

MULTIPLE SEQUENCE ALIGNMENT

Ofer Gill (gill@cs.nyu.edu)

Alyssa Lees(lees@cs.nyu.edu)

Aris Tsirigos(tsirigos@cs.nyu.edu)

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Introduction: Multiple Sequence Alignment poses a challenging and fascinating endeavor in computational biology. The computational methods use in multiple sequence alignments have tremendous importance in solving a series of related

biological problems

For example, a great discovery in molecular biology was the surprising similarity between the DNA sequences of distinct organisms. In fact, similar genes often perform identical functions across different species. In other instances, similar genes evolve or mutate in different species and therefore perform altered functions. Simultaneous alignment of nucleic acid or amino acid sequences allows the examination of the evolutions of mutations among similar genes (Mount, 141).

The ability to mathematically distinguish between gene sequences is also of great use in phylogenetic analysis. Aligned sequences yield predictions in each column of the mutation that occurred at a given site during the evolution of the sequence family. While prior knowledge of the actual nature of an evolutionary tree is needed for proper assessment, multiple sequence alignment algorithms are of great use in constructing the exact nature of evolutionary mutations.

One subsection of multiple sequence alignment algorithms focuses solely on the localized alignments of a subset of each sequence. Instead of examining the global alignment, which includes the relationship of all parts of a sequence, localized analysis removes highly conserved regions in the alignments. These highly conserved subsequences are used to build a “profile”. Once established a profile is used to search a target sequence for possible matches (Mount, 162). A related type of analysis uses blocks to identify motifs in protein sequences. Proteins have higher level structures and a motif is a certain combination of these structures (such as a helix-loop-helix structure). (Setubal, 253). Motifs are extremely important as potential binding sites and the discovery of such structures by pattern matching in related proteins is of great importance.

Generally, if the structure of one of more members of an alignment is known, it is possible to predict the amino acids that hold the same relationships in other

proteins. These alignments can uncover both underlying structural and functional relationships. One example, is that aligned promoters of a set of similarly regulated genes may reveal consensus-binding sites for regulatory proteins. In addition, once a consensus pattern has been found between sequence, database searching can be performed to find related sequence in other organisms.

The importance of multiple string alignment is indisputable. However, implementing efficient algorithms poses several computational difficulties.

As expected, the problem of sequencing several genes simultaneously poses new obstacles when compared to the standard two-sequence case. The different types of multiple sequence alignment algorithms can be divided into classes: 1) global alignment algorithms that progressively align a series of sequences 2) iterative methods that make an initial alignment and then revise 3) statistical methods. In this project we are mainly focusing on the comparison between progressive global alignments, iterative methods and statistical algorithms.

Below is a table we created to summarize the differences between the varying approaches to multiple sequence alignment.

MSA TYPE	SIZE	METHOD	SOFTWARE	FUNCTION	PROBLEMS
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Global Alignments	3-4 sequences or <10 small ones	Modified dynamic programming for pair-wise algorithm with a set scoring matrix	CLUSTALW, MSA	Building phylogenetic trees, Comparing distance between protein sequences	Only small # of sequences can be used. Final msa dependent on initial pair-wise alignment. Hard to make accurate gap penalties.
Iterative Methods	< 20 sequence	Correct problem in global alignments of final msa based on initial pair-wise alignment. Genetic algorithm generates many alignments that simulate gap insertion and recombination events. Revise alignment iteratively.	DIALIGN, PRRP, SAGA genetic algorithm, MultAlin	Improves overall alignment score of msa. Basically used for global alignment purposes such as building phylogenetic trees. Produces alignments by simulating evolutionary changes in sequences.	Slow. Alignments are not guaranteed to be optimal.
Statistical Algorithms (HMM)	Large # of sequences.	Using priors and a training set of sequences, train set model until it converges. Once model has been created, use other data sequences to create msa. Profile HMMs used for both global/local alignment EM/MEME algorithms used for local	eMOTIF, GIBBS, HMMER, MACAW, MEME, SAM	Generally used for local alignment. In a given sequence of proteins find common substrings to all sequences (motifs). HMMs also used to create most probable MSA for a given family of sequences. Model used to search database for common sequences	Large number of sequences are required. HMMs provide better msa than other methods, no sequence order is required, however if inappropriate initial or prior conditions are used results could be nonsense.

Problem: In this project, we explore the different methods of multiple sequence alignment. Using existing data for a variety of protein sequences, we sample algorithms that use progressive global alignment methods (i.e. global dynamic programming), iterative methods, and statistical methods. In attempting to program, a couple of the methods ourselves, we have drawn conclusions about some of the computational difficulties that multiple sequence alignment include. In addition, by exploring examples from each subtype of algorithms, we can draw conclusions on the usefulness and effectiveness of all such methods.

Background on Multiple Sequence Alignment Methods:

Global Alignment (dynamic programming) –

When solving the computational problem of multiple sequence alignment, a natural generalization is to expand the two-sequence case. The basic algorithm for the global comparison of two sequences, is to assign a score. A positive number is assigned for a match between the two base pairs or proteins in a sequence, a negative number for a mismatch and a more severe penalty for a gap. A standard application of dynamic programming is used to calculate the score with gap penalties/etc for the entire sequence (Setubal, 50).

In the multiple sequence case, the issue of scoring becomes more complex.

With several sequences, scores are calculated by assigning a score to each column. The sum-of-pairs or SP measure is often used to calculate values for a sequence. The sum-of-pairs function is the sum of pairwise scores of all pairs of symbols in a given column. A k-dimensional array would be an obvious solution for dynamic programming, but it will quickly eat up time and space. A standard application of dynamic programming for multiple sequences takes exponential time. Even with time saving measures, a multiple sequence alignment of three sequences takes $O(n^3)$ time. As a result, only 3 or 4 sequences can be realistically used when implementing a global dynamic programming algorithm.

Due to the slow nature of dynamic programming algorithms, heuristics are often used to give reasonable approximations quickly.. One such algorithm is Star Alignment, which consists of building a multiple alignment based upon pairwise alignments between a fixed sequence of the input set. The result is a feasible polynomial time algorithm. Another approach to the global alignment problem is Tree alignments, where a weight is computed for each edge of a tree. The star alignment is a particular case of the tree alignment algorithm, in which the star is the tree(Setubal, 79).

In general, the major problems with the global alignment approach are that only a few sequences (even with speedy heuristics) can be sequenced at once. Pure dynamic programming yields accurate results, but is simply too slow without heuristics to approximate the heavy computation. In addition the heuristic approaches, yield good answers, but are often dependent on the initial sequences compared. A bad choice for the first sequence can yield an inaccurate result.

Our representative of this genre of multiple sequence alignment algorithms is the implementation of software CLUSLAW on the gene data (collected and listed below). CLUSTLAW works as follows :

ClustalW is a multiple sequence alignment program which aligns proteins in the following steps:

1. Pairwise alignments of all the sequences are performed with scores recorded
2. A phylogenetic tree is produced based on these scores, using progressive alignment and dynamic programming methods. In general, the closer-related sequences are placed closer to one another in the tree.
3. Using this tree, the sequences are aligned.

The genetic distance is the number of mismatched positions in an alignment (not including gaps) divided by the total number of matched positions. Sequences contributions are weighted based on their relationships from the tree. Weights are based on the distance of each sequence from the root of the tree.

Gaps provide a penalty to the score. There is a penalty for opening a gap within a sequence alignment, opening a gap adjacent to another gap, and enhancing or shrinking already present gaps. Tables based on observed gaps for certain proteins are also utilized in calculating this penalty, and these tables also provide an intuition of the correct alignment. The penalties are customizable, but for purposes of this experiment, the default values for ClustalW 1.82 have been chosen.

ClustalW works well in alignment when protein sequences are closely matched to one another. However, in cases where the sequences are far apart from one another when pairwise-aligned, more errors are made, and these errors are propagated to the tree construction, as well as the final results.

Iterative Methods:

The main of example of iterative methods in the paper is our basic implementation of the SAGA algorithm. SAGA is a genetic algorithm that simulated

changes in a group of alignments in an evolutionary manner. In this project, we wrote a simplified version of this algorithm (the code is attached at the end of the paper as Appendix A). The program is written in the language K.

Statistical Methods:HMM

Local Alignment : Searching for Motifs and Blocks

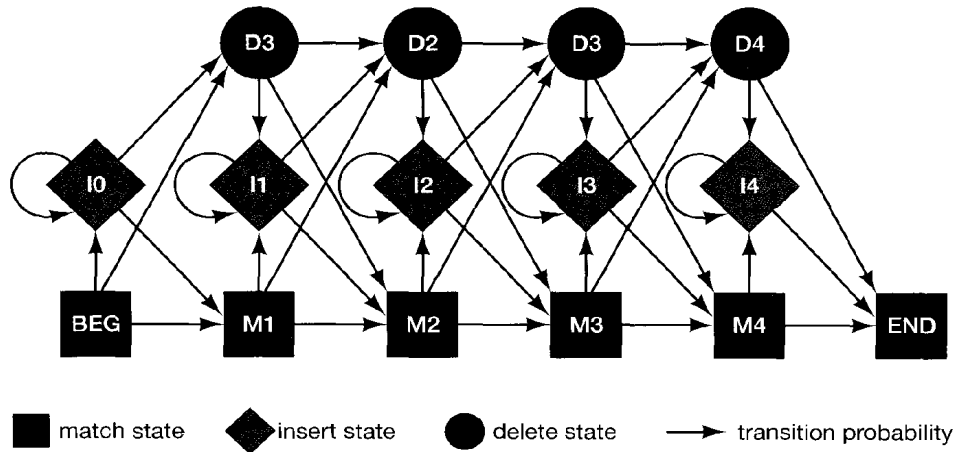
Primarily consisting of the EM algorithm(or MEME algorithm), this category of methods are used on a set of sequences that are expected to have a common subsequence that is not readily recognizable. Initially a guess is made to the location and size of a site of interest in each of the sequences. These sites are aligned for all sequences. The EM algorithms then consists of the two steps: the 'E' or expectation step and the 'M', maximization step. In the expectation step, the conditional probabilities of finding the site at each of the positions in the sequence are calculated. In the maximization step, the next counts of bases or amino acids for each position in the site found in the expectation step are substituted for the previous set. The expectation is step is then repeated with the new counts. The algorithm repeats the two steps until the results converge (Koski, 87).

MEME (Multiple EM for Motif Elicitation) is a common software tool to perform local multiple sequence alignments using the EM algorithm. The software algorithm searches over a range of possible motif widths. The most probably motif width for each profile is found by calculating the loglikelihood score after the first iteration of the EM algorithm. The remaining iterations of the algorithm find the best EM estimate for the given width. The software supports searching for one expected occurrence of a motif per a sequence, a search for zero or one occurrence of a motif per sequence, and finally for a motif to appear any number of times per sequence.

Global Alignment (and local): Building Model and creating MSA with HMM

A Hidden Markov Model uses statistics and prior information about a set of sequences to create all possible combinations of matches, mismatches, and gaps in ultimately creating an alignment. HMMs require a large number of sequences (typically 20-100) in order to “train” the model, but no insertion/deletion penalties are needed and no sequence ordering is required. The results of Hidden Markov Models are comparable if not better than other multiple sequence alignment methods (Mount, 185).

In particular, a certain structured Hidden Markov Model called a profile HMM is used to model multiple alignments. For the moment we will assume that a correct multiple alignment is given. Using this alignment, a profile HMM can be built and used to find and score potential matches to new sequences. The standard structure of the profile HMM consists of a series of N identical match states that are separated by transition probabilities of 1. The model deals with gaps, by treating insertions and deletions separately. The standard model is illustrated below, where match states represent the mostly conserved positions in the sequence family, the insert states represent subsequences that have been inserted in some members of the family and the delete states are silent states representing subsequences that have been deleted in some members of the family (Durbin, 104).



For a given sequence alignment, the most probable path through the model is determined by a decoding algorithm. A common solution is the Viterbi algorithm which finds the most probable path through the profile HMM recursively. A multiple sequence alignment is created by calculating a viterbi alignment for each individual sequence. The residues aligned to the same profile HMM match state are aligned in columns. This gives rise to an important difference between HMM multiple alignments and msa's created by traditional methods. The choice of where or how to put the “insert” residues in the alignment is arbitrary. The insert states are considered to represent segments of a sequence which are unconverted and not meaningfully alignable. According to Durbin, this is a biologically more realistic view of alignment. Other msa algorithms align entire sequences regardless of whether the sequences are meaningfully alignable (Durbin, 151).

In this project, two different methods of exploring HMMs were utilized. Our group initially begin by attempting to code a Multiple Sequence Alignment Algorithm using profile HMMs. The algorithm followed the following procedure:

- 1) First a length of the profile HMM was determined by averaging the length of all the sequences in a given gene family. All other parameters were initialized.
- 2) The model was trained with a subset of the data sequences. The estimated model

was created using a variation of the Baum-Welch algorithm. First a forward algorithm for profile HMMs was used and then a backward algorithm. The forward and backward algorithms were then combined to estimate the emission and transition probabilities using the Baum-Welch Re-Estimation Equations. The emission probabilities are defined to be the probability of seeing a certain symbol (in this case an amino acid), given the fact that we are in a given state. The transition probabilities are the probabilities of entering state i , given that we have started in state j . With Baum-Welch, we improve with each iteration of the probability of a given sequence being observed. The iteration stops when a limiting probability is achieved (the model should eventually converge).

- 3) Finally, all sequences not in the training set are aligned to the final model using the Viterbi algorithm and a multiple alignment is built.

Unfortunately, the project of coding a HMM algorithm in matlab was too ambitious for the limited time allotted. While we were somewhat successful in attempting to write code to train a model, Matlab was simply too slow to get any meaningful output. For example, we were able to write preliminary code that created a HMM profile of an imaginary sequence of a few states. However, even the smallest gene sequences in our data set required a profile of a minimum of 1500 states. This was far too difficult to manage efficiently in matlab.

Unable to write functional matlab code to create multiple sequence alignments with HMMs, we tested the data using the program HMMER. The HMMER software uses an approach listed above to create profile hidden Markov models (profile HMMs) to do sensitive database searching using static descriptions of a sequence family's consensus.

Data:

The data for all experiments with existing software and code we constructed ourselves are amino acid sequences found on various websites. Below we have listed brief descriptions of each of the genes used in this project.

Gene: BACE

Description: Beta-secretase precursor protein found in brain tissue. Responsible for proteolytic processing of the Amyloid Precursor Protein (APP), which generates amyloid beta peptide (Abeta). And, Abeta is an early and critical feature of Alzheimer's disease. Development of BACE inhibitors might assist treatment of Alzheimer's disease.

BACE cleaves at the Amino Terminus of the Abeta peptide sequence, between residues 671 and 672 of APP, leading to the generation and extracellular release of beta-cleaved soluble APP, as well as cell-associated carboxy-terminal fragment which is later released by gamma-secretase.

Gene: CTSE or CATE

Description: The predicted sequence of human gastric cathepsin E (CTSE) was determined by analysis of cDNA clones isolated from a library constructed with poly(A+) RNA from a gastric adenocarcinoma cell line. The CTSE cDNA clones were identified using a set of complementary 18-base oligonucleotide probes specific for a 6-residue sequence surrounding the first active site of all previously characterized human aspartic proteinases. The CTSE gene was localized to human chromosome 1 by concurrent cytogenetic and cDNA probe analyses of a panel of human x mouse somatic cell hybrids.

The intracellular location and distribution of CTSE in lymphoid-

associated tissue causes scientists to believe that it may have a role in immune function. CTSE is a member of the Peptidase family A1 (Pepsin).

Gene: GLTA or CISO

Description: This gene is a member of the citrate synthase family, which is found in nearly all cells capable of oxidative metabolism. GLTA encodes citrate synthase from a novel bacterial isolate (DS2-3R) from Antarctica, and has been cloned, sequenced and over-expressed in *Escherichia coli*.

Both the recombinant and the native enzymes were purified from DS2-3R, and are cold-active with a temperature optimum of 31 degrees C. In addition the enzymes are rapidly inactivated at 45 degrees C, and show significant activity at 10 degrees C and below.

Gene: CS (Citrate synthase, mitochondrial [Precursor])

Description: This gene is another member of the citrate synthase family. The nucleotide sequence encoding the CS gene was determined from the sequencing of the CS cDNA isolated from a human heart cDNA library. The primary sequence of CS deduced from its nucleotide sequence reveals a highly conserved, albeit slightly larger, protein of 466 amino acids, with 95% homology to its pig homologue. The data also indicates that the human genomic CS gene contains no introns, and confirms the location of the human CS gene on chromosome 12.

Gene: POL (Protease)

Description: This gene belongs to the Peptidase family A2, AKA the RetroPepsin family. This gene is found in immune-deficiency viruses such as HIV-1, HIV-2 / SIVSMM / MAC, SIVAGM, SIVMND, LV1-1KS1, FIV, EAIV, and BIV. It is being

analyzed for purposes of treating HIV. A branching order has yet to be found among differing groups of immune-deficiency viruses.

Experiments:

1. Global Alignment – CLUSTALW SOFTWARE:

The experiment consisted of simply running software on all of the gene data listed above. The print outs for each of the CLUSTALW runs on each gene family are attached at the end of this document.

Since the experiments conducted in this report involve closely related proteins, ClustalW worked well on them. Based on the results, within the BACE, CS, GLTA, CATE, and POL proteins, the sequences aligned fairly well. In the BACE, CATE, and POL experiments, the sequences aligned with 10% distances from one another or less.

In the CS experiment, all sequences aligned with less than 10% distances, except CISY_DAUCA which came up around 34.6% distance. In the GLTA experiment, only four genes aligned with less than 10% distance, with all the others aligning with 10-28% distance.

In the CISY experiment, which uses both GLTA and CS proteins, the tree structures produced matched those of GLTA and CS, with the exception of CISY_DAUCA. Furthermore, the sequence distances measured were roughly the same as the GLTA and CS counterparts, with the exception of CISY_DAUCA, whose distance came out fairly lower in the CISY experiment. The explanation for CISY_DAUCA's change of location in the tree and lower distance is probably due to its close match with the GLTA proteins, in spite of CISY_DAUCA being a CS protein.

2. Iterative – SAGA genetic algorithm implementation

simple Genetic Algorithm for the MSA problem

We developed a program in K that implements a very basic version of the genetic algorithm described in [1]. Given the initial sequences, a population of MSAs is created and then evolved through various random “evolutionary” events called operators. In this program, we incorporated three operators:

- Recombination (crossover)
- Gap insertion
- Block shuffling

The operators act on MSAs that are chosen randomly according to their weights (scores). Each generation of MSAs comprises the best scoring 50% of MSAs from the previous generation and another 50% of mutated MSAs generated with the use of the three operators. We tested our program with the first 60 characters of the following proteins:

Name: CARP_CANTR

WebID: Q00663

Gene: SAPT1.

FoundIn: Candida tropicalis (Yeast)

Size=394

Sequence=

```
MATIFLFTKN VFIALAFALF AQGLTIPDGI EKRTDKVVSL DFTVIRKPFN ATAHRLIQKR
SDVPTTLINE GPSYAADIVV GSNQQKQTVV IDTGSSDLWV VDTDAECQVT YSGQTNNFCK
QEGTFDPSSS SSAQNLNQDF SIEYDLTSS QGSFYKDTVG FGGISIKNQQ FADVTTTSVD
QGIMGIGFTA VEAGYNLYSN VPVTLKKQGI INKNAYSCDL NSEDASTGKI IFGGVDNAKY
TGTLTALPVT SSVELRVHLG SINFDGTSVS TNADVVLDSG TTITYFSQST ADKFARIVGA
TWDSRNEIYR LPSCDLGDA VVNFQDQVVKI TVPLSELILK DSDSSICYFG ISRNDANILG
DNFLRRAYIV YLDDKTISL AQVKYTSSSD ISAL
```

Name: CARP_CRYPA

WebID: P11838

Gene: EAPA

FoundIn: parasitica

Size=419

Sequence=

```
MSSPLKNALV TAMPLAGGALS SPTKQHVGP VNASPEVGP KYSFKQVRNP NYKFNGLPSV
KKTYLKYGVP IPAWLEDAVQ NSTSGLAERS TGSATTPID SLDDAYITPV QIGTPAQLN
LDFDTGSSDL WVFSSSETTAS EVDGQTIYTP SKSTTAKLLS GATWSISYGD GSSSSGDVYT
DTVSVGGLTV TGQAVESAKK VSSSFTEDST IDGLLGLAFS TLNTVSPTQQ KTFDFNAKAS
LDSPVFTADL GYHAPGTYNF GFIDTTAYTG SITYTAVSTK QGFWEWTSTG YAVGSGTFKS
TSIDGIADTG TLLYLPA TV VSAYWAQVSG AKSSSSVGGY VFPCSATLPS FTFGVGSARI
VIPGDYIDFG PISTGSSSCF GGIQSSAGIG INIFGDVALK AAFVVFNGAT TPTLGFASK
```

Name: CARP_NEUCR

WebID: Q01294

Gene: PEP-4.

FoundIn: Neurospora crassa

Size=396

Sequence=

```
MKGALLTAAM LLGSAQAGVH TMKLKKVPLA DELESVPIDV QVQHLGQKYT GLRTEHTQA
MFKATDAQVS GNHPVPITNF MNAQYFSEIT IGTPPQTFKV VLDTGSSNLW VPSSQCGSIA
CYLHNKYESS ESSTYKKNGT SFKIEYSGS LSGFVSQDRM TIGDITINDQ LFAEATSEPG
LAFAFGRFDG ILGLGYDRLA VPGITPPFYK MVEQKLVDEP VFSFYLDQD GESEVVFVGGV
```

NKDRYTGKIT TIPLRRKAYW EVDFDAIGYG KDFAELEGHG VILDTGTS LI ALPSQLA EML
NAQIGAKKSW NGQFTIDCGK KSSLEDVTFT LAGYNFTLGP EDYILEASGS CLSTFMGMDM
PAPVGPLAIL GDAFLRKYY S IYDLGADTVG IATAKR

Name: CARP_RHICH

WebID: P06026

Gene:

FoundIn: Rhizopus chinensis (Bread mold)

Size=393

Sequence=

MKFTLISSCI AIAALAVAVD AAPGEEKKISI PLAKNP NYKP SAKNAIQKAI AKYNKHKINT
STGGIVPDAG VGTVPMTDYG NDVEYYGQVT IGTPGK KFN L DFDTGSSDLW IASTLCTNCG
SRQTKYDPKQ SSTYQADGRT WSISYGDGSS ASGILAKDNV NLGGLLIKQ TIELAKREAA
SFANGPNDGL LGLGFD TITT VRGVKTPMDN LISQGLISRP IFGVYLGKAS NGGGGEYIFG
GYDSTKFKGS LTTVPIDNSR GWWGITVDRA TVGTSTVASS FDGILDTGTT LLILPNNVAA
SVARAYGASD NGDGYTISC DTSRFKPLVF SINGASFQVS PDSLVFEEYQ GQCIAGFGYG
NFDFAIIGDT FLKNNYVVFN QGVPEVQIAP VAQ

We used 30 generations of 100 MSAs each and we achieved a score of 63 compared to 84 by CLUSTALW. The scoring array used was a standard PAM250 array. Here is the output:

s: optimize[Snum;30;100]

0

"BEST SCORE: -32"

("-MATIFLFTKNVFIALAFALFAQGLTIPDGIEKRTDKVVS LDFTVIRKPFNATAHRLIQKR-----"
"-----MSSPLKNALVTAMLAGGALSSPTKQHV GIPVNASPEVGP GKYSFKQVRNP NYKFNGPLSV--"
"-----MKGALLTAAMLLGSAQAGVHTMKLKKVPLADELESVPIDVQVQHLGQKYTGLR TESHTQA"
"-----MKFTLISSCIAIAALAVAVDAAPGEEKKISIPLAKNP NYKPSAKNAIQKAI AKYNKHKINT---")

1

"BEST SCORE: -32"

("-MATIFLFTKNVFIALAFALFAQGLTIPDGIEKRTDKVVS LDFTVIRKPFNATAHRLIQKR-----"
"-----MSSPLKNALVTAMLAGGALSSPTKQHV GIPVNASPEVGP GKYSFKQVRNP NYKFNGPLSV--"
"-----MKGALLTAAMLLGSAQAGVHTMKLKKVPLADELESVPIDVQVQHLGQKYTGLR TESHTQA"
"-----MKFTLISSCIAIAALAVAVDAAPGEEKKISIPLAKNP NYKPSAKNAIQKAI AKYNKHKINT---")

2

"BEST SCORE: -32"

("-MATIFLFTKNVFIALAFALFAQGLTIPDGIEKRTDKVVS LDFTVIRKPFNATAHRLIQKR-----"
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"-----MKGALLTAAMLLGSAQAGVHTMKLKKVPLADELESVPIDVQVQHLGQKYTGLR TESHTQA"
"-----MKFTLISSCIAIAALAVAVDAAPGEEKKISIPLAKNP NYKPSAKNAIQKAI AKYNKHKINT---")

3

"BEST SCORE: -32"

("-MATIFLFTKNVFIALAFALFAQGLTIPDGIEKRTDKVVS LDFTVIRKPFNATAHRLIQKR-----"
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"-----MKGALLTAAMLLGSAQAGVHTMKLKKVPLADELESVPIDVQVQHLGQKYTGLR TESHTQA"
"-----MKFTLISSCIAIAALAVAVDAAPGEEKKISIPLAKNP NYKPSAKNAIQKAI AKYNKHKINT---")

4

"BEST SCORE: -13"

("MATIFLF-TKNVFIALAFALFAQGLTIPDGIEKRTDKVVS LDFTVIRKPFNATAHRLIQKR--"
"M-SSPLK-NALVTAMLAGGALSSPTKQHV GIPVNASPEVGP GKYSFKQVRNP NYKFNGPLSV-"
"M-KGALLTAAMLLGSAQAGVHTMKLKKVPLADELESVPIDVQVQHLGQKYTGLRT-ESHTQ-A"
"M-KFTLISSCIAIAALAVAVDAAPGEEKKISIPLAKNP NYKPSAKNAIQKAI AKYN-KHKIN-T")

5

"BEST SCORE: -13"

("MATIFLF-TKNVFIALAFALFAQGLTIPDGIEKRTDKVVS LDFTVIRKPFNATAHRLIQKR--"
"M-SSPLK-NALVTAMLAGGALSSPTKQHV GIPVNASPEVGP GKYSFKQVRNP NYKFNGPLSV-"
"M-KGALLTAAMLLGSAQAGVHTMKLKKVPLADELESVPIDVQVQHLGQKYTGLRT-ESHTQ-A"
"M-KFTLISSCIAIAALAVAVDAAPGEEKKISIPLAKNP NYKPSAKNAIQKAI AKYN-KHKIN-T")

6

"BEST SCORE: 13"
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"MK---GALLTAAMLLGSAQAGVHTMKLKKVPLADELESVPIDVQVQHLGQKYTG-LRTE--SHTQA"
"MKFTLISSCIAIAALAVAVDAAPGEKKISIPAKNPYKPSAKNAIQKAIKYN-KHKI--NT---")

7

"BEST SCORE: 13"
("MATIF--LFTK-NVFIALAFALFAQGLTIPDGIEKRTDKVVSLDFTVIRKPFNATAHRLIQKR---"
"MSSPLKNALVT-AMLAGGALSSPTKQHVGPVNASPEVGPVKYSFKQVRNPNYKFNGPL--SV---"
"MK---GALLTAAMLLGSAQAGVHTMKLKKVPLADELESVPIDVQVQHLGQKYTG-LRTE--SHTQA"
"MKFTLISSCIAIAALAVAVDAAPGEKKISIPAKNPYKPSAKNAIQKAIKYN-KHKI--NT---")

8

"BEST SCORE: 13"
("MATIF--LFTK-NVFIALAFALFAQGLTIPDGIEKRTDKVVSLDFTVIRKPFNATAHRLIQKR---"
"MSSPLKNALVT-AMLAGGALSSPTKQHVGPVNASPEVGPVKYSFKQVRNPNYKFNGPL--SV---"
"MK---GALLTAAMLLGSAQAGVHTMKLKKVPLADELESVPIDVQVQHLGQKYTG-LRTE--SHTQA"
"MKFTLISSCIAIAALAVAVDAAPGEKKISIPAKNPYKPSAKNAIQKAIKYN-KHKI--NT---")

9

"BEST SCORE: 17"
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"M-KGAL---LTAAMLLGSAQAGVHTMKLKKVPLADELESVPIDVQVQHLGQKYTGRLTESHTQA"
"MKFTLISSCIAIAALAVAVDAAPGEKKISIPAKNPYKPSAKNAIQKAIKYNK---HKINT-")

10

"BEST SCORE: 17"
("M-ATIF---LFTKNVFIALAFALFAQGLTIPDGIEKRTDKVVSLDFTVIRKPFNATAHRLIQKR"
"M-SSPLKNALVTAMLAGGALSSPTKQHVGPVNASPEVGPVKYSFKQVRNPNYKF---NGPLSV"
"M-KGAL---LTAAMLLGSAQAGVHTMKLKKVPLADELESVPIDVQVQHLGQKYTGRLTESHTQA"
"MKFTLISSCIAIAALAVAVDAAPGEKKISIPAKNPYKPSAKNAIQKAIKYNK---HKINT-")

11

"BEST SCORE: 17"
("M-ATIF---LFTKNVFIALAFALFAQGLTIPDGIEKRTDKVVSLDFTVIRKPFNATAHRLIQKR"
"M-SSPLKNALVTAMLAGGALSSPTKQHVGPVNASPEVGPVKYSFKQVRNPNYKF---NGPLSV"
"M-KGAL---LTAAMLLGSAQAGVHTMKLKKVPLADELESVPIDVQVQHLGQKYTGRLTESHTQA"
"MKFTLISSCIAIAALAVAVDAAPGEKKISIPAKNPYKPSAKNAIQKAIKYNK---HKINT-")

12

"BEST SCORE: 17"
("M-ATIF---LFTKNVFIALAFALFAQGLTIPDGIEKRTDKVVSLDFTVIRKPFNATAHRLIQKR"
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"M-KGAL---LTAAMLLGSAQAGVHTMKLKKVPLADELESVPIDVQVQHLGQKYTGRLTESHTQA"
"MKFTLISSCIAIAALAVAVDAAPGEKKISIPAKNPYKPSAKNAIQKAIKYNK---HKINT-")

13

"BEST SCORE: 17"
("M-ATIF---LFTKNVFIALAFALFAQGLTIPDGIEKRTDKVVSLDFTVIRKPFNATAHRLIQKR"
"M-SSPLKNALVTAMLAGGALSSPTKQHVGPVNASPEVGPVKYSFKQVRNPNYKF---NGPLSV"
"M-KGAL---LTAAMLLGSAQAGVHTMKLKKVPLADELESVPIDVQVQHLGQKYTGRLTESHTQA"
"MKFTLISSCIAIAALAVAVDAAPGEKKISIPAKNPYKPSAKNAIQKAIKYNK---HKINT-")

14

"BEST SCORE: 17"
("M-ATIF---LFTKNVFIALAFALFAQGLTIPDGIEKRTDKVVSLDFTVIRKPFNATAHRLIQKR"
"M-SSPLKNALVTAMLAGGALSSPTKQHVGPVNASPEVGPVKYSFKQVRNPNYKF---NGPLSV"
"M-KGAL---LTAAMLLGSAQAGVHTMKLKKVPLADELESVPIDVQVQHLGQKYTGRLTESHTQA"
"MKFTLISSCIAIAALAVAVDAAPGEKKISIPAKNPYKPSAKNAIQKAIKYNK---HKINT-")

15

"BEST SCORE: 41"
("MATIFLFTKNVFIALAFALFAQGL--TIPDGIEKRTDKV-VSLDFTVIRKPFNATAHRLIQKR-"
"MS-SPLKNALVTAMLAGGALSSPTKQHVGPVNASPE---VGPVKYSFKQVRNPNYKFNGPLSV"
"MKGALLTAAMLLGSAQAGVHTMKLKK---VPLADELESVPIDVQVQHLGQKYTGRLTESHTQA-"
"MKFTLISSCIAIAALAVAVDAAPGEKKISIPAKNPYKPSAKNAIQKAIKYNKHKINT-")

16

"BEST SCORE: 41"
("MATIFLFTKNVFIALAFALFAQGL--TIPDGIEKRTDKV-VSLDFTVIRKPFNATAHRLIQKR-"
"MS-SPLKNALVTAMLAGGALSSPTKQHVGPVNASPE---VGPGKYSFKQVRNPYKFNGLPSV"
"MKGALLTAAMLLGSAQAGVHTMKLKK---VPLADELESVPIDVQVQHLGQKYTGLRTEHTQA-"
"MKFTLISSCIAIALAVAVDAAPGEKKISIPAKNPN---YKPSAKNAIQKAIKYNKHKINT-")

17

"BEST SCORE: 41"
("MATIFLFTKNVFIALAFALFAQGL--TIPDGIEKRTDKV-VSLDFTVIRKPFNATAHRLIQKR-"
"MS-SPLKNALVTAMLAGGALSSPTKQHVGPVNASPE---VGPGKYSFKQVRNPYKFNGLPSV"
"MKGALLTAAMLLGSAQAGVHTMKLKK---VPLADELESVPIDVQVQHLGQKYTGLRTEHTQA-"
"MKFTLISSCIAIALAVAVDAAPGEKKISIPAKNPN---YKPSAKNAIQKAIKYNKHKINT-")

18

"BEST SCORE: 41"
("MATIFLFTKNVFIALAFALFAQGL--TIPDGIEKRTDKV-VSLDFTVIRKPFNATAHRLIQKR-"
"MS-SPLKNALVTAMLAGGALSSPTKQHVGPVNASPE---VGPGKYSFKQVRNPYKFNGLPSV"
"MKGALLTAAMLLGSAQAGVHTMKLKK---VPLADELESVPIDVQVQHLGQKYTGLRTEHTQA-"
"MKFTLISSCIAIALAVAVDAAPGEKKISIPAKNPN---YKPSAKNAIQKAIKYNKHKINT-")

19

"BEST SCORE: 41"
("MATIFLFTKNVFIALAFALFAQGL--TIPDGIEKRTDKV-VSLDFTVIRKPFNATAHRLIQKR-"
"MS-SPLKNALVTAMLAGGALSSPTKQHVGPVNASPE---VGPGKYSFKQVRNPYKFNGLPSV"
"MKGALLTAAMLLGSAQAGVHTMKLKK---VPLADELESVPIDVQVQHLGQKYTGLRTEHTQA-"
"MKFTLISSCIAIALAVAVDAAPGEKKISIPAKNPN---YKPSAKNAIQKAIKYNKHKINT-")

20

"BEST SCORE: 41"
("MATIFLFTKNVFIALAFALFAQGL--TIPDGIEKRTDKV-VSLDFTVIRKPFNATAHRLIQKR-"
"MS-SPLKNALVTAMLAGGALSSPTKQHVGPVNASPE---VGPGKYSFKQVRNPYKFNGLPSV"
"MKGALLTAAMLLGSAQAGVHTMKLKK---VPLADELESVPIDVQVQHLGQKYTGLRTEHTQA-"
"MKFTLISSCIAIALAVAVDAAPGEKKISIPAKNPN---YKPSAKNAIQKAIKYNKHKINT-")

21

"BEST SCORE: 63"
("MATIFLFTKNVFIA---LAFALFAQGLTIPDGIEKRTDKVVSLDFTVIRKPFNATA--HRLIQKR-----"
"MS---SPLKNALVT---A--MLAGGALSSPTKQHVGPVNASPEVGPYKYSFKQVRNPYKFNGLPSV----"
"M-----KGALLTA---AMLLGSAQAGVHTMKLKKVPLADELESVPIDVQVQHL--GQKYTGLRTEHTQA"
"M-----KFTLISSCIAIALAVAVDAAPGEKKISIPAKNPNYKPSAKNAI----QKAIKYNKHKINT")

22

"BEST SCORE: 63"
("MATIFLFTKNVFIA---LAFALFAQGLTIPDGIEKRTDKVVSLDFTVIRKPFNATA--HRLIQKR-----"
"MS---SPLKNALVT---A--MLAGGALSSPTKQHVGPVNASPEVGPYKYSFKQVRNPYKFNGLPSV----"
"M-----KGALLTA---AMLLGSAQAGVHTMKLKKVPLADELESVPIDVQVQHL--GQKYTGLRTEHTQA"
"M-----KFTLISSCIAIALAVAVDAAPGEKKISIPAKNPNYKPSAKNAI----QKAIKYNKHKINT")

23

"BEST SCORE: 63"
("MATIFLFTKNVFIA---LAFALFAQGLTIPDGIEKRTDKVVSLDFTVIRKPFNATA--HRLIQKR-----"
"MS---SPLKNALVT---A--MLAGGALSSPTKQHVGPVNASPEVGPYKYSFKQVRNPYKFNGLPSV----"
"M-----KGALLTA---AMLLGSAQAGVHTMKLKKVPLADELESVPIDVQVQHL--GQKYTGLRTEHTQA"
"M-----KFTLISSCIAIALAVAVDAAPGEKKISIPAKNPNYKPSAKNAI----QKAIKYNKHKINT")

24

"BEST SCORE: 63"
("MATIFLFTKNVFIA---LAFALFAQGLTIPDGIEKRTDKVVSLDFTVIRKPFNATA--HRLIQKR-----"
"MS---SPLKNALVT---A--MLAGGALSSPTKQHVGPVNASPEVGPYKYSFKQVRNPYKFNGLPSV----"
"M-----KGALLTA---AMLLGSAQAGVHTMKLKKVPLADELESVPIDVQVQHL--GQKYTGLRTEHTQA"
"M-----KFTLISSCIAIALAVAVDAAPGEKKISIPAKNPNYKPSAKNAI----QKAIKYNKHKINT")

25

"BEST SCORE: 63"
("MATIFLFTKNVFIA---LAFALFAQGLTIPDGIEKRTDKVVSLDFTVIRKPFNATA--HRLIQKR-----"
"MS---SPLKNALVT---A--MLAGGALSSPTKQHVGPVNASPEVGPYKYSFKQVRNPYKFNGLPSV----"
"M-----KGALLTA---AMLLGSAQAGVHTMKLKKVPLADELESVPIDVQVQHL--GQKYTGLRTEHTQA"
"M-----KFTLISSCIAIALAVAVDAAPGEKKISIPAKNPNYKPSAKNAI----QKAIKYNKHKINT")

26

"BEST SCORE: 63"

```
("MATIFLFTKNVFIA---LAFALFAQGLTIPDGIEKRTDKVVSLDFTVIRKPFNATA--HRLIQKR-----"  
"MS---SPLKNALVT---A--MLAGGALSSPTKQHVIGIPVNASPEVGPVKYSFKQVRNPYKFNGPLSV----"  
"M-----KGALLTA---AMLLGSAQAGVHTMKLKKVPLADELESVPIDVQVQHL--GQKYTGLRTEHTQA"  
"M-----KFTLISSCIAIAALAVAVDAAPGEKKISIPAKNPYKPSAKNAI-----QKAIKYNKHKINT")
```

27

"BEST SCORE: 63"

```
("MATIFLFTKNVFIA---LAFALFAQGLTIPDGIEKRTDKVVSLDFTVIRKPFNATA--HRLIQKR-----"  
"MS---SPLKNALVT---A--MLAGGALSSPTKQHVIGIPVNASPEVGPVKYSFKQVRNPYKFNGPLSV----"  
"M-----KGALLTA---AMLLGSAQAGVHTMKLKKVPLADELESVPIDVQVQHL--GQKYTGLRTEHTQA"  
"M-----KFTLISSCIAIAALAVAVDAAPGEKKISIPAKNPYKPSAKNAI-----QKAIKYNKHKINT")
```

28

"BEST SCORE: 63"

```
("MATIFLFTKNVFIA---LAFALFAQGLTIPDGIEKRTDKVVSLDFTVIRKPFNATA--HRLIQKR-----"  
"MS---SPLKNALVT---A--MLAGGALSSPTKQHVIGIPVNASPEVGPVKYSFKQVRNPYKFNGPLSV----"  
"M-----KGALLTA---AMLLGSAQAGVHTMKLKKVPLADELESVPIDVQVQHL--GQKYTGLRTEHTQA"  
"M-----KFTLISSCIAIAALAVAVDAAPGEKKISIPAKNPYKPSAKNAI-----QKAIKYNKHKINT")
```

29

"BEST SCORE: 63"

```
("MATIFLFTKNVFIA---LAFALFAQGLTIPDGIEKRTDKVVSLDFTVIRKPFNATA--HRLIQKR-----"  
"MS---SPLKNALVT---A--MLAGGALSSPTKQHVIGIPVNASPEVGPVKYSFKQVRNPYKFNGPLSV----"  
"M-----KGALLTA---AMLLGSAQAGVHTMKLKKVPLADELESVPIDVQVQHL--GQKYTGLRTEHTQA"  
"M-----KFTLISSCIAIAALAVAVDAAPGEKKISIPAKNPYKPSAKNAI-----QKAIKYNKHKINT")
```

[1] C. Notredame and D.G. Higgins, "SAGA: sequence alignment by genetic algorithm," *Nucleic Acids Research*, 1996, Vol. 24, No. 8

3. HMM : HMMER Software

Output from running trials with the HMMER software on several gene families is included at the end of the paper.

As noted in the description earlier in the project, HMM profile alignments differ from the traditional multiple sequence alignments in that alignments are not made for biologically meaningless sequences of insertions.

Results for Base:

Number of sequences: 3
Total # residues: 1503
Smallest: 501
Largest: 501
Average length: 501.0
Alignment length: 501
Average identity: 97%
Most related pair: 99%
Most unrelated pair: 96%
Most distant seq: 96%

Results for Cate:

Number of sequences: 4
Total # residues: 1582

Smallest: 391
Largest: 398
Average length: 395.5
Alignment length: 398
Average identity: 13%
Most related pair: 23%
Most unrelated pair: 7%
Most distant seq: 9%

Results for Cisy:

Number of sequences: 23
Total # residues: 9663
Smallest: 375
Largest: 472
Average length: 420.1
Alignment length: 490
Average identity: 15%
Most related pair: 98%
Most unrelated pair: 3%
Most distant seq: 8%

Results for CS:

Number of sequences: 4
Total # residues: 1835
Smallest: 433
Largest: 472
Average length: 458.8
Alignment length: 472
Average identity: 28%
Most related pair: 96%
Most unrelated pair: 6%
Most distant seq: 9%

Results for GLTA:

Number of sequences: 19
Total # residues: 7828
Smallest: 375
Largest: 437
Average length: 412.0
Alignment length: 455
Average identity: 19%
Most related pair: 98%
Most unrelated pair: 3%
Most distant seq: 8%

Results for POL:

Number of sequences: 53
Total # residues: 53800
Smallest: 100
Largest: 1146
Average length: 1015.1
Alignment length: 1199
Average identity: 16%
Most related pair: 100%
Most unrelated pair: 2%
Most distant seq: 7%

Overall, HMMER performed poorer alignment results in comparison to CLUSTALW.

(Average identity was 20% or lower for all test genes except BACE.) Specifically, areas of the sequences that were aligned with CLUSTALW were not aligned in when HMMER was used.

HMMER uses two modes: An insertion state (areas in lower-case letters) and a match state (areas in upper-case letters). HMMER attempts to align sequences only when it is in match state, and doesn't worry of alignment in the insertion state. According to the results, HMMER was scarcely using the insertion mode, causing portions of the sequences in match mode to match up that shouldn't. Furthermore, in some cases, identical letters were appearing diagonal to one another in the match mode. A little more insertion modes elsewhere would've caused these identical letter portions to align, thus yielding higher average identity percentages.

