

A Poor Mans EVA: Examining the Accuracy of Secondary Structure Prediction

Introduction

One of the best, but perhaps most elusive, things to know about a protein is its structure. Knowing the structure of a protein allows us to infer if not directly see a number of things. For instance, it can tell us how a transcription factor interacts with DNA or how two proteins can combine to form a particular heterodimer. A hallmark of protein activity is an event which causes a conformational change which ultimately results in the proteins altered ability to bind or release or interact in some other way with another protein, ion, or macromolecule. How a protein alters its structure would most likely not be known without solved crystal structures of a given protein. However, obtaining the crystal structure of a protein is a labor-intensive process which can take a number of years to successfully complete. Many investigators with novel proteins would be able to direct their research in a certain direction if they could have a solved structure quickly, but this is usually not possible, and some proteins are nearly impossible to crystallize. In lieu of having an actual structure, the next best thing would be an accurate way to predict protein structure given primary sequence. These predictions could lead an investigator down certain avenues of research that may have been ignored, possibly leading to rapid discoveries and a coveted publication in *Nature* or *Science*.

Although a proteins tertiary structure is usually of the most interest, there can be no prediction of tertiary structure without the prediction of secondary structure. For this fact, an investigation into the accuracy of secondary structure predictors was launched. This is not a novel idea in the world of protein structure prediction in that there is a web-base server that continuously evaluates automatic structure prediction servers named

EVA (<http://cubic.bioc.columbia.edu/eva>), which has collected more than 20,000 secondary structure predictions since June 2000 (1). As EVA analyzes the accuracy of a given structure predictor, it gives it a Q3 score with the current top Q3 score of 74.4 belonging to PROFsec. Furthermore, there are yearly meetings known as CASP (Critical Assessment of Structure Prediction) in which various protein structure prediction programs are put to the test against recently solved sequences. However, there are a number of structure prediction services that are actually overlooked by EVA and CASP and it would be beneficial to examine the accuracy of these systems. Furthermore, there are different approaches to predicting protein structure and a comparison among these models would be beneficial as well. Therefore, I designed a rather rudimentary, but effective method at looking at three different protein secondary structure prediction services, PSIPRED (<http://www.psipred.net>), PROF king (<http://www.aber.ac.uk/~phiwww/prof/>), and the SeqWeb contribution, PeptideStructure (<http://pmgm2.stanford.edu/gcg-bin/seqweb.cgi>).

As mentioned above, there are different approaches to designing algorithms for predicting protein structure. The first method is homology modeling, which essentially builds a model of an unknown protein based on sequence similarity to proteins that already have a known or solved structure (2). A second method is known as ab initio prediction in which protein structure prediction is based purely on first principles without the use of any templates as in homology modeling. The third method is known as sequence-structure threading, or fold recognition which is similar to homology in that a template of already known folds is compared to the unknown protein to derive a structure prediction. A fourth method is docking, but is irrelevant to this discussion in that it is

used for predicting quaternary structure of proteins (protein-protein interactions). It seems as if the method of choice for structure prediction is the “comparative modeling” methods like fold recognition and homology modeling. Many feel that within 10 years, there will be at least one example of most structural folds, which would make comparative modeling very useful (3). Two of the three services analyzed in this paper use comparative modeling, PSIPRED and PROF king. Specifically, they both use homology modeling by searching a database to look for homologous sequences (PSI-BLAST) and then use the known structures of the found sequences to predict secondary structure. PROF king also uses ClustalW for sequence alignments of results obtained from PSI-BLAST whereas PSIPRED uses neural networks to directly analyze the output from PSI-BLAST. The third service, PeptideStructure, I consider to be an ab initio method of structure prediction. Specifically, PeptideStructure uses the Chou-Fasman parameters which assign a set of values (called prediction values) to a residue and then an algorithm is applied to those numbers to determine which areas are alpha-helices and which are beta-strands (or sheets) (4). The details can be cumbersome and won't be discussed further, but the importance lies in the fact that PeptideStructure uses no known protein sequences to make its predictions.

Materials and Methods

Using the NCBI website, (<http://www.ncbi.nlm.nih.gov/entrez/query.fcgi?db=Structure>), 10 different protein sequences with known structures were obtained (See Appendix A for accession numbers and sequences). The proteins picked were of different lengths, from different species, and varied in their secondary structure. The proteins chosen were: RNase Hi, RNase Sa,

Myoglobin, Polio 3C proteinase, Green Fluorescent Protein (GFP), eIF6, Procaspase-7, Procathepsin L, RNA Polymerase, and Trypsin IV. The known secondary structures of each of these proteins were then retrieved from the Protein Data Bank (PDB, <http://www.rcsb.org/pdb/>). Following this, each sequence was run through the three structure predicting services PSIPRED (<http://www.psipred.net>), PROF king (<http://www.aber.ac.uk/~phiwww/prof/>), and PeptideStructure (<http://pmgm2.stanford.edu/gcg-bin/seqweb.cgi>).

After all predictions were retrieved, all sequences were examined by hand. Specifically, analysis was limited to prediction of helices and sheets. The total number of residues that formed alpha-helices or beta-strands were counted and recorded. For each predicted protein structure, the number of correctly predicted residues were then counted and the success of the prediction was expressed as a percent of the total alpha-helices and beta-sheets.

Results

Of the three structure prediction services examined, there appeared to be a clear hierarchy of the accuracy according to my methods of analysis. The first structure prediction service to be examined was the PROF king service. The results are summarized in table 1.

Sequence	Total Scorable Residues	Total Correct	Percent Correct
Ribonuclease Sa	26	12	46.1%
Ribonuclease Hi	93	71	76.3%
Procathepsin L	139	107	76.0%
Hep C RNA Polymerase	303	241	79.5%
Trypsin IV	83	73	87.9%
Procaspase 7	110	85	77.3%

Poliovirus 3C Protease	88	63	71.6%
EIF6	129	100	77.5%
Whale Myoglobin	112	103	92.0%
GFP	124	93	75%

Table 1: Analysis of PROF king protein structure prediction program.

The scores range from a low of 46.1% (from a very small protein) to 92.0% to a larger, but nearly exclusively helical protein. For the most part, the scores fall in the mid to upper 70% range, which is fairly accurate.

After the analysis of PROF king, I then went on to analyze the PeptideStructure service. The results are summarized in Table 2.

Sequence	Total Scorable Residues	Total Correct	Percent Correct
Ribonuclease Sa	26	5	19.2%
Ribonuclease Hi	93	47	50.5%
Procathepsin L	139	ND	ND
Hep C RNA Polymerase	303	ND	ND
Trypsin IV	83	58	69.9%
Procaspase 7	110	65	59.1%
Poliovirus 3C Protease	88	37	42.0%
EIF6	129	76	58.9%
Whale Myoglobin	112	71	63.4%
GFP	124	ND	ND

Table 2: Analysis of PeptideStructure protein structure prediction program. ND=No Data

For this protein prediction program, the scores were significantly lower than the scores that were derived for PROF king. A further problem had with this program was the fact that it was unable to handle 3 proteins because they had unresolved proteins within their sequence, denoted in the protein sequence as X. Therefore, predictions for three protein sequences were unable to be obtained. With a low of 19.2% and a high of only 69.9%, it appears as if this program did not fare well in this rather simple method of analysis.

Lastly, the PSIPRED homology modeling program was also examined as to assess its accuracy. The results for this analysis are summarized in table 3.

Sequence	Total Scorable Residues	Total Correct	Percent Correct
Ribonuclease Sa	26	15	57.7%
Ribonuclease Hi	93	79	84.9%
Procathepsin L	139	119	85.6%
Hep C RNA Polymerase	303	223	73.6%
Trypsin IV	83	78	94.0%
Procaspase 7	110	92	83.6%
Poliovirus 3C Protease	88	63	71.6%
EIF6	129	109	84.5%
Whale Myoglobin	112	103	92%
GFP	124	99	79.84%

Table 3: Analysis of PSIPRED protein structure prediction program

This protein prediction program actually yielded the best results in this method of analysis when compared to the other two programs tested. The low yielded from the analysis of PSIPRED was a high 57.7% with the high being an impressive 94% on a rather large 224 amino acid sequence.

Comparing the results of all three analyses, it appears that under this form of analysis, the PSIPRED surpasses both PROF king and PeptideStructure based on the average of the percent residues correct (Table 4).

Method Analyzed	Total Scorable Residues	Total Correct Residues	Total Percent	Average Percent
PROF King	1207	948	78.5%	75.9%
PeptideStructure	641	359	56.0%	51.9%
PSIPRED	1207	980	81.2%	81.73%

Table 4: Data summary of the three protein structure programs analyzed. Average percent taken as the average percentage of the percent correct field in tables 1-3.

Discussion

From this analysis, there appears not only to be a difference among the three individual programs tested, but also amongst the two types of analyses presented here (ab initio vs. homology modeling). From this analysis, the current strength of homology modeling is brought forward while the fact that ab initio modeling still seems to have quite a ways to go. One obvious shortcoming of the PeptideStructure method is in the method itself. By using the Chao-Fasman method of prediction (which is a number of years old), PeptideStructure will only recognize alpha-helices that are at least 6 residues long and beta-strands that are at least 5 residues long. A quick look at the actual secondary structures actually shows a number of residues that are parts of helices or sheets that are not 5 or 6 residues long and are automatically missed in the PeptideStructure analysis, but are often picked up by the homology modeling programs.

Another obvious fault with the PeptideStructure protein structure prediction program is that it is unable to deal with unknown proteins within a given polypeptide sequence. In many solution structures, there are a couple of unknown proteins, usually identified by the letter X. Three of the proteins used for analysis contained a certain number of unknown proteins to see how analysis would be affected. The two homology modeling programs were able to successfully complete analysis of all 10 proteins whereas the PeptideStructure program was unable to deal with these sequences, yielding no data. This is a very obvious and blatant problem with this particular peptide structure prediction software. It appears as if this inability to deal with the unknown amino acids would cut out a large portion of sequences that could be analyzed. When novel proteins are sequenced, often times not all amino acids can be adequately resolved. Therefore, this program would appear to be useless in the prediction of a number of proteins whose

sequence cannot be completely determined, rendering it nearly useless. However, a surrogate analysis could be performed by replacing the unknown amino acids with another, rather innocuous amino acid, like alanine. This may affect the protein structure predicted in the immediate area of the change, but at least analysis could be performed and the rest of the protein could be analyzed.

From the data presented, it seems that the PSIPRED program is the most accurate program when subjected to this kind of analysis. This may not be the most stringent form of analysis, but it definitely could be useful to know that when you subject one of your protein sequences to one of these programs for analysis, at a basal level, you can know that a little better than three out of every four amino acids is correct when you use PSIPRED or PROF king and barely better than half are actually correct when you use PeptideStructure. As many groups feel, and as this data show, the ab initio procedures of protein secondary structure prediction still have a long way to go before they are accurate.

However, the PSIPRED and PROF king programs are also without their shortfalls. Obviously, neither one was 100% accurate as would be hoped, but that is a somewhat unrealistic expectation for theoretical computational molecular biology. Even though known protein structures were used for this analysis, and these programs all use PSI-BLAST searches to build their databases from, a 100% accurate protein prediction was never gained even though the exact protein should have been found in the PSI-BLAST searches performed by these programs. One would almost think that after finding exact 100% homology between the query sequence and a sequence that exists in a database; one could get a perfect protein prediction. This is most likely an artifact of the

algorithms used for predicting structure. This gave me more of an insight as to how these programs work which is beneficial in that most of the explanations as to the intricacies of algorithms and the programs used for them go over my head. Basically, it appears as if these two programs merely take an average of all the sequences that it finds and this is the output that you end up seeing. There is obviously no perfect prediction and a researcher should obviously use caution when protein prediction programs are used.

As one moves into the analysis of tertiary structure, things become more and more complicated. I would predict that the accuracy would decrease as more complexity is introduced into what is being asked for. However, as more and more protein structures get solved, the number of unknown folds decreases dramatically, increasing the power of homology based modeling not only for the prediction of secondary protein structure, but also for the prediction of tertiary protein structure. One has to wonder that as our knowledge of existing proteins grows, will ab initio structure prediction ever catch up to the homology modeling systems? Also, what accounts for the differences amongst the homology modeling programs? It seems that the biggest difference between PSIPRED and PROF king is the fact that PSIPRED uses a neural network in its analysis of sequences. Is this the main reason that PSIPRED has the highest accuracy rate of over 80% in both categories? PSIPRED has also been shown to receive some of if not the highest scores in the CASP meetings, with its highest honors garnered last year (information from PSIPRED website). Perhaps further development of these neural networks will lead to a continued increase in protein structure prediction like what we have observed since the inception of theoretical computational molecular biology.

Though the analysis was simple, it was effective in showing a large difference between homology modeling and ab initio modeling. The current accuracy of homology modeling was re-enforced; as was the idea that much more development of ab initio prediction is needed. A beneficial avenue to take may be to extend (and also complicate) this analysis not only into fold recognition programs, but also into the analysis of tertiary structure. At some point in the future, it may be possible to try and extend this analysis into three dimensions and actually look at how accurate these programs are at placing an individual amino acid in the correct space in a 3D environment.

