEGRSRDGGLRFGEMERDCQ       1094
tr|C9J2Y9|C9J2Y9_HUMAN              RKITSQIFIGPTYYQRLKHMVDDKIHSRARGPIQILNRQPMEGRSRDGGLRFGEMERDCQ       1087
tr|G8BY61|G8BY61_TETPH              KKLMAQIFFGPTYYQRLRHMVDDKIHARARGPMQVLTRQPVEGRSRDGGLRFGEMERDCM       1138
tr|A0A1X7QYA1|A0A1X7QYA1_9SACH      KKLMAQIFFGPTYYQRLRHMVDDKIHARARGPMQVLTRQPVEGRSRDGGLRFGEMERDCM       1135
tr|J7RV95|J7RV95_KAZNA              KKLMAQIFFGPTYYQRLRHMVDDKIHARARGPMQVLTRQPVEGRSRDGGLRFGEMERDCM       1134
tr|H2AVJ8|H2AVJ8_KAZAF              KKLMAQIFFGPTYYQRLRHMVDDKIHARARGPMQVLTRQPVEGRSRDGGLRFGEMERDCM       1136
sp|Q6FLD5|RPB2_CANGA                KKLMAQIFFGPTYYQRLRHMVDDKIHARARGPMQVLTRQPVEGRSRDGGLRFGEMERDCM       1137
sp|P08518|RPB2_YEAST                KKLMAQIFFGPTYYQRLRHMVDDKIHARARGPMQVLTRQPVEGRSRDGGLRFGEMERDCM       1138
tr|A0A0L8VHA5|A0A0L8VHA5_9SACH      KKLMAQIFFGPTYYQRLRHMVDDKIHARARGPMQVLTRQPVEGRSRDGGLRFGEMERDCM       1138
tr|A0A0L8RB33|A0A0L8RB33_SACEU      KKLMAQIFFGPTYYQRLRHMVDDKIHARARGPMQVLTRQPVEGRSRDGGLRFGEMERDCM       1138
tr|G0VJ71|G0VJ71_NAUCC              KKLMAQIFFGPTYYQRLRHMVDDKIHARARGPMQVLTRQPVEGRSRDGGLRFGEMERDCM       1138
tr|G8ZM49|G8ZM49_TORDC              KKLMAQIFFGPTYYQRLRHMVDDKIHARARGPMQVLTRQPVEGRSRDGGLRFGEMERDCM       1136
tr|A0A1Q3A090|A0A1Q3A090_ZYGRO      KKLMSQIFFGPTYYQRLRHMVDDKIHARARGPMQVLTRQPVEGRSRDGGLRFGEMERDCM       1138
tr|A0A0N7IS35|A0A0N7IS35_9SACH      KKLMSQIFFGPTYYQRLRHMVDDKIHARARGPMQVLTRQPVEGRSRDGGLRFGEMERDCM       1136
tr|A0A212MG88|A0A212MG88_ZYGBA      KKLMSQIFFGPTYYQRLRHMVDDKIHARARGPMQVLTRQPVEGRSRDGGLRFGEMERDCM       1137
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tr|A0A1S7HHE1|A0A1S7HHE1_9SACH      KKLMSQIFFGPTYYQRLRHMVDDKIHARARGPMQVLTRQPVEGRSRDGGLRFGEMERDCM       1137
tr|S6ESB4|S6ESB4_ZYGB2              KKLMSQIFFGPTYYQRLRHMVDDKIHARARGPMQVLTRQPVEGRSRDGGLRFGEMERDCM       1137
tr|B6K5Q5|B6K5Q5_SCHJY              RKLVAQVFLGPTYYQRLKHLVDDKIHARARGPVQILTRQPVEGRSRDGGLRFGEMERDCQ       1127
sp|Q02061|RPB2_SCHPO                RKLVAQVFLGPTYYQRLKHLVDDKIHARARGPVQILTRQPVEGRSRDGGLRFGEMERDCQ       1127
tr|S9R8U4|S9R8U4_SCHOY              RKLVSQVFLGPTYYQRLKHLVDDKIHARARGPVQILTRQPVEGRSRDGGLRFGEMERDCQ       1127
tr|S9W8C6|S9W8C6_SCHCR              RKLVSQVFLGPTYYQRLKHLVDDKIHARARGPVQILTRQPVEGRSRDGGLRFGEMERDCQ       1127
sp|Q8RQE9|RPOB_THET8                EPIEGPIVVGQMFIMKLYHMVEDKMHARSTGPYSLITQQPLGGKAQFGGQRFGEMEVWAL       1040
ASR51304.1                          DKFDRKVTVGYIYMLKLHHLVDDKIHARSIGPYSLVTQQPLGGKAQFGGQRFGEMEVWAL       1310
OXR47929.1                          EQFERPVTVGYMHYLKLHHLVDDKMHARSTGPYSLVTQQPLGGKAQFGGQRFGEMEVWAL       1306
WP_093971860.1                      EQFERPVTVGYMHYLKLHHLVDDKMHARSTGPYSLVTQQPLGGKAQFGGQRFGEMEVWAL       1306
sp|Q2NWR6|RPOB_SODGM                EQFERQVTVGYMYMLKLNHLVDDKMHARSTGSYSLVTQQPLGGKAQFGGQRFGEMEVWAL       1278
sp|B4EYU9|RPOB_PROMH                EQFERQVTVGYMYMLKLNHLVDDKMHARSTGSYSLVTQQPLGGKAQFGGQRFGEMEVWAL       1278
sp|A7FNI3|RPOB_YERP3                EQFERQVTVGYMYMLKLNHLVDDKMHARSTGSYSLVTQQPLGGKAQFGGQRFGEMEVWAL       1278
sp|Q1C1U1|RPOB_YERPA                EQFERQVTVGYMYMLKLNHLVDDKMHARSTGSYSLVTQQPLGGKAQFGGQRFGEMEVWAL       1278
sp|B2K113|RPOB_YERPB                EQFERQVTVGYMYMLKLNHLVDDKMHARSTGSYSLVTQQPLGGKAQFGGQRFGEMEVWAL       1278
sp|A8G8E7|RPOB_SERP5                EQFERQVTVGYMYMLKLNHLVDDKMHARSTGSYSLVTQQPLGGKAQFGGQRFGEMEVWAL       1278
sp|Q6DAN0|RPOB_PECAS                EQFERQVTVGYMYMLKLNHLVDDKMHARSTGSYSLVTQQPLGGKAQFGGQRFGEMEVWAL       1278
sp|C6DHR5|RPOB_PECCP                EKFERQVTVGYMYMLKLNHLVDDKMHARSTGSYSLVTQQPLGGKAQFGGQRFGEMEVWAL       1278
sp|Q7N9A4|RPOB_PHOLL                EQFERQVTVGYMYMLKLNHLVDDKMHARSTGSYSLVTQQPLGGKAQFGGQRFGEMEVWAL       1278
sp|C5BHE3|RPOB_EDWI9                ERFERQVTVGYMYMLKLNHLVDDKMHARSTGSYSLVTQQPLGGKAQFGGQRFGEMEVWAL       1278
sp|A7MQQ9|RPOB_CROS8                EQFERPVTVGYMYMLKLNHLVDDKMHARSTGSYSLVTQQPLGGKAQFGGQRFGEMEVWAL       1278
sp|B5XYF5|RPOB_KLEP3                EQFERPVTVGYMYMLKLNHLVDDKMHARSTGSYSLVTQQPLGGKAQFGGQRFGEMEVWAL       1278
sp|P0A8V2|RPOB_ECOLI                EQFERPVTVGYMYMLKLNHLVDDKMHARSTGSYSLVTQQPLGGKAQFGGQRFGEMEVWAL       1278
sp|C5A0S7|RPOB_ECOBW                EQFERPVTVGYMYMLKLNHLVDDKMHARSTGSYSLVTQQPLGGKAQFGGQRFGEMEVWAL       1278
sp|Q31U10|RPOB_SHIBS                EQFERPVTVGYMYMLKLNHLVDDKMHARSTGSYSLVTQQPLGGKAQFGGQRFGEMEVWAL       1278
sp|Q32AF9|RPOB_SHIDS                EQFERPVTVGYMYMLKLNHLVDDKMHARSTGSYSLVTQQPLGGKAQFGGQRFGEMEVWAL       1278
sp|A8AKT9|RPOB_CITK8                EQFERSVTVGYMYMLKLNHLVDDKMHARSTGSYSLVTQQPLGGKAQFGGQRFGEMEVWAL       1278
sp|B5RFK1|RPOB_SALG2                EQFERPVTVGYMYMLKLNHLVDDKMHARSTGSYSLVTQQPLGGKAQFGGQRFGEMEVWAL       1278
sp|B5BJQ3|RPOB_SALPK                EQFERPVTVGYMYMLKLNHLVDDKMHARSTGSYSLVTQQPLGGKAQFGGQRFGEMEVWAL       1278
sp|B4T0Y9|RPOB_SALNS                EQFERPVTVGYMYMLKLNHLVDDKMHARSTGSYSLVTQQPLGGKAQFGGQRFGEMEVWAL       1278
sp|P06173|RPOB_SALTY                EQFERPVTVGYMYMLKLNHLVDDKMHARSTGSYSLVTQQPLGGKAQFGGQRFGEMEVWAL       1278
                                      :   : .*  .  :* *:*:**:*:*: *  .::.:**: *::: ** ******  .

sp|P30876|RPB2_HUMAN                ACKLLFQELMSMSIAPRMMSV-----------------    1174
tr|G3V8Y5|G3V8Y5_RAT                ACKLLFQELMSMSIAPRMMSV-----------------    1174
tr|A0A250Y753|A0A250Y753_CASCN      ACKLLFQELMSMSIAPRMMSV-----------------    1174
tr|A0A1U7R4C7|A0A1U7R4C7_MESAU      ACKLLFQELMSMSIAPRMMSV-----------------    1174
tr|A0A286XIQ9|A0A286XIQ9_CAVPO      ACKLLFQELMSMSIAPRMMSV-----------------    1174
tr|I3M351|I3M351_ICTTR              ACKLLFQELMSMSIAPRMMSV-----------------    1174
tr|G7P5R6|G7P5R6_MACFA              ACKLLFQELMSMSIAPRMMSV-----------------    1174
tr|H2QPI8|H2QPI8_PANTR              ACKLLFQELMSMSIAPRMMSV-----------------    1174
tr|A0A1U7V0T5|A0A1U7V0T5_TARSY      ACKLLFQELMSMSIAPRMMSV-----------------    1174
tr|A0A1S2ZSL2|A0A1S2ZSL2_ERIEU      ACKLLFQELMSMSIAPRMMSV-----------------    1174
tr|A0A0D9QYL1|A0A0D9QYL1_CHLSB      ACKLLFQELMSMSIAPRMMSV-----------------    1167
tr|A0A2K5ZNR7|A0A2K5ZNR7_MANLE      ACKLLFQELMSMSIAPRMMSV-----------------    1167
tr|A0A2I2ZIU3|A0A2I2ZIU3_GORGO      ACKLLFQELMSMSIAPRMMSV-----------------    1174
tr|A0A1D5QGA5|A0A1D5QGA5_MACMU      ACKLLFQELMSMSIAPRMMSV-----------------    1174
tr|A0A2J8S2N1|A0A2J8S2N1_PONAB      ACKLLFQELMSMSIAPRMMSV-----------------    1174
tr|A0A2K5K5J5|A0A2K5K5J5_COLAP      ACKLLFQELMSMSIAPRMMSV-----------------    1174
tr|A0A2J8PEW7|A0A2J8PEW7_PANTR      ACKLLFQELMSMSIAPRMMSV-----------------    1167
tr|A0A2K5CY83|A0A2K5CY83_AOTNA      ACKLLFQELMSMSIAPRMMSV-----------------    1174
tr|A0A096NEY4|A0A096NEY4_PAPAN      ACKLLFQELMSMSIAPRMMSV-----------------    1174
tr|C9J2Y9|C9J2Y9_HUMAN              ACKLLFQELMSMSIAPRMMSV-----------------    1167
tr|G8BY61|G8BY61_TETPH              AAKLLFQELMAMNITPRLYTDRSKNF------------    1224
tr|A0A1X7QYA1|A0A1X7QYA1_9SACH      AAKLLFQELMAMNITPRLYTDRSRDF------------    1221
tr|J7RV95|J7RV95_KAZNA              AAKLLFQELMAMNITPRLYTDRSRDF------------    1220
tr|H2AVJ8|H2AVJ8_KAZAF              AAKLLFQELMAMNITPRLFTDRSRDF------------    1222
sp|Q6FLD5|RPB2_CANGA                AAKLLFQELMAMNITPRLYTDRSRDF------------    1223
sp|P08518|RPB2_YEAST                AAKLLFQELMAMNITPRLYTDRSRDF------------    1224
tr|A0A0L8VHA5|A0A0L8VHA5_9SACH      AAKLLFQELMAMNITPRLYTDRSRDF------------    1224
tr|A0A0L8RB33|A0A0L8RB33_SACEU      AAKLLFQELMAMNITPRLYTDRSRDF------------    1224
tr|G0VJ71|G0VJ71_NAUCC              AAKLLFQELMAMNITPRLYTERSRDF------------    1224
tr|G8ZM49|G8ZM49_TORDC              AAKLLFQELMAMNITPRLYTDRSRDF------------    1222
tr|A0A1Q3A090|A0A1Q3A090_ZYGRO      AAKLLFQELMAMNITPRLYTDRSKDF------------    1224
tr|A0A0N7IS35|A0A0N7IS35_9SACH      AAKLLFQELMAMNITPRLYTDRSKDF------------    1222
tr|A0A212MG88|A0A212MG88_ZYGBA      AAKLLFQELMAMNITPRLYTDRSKDF------------    1223
tr|A0A1S7HHE1|A0A1S7HHE1_9SACH      AAKLLFQELMAMNITPRLYTDRSKDF------------    1223
tr|S6ESB4|S6ESB4_ZYGB2              AAKLLFQELMAMNITPRLYTDRSKDF------------    1223
tr|B6K5Q5|B6K5Q5_SCHJY              AAKLLFQELMSMNIAPRLFTKSHH--------------    1210
sp|Q02061|RPB2_SCHPO                AAKLLFQELMSMNIAPRLFTKNHK--------------    1210
tr|S9R8U4|S9R8U4_SCHOY              AAKLLFQELMSMNIAPRLFTKNHKI-------------    1211
tr|S9W8C6|S9W8C6_SCHCR              AAKLLFQELMSMNIAPRLFTKNHKN-------------    1211
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sp|Q8RQE9|RPOB_THET8          SFRVLVKELQALALDVQTLDEKDN--PVDIFEGLASKR   1119
ASR51304.1                    SFNVLVKEMRSLGLNVELNSIDALPDPDEIAEAAE---   1388
OXR47929.1                    SFNVLVKEIRSLSLDMDLERN-----------------   1370
WP_093971860.1                SFNVLVKEIRSLSLDMDLERN-----------------   1370
sp|Q2NWR6|RPOB_SODGM          SFNVLLKEIRSLGINIELEED-----------------   1342
sp|B4EYU9|RPOB_PROMH          SFNVLLKEIRSLGINIELEDE-----------------   1342
sp|A7FNI3|RPOB_YERP3          SFNVLLKEIRSLGINIELEEE-----------------   1342
sp|Q1C1U1|RPOB_YERPA          SFNVLLKEIRSLGINIELEEE-----------------   1342
sp|B2K113|RPOB_YERPB          SFNVLLKEIRSLGINIELEEE-----------------   1342
sp|A8G8E7|RPOB_SERP5          SFNVLLKEIRSLGINIELEGE-----------------   1342
sp|Q6DAN0|RPOB_PECAS          SFNVLLKEIRSLGINIELEEK-----------------   1342
sp|C6DHR5|RPOB_PECCP          SFNVLLKEIRSLGINIELEEE-----------------   1342
sp|Q7N9A4|RPOB_PHOLL          SFNVLLKEIRSLGINIELEGE-----------------   1342
sp|C5BHE3|RPOB_EDWI9          SFNVLLKEIRSLGINIELEDE-----------------   1342
sp|A7MQQ9|RPOB_CROS8          SFNVLLKEIRSLGINIELEDE-----------------   1342
sp|B5XYF5|RPOB_KLEP3          SFNVLLKEIRSLGINIELEDE-----------------   1342
sp|P0A8V2|RPOB_ECOLI          SFNVLLKEIRSLGINIELEDE-----------------   1342
sp|C5A0S7|RPOB_ECOBW          SFNVLLKEIRSLGINIELEDE-----------------   1342
sp|Q31U10|RPOB_SHIBS          SFNVLLKEIRSLGINIELEDE-----------------   1342
sp|Q32AF9|RPOB_SHIDS          SFNVLLKEIRSLGINIELEDE-----------------   1342
sp|A8AKT9|RPOB_CITK8          SFNVLLKEIRSLGINIELEDE-----------------   1342
sp|B5RFK1|RPOB_SALG2          SFNVLLKEIRSLGINIELEDE-----------------   1342
sp|B5BJQ3|RPOB_SALPK          SFNVLLKEIRSLGINIELEDE-----------------   1342
sp|B4T0Y9|RPOB_SALNS          SFNVLLKEIRSLGINIELEDE-----------------   1342
sp|P06173|RPOB_SALTY          SFNVLLKEIRSLGINIELEDE-----------------   1342
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Fig. 5 Mix and Match analysis of the initiation subunits β of *E. coli* and Rpb2 of yeast RNAP-II
For legends follow Figures 3-5.