Conclusions:

As expected, the results from the progressive method global alignment based software, CLUSTALW, were favorable. The multiple sequence alignments generated for the various genes scored relatively well. However, the success of CLUSTALW may come from the fact that all the genes in each family are closely related and only a small number of sequences were given as input for each trial.

The results of the tests using Hidden Markov Model software, HMMER were disappointing in comparison. The multiple sequence alignments produced yielded poor percentages of matching. Combined with the fact that the HMMER produced multiple sequence alignments were often worse the progressive method based alignments made with CLUSTALW, a closer examination of the HMM algorithm used should be made.

One possible problem was that each data family fed into the HMMER program had a relatively small number of sequences. In the literature researched, Hidden Markov Models typically need between 20- 200 training sequences in order to produce an accurate model.

One conclusion may be that we simply to not give the software enough data.

After looking at the results from HMMER, it seems that another problem

was that some of the match states are redundant and should be absorbed in an insert state. Durbin suggests that such problems may occur because the initial choice for the length of the model was inappropriate or because local optima were encountered during the initial training of the HMM profile. A possible solution to this problem is to adaptively modify a model's structure while it is being trained.

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13. <http://www.genome.ad.jp>
14. <http://www.ncbi.nlm.nih.gov>

Appendix A - Source Code (align.k):

```

=====
=====
/ FUNCTION: SP[msa]
/
/-----/
/ Calculates the score of a multiple sequence alignment (msa)
/
/=====
=====
SP: { [msa]
  n: #msa
  pairs: ,/{ [x] :(x,/:((x+1)+!(n-x+1)))}'!n
  :+/( {[v] :+/(PAM250 ./: (+v))}'(msa[pairs]))
}

/=====
=====
/ FUNCTION: init
/
/-----/
/ Creates the initial population (generation 0)
/
/=====
=====
init: {
  G:: npop#0
  k: 0
  do[ npop
    offs: nseq _draw 10
    randomly select offsets
    max: |offs+#:'S
  / add offsets at the beginning and then pad the sequences
    G[k]:: { [i] :((offs[i]#20),S[i],(((max-offs[i])-#S[i])#20))}'!nseq
    k+: 1
  ]

```

```
}
```

```
/=====
=====
/ FUNCTION: straln
/
/-----/
/ Converts an alignment from numerical to letter format
/
/=====
=====
straln: { [msa]
:([v]:nucleotides[v])'msa)
}
```

```
/=====
=====
/ FUNCTION: choose_op
/
/-----/
/ Choose an operator according to the weights
/
/=====
=====
choose_op: {
:((+\w_op)>*(1 _draw +/\w_op))?1
}
```

```
/=====
=====
/ FUNCTION: choose_parent
/
/-----/
/ Choose a parent according to the weights
/
/=====
```

```

=====
choose_parent: {
  pid: ((+\w_msa)>*(1 _draw +/\w_msa))?1
  w_msa[pid]:: w_msa[pid]-1
  :pid
}

/=====
=====
/ FUNCTION: insert_gaps
/
/-----/
/ Operator for inserting gaps
/
/=====
=====
insert_gaps: { [pid]
/ Split sequences in two clusters according to their distance
pairs:/(!nseq),/:(!nseq))
sco: SP'G[pid][pairs]
poles: pairs[sco?&/sco]
i: 0
cluster1: !0
cluster2: !0
do[nseq
  :[SP[G[pid][poles[0],i]]>SP[G[pid][poles[1],i]]; cluster1,: i; cluster2,: i]
  i+: 1
]

gaps: *(1 _draw 5)+1

n: #G[pid][0]
pos1: 0
pos2: n-pos1
bestscore: -1000
bestmsa: G[pid]
while[pos1<n
  msa: G[pid]
  r: pos1+!(n-pos1)
  msa[cluster1]: {[i] :(msa[i][!pos1],(gaps#20),msa[i][r])}'cluster1
  r: pos2+!(n-pos2)
  msa[cluster2]: {[i] :(msa[i][!pos2],(gaps#20),msa[i][r])}'cluster2
  pos1+: 1
  pos2-: 1
  if[~test_msa[msa]; (\ "ERROR (INSERTGAP)"; G[-1])]
  score: SP[msa]

```

```

    if[score>bestscore; (bestmsa: msa; bestscore: score)]
  ]
/ \bestscore
:bestmsa
}

/=====
=====/
/ FUNCTION: shuffle_blocks
/
/-----/
/ Operator for shuffling blocks
/
/=====
=====/
shuffle_blocks: { [pid]
  bestscore: -1000
  bestmsa: G[pid]
  bounds: {[v] :&~(v=(0,v[!(-1+#v)]))}'(G[pid]=20) / get space block
bounds
k: 0
while[k<nseq
  msa: G[pid]
  hcut: ?(( _ nseq%2) _draw nseq)
  j: 0
  while[j<#hcut
    jj: hcut[j]
    if[1<#bounds[jj]
      i: 2*(*(1 _draw ( _ (#bounds[jj])%2))) / choose block to be
shifted
      shift: *(1 _draw 2) / shift left or right?
      lbound: bounds[jj][i]
      rbound: bounds[jj][i+1]
      if[lbound=0; shift: 0]
      lbound-: shift / left
block bound
      rbound-: shift / right
block bound
      t: msa[jj;lbound] / swap
      msa[jj;lbound]: msa[jj;rbound]
      msa[jj;rbound]: t
    ]
    j+: 1
  ]
]

if[~test_msa[msa]; (\ "ERROR (SHUFFLEBLOCK)"; G[-1])]

```

```

    score: SP[msa]
    if[score>bestscore; (bestmsa: msa; bestscore: score)]
    k+: 1
  ]
/ \./(">>", $bestscore)

:bestmsa
}

```

```

/=====
=====
/ FUNCTION: recombine
/
/-----
/ Operator for recombining two alignments
/
/=====
=====
recombine: { [pid]
  msa1: G[pid[0]]
  msa2: G[pid[1]]
  bestscore: -1000
  bestmsa: msa1
  i: 1
  do[i<#*msa1
    msa11: +(msa1)[!i]
    msa12: +(msa1)[i+!(#*msa1)-i]

    split: {[i] :*&(+\~msa2[i]=20)=(1+~/~msa11[i]=20)}!#msa1

    msa21: msa2 @' (!:split)
    msa22: msa2 @' (split+!:(#:'msa2)-split))

    msa: msa11 , ' msa22
    msa: msa , ' ((/#:'msa)-(#:'msa))#20
    if[~test_msa[msa]; (\ "ERROR (RECOMBINE)"; G[-1])]
    score: SP[msa]
    if[score>bestscore; (bestmsa: msa; bestscore: score)]

    msa: msa21 , ' msa12
    msa: msa , ' ((/#:'msa)-(#:'msa))#20
    if[~test_msa[msa]; (\ "ERROR (RECOMBINE)"; G[-1])]
    score: SP[msa]
    if[score>bestscore; (bestmsa: msa; bestscore: score)]

```

```
    i+: 1
  ]

:bestmsa
}
```

```
=====
=====
/ FUNCTION: localopt
/
/-----/
/ Operator for local optimization
/
=====
=====
localopt: { [pid]
  bestscore: -1000
  bestmsa: G[pid]
  i: 0
/ do[i<#*msa1
  msa: G[pid]
  x: *(1 _draw #*msa)
  v: (x++nseq#(!5))
  lsa: msa @' v

/ SOS: NOT FINISHED

  if[~test_msa[msa]; (\"ERROR (LOCALOPT)\"; G[-1])]
  score: SP[msa]
  if[score>bestscore; (bestmsa: msa; bestscore: score)]

  i+: 1
/ ]

:bestmsa
}
```

```
=====
=====
/ FUNCTION: make_child
```

/

```
-----/
/ Make a child given the operator and the parent(s)
/
=====
=====
make_child: { [op;pid]
  ::[op=0; insert_gaps[pid]; op=1; shuffle_blocks[pid]; op=2; recombine[pid]; op=3;
  localopt[pid]; G[pid]]
}
```

```
=====
=====
/ FUNCTION: update_wop
/
-----/
/ Update operator weights
/
=====
=====
update_wop: {

}
```

```
=====
=====
/ FUNCTION: test_msa
/
-----/
/ Test an alignment against the original
/
=====
=====
test_msa: { [msa]
  :S~(msa @' &:'~msa=20)
}
```

```

/=====
=====
/ FUNCTION: optimize
/
/-----/
/ Optimize the alignment
/
/=====
=====
optimize: { [msa;generations;population]
  S:: msa
  nseq:: #msa
           / get number of sequences
  ngen:: generations
number of generations
  npop:: population
population size

  init[]
initialize the population
  g: 0
  w_op:: nop#100
initialize operator weights
  credits_op:: nop#0
attributed to operators

while[g<ngen
  if[(g!10)=0; update_wop[]; credits_op:: nop#0]

  scores:: SP'G
  index: >scores
alignments according to score
  scores:: scores[index]
  G:: G[index]
  w_msa:: _(1000*scores)%+scores
each alignment

  \g
  \,/"BEST SCORE: ", $*scores)
  \straln[*G]

  c: _ npop%2

  while[c<npop

/ Choose operators, parents and make child
  op: choose_op[]
  pid: choose_parent[]

```

```

    if[op=2; pid,: choose_parent[]
    child: make_child[op;pid]
    child: +(child)[&~(&/child=20)] / get rid of aligned
space blocks

/ Accept only if not duplicate
    if[~/(child ~/: G[!c])
    G[c]:: child

/ SOS: Update entire list of related operators
    if[SP[G[c]]>SP[G[*pid]]; credits_op[op]:: credits_op[op]+16]
    c+: 1
    ]
    ]
    g+: 1
    ]
    :*G
}

```

```

/=====
=====/
/ MAIN PROGRAM
/
/-----/
/ Optimizes Multiple Sequence Alignment of proteins using a Genetic Algorithm
/
/=====
=====/

```

```

/-----/
/   A C D E F G H I K L M N P Q R S T V W Y -
/-----/
PAM250:: ( 2 -2 0 0 -4 1 -1 -1 -1 -2 -1 0 1 0 -2 1 1 0 -6 -3 -1
-2 12 -5 -5 -4 -3 -3 -2 -5 -6 -5 -4 -3 -5 -4 0 -2 -2 -8 0 -1
0 -5 4 3 -6 1 1 -2 0 -4 -3 2 -1 2 -1 0 0 -2 -7 -4 -1
0 -5 3 4 -5 0 1 -2 0 -3 -2 1 -1 2 -1 0 0 -2 -7 -4 -1
-4 -4 -6 -5 9 -5 -2 1 -5 2 0 -4 -5 -5 -4 -3 -3 -1 0 7 -1
1 -3 1 0 -5 5 -2 -3 -2 -4 -3 0 -1 -1 -3 1 0 -1 -7 -5 -1
-1 -3 1 1 -2 -2 6 -2 0 -2 -2 2 0 3 2 -1 -1 -2 -3 0 -1
-1 -2 -2 -2 1 -3 -2 5 -2 2 2 -2 -2 -2 -2 -1 0 4 -5 -1 -1
-1 -5 0 0 -5 -2 0 -2 5 -3 0 1 -1 1 3 0 0 -2 -3 -4 -1
-2 -6 -4 -3 2 -4 -2 2 -3 6 4 -3 -3 -2 -3 -3 -2 2 -2 -1 -1
-1 -5 -3 -2 0 -3 -2 2 0 4 6 -2 -2 -1 0 -2 -1 2 -4 -2 -1

```

```

0 -4 2 1 -4 0 2 -2 1 -3 -2 2 -1 1 0 1 0 -2 -4 -2 -1
1 -3 -1 -1 -5 -1 0 -2 -1 -3 -2 -1 6 0 0 1 0 -1 -6 -5 -1
0 -5 2 2 -5 -1 3 -2 1 -2 -1 1 0 4 1 -1 -1 -2 -5 -4 -1
-2 -4 -1 -1 -4 -3 2 -2 3 -3 0 0 0 1 6 0 -1 -2 2 -4 -1
1 0 0 0 -3 1 -1 -1 0 -3 -2 1 1 -1 0 2 1 -1 -2 -3 -1
1 -2 0 0 -3 0 -1 0 0 -2 -1 0 0 -1 -1 1 3 0 -5 -3 -1
0 -2 -2 -2 -1 -1 -2 4 -2 2 2 -2 -1 -2 -2 -1 0 4 -6 -2 -1
-6 -8 -7 -7 0 -7 -3 -5 -3 -2 -4 -4 -6 -5 2 -2 -5 -6 17 0 -1
-3 0 -4 -4 7 -5 0 -1 -4 -1 -2 -2 -5 -4 -4 -3 -3 -2 0 10 -1
-1 -1 -1 -1 -1 -1 -1 -1 -1 -1 -1 -1 -1 -1 -1 -1 -1 -1 -1 -1 0)

```

nop:: 3

/ number operators

nucleotides:: "ACDEFGHIKLMNPQRSTVWY-" /

nucleotide letter codes

inpfile:: "seq-2"

if[0<#_i; inpfile:: _i[0]]

Salpha: 0: inpfile / read

sequences from file

Snum: nucleotides ?/: Salpha /

convert to numerical format

msa: optimize[Snum;1000;100]

Appendix B - Test Data Results:

HMMER ALIGNMENTS: Base Gene

STOCKHOLM 1.0
#-GF AU HMMER 2.2g

#=GS sp|P56817|BACE_HUMAN AC BACE (EC 4.1.3.7) - Homo sapiens (Human) .
#=GS sp|P56818|BACE_MOUSE AC BACE (EC 4.1.3.7) - Mus musculus (Mouse) .
#=GS sp|P56819|BACE_RAT AC BACE (EC 4.1.3.7) - Rattus norvegicus (Rat) .

```

sp|P56817|BACE_HUMAN MAQALPWLWLVWGAGVLPAGHTQHGIRLPLRSLGGAPLGLRPLRETDEE
sp|P56818|BACE_MOUSE MAPALHWLWLVVWVSGMLPAQGTGLGIRLPLRSLGGAPLGLRPLRETDEE
sp|P56819|BACE_RAT MAPALRWLWLVVWVSGMLPAQGTGLGIRLPLRSLGGAPLGLRPLRETDEE
#=-GC RF
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX

```

```

sp|P56817|BACE_HUMAN PEEPGRRGFSFVEMVDNLRGKSGQGYVEMTVGSPPTLNILVDTGSSNFA
sp|P56818|BACE_MOUSE SEEPGRRGFSFVEMVDNLRGKSGQGYVEMTVGSPPTLNILVDTGSSNFA
sp|P56819|BACE_RAT PEEPGRRGFSFVEMVDNLRGKSGQGYVEMTVGSPPTLNILVDTGSSNFA
#=-GC RF
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX

```

```

sp|P56817|BACE_HUMAN VGAAPHPFLHRYRQQLSSTYRDLRKGVYVPTYQGWEGELGTDLVSIPH
sp|P56818|BACE_MOUSE VGAAPHPFLHRYRQQLSSTYRDLRKGVYVPTYQGWEGELGTDLVSIPH
sp|P56819|BACE_RAT VGAAPHPFLHRYRQQLSSTYRDLRKSIVYVPTYQGWEGELGTDLVSIPH
#=-GC RF
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX

```

```

sp|P56817|BACE_HUMAN GPNVTVRANIAAITESDKFFINGSNWEGILGLAYAEIARPDSDLEPFDFS
sp|P56818|BACE_MOUSE GPNVTVRANIAAITESDKFFINGSNWEGILGLAYAEIARPDSDLEPFDFS
sp|P56819|BACE_RAT GPNVTVRANIAAITESDKFFINGSNWEGILGLAYAEIARPDSDLEPFDFS
#=-GC RF
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX

```

```

sp|P56817|BACE_HUMAN LVKQTHVPLNLSLQLCGAGFPLNQSEVLASVGGSMIIGGDHSLYTGSLW
sp|P56818|BACE_MOUSE LVKQTHIPNIFSLQLCGAGFPLNQTEALASVGGSMIIGGDHSLYTGSLW
sp|P56819|BACE_RAT LVKQTHIPNIFSLQLCGAGFPLNQTEALASVGGSMIIGGDHSLYTGSLW
#=-GC RF
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX

```

```

sp|P56817|BACE_HUMAN YTPIRREWYEVIVRVEINGQDLKMDCKEYNYDKSIVDSGTTNLRPKK
sp|P56818|BACE_MOUSE YTPIRREWYEVIVRVEINGQDLKMDCKEYNYDKSIVDSGTTNLRPKK
sp|P56819|BACE_RAT YTPIRREWYEVIVRVEINGQDLKMDCKEYNYDKSIVDSGTTNLRPKK
#=-GC RF
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX

```

```

sp|P56817|BACE_HUMAN VFEEAAVKSIIKAASSTEFKPDGFVWLGELVCWQAGTTPWNIFPVISLYLMG
sp|P56818|BACE_MOUSE VFEEAAVKSIIKAASSTEFKPDGFVWLGELVCWQAGTTPWNIFPVISLYLMG
sp|P56819|BACE_RAT VFEEAAVKSIIKAASSTEFKPDGFVWLGELVCWQAGTTPWNIFPVISLYLMG
#=-GC RF
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX

```

```

sp|P56817|BACE_HUMAN EVTNQSFRTILPQQYLRPVEDVATSQDDCYKFAISQSTGTVMGAVIME

```


CLUSTALW ALIGNMENTS: BASE GENE

CLUSTAL W (1.82) Multiple Sequence Alignments

Sequence format is Pearson

Sequence 1: sp|P56817|BACE_HUMAN 501 aa

Sequence 2: sp|P56819|BACE_RAT 501 aa

Sequence 3: sp|P56818|BACE_MOUSE 501 aa

Start of Pairwise alignments

Aligning...

Sequences (1:2) Aligned. Score: 96

Sequences (1:3) Aligned. Score: 96

Sequences (2:3) Aligned. Score: 99

Guide tree file created: [ebi/extserv/old-work/912189.571194.dnd]

Start of Multiple Alignment

There are 2 groups

Aligning...

Group 1: Sequences: 2 Score:10946

Group 2: Sequences: 3 Score:10809

Alignment Score 9380

//

CLUSTAL W (1.82) multiple sequence alignment

```
sp|P56819|BACE_RAT MAPALRWLLLWVSGMLPAQGTHLGIRLPLRSLGAPPLGLRLPRETDEEPEEPGRRGSF 60
sp|P56818|BACE_MOUSE MAPALHWLLLWVSGMLPAQGTHLGIRLPLRSLGAPPLGLRLPRETDEESEEPPGRRGSF 60
sp|P56817|BACE_HUMAN MAQALPWLLLWMGAGVLPAGHTQHGIRLPLRSLGGAPLGLRLPRETDEEPEEPGRRGSF 60
*****
sp|P56819|BACE_RAT VEMVDNLRGKSGQGYVEMTVGSPPTLNILVDTGSSNFVGAAPHFLHRYYQRQLSST 120
sp|P56818|BACE_MOUSE VEMVDNLRGKSGQGYVEMTVGSPPTLNILVDTGSSNFVGAAPHFLHRYYQRQLSST 120
sp|P56817|BACE_HUMAN VEMVDNLRGKSGQGYVEMTVGSPPTLNILVDTGSSNFVGAAPHFLHRYYQRQLSST 120
*****
sp|P56819|BACE_RAT YRDLRKSIVYVPYVTPYQGWEGELGTDLVSIHPGNVTVRANIAAITESDKFFINGSNWEGIL 180
sp|P56818|BACE_MOUSE YRDLRKGIVYVPYVTPYQGWEGELGTDLVSIHPGNVTVRANIAAITESDKFFINGSNWEGIL 180
sp|P56817|BACE_HUMAN YRDLRKGIVYVPYVTPYQGWEGELGTDLVSIHPGNVTVRANIAAITESDKFFINGSNWEGIL 180
*****
sp|P56819|BACE_RAT GLAYAEIARPDSDLVVKQTHIPNIFSLQLCGAGFPLNQTEALASVGGSMIIGGI 240
sp|P56818|BACE_MOUSE GLAYAEIARPDSDLVVKQTHIPNIFSLQLCGAGFPLNQTEALASVGGSMIIGGI 240
sp|P56817|BACE_HUMAN GLAYAEIARPDSDLVVKQTHVFNLFSLQLCGAGFPLNQSEVLASVGGSMIIGGI 240
*****
sp|P56819|BACE_RAT DHSLYTGLWYTPIRREWYVEVIVRVEINGQDLKMDCKEYNYDKSIVDSGTTNLRPKK 300
sp|P56818|BACE_MOUSE DHSLYTGLWYTPIRREWYVEVIVRVEINGQDLKMDCKEYNYDKSIVDSGTTNLRPKK 300
sp|P56817|BACE_HUMAN DHSLYTGLWYTPIRREWYVEVIVRVEINGQDLKMDCKEYNYDKSIVDSGTTNLRPKK 300
*****
sp|P56819|BACE_RAT VFEAAVKSIIKASSTKFPDGFWLGEQLVCWQAGITTPWNIFPVISLYLMGEVTNQSFRT 360
sp|P56818|BACE_MOUSE VFEAAVKSIIKASSTKFPDGFWLGEQLVCWQAGITTPWNIFPVISLYLMGEVTNQSFRT 360
sp|P56817|BACE_HUMAN VFEAAVKSIIKASSTKFPDGFWLGEQLVCWQAGITTPWNIFPVISLYLMGEVTNQSFRT 360
*****
sp|P56819|BACE_RAT ILPQYLRPVEDVATSDDCYKFAVSQSSTGTVMGAVIMEGFYVVFDRARKRIGFAVSAC 420
sp|P56818|BACE_MOUSE ILPQYLRPVEDVATSDDCYKFAVSQSSTGTVMGAVIMEGFYVVFDRARKRIGFAVSAC 420
sp|P56817|BACE_HUMAN ILPQYLRPVEDVATSDDCYKFAISQSSTGTVMGAVIMEGFYVVFDRARKRIGFAVSAC 420
*****
sp|P56819|BACE_RAT HVHDEFRTAAVEGPFVTDMEDCGYNIPQTDDESTLMTIAYVMAAICALFMLPLCLMVCQW 480
sp|P56818|BACE_MOUSE HVHDEFRTAAVEGPFVTDMEDCGYNIPQTDDESTLMTIAYVMAAICALFMLPLCLMVCQW 480
sp|P56817|BACE_HUMAN HVHDEFRTAAVEGPFVTDMEDCGYNIPQTDDESTLMTIAYVMAAICALFMLPLCLMVCQW 480
*****
sp|P56819|BACE_RAT RCLRCLRQHDDFADDISLLK 501
sp|P56818|BACE_MOUSE RCLRCLRQHDDFADDISLLK 501
sp|P56817|BACE_HUMAN RCLRCLRQHDDFADDISLLK 501
*****
```

//

```
(
sp|P56817|BACE_HUMAN:0.03293,
sp|P56819|BACE_RAT:0.00299,
sp|P56818|BACE_MOUSE:0.00299);
//|----- sp|P56817|BACE_HUMAN:0.03293
|----- sp|P56819|BACE_RAT:0.00299
|----- sp|P56818|BACE_MOUSE:0.00299
```

CLUSTALW ALIGNMENTS: CATE GENE

CLUSTAL W (1.82) Multiple Sequence Alignments

Sequence format is Pearson

Sequence 1: sp|P14091|CATE_HUMAN 396 aa

Sequence 2: sp|P43159|CATE_RABIT 396 aa

Sequence 3: sp|P16228|CATE_RAT 398 aa

Sequence 4: sp|P70269|CATE_MOUSE 397 aa

Sequence 5: sp|P25796|CATE_CAVPO 391 aa

Start of Pairwise alignments

Aligning...

Sequences (1:2) Aligned. Score: 85

Sequences (1:3) Aligned. Score: 83

Sequences (1:4) Aligned. Score: 82

Sequences (1:5) Aligned. Score: 84

Sequences (2:3) Aligned. Score: 82

Sequences (1:4) Aligned. Score: 91
Sequences (1:5) Aligned. Score: 18
Sequences (1:6) Aligned. Score: 19
Sequences (1:7) Aligned. Score: 19
Sequences (1:8) Aligned. Score: 19
Sequences (1:9) Aligned. Score: 21
Sequences (1:10) Aligned. Score: 19
Sequences (1:11) Aligned. Score: 21
Sequences (1:12) Aligned. Score: 19
Sequences (1:13) Aligned. Score: 18
Sequences (1:14) Aligned. Score: 17
Sequences (1:15) Aligned. Score: 20
Sequences (1:16) Aligned. Score: 24
Sequences (1:17) Aligned. Score: 19
Sequences (1:18) Aligned. Score: 18
Sequences (1:19) Aligned. Score: 21
Sequences (1:20) Aligned. Score: 21
Sequences (1:21) Aligned. Score: 22
Sequences (1:22) Aligned. Score: 18
Sequences (1:23) Aligned. Score: 20
Sequences (2:3) Aligned. Score: 60
Sequences (2:4) Aligned. Score: 59
Sequences (2:5) Aligned. Score: 20
Sequences (2:6) Aligned. Score: 20
Sequences (2:7) Aligned. Score: 19
Sequences (2:8) Aligned. Score: 19
Sequences (2:9) Aligned. Score: 21
Sequences (2:10) Aligned. Score: 19
Sequences (2:11) Aligned. Score: 18
Sequences (2:12) Aligned. Score: 20
Sequences (2:13) Aligned. Score: 19
Sequences (2:14) Aligned. Score: 17
Sequences (2:15) Aligned. Score: 21
Sequences (2:16) Aligned. Score: 23
Sequences (2:17) Aligned. Score: 19
Sequences (2:18) Aligned. Score: 17
Sequences (2:19) Aligned. Score: 18
Sequences (2:20) Aligned. Score: 21
Sequences (2:21) Aligned. Score: 22
Sequences (2:22) Aligned. Score: 18
Sequences (2:23) Aligned. Score: 20
Sequences (3:4) Aligned. Score: 95
Sequences (3:5) Aligned. Score: 18
Sequences (3:6) Aligned. Score: 20
Sequences (3:7) Aligned. Score: 20
Sequences (3:8) Aligned. Score: 17
Sequences (3:9) Aligned. Score: 21
Sequences (3:10) Aligned. Score: 20
Sequences (3:11) Aligned. Score: 21
Sequences (3:12) Aligned. Score: 18
Sequences (3:13) Aligned. Score: 17
Sequences (3:14) Aligned. Score: 17
Sequences (3:15) Aligned. Score: 21
Sequences (3:16) Aligned. Score: 23
Sequences (3:17) Aligned. Score: 19
Sequences (3:18) Aligned. Score: 18
Sequences (3:19) Aligned. Score: 21
Sequences (3:20) Aligned. Score: 21
Sequences (3:21) Aligned. Score: 24
Sequences (3:22) Aligned. Score: 18
Sequences (3:23) Aligned. Score: 19
Sequences (4:5) Aligned. Score: 20
Sequences (4:6) Aligned. Score: 20
Sequences (4:7) Aligned. Score: 19
Sequences (4:8) Aligned. Score: 18
Sequences (4:9) Aligned. Score: 21
Sequences (4:10) Aligned. Score: 20
Sequences (4:11) Aligned. Score: 22
Sequences (4:12) Aligned. Score: 18
Sequences (4:13) Aligned. Score: 17
Sequences (4:14) Aligned. Score: 18
Sequences (4:15) Aligned. Score: 20
Sequences (4:16) Aligned. Score: 24
Sequences (4:17) Aligned. Score: 18
Sequences (4:18) Aligned. Score: 19
Sequences (4:19) Aligned. Score: 22
Sequences (4:20) Aligned. Score: 21
Sequences (4:21) Aligned. Score: 22
Sequences (4:22) Aligned. Score: 19
Sequences (4:23) Aligned. Score: 18
Sequences (5:6) Aligned. Score: 32
Sequences (5:7) Aligned. Score: 31
Sequences (5:8) Aligned. Score: 30
Sequences (5:9) Aligned. Score: 35
Sequences (5:10) Aligned. Score: 33
Sequences (5:11) Aligned. Score: 30
Sequences (5:12) Aligned. Score: 29
Sequences (5:13) Aligned. Score: 29
Sequences (5:14) Aligned. Score: 58
Sequences (5:15) Aligned. Score: 32
Sequences (5:16) Aligned. Score: 37
Sequences (5:17) Aligned. Score: 29
Sequences (5:18) Aligned. Score: 29
Sequences (5:19) Aligned. Score: 30
Sequences (5:20) Aligned. Score: 32
Sequences (5:21) Aligned. Score: 36
Sequences (5:22) Aligned. Score: 30
Sequences (5:23) Aligned. Score: 36
Sequences (6:7) Aligned. Score: 65
Sequences (6:8) Aligned. Score: 66
Sequences (6:9) Aligned. Score: 50
Sequences (6:10) Aligned. Score: 64
Sequences (6:11) Aligned. Score: 65
Sequences (6:12) Aligned. Score: 44
Sequences (6:13) Aligned. Score: 43
Sequences (6:14) Aligned. Score: 31
Sequences (6:15) Aligned. Score: 74

Sequences (6:16) Aligned. Score: 31
Sequences (6:17) Aligned. Score: 65
Sequences (6:18) Aligned. Score: 60
Sequences (6:19) Aligned. Score: 66
Sequences (6:20) Aligned. Score: 34
Sequences (6:21) Aligned. Score: 35
Sequences (6:22) Aligned. Score: 29
Sequences (6:23) Aligned. Score: 35
Sequences (7:8) Aligned. Score: 71
Sequences (7:9) Aligned. Score: 48
Sequences (7:10) Aligned. Score: 62
Sequences (7:11) Aligned. Score: 67
Sequences (7:12) Aligned. Score: 42
Sequences (7:13) Aligned. Score: 42
Sequences (7:14) Aligned. Score: 30
Sequences (7:15) Aligned. Score: 64
Sequences (7:16) Aligned. Score: 33
Sequences (7:17) Aligned. Score: 76
Sequences (7:18) Aligned. Score: 60
Sequences (7:19) Aligned. Score: 69
Sequences (7:20) Aligned. Score: 36
Sequences (7:21) Aligned. Score: 37
Sequences (7:22) Aligned. Score: 33
Sequences (7:23) Aligned. Score: 34
Sequences (8:9) Aligned. Score: 49
Sequences (8:10) Aligned. Score: 58
Sequences (8:11) Aligned. Score: 64
Sequences (8:12) Aligned. Score: 42
Sequences (8:13) Aligned. Score: 42
Sequences (8:14) Aligned. Score: 31
Sequences (8:15) Aligned. Score: 66
Sequences (8:16) Aligned. Score: 33
Sequences (8:17) Aligned. Score: 78
Sequences (8:18) Aligned. Score: 61
Sequences (8:19) Aligned. Score: 64
Sequences (8:20) Aligned. Score: 37
Sequences (8:21) Aligned. Score: 35
Sequences (8:22) Aligned. Score: 32
Sequences (8:23) Aligned. Score: 35
Sequences (9:10) Aligned. Score: 46
Sequences (9:11) Aligned. Score: 48
Sequences (9:12) Aligned. Score: 43
Sequences (9:13) Aligned. Score: 43
Sequences (9:14) Aligned. Score: 33
Sequences (9:15) Aligned. Score: 48
Sequences (9:16) Aligned. Score: 35
Sequences (9:17) Aligned. Score: 48
Sequences (9:18) Aligned. Score: 48
Sequences (9:19) Aligned. Score: 47
Sequences (9:20) Aligned. Score: 32
Sequences (9:21) Aligned. Score: 38
Sequences (9:22) Aligned. Score: 32
Sequences (9:23) Aligned. Score: 38
Sequences (10:11) Aligned. Score: 60
Sequences (10:12) Aligned. Score: 43
Sequences (10:13) Aligned. Score: 45
Sequences (10:14) Aligned. Score: 30
Sequences (10:15) Aligned. Score: 65
Sequences (10:16) Aligned. Score: 34
Sequences (10:17) Aligned. Score: 61
Sequences (10:18) Aligned. Score: 56
Sequences (10:19) Aligned. Score: 60
Sequences (10:20) Aligned. Score: 38
Sequences (10:21) Aligned. Score: 36
Sequences (10:22) Aligned. Score: 33
Sequences (10:23) Aligned. Score: 36
Sequences (11:12) Aligned. Score: 41
Sequences (11:13) Aligned. Score: 41
Sequences (11:14) Aligned. Score: 29
Sequences (11:15) Aligned. Score: 69
Sequences (11:16) Aligned. Score: 34
Sequences (11:17) Aligned. Score: 67
Sequences (11:18) Aligned. Score: 59
Sequences (11:19) Aligned. Score: 96
Sequences (11:20) Aligned. Score: 33
Sequences (11:21) Aligned. Score: 35
Sequences (11:22) Aligned. Score: 30
Sequences (11:23) Aligned. Score: 35
Sequences (12:13) Aligned. Score: 98
Sequences (12:14) Aligned. Score: 29
Sequences (12:15) Aligned. Score: 45
Sequences (12:16) Aligned. Score: 35
Sequences (12:17) Aligned. Score: 43
Sequences (12:18) Aligned. Score: 45
Sequences (12:19) Aligned. Score: 41
Sequences (12:20) Aligned. Score: 35
Sequences (12:21) Aligned. Score: 36
Sequences (12:22) Aligned. Score: 28
Sequences (12:23) Aligned. Score: 36
Sequences (13:14) Aligned. Score: 30
Sequences (13:15) Aligned. Score: 44
Sequences (13:16) Aligned. Score: 35
Sequences (13:17) Aligned. Score: 42
Sequences (13:18) Aligned. Score: 45
Sequences (13:19) Aligned. Score: 41
Sequences (13:20) Aligned. Score: 35
Sequences (13:21) Aligned. Score: 36
Sequences (13:22) Aligned. Score: 28
Sequences (13:23) Aligned. Score: 36
Sequences (14:15) Aligned. Score: 29
Sequences (14:16) Aligned. Score: 39
Sequences (14:17) Aligned. Score: 32
Sequences (14:18) Aligned. Score: 29
Sequences (14:19) Aligned. Score: 29
Sequences (14:20) Aligned. Score: 32
Sequences (14:21) Aligned. Score: 37
Sequences (14:22) Aligned. Score: 30

Sequences (14:23) Aligned. Score: 36
 Sequences (15:16) Aligned. Score: 32
 Sequences (15:17) Aligned. Score: 68
 Sequences (15:18) Aligned. Score: 58
 Sequences (15:19) Aligned. Score: 68
 Sequences (15:20) Aligned. Score: 34
 Sequences (15:21) Aligned. Score: 36
 Sequences (15:22) Aligned. Score: 30
 Sequences (15:23) Aligned. Score: 35
 Sequences (16:17) Aligned. Score: 35
 Sequences (16:18) Aligned. Score: 34
 Sequences (16:19) Aligned. Score: 33
 Sequences (16:20) Aligned. Score: 44
 Sequences (16:21) Aligned. Score: 42
 Sequences (16:22) Aligned. Score: 40
 Sequences (16:23) Aligned. Score: 42
 Sequences (17:18) Aligned. Score: 61
 Sequences (17:19) Aligned. Score: 68
 Sequences (17:20) Aligned. Score: 37
 Sequences (17:21) Aligned. Score: 37
 Sequences (17:22) Aligned. Score: 33
 Sequences (17:23) Aligned. Score: 36
 Sequences (18:19) Aligned. Score: 59
 Sequences (18:20) Aligned. Score: 34
 Sequences (18:21) Aligned. Score: 35
 Sequences (18:22) Aligned. Score: 32
 Sequences (18:23) Aligned. Score: 38
 Sequences (19:20) Aligned. Score: 33
 Sequences (19:21) Aligned. Score: 36
 Sequences (19:22) Aligned. Score: 30
 Sequences (19:23) Aligned. Score: 35
 Sequences (20:21) Aligned. Score: 35
 Sequences (20:22) Aligned. Score: 58
 Sequences (20:23) Aligned. Score: 34
 Sequences (21:22) Aligned. Score: 30
 Sequences (21:23) Aligned. Score: 51
 Sequences (22:23) Aligned. Score: 31

Guide tree file created: [/ebi/extserv/old-work/26039.6435.dnd]
 Start of Multiple Alignment

There are 22 groups

Aligning...

Group 1: Sequences: 2 Score:8153
 Group 2: Sequences: 3 Score:7766
 Group 3: Sequences: 2 Score:8507
 Group 4: Sequences: 3 Score:8379
 Group 5: Sequences: 2 Score:9195
 Group 6: Sequences: 5 Score:7893
 Group 7: Sequences: 8 Score:7507
 Group 8: Sequences: 9 Score:7534
 Group 9: Sequences: 10 Score:6881
 Group 10: Sequences: 2 Score:9191
 Group 11: Sequences: 12 Score:6515
 Group 12: Sequences: 2 Score:6387
 Group 13: Sequences: 2 Score:6513
 Group 14: Sequences: 3 Score:5633
 Group 15: Sequences: 5 Score:4099
 Group 16: Sequences: 2 Score:6454
 Group 17: Sequences: 7 Score:5300
 Group 18: Sequences: 19 Score:3525
 Group 19: Sequences: 2 Score:9898
 Group 20: Sequences: 3 Score:9014
 Group 21: Sequences: 4 Score:8043
 Group 22: Sequences: 23 Score:3066

Alignment Score 194699

CLUSTAL-Alignment file created [/ebi/extserv/old-work/26039.6435.aln]

//

CLUSTAL W (1.82) multiple sequence alignment

```

sp|P20902|CISY_ACIAN      -----SEATGKK-----AVLHLDGKE-IELPIYSGTLGPD 29
sp|P14165|CISY_PSEAE     -----MADKK-----AQLIEGSAPVELPVLSGTMGPD 28
sp|P18789|CISY_COXBU     -----MSNRK-----AKLSFENQS-VEFPIYSPITLGD 27
sp|P94325|CISY_BRAJA     -----MDAKASNKT-----ATLTVG-NKNYDLPHSGSVGP 31
sp|O33915|CISY_RHIME     -----MSEKS-----ATVTFG-GKSADLPVRSVSGIGPD 27
sp|P51033|CISY_BARHE     -----MSKNK-----AHITVN-DKKIELSVRKGTLGPD 27
sp|P00891|CISY_ECOLI     -----MADTK-----AKLTLNGDTAVELDLVKGTLGQD 28
sp|O68883|CISY_SALTY     -----MADTK-----AKITLTGDTTIELDLVKGTLGQD 28
sp|P09948|CISY_RICPR     -----MTNGNNNLEFAELKIR-GKLFKLPILKASIGKD 33
sp|P42457|CISY_CORGL     -----MFERDIVATDNNK-----AVLHYPGGE-FEMDIEASEGNN 35
sp|Q9ZN37|CISY_HELPI     -----MSVTL-----INNENNARYEFETIETRGP 26
sp|P56062|CISY_HELPY     -----MSVTL-----VNNENNARYEFETIETRGP 26
sp|O34002|CISY_ABDS2     -----
sp|P26491|CISY_MYCSM     -----
sp|P80148|CISY_SULSO     -----
sp|P21553|CISY_THEAC     -----
sp|Q53554|CISY_PYRFU     -----
sp|Q59977|CISY_SYNY3     -----
sp|P51045|CISY_THIFE     -----
sp|O75390|CISY_HUMAN     MALLTAAARLLGTKN-----ASCLVLAARHASASNTLKDILADLPKEQARIKTF 52
sp|P00889|CISY_PIG       MALLTAAARLFGAKN-----ASCLVLAARHASASNTLKDILADLPKEQARIKTF 52
sp|P23007|CISY_CHICK     -----ASSTNLKDVLAALIPKEQARIKTF 25
sp|O80433|CISY_DAUCA     MVFFRSVLLNKLRSRAVQSNLSNTVRFVQVTSASDLDRSOLKELIPEQERIKKL 60

sp|P20902|CISY_ACIAN     VIDVKDVLAS-GHFTFDPGFMATASCESKITFIDGDKGILLHRGYPIDQLATQAD---- 83
sp|P14165|CISY_PSEAE     VVDVRLGTAT-GHFTFDPGFMSTASCESKITIDGDKGVLLHRGYPIQLAEKSD---- 82
sp|P18789|CISY_COXBU     VIDVKTLDGNH-GAYALDVGFYSTAACESKITFIDGEGKILLYRGYPIDQLADKSD---- 81
sp|P94325|CISY_BRAJA     VIDIGKLYGQSGLFTYDPGFTSTASCQSKITYIDGDAAGVLEIRGYPIQLAEHGD---- 86
sp|O33915|CISY_RHIME     VVDIGSLYKQTTMFTYDPGFTSTASCESKITIDGDEGVLLHRGFPIQLAEHGD---- 82
sp|P51033|CISY_BARHE     VIEIASLYKETDTFTYDPGFTSTASCESKITIDGNEGILLYRGYPIDQLAEKGD---- 82
sp|P00891|CISY_ECOLI     VIDIRTLGSK-GVFTFDPGFTSTASCESKITFIDGDEGILLHRGFPIQLATDSN---- 82
sp|O68883|CISY_SALTY     VIDIRSLGSK-GVFTFDPGFTSTASCESKITFIDGDEGILLHRGFPIQLATDSN---- 82
sp|P09948|CISY_RICPR     VIDISRVSAEADYFTYDPGFMSTASCQSTITYIDGDKGLWYRGYDIKDLAEKSD---- 88
sp|P42457|CISY_CORGL     GVVVLGKMLSETGLITFDPGYVSTGSTEKSKITYIDGDAAGILYRGYDIADLAENAT---- 90
sp|Q9ZN37|CISY_HELPI     AVDFSKLFETTGFFSYDPGYSSTAGCQSKISYINGKKGELYRGRHRIEDLVAKYK---- 81
sp|P56062|CISY_HELPY     AVDFSKLFETTGFFSYDPGYSSTAGCQSKISYINGKKGELYRGRHRIEDLVAKYK---- 81

```



```

sp|P80148|CISY_SULSO:0.19140,
sp|P21553|CISY_THEAC:0.22770)
:0.08464)
:0.02693)
:0.00738,
(
sp|Q59977|CISY_SYNY3:0.24166,
sp|P51045|CISY_THIFE:0.24538)
:0.05308)
:0.00732)
:0.05339,
(
sp|Q9ZN37|CISY_HELPI:0.00816,
sp|P56062|CISY_HELPY:0.00827)
:0.27681)
:0.01930,
sp|P42457|CISY_CORGL:0.25348)
:0.05572,
sp|P09948|CISY_RICPR:0.20267)
:0.02580,
(
(
sp|P51033|CISY_BARHE:0.12911,
(
sp|P94325|CISY_BRAJA:0.11836,
sp|O33915|CISY_RHIME:0.10075)
:0.02057)
:0.03308,
(
sp|P00891|CISY_ECOLI:0.02031,
sp|O68883|CISY_SALTY:0.01950)
:0.14263)
:0.01434)
:0.01050,
(
sp|P20902|CISY_ACIAN:0.13006,
sp|P14165|CISY_PSEAE:0.12526)
:0.02760,
sp|P18789|CISY_COXBU:0.19612);
//

```

CLUSTALW ALIGNMENT: CS GENE Part 2
CLUSTAL W (1.82) Multiple Sequence Alignments

```

Sequence format is Pearson
Sequence 1: sp|P23007|CISY_CHICK 433 aa
Sequence 2: sp|O80433|CISY_DAUCA 472 aa
Sequence 3: sp|O75390|CISY_HUMAN 466 aa
Sequence 4: sp|P00889|CISY_PIG 464 aa
Start of Pairwise alignments
Aligning...
Sequences (1:2) Aligned. Score: 61
Sequences (1:3) Aligned. Score: 89
Sequences (1:4) Aligned. Score: 91
Sequences (2:3) Aligned. Score: 60
Sequences (2:4) Aligned. Score: 59
Sequences (3:4) Aligned. Score: 95
Guide tree file created: [/ebi/extserv/old-work/731574.586005.dnd]
Start of Multiple Alignment
There are 3 groups
Aligning...
Group 1: Sequences: 2 Score:9898
Group 2: Sequences: 3 Score:9011
Group 3: Sequences: 4 Score:8062
Alignment Score 13044
CLUSTAL-Alignment file created [/ebi/extserv/old-work/731574.586005.aln]
//