References

1. Rost Burkhard and Eyrich Volker A. EVA: Large-Scale Analysis of Secondary Structure Prediction. *Proteins: Structure, Function, and Genetics Suppl* 2001; 5: 192-199.
2. Marti-Renom Marc A., Stuart Ashley C., Fiser Andras, Sanchez Roberto, Melo Francisco, Sali Andrej. Comparative Protein Structure Modeling of Genes and Genomes. *Annu. Rev. Biophys. Biomol. Struct.* 2000; 29:291-325.
3. Sanchez Roberto, Sali A. Advances in Comparative Protein-Structure Modeling. *Curr. Opin. Struct. Biol.* 7:206-214.
4. Privelige P., Jr, Fasman G.D. Chou-Fasman Prediction of Secondary Structure, in *Prediction of Protein Structure and the Principles of Protein Conformation*, ed. G.B. Fasman (ISBN 0-306-43131-9, Plenum, New York) (1989) 1-91.

Appendix A

Procaspase-7 Chain A

>gi|18158705

SIKTTRDRVPTYQYNMNFEEKLGKCI IINNKNFDKVTGMGVRNGTDKDAEALFKCFRSLGFDVIVYNDSC
AKMQDLLKKASEEDHTNAACFACILLSHGEENVIYKGDGVTP IKDLTAHFRGDRCKTLLEKPKLFFIQAA
RGTELDGDIQADSGPINDTDANPRYKIPVEADFLFAYSTVPGYYSWRSPGRGSWFVQALCSILEEHGKDL
EIMQILTRVNDRVARHFESQSDDPHFHEKKQIPCVVSMMLTKELYFSQLEHHHHHH

Sperm Whale Myoglobin, Chain A

>gi|18655862

VLSEGEWQLVLHVWAKVEADVAGHGQDILIRLFKSHPETLEKDFRFKHLKTEAEMKASEDLKKHGVTVLT
ALGAILKKKGHHEAELKPLAQSHATKHKIPIKYLEFISEAIIHVLHSRHPGDFGADAQGAMNKALELFRK
DIAAKYKELGYQG

S. cerevisiae eif6

>gi|11513605

MATRTQFENSNEIGVFSKLTNTYCLVAVGGSENFYSAFEAELGDAIPIVHTTIAGTRIIIGRMTAGNRRGL
LVPTQTDDQELQHLRNSLPDSVKIQRVEERLSALGNVICNDYVALVHPDIDRETEELISDVLGVEVFRQ
TISGNILVGSYCSLSNQGLVHPQTSVQDQEELSSLLQVPLVAGTVNRRGSSVVGAGMVVNDYLAVTGLDT
TAPELSVIESIFRL

Procathepsin L (human)

>gi|5822035

SLTFDHSLEAQWTKWKAMHNRLYGMNEEGWRRRAVWEKNMKMIELHNQEYREGKHSFTMAMNAFGDMTSEE
FRQVMNGFQNRKPRKGKVFQEPLFYEA PRSVDWREKGYVTPVKNQGCQSXWAFSATGALEGQMFRTGR
LISLSEQNLVDCSGPQGNEGCNGGLMDYAFQYVQDNGGLDSEESYPYEATEESCKYNPKYSVANDAGFVD
IPKQEKALMKAVATVGPISVAIDAGHESFLFYKEGIYFEPDCSSEDMDHGVLVVGYGFEFESTESDNKYWL
VKNSWGEWGMGGYVKMAKDRRNHCGIASAASYPTV

Human Trypsin IV

>gi|20149993

IVGGYTCEENSLPYQVSLNSGSHFCGGSLISEQWVVSAAHCYKTRIQVRLGEHNIKVLEGNEQFINAVKI
IRHPKYNRDTLDNDIMLIKLS SPAVINARVSTISLPTAPPAAGTECLISGWGNTLSFGADYPDELKCLDA
PVLTAECKASYPGKITNSMFCVGFLEGGKDCQRDSGGPVVVCNGQLQGVVSWGHGCAWKNRPGVYTKVY
NYVDWIKDTIAANS

Hepatitis C RNA pol w/UTP and Mn

>gi|20663766

SXSYTWTGALITPCAEEESKLPINALSNSLLRHHNXVYATTSRSAGLRQKKVTFDRLQVLDHHRDVLKE
XKAKASTVKAKLLSVEEACKLTPPHSAKSKFGYGAKDVRNLSSKAVNHIHSVWKDLLEDTVTPIDTTIXA
KNEVFCVQPEKGGKPARLIVFPDLGVRVCEKXALYDVVSTLPQVVXGSSYGFQYSPGQRFVFLVNTWKS
KKNPXGFSYDTRCFDSTVTENDIRVEESIYQCCDLAPPEARQAIAKSLTERLYIGGPLTNSKGQNCGYRRCR
ASGVLTTSCGNTLTCYLKASAAACRAAKLQDCTXLVNGDDLVIICESAGTQEDAASLRVFTAXTRY SAPP
GDPPQPEYDLELITSCSSNVSAHDASGKRYYLTRDPTPLARA AWETARHTPVNSWLGNIIXYAPTLW
ARXILXTHFFSILLAQEQLKALDCQIYGACYSIEPLDLPQIIERLHGLSAFSLHSYSPGEINRVASCLR
KLGVPPLRVWRHRARSVRARLLSQGGRAATCGKYLFNWA VK

Poliovirus 3c proteinase

>gi|20664254

GPGFDYAVAMAKRNIVTATTSKGEFTMLGVHDNVAI LPTHASPGESIVIDGKEVEILDAKALEDDQAGTNL
EITITLKRNEKFRDIRPHIPTQITETNDGV LIVNTSKYPNMYVPVGAVTEQGYLNLGGRQTARTLMYNF
PTRAGQCGGVITCTGKVI GMHVGGNGSHGFAAALKRSYFTQSQ

Streptomyces aureofaciens Ribonuclease Sa Chain A

>gi|17942897

DVSGTVCLSLPPEATDTLNLIASDGPFPYSQDGVVFNRESVLPTQSYGYYHEYTVITPGARTRGTRRI
ITGEATQEDYYTGDHYATFSLIDQTC

E. Coli D10a RNase Hi

>gi|20150465

MLKQVEIFTAGSALGNPGPGGYGAILRYRGREKTFSSAGYTRTTNNRMELMAAIVALEALKEHAEVILSTD
SQYVRQGITQWIHNWKKRGWKTADKKPVKNVDLWQRLDAALGQHQIKWEWVKGHAGHPENERADELAAAA
AMNPTLEDTGYYQVEV

Aequorea Victoria GFP

>gi|17943298

MSKGEELFTGVVPILEVELDGDVNGHKFSVSGEGEGDATYGKLTLLKFICTTGKLPVPWPTLVTTFFXVQCFS
RYPDHMKRHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTLVNRIELKIDFKEDGNILGHKLE
YNYNSHNVYIMADKQKNGIKVNFKIRHNIEDGSVQLADHYQQNTPIGDGPVLLPDNHYLSTQSALSKDPN
EKRDHMLLEFVTAAGITHGMDELYK

Appendix B: Solved Structures

Poliovirus 3C Proteinase Secondary Stx

```
1  GPGFDYAVAM  AKRNIVTATT  SKGEFTMLGV  HDNVAILPTH  ASPGESIVID
    SSSHHHHH  HHHHEEEEEEE  TTEEEEEEE  EETEEEEEGG  G  SEEEE
51  GKEVEILDAK  ALEDQAGTNL  EITIIITLKR  EKFRDIRPHI  PTQITETNDG
    TEEEESEEE  E B TTS B    EEEEE   S   B   GGGB  SS   BSSE
101 VLIVNTSKYP  NMYVPVGAVT  EQGYLNLGGR  QTARTLMYNF  PTRAGQCGGV
    EEEE  SSSS  SEEEE  B  EE  E  B  EEETTE  EE  SEEEE  TTTTT  E
    151 ITCTGKVIGM  HVGNGSHGF  AAALKRSYFT  QSQ
        EEETTEE  EE  E  EEETTEE  EEE  GGG
```

S. cerevesiae eif6 Secondary Stx

```
1  MATRTQFENS  NEIGVFSKLT  NTYCLVAVGG  SENFYSAFEA  ELGDAIPIVH
    EEEE  BTTB  HHHHEEE  SEEEEETT  HHHHHHHH  HHTTTSEEE
51  TTIAGTRIIG  RMTAGNRRGL  LVPTQTTDQE  LQHLRNSLPD  SVKIQRVEER
    E  BTTBS  HH  HHEEE  SSEE  EEETT  HHH  HHHHHHS  T  TSEEEEE
101 LSALGNVICC  NDYVALVHPD  IDRETEELIS  DVLGVEVFRQ  TISGNILVGS
    SS  HHHHEEE  SEEEEETT  HHHHHHHH  HHHTSEEEEE  BTTBS  GGG
151 YCSLSNQGL  VHPQTSVQDQ  EELSSLLQVP  LVAGTVNRGS  SVVGAGMVVN
    SEEE  SEEEE  E  TT  HHHH  HHHHHHTSE  EEE  BTTTB  S  HHHHEEE
    201 DYLAVTGLDT  TAPELSVIES  IFRL
        SS  EEEETT  HHHHHHHH  HTTT
```

Green Fluorescent Protein Solved Structure

```
1  MSKGEELFTG  VVPILEVELD  DVNGHKFSVS  GEGEGDATYG  KLTLKFICTT
    GGGGGSS  EEEEEEEEE  ETTTEEEEE  EEEEEGGGT  EEEEEETT
51  GKLPVPWPTL  VTTFXVQCFS  RYPDHMKRHD  FFKSAMPEGY  VQERTIFFKD
    SS  SS  HHHH  TTTS  GGG  B  GGGGG  HHHHTTTT  E  EEEEEETT
101 DGNYKTRAEV  KFEGDTLVNR  IELKGIDFKE  DGNILGHKLE  YNYNSHNVYI
    S  EEEEEEE  EETTTEEEE  EEEEEES  T  TSTTTTT  B  S  EEEEE
151 MADKQKNGIK  VNFKIRHNIE  DGSVQLADHY  QQNTPIGDGP  VLLPDNHYLS
    EEEGGTTEE  EEEEEEEET  TS  EEEEE  EEEEESS  S  SEEEE
    201 TQSALSKDPN  EKRDHMVLE  FVTAAGITHG  MDELYK
        EEEEE  TT  SEEEEEE  EEEEE
```

Hepatitis C RNA Polymerase Secondary Stx

```
1  SXSYTWTGAL  ITPCAAESK  LPINALSNL  LRHHNXVYAT  TSRSAGLRQK
    B  EEE  S    SS  B    HHHHHH  S  GGEEE  GGGHHHHH
51  KVTFDRLQVL  DDHYRDVLKE  XKAKASTVKA  KLLSVEEACK  LTPPHSAKSK
    HT  B    HHHHHHHH  HHHHHTT  B    HHHHHH  TTTTTS  T
101 FGYGAKDVRN  LSSKAVNHIH  SVWKDLEDT  VTPIDTTIXA  KNEVFCVQPE
    TS  HHHHT  T  HHHHHHHH  HHHHHHHH  S  SS  EEEEE  EEE  BT
151 KGGRKPARLI  VFPDLGVRVC  EKXALYDVVS  TLPQVVXGSS  YGFQYSPGQR
    TTBS  EE  EEE  HHHHHH  HHHHHTTTT  THHHHHGGG  BGGG  HHHH
201 VEFLVNTWKS  KKNPXGFSYD  TRCFDSTVTE  NDIRVEESIY  QCCLAPEAR
    HHHHHHHH  TTTEEEEE  ETTHHHHTH  HHHHHHHH  TTSB  HHHH
251 QAIKSLTERL  YIGGPLTNSK  GQNCGYRRCR  ASGVLTTSCG  NTLTCYLKAS
    HHHHHHHH  TS  EEEE  TT  S  B  EEE  S  TTTTTHHH  HHHHHHHH
301 AACRAAKLQD  CTXLVNGDDL  VVICESAGTQ  EDAASLRVFT  EAXTRYAPP
    HHHHHTT  SS  EEEETT  EEEEE  HH  HHHHHHHH  HHHHHTT  B
```

351 GDPPQPEYDL ELITSCSSNV SVAHDASGKR VYYLTRDPTT PLARAAWETA
SS BS G GG BTTEEE EEEE TT E EEEEE HHH HHHHHHHHHH
401 RHTPVNSWLG NIIXYAPTLW ARXILXTHFF SILLAQEQL KALDCQIYGA
S S HHHH HHHHTTTSHH HHHTHHHHHH HHHHTTTTTT EEEEEETE
451 CYSIEPLDLP QIIERLHGLS AFSLHSYSPG EINRVASCLR KLGVPPLRVW
EEEE GGGHH HHHHHHHH GG GGT B HH HHHHHHHHHH HHT HHHH
501 RHRARSVRAR LLSQGGRAAT CGKYLFWAV K
HHHHHHHHHH HHTTTTHHHHH HHHHTGGG

Sperm Whale Met-Myoglobin Secondary Structure

1 VLSEGEWQLV LHVWAKVEAD VAGHGQDILI RLFKSHPETL EKFDKFKHLK
HHHHHHHH HHHHHHHHTTS HHHHHHHHHH HHHHTHHHHH TTTTTTTT
51 TEAEMKASED LKKHGVTVLT ALGAILKKKG HHEAELKPLA QSHATKHKIP
SHHHHHHTHH HHHHHHHHHH HHHHHHTTTT TTHHHHTHHH HHHHHTS
101 IKYLEFISEA IIVLHSRHP GDFGADAQGA MNKALELFRK DIAAKYKELG
HHHHHHHHHH HHHHHHHHTT TTTTHHHHHH HHHHHHHHHH HHHHHHHHT
151 YQG