Figure 6 shows the mix and match analysis of the elongation subunits from pro- and eukaryotes MSU RNAPs. The active site regions are highlighted in yellow and the representative sequences are highlighted in yellow. In eukaryotic elongation subunits, the catalytic region is brought to the N-terminal region whereas it is found very close to the C-terminal region. There are 4 Cs at the N-terminal region in prokaryotic elongation subunits (out of which 2 are aligning in both) suggesting a possible additional Zn binding region. There are a very few motifs aligning in both. Significant among them are –GHIELA-, -NLM/LGKRVDF/YS-, possible metal binding region -DFDGDE/QM-, -DTAV/LKTAE/NT/SGYI/L-, -L/V/IAAQSIGEPA/GTQM/LTL/MXTFH-. The metal binding region -NADFDGD- is aligning in both and placed in the middle of the enzyme. The C-terminal ends in eukaryotes usually end in -PDDSDE/DE/DN- (except in yeasts and Alligator) and -GSDNE/D- in prokaryotes, suggesting a possible metal binding site (DxD) at the ends. It is interesting to note that the prokaryotic active site is placed at the C-terminal region (~900 amino acids) whereas the eukaryotic active site is placed at the N-terminal region (~90 amino acids) with their built-in Zn binding motifs.

CLUSTAL O(1.2.4):MSA of eubacterial β’ and eukaryotic Rpb1 subunits 6

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tr|A0A1U8DYN0|A0A1U8DYN0_ALLSI      DPRQGVIERTGR---------------CQTCA-GNM--TECPGHFGHIELAKPVFHVGFL       99
tr|A0A1L8H4P4|A0A1L8H4P4_XENLA      DPRQGVIERSGR---------------CQTCA-GNM--TECPGHFGHVELAKPVYHVGFL       98
tr|H9GLG5|H9GLG5_ANOCA              DPRQGVIERTGR---------------CQTCA-GNM--TECPGHFGHIELAKPVFHVGFL       99
tr|H2R1J6|H2R1J6_PANTR              DPRQGVIERTGR---------------CQTCA-GNM--TECPGHFGHIELAKPVFHVGFL       100
sp|P08775|RPB1_MOUSE                DPRQGVIERTGR---------------CQTCA-GNM--TECPGHFGHIELAKPVFHVGFL       100
tr|G1MCZ1|G1MCZ1_AILME              DPRQGVIERTGR---------------CQTCA-GNM--TECPGHFGHIELAKPVFHVGFL       100
tr|O08847|O08847_MOUSE              DPRQGVIERTGR---------------CQTCA-GNM--TECPGHFGHIELAKPVFHVGFL       100
tr|S7PWZ6|S7PWZ6_MYOBR              DPRQGVIERTGR---------------CQTCA-GNM--TECPGHFGHIELAKPVFHVGFL       100
tr|D4A5A6|D4A5A6_RAT                DPRQGVIERTGR---------------CQTCA-GNM--TECPGHFGHIELAKPVFHVGFL       100
tr|A0A1S3EWL2|A0A1S3EWL2_DIPOR      DPRQGVIERTGR---------------CQTCA-GNM--TECPGHFGHIELAKPVFHVGFL       100
sp|P11414|RPB1_CRIGR                DPRQGVIERTGR---------------CQTCA-GNM--TECPGHFGHIELAKPVFHVGFL       100
tr|O35559|O35559_CRIGR              DPRQGVIERTGR---------------CQTCA-GNM--TECPGHFGHIELAKPVFHVGFL       100
tr|A0A2I3M9H2|A0A2I3M9H2_PAPAN      DPRQGVIERTGR---------------CQTCA-GNM--TECPGHFGHIELAKPVFHVGFL       100
tr|F7HB40|F7HB40_MACMU              DPRQGVIERTGR---------------CQTCA-GNM--TECPGHFGHIELAKPVFHVGFL       100
tr|A0A2K6RYW9|A0A2K6RYW9_SAIBB      DPRQGVIERTGR---------------CQTCA-GNM--TECPGHFGHIELAKPVFHVGFL       100
tr|W5N8Z6|W5N8Z6_LEPOC              DPRQGVIERSGR---------------CQTCAAGNM--TECPGHFGHIELAKPVFHVGFI       99
tr|I3JRW6|I3JRW6_ORENI              DPRQGVIERTGR---------------CQTCA-GNM--TECPGHFGHIELAKPVFHVGFI       98
tr|A0A0R4IMS9|A0A0R4IMS9_DANRE      DPRQGVIERSGR---------------CQTCA-GNM--TECPGHFGHIELAKPVFHVGFI       98
tr|A0A1A7X327|A0A1A7X327_9TELE      DPRQGVIERSGR---------------CQTCA-GNM--TECPGHFGHIELAKPVFHVGFI       98
tr|A0A1A8UKD7|A0A1A8UKD7_NOTFU      DPRQGVIERTGR---------------CQTCA-GNM--TECPGHFGHIELAKPVFHVGFI       98
tr|A0A1A8ER05|A0A1A8ER05_9TELE      DPRQGVIERTGR---------------CQTCA-GNM--TECPGHFGHIELAKPVFHVGFI       98
tr|A0A1A8DQ60|A0A1A8DQ60_9TELE      DPRQGVIERTGR---------------CQTCA-GNM--TECPGHFGHIELAKPVFHVGFI       98
tr|A0A1A8NSR8|A0A1A8NSR8_9TELE      DPRQGVIERTGR---------------CQTCA-GNM--TECPGHFGHIELAKPVFHVGFI       98
tr|A0A1W4YLM7|A0A1W4YLM7_9TELE      DPRQGVIERTGR---------------CQTCA-GNM--TECPGHFGHIELAKPVFHVGFI       98
tr|A0A1M8A6L7|A0A1M8A6L7_MALS4      DPRLGTIDRNYK---------------CQTCGE-GQ--AECPGHFGHIDLARPVFHVGFL       98
sp|P04050|RPB1_YEAST                DPRLGSIDRNLK---------------CQTCQE-GM--NECPGHFGHIDLAKPVFHVGFI       96
tr|A0A1B2J8C6|A0A1B2J8C6_PICPA      DPKLGSIDRNFK---------------CQTCGE-GM--AECPGHFGHMELAKPVFHIGFI       96
tr|F2QW17|F2QW17_KOMPC              DPKLGSIDRNFK---------------CQTCGE-GM--AECPGHFGHMELAKPVFHIGFI       96
tr|A3GID7|A3GID7_PICST              DPRLGSIDRNFR---------------CQTCGE-DM--AECPGHFGHIELAKPVFHIGFI       97
tr|A0A1D8PUA6|A0A1D8PUA6_CANAL      DPRLGSIDRNFR---------------CQTCGE-DM--AECPGHFGHIELAKPVFHIGFI       97
tr|G8BEH9|G8BEH9_CANPC              DPRLGSIDRNFK---------------CQTCGE-DM--AECPGHFGHIELAKPVFHIGFI       976,19
AEG34223.1                          DERIFGPIKDYECACGKYKRQRFEGKVCERCGVEVTKSIVRRYRMGHIELATPAAHIWFV       105
ASR51305.1                          CARIFGPVKDYECLCGKYKRMKYKGIVCEKCGVEVTVTKVRRERMGHIELAAPVAHIWFL       117
OXR47930.1                          CAKIFGPIKDYECLCGKYKRLKHRGVICEKCGVEVTVAKVRRERMGHIELASPVAHIWFL       117
sp|A7MQQ8|RPOC_CROS8                CARIFGPVKDYECLCGKYKRLKHRGVICEKCGVEVTQTKVRRERMGHIELASPTAHIWFL       117
sp|Q32AG0|RPOC_SHIDS                CARIFGPVKDYECLCGKYKRLKHRGVICEKCGVEVTQTKVRRERMGHIELASPTAHIWFL       117
sp|Q0SY12|RPOC_SHIF8                CARIFGPVKDYECLCGKYKRLKHRGVICEKCGVEVTQTKVRRERMGHIELASPTAHIWFL       117
sp|B2TWH4|RPOC_SHIB3                CARIFGPVKDYECLCGKYKRLKHRGVICEKCGVEVTQTKVRRERMGHIELASPTAHIWFL       117
sp|P0A8T7|RPOC_ECOLI                CARIFGPVKDYECLCGKYKRLKHRGVICEKCGVEVTQTKVRRERMGHIELASPTAHIWFL       117
sp|Q3YUZ6|RPOC_SHISS                CARIFGPVKDYECLCGKYKRLKHRGVICEKCGVEVTQTKVRRERMGHIELASPTAHIWFL       117
sp|B1XBZ0|RPOC_ECODH                CARIFGPVKDYECLCGKYKRLKHRGVICEKCGVEVTQTKVRRERMGHIELASPTAHIWFL       117
sp|A8A787|RPOC_ECOHS                CARIFGPVKDYECLCGKYKRLKHRGVICEKCGVEVTQTKVRRERMGHIELASPTAHIWFL       117
tr|A0A237JUP3|A0A237JUP3_SHISO      CARIFGPVKDYECLCGKYKRLKHRGVICEKCGVEVTQTKVRRERMGHIELASPTAHIWFL       117
tr|A0A0F1RBF2|A0A0F1RBF2_ENTAS      CARIFGPVKDYECLCGKYKRLKHRGVICEKCGVEVTQTKVRRERMGHIELASPTAHIWFL       117
tr|A0A1B3EWG0|A0A1B3EWG0_ENTCL      CARIFGPVKDYECLCGKYKRLKHRGVICEKCGVEVTQTKVRRERMGHIELASPTAHIWFL       117
tr|A0A0F0XM62|A0A0F0XM62_9ENTR      CARIFGPVKDYECLCGKYKRLKHRGVICEKCGVEVTQTKVRRERMGHIELASPTAHIWFL       117
sp|Q5PK92|RPOC_SALPA                CARIFGPVKDYECLCGKYKRLKHRGVICEKCGVEVTQTKVRRERMGHIELASPTAHIWFL       117
sp|A9MHE9|RPOC_SALAR                CARIFGPVKDYECLCGKYKRLKHRGVICEKCGVEVTQTKVRRERMGHIELASPTAHIWFL       117
tr|A0A232XM43|A0A232XM43_SALMU      CARIFGPVKDYECLCGKYKRLKHRGVICEKCGVEVTQTKVRRERMGHIELASPTAHIWFL       117
tr|B5RFK0|B5RFK0_SALG2              CARIFGPVKDYECLCGKYKRLKHRGVICEKCGVEVTQTKVRRERMGHIELASPTAHIWFL       117
sp|P0A2R5|RPOC_SALTI                CARIFGPVKDYECLCGKYKRLKHRGVICEKCGVEVTQTKVRRERMGHIELASPTAHIWFL       117
sp|Q57H68|RPOC_SALCH                CARIFGPVKDYECLCGKYKRLKHRGVICEKCGVEVTQTKVRRERMGHIELASPTAHIWFL       117
sp|P0A2R4|RPOC_SALTY                CARIFGPVKDYECLCGKYKRLKHRGVICEKCGVEVTQTKVRRERMGHIELASPTAHIWFL       117
sp|A6TGP1|RPOC_KLEP7                CARIFGPVKDYECLCGKYKRLKHRGVICEKCGVEVTQTKVRRERMGHIELACPTAHIWFL       117
tr|A0A0J2K6S7|A0A0J2K6S7_9ENTR      CARIFGPVKDYECLCGKYKRLKHRGVICEKCGVEVTQTKVRRERMGHIELASPTAHIWFL       117
tr|A0A0G3RZQ0|A0A0G3RZQ0_KLEOX      CARIFGPVKDYECLCGKYKRLKHRGVICEKCGVEVTQTKVRRERMGHIELASPTAHIWFL       117
tr|A0A212HDS5|A0A212HDS5_9ENTR      CARIFGPVKDYECLCGKYKRLKHRGVICEKCGVEVTQTKVRRERMGHIELASPTAHIWFL       117
tr|A0A1R0FP41|A0A1R0FP41_CITBR      CARIFGPVKDYECLCGKYKRLKHRGVICEKCGVEVTQTKVRRERMGHIELASPTAHIWFL       117
tr|A0A078LHA5|A0A078LHA5_CITKO      CARIFGPVKDYECLCGKYKRLKHRGVICEKCGVEVTQTKVRRERMGHIELASPTAHIWFL       117
sp|A8AKT8|RPOC_CITK8                CARIFGPVKDYECLCGKYKRLKHRGVICEKCGVEVTQTKVRRERMGHIELASPTAHIWFL       117
                                      :     :  .               *: *            ::**::** *. *: *:


tr|A0A1U8DYN0|A0A1U8DYN0_ALLSI      ATMVDNELPGLPRAMQKSGRPLKSLKQRLKGKEGRVRGNLMGKRVDFSARTVITPDPNLS       373
tr|A0A1L8H4P4|A0A1L8H4P4_XENLA      ATMVDNEIPGLPRAMQKSGRPLKSVKQRLKGKEGRVRGNLMGKRVDFSARTVITPDPNLS       372
tr|H9GLG5|H9GLG5_ANOCA              ATMVDNELPGLPRAMQKSGRPLKSLKQRLKGKEGRVRGNLMGKRVDFSARTVITPDPNLS       373
tr|H2R1J6|H2R1J6_PANTR              ATMVDNELPGLPRAMQKSGRPLKSLKQRLKGKEGRVRGNLMGKRVDFSARTVITPDPNLS       374
sp|P08775|RPB1_MOUSE                ATMVDNELPGLPRAMQKSGRPLKSLKQRLKGKEGRVRGNLMGKRVDFSARTVITPDPNLS       374
tr|G1MCZ1|G1MCZ1_AILME              ATMVDNELPGLPRAMQKSGRPLKSLKQRLKGKEGRVRGNLMGKRVDFSARTVITPDPNLS       374
tr|O08847|O08847_MOUSE              ATMVDNELPGLPRAMQKSGRPLKSLKQRLKGKEGRVRGNLMGKRVDFSARTVITPDPNLS       374
tr|S7PWZ6|S7PWZ6_MYOBR              ATMVDNELPGLPRAMQKSGRPLKSLKQRLKGKEGRVRGNLMGKRVDFSARTVITPDPNLS       374
tr|D4A5A6|D4A5A6_RAT                ATMVDNELPGLPRAMQKSGRPLKSLKQRLKGKEGRVRGNLMGKRVDFSARTVITPDPNLS       374
tr|A0A1S3EWL2|A0A1S3EWL2_DIPOR      ATMVDNELPGLPRAMQKSGRPLKSLKQRLKGKEGRVRGNLMGKRVDFSARTVITPDPNLS       374
sp|P11414|RPB1_CRIGR                ATMVDNELPGLPRAMQKSGRPLKSLKQRLKGKEGRVRGNLMGKRVDFSARTVITPDPNLS       374
tr|O35559|O35559_CRIGR              ATMVDNELPGLPRAMQKSGRPLKSLKQRLKGKEGRVRGNLMGKRVDFSARTVITPDPNLS       374
tr|A0A2I3M9H2|A0A2I3M9H2_PAPAN      ATMVDNELPGLPRAMQKSGRPLKSLKQRLKGKEGRVRGNLMGKRVDFSARTVITPDPNLS       374
tr|F7HB40|F7HB40_MACMU              ATMVDNELPGLPRAMQKSGRPLKSLKQRLKGKEGRVRGNLMGKRVDFSARTVITPDPNLS       374
tr|A0A2K6RYW9|A0A2K6RYW9_SAIBB      ATMVDNELPGLPRAMQKSGRPLKSLKQRLKGKEGRVRGNLMGKRVDFSARTVITPDPNLS       374
tr|W5N8Z6|W5N8Z6_LEPOC              ATMVDNELPGLPRAMQKSGRPLKSIKQRLKGKEGRVRGNLMGKRVDFSARTVITPDPNLQ       373
tr|I3JRW6|I3JRW6_ORENI              ATMVDNELPGLPRAMQKSGRPLKSIKQRLKGKEGRVRGNLMGKRVDFSARTVITPDPNLQ       372
tr|A0A0R4IMS9|A0A0R4IMS9_DANRE      ATMVDNELPGLPRAMQKSGRPLKSIKQRLKGKEGRVRGNLMGKRVDFSARTVITPDPNLQ       371
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tr|A0A1A7X327|A0A1A7X327_9TELE      ATMVDNELPGLPRAMQKSGRPLKSIKQRLKGKEGRVRGNLMGKRVDFSARTVITPDPNLQ        372
tr|A0A1A8UKD7|A0A1A8UKD7_NOTFU      ATMVDNELPGLPRAMQKSGRPLKSLKQRLKGKEGRVRGNLMGKRVDFSARTVITPDPNLQ        372
tr|A0A1A8ER05|A0A1A8ER05_9TELE      ATMVDNELPGLPRAMQKSGRPLKSIKQRLKGKEGRVRGNLMGKRVDFSARTVITPDPNLQ        372