```

CLUSTAL W (1.82) multiple sequence alignment

```

sp|O75390|CISY_HUMAN MALLTAAARLLGTKN-----ASCLVLAARHASASSTNLKDILADLIPKEQARIKTFR 52

```

```

sp|P00889|CISY_PIG  MALLTAAARLFGAKN-----ASCLVLAARHASASSTNLKDILADLIPKEQARIKTFR 52
sp|P23007|CISY_CHICK -----ASSTNLKDVLAALIPKEQARIKTFR 25
sp|O80433|CISY_DAUCA  MVFFRSVSLNKLRSRAVQSQNSLNTVRFVQVTSASDLDLRSQKELIPEQERIKKLK 60
      **.*.* **.*.* **.*.* **.*.*

sp|O75390|CISY_HUMAN  QQHGKTVVVGQITVDMMYGGMRGMKGLVYETSVLDPDEGIRFRGFSIPECQKLLPKAKGGE 112
sp|P00889|CISY_PIG  QQHGNTVVVGQITVDMMYGGMRGMKGLVYETSVLDPDEGIRFRGFSIPECQKMLPKAKGGE 112
sp|P23007|CISY_CHICK  QQHGHTALGQITVDMYSYGGMRGMKGLVYETSVLDPDEGIRFRGFSIPECQKLLPKGGXGG 85
sp|O80433|CISY_DAUCA  AEHGKVVQLGNTVDMVLGGMRGMTGLLWETSLLDPEEGIRFRGLSIPECQKLLPGAKPGG 120
      **.*.* **.*.* **.*.* **.*.* **.*.* **.*.* **.*.* **.*.*

sp|O75390|CISY_HUMAN  EPLPEGLFWLLVTGCIPTTEEQVSWLSKEWAKRAALPSHVVTMLDNFPTNLHPMSQLSAAV 172
sp|P00889|CISY_PIG  EPLPEGLFWLLVTGQIPTTEEQVSWLSKEWAKRAALPSHVVTMLDNFPTNLHPMSQLSAAI 172
sp|P23007|CISY_CHICK  EPLPEGLFWLLVTGQIPTGAQVSWLSKEWAKRAALPSHVVTMLDNFPTNLHPMSQLSAAI 145
sp|O80433|CISY_DAUCA  EPLPEGLFWLLVTGKVPTEQVDALSaelRSRAAVPEHVYKTDALPVT AHPMTQFATGV 180
      ***** **.*.* **.*.* **.*.* **.*.* **.*.* **.*.* **.*.*

sp|O75390|CISY_HUMAN  TALNSESNFQAQYARGISRTKYWELIYEDSVDLIAKLPVAAKIYRNLYWEGSSIGAI 232
sp|P00889|CISY_PIG  TALNSESNFARA YAEGIHRTKYWELIYEDCMDLIAKLPVAAKIYRNLYREGSSIGAI 232
sp|P23007|CISY_CHICK  TALNSESNFARA YAEGLRRTKYWEMVYESAMDLIAKLPVAAKIYRNLYRAGSSIGAI 205
sp|O80433|CISY_DAUCA  MALQVQSEFQKAYEKGIHRTKYWEPTIYEDSITLIAQLPVVAAIYRRMYKNGQSISTDD 240
      **.*.* **.*.* **.*.* **.*.* **.*.* **.*.* **.*.* **.*.*

sp|O75390|CISY_HUMAN  NLDWSHNFTNMLGYTDHQTFLMRLYLTIHSDHEGNGVSAHTSHLVGSALSDPYLSFAAA 292
sp|P00889|CISY_PIG  KLDWSHNFTNMLGYTDAQFTFLMRLYLTIHSDHEGNGVSAHTSHLVGSALSDPYLSFAAA 292
sp|P23007|CISY_CHICK  KLDWSHNFTNMLGYTDAQFTFLMRLYLTIHSDHEGNGVSAHTSHLVGSALSDPYLSFAAA 265
sp|O80433|CISY_DAUCA  -LDYGANFAHMLGYDPSMQELMRLYVTIHTDHEGNGVSAHTSHLVASALSDPYLSFAAA 299
      **.*.* **.*.* **.*.* **.*.* **.*.* **.*.* **.*.* **.*.*

sp|O75390|CISY_HUMAN  MNLGAGPLHGLANQEVLVWLTQLQKEVGDVSDKLRDYIWNLTNSGRVVPYGHAVLRK 352
sp|P00889|CISY_PIG  MNLGAGPLHGLANQEVLVWLTQLQKEVGDVSDKLRDYIWNLTNSGRVVPYGHAVLRK 352
sp|P23007|CISY_CHICK  MNLGAGPLHGLANQEVLVWLTQLQKAXXAGADASLRDYIWNLTNSGRVVPYGHAVLRK 325
sp|O80433|CISY_DAUCA  LNGLAGPLHGLANQEVLLWIKSVVSECGENVTKQLKDYIWKTLNSGKVPYGHGVLRN 359
      ***** **.*.* **.*.* **.*.* **.*.* **.*.* **.*.* **.*.*

sp|O75390|CISY_HUMAN  TDPRYTCQREFALKHLPNDPMPFKLV AQLYKIVPNVLEQGKAKNPWPNVDAHSGVLLQYY 412
sp|P00889|CISY_PIG  TDPRYTCQREFALKHLPNDPMPFKLV AQLYKIVPNVLEQGKAKNPWPNVDAHSGVLLQYY 412
sp|P23007|CISY_CHICK  TDPRYTCQREFALKHLPNDPMPFKLV AQLYKIVPNVLEQGAANPWPVNDVDAHSGVLLQYY 385
sp|O80433|CISY_DAUCA  TDPRYTCQREFALKHLPDDPLFQLVSNLFEVVPILTELKVKNPWPNVDAHSGVLLNHY 419
      ***** **.*.* **.*.* **.*.* **.*.* **.*.* **.*.* **.*.*

sp|O75390|CISY_HUMAN  GMTEMNYYTVLFGVSRALGVLAQLIWSRALGFPLERPKSMSTEGMLKFDVDSKSG 466
sp|P00889|CISY_PIG  GMTEMNYYTVLFGVSRALGVLAQLIWSRALGFPLERPKSMSTDGLIKLVDSK- 464
sp|P23007|CISY_CHICK  GMTEMNYYTVLFGVSRALGVLAQLIWSRALGFPLERPKSMSTDGLIAL----- 433
sp|O80433|CISY_DAUCA  GLTEARYYTVLFGVSRALGVLAQLIWSRALGFPLERPKSVTMEWLENHCKKSS- 472
      **.* **.*.* **.*.* **.*.* **.*.* **.*.* **.*.* **.*.*

//
(
(
sp|P23007|CISY_CHICK:0.03733,
sp|O80433|CISY_DAUCA:0.34604)
:0.03349,
sp|O75390|CISY_HUMAN:0.02528,
sp|P00889|CISY_PIG:0.01782);
//

```

CLUSTAL ALIGNMENT :GLTA GENE

CLUSTAL W (1.82) Multiple Sequence Alignments

Sequence format is Pearson

Sequence 1:	sp O34002 CISY_ABDS2	379 aa
Sequence 2:	sp P20902 CISY_ACIAN	423 aa
Sequence 3:	sp P51033 CISY_BARHA	431 aa
Sequence 4:	sp P94325 CISY_BRAJA	434 aa
Sequence 5:	sp P42457 CISY_CORGL	437 aa
Sequence 6:	sp P18789 CISY_COXBU	430 aa
Sequence 7:	sp P00891 CISY_ECOLI	427 aa
Sequence 8:	sp Q9Z37 CISY_HELPI	426 aa
Sequence 9:	sp P56062 CISY_HELPI	426 aa
Sequence 10:	sp P26491 CISY_MYCSM	375 aa
Sequence 11:	sp P14165 CISY_PSEAE	428 aa
Sequence 12:	sp Q53554 CISY_PYRFU	376 aa
Sequence 13:	sp O33915 CISY_RHIME	429 aa

Sequence 14: sp|P09948|CISY_RICPR 436 aa
Sequence 15: sp|O68883|CISY_SALTY 427 aa
Sequence 16: sp|P80148|CISY_SULSO 377 aa
Sequence 17: sp|Q59977|CISY_SYNY3 397 aa
Sequence 18: sp|P21553|CISY_THEAC 384 aa
Sequence 19: sp|P51045|CISY_THIFE 386 aa

Start of Pairwise alignments

Aligning...

Sequences (1:2) Aligned. Score: 32
Sequences (1:3) Aligned. Score: 31
Sequences (1:4) Aligned. Score: 30
Sequences (1:5) Aligned. Score: 35
Sequences (1:6) Aligned. Score: 33
Sequences (1:7) Aligned. Score: 30
Sequences (1:8) Aligned. Score: 29
Sequences (1:9) Aligned. Score: 29
Sequences (1:10) Aligned. Score: 58
Sequences (1:11) Aligned. Score: 32
Sequences (1:12) Aligned. Score: 37
Sequences (1:13) Aligned. Score: 29
Sequences (1:14) Aligned. Score: 29
Sequences (1:15) Aligned. Score: 30
Sequences (1:16) Aligned. Score: 32
Sequences (1:17) Aligned. Score: 36
Sequences (1:18) Aligned. Score: 30
Sequences (1:19) Aligned. Score: 36
Sequences (2:3) Aligned. Score: 65
Sequences (2:4) Aligned. Score: 66
Sequences (2:5) Aligned. Score: 50
Sequences (2:6) Aligned. Score: 64
Sequences (2:7) Aligned. Score: 65
Sequences (2:8) Aligned. Score: 44
Sequences (2:9) Aligned. Score: 43
Sequences (2:10) Aligned. Score: 31
Sequences (2:11) Aligned. Score: 74
Sequences (2:12) Aligned. Score: 31
Sequences (2:13) Aligned. Score: 65
Sequences (2:14) Aligned. Score: 60
Sequences (2:15) Aligned. Score: 66
Sequences (2:16) Aligned. Score: 34
Sequences (2:17) Aligned. Score: 35
Sequences (2:18) Aligned. Score: 29
Sequences (2:19) Aligned. Score: 35
Sequences (3:4) Aligned. Score: 71
Sequences (3:5) Aligned. Score: 48
Sequences (3:6) Aligned. Score: 62
Sequences (3:7) Aligned. Score: 67
Sequences (3:8) Aligned. Score: 42
Sequences (3:9) Aligned. Score: 42
Sequences (3:10) Aligned. Score: 30
Sequences (3:11) Aligned. Score: 64
Sequences (3:12) Aligned. Score: 33
Sequences (3:13) Aligned. Score: 76
Sequences (3:14) Aligned. Score: 60
Sequences (3:15) Aligned. Score: 69
Sequences (3:16) Aligned. Score: 36
Sequences (3:17) Aligned. Score: 37
Sequences (3:18) Aligned. Score: 33
Sequences (3:19) Aligned. Score: 34
Sequences (4:5) Aligned. Score: 49
Sequences (4:6) Aligned. Score: 58
Sequences (4:7) Aligned. Score: 64
Sequences (4:8) Aligned. Score: 42
Sequences (4:9) Aligned. Score: 42
Sequences (4:10) Aligned. Score: 31
Sequences (4:11) Aligned. Score: 66
Sequences (4:12) Aligned. Score: 33
Sequences (4:13) Aligned. Score: 78
Sequences (4:14) Aligned. Score: 61
Sequences (4:15) Aligned. Score: 64
Sequences (4:16) Aligned. Score: 37
Sequences (4:17) Aligned. Score: 35
Sequences (4:18) Aligned. Score: 32
Sequences (4:19) Aligned. Score: 35
Sequences (5:6) Aligned. Score: 46
Sequences (5:7) Aligned. Score: 48
Sequences (5:8) Aligned. Score: 43
Sequences (5:9) Aligned. Score: 43
Sequences (5:10) Aligned. Score: 33
Sequences (5:11) Aligned. Score: 48
Sequences (5:12) Aligned. Score: 35
Sequences (5:13) Aligned. Score: 48
Sequences (5:14) Aligned. Score: 48
Sequences (5:15) Aligned. Score: 47
Sequences (5:16) Aligned. Score: 32
Sequences (5:17) Aligned. Score: 38
Sequences (5:18) Aligned. Score: 32
Sequences (5:19) Aligned. Score: 38
Sequences (6:7) Aligned. Score: 60
Sequences (6:8) Aligned. Score: 43
Sequences (6:9) Aligned. Score: 45
Sequences (6:10) Aligned. Score: 30
Sequences (6:11) Aligned. Score: 65
Sequences (6:12) Aligned. Score: 34
Sequences (6:13) Aligned. Score: 61
Sequences (6:14) Aligned. Score: 56
Sequences (6:15) Aligned. Score: 60
Sequences (6:16) Aligned. Score: 38
Sequences (6:17) Aligned. Score: 36
Sequences (6:18) Aligned. Score: 33
Sequences (6:19) Aligned. Score: 36
Sequences (7:8) Aligned. Score: 41
Sequences (7:9) Aligned. Score: 41
Sequences (7:10) Aligned. Score: 29
Sequences (7:11) Aligned. Score: 69
Sequences (7:12) Aligned. Score: 34
Sequences (7:13) Aligned. Score: 67

Sequences (7:14) Aligned. Score: 59
Sequences (7:15) Aligned. Score: 96
Sequences (7:16) Aligned. Score: 33
Sequences (7:17) Aligned. Score: 35
Sequences (7:18) Aligned. Score: 30
Sequences (7:19) Aligned. Score: 35
Sequences (8:9) Aligned. Score: 98
Sequences (8:10) Aligned. Score: 29
Sequences (8:11) Aligned. Score: 45
Sequences (8:12) Aligned. Score: 35
Sequences (8:13) Aligned. Score: 43
Sequences (8:14) Aligned. Score: 45
Sequences (8:15) Aligned. Score: 41
Sequences (8:16) Aligned. Score: 35
Sequences (8:17) Aligned. Score: 36
Sequences (8:18) Aligned. Score: 28
Sequences (8:19) Aligned. Score: 36
Sequences (9:10) Aligned. Score: 30
Sequences (9:11) Aligned. Score: 44
Sequences (9:12) Aligned. Score: 35
Sequences (9:13) Aligned. Score: 42
Sequences (9:14) Aligned. Score: 45
Sequences (9:15) Aligned. Score: 41
Sequences (9:16) Aligned. Score: 35
Sequences (9:17) Aligned. Score: 36
Sequences (9:18) Aligned. Score: 28
Sequences (9:19) Aligned. Score: 36
Sequences (10:11) Aligned. Score: 29
Sequences (10:12) Aligned. Score: 39
Sequences (10:13) Aligned. Score: 32
Sequences (10:14) Aligned. Score: 29
Sequences (10:15) Aligned. Score: 29
Sequences (10:16) Aligned. Score: 32
Sequences (10:17) Aligned. Score: 37
Sequences (10:18) Aligned. Score: 30
Sequences (10:19) Aligned. Score: 36
Sequences (11:12) Aligned. Score: 32
Sequences (11:13) Aligned. Score: 68
Sequences (11:14) Aligned. Score: 58
Sequences (11:15) Aligned. Score: 68
Sequences (11:16) Aligned. Score: 34
Sequences (11:17) Aligned. Score: 36
Sequences (11:18) Aligned. Score: 30
Sequences (11:19) Aligned. Score: 35
Sequences (12:13) Aligned. Score: 35
Sequences (12:14) Aligned. Score: 34
Sequences (12:15) Aligned. Score: 33
Sequences (12:16) Aligned. Score: 44
Sequences (12:17) Aligned. Score: 42
Sequences (12:18) Aligned. Score: 40
Sequences (12:19) Aligned. Score: 42
Sequences (13:14) Aligned. Score: 61
Sequences (13:15) Aligned. Score: 68
Sequences (13:16) Aligned. Score: 37
Sequences (13:17) Aligned. Score: 37
Sequences (13:18) Aligned. Score: 33
Sequences (13:19) Aligned. Score: 36
Sequences (14:15) Aligned. Score: 59
Sequences (14:16) Aligned. Score: 34
Sequences (14:17) Aligned. Score: 35
Sequences (14:18) Aligned. Score: 32
Sequences (14:19) Aligned. Score: 38
Sequences (15:16) Aligned. Score: 33
Sequences (15:17) Aligned. Score: 36
Sequences (15:18) Aligned. Score: 30
Sequences (15:19) Aligned. Score: 35
Sequences (16:17) Aligned. Score: 35
Sequences (16:18) Aligned. Score: 58
Sequences (16:19) Aligned. Score: 34
Sequences (17:18) Aligned. Score: 30
Sequences (17:19) Aligned. Score: 51
Sequences (18:19) Aligned. Score: 31

Guide tree file created: [./ebi/extserv/old-work/598348.37290.dnd]

Start of Multiple Alignment

There are 18 groups

Aligning...

Group 1: Sequences: 2 Score:8153
Group 2: Sequences: 3 Score:7763
Group 3: Sequences: 2 Score:8507
Group 4: Sequences: 3 Score:8382
Group 5: Sequences: 2 Score:9195
Group 6: Sequences: 5 Score:7896
Group 7: Sequences: 8 Score:7484
Group 8: Sequences: 9 Score:7533
Group 9: Sequences: 10 Score:6881
Group 10: Sequences: 2 Score:9191
Group 11: Sequences: 12 Score:6515
Group 12: Sequences: 2 Score:6454
Group 13: Sequences: 14 Score:5253
Group 14: Sequences: 2 Score:6513
Group 15: Sequences: 3 Score:5634
Group 16: Sequences: 17 Score:3861
Group 17: Sequences: 2 Score:6387
Group 18: Sequences: 19 Score:3993
Alignment Score 171309

//

CLUSTAL W (1.82) multiple sequence alignment

```

sp|P20902|CISY_ACIAN -----SEATGKK-----AVLHLDGKE-IELPIYSGTLGPDVIDVKDVLAS-GHFTFDPG 47
sp|P14165|CISY_PSEAE -----MADKK-----AQLIEGSA PVLPVLSGTMGPDVVDVRLTAT-GHFTFDPG 46
sp|P18789|CISY_COXBU -----MSNRK-----AKLSFENQS-VEFPIYSPTLGKDVIVKTLGNH-GAYALDVG 45
sp|P94325|CISY_BRAJA -----MDAKASNKT-----ATLTVG-NKNYDLPIHSGSVGPDVIDIGKLYGQSGFLTYPG 50
sp|O33915|CISY_RHME -----MSEKS-----ATVTFG-GKSADLPVRSIGSPDVIDIGSLYKQTMFTYDYG 46
sp|P51033|CISY_BARHE -----MSKNK-----AHITVN-DKKIELSVRKGTLGPDVIELASLYKETDTFTYDYG 46
sp|P00891|CISY_ECOLI -----MADTK-----AKLTLNGDTAVELDVLKGTGQDVIDIRTLGSK-GVFTFDPG 46

```

sp|O68883|CISY_SALTY -----MADTK-----AKITLTGDTTIELDVLKGTGQDVIDIRSLGSK-GVFTFDPG 46
sp|P09948|CISY_RICPR -----MTNGNNNLEFAELKIR-GKLFKLPILKASIGKQDVIDISRVSAEADYFTYDPG 52
sp|P42457|CISY_CORGL MFERDVIATDNNK-----AVLHYPGGE-FEMDIIASEGNNGVVLGKMLSETGLITFDPG 54
sp|Q9Z937|CISY_HELPI -----MSVTL-----INNENNARYEFETIECTRGPKAVDFSKLFETTGFSSYDPG 45
sp|P56062|CISY_HELPI -----MSVTL-----VNNENNERYEFETIESTRGPKAVDFSKLFETTGFSSYDPG 45
sp|Q59977|CISY_SYNY3 -----MNYMMDNEVFKEG 14
sp|P51045|CISY_THIFE -----MAEPN-FAPG 9
sp|P80148|CISY_SULSO -----MSVVSVKG 7
sp|P21553|CISY_THEAC -----PETEISIKG 9
sp|Q53554|CISY_PYRFU -----NTEKYLAKG 9
sp|O34002|CISY_ABD52 -----MT-----EPTIHKG 9
sp|P26491|CISY_MYCSM -----MTTATESEAPRIHKG 15

*

sp|P20902|CISY_ACIAN FMATASCESKITIDGDKGILLHRGYPIDQLATQAD-YLETCLLLNGELP-TAEQKVEF 105
sp|P14165|CISY_PSEAE FMSTASCESKITIDGDKGVLLHRGYPIEQLAEKSD-YLETCLLLNGELP-TAAQKEQF 104
sp|P18789|CISY_COXBU FYSTAACESKITIDGEGKILLYRGYPIDQLADKSD-YMEVCYLLMYGELP-NKGEKEKF 103
sp|P94325|CISY_BRAJA FTSTASCSQSKITYIDGDAVGLYRGYPIDQLAENG-FLETCYLLLYGNLP-TAAQKKDF 108
sp|O33915|CISY_RHIME FTSTASCESKITIDGDEGVLLHRGFPIEQLAEHGD-FLEVYLLLYGELP-TKAQKADF 104
sp|P51033|CISY_BARHE FTSTASCESKITIDGNEGILLYRGYPIDQLAEKSD-FLESCYLLLYGELP-TKQEKIDF 104
sp|P00891|CISY_ECOLI FTSTASCESKITIDGDEGILLHRGFPIDQLATDSN-YLEVYLLLYGELP-TQEQYDEF 104
sp|O68883|CISY_SALTY FTSTASCESKITIDGDEGILLHRGFPIDQLATDSN-YLEVYLLLYGELP-TQEQYDEF 104
sp|P09948|CISY_RICPR FMSTASCSQSKITYIDGDKGILWYRGYDIKDLAEKSD-FLEVA YLMIY GELP-SSDQYCNF 110
sp|P42457|CISY_CORGL YVSTGSTEKITIDGDAAGILYRGYDIADLAENAT-FNEVSYLLINGELP-TPDELHKF 112
sp|Q9Z937|CISY_HELPI YSSTAGCQSKISYINGKKGELYYRGHRIEDLVAKYK-YVDVCKLLLTGELPKNQDESLEF 104
sp|P56062|CISY_HELPI YSSTAGCQSKISYVNGKKGELYYRGHRIEDLVAKYK-YVDVCKLLLTGELPKNQDESLEF 104
sp|Q59977|CISY_SYNY3 LAGVPAAKSRVSHVDGTDGILEYRGIRIEELAKSS-FIEVAYLLIWGKLP-TQAEIEEF 72
sp|P51045|CISY_THIFE LEGVAATQSSISNIDGAAGLLSYRGAIAADLAHSS-FEEVALLLDGVLG-GAADLERF 67
sp|P80148|CISY_SULSO LENVIKVTLNLFIDGEGKILYRGYNIEDLVNYS-GS-YEETIYLLMYGKLP-TKELNDL 65
sp|P21553|CISY_THEAC LEDVNIWTRLTIDGNGKILYRGYSVEDIAGSAQDEEIQYLLFYGNLP-TEQELRKY 68
sp|Q53554|CISY_PYRFU LEDVYIDQTNICYIDGKGEKLYRGYSVEELAELEST-FEEVYLLWVGKLP-SLSELENF 67
sp|O34002|CISY_ABD52 LAGVADTVTAISKVNSDTNLLYRGYPVQELAAKCS-FEQVAYLLWNSLP-NDELKAF 67
sp|P26491|CISY_MYCSM LAGVVVDTAISKVNPETNSLTYRGYPVQDLAAQCS-FEQVAYLLWHGELP-TD-QLALF 72

*: * : : : : *

sp|P20902|CISY_ACIAN DAKVRAHTMVDHQVSRFFNGFRDHPMAIMVGVVGSALFYHNNLDIEDIN-----HRE 160
sp|P14165|CISY_PSEAE VGTIKNHTMVHEQLKTFNFRDHPMAVMCGVIGALSIFYHDSLDINNPK-----HRE 159
sp|P18789|CISY_COXBU VRTIKEHTSVYEQVTKFFNGFHYDAHPMAMVLTIGALSIFYHSDALDITKPA-----DRE 158
sp|P94325|CISY_BRAJA DDRVIHTMVHEQMARFFQFRDHPMAVMVAVSVALAIFYHSDIDNDPK-----QRM 163
sp|O33915|CISY_RHIME DYRVTHHTMVHEQMSRFFTGFRDHPMAVMCGVGSALFYHSDITDTPH-----QRM 159
sp|P51033|CISY_BARHE DRCIMQHTMVHEQFARFFHFRDHPMAVMIACLGAMSIFYHSDIDDPQ-----QRM 159
sp|P00891|CISY_ECOLI KTTVTRHTMIHEQITRLFHAFRRDHPMAVMCGITGALAIFYHSDLDVNNPR-----HRE 159
sp|O68883|CISY_SALTY RTTVTRHTMIHEQITRLFHAFRRDHPMAVMCGITGALAIFYHSDLDVNNPR-----HRE 159
sp|P09948|CISY_RICPR TKKV AHHSVLNERLHYLFQTFSSHPMAIMLAAGVLSALFYHSDLDVNNPR-----DYE 164
sp|P42457|CISY_CORGL NDEIRHHTLLDEDKQFNVPFRDHPMATLASSVNLSTYQDQLNPLDEA-----QLD 167
sp|Q9Z937|CISY_HELPI EELRHRSFVHESLLNMFSAFNSAHPMAKLSGGVLSILSTLYSTHQNMTHEE-----DYQ 159
sp|P56062|CISY_HELPI EELRHRSFVHESLLNMFSAFNSAHPMAKLSGGVLSILSTLYSTHQNMTHEE-----DYQ 159
sp|Q59977|CISY_SYNY3 YEIRTHRRIKYHIRDMMKCFPETGHPMDALQTSAAALGLFYA-RRALDDPK-----YIR 126
sp|P51045|CISY_THIFE DHGLRAHRQVQYKYNVREIMKMPVGTGHPMDMLHCAVASLGMFYP-QQELSDAERGNLHLD 126
sp|P80148|CISY_SULSO KAKLNEEYVQEVLDLTYLMPKEADAIGLEVTGAALASIDKN-FKW-KENDK-----117
sp|P21553|CISY_THEAC KETVQKGYKIPDFVINAIQRLPRESDAVAMQMAA-AAMAASETK-FKWNKDTR-----121
sp|Q53554|CISY_PYRFU IAKFLAKSRGLPKEVIEIMEALPKNTHPMGALRTHIISYLGNDSDGIPVTEEVY-----122
sp|O34002|CISY_ABD52 VNFERSHRKLDENVKGAIDLSTACHPMDVARTAVSVLGANHARAQDSSPEAN-----L 121
sp|P26491|CISY_MYCSM SQRERASRRIDRSMQALLAKLPDNCHPMDVVRTAISYLGAEDEEDVDTAEAN-----Y 126

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sp|P14165|CISY_PSEAE VSAHRLIAKMPTIAAMVYKYSKGEPMYPRNDLNYAENFLHMMFATPADRYK-----211
sp|P18789|CISY_COXBU LSAIRLIAKMPTLAAMVYKYSIGQPFMHPRAMNYAENFLHMLFGTPEETE-----210
sp|P94325|CISY_BRAJA IASMRMIAKIPTLAAMAYKYTIGQPFVYKNSLKFENFLHMCFAVSCVEEYK-----215
sp|O33915|CISY_RHIME VASLRMIAKMPTIAAMAYKYHIGQPFVYKNSLKFENFLHMCFAVSCVEEYV-----211
sp|P51033|CISY_BARHE IASIRLISKVPTLAAMAYKYSIGQAFVYPRNDLSY AANFLRMCFSVPCVEEYK-----211
sp|P00891|CISY_ECOLI IAAFRLLSKMPTMAAMCYKYSIGQPFVYPRNDLSY AAGNLFNMMFSTPCPEYE-----211
sp|O68883|CISY_SALTY IAAFRLLSKMPTMAAMCYKYSIGQPFVYPRNDLSY AAGNLFNMMFSTPCPEYE-----211
sp|P09948|CISY_RICPR LTAIRMIAKIPTIAAMVYKYSIGQPFYPRNDLDFENFLHMMFATPCTKYK-----216
sp|P42457|CISY_CORGL KATVRLMAKVPMLAAYAHRAKRGAPYMPDNLNARENFLRMMFGYPTPEYE-----219
sp|Q9Z937|CISY_HELPI TMARRIVAKIPTLAICYRNEVGAPIYPIARSYVENILFMLRGPYSRLKHTTQGEVE 219
sp|P56062|CISY_HELPI TMARRIVAKIPTLAICYRNEVGAPIYPIARSYVENILFMLRGPYSRLKHTTQGEVE 219
sp|Q59977|CISY_SYNY3 AA VVRLAKIPTMVA AFHMIREGNDPIQNDKLDYASNFLYMLTEKE-----173
sp|P51045|CISY_THIFE AMAMRIARMPTIAMWEQMRFGNDPISPRDLSHAANFLYMLSGRE-----173
sp|P80148|CISY_SULSO EKAIISHAKMATLVANVYRRKEGKPRIPEPSDFSAKSLASFARE-----164
sp|P21553|CISY_THEAC DVAAEMIGRMSAITVNVYRHIMNMPAELPKPSDSYAESFLNAAFGRK-----168
sp|Q53554|CISY_PYRFU RIGISVTAKIPTIVANWYRIKNGLEYVPPKELSHAANFLYMLHGEE-----169
sp|O34002|CISY_ABD52 EKAMSLLA TFPVAVYDQRRRRGEELIEPRELDYASNFLWMTFGEEA-----169
sp|P26491|CISY_MYCSM AKSLRMFAVLPTIVATDIRRRQGLTPIPPHSQGLY AQNLFNMMCFGEVP-----174

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sp|P20902|CISY_ACIAN VNPVLRAMDRIFTLHADHEQNASTSTVRLAGSTGANPYACISAGISALWGAHGGANEA 273
sp|P14165|CISY_PSEAE ISPVLAKAMDRIFILHADHEQNASTSTVRLAGSSGANPFACIASGIALWGAHGGANEA 271
sp|P18789|CISY_COXBU PDPVLRAMDRIFILHADHEQNASTSTVRLAGSTGANPFACIASGIALWGAHGGANEA 270
sp|P94325|CISY_BRAJA INPVLADALDKIFILHADHEQNASTSTVRIAGSSGANPFACIASGIALWGAHGGANEA 275
sp|O33915|CISY_RHIME VNPVLRAMDRIFILHADHEQNASTSTVRLAGSSGANPFACIASGIALWGAHGGANEA 271
sp|P51033|CISY_BARHE INPVLTRAMDRIFILHADHEQNASTSTVRLAGSSGANPFACIASGIALWGAHGGANEA 271
sp|P00891|CISY_ECOLI VNPILERAMDRILILHADHEQNASTSTVRLAGSSGANPFACIASGIALWGAHGGANEA 271
sp|O68883|CISY_SALTY VNPVLERAMDRILILHADHEQNASTSTVRLAGSSGANPFACIASGIALWGAHGGANEA 271
sp|P09948|CISY_RICPR VNPPIKALNLIKIFILHADHEQNASTSTVRIAGSSGANPFACISGIALWGAHGGANEA 276
sp|P42457|CISY_CORGL IDPIMVKALDKLLILHADHEQNCSTSTVIRMIQAQANMFVSIAGGINALSGLHGGANQA 279
sp|Q9Z937|CISY_HELPI ITPLEVEAFDKILTILHADHQNASTSTVIRNVASTGVHPYAAISAGISALWGLHGGANEK 279
sp|P56062|CISY_HELPI ITPLEVEAFDKILTILHADHQNASTSTVIRNVASTGVHPYAAISAGISALWGLHGGANEK 279
sp|Q59977|CISY_SYNY3 PDPFAAKVFDVCLTLHAHEMNSTFSARVASTLTDYPAVVASAVGLTLAGPLHGGANEE 233
sp|P51045|CISY_THIFE PDPFAAKVFDVCLTLHAHEMNSTFSARVASTLTDYPAVVASAVGLTLAGPLHGGANEE 233
sp|P80148|CISY_SULSO PTTDEINAMDKALILYTDHEVPASTTAAALVASTLSDMYSSLTAAALAKGPLHGGAAEE 224
sp|P21553|CISY_THEAC PTTDEINAMDKALILYTDHEVPASTTAAALVASTLSDMYSSLTAAALAKGPLHGGAAEE 228
sp|Q53554|CISY_PYRFU PPKWEKAMDVVALILYAEHEINASTLAVMTVGSTLSDYYSAILAGICALKGIHGGAVEE 229
sp|O34002|CISY_ABD52 -APEVVEAFNVSMILYAEHFNASTFTARVITSLADLHSAVTGAIGALKGPLHGGANEA 228
sp|P26491|CISY_MYCSM -EPVVVRAFEQSMVLYAEHFNASTFAARVVTSTQSDIYSAVTAAGIALKGPLHGGANEA 233

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sp|P20902|CISY_ACIAN VLKMLDEIGSVE-----NVAEFMEKVKRKE--VKLMGFGRVYKFNDFPRAKVMKQTC 324
sp|P14165|CISY_PSEAE VLRMLDEIGDVS-----NIDKFVEKAKDKNDPFLMGFGRVYKFNDFPRAKVMKQTC 324
sp|P18789|CISY_COXBU ALNMLRKIGDEK-----NIGQYIKKAKDKNDPFLMGFGRVYKFNDFPRAKVMKQTCY 323
sp|P94325|CISY_BRAJA CLAMLGEIGSVD-----KIPEFIKAKDKNDPFLMGFGRVYKFNDFPRAKVMKQTC 328
sp|O33915|CISY_RHIME ALNMLAEIGTVD-----RIPEYITKAKDKNDPFLMGFGRVYKFNDFPRAKVMKQTC 324
sp|P51033|CISY_BARHE CLKMLQEIGSVE-----RIPEFIARAKDKNDPFLMGFGRVYKFNDFPRAKVMKQTC 324
sp|P00891|CISY_ECOLI ALKMLEEISSVK-----HIPEFRRAKDKNDPFLMGFGRVYKFNDFPRAVMRETCH 324
sp|O68883|CISY_SALTY ALKMLEEISSVK-----HIPEFRRAKDKNDPFLMGFGRVYKFNDFPRAVMRETCH 324
sp|P09948|CISY_RICPR VINMLKEIGSVE-----NIPKYVAKAKDKNDPFLMGFGRVYKFNDFPRAAVLKETCG 329


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sp|O68883|CISY_SALTY:0.01938)
:0.14278)
:0.01434)
:0.01050,
(
sp|P20902|CISY_ACIAN:0.13002,
sp|P14165|CISY_PSEAE:0.12530)
:0.02793,
sp|P18789|CISY_COXBU:0.19579);
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CLUSTALW ALIGNMENT: POL GENE
CLUSTAL W (1.82) Multiple Sequence Alignments

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Sequence format is Pearson
Sequence 1: sp|P19560|POL_BIV06 1056 aa
Sequence 2: sp|P19561|POL_BIV27 1056 aa
Sequence 3: sp|P33459|POL_CAEEVC 1109 aa
Sequence 4: sp|P19199|POL_COYMV 1886 aa
Sequence 5: sp|P11204|POL_EIAV9 1146 aa
Sequence 6: sp|P32542|POL_EIAVC 1146 aa
Sequence 7: sp|P03371|POL_EIAVY 1145 aa
Sequence 8: sp|P16088|POL_FIVPE 1124 aa
Sequence 9: sp|P19028|POL_FIVSD 1124 aa
Sequence 10: sp|P31822|POL_FIVT2 1124 aa
Sequence 11: sp|P03369|POL_HV1A2 1003 aa
Sequence 12: sp|P03366|POL_HV1B1 1015 aa
Sequence 13: sp|P04587|POL_HV1B5 1015 aa
Sequence 14: sp|P03367|POL_HV1BR 1015 aa
Sequence 15: sp|P05960|POL_HV1C4 118 aa
Sequence 16: sp|P04589|POL_HV1EL 1002 aa
Sequence 17: sp|P04585|POL_HV1H2 1003 aa
Sequence 18: sp|P12498|POL_HV1J3 100 aa
Sequence 19: sp|P20875|POL_HV1JR 1007 aa
Sequence 20: sp|P04588|POL_HV1MA 1002 aa
Sequence 21: sp|P05961|POL_HV1MN 1006 aa
Sequence 22: sp|P12497|POL_HV1N5 1003 aa
Sequence 23: sp|P18802|POL_HV1ND 1002 aa
Sequence 24: sp|P20892|POL_HV1OY 1003 aa
Sequence 25: sp|P03368|POL_HV1PV 1015 aa
Sequence 26: sp|P05959|POL_HV1RH 1002 aa
Sequence 27: sp|P24740|POL_HV1U4 1002 aa
Sequence 28: sp|P35963|POL_HV1Y2 1003 aa
Sequence 29: sp|P12499|POL_HV1Z2 1002 aa
Sequence 30: sp|P18096|POL_HV2BE 1142 aa
Sequence 31: sp|P24107|POL_HV2CA 1034 aa
Sequence 32: sp|P17757|POL_HV2D1 1073 aa
Sequence 33: sp|P15833|POL_HV2D2 1058 aa
Sequence 34: sp|P18042|POL_HV2G1 1049 aa
Sequence 35: sp|Q74120|POL_HV2KR 1035 aa
Sequence 36: sp|P05962|POL_HV2NZ 1035 aa
Sequence 37: sp|P04584|POL_HV2RO 1036 aa
Sequence 38: sp|P12451|POL_HV2SB 1035 aa
Sequence 39: sp|P20876|POL_HV2ST 1055 aa
Sequence 40: sp|P16901|POL_OMVVS 1086 aa
Sequence 41: sp|P27502|POL_RTBPV 1675 aa
Sequence 42: sp|P27973|POL_SIVA1 1047 aa
Sequence 43: sp|P27980|POL_SIVAG 1046 aa
Sequence 44: sp|Q02836|POL_SIVAI 1057 aa

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Sequence 45: sp|P05895|POL_SIVAT 1061 aa
Sequence 46: sp|P17283|POL_SIVCZ 1027 aa
Sequence 47: sp|P22382|POL_SIVGB 1009 aa
Sequence 48: sp|P05896|POL_SIVM1 1056 aa
Sequence 49: sp|P05897|POL_SIVMK 1054 aa
Sequence 50: sp|P12502|POL_SIVS4 1019 aa
Sequence 51: sp|P19505|POL_SIVSP 1022 aa
Sequence 52: sp|P23426|POL_VILV1 1105 aa
Sequence 53: sp|P23427|POL_VILV2 1105 aa
Sequence 54: sp|P35956|POL_VILVK 1101 aa
Sequence 55: sp|P03370|POL_VILV 1105 aa

Start of Pairwise alignments

Aligning...

Sequences (1:2) Aligned. Score: 99
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Sequences (1:5) Aligned. Score: 33
Sequences (1:6) Aligned. Score: 33
Sequences (1:7) Aligned. Score: 32
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Guide tree file created: [/ebi/extserv/old-work/270606.86523.dnd]

Start of Multiple Alignment

There are 54 groups

Aligning...