Human Procaspase-7 Secondary Stx

1 SIKTTRDRVP TYQYNMNF EK LGKCIINNK NFDKVTGMGV RNGTHDKDAEA
S SSB SSB EEEEEEE GGGT TTHHHHHHH
51 LFKCFRSLGF DVIVYND CSC AKMQDLLKKA SEEDHTNAAC FACILLSHGE
HHHHHHHHTE EEEEEES H HHHHHHHHHH HHS TTBSE EEEEEEEEE
101 ENVIYKGDGV TPIKDLTAHF RGDRCKTLE KPKLFFIQAA RGTLEDGDIQ
SSEEE SSSE EEHHHHHHHT TTTTTGGGT SEEEEEEEEE S S
151 ADSGPINDTD ANPRYKIPVE ADFLFAYSTV PGYYSWRSPG RGSWFVQALC
S TTEEEEEEE SS HHHHHHH
201 SILEEHGKDL EIMQILTRVN DRVARHFESQ SDDPHFHEKK QIPCVM SMLT
HHHHHHHTTT TTHHHHHHHH HHHHHHTTS SSTT EEEE S
251 KELYFSQLEH HHHHH
SB S SS

Procathepsin L Secondary Stx

1 SLTFDHSLEA QWTKWKAMHN RLYGMNEEGW RRAVWEKNMK MIELHNQEYR
GGGHH HHHHHHHHTT TTHHHH HHHHHHHHHH HHHHHHHHHH
51 EGKHSFTMAM NAFGDMTSEE FRQVMNGFQN RKPRKGKVFQ EPLFYEAPRS
TT SEEE TTTT HHH HHHHT B S EE TT S
101 VDWREKGYVT PVKNQGQCGS XWAFSATGAL EGQMFRTGR LISLSEQNLV
EEGGGGT B SSS HHHHHHHHHH HHHHHHHHS B HHHHH
151 DCSGPQGN EG CNGGLMDYAF QYVQDNGGLD SEESYPYEAT EESCKYNPKY
HHGGGGT G GG B HHHHH HHHHHHT EE ETTTS SS GGG
201 SVANDAGFVD IPKQEKALMK AVATVGPISV AIDAGHESFL FYKEGIYFEP
B B EEE S HHHHH HHHHH EEE EE SHHHH TB EEEE T
251 DCSSDMDHG VLVVGYGFES TESDNNKYWL VKNSWGEEWG MGGYVKMAKD
T SS EE EEE EEEEE SS EEEEE EE SB TTST BTTEEEEE S
301 RRNHCGIASA ASYPTV
SSSGGGTTTS EEE

Appendix C: Seqweb Results

S. cerevisiae eIF6					49	V	B	B	-0.600
SeqWeb Prediction					50	H	B	B	-0.600
Pos	AA	CF-Pred	GORPred	AI-Ind	51	T	B	B	-0.600
..					52	T	B	B	-0.600
1	M	.	B	0.600	53	I	B	.	-0.300
2	A	.	B	0.600	54	A	B	.	0.300
3	T	.	B	0.900	55	G	B	.	-0.450
4	R	.	B	0.600	56	T	B	B	-0.600
5	T	.	B	0.900	57	R	B	B	-0.600
6	Q	.	.	0.900	58	I	B	B	0.300
7	F	.	.	0.900	59	I	B	B	-0.300
8	E	.	.	0.900	60	G	.	B	-0.300
9	N	.	.	0.900	61	R	.	B	-0.600
10	S	T	.	1.300	62	M	.	B	-0.300
11	N	T	.	1.150	63	T	.	.	0.750
12	E	.	.	0.450	64	A	t	.	1.100
13	I	.	T	-0.050	65	G	t	.	1.100
14	G	.	T	-0.200	66	N	t	T	1.500
15	V	B	.	-0.600	67	R	.	T	1.300
16	F	B	.	-0.600	68	R	B	T	1.150
17	S	B	.	-0.600	69	G	B	T	0.850
18	K	B	T	0.400	70	L	B	B	-0.300
19	L	B	T	1.000	71	L	B	B	-0.600
20	T	B	T	1.300	72	V	B	B	-0.450
21	N	B	T	1.150	73	P	.	B	-0.450
22	T	B	T	-0.050	74	T	.	B	0.000
23	Y	B	B	-0.600	75	Q	.	.	0.900
24	C	B	B	-0.600	76	T	.	.	0.900
25	L	B	B	-0.600	77	T	T	.	1.300
26	V	B	B	-0.600	78	D	T	.	1.300
27	A	B	B	-0.600	79	Q	H	B	0.900
28	V	B	B	-0.600	80	E	H	B	0.900
29	G	t	.	-0.250	81	L	H	B	0.750
30	G	t	.	0.650	82	Q	H	B	0.750
31	S	t	.	0.650	83	H	H	.	0.750
32	E	t	.	1.100	84	L	H	.	0.750
33	N	t	.	1.100	85	R	t	T	1.350
34	F	t	.	0.950	86	N	t	T	1.500
35	Y	t	.	0.500	87	S	.	.	0.900
36	S	H	.	0.300	88	L	.	.	0.900
37	A	H	H	-0.600	89	P	T	.	0.850
38	F	H	H	0.300	90	D	T	.	0.850
39	E	H	H	-0.300	91	S	h	.	-0.150
40	A	H	H	-0.300	92	V	h	B	0.750
41	E	H	H	0.300	93	K	h	B	0.900
42	L	H	H	0.300	94	I	h	B	-0.150
43	G	H	H	-0.450	95	Q	h	B	0.600
44	D	H	H	-0.300	96	R	h	B	0.900
45	A	H	H	-0.600	97	V	h	B	0.900
46	I	H	H	-0.600	98	E	h	B	0.900
47	P	.	B	-0.600	99	E	h	B	0.900
48	I	B	B	-0.600	100	R	h	B	0.600
					101	L	h	T	0.700

Randal C. Cevallos

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Final Project

102	S	h	T	0.100	158	G	T	T	1.250
103	A	h	T	0.100	159	G	t	T	1.050
104	L	h	T	-0.200	160	L	.	.	0.450
105	G	.	T	-0.200	161	V	h	.	0.300
106	N	.	T	-0.200	162	H	h	.	0.450
107	V	B	B	-0.600	163	P	h	.	0.600
108	I	B	B	-0.600	164	Q	h	.	0.600
109	C	B	B	-0.600	165	T	h	.	0.900
110	C	B	B	-0.600	166	S	h	.	0.900
111	N	B	T	-0.200	167	V	h	.	0.900
112	D	.	T	0.100	168	Q	h	.	0.900
113	Y	B	B	-0.600	169	D	h	H	0.900
114	V	B	B	-0.600	170	Q	h	H	0.900
115	A	B	B	-0.600	171	E	h	H	0.900
116	L	B	B	-0.600	172	E	h	H	0.900
117	V	B	B	-0.600	173	L	h	H	0.750
118	H	B	B	-0.600	174	S	.	H	-0.150
119	P	T	.	0.250	175	S	.	H	-0.600
120	D	T	.	1.300	176	L	B	H	-0.600
121	I	h	.	0.900	177	L	B	H	-0.600
122	D	h	H	0.900	178	Q	B	B	-0.600
123	R	h	H	0.900	179	V	B	B	-0.600
124	E	h	H	0.900	180	P	B	B	-0.600
125	T	h	H	0.900	181	L	B	B	-0.600
126	E	h	H	0.750	182	V	B	B	-0.600
127	E	h	H	0.750	183	A	B	B	-0.600
128	L	h	H	0.750	184	G	B	B	-0.600
129	I	h	H	-0.300	185	T	B	B	-0.150
130	S	h	H	-0.600	186	V	B	B	0.750
131	D	h	H	-0.600	187	N	t	.	1.100
132	V	h	H	-0.600	188	R	T	T	1.550
133	L	h	H	-0.600	189	G	T	T	1.250
134	G	.	H	-0.600	190	S	t	.	0.650
135	V	h	H	-0.600	191	S	t	.	0.050
136	E	h	B	-0.600	192	V	.	B	-0.450
137	V	h	B	0.300	193	V	.	B	-0.600
138	F	h	B	0.450	194	G	.	B	-0.600
139	R	h	B	0.450	195	A	t	B	-0.400
140	Q	h	B	-0.150	196	G	t	B	-0.400
141	T	h	.	0.600	197	M	B	B	-0.600
142	I	h	.	0.750	198	V	B	B	-0.600
143	S	t	.	0.050	199	V	B	B	-0.300
144	G	t	T	0.150	200	N	B	B	-0.600
145	N	t	T	0.000	201	D	B	B	-0.600
146	I	.	B	-0.600	202	Y	B	B	-0.600
147	L	.	B	-0.600	203	L	B	B	-0.300
148	V	.	B	-0.600	204	A	B	B	-0.600
149	G	.	B	-0.600	205	V	B	B	-0.600
150	S	T	B	-0.200	206	T	B	B	-0.600
151	Y	T	B	-0.200	207	G	.	B	-0.450
152	C	t	T	0.300	208	L	.	.	-0.150
153	S	t	T	0.900	209	D	.	.	0.450
154	L	t	T	1.200	210	T	.	.	0.600
155	S	T	T	1.250	211	T	h	.	0.900
156	N	T	T	1.550	212	A	h	.	0.900
157	Q	T	T	1.250	213	P	h	H	0.450

214	E	h	H	-0.450	220	S	h	H	-0.600
215	L	h	H	-0.600	221	I	h	H	-0.450
216	S	h	H	-0.600	222	F	h	H	-0.150
217	V	h	H	-0.600	223	R	h	H	-0.450
218	I	h	H	-0.600	224	L	h	H	-0.450
219	E	h	H	-0.600					

Whale Myoglobin SeqWeb Prediction

Pos	AA	CF-Pred	GORPred	AI-					
Ind	..								
					43	F	H	H	0.900
					44	D	H	H	0.900
					45	R	H	H	0.900
1	V	h	.	-0.450	46	F	H	H	0.750
2	L	h	.	-0.450	47	K	H	H	0.900
3	S	h	.	0.450	48	H	H	H	0.750
4	E	h	H	0.450	49	L	H	H	0.900
5	G	h	H	0.900	50	K	H	H	0.900
6	E	h	H	0.900	51	T	H	H	0.900
7	W	B	H	0.600	52	E	H	H	0.900
8	Q	B	H	-0.600	53	A	H	H	0.900
9	L	B	H	-0.300	54	E	H	H	0.750
10	V	B	H	-0.600	55	M	H	H	0.900
11	L	B	H	-0.600	56	K	H	H	0.900
12	H	B	H	-0.600	57	A	H	H	0.900
13	V	B	H	-0.600	58	S	H	H	0.900
14	W	H	H	-0.600	59	E	H	H	0.900
15	A	H	H	0.300	60	D	H	H	0.900
16	K	H	H	-0.600	61	L	H	H	0.900
17	V	H	H	0.750	62	K	H	H	0.900
18	E	H	H	-0.300	63	K	H	H	0.750
19	A	H	H	-0.300	64	H	H	H	0.750
20	D	H	H	-0.600	65	G	.	H	0.600
21	V	H	H	0.300	66	V	B	B	-0.600
22	A	H	H	-0.300	67	T	B	B	-0.600
23	G	.	H	0.600	68	V	B	B	-0.600
24	H	t	H	0.950	69	L	B	B	-0.600
25	G	t	.	0.950	70	T	B	H	-0.600
26	Q	t	.	0.650	71	A	H	H	-0.600
27	D	t	B	0.050	72	L	H	H	-0.600
28	I	B	B	-0.300	73	G	H	H	-0.600
29	L	B	B	-0.600	74	A	H	H	-0.600
30	I	B	B	-0.600	75	I	H	H	-0.600
31	R	B	B	-0.600	76	L	H	H	0.450
32	L	B	B	-0.600	77	K	H	H	0.600
33	F	B	.	0.450	78	K	H	H	0.900
34	K	.	.	0.750	79	K	H	H	0.900
35	S	.	.	0.900	80	G	H	H	0.900
36	H	.	.	0.900	81	H	H	H	0.750
37	P	T	.	1.300	82	H	H	H	0.750
38	E	T	H	1.300	83	E	H	H	0.750
39	T	H	H	0.900	84	A	H	H	0.750
40	L	H	H	0.900	85	E	H	H	0.750
41	E	H	H	0.900	86	L	H	H	0.450
42	K	H	H	0.900	87	K	H	H	-0.150

88	P	h	H	0.450	121	G	T	T	1.550
89	L	h	H	0.600	122	D	t	T	1.350
90	A	h	H	0.750	123	F	t	.	0.950
91	Q	h	H	0.300	124	G	.	.	0.300
92	S	h	H	0.450	125	A	H	H	0.600
93	H	h	H	0.750	126	D	H	H	0.300
94	A	h	H	0.900	127	A	H	H	0.450
95	T	h	H	0.900	128	Q	H	H	0.450
96	K	h	H	0.900	129	G	H	H	0.600
97	H	h	H	0.900	130	A	H	H	0.750
98	K	h	.	0.750	131	M	H	H	0.600
99	I	h	B	0.750	132	N	H	H	-0.300
100	P	.	B	0.750	133	K	H	H	0.450
101	I	.	B	-0.300	134	A	H	H	-0.300
102	K	.	B	-0.150	135	L	H	H	-0.300
103	Y	.	B	-0.300	136	E	H	H	-0.300
104	L	H	H	-0.600	137	L	H	H	-0.300
105	E	H	H	-0.300	138	F	H	H	0.750
106	F	H	H	-0.300	139	R	H	H	0.750
107	I	H	H	-0.600	140	K	H	H	-0.150
108	S	H	H	-0.600	141	D	H	H	0.600
109	E	H	H	-0.600	142	I	H	H	0.750
110	A	B	H	-0.600	143	A	H	H	0.600
111	I	B	H	-0.600	144	A	H	H	0.750
112	I	B	H	-0.600	145	K	H	H	0.750
113	H	B	H	-0.600	146	Y	H	H	0.900
114	V	B	H	-0.600	147	K	H	H	0.900
115	L	B	H	-0.300	148	E	H	H	0.900
116	H	B	.	0.600	149	L	H	T	1.150
117	S	t	.	0.950	150	G	.	T	1.150
118	R	t	.	1.100	151	Y	.	T	1.150
119	H	t	.	1.100	152	Q	.	T	0.850
120	P	T	T	1.700	153	G	.	.	0.900

Polio 3c Proteinase**SeqWeb Prediction**

Pos AA CF-Pred GORPred AI-Ind ..