tr|A0A1A8DQ60|A0A1A8DQ60_9TELE      ATMVDNELPGLPRAMQKSGRPLKSLKQRLKGKEGRVRGNLMGKRVDFSARTVITPDPNLQ        372
tr|A0A1A8NSR8|A0A1A8NSR8_9TELE      ATMVDNELPGLPRAMQKSGRPLKSLKQRLKGKEGRVRGNLMGKRVDFSARTVITPDPNLQ        372
tr|A0A1W4YLM7|A0A1W4YLM7_9TELE      ATMVDNELPGLPRAMQKSGRPLKSIKQRLKGKEGRVRGNLMGKRVDFSARTVITPDPNLQ        372
tr|A0A1M8A6L7|A0A1M8A6L7_MALS4      ATYMDNDIAGLPQSLQSSGRPVKAIRARLKGKEGRLRGNLMGKRVDFSARTVITGDPNLE        374
sp|P04050|RPB1_YEAST                ATYMDNDIAGQPQALQKSGRPVKSIRARLKGKEGRIRGNLMGKRVDFSARTVISGDPNLE        360
tr|A0A1B2J8C6|A0A1B2J8C6_PICPA      ATYMDNDIAGQPQALQKSGRPVKAIRARLKGKEGRLRGNLMGKRVDFSARTVISGDPNLE        361
tr|F2QW17|F2QW17_KOMPC              ATYMDNDIAGQPQALQKSGRPVKAIRARLKGKEGRLRGNLMGKRVDFSARTVISGDPNLE        361
tr|A3GID7|A3GID7_PICST              ATYMDNDIAGQPQALQKTGRPIKSIRARLKGKEGRLRGNLMGKRVDFSARTVISGDPNLD        360
tr|A0A1D8PUA6|A0A1D8PUA6_CANAL      ATYMDNDIAGQPQALQKTGRPIKSIRARLKGKEGRLRGNLMGKRVDFSARTVISGDPNLD        360
tr|G8BEH9|G8BEH9_CANPC              ATYMDNDIAGQPQALQKTGRPIKSIRARLKGKEGRLRGNLMGKRVDFSARTVISGDPNLD        360
AEG34223.1                          DALLDNGRRGAPVTNPGSDRPLRSLTDILSGKQGRFRQNLLGKRVDYSGRSVIVVGPQLK        638
ASR51305.1                          DALFDNGRRGRIITG-ANKRPLKSLSDMLKGKQGRFRQNLLGKRVDYSGRSVIVTGPELK        363
OXR47930.1                          DSLLDNGRRGKAMTG-ANKRQLKSLADMIKGKSGRFRQNLLGKRVDYSGRSVIVVGPQLK        362
sp|A7MQQ8|RPOC_CROS8                DALLDNGRRGRAITG-SNKRPLKSLADMIKGKQGRFRQNLLGKRVDYSGRSVITVGPYLR        362
sp|Q32AG0|RPOC_SHIDS                DALLDNGRRGRAITG-SNKRPLKSLADMIKGKQGRFRQNLLGKRVDYSGRSVITVGPYLR        362
sp|Q0SY12|RPOC_SHIF8                DALLDNGRRGRAITG-SNKRPLKSLADMIKGKQGRFRQNLLGKRVDYSGRSVITVGPYLR        362
sp|B2TWH4|RPOC_SHIB3                DALLDNGRRGRAITG-SNKRPLKSLADMIKGKQGRFRQNLLGKRVDYSGRSVITVGPYLR        362
sp|P0A8T7|RPOC_ECOLI                DALLDNGRRGRAITG-SNKRPLKSLADMIKGKQGRFRQNLLGKRVDYSGRSVITVGPYLR        362
sp|Q3YUZ6|RPOC_SHISS                DALLDNGRRGRAITG-SNKRPLKSLADMIKGKQGRFRQNLLGKRVDYSGRSVITVGPYLR        362
sp|B1XBZ0|RPOC_ECODH                DALLDNGRRGRAITG-SNKRPLKSLADMIKGKQGRFRQNLLGKRVDYSGRSVITVGPYLR        362
sp|A8A787|RPOC_ECOHS                DALLDNGRRGRAITG-SNKRPLKSLADMIKGKQGRFRQNLLGKRVDYSGRSVITVGPYLR        362
tr|A0A237JUP3|A0A237JUP3_SHISO      DALLDNGRRGRAITG-SNKRPLKSLADMIKGKQGRFRQNLLGKRVDYSGRSVITVGPYLR        362
tr|A0A0F1RBF2|A0A0F1RBF2_ENTAS      DALLDNGRRGRAITG-SNKRPLKSLADMIKGKQGRFRQNLLGKRVDYSGRSVITVGPYLR        362
tr|A0A1B3EWG0|A0A1B3EWG0_ENTCL      DALLDNGRRGRAITG-SNKRPLKSLADMIKGKQGRFRQNLLGKRVDYSGRSVITVGPYLR        362
tr|A0A0F0XM62|A0A0F0XM62_9ENTR      DALLDNGRRGRAITG-SNKRPLKSLADMIKGKQGRFRQNLLGKRVDYSGRSVITVGPYLR        362
sp|Q5PK92|RPOC_SALPA                DALLDNGRRGRAITG-SNKRPLKSLADMIKGKQGRFRQNLLGKRVDYSGRSVITVGPYLR        362
sp|A9MHE9|RPOC_SALAR                DALLDNGRRGRAITG-SNKRPLKSLADMIKGKQGRFRQNLLGKRVDYSGRSVITVGPYLR        362
tr|A0A232XM43|A0A232XM43_SALMU      DALLDNGRRGRAITG-SNKRPLKSLADMIKGKQGRFRQNLLGKRVDYSGRSVITVGPYLR        362
tr|B5RFK0|B5RFK0_SALG2              DALLDNGRRGRAITG-SNKRPLKSLADMIKGKQGRFRQNLLGKRVDYSGRSVITVGPYLR        362
sp|P0A2R5|RPOC_SALTI                DALLDNGRRGRAITG-SNKRPLKSLADMIKGKQGRFRQNLLGKRVDYSGRSVITVGPYLR        362
sp|Q57H68|RPOC_SALCH                DALLDNGRRGRAITG-SNKRPLKSLADMIKGKQGRFRQNLLGKRVDYSGRSVITVGPYLR        362
sp|P0A2R4|RPOC_SALTY                DALLDNGRRGRAITG-SNKRPLKSLADMIKGKQGRFRQNLLGKRVDYSGRSVITVGPYLR        362
sp|A6TGP1|RPOC_KLEP7                DALLDNGRRGRAITG-SNKRPLKSLADMIKGKQGRFRQNLLGKRVDYSGRSVITVGPYLR        362
tr|A0A0J2K6S7|A0A0J2K6S7_9ENTR      DALLDNGRRGRAITG-SNKRPLKSLADMIKGKQGRFRQNLLGKRVDYSGRSVITVGPYLR        362
tr|A0A0G3RZQ0|A0A0G3RZQ0_KLEOX      DALLDNGRRGRAITG-SNKRPLKSLADMIKGKQGRFRQNLLGKRVDYSGRSVITVGPYLR        362
tr|A0A212HDS5|A0A212HDS5_9ENTR      DALLDNGRRGRAITG-SNKRPLKSLADMIKGKQGRFRQNLLGKRVDYSGRSVITVGPYLR        362
tr|A0A1R0FP41|A0A1R0FP41_CITBR      DALLDNGRRGRAITG-SNKRPLKSLADMIKGKQGRFRQNLLGKRVDYSGRSVITVGPYLR        362
tr|A0A078LHA5|A0A078LHA5_CITKO      DALLDNGRRGRAITG-SNKRPLKSLADMIKGKQGRFRQNLLGKRVDYSGRSVITVGPYLR        362
sp|A8AKT8|RPOC_CITK8                DALLDNGRRGRAITG-SNKRPLKSLADMIKGKQGRFRQNLLGKRVDYSGRSVITVGPYLR        362
                                     : .**   *   :   . * ::::   :.**.**.* **:*****:*.*:**  .* *

tr|A0A1U8DYN0|A0A1U8DYN0_ALLSI      PSDLHLQIGYKVERHMCDGDIVIFNRQPTLHKMSMMGHRVRILPWSTFRLNLSVTTPYNA        493
tr|A0A1L8H4P4|A0A1L8H4P4_XENLA      PSDLHLQIGYKVERHMCDGDIVIFNRQPTLHKMSMMGHRVRILPWSTFRLNLSVTTPYNA        492
tr|H9GLG5|H9GLG5_ANOCA              PSDLHLQIGYKVERHMCDGDIVIFNRQPTLHKMSMMGHRVRILPWSTFRLNLSVTTPYNA        493
tr|H2R1J6|H2R1J6_PANTR              PSDLHLQTGYKVERHMCDGDIVIFNRQPTLHKMSMMGHRVRILPWSTFRLNLSVTTPYNA        494
sp|P08775|RPB1_MOUSE                PSDLHLQTGYKVERHMCDGDIVIFNRQPTLHKMSMMGHRVRILPWSTFRLNLSVTTPYNA        494
tr|G1MCZ1|G1MCZ1_AILME              PSDLHLQTGYKVERHMCDGDIVIFNRQPTLHKMSMMGHRVRILPWSTFRLNLSVTTPYNA        494
tr|O08847|O08847_MOUSE              PSDLHLQTGYKVERHMCDGDIVIFNRQPTLHKMSMMGHRVRILPWSTFRLNLSVTTPYNA        494
tr|S7PWZ6|S7PWZ6_MYOBR              PSDLHLQTGYKVERHMCDGDIVIFNRQPTLHKMSMMGHRVRILPWSTFRLNLSVTTPYNA        494
tr|D4A5A6|D4A5A6_RAT                PSDLHLQTGYKVERHMCDGDIVIFNRQPTLHKMSMMGHRVRILPWSTFRLNLSVTTPYNA        494
tr|A0A1S3EWL2|A0A1S3EWL2_DIPOR      PSDLHLQTGYKVERHMCDGDIVIFNRQPTLHKMSMMGHRVRILPWSTFRLNLSVTTPYNA        494
sp|P11414|RPB1_CRIGR                PSDLHLQTGYKVERHMCDGDIVIFNRQPTLHKMSMMGHRVRILPWSTFRLNLSVTTPYNA        494
tr|O35559|O35559_CRIGR              PSDLHLQTGYKVERHMCDGDIVIFNRQPTLHKMSMMGHRVRILPWSTFRLNLSVTTPYNA        494
tr|A0A2I3M9H2|A0A2I3M9H2_PAPAN      PSDLHLQTGYKVERHMCDGDIVIFNRQPTLHKMSMMGHRVRILPWSTFRLNLSVTTPYNA        494
tr|F7HB40|F7HB40_MACMU              PSDLHLQTGYKVERHMCDGDIVIFNRQPTLHKMSMMGHRVRILPWSTFRLNLSVTTPYNA        494
tr|A0A2K6RYW9|A0A2K6RYW9_SAIBB      PSDLHLQTGYKVERHMCDGDIVIFNRQPTLHKMSMMGHRVRILPWSTFRLNLSVTTPYNA        494
tr|W5N8Z6|W5N8Z6_LEPOC              PSDLHLQIGYKVERHMCDGDIVIFNRQPTLHKMSMMGHRVRILPWSTFRLNLSVTTPYNA        493
tr|I3JRW6|I3JRW6_ORENI              PSDLHLQIGYKVERHMCDGDIVIFNRQPTLHKMSMMGHRVRILPWSTFRLNLSVTTPYNA        492
tr|A0A0R4IMS9|A0A0R4IMS9_DANRE      PSDLHLQIGYKVERHMCDGDIIVFNRQPTLHKMSMMGHRVRILPWSTFRLNLSVTTPYNA        491
tr|A0A1A7X327|A0A1A7X327_9TELE      PSDLHLQIGYKVERHMCEGDIVIFNRQPTLHKMSMMGHRVRILPWSTFRLNLSVTTPYNA        492
tr|A0A1A8UKD7|A0A1A8UKD7_NOTFU      PSDLHLQIGYKVERHMCDGDIVIFNRQPTLHKMSMMGHRVRILPWSTFRLNLSVTTPYNA        492
tr|A0A1A8ER05|A0A1A8ER05_9TELE      PSDLHLQIGYKVERHMCDGDIVIFNRQPTLHKMSMMGHRVRILPWSTFRLNLSVTTPYNA        492
tr|A0A1A8DQ60|A0A1A8DQ60_9TELE      PSDLHLQIGYKVERHMCDGDIVIFNRQPTLHKMSMMGHRVRILPWSTFRLNLSVTTPYNA        492
tr|A0A1A8NSR8|A0A1A8NSR8_9TELE      PSDLHLQIGYKVERHMCDGDIVIFNRQPTLHKMSMMGHRVRILPWSTFRLNLSVTTPYNA        492
tr|A0A1W4YLM7|A0A1W4YLM7_9TELE      PSDLHLQIGYKVERHMCDGDIIIFNRQPTLHKMSMMGHRVRILPWSTFRLNLSVTTPYNA        492
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sp|P04050|RPB1_YEAST                AGDIQLQYGWKVERHIMDNDPVLFNRQPSLHKMSMMAHRVKVIPYSTFRLNLSVTSPYNA        480
tr|A0A1B2J8C6|A0A1B2J8C6_PICPA      AGDIVLQYGWKVERHLMDDDPVLFNRQPSLHKMSMMAHRVKVMPYSTFRLNLSVTSPYNA        481
tr|F2QW17|F2QW17_KOMPC              AGDIVLQYGWKVERHLMDDDPVLFNRQPSLHKMSMMAHRVKVMPYSTFRLNLSVTSPYNA        481
tr|A3GID7|A3GID7_PICST              AGDIALQYGWKVERHLMDNDPVLFNRQPSLHKMSMMAHRVKVMPYSTFRLNLSVTSPYNA        480
tr|A0A1D8PUA6|A0A1D8PUA6_CANAL      AGDIALQYGWKVERHLMDDDPVLFNRQPSLHKMSMMAHRVRVMPYSTFRLNLSVTSPYNA        480
tr|G8BEH9|G8BEH9_CANPC              AGDIALQYGWKVERHLMDDDPVLFNRQPSLHKMSMMAHRVKVMPYSTFRLNLSVTSPYNA        480
AEG34223.1                          QRDI-KDEVWDALEEVIHGKVVLLNRAPTLHRLGIQAFQPVLVEGQSIQLHPLVCEAFNA        738
ASR51305.1                          ER----KEVWDILDEVIREHPVMLNRAPTLHRLGIQAFEPVLIEGKAIQLHPLVCSAFNA        460
OXR47930.1                          QE----PVVWDILEEVIREHPVMLNRAPTLHRLGIQAFEPVLIEGKAIQLHPLVCAAFNA        459
sp|A7MQQ8|RPOC_CROS8                EE----AVVWDILDEVIREHPVLLNRAPTLHRLGIQAFEPVLIEGKAIQLHPLVCAAYNA        459
sp|Q32AG0|RPOC_SHIDS                EE----AVVWDILDEVIREHPVLLNRAPTLHRLGIQAFEPVLIEGKAIQLHPLVCAAYNA        459
sp|Q0SY12|RPOC_SHIF8                EE----AVVWDILDEVIREHPVLLNRAPTLHRLGIQAFEPVLIEGKAIQLHPLVCAAYNA        459
sp|B2TWH4|RPOC_SHIB3                EE----AVVWDILDEVIREHPVLLNRAPTLHRLGIQAFEPVLIEGKAIQLHPLVCAAYNA        459
sp|P0A8T7|RPOC_ECOLI                EE----AVVWDILDEVIREHPVLLNRAPTLHRLGIQAFEPVLIEGKAIQLHPLVCAAYNA        459
sp|Q3YUZ6|RPOC_SHISS                EE----AVVWDILDEVIREHPVLLNRAPTLHRLGIQAFEPVLIEGKAIQLHPLVCAAYNA        459
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sp|B1XBZ0|RPOC_ECODH                EE----AVVWDILDEVIREHPVLLNRAPTLHRLGIQAFEPVLIEGKAIQLHPLVCAAYNA       459
sp|A8A787|RPOC_ECOHS                EE----AVVWDILDEVIREHPVLLNRAPTLHRLGIQAFEPVLIEGKAIQLHPLVCAAYNA       459
tr|A0A237JUP3|A0A237JUP3_SHISO      EE----AVVWDILDEVIREHPVLLNRAPTLHRLGIQAFEPVLIEGKAIQLHPLVCAAYNA       459
tr|A0A0F1RBF2|A0A0F1RBF2_ENTAS      EE----AVVWDILDEVIREHPVLLNRAPTLHRLGIQAFEPVLIEGKAIQLHPLVCAAYNA       459
tr|A0A1B3EWG0|A0A1B3EWG0_ENTCL      EE----AVVWDILDEVIREHPVLLNRAPTLHRLGIQAFEPVLIEGKAIQLHPLVCAAYNA       459
tr|A0A0F0XM62|A0A0F0XM62_9ENTR      EE----AVVWDILDEVIREHPVLLNRAPTLHRLGIQAFEPVLIEGKAIQLHPLVCAAYNA       459
sp|Q5PK92|RPOC_SALPA                EE----AVVWDILDEVIREHPVLLNRAPTLHRLGIQAFEPVLIEGKAIQLHPLVCAAYNA       459
sp|A9MHE9|RPOC_SALAR                EE----AVVWDILDEVIREHPVLLNRAPTLHRLGIQAFEPVLIEGKAIQLHPLVCAAYNA       459
tr|A0A232XM43|A0A232XM43_SALMU      EE----AVVWDILDEVIREHPVLLNRAPTLHRLGIQAFEPVLIEGKAIQLHPLVCAAYNA       459
tr|B5RFK0|B5RFK0_SALG2              EE----AVVWDILDEVIREHPVLLNRAPTLHRLGIQAFEPVLIEGKAIQLHPLVCAAYNA       459
sp|P0A2R5|RPOC_SALTI                EE----AVVWDILDEVIREHPVLLNRAPTLHRLGIQAFEPVLIEGKAIQLHPLVCAAYNA       459
sp|Q57H68|RPOC_SALCH                EE----AVVWDILDEVIREHPVLLNRAPTLHRLGIQAFEPVLIEGKAIQLHPLVCAAYNA       459
sp|P0A2R4|RPOC_SALTY                EE----AVVWDILDEVIREHPVLLNRAPTLHRLGIQAFEPVLIEGKAIQLHPLVCAAYNA       459
sp|A6TGP1|RPOC_KLEP7                EE----AVVWDILDEVIREHPVLLNRAPTLHRLGIQAFEPVLIEGKAIQLHPLVCAAYNA       459