Group 1: Sequences: 2 Score:23155
Group 2: Sequences: 2 Score:21467
Group 3: Sequences: 2 Score:22105
Group 4: Sequences: 3 Score:21797
Group 5: Sequences: 4 Score:21882
Group 6: Sequences: 5 Score:21916
Group 7: Sequences: 2 Score:2103
Group 8: Sequences: 3 Score:2238
Group 9: Sequences: 8 Score:2161
Group 10: Sequences: 9 Score:10547
Group 11: Sequences: 11 Score:11564
Group 12: Sequences: 2 Score:21617
Group 13: Sequences: 13 Score:13598
Group 14: Sequences: 14 Score:14670
Group 15: Sequences: 2 Score:21606
Group 16: Sequences: 3 Score:21544
Group 17: Sequences: 17 Score:14978
Group 18: Sequences: 18 Score:15849
Group 19: Sequences: 19 Score:16071
Group 20: Sequences: 20 Score:15927
Group 21: Sequences: 2 Score:22182
Group 22: Sequences: 3 Score:22272
Group 23: Sequences: 2 Score:21850
Group 24: Sequences: 3 Score:21817
Group 25: Sequences: 2 Score:21848
Group 26: Sequences: 3 Score:21806
Group 27: Sequences: 6 Score:21488
Group 28: Sequences: 9 Score:21450
Group 29: Sequences: 2 Score:22032
Group 30: Sequences: 2 Score:22125
Group 31: Sequences: 4 Score:21178
Group 32: Sequences: 13 Score:20350
Group 33: Sequences: 14 Score:20427
Group 34: Sequences: 2 Score:21429
Group 35: Sequences: 3 Score:20983
Group 36: Sequences: 4 Score:19467
Group 37: Sequences: 5 Score:17489
Group 38: Sequences: 19 Score:16470
Group 39: Sequences: 39 Score:12876
Group 40: Sequences: 2 Score:24113
Group 41: Sequences: 3 Score:24165
Group 42: Sequences: 4 Score:24108
Group 43: Sequences: 5 Score:22515
Group 44: Sequences: 6 Score:21508
Group 45: Sequences: 2 Score:24026
Group 46: Sequences: 3 Score:23122
Group 47: Sequences: 9 Score:15478
Group 48: Sequences: 2 Score:25026
Group 49: Sequences: 3 Score:24906
Group 50: Sequences: 12 Score:15483
Group 51: Sequences: 51 Score:9302
Group 52: Sequences: 53 Score:10247
Group 53: Delayed
Group 54: Delayed
Sequence:4 Score:7141
Sequence:41 Score:7719
Alignment Score 4144260

CLUSTAL-Alignment file created [/ebi/extserv/old-work/270606.86523.aln]

//

CLUSTAL W (1.82) multiple sequence alignment

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sp|P19560|POL_BIV06 -----
sp|P19561|POL_BIV27 -----
sp|P20875|POL_HV1JR -----FFR-----EDLAFI--- 9
sp|P05961|POL_HV1MN -----FFR-----EDLAFI--- 9
sp|P03366|POL_HV1B1 -----FFR-----EDLAFI--- 9
sp|P03368|POL_HV1PV -----FFR-----EDLAFI--- 9
sp|P04585|POL_HV1H2 -----FFR-----EDLAFI--- 9
sp|P04587|POL_HV1B5 -----FFR-----EDLAFI--- 9
sp|P03367|POL_HV1BR -----FFR-----EDLAFI--- 9
sp|P05960|POL_HV1C4 -----FFR-----EDLAFI--- 9
sp|P12498|POL_HV1J3 -----FFR-----EDLAFI--- 9
sp|P12497|POL_HV1N5 -----FFR-----EDLAFI--- 9
sp|P35963|POL_HV1Y2 -----FFR-----EDLAFI--- 9
sp|P03369|POL_HV1A2 -----FFR-----EDLAFI--- 9
sp|P20892|POL_HV1OY -----FFR-----EDLAFI--- 9
sp|P05959|POL_HV1RH -----FFR-----ENLAFI--- 9
sp|P04589|POL_HV1EL -----FFR-----ENLAFI--- 9
sp|P12499|POL_HV1Z2 -----FFR-----EDLAFI--- 9
sp|P18802|POL_HV1ND -----FFR-----EDLAFI--- 9
sp|P04588|POL_HV1MA -----FFR-----ENLAFI--- 9
sp|P24740|POL_HV1U4 -----FFR-----ENLAFI--- 9
sp|P17283|POL_SIVCZ -----STKKKRLLA V WARGTPNERLHRKTGEFFR-----ERLAFI--- 35
sp|P17757|POL_HV2D1 VLELWKG G T L G E T V P S T Q K T G L L E V W Q V R T H H G K L P G K T G R F F R D G P T G K - A A P Q L P --- 56
sp|P18042|POL_HV2G1 -----M W Q D R T R H G K M P R K T G R F F R D G S M G K - E A P Q L P --- 32
sp|P18096|POL_HV2BE -----K T G L L E V W Q A R T H H G K L P G K T G R F F R V G P T G K - E A S Q L P --- 38
sp|P24107|POL_HV2CA -----T G G F F R D W P L G K - E A P Q F P --- 18
sp|P05962|POL_HV2NZ -----T G W F F R D W P L G K - E G P Q L P --- 18
sp|P04584|POL_HV2RO -----T G R F F R T G P L G K - E A P Q L P --- 18
sp|Q74120|POL_HV2KR -----T G W F F R D W P M G K - E A S Q L P --- 18
sp|P20876|POL_HV2ST -----K T R L L E M W Q G R T H H G K M P R K T G G F F R V G P M G K - E A P Q F P --- 38
sp|P12451|POL_HV2SB -----T G W F F R A W T M G K - E A P Q L P --- 18
sp|P05896|POL_SIVM1 VLELW E G R T L C K A M Q S P K K T G M L E M W K N G P C Y G Q M P K T G G F F R P W P L G K - E A P Q F P --- 56
sp|P05897|POL_SIVM2 VLELW E G G T L C K A M Q S P K K T E M L E M W K N G P C Y G Q M P R Q T G R F F R P W S M G K - E A P Q F P --- 56
sp|P12502|POL_SIVS4 -----K T G G F F R A W P M G K - E A P Q F P --- 19
sp|P19505|POL_SIVSP -----M P R K T S G F F R A W P M G K - E A P Q F P --- 22
sp|P15833|POL_HV2D2 -----K T G M L E M W K N R T H H V K M P R K T G G F F R V R T L G K - E A S Q L P --- 38
sp|P27980|POL_SIVAG -----T K K D E M L E M W E T R A F S K R L Q R - T G K F F R V W P V D G S E T Q K F S --- 40
sp|P05895|POL_SIVAT -----L W K I W P Y A K T M S G T K E N K M S K V W K I G T P S K R L Q G - T G E F F R V W T V D G G K T E K F S --- 53
sp|P27973|POL_SIVA1 -----M W K A R A L S K R L Q G - T G E F F R V W P V D G D K T K K F S --- 32
sp|Q02836|POL_SIVA1 -----V R Q N W P Y G K R L Q E W T G K F F R V W P L G R S E T K K F C A I Q 36
sp|P22382|POL_SIVGB -----F F R V W P L G S L Q T G E L S --- 16
sp|P23427|POL_VILV2 -----
sp|P35956|POL_VILVK -----
sp|P03370|POL_VILV -----
sp|P23426|POL_VILV1 -----
sp|P16901|POL_OMVVS -----
sp|P33459|POL_CAEVC -----
sp|P16088|POL_FIVPE -----
sp|P19028|POL_FIVSD -----
sp|P31822|POL_FIVT2 -----
sp|P11204|POL_EIAV9 -----T A W T F L K A M Q K C S K K R E A R G S R E A P E T N - F 29
sp|P32542|POL_EIAVC -----T A W T F L K A M Q K C S K K R E A R G S R E A P E T N - F 29
sp|P03371|POL_EIAV5 -----T A W T F L K A M Q K C S K K R E A R G S R E A P E T N - F 29
sp|P19199|POL_COYMV -----M A T R R L P A V T Q T D G S R T A T E S G V P E Y E D Q I R S Y R N D Q R R R H I W A G R G 47
sp|P27502|POL_RTBPV -----M S L R P F T G T S R T I T Q D S T S E S N I K K G K N S T K R E L I E E V D V N Q E V E N F 47

sp|P19560|POL_BIV06 TAKM L P L W Q T W P P S K K -----L Q V K K R E V L L C P L W A E E P T T E Q F S P E Q H 44
sp|P19561|POL_BIV27 TAKM L P L W Q T W P P S K K -----L Q V K K R E V L L C P L W A E E P T T E Q F S P E Q H 44
sp|P20875|POL_HV1JR QG K A R E F S S E Q T R A N -----S P T R R E L Q V W G R D N S N S L S E A G E A G A D 51
sp|P05961|POL_HV1MN QG K A - E F S S E Q N R A N -----S P T R R E L Q V W G R D N S N S L S E A G E E A G D D 50
sp|P03366|POL_HV1B1 QG K A R E F S S E Q T R A N S P T I S S E Q T R -----A N S P T R R E L Q V W G R D N S N S P S E A -----G A D 59
sp|P03368|POL_HV1PV QG K A R E F S S E Q T R A N S P T I S S E Q T R -----A N S P T R R E L Q V W G R D N S N S P S E A -----G A D 59
sp|P04585|POL_HV1H2 QG K A R E F S S E Q T R A N -----S P T R R E L Q V W G R D N S N S P S E A -----G A D 47
sp|P04587|POL_HV1B5 QG K A R E F S S E Q T R A N S P T I S S E Q T R -----A N S P T R R E L Q V W G R D N S N S P S E A -----G A D 59
sp|P03367|POL_HV1BR QG K A R E F S S E Q T R A N S P T I S S E Q T R -----A N S P T R R E L Q V W G R D N S N S L S E A -----G A D 59
sp|P05960|POL_HV1C4 QG K A R E F S S E Q T R A N -----S P T R G E L Q V W G R D N S N S L S E A -----G A E 47
sp|P12498|POL_HV1J3 QG K A R E F S S E Q T R A N -----S P S R G E L Q V W G R D N S N S L S E A -----G A E 47
sp|P12497|POL_HV1N5 QG K A R E F S S E Q T R A N -----S P T R R E L Q V W G R D N S N S L S E A -----G A D 47
sp|P35963|POL_HV1Y2 QG K A R E F S S E Q T R A N -----S P I R R E R Q V W R R D N S N S L S E A -----G A D 47
sp|P03369|POL_HV1A2 QG K A R E F S S E Q T R A N -----S P T R R E L Q V W G G E N S N S L S E A -----G A D 47
sp|P20892|POL_HV1OY QG K A R E F S S E Q T R A N -----S P T S R E L R V W G R D N S N S P S E A -----G A D 47
sp|P05959|POL_HV1RH QG K A G E L S S E Q T R A N -----S P T R R E L Q V W G R D - N S L S E A -----G E D 46
sp|P04589|POL_HV1EL QG K A G E L S P K Q T R A N -----S P T S R E L R V W G R D - N P L S K T ---G A E 46
sp|P12499|POL_HV1Z2 QG K A G E L S S E Q T R A N -----S P T S R E L R V W G R D - N P L S E T ---G A E 46
sp|P18802|POL_HV1ND QG K A G E F S S E Q T R A N -----S P T S R E L R V W G G D - N P L S E T ---G A E 46
sp|P04588|POL_HV1MA QG K A R E F S S E Q T R A N -----S P T S R E L R V W G G D - K T L S E T ---G A E 46
sp|P24740|POL_HV1U4 QG E A R E F S S E Q T R A N -----S P T S R N L W D G G K D - D L P C E T ---G A E 46
sp|P17283|POL_SIVCZ Q R E A R Q L C A E Q N R T N -----G P T D R E L W V P G G R E E P G E E R -----G 71
sp|P17757|POL_HV2D1 R G P S S S G A D T N S T P N -----R S S S G P V G E I Y A A R E K A E R A E G E T I Q G 98
sp|P18042|POL_HV2G1 R G P S S S G A D T N S T P S -----R S S S G S I G K I Y A A G E R A E G A E G E T I Q R 74
sp|P18096|POL_HV2BE R D P S P S G A D T N S T S G -----R S S S G T V G E I Y A A R E K A E G A E G E T I Q R 80
sp|P24107|POL_HV2CA R G P S T G A N T N S T P L -----G S S S G T G E I Y A A R E K A E G A E T E T I Q R 60
sp|P05962|POL_HV2NZ R G P S P A G A N T N S T P L -----G S S S G P T G E I Y A A R K K A K G A E R E T V Q G 60
sp|P04584|POL_HV2RO R G P S S A G A D T N S T P S -----G S S S G T G E I Y A A R E K T E R A E R E T I Q G 60
sp|Q74120|POL_HV2KR R D P S A G A D T N S T P S -----R P S S R P A R E V L A A R E A E A R E A N E T I Q G 60
sp|P20876|POL_HV2ST C G P N P A G A D T N S T P D -----R P S R G P T R E V H A A R E K A E R A E R A E I Q R 80
sp|P12451|POL_HV2SB R G P K F A G A N T N S T P N -----G S S S G P T G E V H A A R E K T E R A E T K T I Q R 60
sp|P05896|POL_SIVM1 H G S S A S G A D A N C S P R -----R T S C G S A K E L H A L G Q A A E R K Q R E A L Q G 98
sp|P05897|POL_SIVM2 H G S S A S G A D A N C S P R -----G P S C G S A K E L H A V G Q A A E R K Q R E A L Q G 98
sp|P12502|POL_SIVS4 H G P D A S G A D T N C S P R -----G S S C G S T E E L H E D G Q K A E G E Q R E T L Q G 61
sp|P19505|POL_SIVSP H G P D A S G A D T N C S P R -----G S S C G S T E E L H E D G Q K A E G E Q R E T L Q G 64
sp|P15833|POL_HV2D2 H D P S A S G S D T I C T P D E P S R G H D T S G G D T I C A P C R S S S G D A E K L H A D G E T T E R E P R E T L Q G 98
sp|P27980|POL_SIVAG R R Y S W G G A N C A P S T E S -----I R P C K E A P A A I C R Q G E A V E G T K E K T T S S 84
sp|P05895|POL_SIVAT R R Y S W S G T E C A S T E R H H -----P I R P S K E A P A A I C R E R E T T E G A K E E S T G N 100
sp|P27973|POL_SIVA1 R H S W S G G T K C A P S T E Q L Y -----T L R P S K E A P A A V C R E R E T N E K S E Q K P P S E 79
sp|Q02836|POL_SIVA1 R H S W S G T I N S P P N G N S -----L R S S K E A P P A V C R E G T A P E R G E R T D K E T 80
sp|P22382|POL_SIVGB -----G T R G D S N S S T -----I R G E T S A E N S E H L S - E I R E R A Q A E D E G G 53
sp|P23427|POL_VILV2 -----T R N N M P S L -----W K K R T Y A K G L P -----A E T A G K Q Q E G 30
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sp|P35956|POL_VILVK -----MPSL-----WKKRTYAKGLP-----AEETAGKQOEG 26
sp|P03370|POL_VILV -----TRNNMPSL-----WKKRTYAKGLP-----AEETAGKQOEG 30
sp|P23426|POL_VILV1 -----TRNNMPSL-----WKKRTYAKGLP-----AEETAGKQOEG 30
sp|P16901|POL_OMVVS -----SNITAGKQOEG 11
sp|P33459|POL_CAEVC -----TRNHMSQL-----WKERTYAKRMQRKERHKGKTAGKREEG 35
sp|P16088|POL_FIVPE -----KEFGKLEG-----GASCSPSESAANNAICTSNGGETIG 35
sp|P19028|POL_FIVSD -----KFKGKLEG-----GASCSPSESAANNAICTSNGGKIIG 35
sp|P31822|POL_FIVT2 -----ENLGKREG-----GASCSPSKPSAANS-TICTSNGGETIR 34
sp|P11204|POL_EIAV9 PDTTEESAQQICCTRD-----SSDSKSVPRSERNKKGIQCQEGSSRG 72
sp|P32542|POL_EIAVC PDTTEESAQQICCTRD-----SSDSKSVPRSERNKKGIQCQEGSSRG 72
sp|P03371|POL_EIAVY PDTTEESAQQICCTRD-----SSDSKSVPRSERNKKGIQCQEGSSRG 72
sp|P19199|POL_COYMV RRLLSIMPGVSSSERILEMQMNPVQLQSRSMNHRAEAVPAEVLYRTFHGVSNNHRYVSHRS 107
sp|P27502|POL_RTBPV DWKLSLGIKPNKLYEKN-----WQEKVKLKQQSIVSAYKEAISVTHNAYTTTL 96

sp|P19560|POL_BIV06 EFCDP-----ICTPSYIRLDKQPFKIVFIGGRVWVWGLVDT 79
sp|P19561|POL_BIV27 EFCDP-----ICTPSYIRLDKQPFKIVFIGGRVWVWGLVDT 79
sp|P20875|POL_HV1JR RQGI-----VSFNFPQITLWQRPLVVTIKIGGQLKEALLDT 86
sp|P05961|POL_HV1MN RQGP-----VSFSPQITLWQRPLVVTIKIGGQLKEALLDT 85
sp|P03366|POL_HV1B1 RQGT-----VSFNFPQITLWQRPLVVTIKIGGQLKEALLDT 94
sp|P03368|POL_HV1PV RQGT-----VSFNFPQITLWQRPLVVTIKIGGQLKEALLDT 94
sp|P04585|POL_HV1H2 RQGT-----VSFNFPQITLWQRPLVVTIKIGGQLKEALLDT 82
sp|P04587|POL_HV1B5 RQGT-----VSFNFPQITLWQRPLVVTIKIGGQLKEALLDT 94
sp|P03367|POL_HV1BR RQGT-----VSFNFPQITLWQRPLVVTIKIGGQLKEALLDT 94
sp|P05960|POL_HV1C4 RQGT-----VSFSPQITLWQRPLVVTIKIGGQLKEALLDT 82
sp|P12498|POL_HV1J3 RQGT-----VSFSPQITLWQRPLVVTIKIGGQLKEALLDT 82
sp|P12497|POL_HV1N5 RQGT-----VSFSPQITLWQRPLVVTIKIGGQLKEALLDT 82
sp|P35963|POL_HV1Y2 RQGT-----VSFSPQITLWQRPLVVTIKIGGQLKEALLDT 82
sp|P03369|POL_HV1A2 RQGT-----VSFNFPQITLWQRPLVVTIRIGGQLKEALLDT 82
sp|P20892|POL_HV1OY RQGT-----VSFNFPQITLWQRPLVVTIKIGGQLKEALLDT 82
sp|P05959|POL_HV1RH RQGT-----VSFSPQITLWQRPLVVTIKIGGQLKEALLDT 81
sp|P04589|POL_HV1EL RQGT-----VSFNFPQITLWQRPLVVAIKIGGQLKEALLDT 81
sp|P12499|POL_HV1Z2 RQGT-----VSFNFPQITLWQRPLVVTIKIGGQLKEALLDT 81
sp|P18802|POL_HV1ND RQGT-----VSFSPQITLWQRPLVVTIKIGGQLKEALLDT 81
sp|P04588|POL_HV1MA RQGI-----VSFSPQITLWQRPLVVTIVRIGGQLKEALLDT 81
sp|P24740|POL_HV1U4 RQGT-----DSFSPQITLWQRPLVVTIKIGGQLKEALLDT 81
sp|P17283|POL_SIVCZ REQS-----ISTNLPQITLWQRPLVPIVVEGQLCEALLDT 106
sp|P17757|POL_HV2D1 GDGGLTAPRAGRDPQRG-----DRGLATPQFSLWKRPPVTAHIEGQPVVLLDT 148
sp|P18042|POL_HV2G1 GDGRLTAPRAGKSTSQRG-----DRGLAAPQFSLWKRPPVTAHIEGQPVVLLDT 124
sp|P18096|POL_HV2BE GDGGLAAPRAERDTSQRG-----DRGLAAPQFSLWKRPPVTAHIEGQPVVLLDT 130
sp|P24107|POL_HV2CA GDRGLTAPRTRRRGPMQGD-----NRGLAAPQFSLWKRPPVTAHIEGQPVVLLDT 110
sp|P05962|POL_HV2NZ SDRGLTAPRAGRDTMQGD-----DRGLAAPQFSLWKRPPVTAHIEGQPVVLLDT 110
sp|P04584|POL_HV2RO SDRGLTAPRAGGDTIQGAT-----NRGLAAPQFSLWKRPPVTAHIEGQPVVLLDT 111
sp|Q74120|POL_HV2KR GDRGLTAPRTRRRDTRQGD-----DRGLAAPQFSLWKRPPVTAHIEGQPVVLLDT 110
sp|P20876|POL_HV2ST SDRGLPAARETRDTMQRD-----DRGLAAPQFSLWKRPPVTAHIEGQPVVLLDT 130
sp|P12451|POL_HV2SB SDRGLAASRRARDTQRD-----DRGLAAPQFSLWKRPPVTAHIEGQPVVLLDT 110
sp|P05896|POL_SIVM1 GD-----RGFAAPQFSLWRRPPVTAHIEGQPVVLLDT 131
sp|P05897|POL_SIVM2 GD-----RGFAAPQFSLWRRPPVTAHIEGQPVVLLDT 131
sp|P12502|POL_SIVS4 GD-----RGFAAPQFSLWRRPPVTAHIEGQPVVLLDT 94
sp|P19505|POL_SIVS5 GD-----GGFAAPQFSLWRRPPVTAHIEGQPVVLLDT 97
sp|P15833|POL_HV2D2 GD-----RGFAAPQFSLWRRPPVTKACIEGQSVVLLDT 131
sp|P27980|POL_SIVAG ESRL-----DRGIFPELWRRPIKTVYIEGVPIKALLDT 119
sp|P05895|POL_SIVAT ESGL-----DRGIFPELWRRPIKTVYIEGVPIKALLDT 135
sp|P27973|POL_SIVA1 ESRL-----ERGIFPELWRRPIKTVYIEGVPIKALLDT 114
sp|Q02836|POL_SIVAI EGER-----SGGCFLELWRRPKRVIIEGTPVQALLDT 115
sp|P22382|POL_SIVGB EER-----GGFSFPEYLSRRPIEIVSVDGVTIRALLDT 87
sp|P23427|POL_VILV2 ATCG-----AVRAPYVVEAPPKIEIKVGTWRWKKLLVDT 64
sp|P35956|POL_VILVK ATCG-----AVRAPYVVEAPPKIEIKVGTWRWKKLLVDT 60
sp|P03370|POL_VILV ATCG-----AVRAPYVVEAPPKIEIKVGTWRWKKLLVDT 64
sp|P23426|POL_VILV1 ATCG-----AVRAPYVVEAPPKIEIKVGTWRWKKLLVDT 64
sp|P16901|POL_OMVVS ATCG-----AVRAPYVVEAPPKIDIKVGTWRWKKLLVDT 45
sp|P33459|POL_CAEVC DTGC-----AVRSSYGITSAAPPVQVRIGSQQRNLLFDT 69
sp|P16088|POL_FIVPE FVNY-----NKVGTITLLEKRPEILFVNGYPIKFLLD 69
sp|P19028|POL_FIVSD FINY-----NKVGTITLLEKRPEILFVNGYPIKFLLD 69
sp|P31822|POL_FIVT2 FINY-----NTIGTTTTLEKRPEIQIFVNGHPKIFLLD 68
sp|P11204|POL_EIAV9 SQPG-----QFVGVTYNLEKRPTTIVLINDTPLNVLLD 106
sp|P32542|POL_EIAVC SQPG-----QFVGVTYNLEKRPTTIVLINDTPLNVLLD 106
sp|P03371|POL_EIAVY SQPG-----QFVGVTYNLEKRPTTIVLINDTPLNVLLD 106
sp|P19199|POL_COYMV EERMMVNVNGSQVDRSFIQESSFEVLSRTGIEFIHIGVMLVRIQILHRKFACTMALIVFRD 167
sp|P27502|POL_RTBPV FPQEVKIVNKQGGK-----LYYHIGMMAIGVKGHLHRRKIGTKVMIMFYDD 141

sp|P19560|POL_BIV06 G---ADEVVLLKNHWDRIKG-----YPGTPI 102
sp|P19561|POL_BIV27 G---ADEVVLLKNHWDRIKG-----YPGTPI 102
sp|P20875|POL_HV1JR G---ADDTVLEDMDLPRG-----WKPK 105
sp|P05961|POL_HV1MN G---ADDTVLEEMNLPRR-----WKPK 104
sp|P03366|POL_HV1B1 G---ADDTVLEEMSLPGR-----WKPK 113
sp|P03368|POL_HV1PV G---ADDTVLEEMSLPGR-----WKPK 113
sp|P04585|POL_HV1H2 G---ADDTVLEEMSLPGR-----WKPK 101
sp|P04587|POL_HV1B5 G---ADDTVLEEMSLPGR-----WKPK 113
sp|P03367|POL_HV1BR G---ADDTVLEEMSLPGR-----WKPK 113
sp|P05960|POL_HV1C4 G---ADDTVLEEMNLPRG-----WKPK 101
sp|P12498|POL_HV1J3 G---ADDTVLEEMNSPGR-----WKPK 100
sp|P12497|POL_HV1N5 G---ADDTVLEEMNLPRG-----WKPK 101
sp|P35963|POL_HV1Y2 G---ADDTVLEEMNLPRG-----WKPK 101
sp|P03369|POL_HV1A2 G---ADDTVLEEMNLPGK-----WKPK 101
sp|P20892|POL_HV1OY G---ADDTVLEEMNLPRG-----WKPK 101
sp|P05959|POL_HV1RH G---ADDTVLEEMNLPGK-----WKPK 100
sp|P04589|POL_HV1EL G---ADDTVLEEMNLPGK-----WKPK 100
sp|P12499|POL_HV1Z2 G---ADDTVLEEMNLPGK-----WKPK 100
sp|P18802|POL_HV1ND G---ADDTVLEEMNLPGK-----WKPK 100
sp|P04588|POL_HV1MA G---ADDTVLEEMNLPGK-----WKPK 100
sp|P24740|POL_HV1U4 G---ADDTVLEEMNLPGK-----WKPK 100
sp|P17283|POL_SIVCZ G---ADDTVIERIQLQGL-----WKPK 125
sp|P17757|POL_HV2D1 G---ADDSIVAGIELGDN-----YTPK 167
sp|P18042|POL_HV2G1 G---ADDSIVAGIELGDN-----YVPK 143
sp|P18096|POL_HV2BE G---ADDSIVAGIELGDN-----YTPK 149
sp|P24107|POL_HV2CA G---ADDSIVAGIELGDN-----YSPK 129
sp|P05962|POL_HV2NZ R---ANDSIVAGIELGDN-----YSPK 129
sp|P04584|POL_HV2RO G---ADDSIVAGIELGDN-----YSPK 130
sp|Q74120|POL_HV2KR G---ADDSIVAGIELGDN-----YSPK 129
sp|P20876|POL_HV2ST G---ADDSIVAGIELGDN-----YSPK 149
sp|P12451|POL_HV2SB G---ADDSIVAGIELGDN-----YSPK 129
sp|P05896|POL_SIVM1 G---ADDSIVAGIELGPH-----YTPK 150

sp|P05897|POL_SIVMK G---ADDSIVTGIELGPH-----YTPK 150
sp|P12502|POL_SIVS4 G---ADDSIVAGIELGPN-----YTPK 113
sp|P19505|POL_SIVSP G---ADDSIVAGIELGPN-----YTPK 116
sp|P15833|POL_HV2D2 G---VDDIVAGIELGPN-----YTPK 150
sp|P27980|POL_SIVAG G---ADDTIIEADLQLS-----GTWPK 140
sp|P05895|POL_SIVAT G---ADDTIIEADLQLS-----GPWRPK 156
sp|P27973|POL_SIVA1 G---ADDTIIEADLQLS-----GSWRPK 135
sp|Q02836|POL_SIVA1 G---ADDTIIEADLQLS-----HKPWRSK 138
sp|P22382|POL_SIVGB G---ADDTIIEADLQLS-----GNWQPK 108
sp|P23427|POL_VILV2 G---ADKTIVTSHDM-----SGIPKGR 84
sp|P35956|POL_VILVK G---ADKTIVTSHDM-----SGIPKGR 80
sp|P03370|POL_VILV G---ADKTIVTSHDM-----SGIPKGR 84
sp|P23426|POL_VILV1 G---ADKTIVTSHDM-----SGIPKGR 84
sp|P16901|POL_OMVVS G---ADRTIVRYHDN-----SGIPTGR 65
sp|P33459|POL_CAEVC G---ADRTIVRWHEG-----SGNPAGR 89
sp|P16088|POL_FIVPE G---ADITILNRRDFQ--VK-----NSIENGRQ 92
sp|P19028|POL_FIVSD G---ADITILNRRDFQ--VK-----NSIENGRQ 92
sp|P31822|POL_FIVT2 G---ADITILNRRDFQ--IG-----NSIENGRQ 91
sp|P11204|POL_EIAV9 G---ADTSVLTAAHYNRLKY-----RGRKYOGT 131
sp|P32542|POL_EIAVC G---ADTSVLTAAHYNRLKY-----RGRKYOGT 131
sp|P03371|POL_EIAVY G---ADTSVLTAAHYNRLKY-----RGRKYOGT 131
sp|P19199|POL_COVMY TRWSDRAVLAAMEIDLSEGNQIVYVLPDMMTKISFYRHQICVMTKGYDGWQEDNLL 227
sp|P27502|POL_RTBPV SFGKAREASIGSIEMDMNAGCGVFYSCPDFAKYIKDLSHLKIGIQLG--YENYEGKNLS 199

sp|P19560|POL_BIV06 KQIGVNGVNVAKRKRTHVEVRFKDK-----TGI 129
sp|P19561|POL_BIV27 KQIGVNGVNVAKRKRTHVEVRFKDK-----TGI 129
sp|P20875|POL_HV1JR MIGGIGGFIKVRQYDQIPDIECGH-----KAV 132
sp|P05961|POL_HV1MN MIGGIGGFIKVRQYDQITIGICGH-----KAI 131
sp|P03366|POL_HV1B1 MIGGIGGFIKVRQYDQILIEICGH-----KAI 140
sp|P03368|POL_HV1PV MIGGIGGFIKVRQYDQILIEICGH-----KAI 140
sp|P04585|POL_HV1H2 MIGGIGGFIKVRQYDQILIEICGH-----KAI 128
sp|P04587|POL_HV1B5 MIGGIGGFIKVRQYDQILIEICGH-----KAI 140
sp|P03367|POL_HV1BR MIGGIGGFIKVRQYDQILIEICGH-----KAI 140
sp|P05960|POL_HV1C4 MIGGIGGFIKVRQYDEV-----118
sp|P12498|POL_HV1J3 -----
sp|P12497|POL_HV1N5 MIGGIGGFIKVRQYDQILIEICGH-----KAI 128
sp|P35963|POL_HV1Y2 MIGGIGGFIKVRQYDQIPDIECGH-----KAI 128
sp|P03369|POL_HV1A2 MIGGIGGFIKVRQYDQIPVEICGH-----KAI 128
sp|P20892|POL_HV1OY MIGGIGGFIKVRQYDQILIEICGH-----KAI 128
sp|P05959|POL_HV1RH MIGGIGGFIKVRQYDQILIEICGH-----KAI 127
sp|P04589|POL_HV1EL MIGGIGGFIKVRQYDQIPDIECGH-----KAI 127
sp|P12499|POL_HV1Z2 MIGGIGGFIKVRQYDQILIEICGH-----KAI 127
sp|P18802|POL_HV1ND MIGGIGGFIKVRQYDQILIEICGY-----KAM 127
sp|P04588|POL_HV1MA MIGGIGGFIKVRQYDQILIEICGK-----KAI 127
sp|P24740|POL_HV1U4 IIGGIGGFIKVRQYDQILIEICGK-----KTI 127
sp|P17283|POL_SIVCZ MIGGIGGFIKVRQYDQILIEICGR-----KVV 152
sp|P17757|POL_HV2D1 IVGGIGGFINTKEYKNEIKVNLK-----RVR 194
sp|P18042|POL_HV2G1 IVGGIGGFINTKEYKNEIKVNLK-----RVR 170
sp|P18096|POL_HV2B2 IVGGIGGFINTKEYKNEIKVNLK-----RVR 176
sp|P24107|POL_HV2CA IVGGIGGFINTKEYKNEIEVLGK-----RVR 156
sp|P05962|POL_HV2NC IVGGIGGFINTKEYKNEIEVLGK-----RVR 156
sp|P04584|POL_HV2R0 IVGGIGGFINTKEYKNEIEVLGK-----KVR 157
sp|Q74120|POL_HV2KR IVGGIGGFINTKEYKNEIKVNLK-----KVK 156
sp|P20876|POL_HV2ST IVGGIGGFINTKEYKNEIRVNLK-----RVR 176
sp|P12451|POL_HV2SB IVGGIGGFINTKEYKNEIRVNLK-----RVR 156
sp|P05896|POL_SIVM1 IVGGIGGFINTKEYKNEIEVLGK-----RIK 177
sp|P05897|POL_SIVMK IVGGIGGFINTKEYKNEIEVLGK-----RIK 177
sp|P12502|POL_SIVS4 IVGGIGGFINTKEYKDVKIKVLGK-----VIK 140
sp|P19505|POL_SIVSP IVGGIGGFINTKEYKDVKIKVLGK-----VIK 143
sp|P15833|POL_HV2D2 IVGGIGGFINTKEYKDVIEVVGK-----RVR 177
sp|P27980|POL_SIVAG IIGGIGGGLNVKEYSDREVLEDK-----ILR 167
sp|P05895|POL_SIVAT IIGGIGGGLNVKEYSDREVLEDK-----ILR 183
sp|P27973|POL_SIVA1 IVGGIGGGLNVKEYSDREVLEDK-----ILR 162
sp|Q02836|POL_SIVA1 VVGIGGGHVKEYQGVQVLEDK-----IIT 165
sp|P22382|POL_SIVGB IIGGIGGNLRVKQYDQNVVEIRGK-----GTF 135
sp|P23427|POL_VILV2 ILQGIGGHEGEKWEQVHLQYKDK-----MIK 111
sp|P35956|POL_VILVK ILQGIGGHEGEKWEQVHLQYKDK-----HIR 107
sp|P03370|POL_VILV ILQGIGGHEGEKWEQVHLQYKDK-----MIK 111
sp|P23426|POL_VILV1 ILQGIGGHEGEKWEQVHLQYKDK-----HIR 111
sp|P16901|POL_OMVVS KLQIGGIGHEGEKWDKVVQYKKE-----RIE 92
sp|P33459|POL_CAEVC KLQIGGIGVEGEKWNVELEYKGE-----TRK 116
sp|P16088|POL_FIVPE NMIGVGGKRGNTNYNVHLEIRDENYKTQ-----CIF 124
sp|P19028|POL_FIVSD NMIGVGGKRGNTNYNVHLEIRDENYKTQ-----CIF 124
sp|P31822|POL_FIVT2 NMIGVGGKRGNTNYNVHLEIRDENYRMO-----CIF 123
sp|P11204|POL_EIAV9 GHGIVGGNVET-FSTPVTIKKGR-----HIK 157
sp|P32542|POL_EIAVC GHGIVGGNVET-FSTPVTIKKGR-----HIK 157
sp|P03371|POL_EIAVY GHGIVGGNVET-FSTPVTIKKGR-----HIK 157
sp|P19199|POL_COVMY ITRGLTGRLSNTPNSVGFAYDVKAMVEHLQSNVKAIGKEKWDKRFHNG---QWNIPEK 284
sp|P27502|POL_RTBPV VAIKTIGRLTNTQSKYKINVKDIVEQISSQGIMVAPMEIDSSHLDGNEWDLKFLNHE 259

sp|P19560|POL_BIV06 IDVLFSDTP--VNLFGRLSLLRSIVTCFTLLVHTEK--IEPLPVKVRGP-----173
sp|P19561|POL_BIV27 IDVLFSDTP--VNLFGRLSLLRSIVTCFTLLVHTEK--IEPLPVKVRGP-----173
sp|P20875|POL_HV1JR GTVLVGPTP--VNIIGRNLTLQIG--CTLNFPISP-IETVPVKLKPMD-----176
sp|P05961|POL_HV1MN GTVLVGPTP--VNIIGRNLTLQIG--CTLNFPISP-IETVPVKLKPMD-----175
sp|P03366|POL_HV1B1 GTVLVGPTP--VNIIGRNLTLQIG--CTLNFPISP-IETVPVKLKPMD-----184
sp|P03368|POL_HV1PV GTVLVGPTP--VNIIGRNLTLQIG--CTLNFPISP-IETVPVKLKPMD-----184
sp|P04585|POL_HV1H2 GTVLVGPTP--VNIIGRNLTLQIG--CTLNFPISP-IETVPVKLKPMD-----172
sp|P04587|POL_HV1B5 GTVLVGPTP--VNIIGRNLTLQIG--CTLNFPISP-IETVPVKLKPMD-----184
sp|P03367|POL_HV1BR GTVLVGPTP--VNIIGRNLTLQIG--CTLNFPISP-IETVPVKLKPMD-----184
sp|P05960|POL_HV1C4 -----
sp|P12498|POL_HV1J3 -----
sp|P12497|POL_HV1N5 GTVLVGPTP--VNIIGRNLTLQIG--CTLNFPISP-IETVPVKLKPMD-----172
sp|P35963|POL_HV1Y2 GTVLVGPTP--VNIIGRNLTLQIG--CTLNFPISP-IETVPVKLKPMD-----172
sp|P03369|POL_HV1A2 GTVLVGPTP--VNIIGRNLTLQIG--CTLNFPISP-IETVPVKLKPMD-----172
sp|P20892|POL_HV1OY GTVLVGPTP--VNIIGRNLTLQIG--CTLNFPISP-IETVPVKLKPMD-----172
sp|P05959|POL_HV1RH GTVLVGPTP--VNIIGRNLTLQIG--CTLNFPISP-IETVPVKLKPMD-----171
sp|P04589|POL_HV1EL GTVLVGPTP--VNIIGRNLTLQIG--CTLNFPISP-IETVPVKLKPMD-----171
sp|P12499|POL_HV1Z2 GTVLVGPTP--VNIIGRNLTLQIG--CTLNFPISP-IETVPVKLKPMD-----171
sp|P18802|POL_HV1ND GTVLVGPTP--VNIIGRNLTLQIG--CTLNFPISP-IETVPVKLKPMD-----171
sp|P04588|POL_HV1MA GTVLVGPTP--VNIIGRNLTLQIG--CTLNFPISP-IETVPVKLKPMD-----171
sp|P24740|POL_HV1U4 GTVLVGPTP--VNIIGRNLTLQIG--CTLNFPISP-IETVPVKLKPMD-----171
sp|P17283|POL_SIVCZ GTVLVGPTP--VNIIGRNLTLQIG--CTLNFPISP-IETVPVKLKPMD-----196

sp|P17757|POL_HV2D1 ATIMTGDTP---INIFGRNLTALG--MSLNLPAK-LDPIKVTLPKPKGD----- 238
 sp|P18042|POL_HV2G1 ATIMTGDTP---INIFGRNLTALG--MSLNLPAK-IEPIKVTLPKPKGD----- 214
 sp|P18096|POL_HV2BE ATIMTGDTP---INIFGRNLTALG--MSLNLPAK-IEPIKVTLPKPKGD----- 220
 sp|P24107|POL_HV2CA ATIMTGDTP---INIFGRNLTALG--MSLNLPAK-IEPIKIMLKPKGD----- 200
 sp|P05962|POL_HV2NZ ATIMTGDTP---INIFGRNLTALG--MSLNLPAK-IEPIKIMLKPKGD----- 200
 sp|P04584|POL_HV2RO ATIMTGDTP---INIFGRNLTALG--MSLNLPAK-VEPIKIMLKPKGD----- 201
 sp|Q74120|POL_HV2KR ATIMTGDTP---INIFGRNLTALG--MSLNLPAK-VDPKIVLKPKGD----- 200
 sp|P20876|POL_HV2ST ATIMTGDTP---INIFGRNLTALG--MSLNLPAK-IEPIKIMLKPKGD----- 220
 sp|P12451|POL_HV2SB ATIMTGDTP---INIFGRNLTALG--MSLNLPAK-IEPVKVTLPKPKGD----- 200
 sp|P05896|POL_SIVM1 GTIMTGDTP---INIFGRNLTALG--MSLNLPAK-VEPVKSPLKPKGD----- 221
 sp|P05897|POL_SIVMK RTIMTGDTP---INIFGRNLTALG--MSLNLPAK-VEPVKVALKPKGV----- 221
 sp|P12502|POL_SIVS4 GTIMTGDTP---INIFGRNLTALG--MSLNLPAK-VEPIKVTLPKPKGE----- 184
 sp|P19505|POL_SIVSP GTIMTGDTP---INIFGRNLTALG--MSLNLPAK-VEPIKVTLPKPKGD----- 187
 sp|P15833|POL_HV2D2 ATIMTGDTP---INIFGRNLTALG--MTLNFPAK-VEPVKVELKPKGD----- 221
 sp|P27980|POL_SIVAG GTILIGSTP---INIFGRNLTALG--VMGQVLEQ-IPITPVKLEKGEAR----- 213
 sp|P05895|POL_SIVAT GTILIGSTP---INIFGRNLTALG--VMGQVLEQ-IPVTPVLEKGEAR----- 229
 sp|P27973|POL_SIVA1 GTVLLGATP---INIFGRNLTALG--VMGQVLSQ-IPITPVLEKGEAR----- 208
 sp|Q02836|POL_SIVAI GSILIGSTP---INIFGRNLTALG--VMGQVLSQ-IEFTKVTLPKPKGD----- 211
 sp|P22382|POL_SIVGB GTVLLGATP---INIFGRNLTALG--VMGQVLSQ-IPITPVLEKPKGV----- 181
 sp|P23427|POL_VILV2 GTIVVLATS--PVEVLRDNMRELIGLIMANLEEKKIPSTRVRLKEGCK----- 159
 sp|P35956|POL_VILVK GTIVVLATS--PVEVLRDNMRELIGLIMANLEEKKIPSTRVRLKEGCK----- 155
 sp|P03370|POL_VILV GTIVVLATS--PVEVLRDNMRELIGLIMANLEEKKIPSTRVRLKEGCK----- 159
 sp|P23426|POL_VILV1 GTIVVLATS--PVEVLRDNMRELIGLIMANLEEKKIPSTRVRLKEGCK----- 159
 sp|P16901|POL_OMVVS GTIVVLPSS--PVEVLRDNMRELIGLIMANLEEKKIPSTRVRLKEGCK----- 140
 sp|P33459|POL_CAEVC GTIVVLPSS--PVEVLRDNMRELIGLIMANLEEKKIPSTRVRLKEGCK----- 164
 sp|P16088|POL_FIVPE GNVCVLEDNSLIQPLLGRDNMIFKFNIRLVMAQISDK-IPVVKVMKMDPNK----- 173
 sp|P19028|POL_FIVSD GNVCVLEDNSLIQPLLGRDNMIFKFNIRLVMAQISDK-IPVVKVMKMDPNK----- 173
 sp|P31822|POL_FIVT2 GNVCVLEDNSLIQPLLGRDNMIFKFNIRLVMAQISDK-IPVVKVMKMDPTQ----- 172
 sp|P11204|POL_EIAV9 TRMLVADIP--VTILGRDILQDLGAKLVLAQLSKE-IFKFRKIELKEGTM----- 203
 sp|P32542|POL_EIAVC TRMLVADIP--VTILGRDILQDLGAKLVLAQLSKE-IFKFRKIELKEGTM----- 203
 sp|P03371|POL_EIAVY TRMLVADIP--VTILGRDILQDLGAKLVLAQLSKE-IFKFRKIELKEGTM----- 203
 sp|P19199|POL_COYMV VVVVPMQPTMKA VSNYDGTSLRFSNYAAAASSTKPPQYNEKDEEINENEDEQEIHSLNLL 344
 sp|P27502|POL_RTBPV NTSRVPKALYQNLQGGESLRFNSYKQTRMHDPTENNSDEDEDLKILGEQLN----- 312

sp|P19560|POL_BIV06 -----
 sp|P19561|POL_BIV27 -----
 sp|P20875|POL_HV1JR -----
 sp|P05961|POL_HV1MN -----
 sp|P03366|POL_HV1B1 -----
 sp|P03368|POL_HV1PV -----
 sp|P04585|POL_HV1H2 -----
 sp|P04587|POL_HV1B5 -----
 sp|P03367|POL_HV1BR -----
 sp|P05960|POL_HV1C4 -----
 sp|P12498|POL_HV1J3 -----
 sp|P12497|POL_HV1N5 -----
 sp|P35963|POL_HV1Y2 -----
 sp|P03369|POL_HV1A2 -----
 sp|P20892|POL_HV1OY -----
 sp|P05959|POL_HV1RH -----
 sp|P04589|POL_HV1EL -----
 sp|P12499|POL_HV1Z2 -----
 sp|P18802|POL_HV1ND -----
 sp|P04588|POL_HV1MA -----
 sp|P24740|POL_HV1U4 -----
 sp|P17283|POL_SIVCZ -----
 sp|P17757|POL_HV2D1 -----
 sp|P18042|POL_HV2G1 -----
 sp|P18096|POL_HV2BE -----
 sp|P24107|POL_HV2CA -----
 sp|P05962|POL_HV2NZ -----
 sp|P04584|POL_HV2RO -----
 sp|Q74120|POL_HV2KR -----
 sp|P20876|POL_HV2ST -----
 sp|P12451|POL_HV2SB -----
 sp|P05896|POL_SIVM1 -----
 sp|P05897|POL_SIVMK -----
 sp|P12502|POL_SIVS4 -----
 sp|P19505|POL_SIVSP -----
 sp|P15833|POL_HV2D2 -----
 sp|P27980|POL_SIVAG -----
 sp|P05895|POL_SIVAT -----
 sp|P27973|POL_SIVA1 -----
 sp|Q02836|POL_SIVAI -----
 sp|P22382|POL_SIVGB -----
 sp|P23427|POL_VILV2 -----
 sp|P35956|POL_VILVK -----
 sp|P03370|POL_VILV -----
 sp|P23426|POL_VILV1 -----
 sp|P16901|POL_OMVVS -----
 sp|P33459|POL_CAEVC -----
 sp|P16088|POL_FIVPE -----
 sp|P19028|POL_FIVSD -----
 sp|P31822|POL_FIVT2 -----
 sp|P11204|POL_EIAV9 -----
 sp|P32542|POL_EIAVC -----
 sp|P03371|POL_EIAVY -----
 sp|P19199|POL_COYMV NDEESTDEEYQYQRYAWSQVGDSTFYDDTGVVWEEDRCNDLPEYVPESETPTIDE 404
 sp|P27502|POL_RTBPV -----

sp|P19560|POL_BIV06 -----GPKVPQWPLTK----- 184
 sp|P19561|POL_BIV27 -----GPKVPQWPLTK----- 184
 sp|P20875|POL_HV1JR -----GPKVKQWPLTE----- 187
 sp|P05961|POL_HV1MN -----GPKVKQWPLTE----- 186
 sp|P03366|POL_HV1B1 -----GPKVKQWPLTE----- 195
 sp|P03368|POL_HV1PV -----GPKVKQWPLTE----- 195
 sp|P04585|POL_HV1H2 -----GPKVKQWPLTE----- 183
 sp|P04587|POL_HV1B5 -----GPKVKQWPLTE----- 195
 sp|P03367|POL_HV1BR -----GPKVKQWPLTE----- 195
 sp|P05960|POL_HV1C4 -----
 sp|P12498|POL_HV1J3 -----
 sp|P12497|POL_HV1N5 -----GPKVKQWPLTE----- 183