1	G	.	.	-0.150	19	T	h	.	0.600
2	P	T	.	1.150	20	T	t	.	1.100
3	G	T	.	1.150	21	S	t	.	1.100
4	F	B	.	0.450	22	K	T	.	1.300
5	D	B	H	-0.300	23	G	T	.	1.300
6	Y	B	H	-0.600	24	E	.	.	0.750
7	A	B	H	-0.600	25	F	B	.	-0.300
8	V	B	H	-0.600	26	T	B	.	-0.600
9	A	.	H	-0.600	27	M	B	.	-0.600
10	M	.	H	-0.600	28	L	B	.	-0.600
11	A	.	H	0.450	29	G	B	.	-0.300
12	K	.	H	0.450	30	V	B	.	0.300
13	R	.	H	-0.300	31	H	B	.	-0.300
14	N	.	H	0.450	32	D	h	.	0.300
15	I	.	B	0.300	33	N	h	B	-0.600
16	V	.	B	-0.300	34	V	h	B	-0.600
17	T	.	B	-0.600	35	A	h	B	-0.600
18	A	.	B	-0.450	36	I	h	B	-0.600

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Bioc 218

Final Project

37	L	h	B	-0.600	93	Q	.	.	0.600
38	P	.	B	-0.600	94	I	.	.	0.900
39	T	.	.	-0.450	95	T	.	.	0.900
40	H	.	.	0.600	96	E	.	.	0.900
41	A	t	.	0.950	97	T	t	T	1.500
42	S	t	.	1.100	98	N	T	T	1.700
43	P	T	.	1.300	99	D	T	T	1.550
44	G	T	T	1.250	100	G	T	T	0.350
45	E	.	T	0.250	101	V	B	B	-0.600
46	S	.	H	-0.450	102	L	B	B	-0.600
47	I	.	H	-0.600	103	I	B	B	-0.600
48	V	.	H	-0.600	104	V	B	B	-0.600
49	I	.	H	-0.600	105	N	B	B	-0.450
50	D	t	H	0.050	106	T	B	T	1.000
51	G	t	H	0.050	107	S	t	T	1.500
52	K	H	H	0.900	108	K	t	T	1.500
53	E	H	H	0.750	109	Y	t	.	1.100
54	V	H	H	-0.300	110	P	T	T	1.700
55	E	H	H	0.300	111	N	T	T	1.550
56	I	H	H	-0.600	112	M	B	B	0.450
57	L	H	H	-0.600	113	Y	B	B	-0.300
58	D	H	H	-0.300	114	V	B	B	-0.600
59	A	H	H	-0.600	115	P	B	B	-0.600
60	K	H	H	-0.150	116	V	B	B	-0.600
61	A	H	H	0.750	117	G	B	B	-0.600
62	L	H	H	0.900	118	A	B	B	-0.600
63	E	H	H	0.750	119	V	B	B	-0.300
64	D	H	H	0.750	120	T	B	B	0.450
65	Q	H	H	0.900	121	E	.	B	0.600
66	A	H	H	0.900	122	Q	t	B	0.800
67	G	.	.	0.750	123	G	t	B	1.100
68	T	t	.	0.950	124	Y	.	B	0.600
69	N	t	.	0.050	125	L	.	.	0.300
70	L	.	.	0.300	126	N	.	.	-0.300
71	E	.	.	-0.600	127	L	t	.	0.500
72	I	B	.	-0.600	128	G	t	.	1.100
73	T	B	.	-0.600	129	G	t	.	0.950
74	I	B	.	-0.600	130	R	t	.	1.100
75	I	B	.	-0.600	131	Q	b	.	0.900
76	T	B	.	-0.600	132	T	b	B	0.900
77	L	B	.	-0.150	133	A	b	B	0.900
78	K	h	.	0.900	134	R	b	B	0.450
79	R	h	T	1.300	135	T	b	B	-0.300
80	N	h	T	1.300	136	L	b	B	0.450
81	E	h	T	1.300	137	M	b	B	0.300
82	K	h	T	1.300	138	Y	b	B	-0.300
83	F	h	T	1.300	139	N	b	.	-0.150
84	R	h	T	1.300	140	F	b	.	0.750
85	D	h	T	1.300	141	P	.	T	1.300
86	I	h	T	1.300	142	T	.	T	1.150
87	R	h	.	0.750	143	R	.	T	1.300
88	P	.	.	0.750	144	A	t	T	1.350
89	H	.	.	0.600	145	G	t	T	1.350
90	I	.	.	0.900	146	Q	T	T	1.550
91	P	.	.	0.450	147	C	T	T	0.350
92	T	.	.	0.450	148	G	t	T	0.150

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149	G	t	B	-0.400	167	S	T	.	1.150
150	V	B	B	-0.600	168	H	T	.	1.000
151	I	B	B	-0.600	169	G	.	.	-0.300
152	T	B	B	-0.600	170	F	H	H	-0.600
153	C	B	B	-0.600	171	A	H	H	-0.600
154	T	B	B	-0.450	172	A	H	H	-0.600
155	G	B	T	-0.050	173	A	H	H	-0.600
156	K	B	T	-0.050	174	L	H	H	0.450
157	V	B	B	-0.600	175	K	H	H	0.600
158	I	B	B	-0.300	176	R	t	T	1.200
159	G	B	B	-0.600	177	S	t	T	1.500
160	M	B	B	-0.600	178	Y	B	T	1.300
161	H	B	B	-0.600	179	F	B	T	1.300
162	V	B	.	0.300	180	T	B	T	1.300
163	G	t	.	0.650	181	Q	B	T	1.300
164	G	T	.	1.150	182	S	B	.	0.900
165	N	T	.	1.150	183	Q	.	.	0.900
166	G	T	.	1.150					

Procaspase-7

SeqWeb Prediction

Pos	AA	CF-Pred	GORPred	AI-Ind					
1	S	.	.	0.600	34	K	.	B	0.750
2	I	.	T	1.300	35	V	.	B	-0.150
4	T	.	T	1.300	36	T	.	B	0.450
5	T	.	T	1.300	37	G	.	B	-0.450
6	R	t	T	1.500	38	M	.	B	-0.600
7	D	t	T	1.500	39	G	.	B	0.300
8	R	B	T	1.300	40	V	.	.	0.450
9	V	B	.	0.900	41	R	T	.	0.850
10	P	B	.	0.900	42	N	T	.	1.300
11	T	B	.	0.900	43	G	t	.	1.100
12	Y	B	T	1.150	44	T	H	.	0.900
13	Q	B	T	1.150	45	D	H	.	0.900
14	Y	B	T	1.150	46	K	H	H	0.900
15	N	.	.	0.750	47	D	H	H	0.900
16	M	H	.	0.750	48	A	H	H	0.900
17	N	H	H	0.750	49	E	H	H	0.300
18	F	H	H	0.600	50	A	b	H	0.300
19	E	H	H	0.300	51	L	b	H	-0.600
20	K	H	H	0.900	52	F	b	H	-0.600
21	L	H	H	0.450	53	K	b	H	-0.600
22	G	.	H	0.450	54	C	b	H	-0.300
23	K	.	H	-0.600	55	F	b	H	-0.300
24	C	B	B	-0.600	56	R	b	T	0.700
25	I	B	B	-0.600	57	S	B	T	-0.200
26	I	B	B	-0.600	58	L	B	T	0.100
27	I	B	B	-0.600	59	G	B	T	0.100
28	N	B	B	0.300	60	F	B	T	-0.200
29	N	t	T	1.200	61	D	B	B	-0.600
30	K	T	T	1.700	62	V	B	B	-0.600
31	N	T	T	1.700	63	I	B	B	-0.600
32	F	t	T	1.500	64	V	B	B	-0.300
33	D	t	T	1.500	65	Y	B	T	-0.200

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66	N	T	T	0.500	122	G	t	T	1.350
67	D	T	T	0.500	123	D	t	T	1.500
68	C	T	T	1.100	124	R	t	T	1.500
69	S	t	T	1.200	125	C	b	T	1.150
70	C	t	H	-0.100	126	K	b	H	0.450
71	A	H	H	-0.300	127	T	b	H	0.450
72	K	H	H	0.600	128	L	b	H	0.600
73	M	H	H	0.450	129	L	b	H	0.900
74	Q	H	H	-0.150	130	E	H	H	0.900
75	D	H	H	0.750	131	K	H	H	0.600
76	L	H	H	0.900	132	P	H	H	0.600
77	L	H	H	0.900	133	K	H	H	0.450
78	K	H	H	0.450	134	L	H	H	-0.600
79	K	H	H	0.600	135	F	H	H	-0.600
80	A	H	H	0.900	136	F	H	H	-0.600
81	S	H	H	0.900	137	I	H	H	-0.600
82	E	H	H	0.900	138	Q	H	H	-0.600
83	E	H	H	0.900	139	A	H	H	-0.300
84	D	H	H	0.900	140	A	H	.	0.450
85	H	H	H	0.900	141	R	t	.	1.100
86	T	T	H	1.300	142	G	t	.	0.650
87	N	T	H	1.000	143	T	h	.	0.900
88	A	B	H	-0.300	144	E	h	.	0.900
89	A	B	H	-0.600	145	L	h	.	0.900
90	C	B	H	-0.600	146	D	h	T	0.850
91	F	B	H	-0.600	147	D	h	T	1.150
92	A	B	H	-0.600	148	G	h	T	0.850
93	C	B	H	-0.600	149	I	h	.	0.750
94	I	B	H	-0.600	150	Q	h	.	0.750
95	L	B	H	-0.600	151	A	h	.	0.450
96	L	B	H	-0.600	152	D	h	.	0.600
97	S	t	.	-0.400	153	S	T	.	0.850
98	H	t	.	0.950	154	G	T	.	0.850
99	G	.	.	0.900	155	P	.	.	0.750
100	E	.	.	0.900	156	I	.	.	0.750
101	E	.	.	0.750	157	N	.	.	0.900
102	N	B	T	0.700	158	D	t	T	1.500
103	V	B	T	1.000	159	T	T	T	1.700
104	I	B	T	1.000	160	D	T	T	1.700
105	Y	B	T	1.000	161	A	t	.	1.100
106	G	B	T	0.850	162	N	t	.	1.100
107	K	T	T	1.250	163	P	T	T	1.700
108	D	T	T	1.550	164	R	T	T	1.700
109	G	.	T	1.300	165	Y	t	T	1.500
110	V	.	B	0.450	166	K	h	B	0.900
111	T	.	B	0.450	167	I	h	B	0.750
112	P	h	B	0.450	168	P	h	B	-0.300
113	I	h	B	-0.150	169	V	h	B	0.300
114	K	h	B	0.450	170	E	h	H	-0.600
115	D	h	B	-0.150	171	A	h	H	-0.600
116	L	h	.	0.450	172	D	h	H	-0.600
117	T	h	.	0.300	173	F	B	H	-0.600
118	A	h	.	0.600	174	L	B	H	-0.600
119	H	h	T	0.700	175	F	B	H	-0.600
120	F	h	T	1.000	176	A	B	H	-0.600
121	R	t	T	1.500	177	Y	B	T	-0.200

178	S	.	T	-0.200	222	R	h	.	0.750
179	T	.	.	-0.150	223	V	h	.	0.750
180	V	.	.	0.450	224	A	h	.	0.600
181	P	T	T	1.250	225	R	h	.	0.600
182	G	T	T	1.250	226	H	h	.	0.450
183	Y	t	T	1.050	227	F	h	T	1.150
184	Y	t	T	1.350	228	E	h	T	1.300
185	S	.	T	1.150	229	S	h	T	1.300
186	W	.	T	1.150	230	Q	t	T	1.500
187	R	.	.	0.900	231	S	t	T	1.500
188	S	.	.	0.900	232	D	T	.	1.300
189	P	T	T	1.700	233	D	T	.	1.300
190	G	T	T	1.700	234	P	h	.	0.900
191	R	T	T	1.550	235	H	h	.	0.750
192	G	T	T	1.550	236	F	h	T	1.150
193	S	t	T	1.050	237	H	h	T	1.150
194	W	h	B	0.300	238	E	h	T	1.300
195	F	h	B	-0.600	239	K	h	T	1.300
196	V	h	B	-0.600	240	K	h	T	1.300
197	Q	h	B	-0.600	241	Q	B	T	1.150
198	A	h	.	-0.600	242	I	B	.	0.300
199	L	h	.	-0.600	243	P	B	B	-0.600
200	C	h	.	-0.600	244	C	B	B	-0.600
201	S	h	H	-0.600	245	V	B	B	-0.600
202	I	h	H	-0.600	246	V	B	B	-0.600
203	L	h	H	0.300	247	S	B	B	-0.600
204	E	h	H	0.300	248	M	H	B	-0.600
205	E	h	H	0.900	249	L	H	H	-0.150
206	H	h	H	0.900	250	T	H	H	-0.150
207	G	.	H	0.900	251	K	H	H	0.000
208	K	t	H	1.100	252	E	H	H	-0.150
209	D	t	H	0.950	253	L	H	H	0.750
210	L	.	H	0.300	254	Y	.	H	0.750
211	E	.	H	0.600	255	F	h	H	-0.300
212	I	B	H	-0.600	256	S	h	H	-0.150
213	M	B	H	-0.600	257	Q	h	H	0.600
214	Q	B	H	-0.600	258	L	h	H	0.750
215	I	B	H	-0.600	259	E	h	H	0.750
216	L	B	H	-0.600	260	H	h	H	0.750
217	T	B	.	-0.300	261	H	h	H	0.750
218	R	B	.	0.000	262	H	h	H	0.900
219	V	B	.	0.900	263	H	h	H	0.900
220	N	t	T	1.500	264	H	h	.	0.900
221	D	t	T	1.350	265	H	h	.	0.900

Human Trypsin IV**SeqWeb Prediction**

Pos AA CF-Pred GORPred AI-Ind ..