tr|A0A0J2K6S7|A0A0J2K6S7_9ENTR      EE----AVVWDILDEVIREHPVLLNRAPTLHRLGIQAFEPVLIEGKAIQLHPLVCAAYNA       459
tr|A0A0G3RZQ0|A0A0G3RZQ0_KLEOX      EE----AVVWDILDEVIREHPVLLNRAPTLHRLGIQAFEPVLIEGKAIQLHPLVCAAYNA       459
tr|A0A212HDS5|A0A212HDS5_9ENTR      EE----AVVWDILDEVIREHPVLLNRAPTLHRLGIQAFEPVLIEGKAIQLHPLVCAAYNA       459
tr|A0A1R0FP41|A0A1R0FP41_CITBR      EE----AVVWDILDEVIREHPVLLNRAPTLHRLGIQAFEPVLIEGKAIQLHPLVCAAYNA       459
tr|A0A078LHA5|A0A078LHA5_CITKO      EE----AVVWDILDEVIREHPVLLNRAPTLHRLGIQAFEPVLIEGKAIQLHPLVCAAYNA       459
sp|A8AKT8|RPOC_CITK8                EE----AVVWDILDEVIREHPVLLNRAPTLHRLGIQAFEPVLIEGKAIQLHPLVCAAYNA       459
                                             :    .:   . :::** *:**::.: ...  ::  .:::*:  *   :**

tr|A0A1U8DYN0|A0A1U8DYN0_ALLSI      DFDGDEMNLHLPQSLETRAEIQELAMVPRMIVTPQSNRPVMGIVQDTLTAVRKFTKRDVF       553
tr|A0A1L8H4P4|A0A1L8H4P4_XENLA      DFDGDEMNLHLPQSLETRAEIQELAMVPRMIVTPQSNRPVMGIVQDTLTAVRKFTKRDVF       552
tr|H9GLG5|H9GLG5_ANOCA              DFDGDEMNLHLPQSLETRAEIQELAMVPRMIVTPQSNRPVMGIVQDTLTAVRKFTKRDVF       553
tr|H2R1J6|H2R1J6_PANTR              DFDGDEMNLHLPQSLETRAEIQELAMVPRMIVTPQSNRPVMGIVQDTLTAVRKFTKRDVF       554
sp|P08775|RPB1_MOUSE                DFDGDEMNLHLPQSLETRAEIQELAMVPRMIVTPQSNRPVMGIVQDTLTAVRKFTKRDVF       554
tr|G1MCZ1|G1MCZ1_AILME              DFDGDEMNLHLPQSLETRAEIQELAMVPRMIVTPQSNRPVMGIVQDTLTAVRKFTKRDVF       554
tr|O08847|O08847_MOUSE              DFDGDEMNLHLPQSLETRAEIQELAMVPRMIVTPQSNRPVMGIVQDTLTAVRKFTKRDVF       554
tr|S7PWZ6|S7PWZ6_MYOBR              DFDGDEMNLHLPQSLETRAEIQELAMVPRMIVTPQSNRPVMGIVQDTLTAVRKFTKRDVF       554
tr|D4A5A6|D4A5A6_RAT                DFDGDEMNLHLPQSLETRAEIQELAMVPRMIVTPQSNRPVMGIVQDTLTAVRKFTKRDVF       554
tr|A0A1S3EWL2|A0A1S3EWL2_DIPOR      DFDGDEMNLHLPQSLETRAEIQELAMVPRMIVTPQSNRPVMGIVQDTLTAVRKFTKRDVF       554
sp|P11414|RPB1_CRIGR                DFDGDEMNLHLPQSLETRAEIQELAMVPRMIVTPQSNRPVMGIVQDTLTAVRKFTKRDVF       554
tr|O35559|O35559_CRIGR              DFDGDEMNLHLPQSLETRAEIQELAMVPRMIVTPQSNRPVMGIVQDTLTAVRKFTKRDVF       554
tr|A0A2I3M9H2|A0A2I3M9H2_PAPAN      DFDGDEMNLHLPQSLETRAEIQELAMVPRMIVTPQSNRPVMGIVQDTLTAVRKFTKRDVF       554
tr|F7HB40|F7HB40_MACMU              DFDGDEMNLHLPQSLETRAEIQELAMVPRMIVTPQSNRPVMGIVQDTLTAVRKFTKRDVF       554
tr|A0A2K6RYW9|A0A2K6RYW9_SAIBB      DFDGDEMNLHLPQSLETRAEIQELAMVPRMIVTPQSNRPVMGIVQDTLTAVRKFTKRDVF       554
tr|W5N8Z6|W5N8Z6_LEPOC              DFDGDEMNLHLPQSLETRAEIQELAMVPRMIVTPQSNRPVMGIVQDTLTAVRKFTKRDVF       553
tr|I3JRW6|I3JRW6_ORENI              DFDGDEMNLHLPQSLETRAEIQELAMVPRMIVTPQSNRPVMGIVQDTLTAVRKFTKRDVF       552
tr|A0A0R4IMS9|A0A0R4IMS9_DANRE      DFDGDEMNLHLPQSLETRAEIQELAMVPRMIVTPQSNRPVMGIVQDTLTAVRKFTKRDVF       551
tr|A0A1A7X327|A0A1A7X327_9TELE      DFDGDEMNLHLPQSLETRAEIQELAMVPRMIVTPQSNRPVMGIVQDTLTAVRKFTKRDVF       552
tr|A0A1A8UKD7|A0A1A8UKD7_NOTFU      DFDGDEMNLHLPQSLETRAEIQELAMVPRMIVTPQSNRPVMGIVQDTLTAVRKFTKRDVF       552
tr|A0A1A8ER05|A0A1A8ER05_9TELE      DFDGDEMNLHLPQSLETRAEIQELAMVPRMIVTPQSNRPVMGIVQDTLTAVRKFTKRDVF       552
tr|A0A1A8DQ60|A0A1A8DQ60_9TELE      DFDGDEMNLHLPQSLETRAEIQELAMVPRMIVTPQSNRPVMGIVQDTLTAVRKFTKRDVF       552
tr|A0A1A8NSR8|A0A1A8NSR8_9TELE      DFDGDEMNLHLPQSLETRAEIQELAMVPRMIVTPQSNRPVMGIVQDTLTAVRKFTKRDVF       552
tr|A0A1W4YLM7|A0A1W4YLM7_9TELE      DFDGDEMNLHLPQSLETRAEIQELAMVPRMIVTPQSNRPVMGIVQDTLTAVRKFTKRDVF       552
tr|A0A1M8A6L7|A0A1M8A6L7_MALS4      DFDGDEMNLHVPQSEEARAELAQIAWVPRQIVSPQANKPVMGIVQDTLCGIRKFTLRDCL       553
sp|P04050|RPB1_YEAST                DFDGDEMNLHVPQSEETRAELSQLCAVPLQIVSPQSNKPCMGIVQDTLCGIRKLTLRDTF       540
tr|A0A1B2J8C6|A0A1B2J8C6_PICPA      DFDGDEMNLHVPQSEETRAELSQLCAVPLQIVSPQSNKPVMGIVQDTLCGVRKMTLRDTF       541
tr|F2QW17|F2QW17_KOMPC              DFDGDEMNLHVPQSEETRAELSQLCAVPLQIVSPQSNKPVMGIVQDTLCGVRKMTLRDTF       541
tr|A3GID7|A3GID7_PICST              DFDGDEMNLHVPQSPETRAELSEICAVPLQIVSPQSNKPVMGIVQDTLCGIRKMTLRDNF       540
tr|A0A1D8PUA6|A0A1D8PUA6_CANAL      DFDGDEMNLHVPQSPETRSELSQICAVPLQIVSPQSNKPVMGIVQDTLCGIRKMTLRDIF       540
tr|G8BEH9|G8BEH9_CANPC              DFDGDEMNLHVPQSPETRSELSQICAVPLQIVSPQSNKPVMGIVQDTLCGIRKMTLRDIF       540
AEG34223.1                          DFDGDQMAVHVPLSSFAQAEARIQMLSAHNLLSPASGEPLAKPSRDIILGLYYITQVR-K       797
ASR51305.1                          DFDGDQMAVHVPLSLEAQLEARVLMMSTNNILSPANGKPIIVPSQDMVLGLYYLSMDR-E       519
OXR47930.1                          DFDGDQMAVHVPLSLEAQLEARTLMLASNNVLFPANGEPSIVPSQDIVLGLYYTTRER-I       518
sp|A7MQQ8|RPOC_CROS8                DFDGDQMAVHVPLTLEAQLEARALMMSTNNILSPANGEPIIVPSQDVVLGLYYMTRDK-I       518
sp|Q32AG0|RPOC_SHIDS                DFDGDQMAVHVPLTLEAQLEARALMMSTNNILSPANGEPIIVPSQDVVLGLYYMTRDC-V       518
sp|Q0SY12|RPOC_SHIF8                DFDGDQMAVHVPLTLEAQLEARALMMSTNNILSPANGEPIIVPSQDVVLGLYYMTRDC-V       518
sp|B2TWH4|RPOC_SHIB3                DFDGDQMAVHVPLTLEAQLEARALMMSTNNILSPANGEPIIVPSQDVVLGLYYMTRDC-V       518
sp|P0A8T7|RPOC_ECOLI                DFDGDQMAVHVPLTLEAQLEARALMMSTNNILSPANGEPIIVPSQDVVLGLYYMTRDC-V       518
sp|Q3YUZ6|RPOC_SHISS                DFDGDQMAVHVPLTLEAQLEARALMMSTNNILSPANGEPIIVPSQDVVLGLYYMTRDC-V       518
sp|B1XBZ0|RPOC_ECODH                DFDGDQMAVHVPLTLEAQLEARALMMSTNNILSPANGEPIIVPSQDVVLGLYYMTRDC-V       518
sp|A8A787|RPOC_ECOHS                DFDGDQMAVHVPLTLEAQLEARALMMSTNNILSPANGEPIIVPSQDVVLGLYYMTRDC-V       518
tr|A0A237JUP3|A0A237JUP3_SHISO      DFDGDQMAVHVPLTLEAQLEARALMMSTNNILSPANGEPIIVPSQDVVLGLYYMTRDC-V       518
tr|A0A0F1RBF2|A0A0F1RBF2_ENTAS      DFDGDQMAVHVPLTLEAQLEARALMMSTNNILSPANGEPIIVPSQDVVLGLYYMTRDC-V       518
tr|A0A1B3EWG0|A0A1B3EWG0_ENTCL      DFDGDQMAVHVPLTLEAQLEARALMMSTNNILSPANGEPIIVPSQDVVLGLYYMTRDC-V       518
tr|A0A0F0XM62|A0A0F0XM62_9ENTR      DFDGDQMAVHVPLTLEAQLEARALMMSTNNILSPANGEPIIVPSQDVVLGLYYMTRDC-V       518
sp|Q5PK92|RPOC_SALPA                DFDGDQMAVHVPLTLEAQLEARALMMSTNNILSPANGEPIIVPSQDVVLGLYYMTRDC-V       518
sp|A9MHE9|RPOC_SALAR                DFDGDQMAVHVPLTLEAQLEARALMMSTNNILSPANGEPIIVPSQDVVLGLYYMTRDC-V       518
tr|A0A232XM43|A0A232XM43_SALMU      DFDGDQMAVHVPLTLEAQLEARALMMSTNNILSPANGEPIIVPSQDVVLGLYYMTRDC-V       518
tr|B5RFK0|B5RFK0_SALG2              DFDGDQMAVHVPLTLEAQLEARALMMSTNNILSPANGEPIIVPSQDVVLGLYYMTRDC-V       518
sp|P0A2R5|RPOC_SALTI                DFDGDQMAVHVPLTLEAQLEARALMMSTNNILSPANGEPIIVPSQDVVLGLYYMTRDC-V       518
sp|Q57H68|RPOC_SALCH                DFDGDQMAVHVPLTLEAQLEARALMMSTNNILSPANGEPIIVPSQDVVLGLYYMTRDC-V       518
sp|P0A2R4|RPOC_SALTY                DFDGDQMAVHVPLTLEAQLEARALMMSTNNILSPANGEPIIVPSQDVVLGLYYMTRDC-V       518
sp|A6TGP1|RPOC_KLEP7                DFDGDQMAVHVPLTLEAQLEARALMMSTNNILSPANGEPIIVPSQDVVLGLYYMTRDS-V       518
tr|A0A0J2K6S7|A0A0J2K6S7_9ENTR      DFDGDQMAVHVPLTLEAQLEARALMMSTNNILSPANGEPIIVPSQDVVLGLYYMTRDC-V       518
tr|A0A0G3RZQ0|A0A0G3RZQ0_KLEOX      DFDGDQMAVHVPLTLEAQLEARALMMSTNNILSPANGEPIIVPSQDVVLGLYYMTRDC-V       518
tr|A0A212HDS5|A0A212HDS5_9ENTR      DFDGDQMAVHVPLTLEAQLEARALMMSTNNILSPANGEPIIVPSQDVVLGLYYMTRDC-V       518
tr|A0A1R0FP41|A0A1R0FP41_CITBR      DFDGDQMAVHVPLTLEAQLEARALMMSTNNILSPANGEPIIVPSQDVVLGLYYMTRDC-V       518
tr|A0A078LHA5|A0A078LHA5_CITKO      DFDGDQMAVHVPLTLEAQLEARALMMSTNNILSPANGEPIIVPSQDVVLGLYYMTRDC-V       518
sp|A8AKT8|RPOC_CITK8                DFDGDQMAVHVPLTLEAQLEARALMMSTNNILSPANGEPIIVPSQDVVLGLYYMTRDC-V       518
                                    *****:* :*:* :  :: *          :: *  ..*     :* : .:   :
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tr|A0A1U8DYN0|A0A1U8DYN0_ALLSI      REGLIDTAVKTAETGYIQRRLIKSMESVMVKYDATVRNSINQVVQLRYGEDGLAGESVEF       911
tr|A0A1L8H4P4|A0A1L8H4P4_XENLA      REGLIDTAVKTAETGYIQRRLIKSMESVMVKYDATVRNSINQVVQLRYGEDGLAGEGVEF       901
tr|H9GLG5|H9GLG5_ANOCA              REGLIDTAVKTAETGYIQRRLIKSMESVMVKYDATVRNSINQVVQLRYGEDGLAGESVEF       902
tr|H2R1J6|H2R1J6_PANTR              REGLIDTAVKTAETGYIQRRLIKSMESVMVKYDATVRNSINQVVQLRYGEDGLAGESVEF       903
sp|P08775|RPB1_MOUSE                REGLIDTAVKTAETGYIQRRLIKSMESVMVKYDATVRNSINQVVQLRYGEDGLAGESVEF       903
tr|G1MCZ1|G1MCZ1_AILME              REGLIDTAVKTAETGYIQRRLIKSMESVMVKYDATVRNSINQVVQLRYGEDGLAGESVEF       903
tr|O08847|O08847_MOUSE              REGLIDTAVKTAETGYIQRRLIKSMESVMVKYDATVRNSINQVVQLRYGEDGLAGESVEF       903
tr|S7PWZ6|S7PWZ6_MYOBR              REGLIDTAVKTAETGYIQRRLIKSMESVMVKYDATVRNSINQVVQLRYGEDGLAGESVEF       903
tr|D4A5A6|D4A5A6_RAT                REGLIDTAVKTAETGYIQRRLIKSMESVMVKYDATVRNSINQVVQLRYGEDGLAGESVEF       903
tr|A0A1S3EWL2|A0A1S3EWL2_DIPOR      REGLIDTAVKTAETGYIQRRLIKSMESVMVKYDATVRNSINQVVQLRYGEDGLAGESVEF       903
sp|P11414|RPB1_CRIGR                REGLIDTAVKTAETGYIQRRLIKSMESVMVKYDATVRNSINQVVQLRYGEDGLAGESVEF       903
tr|O35559|O35559_CRIGR              REGLIDTAVKTAETGYIQRRLIKSMESVMVKYDATVRNSINQVVQLRYGEDGLAGESVEF       903
tr|A0A2I3M9H2|A0A2I3M9H2_PAPAN      REGLIDTAVKTAETGYIQRRLIKSMESVMVKYDATVRNSINQVVQLRYGEDGLAGESVEF       902
tr|F7HB40|F7HB40_MACMU              REGLIDTAVKTAETGYIQRRLIKSMESVMVKYDATVRNSINQVVQLRYGEDGLAGESVEF       903
tr|A0A2K6RYW9|A0A2K6RYW9_SAIBB      REGLIDTAVKTAETGYIQRRLIKSMESVMVKYDATVRNSINQVVQLRYGEDGLAGESVEF       903
tr|W5N8Z6|W5N8Z6_LEPOC              REGLIDTAVKTAETGYIQRRLIKSMESVMVKYDATVRNSINQVVQLRYGEDGLAGEAVEF       902
tr|I3JRW6|I3JRW6_ORENI              REGLIDTAVKTAETGYIQRRLIKSMESVMVKYDGTVRNSINQVVQLRYGEDGLAGENVEF       901
tr|A0A0R4IMS9|A0A0R4IMS9_DANRE      REGLIDTAVKTAETGYIQRRLIKSMESVMVKYDATVRNSINQVVQLRYGEDGLAGEAVEF       900
tr|A0A1A7X327|A0A1A7X327_9TELE      REGLIDTAVKTAETGYIQRRLIKSMESVMVKYDATVRNSINQVVQLRYGEDGLAGENVEF       901
tr|A0A1A8UKD7|A0A1A8UKD7_NOTFU      REGLIDTAVKTAETGYIQRRLIKSMESVMVKYDATVRNSINQVVQLRYGEDGLAGENVEF       901
tr|A0A1A8ER05|A0A1A8ER05_9TELE      REGLIDTAVKTAETGYIQRRLIKSMESVMVKYDATVRNSINQVVQLRYGEDGLAGENVEF       901
tr|A0A1A8DQ60|A0A1A8DQ60_9TELE      REGLIDTAVKTAETGYIQRRLIKSMESVMVKYDATVRNSINQVVQLRYGEDGLAGENVEF       901
tr|A0A1A8NSR8|A0A1A8NSR8_9TELE      REGLIDTAVKTAETGYIQRRLIKSMESVMVKYDATVRNSINQVVQLRYGEDGLAGENVEF       901
tr|A0A1W4YLM7|A0A1W4YLM7_9TELE      REGLIDTAVKTAETGYIQRRLIKSMESVMVKYDATVRNSINQVVQLRYGEDGLAGEAVEF       901
tr|A0A1M8A6L7|A0A1M8A6L7_MALS4      REGLIDTAVKTAETGYIQRRLVKALEDVTICYDGTVRNSTNNVIEFAYGEDGIDGAMVER       894
sp|P04050|RPB1_YEAST                REGLIDTAVKTAETGYIQRRLVKALEDIMVHYDNTTRNSLGNVIQFIYGEDGMDAAHIEK       880
tr|A0A1B2J8C6|A0A1B2J8C6_PICPA      REGLIDTAVKTAETGYIQRRLVKALEDIMVHYDGTTRNSLGDIIQFLYGEDGLDGTQVER       881