sp P35963 POL_HV1Y2	-----GPKVKQWPLTE-----	183
sp P03369 POL_HV1A2	-----GPKVKQWPLTE-----	183
sp P20892 POL_HV1OY	-----GPKVKQWPLTE-----	183
sp P05959 POL_HV1RH	-----GPKVKQWPLTE-----	182
sp P04589 POL_HV1EL	-----GPKVKQWPLTE-----	182
sp P12499 POL_HV1Z2	-----GPKVKQWPLTE-----	182
sp P18802 POL_HV1ND	-----GPKVKQWPLTE-----	182
sp P04588 POL_HV1MA	-----GPRVKQWPLTE-----	182
sp P24740 POL_HV1U4	-----GPKVKQWPLTE-----	182
sp P17283 POL_SIVCZ	-----GPKVKQWPLSA-----	207
sp P17757 POL_HV2D1	-----GPRKQWPLTK-----	249
sp P18042 POL_HV2G1	-----GPRKQWPLTK-----	225
sp P18096 POL_HV2BE	-----GPRKQWPLTK-----	231
sp P24107 POL_HV2CA	-----GPRKQWPLTK-----	211
sp P05962 POL_HV2NZ	-----GPRKQWPLTK-----	211
sp P04584 POL_HV2RO	-----GPKLRQWPLTK-----	212
sp Q74120 POL_HV2KR	-----GPKVRQWPLTK-----	211
sp P20876 POL_HV2ST	-----GPKLRQWPLTK-----	231
sp P12451 POL_HV2SB	-----GPKQRQWPLTR-----	211
sp P05896 POL_SIVM1	-----GPKLKQWPLSK-----	232
sp P05897 POL_SIVMK	-----GPKLKQWPLSK-----	232
sp P12502 POL_SIVS4	-----GPKLRQWPLSK-----	195
sp P19505 POL_SIVSP	-----GPKLRQWPLSK-----	198
sp P15833 POL_HV2D2	-----GPKIRQWPLSR-----	232
sp P27980 POL_SIVAG	-----GPFKQWPLSK-----	224
sp P05895 POL_SIVAT	-----GPCVRQWPLSK-----	240
sp P27973 POL_SIVA1	-----GPRKQWPLSK-----	219
sp Q02836 POL_SIVAI	-----GPKLKQWPLSR-----	222
sp P22382 POL_SIVGB	-----GPRKQWPLSK-----	192
sp P23427 POL_VILV2	-----GPHIAQWPLTQ-----	170
sp P35956 POL_VILVK	-----GPHIAQWPLTQ-----	166
sp P03370 POL_VILV	-----GPHIAQWPLTQ-----	170
sp P23426 POL_VILV1	-----GPHIAQWPLTQ-----	170
sp P16901 POL_OMVVS	-----GPHIAQWPLTQ-----	151
sp P33459 POL_CAEVC	-----GPHVPQWPLTE-----	175
sp P16088 POL_FIVPE	-----GPKIKQWPLTN-----	184
sp P19028 POL_FIVSD	-----GPKIKQWPLSN-----	184
sp P31822 POL_FIVT2	-----GPKIKQWPLSN-----	183
sp P11204 POL_EIAV9	-----GPKIPQWPLTK-----	214
sp P32542 POL_EIAVC	-----GPKIPQWPLTK-----	214
sp P03371 POL_EIAVY	-----GPKIPQWPLTK-----	214
sp P19199 POL_COYMV	SEAIHDEFLEHAYEQRCDSDLSQSGDPRKYEYPTPQSSPEHLDNESRSSSSASSTSMQ 664	
sp P27502 POL_RTBPV	-----IKMARFYTMQTPEEELREVIQQLER-----	337

sp P19560 POL_BIV06	----EKYQALKEIVKDLLAEGKISEAAWDPNPNYPVVFVIKKKGTGRWR-----	228
sp P19561 POL_BIV27	----EKYQALKEIVKDLLAEGKISEAAWDPNPNYPVVFVIKKKGTGRWR-----	228
sp P20875 POL_HV1JR	----EKIKALVEICTEMEKEGKISKIGPENPNYPVFAIKKDKSTKWR-----	231
sp P05961 POL_HV1MN	----EKIKALVEICTEMEKEGKISKIGPENPNYPVFAIKKDKSTKWR-----	230
sp P03366 POL_HV1B1	----EKIKALVEICTEMEKEGKISKIGPENPNYPVFAIKKDKSTKWR-----	239
sp P03368 POL_HV1PV	----EKIKALVEICTEMEKEGKISKIGPENPNYPVFAIKKDKSTKWR-----	239
sp P04585 POL_HV1H2	----EKIKALVEICTEMEKEGKISKIGPENPNYPVFAIKKDKSTKWR-----	227
sp P04587 POL_HV1B5	----EKIKALVEICTEMEKEGKISKIGPENPNYPVFAIKKDKSTKWR-----	239
sp P03367 POL_HV1BR	----EKIKALVEICTEMEKEGKISKIGPENPNYPVFAIKKDKSTKWR-----	239
sp P05960 POL_HV1C4	-----	
sp P12498 POL_HV1J3	-----	
sp P12497 POL_HV1N5	----EKIKALVEICTEMEKEGKISKIGPENPNYPVFAIKKDKSTKWR-----	227
sp P35963 POL_HV1Y2	----EKIKALVEICTEMEKEGKISKIGPENPNYPVFAIKKDKSTKWR-----	227
sp P03369 POL_HV1A2	----EKIKALVEICTEMEKEGKISKIGPENPNYPVFAIKKDKSTKWR-----	227
sp P20892 POL_HV1OY	----EKIKALVEICTEMEKEGKISKIGPENPNYPVFAIKKDKSTKWR-----	227
sp P05959 POL_HV1RH	----EKIKALVEICTEMEKEGKISKIGPENPNYPVFAIKKDKSTKWR-----	226
sp P04589 POL_HV1EL	----EKIKALTEICTEMEKEGKISRIGPENPNYPVFAIKKDKSTKWR-----	226
sp P12499 POL_HV1Z2	----EKIKALTEICTEMEKEGKISRIGPENPNYPVFAIKKDKSTKWR-----	226
sp P18802 POL_HV1ND	----EKIKALTEICTEMEKEGKISRIGPENPNYPVFAIKKDKSTKWR-----	226
sp P04588 POL_HV1MA	----EKIKALTEICKDMEKEGKILKIGPENPNYPVFAIKKDKSTKWR-----	226
sp P24740 POL_HV1U4	----EKIKALTEICQEMEKEGKISKIGPENPNYPVFAIKKDKSTKWR-----	226
sp P17283 POL_SIVCZ	----EKIKALTEICQEMEKEGKISKIGPENPNYPVFAIKKDKSTKWR-----	251
sp P17757 POL_HV2D1	----EKIEALKEICEKMEREGQLEEAAPTNPYNTPTFAIKKDKNKWR-----	293
sp P18042 POL_HV2G1	----EKIEALKEICEKMEREGQLEEAAPTNPYNTPTFAIKKDKNKWR-----	269
sp P18096 POL_HV2BE	----EKIEALKEICEKMEREGQLEEAAPTNPYNTPTFAIKKDKNKWR-----	275
sp P24107 POL_HV2CA	----EKIEALKEICEKMEREGQLEEAAPTNPYNTPTFAIKKDKNKWR-----	255
sp P05962 POL_HV2NZ	----EKIEALKEICEKMEREGQLEEAAPTNPYNTPTFAIKKDKNKWR-----	255
sp P04584 POL_HV2RO	----EKIEALKEICEKMEREGQLEEAAPTNPYNTPTFAIKKDKNKWR-----	256
sp Q74120 POL_HV2KR	----EKIEALKEICEKMEREGQLEEAAPTNPYNTPTFAIKKDKNKWR-----	255
sp P20876 POL_HV2ST	----EKIEALKEICEKMEREGQLEEAAPTNPYNTPTFAIKKDKNKWR-----	275
sp P12451 POL_HV2SB	----EKIEALREICEKMEREGQLEEAAPTNPYNTPTFAIKKDKNKWR-----	255
sp P05896 POL_SIVM1	----EKIALREICEKMEKDGQLEEAAPTNPYNTPTFAIKKDKNKWR-----	276
sp P05897 POL_SIVMK	----EKIALREICEKMEKDGQLEEAAPTNPYNTPTFAIKKDKNKWR-----	276
sp P12502 POL_SIVS4	----EKIALREICEKMEKDGQLEEAAPTNPYNTPTFAIKKDKNKWR-----	239
sp P19505 POL_SIVSP	----EKIALREICEKMEKDGQLEEAAPTNPYNTPTFAIKKDKNKWR-----	242
sp P15833 POL_HV2D2	----EKILALKEICEKMEREGQLEEAAPTNPYNTPTFAIKKDKNKWR-----	276
sp P27980 POL_SIVAG	----EKIKALQEICDQLEEGKISKIGGENAYNTPVFAIKKDKSQWR-----	268
sp P05895 POL_SIVAT	----EKIEALQEICDQLEEGKISRIGGENAYNTPVFAIKKDKSQWR-----	284
sp P27973 POL_SIVA1	----EKIALQEICKTLEEEGKLSRIGGENAYNTPVFAIKKDKSQWR-----	263
sp Q02836 POL_SIVAI	----EKIEALTEICQMEEEGKLSRIGGENAYNTPVFAIKKDKTQWR-----	266
sp P22382 POL_SIVGB	----EKIVGLQKICDRLEEEGKISRVDPGNNYNTPTFAIKKDKNWR-----	236
sp P23427 POL_VILV2	----EKLEGLKEIVDRLEKEGKVGGRAPPHWTCNTPTFICIKK-SGKWR-----	213
sp P35956 POL_VILVK	----EKLEGLKEIVDRLEKEGKVGGRAPPHWTCNTPTFICIKK-SGKWR-----	209
sp P03370 POL_VILV	----EKLEGLKEIVDRLEKEGKVGGRAPPHWTCNTPTFICIKK-SGKWR-----	213
sp P23426 POL_VILV1	----EKLEGLKEIVDRLEKEGKVGGRAPPHWTCNTPTFICIKK-SGKWR-----	213
sp P16901 POL_OMVVS	----EKLEGLKEIVDKLEKEGKVGGRAPPHWTCNTPTFICIKK-SGKWR-----	194
sp P33459 POL_CAEVC	----EKIKGLTEIDKLEVEEGKLGKAPPHWTCNTPTFICIKK-SGKWR-----	218
sp P16088 POL_FIVPE	----EKIEALTEIVERLEKEGKVKRADSNPNWNTPTFAIKK-SGKWR-----	227
sp P19028 POL_FIVSD	----EKIEALTEIVERLEREGKVKRADSNPNWNTPTFAIKK-SGKWR-----	227
sp P31822 POL_FIVT2	----EKIEALTDIVERLESEKVKRADSNPNWNTPTFAIKK-SGKWR-----	226
sp P11204 POL_EIAV9	----EKLEGAKEIVQRLLESEGKISEASDNNPNYSPFVIKKR-SGKWR-----	257
sp P32542 POL_EIAVC	----EKLEGAKEIVQRLLESEGKISEASDNNPNYSPFVIKKR-SGKWR-----	257
sp P03371 POL_EIAVY	----EKLEGAKEIVQRLLESEGKISEASDNNPNYSPFVIKKR-SGKWR-----	257
sp P19199 POL_COYMV	DDVEIVRLMKEMRMKQKQKKAQALSSQAQEEPIEENIENKQAQEEPT-----	516
sp P27502 POL_RTBPV	----EKQAMIAKLEAKMKESSMAIVEDNFNPNYELEDYSEYEDLEFEKLGLTGWEDL 393	

sp P19560 POL_BIV06	-----MLMDFRELNKITVKGQEFSTGLPYPPG 255	
sp P19561 POL_BIV27	-----MLMDFRELNKITVKGQEFSTGLPYPPG 255	

sp|P20875|POL_HV1JR -----KLVDFRELNRRTQDFWEVQLGIPHPAG 258
 sp|P05961|POL_HV1MIN -----KLVDFRELNRKKTQDFWEVQLGIPHPAG 257
 sp|P03366|POL_HV1B1 -----KLVDFRELNRKRTQDFWEVQLGIPHPAG 266
 sp|P03368|POL_HV1PV -----KLVDFRELNRKRTQDFWEVQLGIPHPAG 266
 sp|P04585|POL_HV1H2 -----KLVDFRELNRKRTQDFWEVQLGIPHPAG 254
 sp|P04587|POL_HV1B5 -----KLVDFRELNRRTQDFWEVQLGIPHPAG 266
 sp|P03367|POL_HV1BR -----KLVDFRELNRKRTQDFWEVQLGIPHPAG 266
 sp|P05960|POL_HV1C4 -----
 sp|P12498|POL_HV1J3 -----
 sp|P12497|POL_HV1N5 -----KLVDFRELNRKRTQDFWEVQLGIPHPAG 254
 sp|P35963|POL_HV1Y2 -----KLVDFRELNRKRTQDFWEVQLGIPHPAG 254
 sp|P03369|POL_HV1A2 -----KLVDFRELNRKRTQDFWEVQLGIPHPAG 254
 sp|P20892|POL_HV1OY -----KLVDFRELNRKRTQDFWEVQLGIPHPAG 254
 sp|P05959|POL_HV1RH -----KLVDFRELNRKRTQDFWEVQLGIPHPAG 253
 sp|P04589|POL_HV1EL -----KLVDFRELNRKRTQDFWEVQLGIPHPAG 253
 sp|P12499|POL_HV1Z2 -----KLVDFRELNRKRTQDFWEVQLGIPHPAG 253
 sp|P18802|POL_HV1ND -----KLVDFRELNRKRTQDFWEVQLGIPHPAG 253
 sp|P04588|POL_HV1MA -----KLVNFRELNRKRTQDFWEVQLGIPHPAG 253
 sp|P24740|POL_HV1U4 -----KLVDFRELNRKRTQDFWEVQLGIPHTAG 253
 sp|P17283|POL_SIVCZ -----KLVDFRELNRKRTQDFWEVQLGIPHPAG 278
 sp|P17757|POL_HV2D1 -----MLIDFRELNRVTQDFTEIQLGIPHPAG 320
 sp|P18042|POL_HV2G1 -----MLIDFRELNRVTQDFTEIQLGIPHPAG 296
 sp|P18096|POL_HV2BE -----MLIDFRELNRKVTQDFTEIQLGIPHPAG 302
 sp|P24107|POL_HV2CA -----MLIDFRELNRKVTQDFTEIQLGIPHPAG 282
 sp|P05962|POL_HV2NZ -----MLIDFRELNRKVTQDFTEIQLGIPHPAG 282
 sp|P04584|POL_HV2RO -----MLIDFRELNRKVTQDFTEIQLGIPHPAG 283
 sp|Q74120|POL_HV2KR -----MLIDFRELNRKVTQDFTEIQLGIPHPAG 282
 sp|P20876|POL_HV2ST -----MLIDFRELNRKVTQDFTEIQLGIPHPAG 302
 sp|P12451|POL_HV2SB -----MLIDFRELNRKVTQDFTEIQLGIPHPAG 282
 sp|P05896|POL_SIVM1 -----MLIDFRELNRVTQDFTEIQLGIPHPAG 303
 sp|P05897|POL_SIVMK -----MLIHRELNRVTQELVRSPIRHPAG 303
 sp|P12502|POL_SIVS4 -----MLIDFRELNRKVTQDFTEIQLGIPHPAG 266
 sp|P19505|POL_SIVSP -----MLIDFRELNRKVTQDFTEIQLGIPHPAG 269
 sp|P15833|POL_HV2D2 -----MLIDFRELNRKVTQDFTEIQLGIPHPAG 302
 sp|P27980|POL_SIVAG -----MLVDFRELNRKATQDFWEVQLGIPHPAG 295
 sp|P05895|POL_SIVAT -----MLVDFRELNRKATQDFWEVQLGIPHPAG 311
 sp|P27973|POL_SIVAI -----MLVDFRELNRKATQDFWEVQLGIPHPAG 290
 sp|Q02836|POL_SIVAI -----MLVDFRELNRKATQDFWEVQLGIPHPAG 293
 sp|P22382|POL_SIVGB -----KLIDFRELNRKLTQDFHEIQLGIPHPAG 263
 sp|P23427|POL_VILV2 -----MLIDFRELNRKQTEDELAELGLPHPGG 240
 sp|P35956|POL_VILVK -----MLIDFRELNRKQTEDELAELGLPHPGG 236
 sp|P03370|POL_VILV -----MLIDFRELNRKQTEDELAELGLPHPGG 240
 sp|P23426|POL_VILV1 -----MLIDFRELNRKQTEDELAELGLPHPGG 240
 sp|P16901|POL_OMVVS -----MLIDFRELNRKQTEDELAELGLPHPGG 221
 sp|P33459|POL_CAEVC -----MLIDFRELNRKQTEDELAELGLPHPGG 245
 sp|P16088|POL_FIVPE -----MLIDFRELNRKLTQDFHEIQLGIPHPAG 254
 sp|P19028|POL_FIVSD -----MLIDFRELNRKLTQDFHEIQLGIPHPAG 254
 sp|P31822|POL_FIVT2 -----MLIDFRELNRKLTQDFHEIQLGIPHPAG 253
 sp|P11204|POL_EIAV9 -----LLQDLRELNRKTVQVGTISRGLPHPGG 284
 sp|P32542|POL_EIAVC -----LLQDLRELNRKTVQVGTISRGLPHPGG 284
 sp|P03371|POL_EIAVY -----LLQDLRELNRKTVQVGTISRGLPHPGG 284
 sp|P19199|POL_COMVM - - - - -QEEIPTHKENQPEEIHVFEIEPAFKHLAAQLSELVNMAESSGQSGVGFQPPVN 574
 sp|P27502|POL_RTBPV DQDSIETEIEITWENPNQVLRHREIRA YKVSVEQIEDIFGELLKEHGNYDMALKNLEEKYD 453

sp|P19560|POL_BIV06 IKECEHLT-----AIDIKDAYFTIPLHEDFR-----PFTAFSVVPPVN-- 292
 sp|P19561|POL_BIV27 IKECEHLT-----AIDIKDAYFTIPLHEDFR-----PFTAFSVVPPVN-- 292
 sp|P20875|POL_HV1JR LKKKKSVT----VLDVGDAYFSVPLDKDFR-----KYTAFTIPSIN-- 295
 sp|P05961|POL_HV1MIN LKKKKSVT----VLDVGDAYFSVPLDKDFR-----KYTAFTIPSIN-- 294
 sp|P03366|POL_HV1B1 LKKKKSVT----VLDVGDAYFSVPLDEDFR-----KYTAFTIPSIN-- 303
 sp|P03368|POL_HV1PV LKKKKSVT----VLDVGDAYFSVPLDEDFR-----KYTAFTIPSIN-- 303
 sp|P04585|POL_HV1H2 LKKKKSVT----VLDVGDAYFSVPLDEDFR-----KYTAFTIPSIN-- 291
 sp|P04587|POL_HV1B5 LKKKKSVT----VLDVGDAYFSVPLDEDFR-----KYTAFTIPSIN-- 303
 sp|P03367|POL_HV1BR LKKKKSVT----VLDVGDAYFSVPLDEDFR-----KYTAFTIPSIN-- 303
 sp|P05960|POL_HV1C4 -----
 sp|P12498|POL_HV1J3 -----
 sp|P12497|POL_HV1N5 LKQKKSVT----VLDVGDAYFSVPLDKDFR-----KYTAFTIPSIN-- 291
 sp|P35963|POL_HV1Y2 LKQKKSVT----VLDVGDAYFSVPLHEDFR-----KYTAFTIPSIN-- 291
 sp|P03369|POL_HV1A2 LKQKKSVT----VLDVGDAYFSVPLDKDFR-----KYTAFTIPSIN-- 291
 sp|P20892|POL_HV1OY LKQKKSVT----VLDVGDAYFSVPLDKDFR-----KYTAFTIPSIN-- 291
 sp|P05959|POL_HV1RH LKQKKSVT----VLDVGDAYFSVPLDKDFR-----KYTAFTIPSIN-- 290
 sp|P04589|POL_HV1EL LKQKKSVT----VLDVGDAYFSVPLDEDFR-----KYTAFTIPSIN-- 290
 sp|P12499|POL_HV1Z2 LKQKKSVT----VLDVGDAYFSVPLDKDFR-----KYTAFTIPSIN-- 290
 sp|P18802|POL_HV1ND LKQKKSVT----VLDVGDAYFSVPLDEDFR-----KYTAFTIPSIN-- 290
 sp|P04588|POL_HV1MA LKQKKSVT----VLDVGDAYFSVPLDEDFR-----KYTAFTIPSIN-- 290
 sp|P24740|POL_HV1U4 LKQKKSVT----VLDVGDAYFSVPLDEDFR-----KYTAFTIPSIN-- 290
 sp|P17283|POL_SIVCZ LKQKKSVT----VLDVGDAYFSVPLDKDFR-----KYTAFTIPSIN-- 315
 sp|P17757|POL_HV2D1 LAKKKRIT----VLDVGDAYFSIPLHEDFR-----QYTAFTLPSVN-- 357
 sp|P18042|POL_HV2G1 LAKKKRIT----VLDVGDAYFSIPLHEDFR-----QYTAFTLPSVN-- 333
 sp|P18096|POL_HV2BE LAKKKRIS----ILDVGDAYFSIPLHEDFR-----QYTAFTLPAVN-- 339
 sp|P24107|POL_HV2CA LAKKKRIT----VLDVGDAYFSIPLHEDFR-----QYTAFTLPSVN-- 319
 sp|P05962|POL_HV2NZ LAKKKRIT----VLDVGDAYFSIPLHEDFR-----QYTAFTLPSVN-- 319
 sp|P04584|POL_HV2RO LAKKKRIT----VLDVGDAYFSIPLHEDFR-----PYTAFTLPSVN-- 320
 sp|Q74120|POL_HV2KR LAKKKRIT----VLDIGDAYFSIPLHEDFR-----QYTAFTLPTVN-- 319
 sp|P20876|POL_HV2ST LAKKKRIT----VLDVGDAYFSIPLHEDFR-----QYTAFTLPSVN-- 339
 sp|P12451|POL_HV2SB LAKKKRIT----VLDVGDAYFSIPLYEDFR-----QYTAFTLPSVN-- 319
 sp|P05896|POL_SIVM1 LAKKKRIT----VLDIGDAYFSIPLDEEFR-----QYTAFTLPSVN-- 340
 sp|P05897|POL_SIVMK LAKKKRIT----VLDIGDAYFSIPLDEEFR-----QYTAFTLPSVN-- 340
 sp|P12502|POL_SIVS4 LAKRRRIT----VLDVGDAYFSIPLDEEFR-----QYTAFTLPSVN-- 303
 sp|P19505|POL_SIVSP LAKRRRIT----VLDVGDAYFSIPLDEEFR-----QYTAFTLPSVN-- 306
 sp|P15833|POL_HV2D2 VAEKRRIT----VIDVGDAYFSIPLDPNFR-----QYTAFTLPSVN-- 339
 sp|P27980|POL_SIVAG FEKMTFIT----VLDIGDAYYSIPLDPEFR-----KYTAFTIPSVN-- 332
 sp|P05895|POL_SIVAT LRKMRQIT----VLDVGDAYYSIPLDPNFR-----KYTAFTIPTVN-- 348
 sp|P27973|POL_SIVAI LKQKKSVT----VLDVGDAYYSIPLDPEFR-----KYTAFTIPTVN-- 327
 sp|Q02836|POL_SIVAI LKQKKSVT----VIDIGDAYYSIPLCKEFR-----KYTAFTIPSVN-- 330
 sp|P22382|POL_SIVGB IKKCKRIT----VLDIGDAYYSIPLDPDYR-----PYTAFTLPSVN-- 300
 sp|P23427|POL_VILV2 LQRKKHVT----ILDIGDAYFTIPLYEPYR-----QYTCFTMLSPN-- 277
 sp|P35956|POL_VILVK LQRKKHVT----ILDIGDAYFTIPLYEPYR-----QYTCFTMLSPN-- 273
 sp|P03370|POL_VILV LQRKKHVT----ILDIGDAYFTIPLYEPYR-----QYTCFTMLSPN-- 277
 sp|P23426|POL_VILV1 LQRKKHVT----ILDIGDAYFTIPLYEPYR-----QYTCFTMLSPN-- 277
 sp|P16901|POL_OMVVS LQKQKKSVT----ILDIGDAYFTIPLYEPYR-----PYTCFTMLSPN-- 258
 sp|P33459|POL_CAEVC LQKQKKSVT----ILDIGDAYFTIPLYEPYR-----EYTCFTMLSPN-- 282
 sp|P16088|POL_FIVPE LQKQKQVT----VLDIGDAYFTIPLDPDYA-----PYTAFTLPRKN-- 291
 sp|P19028|POL_FIVSD LQKQKQVT----VLDIGDAYFTIPLDPDYA-----PYTAFTLPRKN-- 291

sp|P31822|POL_FIVT2 LQMKKQVT----VLDIGDAYFTIPLDPDYA-----PYTAFTLPRKN-- 290
 sp|P11204|POL_EIAV9 LIKCKHMT----VLDIGDAYFTIPLDPEFR-----PYTAFTIPSIN-- 321
 sp|P32542|POL_EIAVC LIKCKHMT----VLDIGDAYFTIPLDPEFR-----PYTAFTIPSIN-- 321
 sp|P03371|POL_EIAVY LIKCKHMT----VLDIGDAYFTIPLDPEFR-----PYTAFTIPSIN-- 321
 sp|P19199|POL_COYMV AQPVDNMEGPAGYAPATSQATWSNGVNIPVKS-----NFRWKGPGVGNFQLPSAQGK 626
 sp|P27502|POL_RTBPV LDKIEKAKS---IEEIAKSSTSSEIRPTKRPKEEQTAYEDDMRDDWKRKELTVNPIEAS 509

sp|P19560|POL_BIV06 -----REGPIERFQWNVLPQGWVCSP----- 313
 sp|P19561|POL_BIV27 -----REGPIERFQWNVLPQGWVCSP----- 313
 sp|P20875|POL_HV1JR -----NETPGIRYQYNVLPQGWKGS----- 316
 sp|P05961|POL_HV1MN -----NETPGIRYQYNVLPQGWKGS----- 315
 sp|P03366|POL_HV1B1 -----NETPGIRYQYNVLPQGWKGS----- 324
 sp|P03368|POL_HV1PV -----NETPGIRYQYNVLPQGWKGS----- 324
 sp|P04585|POL_HV1H2 -----NETPGIRYQYNVLPQGWKGS----- 312
 sp|P04587|POL_HV1B5 -----NETPGSGYQYNVLPQGWKGS----- 324
 sp|P03367|POL_HV1BR -----NETPGIRYQYNVLPQGWKGS----- 324
 sp|P05960|POL_HV1C4 -----
 sp|P12498|POL_HV1J3 -----
 sp|P12497|POL_HV1N5 -----NETPGIRYQYNVLPQGWKGS----- 312
 sp|P35963|POL_HV1Y2 -----NETPGTRYQYNVLPQGWKGS----- 312
 sp|P03369|POL_HV1A2 -----NETPGIRYQYNVLPQGWKGS----- 312
 sp|P20892|POL_HV1OY -----NETPGIRYQYNVLPQGWKGS----- 312
 sp|P05959|POL_HV1RH -----NETPRIRYQYNVLPQGWKGS----- 311
 sp|P04589|POL_HV1EL -----NETPGIRYQYNVLPQGWKGS----- 311
 sp|P12499|POL_HV1Z2 -----NETPGIRYQYNVLPQGWKGS----- 311
 sp|P18802|POL_HV1ND -----NETPGIRYQYNVLPQGWKGS----- 311
 sp|P04588|POL_HV1MA -----NETPGIRYQYNVLPQGWKGS----- 311
 sp|P24740|POL_HV1U4 -----NETPGVRYQYNVLPQGWKGS----- 311
 sp|P17283|POL_SIVCZ -----NETPGVRYQYNVLPQGWKGS----- 336
 sp|P17757|POL_HV2D1 -----NAEPGKRYVYKVLQGWKGS----- 378
 sp|P18042|POL_HV2G1 -----NAEPGKRYVYKVLQGWKGS----- 354
 sp|P18096|POL_HV2BE -----NMEPGKRYVYKVLQGWKGS----- 360
 sp|P24107|POL_HV2CA -----NAEPGKRYVYKVLQGWKGS----- 340
 sp|P05962|POL_HV2NZ -----NAEPGKRYVYKVLQGWKGS----- 340
 sp|P04584|POL_HV2RO -----NAEPGKRYVYKVLQGWKGS----- 341
 sp|Q74120|POL_HV2KR -----NAEPGKRYVYKVLQGWKGS----- 340
 sp|P20876|POL_HV2ST -----NAEPGKRYVYKVSPOGWKGS----- 360
 sp|P12451|POL_HV2SB -----NAEPGKRYVYKVLQGWKGS----- 340
 sp|P05896|POL_SIVM1 -----NAEPGKRYVYKVLQGWKGS----- 361
 sp|P05897|POL_SIVMK -----NAEPGKRYVYKVLQGWKGS----- 361
 sp|P12502|POL_SIVS4 -----NAEPGKRYVYKVLQGWKGS----- 324
 sp|P19505|POL_SIVSP -----NAEPGKRYVYKVLQGWKGS----- 327
 sp|P15833|POL_HV2D2 -----NAEPGKRYVYKVLQGWKGS----- 360
 sp|P27980|POL_SIVAG -----NQPGTRYQFNCLPQGWKGS----- 353
 sp|P05895|POL_SIVAT -----NQPGIRYQFNCLPQGWKGS----- 369
 sp|P27973|POL_SIV1A -----NEPGIRYQFNCLPQGWKGS----- 348
 sp|Q02836|POL_SIV1A -----NTGPGIRYQFNCLPQGWKGS----- 351
 sp|P22382|POL_SIVGB -----NQAPGKRYMYNVLPQGWKGS----- 321
 sp|P23427|POL_VILV2 -----NLGPCVRYVYKVLQGWKLS----- 298
 sp|P35956|POL_VILVK -----NLGPCVRYVYKVLQGWKLS----- 294
 sp|P03370|POL_VILV -----NLGPCVRYVYKVLQGWKLS----- 298
 sp|P23426|POL_VILV1 -----NLGPCVRYVYKVLQGWKLS----- 298
 sp|P16901|POL_OMVVS -----NLGPCTRYVYKVLQGWKLS----- 279
 sp|P33459|POL_CAEVC -----NLGPCKRYVYKVLQGWKLS----- 303
 sp|P16088|POL_FIVPE -----NAGPGRRFVWCSLPQGWILSP----- 312
 sp|P19028|POL_FIVSD -----NAGPGRRFVWCSLPQGWILSP----- 312
 sp|P31822|POL_FIVT2 -----NAGPGRRYVWCSLPQGWVLS----- 311
 sp|P11204|POL_EIAV9 -----HQEPDKRYVWNCLPQGFVLS----- 342
 sp|P32542|POL_EIAVC -----HQEPDKRYVWNCLPQGFVLS----- 342
 sp|P03371|POL_EIAVY -----HQEPDKRYVWVCLPQGFVLS----- 342
 sp|P19199|POL_COYMV DGAMLVFG-----MNYSPVEFDRWASITRNYISSFNFDGGDKIAWM 668
 sp|P27502|POL_RTBPV KDRNFERIGSSYKKNFYPSRSEILNLDNVPQFYDYDQLVTFWEGIVKNEWEARKKDGMDMW 569

sp|P19560|POL_BIV06 -----AIFYQTTQKIHENIKKSHPDVMLYQYMDLLIGSNRD--DHKQI 355
 sp|P19561|POL_BIV27 -----AIFYQTTQKIHENIKKSHPDVMLYQYMDLLIGSNRD--DHKQI 355
 sp|P20875|POL_HV1JR -----AIFQSSMTKILEPFRKQNPDIIVYQYMDLLYVGSDEIGQHRTK 360
 sp|P05961|POL_HV1MN -----AIFQSSMTKILEPFRKQNPDIIVYQYMDLLYVGSDEIGQHRTK 359
 sp|P03366|POL_HV1B1 -----AIFQSSMTKILEPFRKQNPDIIVYQYMDLLYVGSDEIGQHRTK 368
 sp|P03368|POL_HV1PV -----AIFQSSMTKILEPFRKQNPDIIVYQYMDLLYVGSDEIGQHRTK 368
 sp|P04585|POL_HV1H2 -----AIFQSSMTKILEPFRKQNPDIIVYQYMDLLYVGSDEIGQHRTK 356
 sp|P04587|POL_HV1B5 -----AIFQSSMTKILEPFRKQNPDIIVYQYMDLLYVGSDEIGQHRTK 368
 sp|P03367|POL_HV1BR -----AIFQSSMTKILEPFRKQNPDIIVYQYMDLLYVGSDEIGQHRTK 368
 sp|P05960|POL_HV1C4 -----
 sp|P12498|POL_HV1J3 -----
 sp|P12497|POL_HV1N5 -----AIFQSSMTKILEPFRKQNPDIIVYQYMDLLYVGSDEIGQHRTK 356
 sp|P35963|POL_HV1Y2 -----AIFQSSMTKILEPFRKQNPDIIVYQYMDLLYVGSDEIGQHRTK 356
 sp|P03369|POL_HV1A2 -----AIFQSSMTKILEPFRKQNPDIIVYQYMDLLYVGSDEIGQHRTK 356
 sp|P20892|POL_HV1OY -----AIFQSSMTKILEPFRKQNPDIIVYQYMDLLYVGSDEIGQHRTK 356
 sp|P05959|POL_HV1RH -----AIFQSSMTKILEPFRKQNPDIIVYQYMDLLYVGSDEIGQHRTK 355
 sp|P04589|POL_HV1EL -----AIFQSSMTKILEPFRKQNPDIIVYQYMDLLYVGSDEIGQHRTK 355
 sp|P12499|POL_HV1Z2 -----AIFQSSMTKILEPFRKQNPDIIVYQYMDLLYVGSDEIGQHRTK 355
 sp|P18802|POL_HV1ND -----AIFQSSMTKILEPFRKQNPDIIVYQYMDLLYVGSDEIGQHRTK 355
 sp|P04588|POL_HV1MA -----AIFQSSMTKILEPFRKQNPDIIVYQYMDLLYVGSDEIGQHRTK 355
 sp|P24740|POL_HV1U4 -----SIFQSSMTKILEPFRKQNPDIIVYQYMDLLYVGSDEIGQHRTK 355
 sp|P17283|POL_SIVCZ -----SIFQSSMTKILEPFRKQNPDIIVYQYMDLLYVGSDEIGQHRTK 380
 sp|P17757|POL_HV2D1 -----AIFQFMTRQVLEPFRKANPDVILIQYMDLLIASDRTGLEHDKV 422
 sp|P18042|POL_HV2G1 -----AIFQHTMRQVLEPFRKANPDVILIQYMDLLIASDRTGLEHDKV 398
 sp|P18096|POL_HV2BE -----AIFQYTMROVLEPFRKANPDVILIQYMDLLIASDRTGLEHDKV 404
 sp|P24107|POL_HV2CA -----AIFQYTMROVLEPFRKANPDVILIQYMDLLIASDRTGLEHDKV 384
 sp|P05962|POL_HV2NZ -----AIFQYTMROVLEPFRKANPDVILIQYMDLLIASDRTGLEHDKV 384
 sp|P04584|POL_HV2RO -----AIFQHTMRQVLEPFRKANPDVILIQYMDLLIASDRTGLEHDKV 385
 sp|Q74120|POL_HV2KR -----AIFQHTMRQVLEPFRKANPDVILIQYMDLLIASDRTGLEHDKV 384
 sp|P20876|POL_HV2ST -----AIFQYTMROVLEPFRKANPDVILIQYMDLLIASDRTGLEHDKV 404
 sp|P12451|POL_HV2SB -----AIFQYTMROVLEPFRKANPDVILIQYMDLLIASDRTGLEHDKV 384
 sp|P05896|POL_SIVM1 -----AIFQYTMRHVLEPFRKANPDVILIQYMDLLIASDRTGLEHDKV 405
 sp|P05897|POL_SIVMK -----AIFQYTMRHVLEPFRKANPDVILIQYMDLLIASDRTGLEHDKV 405
 sp|P12502|POL_SIVS4 -----AIFQYTMRVNLEPFRKANPDVILIQYMDLLIASDRTGLEHDKV 368
 sp|P19505|POL_SIVSP -----AIFQHTMRNVLEPFRKANPDVILIQYMDLLIASDRTGLEHDKV 371
 sp|P15833|POL_HV2D2 -----SICQYSMRKVLDPFRKANPDVILIQYMDLLIASDRTGLEHDKV 404
 sp|P27980|POL_SIVAG -----TIFQNTAASILEEIKKELKPLTIVQYMDLLVWGSQEQEYTHDRL 397
 sp|P05895|POL_SIVAT -----TIFQNTAASILEEIKKELKPLTIVQYMDLLVWGSQEQEYTHDRL 413
 sp|P27973|POL_SIV1A -----TIFQNTASKILEEIKKELKPLTIVQYMDLLVWGSQEQEYTHDRL 392

sp|Q02836|POL_SIVAI -----TIFQNTAANILEEIKRHTPGLEIVQYMDLWLASDHDDETRHNQ 395
sp|P22382|POL_SIVGB -----CIFQGTVASLLEVFRKNHPTVQLYQYMDLWLVGSDYTAEEHEKA 365
sp|P23427|POL_VILV2 -----AVYQFTMQKILRGWIEEHPMIQFGIYMDIYIGSDLGLEEHRGI 342
sp|P35956|POL_VILVK -----AVYQFTMQKILRGWIEEHPMIQFGIYMDIYIGSDLGLEEHRGI 338
sp|P03370|POL_VILV -----AVYQFTMQKILRGWIEEHPMIQFGIYMDIYIGSDLGLEEHRGI 342
sp|P23426|POL_VILV1 -----SVYQFTMQKILRGWIEEHPMIQFGIYMDIYIGSDLGLEEHRGI 342
sp|P16901|POL_OMVVS -----SVYQFTMQEILRDWIAKHMPMIQFGIYMDIYIGSDLDIMKHREI 323
sp|P33459|POL_CAEVC -----SVYQFTMQEILEDWIQHPPIQFGIYMDIYIGSDLEIKKHREI 347
sp|P16088|POL_FIVPE -----LIYQSTLDNIHQPFIRQNPQLDIYQYMDIYIGSNLSKKEHKEK 356
sp|P19028|POL_FIVSD -----LIYQSTLDNIHQPFIRQNPQLDIYQYMDIYIGSNLSKKEHKEK 356
sp|P31822|POL_FIVT2 -----LIYQSTLDNIHQPFIRQNPQLDIYQYMDIYIGSNLSKKEHKEK 355
sp|P11204|POL_EIAV9 -----YIYQKTLQEILQPFRRERYPEVQLYQYMDLWLVGSDYTAEEHEKA 386
sp|P32542|POL_EIAVC -----YIYQKTLQEILQPFRRERYPEVQLYQYMDLWLVGSDYTAEEHEKA 386
sp|P03371|POL_EIAVY -----YIYQKTLQEILQPFRRERYPEVQLYQYMDLWLVGSDYTAEEHEKA 386
sp|P19199|POL_COYMV EDLLGETERKIFVSWMRFRKDEYQNLAKIANQDGGTQAILSQIRRIFLGEDPVLGQNTVQ 728
sp|P27502|POL_RTBPV SWMDGRITGLVLYLQDVISKNQAAAYNDIKSRGDRPENFVKMVKDRFLIEDPTDERRAL 629

sp|P19560|POL_BIV06 -----VQEIRDKLSYGFKTPDE---KVQEE-RVKWIGFELTPKKWRFQ 395
sp|P19561|POL_BIV27 -----VQEIRDKLSYGFKTPDE---KVQEE-RVKWIGFELTPKKWRFQ 395
sp|P20875|POL_HV1JR -----IEELRQHLLRWGFTTPDK---KHQKEPPFLWMGYELHPDKWTVQ 401
sp|P05961|POL_HV1MN -----IEELRRHLLRWGFTTPDK---KHQKEPPFLWMGYELHPDKWTVQ 400
sp|P03366|POL_HV1B1 -----IEELRQHLLRWGLTTPDK---KHQKEPPFLWMGYELHPDKWTVQ 409
sp|P03368|POL_HV1PV -----IEELRQHLLRWGLTTPDK---KHQKEPPFLWMGYELHPDKWTVQ 409
sp|P04585|POL_HV1H2 -----IEELRQHLLRWGLTTPDK---KHQKEPPFLWMGYELHPDKWTVQ 397
sp|P04587|POL_HV1B5 -----IEELRQHLLRWGFTTPDK---KHQKEPPFLWMGYELHPDKWTVQ 409
sp|P03367|POL_HV1BR -----IEELRQHLLRWGLTTPDK---KHQKEPPFLWMGYELHPDKWTVQ 409
sp|P05960|POL_HV1C4 -----
sp|P12498|POL_HV1J3 -----
sp|P12497|POL_HV1N5 -----IEELRQHLLRWGFTTPDK---KHQKEPPFLWMGYELHPDKWTVQ 397
sp|P35963|POL_HV1Y2 -----IEELRQHLLRWGFTTPDK---KHQKEPPFLWMGYELHPDKWTVQ 397
sp|P03369|POL_HV1A2 -----IEELRQHLLRWGFTTPDK---KHQKEPPFLWMGYELHPDKWTVQ 397
sp|P20892|POL_HV1OY -----IEELRQHLLRWGFTTPDK---KHQKEPPFLWMGYELHPDKWTVQ 397
sp|P05959|POL_HV1RH -----IEELREHLLRWGFTTPDK---KHQKEPPFLWMGYELHPDKWTVQ 396
sp|P04589|POL_HV1EL -----IEELREHLLRWGFTTPDK---KHQKEPPFLWMGYELHPDKWTVQ 396
sp|P12499|POL_HV1Z2 -----IEELREHLLRWGFTTPDK---KHQKEPPFLWMGYELHPDKWTVQ 396
sp|P18802|POL_HV1ND -----IEELREHLLRWGFTTPDK---KHQKEPPFLWMGYELHPDKWTVQ 396
sp|P04588|POL_HV1MA -----IEELREHLLRWGFTTPDK---KHQKEPPFLWMGYELHPDKWTVQ 396
sp|P24740|POL_HV1U4 -----IEELRAHLLRWGFTTPDK---KHQKEPPFLWMGYELHPDKWTVQ 396
sp|P17283|POL_SIVCZ -----VEELRQHLLRWGFTTPDK---KHQKEPPFLWMGYELHPDKWTVQ 421
sp|P17757|POL_HV2D1 -----VLQKELLNGLGFSTPDE---KFQKDPFQWGMGYELWPTKWKLQ 463
sp|P18042|POL_HV2G1 -----VLQKELLNGLGFSTPDE---KFQKDPFQWGMGYELWPTKWKLQ 439
sp|P18096|POL_HV2BE -----VLQKELLNGLGFSTPDE---KFQKDPFQWGMGYELWPTKWKLQ 445
sp|P24107|POL_HV2CA -----VLQKELLNGLGFSTPDE---KFQKDPFQWGMGYELWPTKWKLQ 425
sp|P05962|POL_HV2NZ -----VLQKELLNGLGFSTPDE---KFQKDPFQWGMGYELWPTKWKLQ 425
sp|P04584|POL_HV2RO -----VLQKELLNGLGFSTPDE---KFQKDPFQWGMGYELWPTKWKLQ 426
sp|Q74120|POL_HV2KR -----VLQKELLNGLGFSTPDE---KFQKDPFQWGMGYELWPTKWKLQ 425
sp|P20876|POL_HV2ST -----VLQKELLNGLGFSTPDE---KFQKDPFQWGMGYELWPTKWKLQ 445
sp|P12451|POL_HV2SB -----VLQKELLNGLGFSTPDE---KFQKDPFQWGMGYELWPTKWKLQ 425
sp|P05896|POL_SIVM1 -----VLQKELLNSIGFSTPEE---KFQKDPFQWGMGYELWPTKWKLQ 446
sp|P05897|POL_SIVMK -----VLQKELLNSIGFSTPEE---KFQKDPFQWGMGYELWPTKWKLQ 446
sp|P12502|POL_SIVS4 -----VLQKELLNSIGFSTPEE---KFQKDPFQWGMGYELWPTKWKLQ 409
sp|P19505|POL_SIVS5 -----VLQKELLNSIGFSTPEE---KFQKDPFQWGMGYELWPTKWKLQ 412
sp|P15833|POL_HV2D2 -----VSQKELLNDMGFSTPEE---KFQKDPFQWGMGYELWPTKWKLQ 445
sp|P27980|POL_SIVAG -----VEQLRMKLSAWGLETPEK---KVQKPPYEWGMGYELWPHKWQIS 438
sp|P05895|POL_SIVAT -----VEQLRKLQAWGLETPEK---KVQKPPYEWGMGYELWPHKWQIS 454
sp|P27973|POL_SIVAI -----VQTLRNRLQEWGLETPEK---KVQREPPFEWGMGYELWPHKWQIS 433
sp|Q02836|POL_SIVAI -----VDIVRKMLLEKGLTTPDK---KVQREPPFEWGMGYELWPHKWQIS 436
sp|P22382|POL_SIVGB -----IVELRALLMTWNETPEK---KYQKEPPFHWMGYELHPDKWKIE 406
sp|P23427|POL_VILV2 -----VNELASYIAQYGFMLPED---KRQEGYPAKWLGFEHLPEKWKQF 383
sp|P35956|POL_VILVK -----VNELASYIAQYGFMLPED---KRQEGYPAKWLGFEHLPEKWKQF 379
sp|P03370|POL_VILV -----VNELASYIAQYGFMLPED---KRQEGYPAKWLGFEHLPEKWKQF 383
sp|P23426|POL_VILV1 -----VNELASYIAQYGFMLPED---KRQEGYPAKWLGFEHLPEKWKQF 383
sp|P16901|POL_OMVVS -----VEELASYIAQYGFMLPEE---KRQEGYPAKWLGFEHLPEKWKQF 364
sp|P33459|POL_CAEVC -----VKDLANVIAQYGFMLPEE---KRQEGYPAKWLGFEHLPEKWKQF 388
sp|P16088|POL_FIVPE -----VEELRKLWWGFTTPED---KLQEEPPYTWGMGYELHPLTWIQT 397
sp|P19028|POL_FIVSD -----VEELRKLWWGFTTPED---KLQEEPPYTWGMGYELHPLTWIQT 397
sp|P31822|POL_FIVT2 -----VEELRKLWWGFTTPED---KLQEEPPYTWGMGYELHPLTWIQT 396
sp|P11204|POL_EIAV9 -----IEELRAILLEEGFETPDD---KLQEVPPYVWLGQYQLCPENWVKVQ 427
sp|P32542|POL_EIAVC -----IEELRAILLEEGFETPDD---KLQEVPPYVWLGQYQLCPENWVKVQ 427
sp|P03371|POL_EIAVY -----IEELRAIL-KQGFETPDD---KLQEVPPYVWLGQYQLCPENWVKVQ 426
sp|P19199|POL_COYMV NIAFRKQLV-CPNYQIRRYLMDYLTLAETGLMWSSETGPAISELFTKMPAAIGER 787
sp|P27502|POL_RTBPV QRLAQREALNCDPTKIQPFMAEYLKKAESA---KKGFDVVYVERLFDRLPEAVGKV 685