1	I	B	T	-0.050	8	E	.	T	1.300
2	V	B	T	-0.050	9	E	.	T	1.150
3	G	B	.	-0.450	10	N	.	T	1.300
4	G	B	.	-0.450	11	S	.	.	0.900
5	Y	B	.	-0.300	12	L	.	.	0.750
6	T	B	.	0.600	13	P	.	T	0.700
7	C	B	T	1.300	14	Y	B	T	0.700

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15	Q	B	B	-0.600	71	I	B	B	0.300
16	V	B	B	0.300	72	R	B	B	0.600
17	S	B	B	0.300	73	H	B	B	0.750
18	L	B	B	0.300	74	P	T	T	1.700
19	N	t	T	0.450	75	K	T	T	1.700
20	S	T	T	1.550	76	Y	t	T	1.500
21	G	T	T	1.250	77	N	.	T	1.300
22	S	t	T	1.050	78	R	T	T	1.700
23	H	t	T	0.900	79	D	T	T	1.700
24	F	t	T	0.300	80	T	.	T	1.300
25	C	t	T	0.900	81	L	.	.	0.900
26	G	T	T	0.350	82	D	t	T	1.350
27	G	T	T	0.350	83	N	t	T	1.050
28	S	t	.	-0.250	84	D	t	T	0.150
29	L	.	.	-0.150	85	I	B	.	-0.600
30	I	.	.	0.450	86	M	B	.	-0.600
31	S	.	.	0.450	87	L	B	.	-0.600
32	E	.	H	-0.450	88	I	B	.	-0.600
33	Q	B	H	-0.600	89	K	B	.	-0.600
34	W	B	H	0.300	90	L	B	.	-0.450
35	V	B	H	-0.300	91	S	.	.	-0.300
36	V	B	H	-0.600	92	S	.	.	-0.150
37	S	B	H	-0.600	93	P	.	.	-0.450
38	A	B	H	-0.600	94	A	B	.	-0.600
39	A	B	H	-0.600	95	V	B	B	-0.600
40	H	B	T	0.700	96	I	B	B	-0.300
41	C	B	T	0.700	97	N	B	B	-0.600
42	Y	B	T	1.150	98	A	B	B	-0.600
43	K	B	T	1.150	99	R	B	B	-0.150
44	T	B	T	1.300	100	V	B	B	-0.300
45	R	B	B	0.900	101	S	B	B	-0.450
46	I	B	B	0.750	102	T	B	B	-0.450
47	Q	B	B	0.300	103	I	B	B	-0.450
48	V	B	B	0.300	104	S	.	B	-0.600
49	R	B	B	-0.300	105	L	.	.	-0.450
50	L	B	.	0.600	106	P	.	.	-0.450
51	G	.	.	0.750	107	T	.	.	0.600
52	E	H	.	0.600	108	A	.	.	0.000
53	H	H	.	0.750	109	P	.	.	0.450
54	N	H	.	0.600	110	P	.	.	-0.150
55	I	H	.	0.300	111	A	.	.	-0.150
56	K	H	.	0.300	112	A	.	.	0.750
57	V	H	.	-0.300	113	G	.	B	0.450
58	L	H	.	-0.150	114	T	t	B	-0.250
59	E	H	H	0.750	115	E	t	B	-0.400
60	G	.	H	0.900	116	C	.	B	-0.600
61	N	.	H	0.900	117	L	.	B	-0.600
62	E	.	H	0.750	118	I	.	B	-0.600
63	Q	B	H	0.900	119	S	.	.	-0.600
64	F	B	H	0.600	120	G	t	T	0.300
65	I	B	H	-0.600	121	W	t	T	1.050
66	N	B	H	-0.300	122	G	.	.	0.450
67	A	B	H	-0.600	123	N	b	.	0.450
68	V	B	H	-0.600	124	T	b	.	-0.150
69	K	B	H	-0.600	125	L	b	.	-0.300
70	I	B	B	-0.600	126	S	b	T	-0.200

127	F	b	T	-0.200	176	D	t	T	1.500
128	G	.	T	0.100	177	S	T	T	1.700
129	A	T	T	1.100	178	G	T	T	1.550
130	D	T	.	1.150	179	G	t	.	0.050
131	Y	.	.	0.900	180	P	.	.	-0.450
132	P	T	.	1.300	181	V	.	B	-0.600
133	D	T	H	1.300	182	V	.	B	-0.600
134	E	H	H	0.750	183	C	t	B	-0.100
135	L	H	H	0.450	184	N	T	B	-0.200
136	K	H	H	0.600	185	G	T	B	0.850
137	C	H	H	-0.300	186	Q	B	B	0.750
138	L	H	H	-0.600	187	L	B	B	0.450
139	D	H	H	-0.600	188	Q	B	B	-0.450
140	A	H	H	-0.600	189	G	B	B	-0.600
141	P	h	H	-0.600	190	V	B	B	-0.600
142	V	h	H	-0.300	191	V	B	B	-0.300
143	L	h	H	-0.600	192	S	.	T	0.100
144	T	h	H	-0.300	193	W	.	T	0.100
145	Q	h	H	-0.450	194	G	t	T	0.300
146	A	h	H	0.900	195	H	t	T	0.900
147	E	h	H	0.600	196	G	t	T	0.900
148	C	h	H	0.600	197	C	t	T	1.200
149	K	h	T	0.700	198	A	.	T	1.000
150	A	h	T	1.000	199	W	.	T	1.000
151	S	h	.	0.900	200	K	t	T	1.500
152	Y	.	.	0.900	201	N	t	T	1.500
153	P	T	T	1.400	202	R	t	.	1.100
154	G	T	T	1.700	203	P	T	T	1.700
155	K	.	T	1.300	204	G	T	T	1.700
156	I	.	T	1.150	205	V	B	T	1.150
157	T	.	B	0.450	206	Y	B	B	-0.300
158	N	.	B	-0.150	207	T	B	B	-0.300
159	S	.	B	-0.600	208	K	B	B	0.450
160	M	B	B	-0.600	209	V	B	B	0.750
161	F	B	B	-0.600	210	Y	B	B	0.300
162	C	B	B	-0.600	211	N	B	B	0.600
163	V	B	B	-0.600	212	Y	B	B	0.450
164	G	B	B	-0.600	213	V	h	B	0.300
165	F	B	B	-0.600	214	D	h	B	0.600
166	L	B	.	-0.600	215	W	h	B	0.600
167	E	t	T	1.050	216	I	h	B	0.750
168	G	t	T	1.500	217	K	h	B	0.300
169	G	t	T	1.500	218	D	h	B	-0.300
170	K	T	T	1.550	219	T	h	B	-0.600
171	D	T	T	1.550	220	I	h	.	0.600
172	S	T	T	1.700	221	A	h	.	0.450
173	C	T	T	1.700	222	A	h	.	-0.450
174	Q	t	T	1.500	223	N	.	.	-0.450
175	R	t	T	1.350	224	S	.	.	0.600

Ribonuclease Sa**SeqWeb Prediction**

Pos AA CF-Pred GORPred AI-Ind ..

1	D	.	T	0.850	3	S	t	T	0.150
2	V	t	T	1.050	4	G	t	B	-0.250

5	T	.	B	-0.450	51	Y	B	T	1.150
6	V	h	B	-0.600	52	Y	B	T	1.150
7	C	h	B	-0.600	53	H	B	B	0.750
8	L	h	B	-0.600	54	E	B	B	0.750
9	S	h	B	-0.600	55	Y	B	B	0.300
10	A	h	.	-0.600	56	T	B	B	0.300
11	L	h	.	-0.150	57	V	B	B	-0.300
12	P	.	.	0.450	58	I	B	B	-0.600
13	P	t	.	0.200	59	T	B	B	-0.600
14	E	t	H	1.100	60	P	T	.	-0.050
15	A	.	H	0.900	61	G	T	.	1.000
16	T	.	H	0.900	62	A	.	.	0.900
17	D	.	H	0.900	63	R	.	.	0.900
18	T	B	H	-0.150	64	T	t	.	1.100
19	L	B	H	-0.600	65	R	t	T	1.500
20	N	B	B	-0.600	66	G	t	T	1.500
21	L	B	B	-0.600	67	T	B	T	1.300
22	I	B	B	-0.600	68	R	B	B	0.750
23	A	B	B	-0.300	69	R	B	B	0.450
24	S	T	T	0.350	70	I	B	B	0.300
25	D	T	T	0.350	71	I	B	B	0.600
26	G	T	.	1.000	72	T	B	.	-0.150
27	P	t	.	1.100	73	G	.	.	-0.450
28	F	t	.	0.950	74	E	H	.	0.600
29	P	T	.	1.150	75	A	H	.	0.900
30	Y	T	T	1.700	76	T	H	.	0.900
31	S	t	T	1.500	77	Q	H	.	0.900
32	Q	T	T	1.700	78	E	H	T	1.300
33	D	T	T	1.250	79	D	H	T	1.300
34	G	t	T	0.150	80	Y	t	T	1.500
35	V	B	B	-0.300	81	Y	t	T	1.500
36	V	B	B	-0.300	82	T	t	T	1.500
37	F	B	B	0.300	83	G	t	T	1.500
38	Q	B	B	0.900	84	D	t	T	1.500
39	N	B	.	0.900	85	H	t	.	0.950
40	R	t	T	1.500	86	Y	B	.	0.750
41	E	t	T	1.500	87	A	B	B	0.600
42	S	.	T	1.150	88	T	B	B	-0.300
43	V	B	.	0.450	89	F	B	B	-0.600
44	L	B	.	0.450	90	S	B	B	-0.600
45	P	B	.	-0.150	91	L	B	T	0.100
46	T	B	T	0.400	92	I	B	T	0.100
47	Q	B	T	1.300	93	D	.	T	0.250
48	S	B	T	1.300	94	Q	t	T	0.150
49	Y	B	T	1.150	95	T	t	T	1.050
50	G	.	T	1.150	96	C	.	T	1.150

Ribonuclease Hi**SeqWeb Prediction**

Pos AA CF-Pred GORPred AI-Ind ..