tr|F2QW17|F2QW17_KOMPC              REGLIDTAVKTAETGYIQRRLVKALEDIMVHYDGTTRNSLGDIIQFLYGEDGLDGTQVER       881
tr|A3GID7|A3GID7_PICST              REGLIDTAVKTAETGYIQRRLVKALEDIMVHYDGTTRNSLGDIIQFVYGEDGIDGTQVEK       880
tr|A0A1D8PUA6|A0A1D8PUA6_CANAL      REGLIDTAVKTAETGYIQRRLVKALEDIMVHYDGTTRNSLGDIIQFIYGEDGIDGTQVEK       880
tr|G8BEH9|G8BEH9_CANPC              REGLIDTAVKTAETGYIQRRLVKALEDIMVHYDGTTRNSLGDIIQFIYGEDGIDATQVEK       880
AEG34223.1                          RKGGADTALRTADSGYLTRKLVDVTHEIVVREADCGTTNYISV-PLFQPDEVT-------       1129
ASR51305.1                          RKGLADTALKTANSGYLTRRLVDVSQDCVIVQEDCGTENALEMRAIVQGGSVI-------       827
OXR47930.1                          RKGLADTALKTANSGYLTRRLVDVTQDLVITETDCGTTSGYTMKALVEGGEVI-------       832
sp|A7MQQ8|RPOC_CROS8                RKGLADTALKTANSGYLTRRLVDVAQDLVVTEDDCGTLEGITMTPVIEGGDVK-------       832
sp|Q32AG0|RPOC_SHIDS                RKGLADTALKTANSGYLTRRLVDVAQDLVVTEDDCGTHEGIMMTPVIEGGDVK-------       832
sp|Q0SY12|RPOC_SHIF8                RKGLADTALKTANSGYLTRRLVDVAQDLVVTEDDCGTHEGIMMTPVIEGGDVK-------       832
sp|B2TWH4|RPOC_SHIB3                RKGLADTALKTANSGYLTRRLVDVAQDLVVTEDDCGTHEGIMMTPVIEGGDVK-------       832
sp|P0A8T7|RPOC_ECOLI                RKGLADTALKTANSGYLTRRLVDVAQDLVVTEDDCGTHEGIMMTPVIEGGDVK-------       832
sp|Q3YUZ6|RPOC_SHISS                RKGLADTALKTANSGYLTRRLVDVAQDLVVTEDDCGTHEGIMMTPVIEGGDVK-------       832
sp|B1XBZ0|RPOC_ECODH                RKGLADTALKTANSGYLTRRLVDVAQDLVVTEDDCGTHEGIMMTPVIEGGDVK-------       832
sp|A8A787|RPOC_ECOHS                RKGLADTALKTANSGYLTRRLVDVAQDLVVTEDDCGTHEGIMMTPVIEGGDVK-------       832
tr|A0A237JUP3|A0A237JUP3_SHISO      RKGLADTALKTANSGYLTRRLVDVAQDLVVTEDDCGTHEGIMMTPVIEGGDVK-------       832
tr|A0A0F1RBF2|A0A0F1RBF2_ENTAS      RKGLADTALKTANSGYLTRRLVDVAQDLVVTEDDCGTLEGITMTPVIEGGDVK-------       832
tr|A0A1B3EWG0|A0A1B3EWG0_ENTCL      RKGLADTALKTANSGYLTRRLVDVAQDLVVTEDDCGTLEGITMTPVIEGGDVK-------       832
tr|A0A0F0XM62|A0A0F0XM62_9ENTR      RKGLADTALKTANSGYLTRRLVDVAQDLVVTEDDCGTLEGITMTPVIEGGDVK-------       832
sp|Q5PK92|RPOC_SALPA                RKGLADTALKTANSGYLTRRLVDVAQDLVVTEDDCGTHEGILMTPVIEGGDVK-------       832
sp|A9MHE9|RPOC_SALAR                RKGLADTALKTANSGYLTRRLVDVAQDLVVTEDDCGTHEGILMTPVIEGGDVK-------       832
tr|A0A232XM43|A0A232XM43_SALMU      RKGLADTALKTANSGYLTRRLVDVAQDLVVTEDDCGTHEGILMTPVIEGGDVK-------       832
tr|B5RFK0|B5RFK0_SALG2              RKGLADTALKTANSGYLTRRLVDVAQDLVVTEDDCGTHEGILMTPVIEGGDVK-------       832
sp|P0A2R5|RPOC_SALTI                RKGLADTALKTANSGYLTRRLVDVAQDLVVTEDDCGTHEGILMTPVIEGGDVK-------       832
sp|Q57H68|RPOC_SALCH                RKGLADTALKTANSGYLTRRLVDVAQDLVVTEDDCGTHEGILMTPVIEGGDVK-------       832
sp|P0A2R4|RPOC_SALTY                RKGLADTALKTANSGYLTRRLVDVAQDLVVTEDDCGTHEGILMTPVIEGGDVK-------       832
sp|A6TGP1|RPOC_KLEP7                RKGLADTALKTANSGYLTRRLVDVAQDLVVTEDDCGTLEGITMTPVIEGGDVK-------       832
tr|A0A0J2K6S7|A0A0J2K6S7_9ENTR      RKGLADTALKTANSGYLTRRLVDVAQDLVVTEDDCGTLEGITMTPVIEGGDVK-------       832
tr|A0A0G3RZQ0|A0A0G3RZQ0_KLEOX      RKGLADTALKTANSGYLTRRLVDVAQDLVVTEDDCGTLEGITMTPVIEGGDVK-------       832
tr|A0A212HDS5|A0A212HDS5_9ENTR      RKGLADTALKTANSGYLTRRLVDVAQDLVVTEDDCGTLEGITMTPVIEGGDVK-------       832
tr|A0A1R0FP41|A0A1R0FP41_CITBR      RKGLADTALKTANSGYLTRRLVDVAQDLVVTEDDCGTLEGITMTPVIEGGDVK-------       832
tr|A0A078LHA5|A0A078LHA5_CITKO      RKGLADTALKTANSGYLTRRLVDVAQDLVVTEDDCGTHEGILMTPVIEGGDVK-------       832
sp|A8AKT8|RPOC_CITK8                RKGLADTALKTANSGYLTRRLVDVAQDLVVTEDDCGTHEGILMTPVIEGGDVK-------       832
                                    *:*  ***::**::**: *:*:.  ..  :        .   :  .    .

tr|A0A1U8DYN0|A0A1U8DYN0_ALLSI      VNGDDPLSRQAQENATLLFNIHLRSTLCARRMIEEFRLSAQAFDWLLGEIESKFNQAIAH       1090
tr|A0A1L8H4P4|A0A1L8H4P4_XENLA      VNGDDPLSRQAQENATLLFNIHLRSTLSSRRMIEEFRLSGEAFDWLLGEIESKFNQAIAH       1080
tr|H9GLG5|H9GLG5_ANOCA              VNGDDPLSKQAQENATLLFNIHLRSTLCSRRMIEEFRLSGEAFDWLLGEIESKFNQAIAH       1081
tr|H2R1J6|H2R1J6_PANTR              VNGDDPLSRQAQENATLLFNIHLRSTLCSRRMAEEFRLSGEAFDWLLGEIESKFNQAIAH       1082
sp|P08775|RPB1_MOUSE                VNGDDPLSRQAQENATLLFNIHLRSTLCSRRMAEEFRLSGEAFDWLLGEIESKFNQAIAH       1082
tr|G1MCZ1|G1MCZ1_AILME              VNGDDPLSRQAQENATLLFNIHLRSTLCSRRMAEEFRLSGEAFDWLLGEIESKFNQAIAH       1082
tr|O08847|O08847_MOUSE              VNGDDPLSRQAQENATLLFNIHLRSTLCSRRMAEEFRLSGEAFDWLLGEIESKFNQAIAH       1082
tr|S7PWZ6|S7PWZ6_MYOBR              VNGDDPLSRQAQENATLLFNIHLRSTLCSRRMAEEFRLSGEAFDWLLGEIESKFNQAIAH       1082
tr|D4A5A6|D4A5A6_RAT                VNGDDPLSRQAQENATLLFNIHLRSTLCSRRMAEEFRLSGEAFDWLLGEIESKFNQAIAH       1082
tr|A0A1S3EWL2|A0A1S3EWL2_DIPOR      VNGDDPLSRQAQENATLLFNIHLRSTLCSRRMAEEFRLSGEAFDWLLGEIESKFNQAIAH       1082
sp|P11414|RPB1_CRIGR                VNGDDPLSRQAQENATLLFNIHLRSTLCSRRMAEEFRLSGEAFDWLLGEIESKFNQAIAH       1082
tr|O35559|O35559_CRIGR              VNGDDPLSRQAQENATLLFNIHLRSTLCSRRMAEEFRLSGEAFDWLLGEIESKFNQAIAH       1082
tr|A0A2I3M9H2|A0A2I3M9H2_PAPAN      VNGDDPLSRQAQENATLLFNIHLRSTLCSRRMAEEFRLSGEAFDWLLGEIESKFNQAIAH       1081
tr|F7HB40|F7HB40_MACMU              VNGDDPLSRQAQENATLLFNIHLRSTLCSRRMAEEFRLSGEAFDWLLGEIESKFNQAIAH       1082
tr|A0A2K6RYW9|A0A2K6RYW9_SAIBB      VNGDDPLSRQAQENATLLFNIHLRSTLCSRRMAEEFRLSGEAFDWLLGEIESKFNQAIAH       1082
tr|W5N8Z6|W5N8Z6_LEPOC              VNGDDPLSRQAQENATLLFNIHLRSTLCSRRMTEEFRLSTEAYEWLLGEIETKFNQSIAH       1081
tr|I3JRW6|I3JRW6_ORENI              VNGDDPLSRQAQQNATLLFNIHLRSTLCSKRMTEEFRLSTEAFDWLLGEIETKFNQSIAH       1080
tr|A0A0R4IMS9|A0A0R4IMS9_DANRE      VNGDDQLSRQAQENATLLFNIHLRSTLCSKRMTEEFRLSTEAFDWLLGEIETKFNQSIAH       1079
tr|A0A1A7X327|A0A1A7X327_9TELE      VNGDDPLSRQAQENATLLFNIHLRSTLCSKRMTEEFRLSTEAFDWLLGEIETKFNQSIVH       1080
tr|A0A1A8UKD7|A0A1A8UKD7_NOTFU      VNGDDPLSRQAQENATLLFNIHLRSTLCSRRMTEEFRLSMEAFDWLLGEIETKFNQSIVH       1080
tr|A0A1A8ER05|A0A1A8ER05_9TELE      VNGDDPLSRQAQENATLLFNIHLRSTLCSRRMTEEFRLSMEAFDWLLGEIETKFNQSIVH       1080
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tr|A0A1A8DQ60|A0A1A8DQ60_9TELE      VNGDDPLSRQAQENATLLFNIHLRSTLCSRRMTEEFRLSMEAFDWLLGEIETKFNQSIVH      1080
tr|A0A1A8NSR8|A0A1A8NSR8_9TELE      VNGDDPLSRQAQENATLLFNIHLRSTLCSRRMTEEFRLSMEAFDWLLGEIETKFNQSIVH      1080
tr|A0A1W4YLM7|A0A1W4YLM7_9TELE      VNGDDPLSRQAQENATLLFNIHLRSTLCSRRMTEEFRLSTEAFEWLLGEIETKFNQAIVH      1080
tr|A0A1M8A6L7|A0A1M8A6L7_MALS4      IRGNDPISRSMQENATLLFKIHMRSFLCTKQVIEVHHLSREAWEWILGEIEGQFARSVAQ      1071
sp|P04050|RPB1_YEAST                LRGKNEIIQNAQRDAVTLFCCLLRSRLATRRVLQEYRLTKQAFDWVLSNIEAQFLRSVVH      1059
tr|A0A1B2J8C6|A0A1B2J8C6_PICPA      LRGENELIKEAQQNATSLFQCLVRARLATRRILEEFRLNRDAFEWVLGTIEAQFQRSLVH      1061
tr|F2QW17|F2QW17_KOMPC              LRGENELIKEAQQNATSLFQCLVRARLATRRILEEFRLNRDAFEWVLGTIEAQFQRSLVH      1061
tr|A3GID7|A3GID7_PICST              VRGDTELVKEAQANATLLFQCLVRSRLASRRVIEEFKLNRSSFEWVVGEIETQFQKSIVH      1060
tr|A0A1D8PUA6|A0A1D8PUA6_CANAL      VRGDTPLVKEAQENATLLFQCLLRSRLAARRVIEEFKLNRASFEWVMGEIETQFQKSIVH      1060
tr|G8BEH9|G8BEH9_CANPC              VRGKTKLAKEAQENATLLFQCLVRSRLAARRVIEEFKLNRSSFDWVLGEIETQFQKSIVH      1060
AEG34223.1                          -GEIQ------EVPVRSPLTCQTRYGVCQKC-----------YGYDLS------MARPVS      1216
ASR51305.1                          -LGLQ------AARIRSPLICEATMGVCGKC-----------YGRDLA------RGTPVN      905
OXR47930.1                          -LGVD------EVKIRTPLTCETRRGLCAHC-----------YGRDLG------RGSLVN      910
sp|A7MQQ8|RPOC_CROS8                -NSVD------SVKVRSVVTCDTDFGVCAHC-----------YGRDLA------RGHIIN      910
sp|Q32AG0|RPOC_SHIDS                -NSVD------AVKVRSVVSCDTDFGVCAHC-----------YGRDLA------RGHIIN      910
sp|Q0SY12|RPOC_SHIF8                -NSVD------AVKVRSVVSCDTDFGVCAHC-----------YGRDLA------RGHIIN      910
sp|B2TWH4|RPOC_SHIB3                -NSVD------AVKVRSVVSCDTDFGVCAYC-----------YGRDLA------RGHIIN      910
sp|P0A8T7|RPOC_ECOLI                -NSVD------AVKVRSVVSCDTDFGVCAHC-----------YGRDLA------RGHIIN      910
sp|Q3YUZ6|RPOC_SHISS                -NSVD------AVKVRSVVSCDTDFGVCAHC-----------YGRDLA------RGHIIN      910
sp|B1XBZ0|RPOC_ECODH                -NSVD------AVKVRSVVSCDTDFGVCAHC-----------YGRDLA------RGHIIN      910
sp|A8A787|RPOC_ECOHS                -NSVD------AVKVRSVVSCDTDFGVCAHC-----------YGRDLA------RGHIIN      910
tr|A0A237JUP3|A0A237JUP3_SHISO      -NSVD------AVKVRSVVSCDTDFGVCAHC-----------YGRDLA------RGHIIN      910
tr|A0A0F1RBF2|A0A0F1RBF2_ENTAS      -NSVD------SVKVRSVVSCDTDFGVCAHC-----------YGRDLA------RGHIIN      910
tr|A0A1B3EWG0|A0A1B3EWG0_ENTCL      -NSVD------SVKVRSVVSCDTDFGVCAHC-----------YGRDLA------RGHIIN      910
tr|A0A0F0XM62|A0A0F0XM62_9ENTR      -NSVD------SVKVRSVVSCDTDFGVCAHC-----------YGRDLA------RGHIIN      910
sp|Q5PK92|RPOC_SALPA                -NSVD------AVKVRSVVSCDTDFGVCAHC-----------YGRDLA------RGHIIN      910
sp|A9MHE9|RPOC_SALAR                -NSVD------AVKVRSVVSCDTDFGVCAHC-----------YGRDLA------RGHIIN      910
tr|A0A232XM43|A0A232XM43_SALMU      -NSVD------AVKVRSVVSCDTDFGVCAHC-----------YGRDLA------RGHIIN      910
tr|B5RFK0|B5RFK0_SALG2              -NSVD------AVKVRSVVSCDTDFGVCAHC-----------YGRDLA------RGHIIN      910
sp|P0A2R5|RPOC_SALTI                -NSVD------AVKVRSVVSCDTDFGVCAHC-----------YGRDLA------RGHIIN      910
sp|Q57H68|RPOC_SALCH                -NSVD------AVKVRSVVSCDTDFGVCAHC-----------YGRDLA------RGHIIN      910
sp|P0A2R4|RPOC_SALTY                -NSVD------AVKVRSVVSCDTDFGVCAHC-----------YGRDLA------RGHIIN      910
sp|A6TGP1|RPOC_KLEP7                -NSVD------SVKVRSVVSCDTDFGVCAHC-----------YGRDLA------RGHLIN      910
tr|A0A0J2K6S7|A0A0J2K6S7_9ENTR      -NSVD------SVKVRSVVSCDTDFGVCAHC-----------YGRDLA------RGHIIN      910
tr|A0A0G3RZQ0|A0A0G3RZQ0_KLEOX      -NSVD------SVKVRSVVSCDTDFGVCAHC-----------YGRDLA------RGHIIN      910
tr|A0A212HDS5|A0A212HDS5_9ENTR      -NSVD------SVKVRSVVSCDTDFGVCAHC-----------YGRDLA------RGHIIN      910
tr|A0A1R0FP41|A0A1R0FP41_CITBR      -NSVD------SVKVRSVVSCDTDFGVCAHC-----------YGRDLA------RGHIIN      910
tr|A0A078LHA5|A0A078LHA5_CITKO      -NSVD------AVKVRSVVSCDTDFGVCAHC-----------YGRDLA------RGHIIN      910
sp|A8AKT8|RPOC_CITK8                -NSVD------AVKVRSVVSCDTDFGVCAHC-----------YGRDLA------RGHIIN      910x16
                                                      .       :.              :   :.