sp|P19560|POL_BIV06 PRQLKIKN--PLTVNELQQLVGNVWVQPEVK-IPLYPLTDLLRD-----KTNLQ 442
sp|P19561|POL_BIV27 PRQLKIKN--PLTVNELQQLVGNVWVQPEVK-IPLYPLTDLLRD-----KTNLQ 442
sp|P20875|POL_HV1JR PIVLPEKD--SWTVNDIQKLVGKLNWASQIYAGIKVQKQCKLLRG-----TKALT 449
sp|P05961|POL_HV1MN PIVLPEKD--SWTVNDIQKLVGKLNWASQIYAGIKVQKQCKLLRG-----TKALT 448
sp|P03366|POL_HV1B1 PIVLPEKD--SWTVNDIQKLVGKLNWASQIYAGIKVQKQCKLLRG-----TKALT 457
sp|P03368|POL_HV1PV PIVLPEKD--SWTVNDIQKLVGKLNWASQIYAGIKVQKQCKLLRG-----TKALT 457
sp|P04585|POL_HV1H2 PIVLPEKD--SWTVNDIQKLVGKLNWASQIYAGIKVQKQCKLLRG-----TKALT 445
sp|P04587|POL_HV1B5 PIVLPEKD--SWTVNDIQKLVGKLNWASQIYAGIKVQKQCKLLRG-----TKALT 457
sp|P03367|POL_HV1BR PIVLPEKD--SWTVNDIQKLVGKLNWASQIYAGIKVQKQCKLLRG-----TKALT 457
sp|P05960|POL_HV1C4 -----
sp|P12498|POL_HV1J3 -----
sp|P12497|POL_HV1N5 PIVLPEKD--SWTVNDIQKLVGKLNWASQIYAGIKVQKQCKLLRG-----TKALT 445
sp|P35963|POL_HV1Y2 PIVLPEKD--SWTVNDIQKLVGKLNWASQIYAGIKVQKQCKLLRG-----TKALT 445
sp|P03369|POL_HV1A2 PIVLPEKD--SWTVNDIQKLVGKLNWASQIYAGIKVQKQCKLLRG-----TKALT 445
sp|P20892|POL_HV1OY PIVLPEKD--SWTVNDIQKLVGKLNWASQIYAGIKVQKQCKLLRG-----TKALT 445
sp|P05959|POL_HV1RH PIVLPEKD--SWTVNDIQKLVGKLNWASQIYAGIKVQKQCKLLRG-----TKALT 444
sp|P04589|POL_HV1EL SIKLPEKE--SWTVNDIQKLVGKLNWASQIYAGIKVQKQCKLLRG-----TKALT 444
sp|P12499|POL_HV1Z2 SIKLPEKE--SWTVNDIQKLVGKLNWASQIYAGIKVQKQCKLLRG-----TKALT 444
sp|P18802|POL_HV1ND PINLPEKE--SWTVNDIQKLVGKLNWASQIYAGIKVQKQCKLLRG-----TKALT 444
sp|P04588|POL_HV1MA PIQLPEKE--SWTVNDIQKLVGKLNWASQIYAGIKVQKQCKLLRG-----AKALT 444
sp|P24740|POL_HV1U4 PIQLPEKE--SWTVNDIQKLVGKLNWASQIYAGIKVQKQCKLLRG-----AKALT 444
sp|P17283|POL_SIVCZ PIQLPEKE--VWTVNDIQKLVGKLNWASQIYAGIKVQKQCKLLRG-----TKALT 469
sp|P17757|POL_HV2D1 KIQLPQKE--IWTVNDIQKLVGKLNWAAQIYPIGKIKTKHLCKLLRG-----KMTLT 511
sp|P18042|POL_HV2G1 KIQLPQKE--IWTVNDIQKLVGKLNWAAQIYPIGKIKTKHLCKLLRG-----KMTLT 487
sp|P18096|POL_HV2BE KIQLPQKE--IWTVNDIQKLVGKLNWAAQIYPIGKIKTKHLCKLLRG-----KMTLT 493
sp|P24107|POL_HV2CA KIQLPQKE--IWTVNDIQKLVGKLNWAAQIYPIGKIKTKHLCKLLRG-----KMTLT 473
sp|P05962|POL_HV2NZ KIQLPQKE--IWTVNDIQKLVGKLNWAAQIYPIGKIKTKHLCKLLRG-----KMTLT 473
sp|P04584|POL_HV2RO KIQLPQKE--IWTVNDIQKLVGKLNWAAQIYPIGKIKTKHLCKLLRG-----KMTLT 474
sp|Q74120|POL_HV2KR KIQLPQKE--IWTVNDIQKLVGKLNWAAQIYPIGKIKTKHLCKLLRG-----KMTLT 473

sp|P20876|POL_HV2ST RIQLPQKE--VWTVNDIQKLVGVLNWAQAQIYPGKIKTRNLRLIRG-----KMTLT 493
sp|P12451|POL_HV2SB KIQLPQKE--VWTVNDIQKLVGVLNWAQAQIYPGKIKTRHCKLIRG-----KMTPT 473
sp|P05896|POL_SIVM1 KIELPQRE--TWTVNDIQKLVGVLNWAQAQIYPGKIKTRHCKLIRG-----KMTLT 494
sp|P05897|POL_SIVM2 KIELPQRE--TWTVNDIQKLVGVLNWAQAQIYPGKIKTRHCKLIRG-----KMTLT 494
sp|P12502|POL_SIVS4 KIELPQRE--TWTVNDIQKLVGVLNWAQAQIYPGKIKTRHCKLIRG-----KMTLT 457
sp|P19505|POL_SIVS5 KIELPQRE--TWTVNDIQKLVGVLNWAQAQIYPGKIKTRHCKLIRG-----KMTLT 460
sp|P15833|POL_HV2D2 KIQLPEKE--VWTVNDIQKLVGVLNWAQAQIYPGKIKTRHCKLIRG-----KMTLT 493
sp|P27980|POL_SIVAG SIELEDEK--EWTVNDIQKLVGVLNWAQAQIYPGKIKTRHCKLIRG-----KKNLL 486
sp|P05895|POL_SIVAT RIQLEEKD--EWTVNDIQKLVGVLNWAQAQIYPGKIKTRHCKLIRG-----KKNLL 502
sp|P27973|POL_SIVA1 SIELEKKE--QWTVNDIQKLVGVLNWAQAQIYPGKIKTRHCKLIRG-----KKNLL 481
sp|Q02836|POL_SIVA1 KIELPLEG--EWTVNDIQKLVGVLNWAQAQIYPGKIKTRHCKLIRG-----KKNLL 485
sp|P22382|POL_SIVG2 KVQLPEAE--QPTVNDIQKLVGVLNWAQAQIYPGKIKTRHCKLIRG-----GLNLT 455
sp|P23427|POL_VILV2 KHTLPEITEGPTLNKQLKLVGDLVWR--QSLIGKSPINILKLMEG-----DRAIQ 432
sp|P35956|POL_VILV3 KHTLPEITEGPTLNKQLKLVGDLVWR--QSLIGKSPINILKLMEG-----DRAIQ 428
sp|P03370|POL_VILV KHTLPEITEGPTLNKQLKLVGDLVWR--QSLIGKSPINILKLMEG-----DRAIQ 432
sp|P23426|POL_VILV1 KHTLPEITEGPTLNKQLKLVGDLVWR--QSLIGKSPINILKLMEG-----DRAIQ 432
sp|P16901|POL_OMVVS KHTLPEITEGPTLNKQLKLVGDLVWR--QSLIGKSPINILKLMEG-----DRAIQ 413
sp|P33459|POL_CAEVC KHTLPELTKGTITLTKLQKLVGDLVWR--QSLIGKSPINILKLMEG-----DREIQ 437
sp|P16088|POL_FIVPE QKQL-DIPE-QPTLNELQKLVGDLVWR--QSLIGKSPINILKLMEG-----NQNLN 445
sp|P19028|POL_FIVSD QKQL-EIPE-KPTLNELQKLVGDLVWR--QSLIGKSPINILKLMEG-----NQNLN 445
sp|P31822|POL_FIVT2 QKQL-EIPE-RPTLNELQKLVGDLVWR--QSLIGKSPINILKLMEG-----DQKLD 444
sp|P11204|POL_EIAV9 KMQLDMVKN--PTLNDVQKLMGNITWSSGVPGLTVKHIAATTGK-----CLELN 475
sp|P32542|POL_EIAVC KMQLDMVKN--PTLNDVQKLMGNITWSSGVPGLTVKHIAATTGK-----CLELN 475
sp|P03371|POL_EIAVY KMQLDMVKN--PTLNDVQKLMGNITWSSGVPGLTVKHIAATTGK-----CLELN 474
sp|P19199|POL_COYMV VAAQYKIMDPTSAVNLPSRVYFTINYLTEQCKEASYMRSKALDFCRDFPIEGYYSRSGE 847
sp|P27502|POL_RTBPV VKADFKDGNYSYEAAGIGIYVSYSTWMAKCKIKTEAKTQKASLAFCR-----SITYTG 740

sp|P19560|POL_BIV06 EKIQLTPEAIKVEEENLKLKDPKWKDRIREGAEVLKIQMVPGRGIVFDLLQDGN----P 498
sp|P19561|POL_BIV27 EKIQLTPEAIKVEEENLKLKDPKWKDRIREGAEVLKIQMVPGRGIVFDLLQDGN----P 498
sp|P20875|POL_HV1JR EVIPLTEAELELAENREILKEPVHGVYDPSKDLIAEIQKQGGQGWTYQIYQEP-FKLN 508
sp|P05961|POL_HV1MN EVIPLTEAELELAENREILKEPVHGVYDPSKDLIAEIQKQGGQGWTYQIYQEP-FKLN 507
sp|P03366|POL_HV1B1 EVIPLTEAELELAENREILKEPVHGVYDPSKDLIAEIQKQGGQGWTYQIYQEP-FKLN 516
sp|P03368|POL_HV1PV EVIPLTEAELELAENREILKEPVHGVYDPSKDLIAEIQKQGGQGWTYQIYQEP-FKLN 516
sp|P04585|POL_HV1H2 EVIPLTEAELELAENREILKEPVHGVYDPSKDLIAEIQKQGGQGWTYQIYQEP-FKLN 504
sp|P04587|POL_HV1B5 EVIPLTEAELELAENREILKEPVHGVYDPSKDLIAEIQKQGGQGWTYQIYQEP-FKLN 516
sp|P03367|POL_HV1BR EVIPLTEAELELAENREILKEPVHGVYDPSKDLIAEIQKQGGQGWTYQIYQEP-FKLN 516
sp|P05960|POL_HV1C4 -----
sp|P12498|POL_HV1J3 -----
sp|P12497|POL_HV1N5 EVVPLTEAELELAENREILKEPVHGVYDPSKDLIAEIQKQGGQGWTYQIYQEP-FKLN 504
sp|P35963|POL_HV1Y2 EVIPLTEAELELAENREILKEPVHGVYDPSKDLIAEIQKQGGQGWTYQIYQEP-FKLN 504
sp|P03369|POL_HV1A2 EVIPLTEAELELAENREILKEPVHGVYDPSKDLIAEIQKQGGQGWTYQIYQEP-FKLN 504
sp|P20892|POL_HV1OY EVIPLTEAELELAENREILKEPVHGVYDPSKDLIAEIQKQGGQGWTYQIYQEP-FKLN 504
sp|P05959|POL_HV1RH EVVQLTKEAELELAENREILKEPVHGVYDPSKDLIAEIQKQGGQGWTYQIYQEP-FKLN 503
sp|P04589|POL_HV1EL EVIPLTEAELELAENREILKEPVHGVYDPSKDLIAEIQKQGGQGWTYQIYQEP-FKLN 503
sp|P12499|POL_HV1Z2 EVIPLTEAELELAENREILKEPVHGVYDPSKDLIAEIQKQGGQGWTYQIYQEP-FKLN 503
sp|P18802|POL_HV1ND EVVPLTEAELELAENREILKEPVHGVYDPSKDLIAEIQKQGGQGWTYQIYQEP-FKLN 503
sp|P04588|POL_HV1MA DIVPLTEAELELAENREILKEPVHGVYDPSKDLIAEIQKQGGQGWTYQIYQEP-FKLN 503
sp|P24740|POL_HV1U4 DIVPLTEAELELAENREILKEPVHGVYDPSKDLIAEIQKQGGQGWTYQIYQEP-FKLN 503
sp|P17283|POL_SIVCZ DVVPLTEAELELAENREIVSPPHGVYDPSKDLIAEIQKQGGQGWTYQIYQEP-FKLN 528
sp|P17757|POL_HV2D1 EEVQWTELAEAELLENKILSQQEQEGYQEEKELEATVQKQDNQWYKIHQ--ERVL 569
sp|P18042|POL_HV2G1 EEVQWTELAEAELLENKILSQQEQEGYQEEKELEATVQKQDNQWYKIHQ--EKIL 545
sp|P18096|POL_HV2BE EEVQWTELAEAELLENKILSQQEQEGYQEEKELEATVQKQDNQWYKIHQ--EKIL 551
sp|P24107|POL_HV2CA EEVQWTELAEAELLENKILSQQEQEGYQEEKELEATVQKQDNQWYKIHQ--EKIL 531
sp|P05962|POL_HV2NZ EEVQWTELAEAELLENKILSQQEQEGYQEEKELEATVQKQDNQWYKIHQ--EKIL 531
sp|P04584|POL_HV2R2 EEVQWTELAEAELLENKILSQQEQEGYQEEKELEATVQKQDNQWYKIHQ--EKIL 532
sp|Q74120|POL_HV2KR EEVQWTELAEAELLENKILSQQEQEGYQEEKELEATVQKQDNQWYKIHQ--EKIL 531
sp|P20876|POL_HV2ST EEVQWTELAEAELLENKILSQQEQEGYQEEKELEATVQKQDNQWYKIHQ--GKIL 551
sp|P12451|POL_HV2SB EEVQWTELAEAELLENKILSQQEQEGYQEEKELEATVQKQDNQWYKIHQ--EKIL 531
sp|P05896|POL_SIVM1 EEVQWTEMAEAEEYENKILSQQEQEGYQEEKELEATVQKQDNQWYKIHQ--DKIL 552
sp|P05897|POL_SIVM2 EAVQWTEMAEAEEYENKILSQQEQEGYQEEKELEATVQKQDNQWYKIHQ--DKIL 552
sp|P12502|POL_SIVS4 EEVQWTEMAEAEEYENKILSQQEQEGYQEEKELEATVQKQDNQWYKIHQ--DKVL 515
sp|P19505|POL_SIVS5 EEVQWTEMAEAEEYENKILSQQEQEGYQEEKELEATVQKQDNQWYKIHQ--DKIL 518
sp|P15833|POL_HV2D2 EEVQWTELAEAELLENKILSQQEQEGYQEEKELEATVQKQDNQWYKIHQ--NKVL 551
sp|P27980|POL_SIVAG ETVTVTEEAEEYENKILSQQEQEGYQEEKELEATVQKQDNQWYKIHQ--GQVL 544
sp|P05895|POL_SIVAT ELVAWTEEAEEYENKILSQQEQEGYQEEKELEATVQKQDNQWYKIHQ--GQVL 560
sp|P27973|POL_SIVA1 DVVEWTEEAEEYENKILSQQEQEGYQEEKELEATVQKQDNQWYKIHQ--GKIL 539
sp|Q02836|POL_SIVA1 EIVVWTEEAEEYENKILSQQEQEGYQEEKELEATVQKQDNQWYKIHQ--GAVL 543
sp|P22382|POL_SIVG2 EKVTMTTEEAELLEYQNKELAEQEGSYDPPNKELYVRFQKTTGGDISFQWQ--NKVL 513
sp|P23427|POL_VILV2 SERYESIHVREWEACRQKLEMEGN--YDDEEKDIYGQLDWG--NKAIEYVVFQ--KGKPL 489
sp|P35956|POL_VILV3 SERYESIHVREWEACRQKLEMEGN--YDDEEKDIYGQLDWG--NKAIEYVVFQ--KGKPL 485
sp|P03370|POL_VILV KHTLPEITEGPTLNKQLKLVGDLVWR--QSLIGKSPINILKLMEG-----DRAIQ 432
sp|P23426|POL_VILV1 SERYESIHVREWEACRQKLEMEGN--YDDEEKDIYGQLDWG--NKAIEYVVFQ--KGKPL 489
sp|P16901|POL_OMVVS SERRIELRHVKEWEECRKLEMEGN--YDDEEKDIYGQLDWG--DKAIEYVVFQ--RGKPL 470
sp|P33459|POL_CAEVC SERKIEEVHVKEWEECRKLEMEGN--YDDEEKDIYGQLDWG--DKAIEYVVFQ--KGKPL 474
sp|P16088|POL_FIVPE STROWTEARLEVQKAKKAEIEQVQLGYDPSKELYAKLSLVGPHQISYQVYQKDPKIL 505
sp|P19028|POL_FIVSD STREWTEARLEVQKAKKAEIEQVQLGYDPSKELYAKLSLVGPHQISYQVYQKDPKIL 505
sp|P31822|POL_FIVT2 SIREWTVAKREVQKAKAEIETQAQLNYYDPPNRGLYAKLSLVGPHQISYQVYQKDPKIL 504
sp|P11204|POL_EIAV9 QKVIWTEEAQKELEENNEKIKNAQGLQYNNPEEEMLCEVEITKNYEATYVIKQS--QGIL 533
sp|P32542|POL_EIAVC QKVIWTEEAQKELEENNEKIKNAQGLQYNNPEEEMLCEVEITKNYEATYVIKQS--QGIL 533
sp|P03371|POL_EIAVY QKVIWTEEAQKELEENNEKIKNAQGLQYNNPEEEMLCEVEITKNYEATYVIKQS--QGIL 532
sp|P19199|POL_COYMV KKKYARKATKYTGKAHDNHRVTKAKYQRCKCYICGQEGHYANQRNKHKDKQQRVAIL 907
sp|P27502|POL_RTBPV DYKRRKILKRVNTYNNKRRNRYRRPSIKKCRCYICQDENHLANRCPRTYNTQARASLI 800

sp|P19560|POL_BIV06 IWGGVKGLN-----YDHSNKIKILRTMNLNRTV 528
sp|P19561|POL_BIV27 IWGGVKGLN-----YDHSNKIKILRTMNLNRTV 528
sp|P20875|POL_HV1JR KTGKYARTR-----GAHTNDVKQLTEAVQKIANES 538
sp|P05961|POL_HV1MN KTGKYARMR-----GAHTNDVKQLTEAVQKIATES 537
sp|P03366|POL_HV1B1 KTGKYARMR-----GAHTNDVKQLTEAVQKITTES 546
sp|P03368|POL_HV1PV KTGKYARMR-----GAHTNDVKQLTEAVQKITTES 546
sp|P04585|POL_HV1H2 KTGKYARMR-----GAHTNDVKQLTEAVQKITTES 534
sp|P04587|POL_HV1B5 KTGKYARMR-----GAHTNDVKQLTEAVQKITTES 546
sp|P03367|POL_HV1BR KTGKYARTR-----GAHTNDVKQLTEAVQKITTES 546
sp|P05960|POL_HV1C4 -----
sp|P12498|POL_HV1J3 -----
sp|P12497|POL_HV1N5 KTGKYARMK-----GAHTNDVKQLTEAVQKIATES 534
sp|P35963|POL_HV1Y2 KTGKYARTR-----GAHTNDVKQLTEAVQKIATES 534
sp|P03369|POL_HV1A2 KTGKYARMR-----GAHTNDVKQLTEAVQKVSTES 534
sp|P20892|POL_HV1OY KTGKYARMR-----GAHTNDVKQLTEAVQKITTES 534
sp|P05959|POL_HV1RH KTGKYARMR-----GAHTNDVKQLTEAVQKVATES 533
sp|P04589|POL_HV1EL KTGKYARMR-----GAHTNDVKQLAEAVQKISTES 533
sp|P12499|POL_HV1Z2 KTGKYARMR-----GAHTNDVKQLAEAVQKISTES 533
sp|P18802|POL_HV1ND KTGKYARTR-----GAHTNDVKQLTEAVQKIATES 533

sp|P04588|POL_HV1MA KTGKYARIK-----SAHTNDVKQLTEAVQKIAQES 533
 sp|P24740|POL_HV1U4 KTGKYARKR-----SAHTNDVKQLTEVQKVSTES 533
 sp|P17283|POL_SIVCZ KTGKYARQR-----SAHTNDIRQLAEAQKIAQES 558
 sp|P17757|POL_HV2D1 KVGKYARIK-----NHTNGVRLLAQVQKIGKEA 599
 sp|P18042|POL_HV2G1 KVGKYARIK-----NHTNGVRLLAQVQKIGKEA 575
 sp|P18096|POL_HV2BE KVGKYARIK-----NHTNGVRLLAQVQKIGKEA 581
 sp|P24107|POL_HV2CA KVGKYARIK-----HTHTNGVRLLAQVQKIGKEA 561
 sp|P05962|POL_HV2NZ KGGKICKDK-----KYPYQVRVLLAQVQKIGKEA 561
 sp|P04584|POL_HV2RO KVGKYAKVK-----NHTNGIRLLAQVQKIGKEA 562
 sp|Q74120|POL_HV2KR KVGKYAKIK-----NHTNGVRLLAHVQKIGKEA 561
 sp|P20876|POL_HV2ST KVGKYAKVK-----NHTNGVRLLAQVQKIGKEA 581
 sp|P12451|POL_HV2SB KVGKYARIK-----NHTNGVRLLAQVQKIGKEA 561
 sp|P05896|POL_SIVM1 KVGKFAKIK-----NHTNGVRLLAHVQKIGKEA 582
 sp|P05897|POL_SIVM2 KVRKFAKIK-----NHTNGVRLLAHVQKIGKEA 582
 sp|P12502|POL_SIVS4 KVGKFAKVK-----NHTNGVRLLAHVQKIGKEA 545
 sp|P19505|POL_SIVS5 KVGKFAKIK-----NHTNGVRLLAHVQKIGKEA 548
 sp|P15833|POL_HV2D2 KVGKYAKVK-----NHTNGVRLLAHVQKIGKEA 581
 sp|P27980|POL_SIVAG KVGKYTKQK-----NHTNEFRVLAGLVQKICKES 574
 sp|P05895|POL_SIVAT KVGKYTKQK-----NHTNELRRLAGLVQKICKES 590
 sp|P27973|POL_SIVA1 KVGKFAKQK-----ATHNELRRLAGLVQKIGKEA 569
 sp|Q02836|POL_SIVA1 KVGRYAKQR-----ETHNDRRLAHLVQKICKES 573
 sp|P22382|POL_SIVGB RAGKYGKQK-----TAHSNDLMLKLAGATQKVGRES 543
 sp|P23427|POL_VILV2 WVNNVHSIK-----NLSQ--AQQIKAAQKLTQEV 517
 sp|P35956|POL_VILVK WVNNVHSIK-----NLSQ--AQQIKAAQKLTQEV 513
 sp|P03370|POL_VILV WVNNVHSIK-----NLSQ--AQQIKAAQKLTQEV 517
 sp|P23426|POL_VILV1 WVNNVHSIK-----NLSQ--AQQIKAAQKLTQEV 517
 sp|P16901|POL_OMVVS WVNNVHNIK-----NLSQ--SQQIKAAQKLTQEV 498
 sp|P33459|POL_CAEVC WVNNVHNIK-----NLSI--PQQVIAAAQKLTQEV 522
 sp|P16088|POL_FIVPE WYGKMSRQK-----KKAENTCDIALRACYKIREES 535
 sp|P19028|POL_FIVSD WYGKMSRQK-----KKAENTCDIALRACYKIREES 535
 sp|P31822|POL_FIVT2 WYGINRQK-----KKAENTCDIALRACYKIREES 534
 sp|P11204|POL_EIAV9 WAGKIMKA-----NKGWSTVKNLMLLQHVATES 563
 sp|P32542|POL_EIAVC WAGKIMKA-----NKGWSTVKNLMLLQHVATES 563
 sp|P03371|POL_EIAVY WAGKIMKA-----NKGWSTVKNLMLLQHVATES 562
 sp|P19199|POL_COVMY QSLDLKENEVVSADDKEEEDDEIFSVLGEEDYQEETIMVLEEDDIQQIHKFSKFGDLS 967
 sp|P27502|POL_RTBPV DGLDEDIVS-----IASDDEIDENFLEHDEFIA 831

sp|P19560|POL_BIV06 -----VIMTGREASFLLPSSSEDWEAALQKEESLTIQFPVKFYRHSCRWT 573
 sp|P19561|POL_BIV27 -----VIMTGREASFLLPSSSEDWEAALQKEESLTIQFPVKFYRHSCRWT 573
 sp|P20875|POL_HV1JR -----IWIWGKIPKFKLPIQKETWETWWTWTEYWQATWIPEWEFVNTPLVK 583
 sp|P05961|POL_HV1MN -----IWIWGKTPKFKLPIQKETWETWWTWTEYXATWIPEWEFVNTPLVK 582
 sp|P03366|POL_HV1B1 -----IWIWGKTPKFKLPIQKETWETWWTWTEYWQATWIPEWEFVNTPLVK 591
 sp|P03368|POL_HV1PV -----IWIWGKTPKFKLPIQKETWETWWTWTEYWQATWIPEWEFVNTPLVK 591
 sp|P04585|POL_HV1H2 -----IWIWGKTPKFKLPIQKETWETWWTWTEYWQATWIPEWEFVNTPLVK 579
 sp|P04587|POL_HV1B5 -----IWIWGKTPKFKLPIQKETWETWWTWTEYWQATWIPEWEFVNTPLVK 591
 sp|P03367|POL_HV1BR -----IWIWGKTPKFKLPIQKETWETWWTWTEYWQATWIPEWEFVNTPLVK 591
 sp|P05960|POL_HV1C4 -----
 sp|P12498|POL_HV1J3 -----
 sp|P12497|POL_HV1N5 -----IWIWGKTPKFKLPIQKETWEAWWTEYWQATWIPEWEFVNTPLVK 579
 sp|P35963|POL_HV1Y2 -----IWIWGKTPKFKLPIQKETWETWWTWTEYWQATWIPEWEFVNTPLVK 579
 sp|P03369|POL_HV1A2 -----IWIWGKIPKFKLPIQKETWEAWWTEYWQATWIPEWEFVNTPLVK 579
 sp|P20892|POL_HV1OY -----IWIWGKTPKFKLPIQKETWEAWWTEYWQATWIPEWEFVNTPLVK 579
 sp|P05959|POL_HV1RH -----IWIWGKTPKFKLPIQKETWEAWWTEYWQATWIPEWEFVNTPLVK 578
 sp|P04589|POL_HV1EL -----IWIWGRTPKFKLPIQKETWETWWEAYWQATWIPEWEFVNTPLVK 578
 sp|P12499|POL_HV1Z2 -----IWIWGKTPKFKLPIQKETWETWWTWTEYWQATWIPEWEFVNTPLVK 578
 sp|P18802|POL_HV1ND -----IWIWGKTPKFKLPIQKETWETWWTWTEYWQATWIPEWEFVNTPLVK 578
 sp|P04588|POL_HV1MA -----IWIWGKTPKFKLPIQKETWEAWWTEYWQATWIPEWEFVNTPLVK 578
 sp|P24740|POL_HV1U4 -----IWIWGKIPKFKLPIQKETWEAWWTEYWQATWIPEWEFVNTPLVK 578
 sp|P17283|POL_SIVCZ -----IWIWGKTPKFKLPIQKESWEAWWTEYWQATWIPEWEFVNTPLVK 603
 sp|P17757|POL_HV2D1 -----LVIWGRVPKFHLPERDTEWQWWDNYWQVTVWPEWDFVSTPLVR 644
 sp|P18042|POL_HV2G1 -----LVIWGRIPKFKLPERETWEQWWDNYWQVTVWPEWDFVSTPLVR 620
 sp|P18096|POL_HV2BE -----LVIWGRIPKFKLPERETWEQWWDNYWQVTVWPEWDFVSTPLVR 626
 sp|P24107|POL_HV2CA -----LVIG-RIPKFKLPEREVWEQWWDNYWQVTVWIPDWFVSTPLVR 605
 sp|P05962|POL_HV2NZ -----LVIWGRIPKFKLPERDTEWQWWDNYWQVTVWIPDWFVSTPLVR 606
 sp|P04584|POL_HV2RO -----LVIWGRIPKFKLPEREWEQWWDNYWQVTVWIPDWFVSTPLVR 607
 sp|Q74120|POL_HV2KR -----LVIWGRIPKFKLPERETWEQWWDNYWQVTVWIPDWFVSTPLVR 606
 sp|P20876|POL_HV2ST -----LVIWGRIPKFKLPERDTEWQWWDNYWQVTVWIPDWFVSTPLVR 626
 sp|P12451|POL_HV2SB -----LVIWGRIPKFKLPERETWEQWWDNYWQVTVWIPDWFVSTPLVR 606
 sp|P05896|POL_SIVM1 -----IWIWQVPKFKLPEREDVWEQWWDNYWQVTVWIPDWFVSTPLVR 627
 sp|P05897|POL_SIVM2 -----IWIWQVPKFKLPEREDVWEQWWDNYWQVTVWIPDWFVSTPLVR 627
 sp|P12502|POL_SIVS4 -----LVIWGEVPKFKLPEREWEQWWDNYWQVTVWIPDWFVSTPLVR 590
 sp|P19505|POL_SIVS5 -----IWIWQVPRFKLPEREWEQWWDNYWQVTVWIPDWFVSTPLVR 593
 sp|P15833|POL_HV2D2 -----LVIWGEIPVFKLPERETWQWWDNYWQVTVWIPDWFVSTPLVR 626
 sp|P27980|POL_SIVAG -----LVIWGEIPVLEPIEREVWEQWWDNYWQVTVWIPDWFVSTPLVR 619
 sp|P05895|POL_SIVAT -----LVIWGEIPVLEPIEREVWEQWWDNYWQVTVWIPDWFVSTPLVR 635
 sp|P27973|POL_SIVA1 -----LVIWGLPTFELPVERDTEWQWWDNYWQVTVWIPDWFVSTPLVR 614
 sp|Q02836|POL_SIVA1 -----LTIWGRRLPRVQLPVDKKTWDMWWDNYWQVTVWIPDWFVSTPLVR 618
 sp|P22382|POL_SIVGB -----IWIWGFVPMQIPTTREIWEWWDNYWQVTVWIPDWFVSTPLVR 588
 sp|P23427|POL_VILV2 -----IIRTGKIPWILLPGREEDWILELQMGNNINWMPFSWCSYKGSVRWK 562
 sp|P35956|POL_VILVK -----IIRTGKIPWILLPGREEDWILELQMGNNINWMPFSWCSYKGSVRWK 558
 sp|P03370|POL_VILV -----IIRTGKIPWILLPGREEDWILELQMGNNINWMPFSWCSYKGSVRWK 562
 sp|P23426|POL_VILV1 -----IIRTGKIPWILLPGREEDWILELQMGNNINWMPFSWCSYKGSVRWK 562
 sp|P16901|POL_OMVVS -----IIRIGKIPWILLPGKEEDWILELQGNITWMPFSWCSYRGSIRWK 543
 sp|P33459|POL_CAEVC -----IIRTGKIPWILLPGKEEDWILELQGNITWMPFSWCSYRGRHTRWR 567
 sp|P16088|POL_FIVPE -----IIRIGKEPRYEIPTSREAWESNLINSPYLKAPPEVEYIHAALNI 580
 sp|P19028|POL_FIVSD -----IIRIGKEPRYEIPTSREAWESNLINSPYLKAPPEVEYIHAALNI 580
 sp|P31822|POL_FIVT2 -----IIRIGKEPRYEIPTSREAWESNLINSPYLKAPPEVEYIHAALSI 579
 sp|P11204|POL_EIAV9 -----ITRVGKCPTEFKVPFTKEQVMWEMQKQ-WYYSWLPEIVYTHQVVDH 607
 sp|P32542|POL_EIAVC -----ITRVGKCPTEFKVPFTKEQVMWEMQKQ-WYYSWLPEIVYTHQVVDH 607
 sp|P03371|POL_EIAVY -----ITRVGKCPTEFKVPFTKEQVMWEMQKQ-WYYSWLPEIVYTHQVVDH 606
 sp|P19199|POL_COVMY RRVNVPNFGPAEVMGLPKSSWRRPIQATLEINCHHNWTAISTQLACRSCKQFLA 1027
 sp|P27502|POL_RTBPV -----HSSQEHEHTWEIGKDKVCEISYFTDYNKTVSCKTCETQYCKT 876

sp|P19560|POL_BIV06 -----SICGPVR-----ENLTTYTDGKKK--KTAADVWCEG--RTKSKVFP 614
 sp|P19561|POL_BIV27 -----SICGPVR-----ENLTTYTDGKKK--KTAADVWCEG--RTKSKVFP 614
 sp|P20875|POL_HV1JR -----LWYQLE--KEPIVGAETFYVDGAANRETKLKGAGYVTRGRQKVVSLTDT 631
 sp|P05961|POL_HV1MN -----LWYQLE--KEPIVGAETFYVDGAANRETKLKGAGYVTRGRQKVVSLTDT 630
 sp|P03366|POL_HV1B1 -----LWYQLE--KEPIVGAETFYVDGAANRETKLKGAGYVTRGRQKVVPLTNT 639
 sp|P03368|POL_HV1PV -----LWYQLE--KEPIVGAETFYVDGAANRETKLKGAGYVTRGRQKVVPLTNT 639
 sp|P04585|POL_HV1H2 -----LWYQLE--KEPIVGAETFYVDGAANRETKLKGAGYVTRGRQKVVTLTDT 627
 sp|P04587|POL_HV1B5 -----LWYQLE--KEPIVGAETFYVDGAANRETKLKGAGYVTRGRQKVVTLTDT 639
 sp|P03367|POL_HV1BR -----LWYQLE--KEPIVGAETFYVDGAANRETKLKGAGYVTRGRQKVVTLTDT 639

sp|P05960|POL_HV1C4
sp|P12498|POL_HV1J3
sp|P12497|POL_HV1N5 -----LWYQLE--KEPIGAETFFYVDGAANRETKLKGAGYVTDGRGKQVPLTDT 627
sp|P35963|POL_HV1Y2 -----LWYQLE--KEPIGAETFFYVDGAANRETKLKGAGYVTDGRGKQVPLTDT 627
sp|P03369|POL_HV1A2 -----LWYQLE--KEPIVGAETFFYVDGAANRETKLKGAGYVTDGRGKQVSIADT 627
sp|P20892|POL_HV1OY -----LWYQLE--KDPIVGAETFFYVDGAANRETKLKGAGYVTDGRGKQVSLTDT 627
sp|P05959|POL_HV1RH -----LWYQLE--KEPIGAETFFYVDGAANRETKLKGAGYVTDGRGKQVPLTDT 626
sp|P04589|POL_HV1EL -----LWYQLE--KEPIGAETFFYVDGAANRETKLKGAGYVTDGRGKQVPLTDT 626
sp|P12499|POL_HV1Z2 -----LWYQLE--KEPIGAETFFYVDGAANRETKLKGAGYVTDGRGKQVPLTDT 626
sp|P18802|POL_HV1ND -----LWYQLE--KEPIGAETFFYVDGAANRETKLKGAGYVTDGRGKQVPLTDT 626
sp|P04588|POL_HV1MA -----LWYQLE--TEPIVGAETFFYVDGAANRETKLKGAGYVTDGRGKQVSLTET 626
sp|P24740|POL_HV1U4 -----LWYQLE--KDPIGAETFFYVDGAANRETKLKGAGYVTDGRGKQVSLTET 626
sp|P17283|POL_SIVCZ -----LWYSLE--TEPIPTDTYVDGAANRETKLKGAGYVTDGKQKQISLENT 651
sp|P17757|POL_HV2D1 -----LTFNVL--GDPIPGTETFFYTDGSCNRQSKGKAGYVTDGRDRVRVLEQT 692
sp|P18042|POL_HV2G1 -----LTFNVL--GDPIVGAETFFYTDGSCNRQSKGKAGYVTDGRGKDKVRLERT 668
sp|P18096|POL_HV2BE -----LTFNVL--GDPIVGAETFFYTDGSCNRQSKGKAGYVTDGRGKDKVRLERT 674
sp|P24107|POL_HV2CA -----LAFNVL--GDPIPGTETFFYTDGSCNRQSKGKAGYVTDGRGKDKVLEQT 653
sp|P05962|POL_HV2NZ -----LAFNVL--GEPVPGAETFFYTDGSCNRQSKGKAGYVTDGRGKDKVLEQT 654
sp|P04584|POL_HV2RO -----LAFNVL--GDPIVGAETFFYTDGSCNRQSKGKAGYVTDGRGKDKVLEQT 655
sp|Q74120|POL_HV2KR -----LAFNVL--KDPIVGAETFFYTDGSCNRQSKGKAGYVTDGRGKDKVLEQT 654
sp|P20876|POL_HV2ST -----LAFNVL--KDPIVGAETFFYTDGSCNRQSKGKAGYVTDGRGKDKVLEQT 674
sp|P12451|POL_HV2SB -----LAFNVL--KDPIVGAETFFYTDGSCNRQSKGKAGYVTDGRGKDKVLEQT 654
sp|P05896|POL_SIVM1 -----LAFNVL--KDPIVGAETFFYTDGSCNRQSKGKAGYVTDGRGKDKVLEQT 675
sp|P05897|POL_SIVM2 -----LAFNVL--KDPIVGAETFFYTDGSCNRQSKGKAGYVTDGRGKDKVLEQT 674
sp|P12502|POL_SIVS4 -----LAFNVL--KEPIVGAETFFYTDGSCNRQSKGKAGYVTDGRGKDKVLEQT 638
sp|P19505|POL_SIVS5 -----LAFNVL--KEPIVGAETFFYTDGSCNRQSKGKAGYVTDGRGKDKVLEQT 641
sp|P15833|POL_HV2D2 -----LAFNVL--KDPIVGAETFFYTDGSCNRQSKGKAGYVTDGRGKDKVLEQT 674
sp|P27980|POL_SIVAG -----LWYTLT--KEPIKEDVYVVDGACNRNSREGKAGYITQYKQVLENT 667
sp|P05895|POL_SIVAT -----LWYTLT--KEPIKEDVYVVDGACNRNSREGKAGYITQYKQVLENT 682
sp|P27973|POL_SIVA1 -----LWYTLT--KEPIKEDVYVVDGACNRNSREGKAGYITQYKQVLENT 662
sp|Q02836|POL_SIVA2 -----LWYTLT--KEPIKEDVYVVDGACNRNSREGKAGYITQYKQVLENT 666
sp|P22382|POL_SIVGB -----EWYSLV--PEPLEGVEYVVDGAANRDSKMGKAGYITDRGFQVVEYENT 636
sp|P23427|POL_VILV2 -----KRVN---IAEVVPGPTYYTDGGKKNRGS--LGYIATGKFRHIEE-G 605
sp|P35956|POL_VILV3 -----KRVN---IAEVVPGPTYYTDGGKKNRGS--LGYIATGKFRHIEE-G 601
sp|P03370|POL_VILV4 -----KRVN---IAEVVPGPTYYTDGGKKNRGS--LGYIATGKFRHIEE-G 605
sp|P23426|POL_VILV1 -----KRVN---IAEVVPGPTYYTDGGKKNRGS--LGYIATGKFRHIEE-G 605
sp|P16901|POL_OMVVS -----KRVN---ITEVVEGPTYYTDGGKKNRGS--LGYIATGKFRHIEE-G 586
sp|P33459|POL_CAIEVC -----KRVN---ITEVVEGPTYYTDGGKKNRGS--LGYIATGKFRHIEE-G 610
sp|P16088|POL_FIVPE -----KRALSMIKDAPIGAETWYIDGGRKLGKAAK--AAYWTDGKWRVMDLE-G 628
sp|P19028|POL_FIVSD -----KRALSMIKDAPIGAETWYIDGGRKLGKAAK--AAYWTDGKWRVMDLE-G 628
sp|P31822|POL_FIVT2 -----KRALSMIQDAPIGAETWYIDGGRKLGKAAK--AAYWTDGKWRVMDLE-G 627
sp|P11204|POL_EIAV9 -----DWRMK--LVEEPTSGITTYTDGGKQNGEGI--AAYVTSNGRTKQKRLGPV 653
sp|P32542|POL_EIAVC -----DWRMK--LVEEPTSGITTYTDGGKQNGEGI--AAYVTSNGRTKQKRLGPV 653
sp|P03371|POL_EIAV5 -----DWRMK--LVEEPTSGITTYTDGGKQNGEGI--AAYVTSNGRTKQKRLGPV 652
sp|P19199|POL_COYMV GYVCHHCHAVYCFMCAEAYHDVQAEKILSKDYSFARGKKGKAVHIEEDEIEGFLISQL 1087
sp|P27502|POL_RTBPV CS-----DQLALEVTEVKKPKTEETMIDDLKLVNKNLEFRVTLKHEKVMQNLQDKFE 929