1	M	H	B	0.600	6	E	H	B	-0.300
2	L	H	B	-0.150	7	I	H	B	-0.600
3	K	H	B	0.450	8	F	H	B	-0.600
4	Q	H	B	-0.150	9	T	H	B	-0.300
5	V	H	B	-0.300	10	A	H	.	-0.600

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11	G	.	.	-0.450	67	L	B	H	0.300
12	S	.	.	-0.450	68	S	B	.	-0.150
13	A	.	.	-0.150	69	T	B	T	0.400
14	L	.	.	-0.150	70	D	t	T	0.600
15	G	.	.	-0.150	71	S	t	T	0.600
16	N	.	.	-0.150	72	Q	B	T	1.000
17	P	T	.	0.250	73	Y	B	T	1.000
18	G	T	.	0.850	74	V	B	.	0.000
19	P	T	.	0.250	75	R	B	T	0.250
20	G	T	.	0.250	76	Q	B	T	-0.050
21	G	T	.	-0.050	77	G	B	T	0.400
22	Y	T	B	-0.200	78	I	B	.	-0.150
23	G	.	B	-0.600	79	T	B	B	-0.450
24	A	B	B	-0.600	80	Q	B	B	-0.600
25	I	B	B	-0.600	81	W	B	B	-0.600
26	L	B	B	-0.300	82	I	B	B	-0.600
27	R	B	B	-0.300	83	H	B	.	-0.600
28	Y	B	B	0.450	84	N	B	T	-0.050
29	R	t	T	1.500	85	W	.	T	0.850
30	G	t	T	1.500	86	K	.	.	0.900
31	R	h	T	1.300	87	K	t	T	1.200
32	E	h	T	1.300	88	R	T	T	1.700
33	K	h	T	1.300	89	G	T	T	1.700
34	T	h	.	0.900	90	W	h	T	1.300
35	F	h	.	0.300	91	K	h	.	0.900
36	S	h	.	-0.300	92	T	h	.	0.900
37	A	h	.	-0.600	93	A	h	T	1.300
38	G	.	.	-0.150	94	D	h	T	1.300
39	Y	.	.	-0.150	95	K	h	.	0.900
40	T	.	.	0.000	96	K	h	.	0.900
41	R	.	.	0.000	97	P	h	.	0.900
42	T	.	.	0.000	98	V	h	.	0.900
43	T	T	.	1.300	99	K	h	B	0.900
44	N	T	.	1.300	100	N	h	B	0.450
45	N	t	.	1.100	101	V	H	B	-0.300
46	R	H	H	0.600	102	D	H	B	-0.300
47	M	H	H	0.450	103	L	H	H	-0.300
48	E	H	H	0.300	104	W	H	H	-0.300
49	L	H	H	0.300	105	Q	H	H	0.300
50	M	H	H	-0.600	106	R	H	H	-0.150
51	A	H	H	-0.600	107	L	H	H	-0.150
52	A	H	H	-0.600	108	D	H	H	0.300
53	I	H	H	-0.600	109	A	H	H	0.300
54	V	H	H	-0.600	110	A	H	H	-0.300
55	A	H	H	-0.600	111	L	H	H	-0.300
56	L	H	H	-0.600	112	G	.	H	-0.600
57	E	H	H	-0.300	113	Q	h	H	-0.600
58	A	H	H	0.600	114	H	h	H	-0.150
59	L	H	H	0.750	115	Q	h	.	-0.150
60	K	H	H	0.600	116	I	h	.	0.450
61	E	H	H	0.750	117	K	h	T	-0.050
62	H	H	H	0.750	118	W	h	T	-0.200
63	A	H	H	0.600	119	E	h	T	0.250
64	E	H	H	-0.300	120	W	h	T	0.700
65	V	B	H	-0.600	121	V	h	.	-0.600
66	I	B	H	-0.300	122	K	h	.	0.300

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Final Project

123	G	.	.	-0.600	140	A	H	H	-0.300
124	H	.	.	-0.300	141	A	H	H	0.300
125	A	t	.	0.500	142	M	H	H	-0.600
126	G	t	.	0.650	143	N	.	.	-0.600
127	H	.	.	0.600	144	P	T	.	0.250
128	P	.	.	0.900	145	T	T	.	1.000
129	E	H	.	0.900	146	L	.	.	0.900
130	N	H	H	0.900	147	E	.	T	1.000
131	E	H	H	0.900	148	D	.	T	1.000
132	R	H	H	0.900	149	T	T	T	1.400
133	A	H	H	0.900	150	G	T	.	1.000
134	D	H	H	0.900	151	Y	B	.	0.450
135	E	H	H	0.900	152	Q	B	B	-0.150
136	L	H	H	0.750	153	V	B	B	-0.150
137	A	H	H	0.600	154	E	B	B	-0.450
138	R	H	H	0.300	155	V	B	B	0.45
139	A	H	H	-0.300					

Appendix D: PROF King results

Trypsin IV prediction												
1	I	C	0.547	50	L	E	0.935	104	S	C	0.524	
2	V	E	0.665	51	G	E	0.868	105	L	C	0.796	
3	G	E	0.579	52	E	E	0.746	106	P	C	0.884	
4	G	C	0.544	53	H	E	0.747	107	T	C	0.889	
5	Y	C	0.628	54	N	E	0.751	108	A	C	0.881	
6	T	C	0.658	55	I	E	0.733	109	P	C	0.889	
7	C	C	0.765	56	K	E	0.733	110	P	C	0.888	
8	E	C	0.847	57	V	E	0.674	111	A	C	0.889	
9	E	C	0.841	58	L	C	0.559	112	A	C	0.876	
10	N	C	0.846	59	E	C	0.812	113	G	C	0.826	
11	S	C	0.850	60	G	C	0.875	114	T	C	0.629	
12	L	C	0.794	61	N	C	0.853	115	E	E	0.764	
13	P	C	0.554	62	E	C	0.717	116	C	E	0.927	
14	Y	E	0.807	63	Q	E	0.592	117	L	E	0.959	
15	Q	E	0.946	64	F	E	0.865	118	I	E	0.957	
16	V	E	0.962	65	I	E	0.900	119	S	E	0.902	
17	S	E	0.960	66	N	E	0.906	120	G	E	0.744	
18	L	E	0.929	67	A	E	0.921	121	W	E	0.611	
19	N	E	0.734	68	V	E	0.906	122	G	E	0.575	
20	S	C	0.625	69	K	E	0.906	123	N	E	0.586	
21	G	C	0.837	70	I	E	0.921	124	T	E	0.491	
22	S	C	0.762	71	I	E	0.900	125	L	C	0.685	
23	H	E	0.493	72	R	E	0.765	126	S	C	0.857	
24	F	E	0.809	73	H	C	0.549	127	F	C	0.882	
25	C	E	0.816	74	P	C	0.790	128	G	C	0.881	
26	G	E	0.733	75	K	C	0.885	129	A	C	0.878	
27	G	E	0.799	76	Y	C	0.885	130	D	C	0.887	
28	S	E	0.874	77	N	C	0.900	131	Y	C	0.869	
29	L	E	0.860	78	R	C	0.883	132	P	C	0.733	
30	I	E	0.768	79	D	C	0.868	133	D	C	0.693	
31	S	C	0.618	80	T	C	0.867	134	E	C	0.657	
32	E	C	0.735	81	L	C	0.862	135	L	C	0.459	
33	Q	C	0.581	82	D	C	0.847	136	K	E	0.747	
34	W	E	0.789	83	N	C	0.780	137	C	E	0.888	
35	V	E	0.910	84	D	C	0.591	138	L	E	0.912	
36	V	E	0.940	85	I	E	0.830	139	D	E	0.888	
37	S	E	0.916	86	M	E	0.951	140	A	E	0.858	
38	A	E	0.811	87	L	E	0.961	141	P	E	0.858	
39	A	E	0.693	88	I	E	0.959	142	V	E	0.822	
40	H	E	0.633	89	K	E	0.920	143	L	E	0.578	
41	C	E	0.484	90	L	E	0.626	144	T	C	0.722	
42	Y	C	0.686	91	S	C	0.692	145	Q	C	0.633	
43	K	C	0.794	92	S	C	0.856	146	A	C	0.492	
44	T	C	0.802	93	P	C	0.833	147	E	C	0.424	
45	R	C	0.693	94	A	C	0.753	148	C	C	0.432	
46	I	E	0.512	95	V	C	0.637	149	K	C	0.413	
47	Q	E	0.847	96	I	C	0.683	150	A	H	0.455	
48	V	E	0.939	97	N	C	0.726	151	S	H	0.403	
49	R	E	0.949	98	A	C	0.618	152	Y	C	0.456	
				99	R	E	0.550	153	P	C	0.785	
				100	V	E	0.752	154	G	C	0.831	
				101	S	E	0.803	155	K	C	0.788	
				102	T	E	0.777	156	I	C	0.764	
				103	I	E	0.671	157	T	C	0.713	

158	N	C	0.508	181	V	E	0.844	204	G	E	0.597
159	S	E	0.723	182	V	E	0.887	205	V	E	0.913
160	M	E	0.907	183	C	E	0.868	206	Y	E	0.967
161	F	E	0.951	184	N	E	0.714	207	T	E	0.965
162	C	E	0.927	185	G	E	0.751	208	K	E	0.927
163	V	E	0.786	186	Q	E	0.885	209	V	E	0.716
164	G	E	0.609	187	L	E	0.922	210	Y	C	0.447
165	F	C	0.492	188	Q	E	0.935	211	N	H	0.480
166	L	C	0.719	189	G	E	0.946	212	Y	H	0.679
167	E	C	0.850	190	V	E	0.940	213	V	H	0.808
168	G	C	0.866	191	V	E	0.922	214	D	H	0.879
169	G	C	0.820	192	S	E	0.803	215	W	H	0.892
170	K	C	0.643	193	W	E	0.521	216	I	H	0.848
171	D	E	0.617	194	G	C	0.630	217	K	H	0.810
172	S	E	0.758	195	H	C	0.709	218	D	H	0.796
173	C	E	0.802	196	G	C	0.702	219	T	H	0.797
174	Q	E	0.780	197	C	C	0.761	220	I	H	0.718
175	R	E	0.558	198	A	C	0.827	221	A	H	0.473
176	D	C	0.726	199	W	C	0.855	222	A	C	0.587
177	S	C	0.846	200	K	C	0.851	223	N	C	0.898
178	G	C	0.816	201	N	C	0.869	224	S	C	0.958
179	G	C	0.649	202	R	C	0.861				
180	P	E	0.705	203	P	C	0.757				

RNase SA Prediction

1	D	C	0.967	32	Q	C	0.872	63	R	C	0.619
2	V	C	0.940	33	D	C	0.857	64	T	C	0.583
3	S	C	0.896	34	G	C	0.674	65	R	C	0.540
4	G	C	0.671	35	V	E	0.735	66	G	E	0.493
5	T	E	0.719	36	V	E	0.908	67	T	E	0.668
6	V	E	0.899	37	F	E	0.921	68	R	E	0.811
7	C	E	0.926	38	Q	E	0.795	69	R	E	0.855
8	L	E	0.853	39	N	C	0.519	70	I	E	0.853
9	S	E	0.570	40	R	C	0.763	71	I	E	0.854
10	A	C	0.651	41	E	C	0.802	72	T	E	0.744
11	L	C	0.842	42	S	C	0.790	73	G	E	0.600
12	P	C	0.895	43	V	C	0.775	74	E	C	0.538
13	P	C	0.789	44	L	C	0.774	75	A	C	0.688
14	E	C	0.694	45	P	C	0.808	76	T	C	0.748
15	A	C	0.696	46	T	C	0.833	77	Q	C	0.654
16	T	C	0.716	47	Q	C	0.827	78	E	C	0.484
17	D	C	0.658	48	S	C	0.826	79	D	E	0.641
18	T	E	0.543	49	Y	C	0.806	80	Y	E	0.756
19	L	E	0.756	50	G	C	0.746	81	Y	E	0.721
20	N	E	0.834	51	Y	C	0.588	82	T	E	0.488
21	L	E	0.851	52	Y	E	0.693	83	G	C	0.760
22	I	E	0.814	53	H	E	0.836	84	D	C	0.766
23	A	E	0.636	54	E	E	0.894	85	H	C	0.547
24	S	C	0.546	55	Y	E	0.938	86	Y	E	0.773
25	D	C	0.788	56	T	E	0.938	87	A	E	0.836
26	G	C	0.869	57	V	E	0.929	88	T	E	0.817
27	P	C	0.889	58	I	E	0.884	89	F	E	0.862
28	F	C	0.878	59	T	E	0.738	90	S	E	0.868
29	P	C	0.883	60	P	E	0.583	91	L	E	0.841
30	Y	C	0.890	61	G	E	0.478	92	I	E	0.745
31	S	C	0.883	62	A	C	0.571	93	D	E	0.573

94 Q C 0.472 95 T C 0.733 96 C C 0.929

RNase Hi Prediction

1	M	C	0.973	53	I	H	0.842	105	Q	H	0.959
2	L	C	0.903	54	V	H	0.844	106	R	H	0.969
3	K	C	0.598	55	A	H	0.824	107	L	H	0.966
4	Q	E	0.841	56	L	H	0.801	108	D	H	0.956
5	V	E	0.913	57	E	H	0.783	109	A	H	0.942
6	E	E	0.936	58	A	H	0.723	110	A	H	0.917
7	I	E	0.930	59	L	H	0.620	111	L	H	0.819
8	F	E	0.859	60	K	H	0.534	112	G	H	0.634
9	T	E	0.658	61	E	H	0.441	113	Q	C	0.688
10	A	C	0.601	62	H	C	0.414	114	H	C	0.884
11	G	C	0.739	63	A	C	0.412	115	Q	C	0.776
12	S	C	0.779	64	E	E	0.483	116	I	E	0.563
13	A	C	0.824	65	V	E	0.622	117	K	E	0.880
14	L	C	0.889	66	I	E	0.680	118	W	E	0.947
15	G	C	0.916	67	L	E	0.687	119	E	E	0.939
16	N	C	0.919	68	S	E	0.567	120	W	E	0.914
17	P	C	0.921	69	T	C	0.671	121	V	E	0.744
18	G	C	0.905	70	D	C	0.821	122	K	C	0.585
19	P	C	0.870	71	S	H	0.590	123	G	C	0.807
20	G	C	0.848	72	Q	H	0.856	124	H	C	0.912
21	G	C	0.756	73	Y	H	0.889	125	A	C	0.923
22	Y	E	0.488	74	V	H	0.941	126	G	C	0.921
23	G	E	0.816	75	R	H	0.942	127	H	C	0.931
24	A	E	0.927	76	Q	H	0.920	128	P	C	0.915
25	I	E	0.949	77	G	H	0.897	129	E	C	0.857
26	L	E	0.930	78	I	H	0.879	130	N	H	0.540
27	R	E	0.848	79	T	H	0.824	131	E	H	0.800
28	Y	E	0.617	80	Q	H	0.702	132	R	H	0.880
29	R	C	0.676	81	W	H	0.598	133	A	H	0.942
30	G	C	0.862	82	I	H	0.616	134	D	H	0.954
31	R	C	0.868	83	H	H	0.669	135	E	H	0.960
32	E	C	0.700	84	N	H	0.572	136	L	H	0.958
33	K	C	0.472	85	W	H	0.492	137	A	H	0.945
34	T	E	0.643	86	K	C	0.509	138	R	H	0.928
35	F	E	0.628	87	K	C	0.628	139	A	H	0.870
36	S	C	0.468	88	R	C	0.779	140	A	H	0.704
37	A	C	0.632	89	G	C	0.812	141	A	C	0.518
38	G	C	0.678	90	W	C	0.689	142	M	C	0.628
39	Y	C	0.708	91	K	C	0.619	143	N	C	0.819
40	T	C	0.796	92	T	C	0.674	144	P	C	0.807
41	R	C	0.805	93	A	C	0.785	145	T	C	0.804
42	T	C	0.795	94	D	C	0.881	146	L	C	0.622
43	T	C	0.716	95	K	C	0.916	147	E	C	0.629
44	N	C	0.730	96	K	C	0.913	148	D	C	0.756
45	N	C	0.675	97	P	C	0.887	149	T	C	0.851
46	R	H	0.484	98	V	C	0.816	150	G	C	0.877
47	M	H	0.633	99	K	C	0.753	151	Y	C	0.826
48	E	H	0.756	100	N	C	0.779	152	Q	C	0.753
49	L	H	0.796	101	V	H	0.706	153	V	C	0.649
50	M	H	0.791	102	D	H	0.873	154	E	C	0.658
51	A	H	0.834	103	L	H	0.923	155	V	C	0.882
52	A	H	0.838	104	W	H	0.946				