tr|A0A1U8DYN0|A0A1U8DYN0_ALLSI      PGEMGGALAAQSLGEPATQMTLNTFHYAGVSAKNVTLGVPR--------LKELINISKKP      1142
tr|A0A1L8H4P4|A0A1L8H4P4_XENLA      PGEMVGALAAQSLGEPATQMTLNTFHYAGVSAKNVTLGVPR--------LKELINISKKP      1132
tr|H9GLG5|H9GLG5_ANOCA              PGEMVGALAAQSLGEPATQMTLNTFHYAGVSAKNVTLGVPR--------LKELINISKKP      1133
tr|H2R1J6|H2R1J6_PANTR              PGEMVGALAAQSLGEPATQMTLNTFHYAGVSAKNVTLGVPR--------LKELINISKKP      1134
sp|P08775|RPB1_MOUSE                PGEMVGALAAQSLGEPATQMTLNTFHYAGVSAKNVTLGVPR--------LKELINISKKP      1134
tr|G1MCZ1|G1MCZ1_AILME              PGEMVGALAAQSLGEPATQMTLNTFHYAGVSAKNVTLGVPR--------LKELINISKKP      1134
tr|O08847|O08847_MOUSE              PGEMVGALAAQSLGEPATQMTLNTFHYAGVSAKNVTLGVPR--------LKELINISKKP      1134
tr|S7PWZ6|S7PWZ6_MYOBR              PGEMVGALAAQSLGEPATQMTLNTFHYAGVSAKNVTLGVPR--------LKELINISKKP      1134
tr|D4A5A6|D4A5A6_RAT                PGEMVGALAAQSLGEPATQMTLNTFHYAGVSAKNVTLGVPR--------LKELINISKKP      1134
tr|A0A1S3EWL2|A0A1S3EWL2_DIPOR      PGEMVGALAAQSLGEPATQMTLNTFHYAGVSAKNVTLGVPR--------LKELINISKKP      1134
sp|P11414|RPB1_CRIGR                PGEMVGALAAQSLGEPATQMTLNTFHYAGVSAKNVTLGVPR--------LKELINISKKP      1134
tr|O35559|O35559_CRIGR              PGEMVGALAAQSLGEPATQMTLNTFHYAGVSAKNVTLGVPR--------LKELINISKKP      1134
tr|A0A2I3M9H2|A0A2I3M9H2_PAPAN      PGEMVGALAAQSLGEPATQMTLNTFHYAGVSAKNVTLGVPR--------LKELINISKKP      1133
tr|F7HB40|F7HB40_MACMU              PGEMVGALAAQSLGEPATQMTLNTFHYAGVSAKNVTLGVPR--------LKELINISKKP      1134
tr|A0A2K6RYW9|A0A2K6RYW9_SAIBB      PGEMVGALAAQSLGEPATQMTLNTFHYAGVSAKNVTLGVPR--------LKELINISKKP      1134
tr|W5N8Z6|W5N8Z6_LEPOC              PGEMVGALAAQSLGEPATQMTLNTFHYAGVSAKNVTLGVPR--------LKELINISKRP      1133
tr|I3JRW6|I3JRW6_ORENI              PGEMVGALAAQSLGEPATQMTLNTFHYAGVSAKNVTLGVPR--------LKELINISKRP      1132
tr|A0A0R4IMS9|A0A0R4IMS9_DANRE      PGEMVGALAAQSLGEPATQMTLNTFHYAGVSAKNVTLGVPR--------LKELINISKRP      1131
tr|A0A1A7X327|A0A1A7X327_9TELE      PGEMVGALAAQSLGEPATQMTLNTFHYAGVSAKNVTLGVPR--------LKELINISKRP      1132
tr|A0A1A8UKD7|A0A1A8UKD7_NOTFU      PGEMVGALAAQSLGEPATQMTLNTFHYAGVSAKNVTLGVPR--------LKELINISKRP      1132
tr|A0A1A8ER05|A0A1A8ER05_9TELE      PGEMVGALAAQSLGEPATQMTLNTFHYAGVSAKNVTLGVPR--------LKELINISKRP      1132
tr|A0A1A8DQ60|A0A1A8DQ60_9TELE      PGEMVGALAAQSLGEPATQMTLNTFHYAGVSAKNVTLGVPR--------LKELINISKRP      1132
tr|A0A1A8NSR8|A0A1A8NSR8_9TELE      PGEMVGALAAQSLGEPATQMTLNTFHYAGVSAKNVTLGVPR--------LKELINISKRP      1132
tr|A0A1W4YLM7|A0A1W4YLM7_9TELE      PGEMVGALAAQSLGEPATQMTLNTFHYAGVSAKNVTLGVPR--------LKELINISKRP      1132
tr|A0A1M8A6L7|A0A1M8A6L7_MALS4      PGEMCGTLAAQSIGEPATQMTLNTFHYAGVSSKNVTLGVPR--------LKEIINCAENI      1123
sp|P04050|RPB1_YEAST                PGEMVGVLAAQSIGEPATQMTLNTFHFAGVASKKVTSGVPR--------LKEILNVAKNM      1111
tr|A0A1B2J8C6|A0A1B2J8C6_PICPA      PGEMVGVIAAQSIGEPATQMTLNTFHYAGVSSKNVTLGVPR--------LKEILNVAKNI      1113
tr|F2QW17|F2QW17_KOMPC              PGEMVGVIAAQSIGEPATQMTLNTFHYAGVSSKNVTLGVPR--------LKEILNVAKNI      1113
tr|A3GID7|A3GID7_PICST              PGEMVGVIAAQSIGEPATQMTLNTFHYAGVSSKNVTLGVPR--------LKEILNVAKNI      1112
tr|A0A1D8PUA6|A0A1D8PUA6_CANAL      PGEMVGVVAAQSIGEPATQMTLNTFHYAGVSSKNVTLGVPR--------LKEILNVAKNI      1112
tr|G8BEH9|G8BEH9_CANPC              PGEMVGVIAAQSIGEPATQMTLNTFHYAGVSSKNVTLGVPR--------LKEILNVAKNI      1112
AEG34223.1                          IGEAVGIVAAQSIGEPGTQLTMRTFHTGGVAG----------------------------      1248
ASR51305.1                          IGEAVGVIAAQSIGEPGTQLTMRTFHIGGAAQLNE-TSNLEAVADGTLQYRDI-PTIVNK      963
OXR47930.1                          RGEAVGVIAAQSIGEPGTQLTMRTFHIGGAASRAAMASSVETKAAGTVSFGVSMRYVTNA      970
sp|A7MQQ8|RPOC_CROS8                KGEAIGVIAAQSIGEPGTQLTMRTFHIGGAASRAAAESSIQVKNKGSIRLSNA-KSVVNS      969
sp|Q32AG0|RPOC_SHIDS                KGEAIGVIAAQSIGEPGTQLTMRTFHIGGAASRAAAESSIQVKNKGSIKLSNV-KSVVNS      969
sp|Q0SY12|RPOC_SHIF8                KGEAIGVIAAQSIGEPGTQLTMRTFHIGGAASRAAAESSIQVKNKGSIKLSNV-KSVVNS      969
sp|B2TWH4|RPOC_SHIB3                KGEAIGVIAAQSIGEPGTQLTMRTFHIGGAASRAAAESSIQVKNKGSIKLSNV-KSVVNS      969
sp|P0A8T7|RPOC_ECOLI                KGEAIGVIAAQSIGEPGTQLTMRTFHIGGAASRAAAESSIQVKNKGSIKLSNV-KSVVNS      969
sp|Q3YUZ6|RPOC_SHISS                KGEAIGVIAAQSIGEPGTQLTMRTFHIGGAASRAAAESSIQVKNKGSIKLSNV-KSVVNS      969
sp|B1XBZ0|RPOC_ECODH                KGEAIGVIAAQSIGEPGTQLTMRTFHIGGAASRAAAESSIQVKNKGSIKLSNV-KSVVNS      969
sp|A8A787|RPOC_ECOHS                KGEAIGVIAAQSIGEPGTQLTMRTFHIGGAASRAAAESSIQVKNKGSIKLSNV-KSVVNS      969
tr|A0A237JUP3|A0A237JUP3_SHISO      KGEAIGVIAAQSIGEPGTQLTMRTFHIGGAASRAAAESSIQVKNKGSIKLSNV-KSVVNS      969
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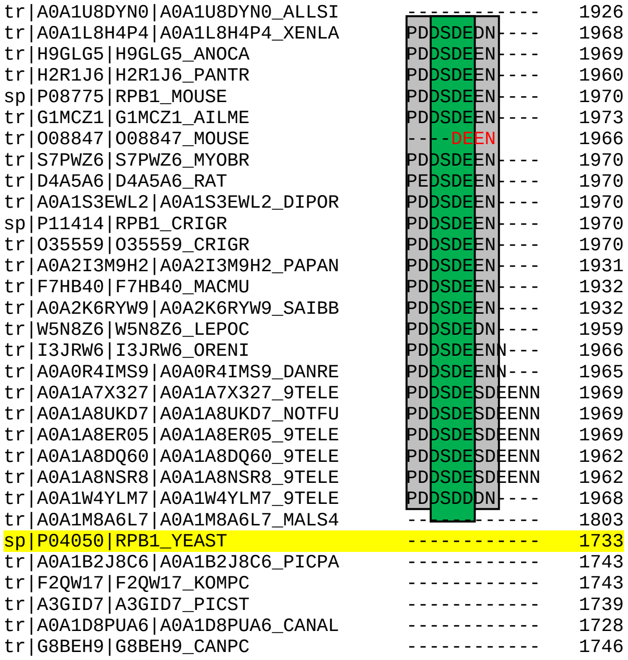
tr|A0A0F1RBF2|A0A0F1RBF2_ENTAS      KGEAIGVIAAQSIGEPGTQLTMRTFHIGGAASRAAAESSIQVKNKGSIKLSNA-KSVVNS       969
tr|A0A1B3EWG0|A0A1B3EWG0_ENTCL      KGEAIGVIAAQSIGEPGTQLTMRTFHIGGAASRAAAESSIQVKNKGSIKLSNA-KSVVNS       969
tr|A0A0F0XM62|A0A0F0XM62_9ENTR      KGEAIGVIAAQSIGEPGTQLTMRTFHIGGAASRAAAESSIQVKNKGSIKLSNA-KSVVNS       969
sp|Q5PK92|RPOC_SALPA                KGEAIGVIAAQSIGEPGTQLTMRTFHIGGAASRAAAESSIQVKNKGSIKLSNV-KSVVNS       969
sp|A9MHE9|RPOC_SALAR                KGEAIGVIAAQSIGEPGTQLTMRTFHIGGAASRAAAESSIQVKNKGSIKLSNV-KSVVNS       969
tr|A0A232XM43|A0A232XM43_SALMU      KGEAIGVIAAQSIGEPGTQLTMRTFHIGGAASRAAAESSIQVKNKGSIKLSNV-KSVVNS       969
tr|B5RFK0|B5RFK0_SALG2              KGEAIGVIAAQSIGEPGTQLTMRTFHIGGAASRAAAESSIQVKNKGSIKLSNV-KSVVNS       969
sp|P0A2R5|RPOC_SALTI                KGEAIGVIAAQSIGEPGTQLTMRTFHIGGAASRAAAESSIQVKNKGSIKLSNV-KSVVNS       969
sp|Q57H68|RPOC_SALCH                KGEAIGVIAAQSIGEPGTQLTMRTFHIGGAASRAAAESSIQVKNKGSIKLSNV-KSVVNS       969
sp|P0A2R4|RPOC_SALTY                KGEAIGVIAAQSIGEPGTQLTMRTFHIGGAASRAAAESSIQVKNKGSIKLSNV-KSVVNS       969
sp|A6TGP1|RPOC_KLEP7                KGEAIGVIAAQSIGEPGTQLTMRTFHIGGAASRAAAESSIQVKNKGSIKLSNA-KSVVNS       969
tr|A0A0J2K6S7|A0A0J2K6S7_9ENTR      KGEAIGVIAAQSIGEPGTQLTMRTFHIGGAASRAAAESSIQVKNKGSIRLSNA-KSVVNS       969
tr|A0A0G3RZQ0|A0A0G3RZQ0_KLEOX      KGEAIGVIAAQSIGEPGTQLTMRTFHIGGAASRAAAESSIQVKNKGSIRLSNA-KSVVNS       969
tr|A0A212HDS5|A0A212HDS5_9ENTR      KGEAIGVIAAQSIGEPGTQLTMRTFHIGGAASRAAAESSIQVKNKGSIRLSNA-KSVVNS       969
tr|A0A1R0FP41|A0A1R0FP41_CITBR      KGEAIGVIAAQSIGEPGTQLTMRTFHIGGAASRAAAESSIQVKNKGSIRLSNA-KSVVNS       969
tr|A0A078LHA5|A0A078LHA5_CITKO      KGEAIGVIAAQSIGEPGTQLTMRTFHIGGAASRAAAESSIQVKNKGSIRLSNA-KSVVNS       969
sp|A8AKT8|RPOC_CITK8                KGEAIGVIAAQSIGEPGTQLTMRTFHIGGAASRAAAESSIQVKNKGSIRLSNA-KSVVNS       969
                                     **  * :****:***.**:*:.*** .*.:

tr|A0A1U8DYN0|A0A1U8DYN0_ALLSI      --WSPS---VGSGMTPGAAGFSPSAASDA-SGFSPGYSPAWSPTPGSPGSPGPSSPY---       1589
tr|A0A1L8H4P4|A0A1L8H4P4_XENLA      --WSPS---IGSGMTPGAAGFSPSAASDA-SGFSPGYSPAWSPTPGSPGSPGPSSPY---       1579
tr|H9GLG5|H9GLG5_ANOCA              --WSPS---VGSGMTPGAAGFSPSAASDA-SGLSPGYSPAWSPTPGSPGSPGPSSPY---       1580
tr|H2R1J6|H2R1J6_PANTR              GLWSPALA-----------------LTYA-SGFSPGYSPAWSPTPGSPGSPGPSSPY---       1571
sp|P08775|RPB1_MOUSE                --WSPSV---GSGMTPGAAGFSPSAASDA-SGFSPGYSPAWSPTPGSPGSPGPSSPY---       1581
tr|G1MCZ1|G1MCZ1_AILME              --WSPSVDITGSGMTPGAAGFSPSAASDA-SGFSPGYSPAWSPTPGSPGSPGPSSPY---       1584
tr|O08847|O08847_MOUSE              --WSPSV---GSGMTPGAAGFSPSAASDA-SGFSPGYSPAWSPTPGSPGSPGPSSPY---       1581
tr|S7PWZ6|S7PWZ6_MYOBR              --WSPSV---GSGMTPGAAGFSPSAASDA-SGFSPGYSPAWSPTPGSPGSPGPSSPY---       1581
tr|D4A5A6|D4A5A6_RAT                --WSPSV---GSGMTPGAAGFSPSAASDA-SGFSPGYSPAWSPTPGSPGSPGPSSPY---       1581
tr|A0A1S3EWL2|A0A1S3EWL2_DIPOR      --WSPSV---GSGMTPGAAGFSPSAASDA-SGFSPGYSPAWSPTPGSPGSPGPSSPY---       1581
sp|P11414|RPB1_CRIGR                --WSPSV---GSGMTPGAAGFSPSAASDA-SGFSPGYSPAWSPTPGSPGSPGPSSPY---       1581
tr|O35559|O35559_CRIGR              --WSPSV---GSGMTPGAAGFSPSAASDA-SGFSPGYSPAWSPTPGSPGSPGPSSPY---       1581
tr|A0A2I3M9H2|A0A2I3M9H2_PAPAN      ------------GMTPGAAGFSPSAASDA-SGFSPGYSPAWSPTPGSPGSPGPSSPY---       1542
tr|F7HB40|F7HB40_MACMU              ------------GMTPGAAGFSPSAASDA-SGFSPGYSPAWSPTPGSPGSPGPSSPY---       1543
tr|A0A2K6RYW9|A0A2K6RYW9_SAIBB      ------------GMTPGAAGFSPSAASDA-SGFSPGYSPAWSPTPGSPGSPGPSSPY---       1543
tr|W5N8Z6|W5N8Z6_LEPOC              --WSPS---VGSGMTPGAAGFSPSAASDA-SGFSPGYSPAWSPTPGSPGSPGPSSPY---       1580
tr|I3JRW6|I3JRW6_ORENI              --WSPS---VGSGMTPGGAGFSPSAASDA-SGFSPGYSPAWSPTPGSPGSPGPASPY---       1579
tr|A0A0R4IMS9|A0A0R4IMS9_DANRE      --WSPS---VGSGMTPGAAGFSPSAASDA-SGFSPGYSPAWSPTPGSPGSPGPASPY---       1578
tr|A0A1A7X327|A0A1A7X327_9TELE      --WSPS---VGSGMTPGAAGFSPSAASDA-SGFSPGYSPAWSPTPGSPGSPGPASPY---       1579
tr|A0A1A8UKD7|A0A1A8UKD7_NOTFU      --WSPS---VGSGMTPGAAGFSPSAASDA-SGFSPGYSPAWSPTPGSPGSPGPASPY---       1579
tr|A0A1A8ER05|A0A1A8ER05_9TELE      --WSPS---VGSGMTPGAAGFSPSAASDA-SGFSPGYSPAWSPTPGSPGSPGPASPY---       1579
tr|A0A1A8DQ60|A0A1A8DQ60_9TELE      --WSPS---VGSGMTPGAAGFSPSAASDA-SGFSPGYSPAWSPTPGSPGSPGPASPY---       1579
tr|A0A1A8NSR8|A0A1A8NSR8_9TELE      --WSPS---VGSGMTPGAAGFSPSAASDA-SGFSPGYSPAWSPTPGSPGSPGPASPY---       1579
tr|A0A1W4YLM7|A0A1W4YLM7_9TELE      --WSPS---VGSGMTPGAAGFSPSAASDA-SGFSPGYSPAWSPTPGSPGSPGPASPY---       1579
tr|A0A1M8A6L7|A0A1M8A6L7_MALS4      ---DDF-----R--VQQQAMFSPLVQVGGDE---GGY----SDYLSAGQSP---------       1542
sp|P04050|RPB1_YEAST                ---N-A-----DLDVKDELMFSPLVDSGSNDAMAGGF----TAYGGADYGEA-TSPF---       1523
tr|A0A1B2J8C6|A0A1B2J8C6_PICPA      ---DEF-----NHDDVADVMFSPMAETGSGDDRSGGL----TEYAGIQSPYQP-------       1527
tr|F2QW17|F2QW17_KOMPC              ---DEF-----NHDDVADVMFSPMAETGSGDDRSGGL----TEYAGIQSPYQP-------       1527
tr|A3GID7|A3GID7_PICST              ---DD------KIQFEEGAGFSPIHTAQVQ-DVSGGL----TSYGGQPTSPSATSPFSYG       1529
tr|A0A1D8PUA6|A0A1D8PUA6_CANAL      ---DE------NIDIDAGAGFSPIHIAQMNEGNIGGL----TSYGGQPTSPAATSPFSYG       1527
tr|G8BEH9|G8BEH9_CANPC              ---DD------RIQVDESAGFSPVHQAPTAEGMNGGL----TSYGGQPTSPSATSPFSYS       1526
AEG34223.1                          GKQA--------------------------------------------------------       1524
ASR51305.1                          ------------------------------------------------------------       1403
OXR47930.1                          GNEE--------------------------------------------------------       1416
sp|A7MQQ8|RPOC_CROS8                GNDNE-------------------------------------------------------       1407
sp|Q32AG0|RPOC_SHIDS                GSDNE-------------------------------------------------------       1407