sp|P19560|POL_BIV06 TNQQAELKAICMALLDGPCK----MNIITDSRYAYEGMREE--PETWAREGIWLEIAKIL 668
sp|P19561|POL_BIV27 TNQQAELKAICMALLDGPCK----MNIITDSRYAYEGMREE--PETWAREGIWLEIAKIL 668
sp|P20875|POL_HV1JR TNQKTELQAIHLALQDSGLE-----VNIIVTDSQYALGHIQA--QPKDSESELVSNQHEQL 684
sp|P05961|POL_HV1MN TNQKTELQAIHLALQDSGLE-----VNIIVTDSQYALGHIQA--QPKDSESELVSNQHEQL 683
sp|P03366|POL_HV1B1 TNQKTELQAIHLALQDSGLE-----VNIIVTDSQYALGHIQA--QPKDSESELVSNQHEQL 692
sp|P03368|POL_HV1PV TNQKTELQAIHLALQDSGLE-----VNIIVTDSQYALGHIQA--QPKDSESELVSNQHEQL 692
sp|P04585|POL_HV1H2 TNQKTELQAIHLALQDSGLE-----VNIIVTDSQYALGHIQA--QPKDSESELVSNQHEQL 680
sp|P04587|POL_HV1B5 TNQKTELQAIHLALQDSGLE-----VNIIVTDSQYALGHIQA--QPKDSESELVSNQHEQL 692
sp|P03367|POL_HV1BR TNQKTELQAIHLALQDSGLE-----VNIIVTDSQYALGHIQA--QPKDSESELVSNQHEQL 692
sp|P05960|POL_HV1C4
sp|P12498|POL_HV1J3
sp|P12497|POL_HV1N5 TNQKTELQAIHLALQDSGLE-----VNIIVTDSQYALGHIQA--QPKDSESELVSNQHEQL 680
sp|P35963|POL_HV1Y2 TNQKTELQAIHLALQDSGLE-----VNIIVTDSQYALGHIQA--QPKDSESELVSNQHEQL 680
sp|P03369|POL_HV1A2 TNQKTELQAIHLALQDSGLE-----VNIIVTDSQYALGHIQA--QPKDSESELVSNQHEQL 680
sp|P20892|POL_HV1OY TNQKTELQAIHLALQDSGLE-----VNIIVTDSQYALGHIQA--QPKDSESELVSNQHEQL 680
sp|P05959|POL_HV1RH TNQKTELQAIHLALQDSGLE-----VNIIVTDSQYALGHIQA--QPKDSESELVSNQHEQL 679
sp|P04589|POL_HV1EL TNQKTELQAIHLALQDSGLE-----VNIIVTDSQYALGHIQA--QPKDSESELVSNQHEQL 679
sp|P12499|POL_HV1Z2 TNQKTELQAIHLALQDSGLE-----VNIIVTDSQYALGHIQA--QPKDSESELVSNQHEQL 679
sp|P18802|POL_HV1ND TNQKTELQAIHLALQDSGLE-----VNIIVTDSQYALGHIQA--QPKDSESELVSNQHEQL 679
sp|P04588|POL_HV1MA TNQKTELQAIHLALQDSGLE-----VNIIVTDSQYALGHIQA--QPKDSESELVSNQHEQL 679
sp|P24740|POL_HV1U4 TNQKTELQAIHLALQDSGLE-----VNIIVTDSQYALGHIQA--QPKDSESELVSNQHEQL 679
sp|P17283|POL_SIVCZ TNQQAELKALLALQDSGPK-----VNIIVDSQYVLMGIVAG--QPTSESNRIVNQHEEM 704
sp|P17757|POL_HV2D1 SNQQAELKALLALQDSGPK-----VNIIVDSQYVLMGIVAG--QPTSESNRIVNQHEEM 745
sp|P18042|POL_HV2G1 TNQQAELKALLALQDSGPK-----VNIIVDSQYVLMGIVAG--QPTSESNRIVNQHEEM 721
sp|P18096|POL_HV2BE TNQQAELKALLALQDSGPK-----VNIIVDSQYVLMGIVAG--QPTSESNRIVNQHEEM 727
sp|P24107|POL_HV2CA TNQQAELKALLALQDSGPK-----VNIIVDSQYVLMGIVAG--QPTSESNRIVNQHEEM 706
sp|P05962|POL_HV2NZ TNQQAELKALLALQDSGPK-----VNIIVDSQYVLMGIVAG--QPTSESNRIVNQHEEM 707
sp|P04584|POL_HV2RO TNQQAELKALLALQDSGPK-----VNIIVDSQYVLMGIVAG--QPTSESNRIVNQHEEM 708
sp|Q74120|POL_HV2KR TNQQAELKALLALQDSGPK-----VNIIVDSQYVLMGIVAG--QPTSESNRIVNQHEEM 707
sp|P20876|POL_HV2ST TNQQAELKALLALQDSGPK-----VNIIVDSQYVLMGIVAG--QPTSESNRIVNQHEEM 727
sp|P12451|POL_HV2SB TNQQAELKALLALQDSGPK-----VNIIVDSQYVLMGIVAG--QPTSESNRIVNQHEEM 707
sp|P05896|POL_SIVM1 TNQQAELKALLALQDSGPK-----VNIIVDSQYVLMGIVAG--QPTSESNRIVNQHEEM 728
sp|P05897|POL_SIVM2 TNQQAELKALLALQDSGPK-----VNIIVDSQYVLMGIVAG--QPTSESNRIVNQHEEM 727
sp|P12502|POL_SIVS4 TNQQAELKALLALQDSGPK-----VNIIVDSQYVLMGIVAG--QPTSESNRIVNQHEEM 691
sp|P19505|POL_SIVS5 TNQQAELKALLALQDSGPK-----VNIIVDSQYVLMGIVAG--QPTSESNRIVNQHEEM 694
sp|P15833|POL_HV2D2 TNQQAELKALLALQDSGPK-----VNIIVDSQYVLMGIVAG--QPTSESNRIVNQHEEM 727
sp|P27980|POL_SIVAG TNQQAELKALLALQDSGPK-----VNIIVDSQYVLMGIVAG--QPTSESNRIVNQHEEM 720
sp|P05895|POL_SIVAT TNQQAELKALLALQDSGPK-----VNIIVDSQYVLMGIVAG--QPTSESNRIVNQHEEM 735
sp|P27973|POL_SIVA1 TNQQAELKALLALQDSGPK-----VNIIVDSQYVLMGIVAG--QPTSESNRIVNQHEEM 715
sp|Q02836|POL_SIVA2 TNQQAELKALLALQDSGPK-----VNIIVDSQYVLMGIVAG--QPTSESNRIVNQHEEM 719
sp|P22382|POL_SIVGB TNQQAELKALLALQDSGPK-----VNIIVDSQYVLMGIVAG--QPTSESNRIVNQHEEM 689
sp|P23427|POL_VILV2 TNQQAELKALLALQDSGPK-----VNIIVDSQYVLMGIVAG--QPTSESNRIVNQHEEM 660
sp|P35956|POL_VILV3 TNQQAELKALLALQDSGPK-----VNIIVDSQYVLMGIVAG--QPTSESNRIVNQHEEM 656
sp|P03370|POL_VILV4 TNQQAELKALLALQDSGPK-----VNIIVDSQYVLMGIVAG--QPTSESNRIVNQHEEM 660
sp|P23426|POL_VILV1 TNQQAELKALLALQDSGPK-----VNIIVDSQYVLMGIVAG--QPTSESNRIVNQHEEM 660
sp|P16901|POL_OMVVS TNQQAELKALLALQDSGPK-----VNIIVDSQYVLMGIVAG--QPTSESNRIVNQHEEM 641
sp|P33459|POL_CAIEVC TNQQAELKALLALQDSGPK-----VNIIVDSQYVLMGIVAG--QPTSESNRIVNQHEEM 665
sp|P16088|POL_FIVPE SNQQAELKALLALQDSGPK-----VNIIVDSQYVLMGIVAG--QPTSESNRIVNQHEEM 680
sp|P19028|POL_FIVSD SNQQAELKALLALQDSGPK-----VNIIVDSQYVLMGIVAG--QPTSESNRIVNQHEEM 680
sp|P31822|POL_FIVT2 SNQQAELKALLALQDSGPK-----VNIIVDSQYVLMGIVAG--QPTSESNRIVNQHEEM 679
sp|P11204|POL_EIAV9 TNQQAELKALLALQDSGPK-----VNIIVDSQYVLMGIVAG--QPTSESNRIVNQHEEM 708
sp|P32542|POL_EIAVC THQVAERMAIQMALEDTRDKQ-----VNIIVDSQYVLMGIVAG--QPTSESNRIVNQHEEM 708
sp|P03371|POL_EIAV5 THQVAERMAIQMALEDTRDKQ-----VNIIVDSQYVLMGIVAG--QPTSESNRIVNQHEEM 707
sp|P19199|POL_COYMV THQVAERMAIQMALEDTRDKQ-----VNIIVDSQYVLMGIVAG--QPTSESNRIVNQHEEM 707
sp|P27502|POL_RTBPV TMQIRNKSEITEIPTSLAMRANESNYIKTSINKTAGCYVETKISFNENRITIALIDSG 989

sp|P19560|POL_BIV06 PFKQYVGVGWPVPAHKGIGGN---TEADEGVKKALEQMAPCSPPEAILLKPGEKQNLGTG- 724
sp|P19561|POL_BIV27 PFKQYVGVGWPVPAHKGIGGN---TEADEGVKKALEQMAPCSPPEAILLKPGEKQNLGTG- 724
sp|P20875|POL_HV1JR IKKEKVYLAWVPAHKGIGGN---EQVDKLVSA GIRKVL----- 719
sp|P05961|POL_HV1MN IKKEKVYLAWVPAHKGIGGN---EQVDKLVSA GIRKVL----- 718
sp|P03366|POL_HV1B1 IKKEKVYLAWVPAHKGIGGN---EQVDKLVSA GIRKIL----- 727
sp|P03368|POL_HV1PV IKKQKVYLAWVPAHKGIGGN---EQVDKLVSA GIRKIL----- 727
sp|P04585|POL_HV1H2 IKKEKVYLAWVPAHKGIGGN---EQVDKLVSA GIRKVL----- 715
sp|P04587|POL_HV1B5 IKKEKVYLAWVPAHKGIGGN---EQVDKLVSA GIRKIL----- 727
sp|P03367|POL_HV1BR IKKEKVYLAWVPAHKGIGGN---EQVDKLVSA GIRKVL----- 727
sp|P05960|POL_HV1C4 -----
sp|P12498|POL_HV1J3 -----
sp|P12497|POL_HV1N5 IKKEKVYLAWVPAHKGIGGN---EQVDGLVSA GIRKVL----- 715
sp|P35963|POL_HV1Y2 IKKEKVYLAWVPAHKGIGGN---EQVDKLVSA GIRKVL----- 715
sp|P03369|POL_HV1A2 IKKEKVYLAWVPAHKGIGGN---EQVDKLVSA GIRKVL----- 715
sp|P20892|POL_HV1OY IKKEKVYLAWVPAHKGIGGN---EQVDKLVSA GIRKVL----- 715
sp|P05959|POL_HV1RH IKKEKVYLAWVPAHKGIGGN---EQVDRLVSTGIRKVL----- 714
sp|P04589|POL_HV1EL IKKEKVYLAWVPAHKGIGGN---EQVDKLVSA GIRKVL----- 714
sp|P12499|POL_HV1Z2 IKKEKVYLAWVPAHKGIGGN---EQVDKLVSA GQIRKVL----- 714
sp|P18802|POL_HV1ND IKKEKVYLAWVPAHKGIGGN---EQVDKLVSA GIRKVL----- 714
sp|P04588|POL_HV1MA IQKDKVYLSWVPAHKGIGGN---EQVDKLVSSGIRKVL----- 714
sp|P24740|POL_HV1U4 IEKEKVYLSWVPAHKGIGGN---EQVDKLVSSGIRKVL----- 714
sp|P17283|POL_SIVCZ IKKEKIYLSWVPAHKGIGGN---EQVDKLVSA GIRKVL----- 739
sp|P17757|POL_HV2D1 IKKEAVYVAWVPAHKGIGGN---QEVDHLVSA GQIRQVL----- 780
sp|P18042|POL_HV2G1 IKKEAVYVAWVPAHKGIGGN---QEVDHLVSA GQIRQVL----- 756
sp|P18096|POL_HV2BE IKKEAVYVAWVPAHKGIGGN---QEVDHLVSA GQIRQVL----- 762
sp|P24107|POL_HV2CA IKKEAIYVAWVPAHKGIGGN---QEVDHLVSA GQIRQVL----- 741
sp|P05962|POL_HV2NZ IKKEAIYVAWVPAHKGIGGN---QEVDHLVSA GQIRQVL----- 742
sp|P04584|POL_HV2RO IKKEAIYVAWVPAHKGIGGN---QEVDHLVSA GQIRQVL----- 743
sp|Q74120|POL_HV2KR IKKETLYVAWVPAHKGIGGN---QEVDHLVSA GQIRQVL----- 742
sp|P20876|POL_HV2ST IKKEAIYVAWVPAHKGIGGN---QEVDHLVSA GQIRQVL----- 762
sp|P12451|POL_HV2SB IKKEAIYVAWVPAHKGIGGN---QEIDHLVSA GQIRQVL----- 742
sp|P05896|POL_SIVM1 IKKTEIYVAWVPAHKGIGGN---QEIDHLVSA GQIRQVL----- 763
sp|P05897|POL_SIVMK IK-VRVYVAWVPALEGIGGN---QEIGPLVSA GQIRQVL----- 761
sp|P12502|POL_SIVS4 IKKEAIYVAWVPAHKGIGGN---QEVDHLVSA GQIRQVL----- 726
sp|P19505|POL_SIVSP IKKEAIYVAWVPAHKGIGGN---QEVDHLVSA GQIRQVL----- 729
sp|P15833|POL_HV2D2 IKKEAVYVGVWVPAHKGIGGN---QEVDHLVSA GQIRQVL----- 762
sp|P27980|POL_SIVAG VQKHQIYLQWVPAHKGIGGN---EEIDKLVSA GMRKIL----- 755
sp|P05895|POL_SIVAT IQKQIYLVQWVPAHKGIGGN---EEIDKLVSA GKIRRVL----- 770
sp|P27973|POL_SIVA1 VQKEAIYLVQWVPAHKGIGGN---EEIDKLVSA GKVRRL----- 750
sp|Q02836|POL_SIVA1 MKKRQVYLQWVPAHKGIGGN---TEIDKLVSA GKIRQL----- 754
sp|P22382|POL_SIVGB KGKEKIYLSWVPAHKGIGGN---EQIDKLVSA GQIRKVL----- 724
sp|P23427|POL_VILV2 HNKEKIGVHVWVPGHKGIPQN---EEDRYISEIFLAKEGRGILQKRAEDAGYDLICP-QE 716
sp|P35956|POL_VILV3 HNKEKIGVHVWVPGHKGIPQN---EEDRYISEIFLAKEGRGILQKRAEDAGYDLICP-QE 712
sp|P03370|POL_VILV HNKEKIGVHVWVPGHKGIPQN---EEDRYISEIFLAKEGRGILQKRAEDAGYDLICP-QE 716
sp|P23426|POL_VILV1 HNKEKIGVHVWVPGHKGIPQN---EEDRYISEIFLAKEGRGILQKRAEDAGYDLICP-QE 716
sp|P16901|POL_OMVVS HDKEQIGVHVWVPGHKGIPQN---EEDRYISEIFLAKEGRGILQKRAEDAGYDLICP-QE 697
sp|P33459|POL_CAIEVC HKKDRIGVHVWVPGHKGIPQN---EEDRYISEIFLAKEGRGILQKRAEDAGYDLICP-QE 721
sp|P16088|POL_FIVPE EKKTAFIDWVWVPGHKGIPGN---EEVDK-LCQTMHIEGDLKRSRSEDAGYDLAA-KE 735
sp|P19028|POL_FIVSD EKKTAFIDWVWVPGHKGIPGN---EEVDK-LCQTMHIEGDLKRTEDAGYDLAA-KE 735
sp|P31822|POL_FIVT2 EKKTAFIDWVWVPGHKGIPGN---EEVDK-LCQTMHIEGDLKRSRSEDAGYDLAA-KE 735
sp|P11204|POL_EIAV9 REKEIVYFAWVWVPGHKGIGCNQLADEAAKIKEEIMLAYQGTQIKEKREDEAGFDLCPV-YD 767
sp|P32542|POL_EIAVC REKEIVYFAWVWVPGHKGIGCNQLADEAAKIKEEIMLAYQGTQIKEKREDEAGFDLCPV-YD 767
sp|P03371|POL_EIAVY REKEIVYFAWVWVPGHKGIGCNQLADEAAKIKEEIMLAYQGTQIKEKREDEAGFDLCPV-YD 766
sp|P19199|POL_COVMV KEETRMAIAQLKEAIVQEEDTIEERCAMILEEKHTENISYATAKAENGLYNVKVGKIP 1207
sp|P27502|POL_RTBPV STHNIICPTLIPASWINNTHR--EHMFVAVDNSKYNLNQELIDDIKLQFQEVDETFG--- 1044

sp|P19560|POL_BIV06 -----IYM 727
sp|P19561|POL_BIV27 -----IYM 727
sp|P20875|POL_HV1JR -----
sp|P05961|POL_HV1MN -----
sp|P03366|POL_HV1B1 -----
sp|P03368|POL_HV1PV -----
sp|P04585|POL_HV1H2 -----
sp|P04587|POL_HV1B5 -----
sp|P03367|POL_HV1BR -----
sp|P05960|POL_HV1C4 -----
sp|P12498|POL_HV1J3 -----
sp|P12497|POL_HV1N5 -----
sp|P35963|POL_HV1Y2 -----
sp|P03369|POL_HV1A2 -----
sp|P20892|POL_HV1OY -----
sp|P05959|POL_HV1RH -----
sp|P04589|POL_HV1EL -----
sp|P12499|POL_HV1Z2 -----
sp|P18802|POL_HV1ND -----
sp|P04588|POL_HV1MA -----
sp|P24740|POL_HV1U4 -----
sp|P17283|POL_SIVCZ -----
sp|P17757|POL_HV2D1 -----
sp|P18042|POL_HV2G1 -----
sp|P18096|POL_HV2BE -----
sp|P24107|POL_HV2CA -----
sp|P05962|POL_HV2NZ -----
sp|P04584|POL_HV2RO -----
sp|Q74120|POL_HV2KR -----
sp|P20876|POL_HV2ST -----
sp|P12451|POL_HV2SB -----
sp|P05896|POL_SIVM1 -----
sp|P05897|POL_SIVMK -----
sp|P12502|POL_SIVS4 -----
sp|P19505|POL_SIVSP -----
sp|P15833|POL_HV2D2 -----
sp|P27980|POL_SIVAG -----
sp|P05895|POL_SIVAT -----
sp|P27973|POL_SIVA1 -----
sp|Q02836|POL_SIVA1 -----
sp|P22382|POL_SIVGB -----
sp|P23427|POL_VILV2 ISIPAGQVKRIAIDLKINLKKDQWAMIGTKSSFANKGVFVQGGHDSGYQGTIQVVIYNS 776
sp|P35956|POL_VILV3 ISIPAGQVKRIAIDLKINLKKDQWAMIGTKSSFANKGVFVQGGHDSGYQGTIQVVIYNS 772
sp|P03370|POL_VILV ISIPAGQVKRIAIDLKINLKKDQWAMIGTKSSFANKGVFVQGGHDSGYQGTIQVVIYNS 776
sp|P23426|POL_VILV1 ISIPAGQVKRIAIDLKINLKKDQWAMIGTKSSFANKGVFVQGGHDSGYQGTIQVVIYNS 776
sp|P16901|POL_OMVVS VCIPAGQVKRIPKINLRLNKEDQWAMVGTKSSFASKGVFVQGGHDSGYQGTIQVVIYNS 757

sp|P33459|POL_CAIEVC VTIPEGQVKCIPIELRLNLKKSQWAMIATKSSMAAKGVFTQGGHDSGYQGQIQVIMYNS 781
sp|P16088|POL_FIVPE IHLLPGEVVKVIPTGVKLMPLPKGYWGLIGKSSIGSKGLDVLGGVIDEGYRGEIGVIMINV 795
sp|P19028|POL_FIVSD IHLLPGEVVKVIPTGVKLMPLPKGHWGLIMGKSSIGSKGLDVLGGVIDEGYRGEIGVIMINL 795
sp|P31822|POL_FIVT2 THLLPGEVRIVPTKTRIMLPKGHWGLIMGKSSIGSKGVLDVLGGVIDEGYRGEIGVIMINL 795
sp|P11204|POL_EIAV9 IMIPVSDTKIIPDVKIQVPPNSFGWVTGKSSMAKQGLLINGHIDEGYTGEIQVICTNI 827
sp|P32542|POL_EIAVC IMIPVSDTKIIPDVKIQVPPNSFGWVTGKSSMAKQGLLINGHIDEGYTGEIQVICTNI 827
sp|P03371|POL_EIAVY IMIPVSDTKIIPDVKIQVPPNSFGWVTGKSSMAKQGLLINGHIDEGYTGEIQVICTNI 826
sp|P19199|POL_COVMV DNMEPYINAIIVDTGATACLIQISAIPENYEDAKVTVNFRSVLIGIGTQMIKAGRILI 1267
sp|P27502|POL_RTBPV -----IKYKL 1049

sp|P19560|POL_BIV06 OQLRPQSFLPRADLP-----VAITGTMVDSELQLQLLNIGTEHIRIQKDEVFMTCFLEN 781
sp|P19561|POL_BIV27 OQLRPQSFLPRADLP-----VAITGTMVDSELQLQLLNIGTEHIRIQKDEVFMTCFLEN 781
sp|P20875|POL_HV1JR -----FLDG 723
sp|P05961|POL_HV1MN -----FLDG 722
sp|P03366|POL_HV1B1 -----FLDG 731
sp|P03368|POL_HV1PV -----FLDG 731
sp|P04585|POL_HV1H2 -----FLDG 719
sp|P04587|POL_HV1B5 -----FLDG 731
sp|P03367|POL_HV1BR -----FLDG 731
sp|P05960|POL_HV1C4 -----
sp|P12498|POL_HV1J3 -----
sp|P12497|POL_HV1N5 -----FLDG 719
sp|P35963|POL_HV1Y2 -----FLDG 719
sp|P03369|POL_HV1A2 -----FLNG 719
sp|P20892|POL_HV1OY -----FLDG 719
sp|P05959|POL_HV1RH -----FLDG 718
sp|P04589|POL_HV1EL -----FLDG 718
sp|P12499|POL_HV1Z2 -----FLDG 718
sp|P18802|POL_HV1ND -----FLDG 718
sp|P04588|POL_HV1MA -----FLDG 718
sp|P24740|POL_HV1U4 -----FLDG 718
sp|P17283|POL_SIVCZ -----FLDG 743
sp|P17757|POL_HV2D1 -----FLEK 784
sp|P18042|POL_HV2G1 -----FLER 760
sp|P18096|POL_HV2BE -----FLEK 766
sp|P24107|POL_HV2CA -----FLEK 745
sp|P05962|POL_HV2NZ -----FLEK 746
sp|P04584|POL_HV2RO -----FLEK 747
sp|Q74120|POL_HV2KR -----FLEK 746
sp|P20876|POL_HV2ST -----FLEK 766
sp|P12451|POL_HV2SB -----FLER 746
sp|P05896|POL_SIVM1 -----FLEK 767
sp|P05897|POL_SIVMK -----FLEK 765
sp|P12502|POL_SIVS4 -----FLKK 730
sp|P19505|POL_SIVSP -----FLEK 733
sp|P15833|POL_HV2D2 -----FLEK 766
sp|P27980|POL_SIVAG -----FLEK 759
sp|P05895|POL_SIVAT -----FLEK 774
sp|P27973|POL_SIVA1 -----FIGR 754
sp|Q02836|POL_SIVAI -----FLDR 758
sp|P22382|POL_SIVGB -----FLQN 728
sp|P23427|POL_VILV2 NNKEVVIPOGRKFAQ-----LILMPLIHEELKPWGETRKRTERGEQGFSTGMV--WIEN 828
sp|P35956|POL_VILVK NNKEVVIPOGRKFAQ-----LILMPLIHEELPWPGETRKRTERGEQGFSTGMV--WIEN 824
sp|P03370|POL_VILV NNKEVVIPOGRKFAQ-----LILMPLIHEELPWPGETRKRTERGEQGFSTGMV--WIEN 828
sp|P23426|POL_VILV1 NNKEVVIPOGRKFAQ-----LILMPLIHEELPWPGETRKRTERGEQGFSTGMV--WIEN 828
sp|P16901|POL_OMVVS NDKEVVIPOGRKFAQ-----LILMPLIHEDELAWGETRRTTERGNQGFSTGAY--WIEN 809
sp|P33459|POL_CAIEVC NKIAVVIPOGRKFAQ-----LILMDKKGKLEPWPGESRKRTERGEKGFSTGMV--WIEN 833
sp|P16088|POL_FIVPE SRKSITLIMERQKIAQ-----LILPCKHEVLEQKGVVMDSERGDNGYVSSWVDR 849
sp|P19028|POL_FIVSD SKKSITLLEQKQKIAQ-----LILPHKHEALEQKGVVMDSERGEKGYGSGTVFSSWVDR 849
sp|P31822|POL_FIVT2 TKKSITLLEQKQKIAQ-----LILPCRHEGLQGEIQMNSERGEKGFSGVSSWVDR 849
sp|P11204|POL_EIAV9 GKSNKLEIEGQKFAQ-----LILQHHSNSRQPWDEKISQKQKGFSTGVF--VVEN 879
sp|P32542|POL_EIAVC GKSNKLEIEGQKFAQ-----LILQHHSNSRQPWDEKISQKQKGFSTGVF--VVEN 879
sp|P03371|POL_EIAVY GKSNKLEIEGQKFAQ-----LILQHHSNSRQPWDEKISQKQKGFSTGVF--VVEN 878
sp|P19199|POL_COVMV GEQYFRMPVTYVMNMGSLSPGIQMIIGCSFIRSLGGLRIEKDIITFKVLTSTIETSRITQ 1327
sp|P27502|POL_RTBPV GQTYVAPKPTKTFIIGHRFLTNENGSVTHKDYITTIQKTTGIYPTARHELKSEFARKHGG 1109

sp|P19560|POL_BIV06 IPSATEDHERWHTSPDILVRQFHLPRRIAKEIVARCQECKR-TTASPV---RGTNPRGRF 837
sp|P19561|POL_BIV27 IPSATEDHERWHTSPDILVRQFHLPKRIAKEIVARCQECKR-TTASPV---RGTNPRGRF 837
sp|P20875|POL_HV1JR IDKAQEEHEKYHSNWRAMASDFNLPPVVAKEIVASCDCQ--LKGEAM---HGQVDCSPG 778
sp|P05961|POL_HV1MN IDKAQEEHEKYHSNWRAMASDFNLPPVVAKEIVASCDCQ--LKGEAM---HGQVDCSPG 777
sp|P03366|POL_HV1B1 IDKAQEEHEKYHSNWRAMASDFNLPPVVAKEIVASCDCQ--LKGEAM---HGQVDCSPG 786
sp|P03368|POL_HV1PV IDKAQEEHEKYHSNWRAMASDFNLPPVVAKEIVASCDCQ--LKGEAM---HGQVDCSPG 786
sp|P04585|POL_HV1H2 IDKAQEEHEKYHSNWRAMASDFNLPPVVAKEIVASCDCQ--LKGEAM---HGQVDCSPG 774
sp|P04587|POL_HV1B5 IDKAQEEHEKYHSNWRAMASDFNLPPVVAKEIVASCDCQ--LKGEAM---HGQVDCSPG 786
sp|P03367|POL_HV1BR IDKAQEEHEKYHSNWRAMASDFNLPPVVAKEIVASCDCQ--LKGEAM---HGQVDCSPG 786
sp|P05960|POL_HV1C4 -----
sp|P12498|POL_HV1J3 -----
sp|P12497|POL_HV1N5 IDKAQEEHEKYHSNWRAMASDFNLPPVVAKEIVASCDCQ--LKGEAM---HGQVDCSPG 774
sp|P35963|POL_HV1Y2 IDKAQEEHEKYHSNWRAMASDFNLPPVVAKEIVASCDCQ--LKGEAM---HGQVDCSPG 774
sp|P03369|POL_HV1A2 IDKAQEEHEKYHSNWRAMASDFNLPPVVAKEIVASCDCQ--LKGEAM---HGQVDCSPG 774
sp|P20892|POL_HV1OY IDKAQEEHEKYHSNWRAMASDFNLPPVVAKEIVASCDCQ--LKGEAM---HGQVDCSPG 774
sp|P05959|POL_HV1RH IDKAQEEHEKYHSNWRAMASDFNLPPVVAKEIVASCDCQ--LKGEAM---HGQVDCSPG 773
sp|P04589|POL_HV1EL IDKAQEEHEKYHSNWRAMASDFNLPPVVAKEIVASCDCQ--LKGEAM---HGQVDCSPG 773
sp|P12499|POL_HV1Z2 IDKAQEEHEKYHSNWRAMASDFNLPPVVAKEIVASCDCQ--LKGEAM---HGQVDCSPG 773
sp|P18802|POL_HV1ND IDKAQEEHEKYHSNWRAMASDFNLPPVVAKEIVASCDCQ--LKGEAM---HGQVDCSPG 773
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sp|P24740|POL_HV1U4 IDKAQEEHEKYHSNWRAMASDFNLPPVVAKEIVASCDCQ--LKGEAM---HGQVDCSPG 773
sp|P17283|POL_SIVCZ IDRAQEEHEKYHSNWRAMASDFNLPPVVAKEIVASCDCQ--VKGEAM---HGQVDCSPG 798
sp|P17757|POL_HV2D1 IEPAQEEHEKYHSNIKELTHKFGIPQLVARQIVNTCAQCC--QKGEAI---HGQVNAEIG 839
sp|P18042|POL_HV2G1 IEPAQEEHEKYHSNIKELTHKFGIPQLVARQIVNTCAQCC--QKGEAI---HGQVNAEIG 815
sp|P18096|POL_HV2BE IEPAQEEHEKYHSNIKELTHKFGIPQLVARQIVNTCAQCC--QKGEAI---HGQVNAEIG 821
sp|P24107|POL_HV2CA IEPAQEEHEKYHSNIKELTHKFGIPQLVARQIVNTCAQCC--QKGEAI---HGQVNAEIG 800
sp|P05962|POL_HV2NZ IEPAQEEHEKYHSNIKELSHKFGIPQLVARQIVNTCAHVQ--QKGEAI---HGQVNAELG 801
sp|P04584|POL_HV2RO IEPAQEEHEKYHSNIKELSHKFGIPQLVARQIVNTCAQCC--QKGEAI---HGQVNAELG 802
sp|Q74120|POL_HV2KR IEPAQEEHEKYHSNIKELSHKFGIPQLVARQIVNTCAQCC--QKGEAI---HGQVDAELG 801
sp|P20876|POL_HV2ST IEPAQEEHEKYHSNIKELSHKFGIPQLVARQIVNTCTQCC--QKGEAI---HGQVNAELG 821
sp|P12451|POL_HV2SB IEPAQEEHEKYHSNIKELAHKFGIPQLVARQIVNTCAQCC--QKGEAI---HGQVNAELG 801
sp|P05896|POL_SIVM1 IEPAQEEHKSYSNIKELVFKFGLPRLVARQIVNTCDKCH--QKGEAI---HGQVNSDLG 822
sp|P05897|POL_SIVMK IEPAQEEHKSYSNIKELVFKFGLPRLVARQIVNTCDKCH--QKGEAI---HGQVNSDLG 820
sp|P12502|POL_SIVS4 IEPAQEEHEKYHSNIKELVFKFGLPRLVARQIVNTCDKCH--QKGEAI---HGQVNAELG 785
sp|P19505|POL_SIVSP IEPAQEEHEKYHSNIKELVFKFGLPRLVARQIVNTCDKCH--QKGEAI---HGQVNAELG 788
sp|P15833|POL_HV2D2 IEPAQEEHEKYHSNIKELVHKFGIPQLVARQIVNSDCDCQ--QKGEAI---HGQVNAELG 821

sp|P27980|POL_SIVAG IEEAQEEHRYHNNWRNLADTYGLPQIVAKEIVAMCPKCQ--IKGEPV---HGQVDASPG 814
sp|P05895|POL_SIVAT IEEAQEKHERYHNNWRNLADTYGLPQIVAKEIVAMCPKCQ--IKGEPV---HGQVDASPG 829
sp|P27973|POL_SIVA1 IEEAQEEHRYHNSNRNLADTFGLPQIVAKEIVAMCPKCQ--VKGEPI---HGQVDASPG 809
sp|Q02836|POL_SIVA1 IEEAQEDHAKYHNNWRSMVQEFGLPNVIAKEIVAAACPKCQ--IRGEPK---HGQVDASIE 813
sp|P22382|POL_SIVGB IEPAQEEHEKYHSNEAQLREKFLPALVAKQIVQSCSKCC--HHGEPI---KGQTDASLG 783
sp|P23427|POL_VILV2 IPLAEEEHNKWHQDAVSLHLEFGIPRTAAEDIVQQCDVQENKMPSTL---RGSNKRIGID 885
sp|P35956|POL_VILVK IPLAEEEHNKWHQDAVSLHLEFGIPRTAAEDIVQQCDVQENKMPSTL---RGSNKRIGID 881
sp|P03370|POL_VILV IPLAEEEHNKWHQDAVSLHLEFGIPRTAAEDIVQQCDVQENKMPSTL---RGSNKRIGID 885
sp|P23426|POL_VILV1 IPLAEEEHNKWHQDAVSLHLEFGIPRTAAEDIVQQCDVQENKMPSTL---RGSNKRIGID 885
sp|P16901|POL_OMVVS IPLAEEEDHSHKWHQDAGSLHLEFGIPRTAAEDIVQQCEVCQENKMPSTL---RGSNKRIGID 866
sp|P33459|POL_CAEVC IPLAEEEDHTKWHQDARSLHLEFEIPRTAAEDIVNQCCEICKEARTPAVI---RGGNKRIGVN 890
sp|P16088|POL_FIVPE IEEAEINHEKHFSDPQYLRTFENLPKMVAEEIIRKCPVCR--IIGEQV---GGQLKIGPG 904
sp|P19028|POL_FIVSD IEEAETNHEKHFSDPQYLRTFENLPKMVAEEIIRKCPVCR--IRGEQV---GGQLKIGPG 904
sp|P31822|POL_FIVT2 IEEAELNHEKHFSDPQYLRTFENLPRIVAEIIRKCPVCR--IRGEQV---GGQLKIRPG 904
sp|P11204|POL_EIAV9 IQEAQDEHENWHTSPKILARNYKIPLTVAKQITQEQCPHCT--KQSGP---AGCVMRSPN 934
sp|P32542|POL_EIAVC IQEAQDEHENWHTSPKILARNYKIPLTVAKQITQEQCPHCT--KQSGP---AGCVMRSPN 934
sp|P03371|POL_EIAVY IQEAQDEHENWHTSPKILARNYKIPLTVAKQITQEQCPHCT--KQSGP---AGCVMRSPN 933
sp|P19199|POL_COYMV VANSIEEELSEDEYLNIAASVETPSFLDQEFARKNKDILLKEMKEMKY---IGENP--ME 1382
sp|P27502|POL_RTBPV RPPLFSNPETYNKIPHLHSYQPQPILGKNEIGNQSLITMVKLEALGFIGDDITKNRT 1169

sp|P19560|POL_BIV06 LWQMDNTHWNKTHIIVAVETNSGLVEAQVIPEETALQVALCILQIQRVTVLH----- 890
sp|P19561|POL_BIV27 LWQMDNTHWNKTHIIVAVETNSGLVEAQVIPEETALQVALCILQIQRVTVLH----- 890
sp|P20875|POL_HV1JR IWQLDCTHLEGGKILVAVHVASGYIEAEVIPAETGQETAYFLLKLAGRWPVTT----- 831
sp|P05961|POL_HV1MN IWQLDCTHLEGGKILVAVHVASGYIEAEVIPAETGQETAYFLLKLAGRWPVKT----- 830
sp|P03366|POL_HV1B1 IWQLDCTHLEGGKILVAVHVASGYIEAEVIPAETGQETAYFLLKLAGRWPVKT----- 839
sp|P03368|POL_HV1PV IWQLDCTHLEGGKILVAVHVASGYIEAEVIPAETGQETAYFLLKLAGRWPVKT----- 839
sp|P04585|POL_HV1H2 IWQLDCTHLEGGKILVAVHVASGYIEAEVIPAETGQETAYFLLKLAGRWPVKT----- 827
sp|P04587|POL_HV1B5 IWQLDCTHLEGGKILVAVHVASGYIEAEVIPAETGQETAYFLLKLAGRWPVKT----- 839
sp|P03367|POL_HV1BR IWQLDCTHLEGGKILVAVHVASGYIEAEVIPAETGQETAYFLLKLAGRWPVKT----- 839
sp|P05960|POL_HV1C4 -----
sp|P12498|POL_HV1J3 -----
sp|P12497|POL_HV1N5 IWQLDCTHLEGGKILVAVHVASGYIEAEVIPAETGQETAYFLLKLAGRWPVKT----- 827
sp|P35963|POL_HV1Y2 IWQLDCTHLEGGKILVAVHVASGYIEAEVIPAETGQETAYFLLKLAGRWPVTT----- 827
sp|P03369|POL_HV1A2 IWQLDCTHLEGGKILVAVHVASGYIEAEVIPAETGQETAYFLLKLAGRWPVKT----- 827
sp|P20892|POL_HV1OY IWQLDCTHLEGGKILVAVHVASGYIEAEVIPAETGQETAYFLLKLAGRWPVKT----- 827
sp|P05959|POL_HV1RH IWQLDCTHLEGGKILVAVHVASGYIEAEVIPAETGQETAYFLLKLAGRWPVKT----- 826
sp|P04589|POL_HV1EL IWQLDCTHLEGGKILVAVHVASGYIEAEVIPAETGQETAYFLLKLAGRWPVKT----- 826
sp|P12499|POL_HV1Z2 IWQLDCTHLEGGKILVAVHVASGYIEAEVIPAETGQETAYFLLKLAGRWPVKT----- 826
sp|P18802|POL_HV1ND IWQLDCTHLEGGKILVAVHVASGYIEAEVIPAETGQETAYFLLKLAGRWPVKT----- 826
sp|P04588|POL_HV1MA IWQLDCTHLEGGKILVAVHVASGYIEAEVIPAETGQETAYFLLKLAGRWPVKT----- 826
sp|P24740|POL_HV1U4 IWQLDCTHLEGGKILVAVHVASGYIEAEVIPAETGQETAYFLLKLAGRWPVKT----- 826
sp|P17283|POL_SIVCZ IWQVDCDTHLEGGKILVAVHVASGYIEAEVIPAETGQETAYFLLKLAGRWPVKT----- 851
sp|P17757|POL_HV2D1 VWQMDCTHLEGGKILVAVHVASGFIEAEVIPAQESGRQTALFLLKLAGRWPVTT----- 892
sp|P18042|POL_HV2G1 VWQMDCTHLEGGKILVAVHVASGFIEAEVIPAQESGRQTALFLLKLAGRWPVTT----- 868
sp|P18096|POL_HV2BE VWQMDCTHLEGGKILVAVHVASGFIEAEVIPAQESGRQTALFLLKLAGRWPVTT----- 874
sp|P24107|POL_HV2CA VWQMDCTHLEGGKILVAVHVASGFIEAEVIPAQESGRQTALFLLKLAGRWPVTT----- 853
sp|P05962|POL_HV2NZ TWQMDCTHLEGGKILVAVHVASGFIEAEVIPAQESGRQTALFLLKLAGRWPVTT----- 854
sp|P04584|POL_HV2RO TWQMDCTHLEGGKILVAVHVASGFIEAEVIPAQESGRQTALFLLKLAGRWPVTT----- 855
sp|Q74120|POL_HV2KR TWQMDCTHLEGGKILVAVHVASGFIEAEVIPAQESGRQTALFLLKLAGRWPVTT----- 854
sp|P20876|POL_HV2ST TWQMDCTHLEGGKILVAVHVASGFIEAEVIPAQESGRQTALFLLKLAGRWPVTT----- 874
sp|P12451|POL_HV2SB TWQMDCTHLEGGKILVAVHVASGFIEAEVIPAQESGRQTALFLLKLAGRWPVTT----- 854
sp|P05896|POL_SIVM1 TWQMDCTHLEGGKILVAVHVASGFIEAEVIPAQESGRQTALFLLKLAGRWPVTT----- 875
sp|P05897|POL_SIVMK TWQMDCTHLEGGKILVAVHVASGFIEAEVIPAQESGRQTALFLLKLAGRWPVTT----- 872
sp|P12502|POL_SIVS4 TWQMDCTHLEGGKILVAVHVASGFIEAEVIPAQESGRQTALFLLKLAGRWPVTT----- 838
sp|P19505|POL_SIVSP TWQMDCTHLEGGKILVAVHVASGFIEAEVIPAQESGRQTALFLLKLAGRWPVTT----- 841
sp|P15833|POL_HV2D2 TWQMDCTHLEGGKILVAVHVASGFIEAEVIPAQESGRQTALFLLKLAGRWPVTT----- 874
sp|P27980|POL_SIVAG VWQMDCTHLEGGKILVAVHVASGFIEAEVIPAQESGRQTALFLLKLAGRWPVTT----- 867
sp|P05895|POL_SIVAT TWQMDCTHLEGGKILVAVHVASGFIEAEVIPAQESGRQTALFLLKLAGRWPVTT----- 882
sp|P27973|POL_SIVA1 VWQMDCTHLEGGKILVAVHVASGFIEAEVIPAQESGRQTALFLLKLAGRWPVTT----- 862
sp|Q02836|POL_SIVA1 TWQMDCTHLEGGKILVAVHVASGFIEAEVIPAQESGRQTALFLLKLAGRWPVTT----- 866
sp|P22382|POL_SIVGB VWQMDCTHLEGGKILVAVHVASGFIEAEVIPAQESGRQTALFLLKLAGRWPVTT----- 836
sp|P23427|POL_VILV2 HWQVDYTHYEDKILVWVETNSGLIYAERVKGETGQEFVQTMKQWYAMFAPKS----- 938
sp|P35956|POL_VILVK HWQVDYTHYEDKILVWVETNSGLIYAERVKGETGQEFVQTMKQWYAMFAPKS----- 934
sp|P03370|POL_VILV HWQVDYTHYEDKILVWVETNSGLIYAERVKGETGQEFVQTMKQWYAMFAPKS----- 938
sp|P23426|POL_VILV1 HWQVDYTHYEDKILVWVETNSGLIYAERVKGETGQEFVQTMKQWYAMFAPKS----- 938
sp|P16901|POL_OMVVS HWQVDYTHYEDKILVWVETNSGLIYAERVKGETGQEFVQTMKQWYAMFAPKS----- 919
sp|P33459|POL_CAEVC HWQVDYTHYENILLVWVETNSGLIYAERVKGETGQEFVQTMKQWYAMFAPKS----- 943
sp|P16088|POL_FIVPE IWQMDCTHFDGKILVAVHVESGYIWAQIISQETADCTVKAVALQLLSAHNVTE----- 957
sp|P19028|POL_FIVSD IWQMDCTHFDGKILVAVHVESGYIWAQIISQETADCTVKAVALQLLSAHNVTE----- 957
sp|P31822|POL_FIVT2 IWQMDCTHFDGKILVAVHVESGYIWAQIISQETADCTVKAVALQLLSAHNVTE----- 957
sp|P11204|POL_EIAV9 HWQADCTHLDNKILTFVESNSGYIHAATLLSKENALCTSLAILEWARLFSPPS----- 987
sp|P32542|POL_EIAVC HWQADCTHLDNKILTFVESNSGYIHAATLLSKENALCTSLAILEWARLFSPPS----- 987
sp|P03371|POL_EIAVY HWQADCTHLDNKILTFVESNSGYIHAATLLSKENALCTSLAILEWARLFSPPS----- 986
sp|P19199|POL_COYMV FWKNNKIKCKLNIINPDIKMGRPIKHVTPGDEEAMTRQINLLQMKVIRPSEKHRSTA 1442
sp|P27502|POL_RTBPV TWVCDFKIINPDINICATIPYTPADKEVFEKQIKELDNKLIKADPTCRHRTAAAFVTR 1229