Hep C RNA pol Prediction

1	S	C	0.966	56	R	E	0.625	111	L	C	0.552
2	X	C	0.744	57	L	C	0.488	112	S	C	0.721
3	S	E	0.621	58	Q	C	0.616	113	S	C	0.640
4	Y	E	0.800	59	V	C	0.734	114	K	H	0.615
5	T	E	0.787	60	L	C	0.813	115	A	H	0.805
6	W	E	0.678	61	D	C	0.788	116	V	H	0.884
7	T	C	0.471	62	D	H	0.749	117	N	H	0.915
8	G	C	0.548	63	H	H	0.809	118	H	H	0.941
9	A	C	0.595	64	Y	H	0.910	119	I	H	0.950
10	L	C	0.633	65	R	H	0.942	120	H	H	0.953
11	I	C	0.695	66	D	H	0.949	121	S	H	0.947
12	T	C	0.774	67	V	H	0.953	122	V	H	0.943
13	P	C	0.717	68	L	H	0.948	123	W	H	0.947
14	C	C	0.718	69	K	H	0.952	124	K	H	0.944
15	A	C	0.612	70	E	H	0.952	125	D	H	0.928
16	A	C	0.611	71	X	H	0.951	126	L	H	0.900
17	E	C	0.697	72	K	H	0.939	127	L	H	0.779
18	E	C	0.799	73	A	H	0.926	128	E	H	0.532
19	S	C	0.890	74	K	H	0.923	129	D	C	0.762
20	K	C	0.912	75	A	H	0.917	130	T	C	0.911
21	L	C	0.907	76	S	H	0.929	131	V	C	0.938
22	P	C	0.868	77	T	H	0.916	132	T	C	0.926
23	I	C	0.745	78	V	H	0.871	133	P	C	0.885
24	N	C	0.741	79	K	H	0.794	134	I	C	0.748
25	A	C	0.764	80	A	H	0.634	135	D	C	0.521
26	L	C	0.627	81	K	C	0.525	136	T	E	0.733
27	S	C	0.570	82	L	C	0.555	137	T	E	0.875
28	N	H	0.504	83	L	C	0.748	138	I	E	0.876
29	S	H	0.685	84	S	C	0.725	139	X	E	0.730
30	L	H	0.742	85	V	H	0.761	140	A	E	0.627
31	L	H	0.680	86	E	H	0.703	141	K	E	0.508
32	R	H	0.567	87	E	H	0.780	142	N	E	0.515
33	H	C	0.613	88	A	H	0.813	143	E	E	0.648
34	H	C	0.831	89	C	H	0.656	144	V	E	0.787
35	N	C	0.859	90	K	C	0.520	145	F	E	0.795
36	X	E	0.511	91	L	C	0.824	146	C	E	0.738
37	V	E	0.883	92	T	C	0.910	147	V	E	0.518
38	Y	E	0.939	93	P	C	0.923	148	Q	C	0.688
39	A	E	0.922	94	P	C	0.831	149	P	C	0.836
40	T	E	0.753	95	H	C	0.658	150	E	C	0.877
41	T	C	0.582	96	S	C	0.587	151	K	C	0.885
42	S	C	0.725	97	A	C	0.516	152	G	C	0.907
43	R	C	0.606	98	K	C	0.500	153	G	C	0.921
44	S	H	0.580	99	S	C	0.477	154	R	C	0.917
45	A	H	0.636	100	K	H	0.473	155	K	C	0.907
46	G	H	0.535	101	F	C	0.512	156	P	C	0.862
47	L	H	0.415	102	G	C	0.692	157	A	C	0.749
48	R	C	0.411	103	Y	C	0.739	158	R	E	0.689
49	Q	C	0.412	104	G	C	0.786	159	L	E	0.876
50	K	C	0.435	105	A	C	0.576	160	I	E	0.889
51	K	E	0.534	106	K	C	0.396	161	V	E	0.795
52	V	E	0.599	107	D	C	0.422	162	F	C	0.568
53	T	E	0.739	108	V	H	0.386	163	P	C	0.823
54	F	E	0.697	109	R	C	0.412	164	D	C	0.875
55	D	E	0.680	110	N	C	0.458	165	L	C	0.863

166 G	C	0.875	223 C	C	0.444	280 R	E	0.662
167 V	C	0.592	224 F	C	0.604	281 A	C	0.509
168 R	C	0.344	225 D	C	0.680	282 S	C	0.665
169 V	H	0.511	226 S	C	0.555	283 G	C	0.521
170 C	H	0.465	227 T	C	0.558	284 V	E	0.647
171 E	H	0.598	228 V	C	0.519	285 L	E	0.700
172 K	H	0.758	229 T	C	0.597	286 T	E	0.677
173 X	H	0.846	230 E	H	0.435	287 T	E	0.559
174 A	H	0.834	231 N	H	0.492	288 S	C	0.576
175 L	H	0.728	232 D	H	0.511	289 C	C	0.742
176 Y	H	0.603	233 I	H	0.645	290 G	C	0.693
177 D	C	0.502	234 R	H	0.746	291 N	H	0.487
178 V	H	0.561	235 V	H	0.891	292 T	H	0.785
179 V	H	0.551	236 E	H	0.925	293 L	H	0.874
180 S	C	0.456	237 E	H	0.933	294 T	H	0.906
181 T	C	0.559	238 S	H	0.942	295 C	H	0.926
182 L	C	0.609	239 I	H	0.933	296 Y	H	0.938
183 P	C	0.434	240 Y	H	0.885	297 L	H	0.937
184 Q	E	0.536	241 Q	H	0.701	298 K	H	0.953
185 V	E	0.756	242 C	H	0.562	299 A	H	0.962
186 V	E	0.807	243 C	C	0.640	300 S	H	0.959
187 X	E	0.644	244 D	C	0.857	301 A	H	0.957
188 G	C	0.524	245 L	C	0.900	302 A	H	0.943
189 S	C	0.534	246 A	C	0.920	303 C	H	0.919
190 S	C	0.460	247 P	H	0.665	304 R	H	0.863
191 Y	E	0.582	248 E	H	0.846	305 A	H	0.773
192 G	E	0.632	249 A	H	0.924	306 A	H	0.509
193 F	E	0.662	250 R	H	0.954	307 K	C	0.754
194 Q	E	0.692	251 Q	H	0.957	308 L	C	0.849
195 Y	C	0.583	252 A	H	0.960	309 Q	C	0.848
196 S	C	0.815	253 I	H	0.953	310 D	C	0.779
197 P	H	0.557	254 K	H	0.954	311 C	C	0.640
198 G	H	0.761	255 S	H	0.945	312 T	E	0.511
199 Q	H	0.845	256 L	H	0.932	313 X	E	0.674
200 R	H	0.924	257 T	H	0.897	314 L	E	0.761
201 V	H	0.952	258 E	H	0.846	315 V	E	0.656
202 E	H	0.959	259 R	H	0.815	316 N	C	0.580
203 F	H	0.956	260 L	H	0.727	317 G	C	0.857
204 L	H	0.957	261 Y	H	0.521	318 D	C	0.894
205 V	H	0.961	262 I	C	0.442	319 D	C	0.616
206 N	H	0.957	263 G	C	0.793	320 L	E	0.840
207 T	H	0.938	264 G	C	0.840	321 V	E	0.928
208 W	H	0.880	265 P	C	0.759	322 V	E	0.936
209 K	H	0.731	266 L	C	0.698	323 I	E	0.929
210 S	H	0.528	267 T	C	0.767	324 C	E	0.873
211 K	C	0.783	268 N	C	0.889	325 E	E	0.578
212 K	C	0.901	269 S	C	0.915	326 S	C	0.754
213 N	C	0.929	270 K	C	0.913	327 A	C	0.868
214 P	C	0.882	271 G	C	0.882	328 G	C	0.902
215 X	C	0.722	272 Q	C	0.757	329 T	C	0.876
216 G	C	0.540	273 N	C	0.516	330 Q	C	0.581
217 F	E	0.610	274 C	E	0.572	331 E	H	0.824
218 S	E	0.630	275 G	E	0.623	332 D	H	0.879
219 Y	E	0.524	276 Y	E	0.637	333 A	H	0.939
220 D	C	0.596	277 R	E	0.659	334 A	H	0.951
221 T	C	0.613	278 R	E	0.714	335 S	H	0.959
222 R	C	0.554	279 C	E	0.725	336 L	H	0.966

337 R	H	0.965	394 R	H	0.758	451 C	E	0.569
338 V	H	0.961	395 A	H	0.729	452 Y	E	0.571
339 F	H	0.954	396 A	H	0.718	453 S	C	0.623
340 T	H	0.949	397 W	H	0.775	454 I	C	0.786
341 E	H	0.938	398 E	H	0.700	455 E	C	0.856
342 A	H	0.892	399 T	H	0.602	456 P	C	0.709
343 X	H	0.757	400 A	C	0.538	457 L	C	0.662
344 T	H	0.629	401 R	C	0.768	458 D	C	0.754
345 R	H	0.535	402 H	C	0.837	459 L	C	0.744
346 Y	C	0.615	403 T	C	0.886	460 P	H	0.848
347 S	C	0.842	404 P	C	0.820	461 Q	H	0.908
348 A	C	0.907	405 V	H	0.498	462 I	H	0.924
349 P	C	0.905	406 N	H	0.693	463 I	H	0.934
350 P	C	0.921	407 S	H	0.734	464 E	H	0.922
351 G	C	0.925	408 W	H	0.844	465 R	H	0.813
352 D	C	0.930	409 L	H	0.851	466 L	H	0.560
353 P	C	0.930	410 G	H	0.799	467 H	C	0.830
354 P	C	0.924	411 N	H	0.715	468 G	C	0.934
355 Q	C	0.901	412 I	H	0.772	469 L	C	0.912
356 P	C	0.770	413 I	H	0.713	470 S	C	0.549
357 E	C	0.574	414 X	H	0.557	471 A	E	0.783
358 Y	C	0.473	415 Y	C	0.674	472 F	E	0.892
359 D	C	0.514	416 A	C	0.856	473 S	E	0.896
360 L	C	0.483	417 P	C	0.772	474 L	E	0.804
361 E	E	0.478	418 T	C	0.668	475 H	E	0.497
362 L	E	0.489	419 L	H	0.590	476 S	C	0.726
363 I	E	0.482	420 W	H	0.473	477 Y	C	0.863
364 T	E	0.572	421 A	H	0.607	478 S	C	0.894
365 S	E	0.557	422 R	H	0.622	479 P	C	0.818
366 C	C	0.466	423 X	H	0.493	480 G	H	0.528
367 S	C	0.629	424 I	H	0.479	481 E	H	0.626
368 S	C	0.725	425 L	C	0.388	482 I	H	0.837
369 N	C	0.695	426 X	C	0.598	483 N	H	0.919
370 V	E	0.483	427 T	H	0.703	484 R	H	0.942
371 S	E	0.611	428 H	H	0.836	485 V	H	0.954
372 V	E	0.735	429 F	H	0.867	486 A	H	0.957
373 A	E	0.806	430 F	H	0.925	487 S	H	0.953
374 H	E	0.690	431 S	H	0.928	488 C	H	0.941
375 D	C	0.550	432 I	H	0.913	489 L	H	0.929
376 A	C	0.802	433 L	H	0.834	490 R	H	0.852
377 S	C	0.888	434 L	H	0.680	491 K	H	0.665
378 G	C	0.864	435 A	H	0.496	492 L	C	0.713
379 K	C	0.593	436 Q	C	0.557	493 G	C	0.913
380 R	E	0.853	437 E	C	0.672	494 V	C	0.933
381 V	E	0.931	438 Q	C	0.720	495 P	C	0.919
382 Y	E	0.944	439 L	C	0.737	496 P	C	0.707
383 Y	E	0.926	440 E	C	0.676	497 L	H	0.676
384 L	E	0.878	441 K	C	0.556	498 R	H	0.794
385 T	E	0.626	442 A	C	0.594	499 V	H	0.892
386 R	C	0.673	443 L	C	0.520	500 W	H	0.937
387 D	C	0.837	444 D	C	0.454	501 R	H	0.946
388 P	C	0.892	445 C	E	0.620	502 H	H	0.948
389 T	C	0.899	446 Q	E	0.682	503 R	H	0.936
390 T	C	0.733	447 I	E	0.651	504 A	H	0.934
391 P	H	0.568	448 Y	E	0.468	505 R	H	0.954
392 L	H	0.606	449 G	C	0.582	506 S	H	0.962
393 A	H	0.643	450 A	C	0.556	507 V	H	0.960