sp|Q0SY12|RPOC_SHIF8                GSDNE-------------------------------------------------------       1407
sp|B2TWH4|RPOC_SHIB3                GSDNE-------------------------------------------------------       1407
sp|P0A8T7|RPOC_ECOLI                GSDNE-------------------------------------------------------       1407
sp|Q3YUZ6|RPOC_SHISS                GSDNE-------------------------------------------------------       1407
sp|B1XBZ0|RPOC_ECODH                GSDNE-------------------------------------------------------       1407
sp|A8A787|RPOC_ECOHS                GSDNE-------------------------------------------------------       1407
tr|A0A237JUP3|A0A237JUP3_SHISO      GSDNE-------------------------------------------------------       1407
tr|A0A0F1RBF2|A0A0F1RBF2_ENTAS      GSDNE-------------------------------------------------------       1407
tr|A0A1B3EWG0|A0A1B3EWG0_ENTCL      GSDNE-------------------------------------------------------       1407
tr|A0A0F0XM62|A0A0F0XM62_9ENTR      GSDNE-------------------------------------------------------       1407
sp|Q5PK92|RPOC_SALPA                GSDNE-------------------------------------------------------       1407
sp|A9MHE9|RPOC_SALAR                GSDNE-------------------------------------------------------       1407
tr|A0A232XM43|A0A232XM43_SALMU      GSDNE-------------------------------------------------------       1407
tr|B5RFK0|B5RFK0_SALG2              GSDNE-------------------------------------------------------       1407
sp|P0A2R5|RPOC_SALTI                GSDNE-------------------------------------------------------       1407
sp|Q57H68|RPOC_SALCH                GSDNE-------------------------------------------------------       1407
sp|P0A2R4|RPOC_SALTY                GSDNE-------------------------------------------------------       1407
sp|A6TGP1|RPOC_KLEP7                GSDND-------------------------------------------------------       1407
tr|A0A0J2K6S7|A0A0J2K6S7_9ENTR      GSDND-------------------------------------------------------       1407
tr|A0A0G3RZQ0|A0A0G3RZQ0_KLEOX      GSDND-------------------------------------------------------       1407
tr|A0A212HDS5|A0A212HDS5_9ENTR      GSDNE-------------------------------------------------------       1407
tr|A0A1R0FP41|A0A1R0FP41_CITBR      GSDND-------------------------------------------------------       1407
tr|A0A078LHA5|A0A078LHA5_CITKO      GSDNE-------------------------------------------------------       1407
sp|A8AKT8|RPOC_CITK8                GSDND-------------------------------------------------------       1407
```



```
tr|A0A1U8DYN0|A0A1U8DYN0_ALLSI      ------------    1926
tr|A0A1L8H4P4|A0A1L8H4P4_XENLA      PDDSDEDN----    1968
tr|H9GLG5|H9GLG5_ANOCA              PDDSDEEN----    1969
tr|H2R1J6|H2R1J6_PANTR              PDDSDEEN----    1960
sp|P08775|RPB1_MOUSE                PDDSDEEN----    1970
tr|G1MCZ1|G1MCZ1_AILME              PDDSDEEN----    1973
tr|O08847|O08847_MOUSE              ----DEEN        1966
tr|S7PWZ6|S7PWZ6_MYOBR              PDDSDEEN----    1970
tr|D4A5A6|D4A5A6_RAT                PEDSDEEN----    1970
tr|A0A1S3EWL2|A0A1S3EWL2_DIPOR      PDDSDEEN----    1970
sp|P11414|RPB1_CRIGR                PDDSDEEN----    1970
tr|O35559|O35559_CRIGR              PDDSDEEN----    1970
tr|A0A2I3M9H2|A0A2I3M9H2_PAPAN      PDDSDEEN----    1931
tr|F7HB40|F7HB40_MACMU              PDDSDEEN----    1932
tr|A0A2K6RYW9|A0A2K6RYW9_SAIBB      PDDSDEEN----    1932
tr|W5N8Z6|W5N8Z6_LEPOC              PDDSDEDN----    1959
tr|I3JRW6|I3JRW6_ORENI              PDDSDEENN---    1966
tr|A0A0R4IMS9|A0A0R4IMS9_DANRE      PDDSDEENN---    1965
tr|A0A1A7X327|A0A1A7X327_9TELE      PDDSDESDEENN    1969
tr|A0A1A8UKD7|A0A1A8UKD7_NOTFU      PDDSDESDEENN    1969
tr|A0A1A8ER05|A0A1A8ER05_9TELE      PDDSDESDEENN    1969
tr|A0A1A8DQ60|A0A1A8DQ60_9TELE      PDDSDESDEENN    1962
tr|A0A1A8NSR8|A0A1A8NSR8_9TELE      PDDSDESDEENN    1962
tr|A0A1W4YLM7|A0A1W4YLM7_9TELE      PDDSDDDN----    1968
tr|A0A1M8A6L7|A0A1M8A6L7_MALS4      ------------    1803
sp|P04050|RPB1_YEAST                ------------    1733
tr|A0A1B2J8C6|A0A1B2J8C6_PICPA      ------------    1743
tr|F2QW17|F2QW17_KOMPC              ------------    1743
tr|A3GID7|A3GID7_PICST              ------------    1739
tr|A0A1D8PUA6|A0A1D8PUA6_CANAL      ------------    1728
tr|G8BEH9|G8BEH9_CANPC              ------------    1746
```

Fig. 6 Mix and Match analysis of the elongation subunits β' of *E. coli* and Rpb1 of yeast RNAP-II.
For legends refer to Figs. 3 and 4

8. Active site analysis of the *S. cerevisiae* MSU RNAP- II

8.1. Catalytic region

It has been found that almost all DNA polymerases and SSU RNAPs use an invariant K for catalysis, i.e., in the initial proton transfer reactions [Palanivelu 2013, 2017]. However, in all MSU RNAPs analyzed, no K was found at the expected distance from the template binding YG/FG pair but an equivalent invariant R (Table 4). However, a detailed analysis has shown that all prokaryotic DNA polymerases II also use an invariant R in catalysis with similar distance conservations [Palanivelu, 2013, 2019] instead of a usual K; interestingly, an enzyme also possesses primase activity and along with associated 3′→5′ exonuclease activity. Table 4 shows the invariant template binding YG pair with its catalytic R in the initiation (β and Rpb2) and in the elongation subunits (β' and Rpb1) of eubacterial and eukaryotic MSU RNAPs, respectively (Figs. 3-7). The catalytic R in both in the initiation and elongation subunits of the MSU RNAPs will serve as a proton abstractor for initiating the catalysis as explained by Palanivelu (2018).

Table 4 Amino acids around the catalytic amino acid K/R and the YG/FG pair in DNA polymerases, SSU and MSU RNAPs.

Polymerase type	Catalytic Region
Viral SSU RNA pol (T7)	$\text{-TR}^{-4}\text{VTKR}^{1}\text{SVMTLAY}^{8}\text{GS-}$
Mitochondrial SSU RNA pol (Yeast)	$\text{-TR}^{-4}\text{KVVKQ}^{1}\text{TVMTNVY}^{8}\text{GV--}$
Chloroplast SSU pol (ARATH)	$\text{-DR}^{-4}\text{KLVKQ}^{1}\text{TVMTSVY}^{8}\text{GV-}$
E. coli DNA pol I (SSU)	$\text{-QR}^{-4}\text{RSAKA}^{1}\text{INFGLIY}^{8}\text{GM-}$
Initiation subunits of MSU RNAPs	
E. coli MSU RNAP β subunit	$\text{-}^{539}\text{TR}^{-8}\text{ERAGFEVRD}^{1}\text{VHPTHY}^{7}\text{G}^{8}\text{RV}^{558}\text{-}$
S. cerevisiae MSU RNAP II Rpb2 subunit	$\text{-}^{851}\text{FR}^{-5}\text{SLFFRS}^{1}\text{YMDQEKKY}^{9}\text{GMSI}^{870}\text{-}$

Human MSU RNAP II Rpb2 subunit	-^{806}FR^{-5}SVFYRS^{1}YKEQESKK^{9}GFDQ^{825}-
Elongation subunits of MSU RNAPs	
E. coli MSU RNAP β’ subunit	-^{833}NSV^{-6}DAVKVRS^{1}VVSC^{5}DTDFGVC^{12}AHC^{15}Y^{16}G^{17}RDL^{861}-
S. cerevisiae MSU RNAP II Rpb1 subunit	-^{55}DPR^{-6}LGSIDRN^{1}LKC^{4}QTC^{7}QEGMNEC^{14}PGHF^{18}G^{19}HI^{84}-
Human MSU RNAP II Rpb1 subunit	-^{59}DPR^{-6}QGVIERT^{1}GRC^{4}QTC^{7}AGNMTEC^{14}PGHF^{18}G^{19}HI^{88}-

NB: MSU RNA polymerases which use R in the catalytic site is shown in bold.
The invariant R, at -6/-7 is not found in β’ subunits of eubacteria
The eukaryotic elongation subunits an FG instead of a YG

Table 4 shows the invariant YG/FG pair and its catalytic R in the initiation and elongation subunits of eubacterial and eukaryotic MSU RNAPs.

It is interesting to note that the YG pair appears to be specific for polymerases using DNA as the template (including the prokaryotic and eukaryotic MSU RNAPs, data not shown) as it is not reported in RNA dependent RNAPs where they use RNA as the template [Tunitskaya and Kochetkov, 2002]. In fact, Kotsyuk et al. (1995) have shown that the DNA dependent T7 RNAP requires both the strands for activity and uses two YG pairs and there was no activity when single-stranded DNA was used as the substrate. However, the eukaryotic initiation subunit Rpb2 uses a functional equivalent FG and the initiation subunit from higher eukaryotes including human uses a completely different pair, KG but followed by an F. The elongation subunits in all eukaryotes use a functionally equivalent FG pair. However, it is interesting to note the catalytic amino acid is R and is completely conserved in all MSU RNAPs II. Three invariant Cs between catalytic R and YG/FG pair in the elongation subunits (β’ and Rpb1) are highly conserved in both pro- and eukaryotes but the three Cs are placed at a different distances as 5+12+15 and 4+7+14 with an 11 amino acids span in both the cases (Table 4). These completely conserved Cs are implicated in Zn binding in the bacterial elongation subunits by crystallographic analysis (Zhang et al 1999).

8.2 Mechanism of NTP and dNTP discrimination in eukaryotic MSU RNA polymerases

NTP and dNTP discrimination in nucleic acid polymerases is usually achieved by base pairing, base stacking, hydrogen bonding and also by specific interaction(s) of completely conserved amino acid(s) in the nucleotide interacting domains**.** A completely conserved R at -5 in the Rpb2 and -6 in Rpb1 is known to participate in the nucleotide discrimination and select only NTPs in the polymerization site (Table 4). Similar absolute conservation is seen in SSU RNAPs from viruses, mitochondria and chloroplasts and DNA polymerases too. A conspicuous absence of an invariant R at the expected distance at -6 in the elongation subunit β’ of eubacterial MSU RNAPs (Table 4) raises the question of how they discriminate the NTPs from dNTPs. Modelling of the substrate NTP bound to the *T. thermophilus* RNAP active site suggests that N^{458} (numbering from *E. coli* RNA polymerase) within a highly conserved sequence motif ^{458}**NADFDGD**^{464} that includes the catalytic Asp triad (D460, D462, D464) could mediate specific recognition of the O2 ribose atom (Svetlov et al 2004; Zhang et al 1999). Functional *in vitro* analysis demonstrated that the substitutions of the corresponding β′ N^{458} residue led to the loss of discrimination between NTP and dNTP substrates as well as to defects in RNA chain extension (Svetlov et al 2004). It is interesting to note that substitution of the corresponding amino acid in yeast Rpb1 (N479Y) is lethal in the same sequence motif ^{478}Y**NADFDGD** in eukaryotes (Trinh et al 2006). The absolutely conserved N in both the cases could discriminate the NTP from dNTP by recognizing the 2’-OH of the ribose and suggested that the crucial N could interact with both the 2’-OH as well 3’-OH (Trinh et al 2006).