sp|P19560|POL_BIV06 -----LHSD-NGPCFTHAHRIENLCKYL----- 912
sp|P19561|POL_BIV27 -----LHSD-NGPCFTHAHRIENLCKYL----- 912
sp|P20875|POL_HV1JR -----IHTD-NGSNFTSTTVKAAACWWAG----- 853
sp|P05961|POL_HV1MN -----IHTD-NGSNFTSTTVKAAACWWAG----- 852
sp|P03366|POL_HV1B1 -----IHTD-NGSNFTSATVKAACWWAG----- 861
sp|P03368|POL_HV1PV -----IHTD-NGSNFTSATVKAACWWAG----- 861
sp|P04585|POL_HV1H2 -----IHTD-NGSNFTSATVKAACWWAG----- 849
sp|P04587|POL_HV1B5 -----IHTD-NGSNFTSATVKAACWWAG----- 861
sp|P03367|POL_HV1BR -----IHTD-NGSNFTSTTVKAAACWWAG----- 861
sp|P05960|POL_HV1C4 -----
sp|P12498|POL_HV1J3 -----
sp|P12497|POL_HV1N5 -----VHTD-NGSNFTSTTVKAAACWWAG----- 849
sp|P35963|POL_HV1Y2 -----IHTD-NGSNFTSATVKAACWWAG----- 849
sp|P03369|POL_HV1A2 -----IHTD-NGSNFTSTTVKAAACWWAG----- 849
sp|P20892|POL_HV1OY -----IHTD-NGSNFTSTTVKAAACWWAG----- 849
sp|P05959|POL_HV1RH -----IHTD-NGSNFTSTTVKAAACWWAG----- 848
sp|P04589|POL_HV1EL -----VHTD-NGSNFTSAAVKAAACWWAG----- 848
sp|P12499|POL_HV1Z2 -----VHTD-NGSNFTSAAVKAAACWWAG----- 848
sp|P18802|POL_HV1ND -----VHTD-NGSNFTSATVKAACWWAG----- 848
sp|P04588|POL_HV1MA -----VHTD-NGSNFTSAAVKAAACWWAN----- 848
sp|P24740|POL_HV1U4 -----IHTD-NGSNFTSAAVKAAACWWAN----- 848
sp|P17283|POL_SIVCZ -----IHTD-NGSNFTSAAVKAAACWWAD----- 873
sp|P17757|POL_HV2D1 -----LHTD-NGSNFTSQEVKMAVWWIG----- 914
sp|P18042|POL_HV2G1 -----LHTD-NGSNFTSQEVKMAVWWIG----- 890
sp|P18096|POL_HV2BE -----LHTD-NGSNFTSQEVKMAVWWIG----- 896
sp|P24107|POL_HV2CA -----LHTD-NGSNFTSQEVKMAVWWIG----- 875

sp|P05962|POL_HV2NZ -----LHTD-NGANFTSQEVKMAVWVWG----- 876
sp|P04584|POL_HV2RO -----LHTD-NGANFTSQEVKMAVWVWG----- 877
sp|Q74120|POL_HV2KR -----LHTD-NGANFTSQEVKMAVWVWG----- 876
sp|P20876|POL_HV2ST -----LHTD-NGANFTSQEVKMAVWVWG----- 896
sp|P12451|POL_HV2SB -----LHTD-NGANFTSQEVKMAVWVWG----- 876
sp|P05896|POL_SIVM1 -----LHTD-NGANFASQEVKMAVWVWG----- 897
sp|P05897|POL_SIVMK -----YTHSNGANFASQEVKMAVWVWG----- 895
sp|P12502|POL_SIVS4 -----LHTD-NGANFTSQEVKMAVWVWG----- 860
sp|P19505|POL_SIVSP -----LHTD-NGANFTSQEVKMAVWVWG----- 863
sp|P15833|POL_HV2D2 -----LHTD-NGANFTSPSVKMAVWVWG----- 896
sp|P27980|POL_SIVAG -----LHTD-NGPNFTSQEVAAMCWWGK----- 889
sp|P05895|POL_SIVAT -----LHTD-NGPNFTSQEVAAMCWWGK----- 904
sp|P27973|POL_SIVA1 -----LHTD-NGPNFTSQEVAAMCWWGK----- 884
sp|Q02836|POL_SIVAI -----LHTD-NGPNFTSQVNAAVCWWGN----- 888
sp|P22382|POL_SIVGB -----LHTD-NGPNFTSQEVETMCWWLG----- 858
sp|P23427|POL_VILV2 -----LQSD-NGPAFVAESTQLLMKYLG----- 960
sp|P35956|POL_VILVK -----LQSD-NGPAFVAESTQLLMKYLG----- 956
sp|P03370|POL_VILV -----LQSD-NGPAFVAESTQLLMKYLG----- 960
sp|P23426|POL_VILV1 -----LQSD-NGPAFVAESTQLLMKYLG----- 960
sp|P16901|POL_OMVVS -----LQSD-NGPAFVAESTQLLMKYLG----- 941
sp|P33459|POL_CAEVC -----LQSD-NGPAFAAESTQLLMQYLG----- 965
sp|P16088|POL_FIVPE -----LQTD-NGPNFKNQKMEGVLYNYMG----- 979
sp|P19028|POL_FIVSD -----LQTD-NGPNFKNQKMEGVLYNYMG----- 979
sp|P31822|POL_FIVT2 -----LQTD-NGPNFKNQKMEGLLNYMG----- 979
sp|P11204|POL_EIAV9 -----LHTD-NGTNFVAEPVVNLLKFLK----- 1009
sp|P32542|POL_EIAV5 -----LHTD-NGTNFVAEPVVNLLKFLK----- 1009
sp|P03371|POL_EIAVC -----LHTD-NGTNFVAEPVVNLLKFLK----- 1008
sp|P19199|POL_COYMV FIVRSGTEIDPITGKEKKGKERMVFNKLLNENTESDQYSLPGINTIISKVGRSKIYSKF 1502
sp|P27502|POL_RTBPV N-----HSEEVAQKPRIVYNYKRLNDNMHTDPFNIPHKISMNLIKANIFSKF 1278

sp|P19560|POL_BIV06 -----ITKTTGIP----YNPQSQGVVERAHRDLK 937
sp|P19561|POL_BIV27 -----ITKTTGIP----YNPQSQGVVERAHRDLK 937
sp|P20875|POL_HV1JR -----IKQEFGIP----YNPQSQGVVSMNKELK 878
sp|P05961|POL_HV1MN -----IKQEFGIP----YNPQSQGVVSMNKELK 877
sp|P03366|POL_HV1B1 -----IKQEFGIP----YNPQSQGVVSMNKELK 886
sp|P03368|POL_HV1PV -----IKQEFGIP----YNPQSQGVVSMNKELK 886
sp|P04585|POL_HV1H2 -----IKQEFGIP----YNPQSQGVVSMNKELK 874
sp|P04587|POL_HV1B5 -----IKQEFGIP----YNPQSQGVVSMNKELK 886
sp|P03367|POL_HV1BR -----IKQEFGIP----YNPQSQGVVSMNKELK 886
sp|P05960|POL_HV1C4 -----
sp|P12498|POL_HV1J3 -----
sp|P12497|POL_HV1N5 -----IKQEFGIP----YNPQSQGVVSMNKELK 874
sp|P35963|POL_HV1Y2 -----IKQEFGIP----YNPQSQGVVSMNKELK 874
sp|P03369|POL_HV1A2 -----IKQEFGIP----YNPQSQGVVSMNKELK 874
sp|P20892|POL_HV1OY -----IKQEFGIP----YNPQSQGVVSMNKELK 874
sp|P05959|POL_HV1RH -----IKQEFGIP----YNPQSQGVVSMNKELK 873
sp|P04589|POL_HV1EL -----IKQEFGIP----YNPQSQGVVSMNKELK 873
sp|P12499|POL_HV1Z2 -----IKQEFGIP----YNPQSQGVVSMNKELK 873
sp|P18802|POL_HV1ND -----IKQEFGIP----YNPQSQGVVSMNKELK 873
sp|P04588|POL_HV1MA -----IKQEFGIP----YNPQSQGVVSMNKELK 873
sp|P24740|POL_HV1U4 -----IQQEFGIP----YNPQSQGVVSMNKELK 873
sp|P17283|POL_SIVC2 -----IKQEFGIP----YNPQSQGVVSMNKELK 898
sp|P17757|POL_HV2D1 -----IEQSFVGP----YNPQSQGVVEAMNHHLK 939
sp|P18042|POL_HV2G1 -----IEQSFVGP----YNPQSQGVVEAMNHHLK 915
sp|P18096|POL_HV2BE -----IEQSFVGP----YNPQSQGVVEAMNHHLK 921
sp|P24107|POL_HV2CA -----IEQTFGVP----YNPQSQGVVEAMNHHLK 900
sp|P05962|POL_HV2NZ -----IEQTFGVP----YNPQSQGVVEAMNHHLK 901
sp|P04584|POL_HV2RO -----IEQSFVGP----YNPQSQGVVEAMNHHLK 902
sp|Q74120|POL_HV2KR -----IEQSFVGP----YNPQSQGVVEAMNHHLK 901
sp|P20876|POL_HV2ST -----IEQSFVGP----YNPQSQGVVEAMNHHLK 921
sp|P12451|POL_HV2SB -----IEQSFVGP----YNPQSQGVVEAMNHHLK 901
sp|P05896|POL_SIVM1 -----IEHTFGVP----YNPQSQGVVEAMNHHLK 922
sp|P05897|POL_SIVMK -----IEAHLWVP----YNPQSQGVVEAMNHHLK 920
sp|P12502|POL_SIVS4 -----IEQTFGVP----YNPQSQGVVEAMNHHLK 885
sp|P19505|POL_SIVSP -----IEQTFGVP----YNPQSQGVVEAMNHHLK 888
sp|P15833|POL_HV2D2 -----IEQTFGVP----YNPQSQGVVEAMNHHLK 921
sp|P27980|POL_SIVAG -----IEHTTGVP----YNPQSQGVVSMNKELK 914
sp|P05895|POL_SIVAT -----IEHTTGIP----YNPQSQGVVSMNKELK 929
sp|P27973|POL_SIVA1 -----VEHTTGVP----YNPQSQGVVSMNKELK 909
sp|Q02836|POL_SIVAI -----IEHTTGIP----YNPQSQGVVSMNKELK 913
sp|P22382|POL_SIVGB -----IEHTTGIP----YNPQSQGVVSMNKELK 883
sp|P23427|POL_VILV2 -----IEHTTGIP----WNPQSQALVERTHQTLLK 985
sp|P35956|POL_VILVK -----IEHTTGIP----WNPQSQALVERTHQTLLK 981
sp|P03370|POL_VILV -----IEHTTGIP----WNPQSQALVERTHQTLLK 985
sp|P23426|POL_VILV1 -----IEHTTGIP----WNPQSQALVERTHQTLLK 985
sp|P16901|POL_OMVVS -----IHTTGIP----WNPQSQALVERTHQTLLK 966
sp|P33459|POL_CAEVC -----VKHTTGIP----WNPQSQALVERAHLK 990
sp|P16088|POL_FIVPE -----VKHKFGIP----GNPQSQALVENVNTLK 1004
sp|P19028|POL_FIVSD -----VKHKFGIP----GNPQSQALVENVNTLK 1004
sp|P31822|POL_FIVT2 -----IKHKLKIP----GNPQSQALVENANNTLK 1004
sp|P11204|POL_EIAV9 -----IAHTTGIP----YHPESQGIVERANRTLK 1034
sp|P32542|POL_EIAVC -----IAHTTGIP----YHPESQGIVERANRTLK 1034
sp|P03371|POL_EIAV5 -----IAHTTGIP----YHPESQGIVERANRTLK 1033
sp|P19199|POL_COYMV DLKSGFWQVAMEEESVPWTAFLAGNKLYEWLVMPFGLKNAPAFQRKMDNVFGTEKIFA 1562
sp|P27502|POL_RTBPV DLKAGFHMMKLDKDFKDWTTFTTCEGLYTWVNCPPFGIANAPCAFQRFMQESFG-DLK 1337

sp|P19560|POL_BIV06 DRLAAYQGDCEVTEAALSALVSLN-KKRGIGGHTPYEYIYSEHTKYQDQLEQQFSKQ 996
sp|P19561|POL_BIV27 DRLAAYQGDCEVTEAALSALVSLN-KKRGIGGHTPYEYIYSEHTKYQDQLEQQFSKQ 996
sp|P20875|POL_HV1JR KIIGQVRDQAEHLKTAVQMAVFIHNFKRKGIGGYSAGERIVDIIATDIQTKELQKQITK 938
sp|P05961|POL_HV1MN KIIGQVRDQAEHLKTAVQMAVFIHNFKRKGIGGYSAGERIVDIIATDIQTKELQKQITK 937
sp|P03366|POL_HV1B1 KIIGQVRDQAEHLKTAVQMAVFIHNFKRKGIGGYSAGERIVDIIATDIQTKELQKQITK 946
sp|P03368|POL_HV1PV KIIGQVRDQAEHLKTAVQMAVFIHNFKRKGIGGYSAGERIVDIIATDIQTKELQKQITK 946
sp|P04585|POL_HV1H2 KIIGQVRDQAEHLKTAVQMAVFIHNFKRKGIGGYSAGERIVDIIATDIQTKELQKQITK 934
sp|P04587|POL_HV1B5 KIIGQVRDQAEHLKTAVQMAVFIHNFKRKGIGGYSAGERIVDIIATDIQTKELQKQITK 946
sp|P03367|POL_HV1BR KIIGQVRDQAEHLKTAVQMAVFIHNFKRKGIGGYSAGERIVDIIATDIQTKELQKQITK 946
sp|P05960|POL_HV1C4 -----
sp|P12498|POL_HV1J3 -----
sp|P12497|POL_HV1N5 KIIGQVRDQAEHLKTAVQMAVFIHNFKRKGIGGYSAGERIVDIIATDIQTKELQKQITK 934
sp|P35963|POL_HV1Y2 KIIGQVRDQAEHLKTAVQMAVFIHNFKRKGIGGYSAGERIVDIIATDIQTKELQKQITK 934
sp|P03369|POL_HV1A2 KIIGQVRDQAEHLKTAVQMAVFIHNFKRKGIGGYSAGERIVDIIATDIQTKELQKQITK 934
sp|P20892|POL_HV1OY KIIGQVRDQAEHLKTAVQMAVFIHNFKRKGIGGYSAGERIVDIIATDIQTKELQKQITK 934
sp|P05959|POL_HV1RH KIIGQVRDQAEHLKTAVQMAVFIHNFKRKGIGGYSAGERIVDIIATDIQTKELQKQITK 933

sp|P04589|POL_HV1EL KHGQVRDQAEHLKTAVQMAVFIHNFKRRGGIGGYSAGERIIDHATDIQTKELQKQHK 933
sp|P12499|POL_HV1Z2 KHGQVRDQAEHLKTAVQMAVFIHNFKRRGGIGGYSAGERIIDHATDIQTKELQKQHK 933
sp|P18802|POL_HV1ND KHGQVRDQAEHLKTAVQMAVFIHNFKRRGGIGGYSAGERIIDHATDIQTKELQKQHK 933
sp|P04588|POL_HV1MA KHGQVREQAHLKTAVQMAVFIHNFKRRGGIGGYSAGERIIDHATDIQTKELQKQHK 933
sp|P24740|POL_HV1U4 KHGQVREQAHLKTAVQMAVFIHNFKRRGGIGGYSAGERIIDHATDIQTKELQKQHK 933
sp|P17283|POL_SIVCZ KHGQVRDQAEHLKTAVQMAVFIHNFKRRGGIGGYSAGERIIDHATDIQTKELQKQHK 933
sp|P17757|POL_HV2D1 NQISRIREQANTTETIVLMAVHCFMNFKRRGGIGDMTPAERLINMITTEQEIQFLQRKNSN 999
sp|P18042|POL_HV2G1 NQISRIREQANTTETIVLMAVHCFMNFKRRGGIGDMTPAERLINMITTEQEIQFLQRKNSN 975
sp|P18096|POL_HV2BE NQISRIREQANTTETIVLMAVHCFMNFKRRGGIGDMTPAERLINMITTEQEIQFLQRKNSN 981
sp|P24107|POL_HV2CA NQISRIREQANTTETIVLMAVHCFMNFKRRGGIGDMTPAERLINMITTEQEIQFLQRKNSN 960
sp|P05962|POL_HV2NZ NQISRIREQANTTETIVLMAVHCFMNFKRRGGIGDMTPAERLINMITTEQEIQFLQRKNSN 961
sp|P04584|POL_HV2RO NQISRIREQANTTETIVLMAVHCFMNFKRRGGIGDMTPAERLINMITTEQEIQFLQRKNSN 962
sp|Q74120|POL_HV2KR NQISRIREQANTTETIVLMAVHCFMNFKRRGGIGDMTPAERLINMITTEQEIQFLQRKNSN 961
sp|P20876|POL_HV2ST NQISRIREQANTTETIVLMAVHCFMNFKRRGGIGDMTPAERLINMITTEQEIQFLQRKNSN 981
sp|P12451|POL_HV2SB NQISRIREQANTTETIVLMAVHCFMNFKRRGGIGDMTPAERLINMITTEQEIQFLQRKNSN 961
sp|P05896|POL_SIVM1 NQISRIREQANTTETIVLMAVHCFMNFKRRGGIGDMTPAERLINMITTEQEIQFLQRKNSN 982
sp|P05897|POL_SIVM2 NQISRIREQANTTETIVLMAVHCFMNFKRRGGIGDMTPAERLINMITTEQEIQFLQRKNSN 980
sp|P12502|POL_SIVS4 TQIDRIREQANSIETIVLMAVHCFMNFKRRGGIGDMTPAERLINMITTEQEIQFLQRKNSN 945
sp|P19505|POL_SIVSP TQIDRIREQANSIETIVLMAVHCFMNFKRRGGIGDMTPAERLINMITTEQEIQFLQRKNSN 948
sp|P15833|POL_HV2D2 NQISRIREQANTTETIVLMAVHCFMNFKRRGGIGDMTPAERLINMITTEQEIQFLQRKNSN 961
sp|P27980|POL_SIVAG EIIGKIRDDCOYTETAVALMAVHCFMNFKRRGGIGDMTPAERLINMITTEQEIQFLQRKNSN 974
sp|P05895|POL_SIVAT EIIGKIRDDCOYTETAVALMAVHCFMNFKRRGGIGDMTPAERLINMITTEQEIQFLQRKNSN 989
sp|P27973|POL_SIVA1 EIIGKIRDDCOYTETAVALMAVHCFMNFKRRGGIGDMTPAERLINMITTEQEIQFLQRKNSN 969
sp|Q02836|POL_SIVA1 EIIGKIRDDCOYTETAVALMAVHCFMNFKRRGGIGDMTPAERLINMITTEQEIQFLQRKNSN 973
sp|P22382|POL_SIVGB ELIEKIREDCCKELKTAVALMAVHCFMNFKRRGGIGDMTPAERLINMITTEQEIQFLQRKNSN 943
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sp|P35956|POL_VILVK NTLEKLIPMFNAFESALAGTLITLNIKRKGGGLTSPMDIFIFNKEQRIQQQSKSKQEKI 1041
sp|P03370|POL_VILV NTLEKLIPMFNAFESALAGTLITLNIKRKGGGLTSPMDIFIFNKEQRIQQQSKSKQEKI 1045
sp|P23426|POL_VILV1 NTLEKLIPMFNAFESALAGTLITLNIKRKGGGLTSPMDIFIFNKEQRIQQQSKSKQEKI 1045
sp|P16901|POL_OMVVS NTIEKFVSMFAFESALAAALITLNIKRKGGGLTSPMDIFIFNKEQRIQQQSKSKQEKI 1026
sp|P33459|POL_CAEVC STLKKFQPFVAVESALAAALITLNIKRKGGGLTSPMDIFIFNKEQRIQQQSKSKQEKI 1050
sp|P16088|POL_FIVPE VVWVHKFLPETTSLDNALALAVHCLNFKRRGGIGDMTPAERLINMITTEQEIQFLQRKNSN 1064
sp|P19028|POL_FIVSD VVWVHKFLPETTSLDNALALAVHCLNFKRRGGIGDMTPAERLINMITTEQEIQFLQRKNSN 1064
sp|P31822|POL_FIVT2 VVWVHKFLPETTSLDNALALAVHCLNFKRRGGIGDMTPAERLINMITTEQEIQFLQRKNSN 1064
sp|P11204|POL_EIAV9 EKIQSHRDNTQTEAALQALALITCNKGRESMGGQTPWEVFITNQAQVIEHKLKLLQQAQSS 1094
sp|P32542|POL_EIACV EKIQSHRDNTQTEAALQALALITCNKGRESMGGQTPWEVFITNQAQVIEHKLKLLQQAQSS 1094
sp|P03371|POL_EIAV9 EKIQSHRDNTQTEAALQALALITCNKGRESMGGQTPWEVFITNQAQVIEHKLKLLQQAQSS 1093
sp|P19199|POL_COYMV YIDDILVSEETAQHSQHLTYMLQLCKENGLILSPTKMKIGTPEIDFLGASLGTCKIKL 1622
sp|P27502|POL_RTBPV LYIDDILVSEETAQHSQHLTYMLQLCKENGLILSPTKMKIGTPEIDFLGASLGTCKIKL 1397

sp|P19560|POL_BIV06 KIEKWYVYRN-RRKEWKGYPY-----K 1016
sp|P19561|POL_BIV27 KIEKWYVYRN-RRKEWKGYPY-----K 1016
sp|P20875|POL_HV1JR IQNFRVYRDRDPIWKGPA-----K 959
sp|P05961|POL_HV1MN IQNFRVYRDRDPIWKGPA-----K 958
sp|P03366|POL_HV1B1 IQNFRVYRDRDPIWKGPA-----K 967
sp|P03368|POL_HV1P1 IQNFRVYRDRDPIWKGPA-----K 967
sp|P04585|POL_HV1H2 IQNFRVYRDRDPIWKGPA-----K 955
sp|P04587|POL_HV1B5 IQNFRVYRDRDPIWKGPA-----K 967
sp|P03367|POL_HV1BR IQNFRVYRDRDPIWKGPA-----K 967
sp|P05960|POL_HV1C4 -----
sp|P12498|POL_HV1J3 -----
sp|P12497|POL_HV1N5 IQNFRVYRDRDPIWKGPA-----K 955
sp|P35963|POL_HV1Y2 IQNFRVYRDRDPIWKGPA-----K 955
sp|P03369|POL_HV1A2 IQNFRVYRDRDPIWKGPA-----K 955
sp|P20892|POL_HV1OY IQNFRVYRDRDPIWKGPA-----K 955
sp|P05959|POL_HV1RH IQNFRVYRDRDPIWKGPA-----K 954
sp|P04589|POL_HV1EL IQNFRVYRDRDPIWKGPA-----K 954
sp|P12499|POL_HV1Z2 IQNFRVYRDRDPIWKGPA-----K 954
sp|P18802|POL_HV1ND IQNFRVYRDRDPIWKGPA-----K 954
sp|P04588|POL_HV1MA IQNFRVYRDRDPIWKGPA-----K 954
sp|P24740|POL_HV1U4 IQNFRVYRDRDPIWKGPA-----K 954
sp|P17283|POL_SIVCZ VQKFRVYRDRDPIWKGPA-----T 979
sp|P17757|POL_HV2D1 FKFQVYVYREGRDQLWKGPG-----E 1020
sp|P18042|POL_HV2G1 FKNFQVYVYREGRDQLWKGPG-----E 996
sp|P18096|POL_HV2BE FKNFQVYVYREGRDQLWKGPG-----E 1002
sp|P24107|POL_HV2CA LKNFRVYFREGRDQLWKGPG-----E 981
sp|P05962|POL_HV2NZ LKNFRVYFREGRDQLWKGPG-----E 982
sp|P04584|POL_HV2RO LKDFRVYFREGRDQLWKGPG-----E 983
sp|Q74120|POL_HV2KR LKNFRVYFREGRDQLWKGPG-----E 982
sp|P20876|POL_HV2ST LQNFVYFREGRDQLWKGPG-----E 1002
sp|P12451|POL_HV2SB LKNFRVYFREGRNQLWQGGP-----E 982
sp|P05896|POL_SIVM1 FKNFRVYVYREGRDQLWKGPG-----E 1003
sp|P05897|POL_SIVM2 FKNFRVYVYREGRDQLWKGPG-----E 1001
sp|P12502|POL_SIVS4 FKNFRVYVYREGRDQLWKGPG-----E 966
sp|P19505|POL_SIVSP FKNFRVYVYREGRDQLWKGPG-----E 969
sp|P15833|POL_HV2D2 FQNFQVYVYREGRDQLWKGPG-----E 1002
sp|P27980|POL_SIVAG ILNFRVYVYREGRDPIWKGPA-----Q 995
sp|P05895|POL_SIVAT ILNFRVYVYREGRDPIWKGPA-----Q 1010
sp|P27973|POL_SIVA1 ILNFRVYVYREGRDPIWKGPA-----R 990
sp|Q02836|POL_SIVA1 ILNFKVYVYREGRDPIWKGPA-----R 994
sp|P22382|POL_SIVGB NLNFKVYVYREGRDQLWKGPG-----I 966
sp|P23427|POL_VILV2 RFCYYRTRKRKRGHPGEWQGPT-----Q 1066
sp|P35956|POL_VILVK RFCYYRTRKRKRGHPGEWQGPT-----Q 1062
sp|P03370|POL_VILV RFCYYRTRKRKRGHPGEWQGPT-----Q 1066
sp|P23426|POL_VILV1 RFCYYRTRKRKRGHPGEWQGPT-----Q 1066
sp|P16901|POL_OMVVS RFCYYRTRKRKRGHPGEWLGPT-----Q 1047
sp|P33459|POL_CAEVC QFCYYRTRKRKRGHPGEWQDQP-----R 1071
sp|P16088|POL_FIVPE QAQWYIYKQD-KDKKWKQGM-----R 1084
sp|P19028|POL_FIVSD QAQWYIYKQD-KDKKWKQGM-----R 1084
sp|P31822|POL_FIVT2 MMQWLYYKQD-KDKKWKQGM-----R 1084
sp|P11204|POL_EIAV9 KKFCFYKIPG--EHDWKGPT-----R 1113
sp|P32542|POL_EIACV KKFCFYKIPG--EHDWKGPT-----R 1113
sp|P03371|POL_EIAV9 KKFCFYKIPG--EHDWKGPT-----R 1112
sp|P19199|POL_COYMV QPHISKICDFSEKLAETPEGMRSWLGILSYARNYIQDIGKLVQPLRQKMAPTGDKRMNP 1682
sp|P27502|POL_RTBPV QPHIVDKIKKFKDKNLNTLKLGLQAYLGLLNARYGKIDLSKLVGPLYKKTGKNGQRIFNK 1457

sp|P19560|POL_BIV06 VLWDGDGAAVIEEEG--KTALYPRHRMRFIPPPDSIQDQSS----- 1056
sp|P19561|POL_BIV27 VLWDGDGAAVIEEEG--KTALYPRHRMRFIPPPDSIQDQSS----- 1056
sp|P20875|POL_HV1JR LLWKEGEAVVIQDNS--DIKVVPRRKAKIIRDYGKQMGAGDDCVASRQDED----- 1007
sp|P05961|POL_HV1MN LLWKEGEAVVIQDNS--DIKVVPRRKAKIIRDYGKQMGAGDDCVASRQDED----- 1006
sp|P03366|POL_HV1B1 LLWKEGEAVVIQDNS--DIKVVPRRKAKIIRDYGKQMGAGDDCVASRQDED----- 1015
sp|P03368|POL_HV1P1 LLWKEGEAVVIQDNS--DIKVVPRRKAKIIRDYGKQMGAGDDCVASRQDED----- 1015

sp|P04585|POL_HV1H2 LLWKGEGAVVIQDNS--DIKVVPRRKAIIIRDYGGKQAGDDCVASRQDED----- 1003
sp|P04587|POL_HV1B5 LLWKGEGAVVIQDNS--DIKVVPRRKAIIIRDYGGKQAGDDCVASRQDED----- 1015
sp|P03367|POL_HV1BR LLWKGEGAVVIQDNS--DIKVVPRRKAIIIRDYGGKQAGDDCVASRQDED----- 1015
sp|P05960|POL_HV1C4 -----
sp|P12498|POL_HV1J3 -----
sp|P12497|POL_HV1N5 LLWKGEGAVVIQDNS--DIKVVPRRKAIIIRDYGGKQAGDDCVASRQDED----- 1003
sp|P35963|POL_HV1Y2 LLWKGEGAVVIQDNS--DIKVVPRRKAIIIRDYGGKQAGDDCVASRQDED----- 1003
sp|P03369|POL_HV1A2 LLWKGEGAVVIQDNS--DIKVVPRRKAIIIRDYGGKQAGDDCVASRQDED----- 1003
sp|P20892|POL_HV1OY LLWKGEGAVVIQDNS--DIKVVPRRKAIIIRDYGGKQAGDDCVASRQDED----- 1003
sp|P05959|POL_HV1RH LLWKGEGAVVIQDNS--DIKVVPRRKAIIIRDYGGKQAGDDCVASRQDED----- 1002
sp|P04589|POL_HV1EL LLWKGEGAVVIQDNS--DIKVVPRRKAIIIRDYGGKQAGDDCVASRQDED----- 1002
sp|P12499|POL_HV1Z2 LLWKGEGAVVIQDNS--DIKVVPRRKAIIIRDYGGKQAGDDCVASRQDED----- 1002
sp|P18802|POL_HV1ND LLWKGEGAVVIQDNS--DIKVVPRRKAIIIRDYGGKQAGDDCVASRQDED----- 1002
sp|P04588|POL_HV1MA LLWKGEGAVVIQDNS--DIKVVPRRKAIIIRDYGGKQAGDDCVASRQDED----- 1002
sp|P24740|POL_HV1U4 LLWKGEGAVVIQDNS--DIKVVPRRKAIIIRDYGGKQAGDDCVASRQDED----- 1002
sp|P17283|POL_SIVCZ LLWKGEGAVVIQDQ--ELKVVPRRKAIIIRDYGGKQAGDDCVASRQDED----- 1027
sp|P17757|POL_HV2D1 LLWKGEGAVVIQDNS--DIKVVPRRKAIIIRDYGGKQAGDDCVASRQDED----- 1073
sp|P18042|POL_HV2G1 LLWKGEGAVVIQDNS--DIKVVPRRKAIIIRDYGGKQAGDDCVASRQDED----- 1049
sp|P18096|POL_HV2BE LLWKGEGAVVIQDNS--DIKVVPRRKAIIIRDYGGKQAGDDCVASRQDED----- 1059
sp|P24107|POL_HV2CA LLWKGEGAVVIQDNS--DIKVVPRRKAIIIRDYGGKQAGDDCVASRQDED----- 1034
sp|P05962|POL_HV2NZ LLWKGEGAVVIQDNS--DIKVVPRRKAIIIRDYGGKQAGDDCVASRQDED----- 1035
sp|P04584|POL_HV2RO LLWKGEGAVVIQDNS--DIKVVPRRKAIIIRDYGGKQAGDDCVASRQDED----- 1036
sp|Q74120|POL_HV2KR LLWKGEGAVVIQDNS--DIKVVPRRKAIIIRDYGGKQAGDDCVASRQDED----- 1035
sp|P20876|POL_HV2ST LLWKGEGAVVIQDNS--DIKVVPRRKAIIIRDYGGKQAGDDCVASRQDED----- 1055
sp|P12451|POL_HV2SB LLWKGEGAVVIQDNS--DIKVVPRRKAIIIRDYGGKQAGDDCVASRQDED----- 1035
sp|P05896|POL_SIVM1 LLWKGEGAVVIQDNS--DIKVVPRRKAIIIRDYGGKQAGDDCVASRQDED----- 1056
sp|P05897|POL_SIVMK LLWKGEGAVVIQDNS--DIKVVPRRKAIIIRDYGGKQAGDDCVASRQDED----- 1054
sp|P12502|POL_SIVS4 LLWKGEGAVVIQDNS--DIKVVPRRKAIIIRDYGGKQAGDDCVASRQDED----- 1019
sp|P19505|POL_SIVSP LLWKGEGAVVIQDNS--DIKVVPRRKAIIIRDYGGKQAGDDCVASRQDED----- 1022
sp|P15833|POL_HV2D2 LLWKGEGAVVIQDNS--DIKVVPRRKAIIIRDYGGKQAGDDCVASRQDED----- 1058
sp|P27980|POL_SIVAG LLWKGEGAVVIQDNS--DIKVVPRRKAIIIRDYGGKQAGDDCVASRQDED----- 1046
sp|P05895|POL_SIVAT LLWKGEGAVVIQDNS--DIKVVPRRKAIIIRDYGGKQAGDDCVASRQDED----- 1061
sp|P27973|POL_SIVA1 LLWKGEGAVVIQDNS--DIKVVPRRKAIIIRDYGGKQAGDDCVASRQDED----- 1047
sp|Q02836|POL_SIVA1 LLWKGEGAVVIQDNS--DIKVVPRRKAIIIRDYGGKQAGDDCVASRQDED----- 1052
sp|P22382|POL_SIVGB LLWKGEGAVVIQDNS--DIKVVPRRKAIIIRDYGGKQAGDDCVASRQDED----- 1009
sp|P23427|POL_VILV2 VLWGGDGAIVVKDRGTDRYLVIANKDVKFIPPPKEIQE----- 1105
sp|P35956|POL_VILVK VLWGGDGAIVVKDRGTDRYLVIANKDVKFIPPPKEIQE----- 1101
sp|P03370|POL_VILV VLWGGDGAIVVKDRGTDRYLVIANKDVKFIPPPKEIQE----- 1105
sp|P23426|POL_VILV1 VLWGGDGAIVVKDRGTDRYLVIANKDVKFIPPPKEIQE----- 1105
sp|P16901|POL_OMVVS VLWGGDGAIVVKDRGTDRYLVIANKDVKFIPPPKEIQE----- 1086
sp|P33459|POL_CAEVC YCGKGEPIVVKDIESEKYLVIPIYKDAKFIPTTKEKE----- 1109
sp|P16088|POL_FIVPE VEYWGQGSVLLKDEE-KGYFLIPRRHRRVPEPCALPEGDE----- 1124
sp|P19028|POL_FIVSD VEYWGQGSVLLKDEE-KGYFLIPRRHRRVPEPCALPEGDE----- 1124
sp|P31822|POL_FIVT2 VEYWGQGSVLLKDEE-KGYFLIPRRHRRVPEPCALPEGDE----- 1124
sp|P11204|POL_EIAV9 VLWGGDGAIVVNDEG-KGHAVPLTRTKLLIKPN----- 1146
sp|P32542|POL_EIAVC VLWGGDGAIVVNDEG-KGHAVPLTRTKLLIKPN----- 1146
sp|P03371|POL_EIAVY VLWGGDGAIVVNDEG-KGHAVPLTRTKLLIKPN----- 1145
sp|P19199|POL_COVMV ETWKMVRRQIKKVKNLPLQLPKDSFHITDGCMTGWGAVCKWKMCKHDPSTERICA 1742
sp|P27502|POL_RTBPV EDWNHIFKIEREVSKIKPLERPKETDYIHITDASEEGWGAIVLCKPDKYSGKDTTEKIAG 1517

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sp|P05961|POL_HV1MN -----
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sp|P03368|POL_HV1PV -----
sp|P04585|POL_HV1H2 -----
sp|P04587|POL_HV1B5 -----
sp|P03367|POL_HV1BR -----
sp|P05960|POL_HV1C4 -----
sp|P12498|POL_HV1J3 -----
sp|P12497|POL_HV1N5 -----
sp|P35963|POL_HV1Y2 -----
sp|P03369|POL_HV1A2 -----
sp|P20892|POL_HV1OY -----
sp|P05959|POL_HV1RH -----
sp|P04589|POL_HV1EL -----
sp|P12499|POL_HV1Z2 -----
sp|P18802|POL_HV1ND -----
sp|P04588|POL_HV1MA -----
sp|P24740|POL_HV1U4 -----
sp|P17283|POL_SIVCZ -----
sp|P17757|POL_HV2D1 -----
sp|P18042|POL_HV2G1 -----
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sp|P24107|POL_HV2CA -----
sp|P05962|POL_HV2NZ -----
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sp|Q74120|POL_HV2KR -----
sp|P20876|POL_HV2ST -----
sp|P12451|POL_HV2SB -----
sp|P05896|POL_SIVM1 -----
sp|P05897|POL_SIVMK -----
sp|P12502|POL_SIVS4 -----
sp|P19505|POL_SIVSP -----
sp|P15833|POL_HV2D2 -----
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sp|P05895|POL_SIVAT -----
sp|P27973|POL_SIVA1 LQDQE----- 1057
sp|Q02836|POL_SIVA1 -----
sp|P22382|POL_SIVGB -----
sp|P23427|POL_VILV2 -----
sp|P35956|POL_VILVK -----
sp|P03370|POL_VILV -----
sp|P23426|POL_VILV1 -----
sp|P16901|POL_OMVVS -----
sp|P33459|POL_CAEVC -----
sp|P16088|POL_FIVPE -----
sp|P19028|POL_FIVSD -----
sp|P31822|POL_FIVT2 -----
sp|P11204|POL_EIAV9 -----
sp|P32542|POL_EIAVC -----
sp|P03371|POL_EIAVY -----

sp|P19199|POL_COYMV YASGSFNPIKSTIDAEIQAAIHGLDKFKIYYLDKKEIIRSDCEAIKFKYNKTNENKPSR 1802
sp|P27502|POL_RTBPV YASGNFGEKKTWTSLDYEIEAINEALNKFQIYLDKDFITRTDCEAIVKGIKTEDYKRSK 1577

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sp|P17757|POL_HV2D1 -----
sp|P18042|POL_HV2G1 -----
sp|P18096|POL_HV2BE KINLVYRKVLDRCYPRLCRHPNT----- 1142
sp|P24107|POL_HV2CA -----
sp|P05962|POL_HV2NZ -----
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sp|Q74120|POL_HV2KR -----
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sp|P27980|POL_SIVAG -----
sp|P05895|POL_SIVAT -----
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sp|Q02836|POL_SIVAI -----
sp|P22382|POL_SIVGB -----
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sp|P35956|POL_VILVK -----
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sp|P16901|POL_OMVVS -----
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sp|P16088|POL_FIVPE -----
sp|P19028|POL_FIVSD -----
sp|P31822|POL_FIVT2 -----
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sp|P32542|POL_EIAVC -----
sp|P03371|POL_EIAVY -----
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sp|P27502|POL_RTBPV TRWIKLRDNLKLDGYKPTFEHIKGNKNFLPNLSREGDFILKCLQNPDESTESYSIDSSSES 1637

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sp|P03368|POL_HV1PV -----
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sp|P04587|POL_HV1B5 -----
sp|P03367|POL_HV1BR -----
sp|P05960|POL_HV1C4 -----
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sp|P12497|POL_HV1N5 -----
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sp|P03369|POL_HV1A2 -----
sp|P20892|POL_HV1OY -----
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sp|P12499|POL_HV1Z2 -----
sp|P18802|POL_HV1ND -----
sp|P04588|POL_HV1MA -----
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sp|P20876|POL_HV2ST -----
sp|P12451|POL_HV2SB -----
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sp|P05897|POL_SIVMK -----
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sp|P19505|POL_SIVSP -----
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sp|P05895|POL_SIVAT -----
sp|P27973|POL_SIVA1 -----
sp|Q02836|POL_SIVAI -----
sp|P22382|POL_SIVGB -----
sp|P23427|POL_VILV2 -----
sp|P35956|POL_VILVK -----

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sp|P03370|POL_VILV -----
sp|P23426|POL_VILV1 -----
sp|P16901|POL_OMVVS -----
sp|P33459|POL_CAEVC -----
sp|P16088|POL_FIVPE -----
sp|P19028|POL_FIVSD -----
sp|P31822|POL_FIVT2 -----
sp|P11204|POL_EIAV9 -----
sp|P32542|POL_EIAVC -----
sp|P03371|POL_EIAVY -----
sp|P19199|POL_COYMV VCNDHGRNLISAVINDIITVLR----- 1886
sp|P27502|POL_RTBPV IPLYIDSKESHIESDDSIPLYRDKLLPLVERLKEKSA 1675
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(
(
(
sp|P19560|POL_BIV06:0.00090,
sp|P19561|POL_BIV27:0.00099)
:0.33629,
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sp|P19199|POL_COYMV:0.37998,
sp|P27502|POL_RTBPV:0.38002)
:0.20132)
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sp|P33459|POL_CAEVC:0.12393,
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sp|P16901|POL_OMVVS:0.06938,
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sp|P23426|POL_VILV1:0.00386,
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sp|P23427|POL_VILV2:0.00086,
sp|P35956|POL_VILVK:0.00277)
:0.00012,
sp|P03370|POL_VILV:0.00079)
:0.00338)
:0.05845)
:0.04841)
:0.21362,
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(
(
sp|P16088|POL_FIVPE:0.02365,
sp|P19028|POL_FIVSD:0.02796)
:0.04373,
sp|P31822|POL_FIVT2:0.07326)
:0.21467)
:0.01074,
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(
(
sp|P11204|POL_EIAV9:0.00045,
sp|P32542|POL_EIAVC:0.00042)
:0.00157,
sp|P03371|POL_EIAVY:0.00367)
:0.31107)
:0.01042)
:0.10268,
(
(
(
(
sp|P18096|POL_HV2BE:0.03656,
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sp|P17757|POL_HV2D1:0.03966,
sp|P18042|POL_HV2G1:0.03470)
:0.00209)
:0.01576,
(
(

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