The highly conserved S/T adjacent (N in *S. cerevisiae*) to the catalytic R in the initiation and elongation subunits likely recognizes the 2’-OH in the NTPs and possibly makes a hydrogen bond and discriminate dNTPs, which lack a 2’-OH (the yeast elongation subunit, Rpb1 could also use the invariant N^{479} to make the necessary H bond with the 2’-OH a well as 3’-OH as shown in elongation subunit β’ of eubacterial MSU RNAPs (Palanivelu 2018). Kaplan et al (2008) have shown by SDM experiments that the completely conserved His1085 both in prokaryotes (β’) and eukaryotes Rpb1 might involve in NTP selection and substitution of Ala or Phe resulted in inviability. This H1085 in the trigger loop (amino acids from 1060 to 1101) was shown to make a contact with the β phosphate either through H-bond or salt bridge and the L1081 was located at the 3’ end of the RNA (Wang et al, 2006). Mix and match analysis also shows and that particular His is completely conserved in both prokaryotes and eukaryotes in highly conserved stretch (Fig. 6). Another amino acid Q1078 in the same block is also shown to be essential and replacing Q1078 in Rpb1 to either N or S is lethal in yeast (Kaplan et al, 2008), consistent with a key role of these residues in NTP/dNTP discrimination.

9. The initiation and elongation subunits work in tandem during transcription cycles in eukaryotic MSU RNAP II

A close similarity is observed between the prokaryotic and eukaryotic transcription cycles. For example, it has been shown in prokaryotes (*E. coli)* that the initiation of transcription by the β subunit is not smooth and it makes many aborted transcripts of sizes 2-7 nts before the elongation step is taken over by the β' subunit (Campbell et al 2001). It was found that RNA/DNA hybrids of less than 8-bp display markedly less stability than those that are 8 bp or longer. In fact, the *E. coli* MSU RNAPs use these short RNA/DNA hybrids of 8 bp or longer for the ternary elongation complex (TEC) formation and further processivity (Kireeva et al 2000). Furthermore, Zaychikov et al (1997) have shown that an ~17 bp region of the DNA called the 'transcription bubble' was melted to expose the template strand for transcription in *E. coli*. MSA analysis agreed with these findings with the 7 amino acid gap between the catalytic R and the template binding YG pair in the initiation subunit β and 17 amino acid gap ('transcription bubble') between the catalytic R and the template binding YG pair in the elongation subunit β' (Table 5) (Palanivelu, 2018).

A similar observation of abortive initiations in eukaryotic Rpb2 was also reported by Pal and Luse, (1997). In addition to, as in prokaryotes, in eukaryotes also a 9 bp DNA-RNA stable hybrid is formed which extends from the active centre at nearly right angles to the entering DNA during the elongation cycle (Gnatt et al, 2001). Fiedler and Timmers (2001) results further support the MSA findings where the transition from abortive to productive elongation cycle occurred once the RNAP register +10 nts (Table 5). These observations are further supported by Luse (2013) who have shown that the promoter clearance was complete with ~ 10 nts. Pal et al (2005) on analyzing the 'transcription bubble' have found that regardless of promoter spacing, the upstream edge of the 'transcription bubble' formed 20 bp from TATA which is in close agreement with MSA analysis data. A similar finding was reported by Giardina and Lis (1993). Furthermore, Holstege et al (1997) analyzed the transcription initiation by the yeast RNAP II in a highly efficient *in vitro* transcription system composed of essentially homogeneous protein preparations and found that the downstream part of the 'transcription bubble' expands in a continuous motion, but the initially opened region on the non-template strand reclosed abruptly when transcription reached 11, which was accompanied by a switch from abortive initiations to productive mRNA synthesis (elongation). MSA analysis agrees with these findings with the 9 amino acid gap between the catalytic R and the template binding YG pair in the initiation subunit Rpb2 and 19 amino acid gap ('transcription bubble') between the catalytic R and the template binding FG pair in the elongation subunit Rpb1. Furthermore, Gnatt et al, found that the contacts to the downstream and upstream parts of the hybrid are made by Rpb1 and Rpb2, respectively, which further supports the tandem arrangement of the initiation and elongation subunits as proposed in this model (Gnatt et al, 2001).

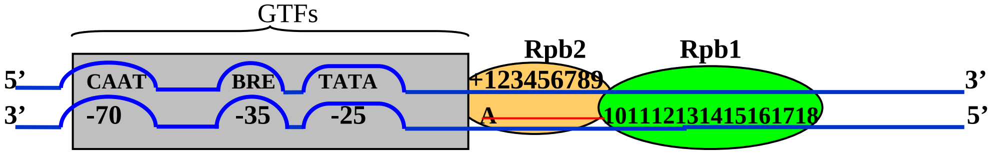


Fig. 7 A consensus model showing pre-initiation, initiation and elongation events by GTFs, Rpb2 and Rpb1 subunits of MSU RNAP- II of *S. cerevisiae*

NB: Thick lines indicate DNA strands and the thin line indicates the mRNA transcript.
A is shown as the first nucleotide at the +1 TSS
GTFs, General Transcription Factors (TFII-D, -A, -B, -F, -E, -H)
BRE, TFII-B Recognition Element (G/C-G/C-G/A-C-G-C-C)

In contrast to prokaryotes, in eukaryotes, it has been found that an A is inserted (and not a usual G, as in prokaryotes) in the initiation site as it invariably uses a G for capping enzyme which is also associated with the RNAP II.

Figure 7 shows a consensus model of the yeast MSU RNAP II subunits, from promoter recognition to initiation and elongation events during the transcription process. This has been confirmed that the RNAP II undergoes abortive initiations until it reached a position beyond +9 (i.e., the distance between the template binding FG pair and the catalytic R), at which stage the RNAP II was released from its promoter contacts and an elongation complex (TEC) is formed and a 20 bp "transcription bubble' formed from the TATA box (Pal et al, 2005). A modular structure is proposed for the initiation and elongation subunits' function in eukaryotes also as suggested by Severinov et al (1996) in prokaryotes.

10. Metal binding sites

The metal binding sites *S. cerevisiae* MSU RNAP II is arrived at from the data obtained by the MSA (this work) and X-ray crystallographic analyses (Zhang et al.1999) and SDM experiments (Svetlov et al, 2004) on eubacterial MSU RNAPs. The eukaryotic Rpb2 and Rpb1 subunits show many possible metal binding sites (highlighted in green). A Mg^{2+} ion binding site is found in the mRNA initiation subunit, Rpb2, from all eukaryotes. Similarly, a Mg^{2+} and a Zn^{2+} binding motifs are also found in the elongation subunits, Rpb1, of all eukaryotic RNAPs II. Crystallographic analysis of the *T. aquaticus* RNAP by Zhang et al, (1999) have shown that the Mg atom is chelated at an absolutely conserved –**NADFDGD**- motif in the β' elongation subunit and surprisingly the same invariant motif is found by MSA in all eukaryotic elongation subunits as well. Moreover, this is one of the regions that align in both the pro- and eukaryotes by mix and match analysis (Fig. 6). Interestingly, substitution of these Ds by A (D→A) gave rise to a dominant lethal phenotype and showed no detectable enzyme activity (Zaychikov et al, 1996). In addition to that, a Zn binding motif is also recognized in the eubacterial and eukaryotic elongation subunits with three conserved Cs. However, their distances arrangements of the three Cs are found to be different (Table 5). Another distinguishing feature between the eukaryotic and eubacterial elongation subunits is the catalytic and Zn binding regions, i.e., in *E. coli* β' subunit, the amino acids 888, 895 and 898 are shown to be involved in Zn binding (Table 5) but in eukaryotic elongation subunits it is placed at the very beginning of the N-terminal and covers the amino acids region 57-82 (Table 5). The Zn binding motif that is located in Rpb1 subunits may play a similar role in the Zn mediated proof-reading function as proposed for DNA polymerases and MSU RNAPs from eubacteria (Palanivelu, 2013, 2018).

Table 5. Metal binding sites in prokaryotic and eukaryotic MSU RNAPs

Subunit (Organism)	**Metal biding site**	**Method and Reference**
β eubacteria (*E. coli*)	-^{671}LEHDDA/ -^{809}GYNFEDS* - (Mg^{2+})	MSA (This communication)
β' eubacteria (*E. coli*)	**-^{458}YNADFDGDQM - (Mg^{2+}) &** **-^{883}RS^{1}VVSC^{5}DTDFGVC^{12}AHC^{15}Y^{16}GR^{901}-(Zn^{2+})***	X-ray crystallographic data (Zhang et al, 1999)
Rpb2 Eukaryote (*S. cerevisiae*)	-^{893}LDDDG^{897}- -^{832}GYNQED*S^{838}-(Mg^{2+})	MSA (This communication)
Rpb1 Eukaryote (*S. cerevisiae*)	**–^{478}YNAD*FD*GDEM^{487}- (Mg^{2+}) &** **-^{56}PR^{-6}LGSIDRN^{1}LKC^{4}QTC^{7}QEGMNEC^{14}PGHF^{18}GH^{83}-(Zn^{2+})**	MSA (This communication)

Possible metal binding sites arrived at by MSA and SDM

NB: The β' and RpB1 elongation subunits of eubacteria and eukaryotes contain both the $Mg^{2+\backslash}$ and Zn^{2+} binding sites. In both the cases, the Zn^{2+} binding site is built in the catalytic region with the 3 invariant Cs which coordinates the Zn atom.

11. Mechanism of Action of the Eukaryotic (*S. cerevisiae*) MSU RNAP II

A minimal number of steps involved in the catalytic cycle of RNAPs consist of NTP selection, Watson-Crick base pairing with the complementary nucleotide to the template, catalysis, pyrophosphate release and translocation. As the catalytic regions are found to be similar in both the initiation and elongation subunits, the polymerization mechanism could be also similar in both the initiation and elongation reactions. Figs. 7 describe the mechanism of action of the initiation and elongation subunits during transcription cycles in *S. cerevisiae.*

11.1 Mechanism of initiation by Rpb2 subunit of S. cerevisiae in MSU RNAP II

Step 1. Enzyme and the NTP at the Entry Site: Template binding pair (Tyr-Gly) and nucleotide discrimination by the invariant amino acids, Watson-Crick base pairing of the incoming NTP with the template DNA. The catalytic site amino acid Arg in positioned for proton abstraction. ATP is the initiating nucleotide.

Step 2. Proton abstraction and nucleophilic attack of the α-phosphate of NTP: Electronic transition at the active site for proton abstraction by the active site Arg and an electrophilic and nucleophilic attack of the incoming NTPs on the 3'-OH.

Step 3. Phosphodiester bond formation: Proton abstraction by the active site amino acid Arg with simultaneous formation of 3'→5' phosphodiester bond with the incoming NTPs.

Step 4. Inorganic pyrophosphate formation and translocation of the enzyme to next nucleotide: Proton transfer from the active site amino acid Arg, formation of inorganic pyrophosphate, active site restoration and translocation of the enzyme to next nucleotide.

11.2 Mechanism of elongation by Rpb1 subunit in yeast MSU RNAP II

Step1: Enzyme and the NTP at the Entry Site: Template binding by the template binding amino acids (Phe- Gly) and nucleotide discrimination by the invariant amino acids, Watson-Crick base pairing of the incoming NTP with the template DNA. The catalytic site amino acid Arg in positioned for proton abstraction.

Step 2. Proton abstraction and nucleophilic attack of α-phosphate of NTP: Electronic transition at the active site for proton abstraction by the active site Arg and an electrophilic and nucleophilic attack of the incoming NTPs on the 3'-OH.

Step 3. Phosphodiester bond formation: Proton abstraction by the active site amino acid Arg with simultaneous formation of 3'→5' phosphodiester bond with the incoming NTPs.

Step 4. Inorganic pyrophosphate formation and translocation of the enzyme to next nucleotide: Proton transfer from the active site amino acid Arg, formation of inorganic pyrophosphate, active site restoration and translocation of the enzyme to next nucleotide.

12. Proof-reading mechanism and Transcription termination in *S. cerevisiae* MSU RNAP II

Maintaining high fidelity during transcription is essential for the accurate transfer of genetic information from DNA to RNA as the first step in gene expression. The proof-reading mechanism is well established in DNA polymerases (Palanivelu 2013). However, it is poorly understood in RNAPs. Transcription accuracy is relatively high, as RNAPs generally misincorporate one wrong nucleotide/~100000 bases. As RNAPs are also Zn metalloenzymes the Zn-mediated deletion of the misincorporated NTP could be a possible mechanism as explained for DNA polymerases and eubacterial MSU RNAPs as both use DNA template to produce a complementary DNA/RNA strand (Palanivelu 2013, 2018). There is no distinct proof-reading domain or separate proof-reading subunit as reported in DNA polymerases. However, in eubacterial and eukaryotic elongation subunits of the MSU RNAPs a highly conserved Zn binding motif built into the catalytic region itself might involve in the proof-reading function (Palanivelu 2018). Presence of two metal ions at the active site is supported by a 2.8 Ǻ difference Fourier map, one persistently bound and the other possibly exchangeable during RNA synthesis (Cramer et al, 2001). When the enzyme stalls due to secondary structures and/or misincorporation, the proof-reading begins with fraying of the misincorporated nucleotide away from the DNA template and subsequent backtracking of RNAP by one position followed by nucleolytic cleavage of a dinucleotide that contains the misincorporated nucleotide (Sydow and Cramer (2009). Sydow and Cramer (2009), have also proposed that the exo- or endonucleolytic cleavage occurs at the same active site that is used for polymerization, which is further confirmed by X-ray crystallographic analysis of the *E. coli* and *T. thermophilus* MSU RNAPs (Zhang et al, 1999) suggesting a possible Zn mediated cleavage. The complete conservation of the active sites and Zn binding motif in all prokaryotic and eukaryotic elongation subunits, found by MSA analysis also further proves this point. The proof-reading mechanism may not be that much important during initiation events by the Rpb1 subunits, as they transcribe only very small regions, i.e., only ~ 10 nts and again such transcripts are well within the 5' untranslated regions of the RNA; so any error it makes may not be deleterious. Furthermore, a Zn binding motif is not found in the active site region of the initiation subunits. However, proof- reading is very important for the elongation subunit, viz., Rpb1 to produce an error–free transcripts, as they are going to be translated into active proteins. Therefore, when the enzyme stalls at the wrong nucleotide, it could backtrack and make an endonucleolytic cleavage or simply remove the wrong nucleotide by exonuclease action (Nudler 2009; Palanivelu 2013). Thus, the fidelity in the transcription is ensured by two mechanisms in MSU RNAPs, viz. by selection of correct NTPs and an efficient Zn mediated proof-reading.

The enzyme could use the same strategy for transcription terminations (intrinsic types) at TTSs. That is, when the enzyme stalls due to the stem-loop structures commonly found at the TTSs, it could backtrack and make an endo- or exonucleolytic cleavage and release the RNA transcript, using the same active site by Zn mediated reaction.

13. Other conserved regions and amino acid(s) in the MSU RNAP II

The above analysis to find out the conserved motifs, active sites and invariant amino acids, with respect to the substrate binding and catalytic region, form only a small region of the MSU RNAPs. Apart from these, there are a large number of single amino acid conservations like Ys, Ws, Cs, Ps and Gs, diads, triads and long stretches of conserved amino acids in all these polymerases (Figs. 4 – 6). The highly conserved stretches of amino acids may represent the different conserved structural motifs such as loops, rudders, jaws, bridge helix, exit/entry points for DNA/RNA, etc. Thus, they could form small functional domains. A good number of completely conserved Ps in these polymerases is implicated in making the necessary bents on the enzyme's structure during unique folding, substrate and template binding. The completely conserved Cs other than the catalytic region may play a role in the formation of disulphide bridges to make the enzyme more compact and stable.

14. CONCLUSIONS

Unlike reported for the DNA polymerases and SSU RNA polymerases, the MSU enzymes of eukaryotic MSU RNAPs are similar to the prokaryotic ones and use an R as the catalytic amino acid. However, they maintain a different distance conservation in the initiation and elongation subunits. An invariant Zn^{2+} binding motif found in the Rpb1 elongation subunits, is proposed to participate in proof-reading function. Therefore, it is clear from this communication that even though the transcription machinery of eukaryotes is much more complex than that of prokaryotes, the general principals of transcription and its regulation are found to be highly preserved. Hence, it is proposed that the MSU RNAP II of eukaryotes may also follow very similar polymerization and proof-reading mechanisms like their counterparts in eubacteria. MSA data and the available experimental data show that both the eubacterial and eukaryotic MSU RNAPs would have evolved from a common ancestor.

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The author declares no conflict of interest

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