508 R	H	0.957	516 G	C	0.920	524 Y	H	0.669
509 A	H	0.957	517 R	H	0.547	525 L	H	0.661
510 R	H	0.957	518 A	H	0.699	526 F	H	0.531
511 L	H	0.937	519 A	H	0.726	527 N	H	0.509
512 L	H	0.905	520 T	H	0.811	528 W	H	0.523
513 S	H	0.770	521 C	H	0.778	529 A	H	0.415
514 Q	C	0.585	522 G	H	0.677	530 V	C	0.615
515 G	C	0.894	523 K	H	0.617	531 K	C	0.943
532								

Procathepsin L Prediction

1 S	C	0.967	46 N	C	0.510	91 E	C	0.723
2 L	C	0.942	47 Q	C	0.710	92 P	C	0.815
3 T	C	0.893	48 E	C	0.769	93 L	C	0.822
4 F	C	0.767	49 Y	C	0.807	94 F	C	0.820
5 D	H	0.618	50 R	C	0.841	95 Y	C	0.875
6 H	H	0.801	51 E	C	0.802	96 E	C	0.899
7 S	H	0.868	52 G	C	0.816	97 A	C	0.908
8 L	H	0.926	53 K	C	0.783	98 P	C	0.856
9 E	H	0.946	54 H	C	0.675	99 R	C	0.737
10 A	H	0.957	55 S	E	0.522	100 S	C	0.622
11 Q	H	0.957	56 F	E	0.757	101 V	C	0.613
12 W	H	0.959	57 T	E	0.838	102 D	C	0.711
13 T	H	0.962	58 M	E	0.776	103 W	C	0.607
14 K	H	0.956	59 A	E	0.622	104 R	C	0.557
15 W	H	0.940	60 M	E	0.428	105 E	C	0.570
16 K	H	0.932	61 N	C	0.487	106 K	C	0.694
17 A	H	0.899	62 A	C	0.603	107 G	C	0.671
18 M	H	0.770	63 F	C	0.563	108 Y	C	0.561
19 H	C	0.529	64 G	C	0.682	109 V	C	0.608
20 N	C	0.836	65 D	C	0.759	110 T	C	0.612
21 R	C	0.869	66 M	C	0.715	111 P	C	0.644
22 L	C	0.802	67 T	C	0.826	112 V	C	0.584
23 Y	C	0.770	68 S	H	0.830	113 K	C	0.575
24 G	C	0.830	69 E	H	0.894	114 N	C	0.773
25 M	C	0.706	70 E	H	0.921	115 Q	C	0.884
26 N	H	0.510	71 F	H	0.944	116 G	C	0.874
27 E	H	0.683	72 R	H	0.932	117 Q	C	0.829
28 E	H	0.820	73 Q	H	0.904	118 C	C	0.818
29 G	H	0.891	74 V	H	0.803	119 G	C	0.792
30 W	H	0.906	75 M	H	0.643	120 S	C	0.697
31 R	H	0.914	76 N	C	0.636	121 X	C	0.419
32 R	H	0.911	77 G	C	0.823	122 W	H	0.546
33 A	H	0.916	78 F	C	0.858	123 A	H	0.573
34 V	H	0.916	79 Q	C	0.819	124 F	H	0.767
35 W	H	0.912	80 N	C	0.786	125 S	H	0.754
36 E	H	0.914	81 R	C	0.830	126 A	H	0.799
37 K	H	0.889	82 K	C	0.878	127 T	H	0.861
38 N	H	0.900	83 P	C	0.878	128 G	H	0.853
39 M	H	0.913	84 R	C	0.861	129 A	H	0.868
40 K	H	0.934	85 K	C	0.840	130 L	H	0.882
41 M	H	0.942	86 G	C	0.825	131 E	H	0.864
42 I	H	0.930	87 K	C	0.734	132 G	H	0.858
43 E	H	0.914	88 V	C	0.651	133 Q	H	0.870
44 L	H	0.860	89 F	C	0.620	134 M	H	0.848
45 H	H	0.704	90 Q	C	0.635	135 F	H	0.732

136 R	H	0.614	193 S	C	0.855	250 P	C	0.716
137 K	H	0.472	194 C	C	0.818	251 D	C	0.774
138 T	C	0.703	195 K	C	0.792	252 C	C	0.805
139 G	C	0.873	196 Y	C	0.782	253 S	C	0.839
140 R	C	0.778	197 N	C	0.821	254 S	C	0.850
141 L	C	0.484	198 P	C	0.865	255 E	C	0.830
142 I	E	0.613	199 K	C	0.867	256 D	C	0.837
143 S	E	0.637	200 Y	C	0.802	257 M	C	0.834
144 L	E	0.473	201 S	C	0.544	258 D	C	0.799
145 S	C	0.598	202 V	E	0.773	259 H	E	0.563
146 E	C	0.483	203 A	E	0.865	260 G	E	0.859
147 Q	C	0.438	204 N	E	0.865	261 V	E	0.931
148 N	C	0.415	205 D	E	0.771	262 L	E	0.953
149 L	E	0.493	206 A	E	0.640	263 V	E	0.948
150 V	E	0.574	207 G	E	0.685	264 V	E	0.916
151 D	E	0.564	208 F	E	0.786	265 G	E	0.838
152 C	C	0.568	209 V	E	0.834	266 Y	E	0.658
153 S	C	0.739	210 D	E	0.722	267 G	C	0.511
154 G	C	0.826	211 I	C	0.559	268 F	C	0.591
155 P	C	0.862	212 P	C	0.777	269 E	C	0.721
156 Q	C	0.877	213 K	C	0.856	270 S	C	0.811
157 G	C	0.895	214 Q	C	0.816	271 T	C	0.865
158 N	C	0.907	215 E	H	0.866	272 E	C	0.888
159 E	C	0.903	216 K	H	0.910	273 S	C	0.889
160 G	C	0.910	217 A	H	0.939	274 D	C	0.888
161 C	C	0.888	218 L	H	0.956	275 N	C	0.888
162 N	C	0.851	219 M	H	0.962	276 N	C	0.797
163 G	C	0.851	220 K	H	0.964	277 K	E	0.513
164 G	C	0.868	221 A	H	0.945	278 Y	E	0.865
165 L	C	0.835	222 V	H	0.925	279 W	E	0.940
166 M	H	0.521	223 A	H	0.823	280 L	E	0.942
167 D	H	0.624	224 T	H	0.590	281 V	E	0.922
168 Y	H	0.833	225 V	C	0.873	282 K	E	0.801
169 A	H	0.910	226 G	C	0.928	283 N	C	0.503
170 F	H	0.932	227 P	C	0.830	284 S	C	0.717
171 Q	H	0.949	228 I	E	0.758	285 W	C	0.795
172 Y	H	0.943	229 S	E	0.923	286 G	C	0.821
173 V	H	0.928	230 V	E	0.961	287 E	C	0.814
174 Q	H	0.876	231 A	E	0.955	288 E	C	0.824
175 D	H	0.714	232 I	E	0.927	289 W	C	0.824
176 N	C	0.581	233 D	E	0.739	290 G	C	0.823
177 G	C	0.848	234 A	C	0.501	291 M	C	0.738
178 G	C	0.906	235 G	C	0.718	292 G	C	0.678
179 L	C	0.849	236 H	C	0.641	293 G	C	0.571
180 D	C	0.770	237 E	H	0.580	294 Y	E	0.762
181 S	C	0.791	238 S	H	0.620	295 V	E	0.897
182 E	C	0.847	239 F	H	0.596	296 K	E	0.923
183 E	C	0.867	240 L	H	0.589	297 M	E	0.913
184 S	C	0.874	241 F	H	0.455	298 A	E	0.773
185 Y	C	0.882	242 Y	H	0.360	299 K	C	0.504
186 P	C	0.877	243 K	C	0.443	300 D	C	0.767
187 Y	C	0.880	244 E	C	0.625	301 R	C	0.875
188 E	C	0.875	245 G	C	0.612	302 R	C	0.882
189 A	C	0.867	246 I	E	0.560	303 N	C	0.852
190 T	C	0.880	247 Y	E	0.667	304 H	C	0.732
191 E	C	0.886	248 F	E	0.580	305 C	C	0.597
192 E	C	0.893	249 E	C	0.569	306 G	C	0.519

307	I	E	0.482	314	P	C	0.653
308	A	E	0.580	315	T	C	0.727
309	S	E	0.579	316	V	C	0.891
310	A	C	0.449				
311	A	C	0.617				
312	S	C	0.642				
313	Y	C	0.660				

Polio 3C proteinase Prediction

1	G	C	0.964	48	V	E	0.938	95	T	C	0.783
2	P	C	0.915	49	I	E	0.906	96	E	C	0.837
3	G	C	0.740	50	D	E	0.668	97	T	C	0.864
4	F	H	0.706	51	G	C	0.585	98	N	C	0.878
5	D	H	0.736	52	K	C	0.622	99	D	C	0.808
6	Y	H	0.825	53	E	C	0.479	100	G	E	0.498
7	A	H	0.882	54	V	E	0.549	101	V	E	0.874
8	V	H	0.893	55	E	E	0.649	102	L	E	0.947
9	A	H	0.868	56	I	E	0.639	103	I	E	0.959
10	M	H	0.842	57	L	E	0.487	104	V	E	0.945
11	A	H	0.713	58	D	C	0.419	105	N	E	0.863
12	K	C	0.548	59	A	E	0.451	106	T	E	0.653
13	R	C	0.842	60	K	E	0.531	107	S	C	0.588
14	N	C	0.876	61	A	E	0.597	108	K	C	0.855
15	I	C	0.544	62	L	E	0.624	109	Y	C	0.891
16	V	E	0.860	63	E	E	0.574	110	P	C	0.840
17	T	E	0.952	64	D	E	0.503	111	N	C	0.597
18	A	E	0.962	65	Q	C	0.445	112	M	E	0.697
19	T	E	0.942	66	A	C	0.777	113	Y	E	0.830
20	T	E	0.813	67	G	C	0.869	114	V	E	0.819
21	S	E	0.510	68	T	C	0.840	115	P	E	0.701
22	K	C	0.808	69	N	C	0.746	116	V	E	0.501
23	G	C	0.793	70	L	E	0.557	117	G	C	0.554
24	E	E	0.577	71	E	E	0.846	118	A	C	0.565
25	F	E	0.876	72	I	E	0.943	119	V	C	0.473
26	T	E	0.934	73	T	E	0.958	120	T	E	0.466
27	M	E	0.957	74	I	E	0.958	121	E	E	0.473
28	L	E	0.937	75	I	E	0.951	122	Q	E	0.505
29	G	E	0.852	76	T	E	0.927	123	G	E	0.559
30	V	E	0.795	77	L	E	0.760	124	Y	E	0.632
31	H	E	0.586	78	K	C	0.572	125	L	E	0.675
32	D	C	0.622	79	R	C	0.769	126	N	E	0.620
33	N	E	0.628	80	N	C	0.815	127	L	C	0.595
34	V	E	0.842	81	E	C	0.781	128	G	C	0.768
35	A	E	0.891	82	K	C	0.711	129	G	C	0.830
36	I	E	0.876	83	F	C	0.624	130	R	C	0.824
37	L	E	0.668	84	R	C	0.477	131	Q	C	0.797
38	P	C	0.570	85	D	C	0.466	132	T	C	0.679
39	T	C	0.736	86	I	C	0.471	133	A	C	0.563
40	H	C	0.791	87	R	C	0.534	134	R	E	0.561
41	A	C	0.840	88	P	C	0.618	135	T	E	0.770
42	S	C	0.879	89	H	C	0.693	136	L	E	0.814
43	P	C	0.896	90	I	C	0.637	137	M	E	0.752
44	G	C	0.873	91	P	C	0.548	138	Y	E	0.609
45	E	C	0.736	92	T	C	0.519	139	N	C	0.473
46	S	E	0.717	93	Q	C	0.589	140	F	C	0.658
47	I	E	0.907	94	I	C	0.684	141	P	C	0.663

142	T	C	0.637	156	K	E	0.536	170	F	H	0.865
143	R	C	0.617	157	V	E	0.887	171	A	H	0.916
144	A	C	0.692	158	I	E	0.938	172	A	H	0.930
145	G	C	0.734	159	G	E	0.964	173	A	H	0.922
146	Q	C	0.727	160	M	E	0.960	174	L	H	0.898
147	C	C	0.704	161	H	E	0.929	175	K	H	0.881
148	G	C	0.663	162	V	E	0.720	176	R	H	0.838
149	G	E	0.701	163	G	C	0.675	177	S	H	0.752
150	V	E	0.910	164	G	C	0.832	178	Y	H	0.627
151	I	E	0.943	165	N	C	0.871	179	F	H	0.500
152	T	E	0.922	166	G	C	0.876	180	T	H	0.476
153	C	E	0.816	167	S	C	0.773	181	Q	C	0.522
154	T	C	0.597	168	H	H	0.548	182	S	C	0.765
155	G	C	0.796	169	G	H	0.734	183	Q	C	0.950
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Whale Myoglobin

1	V	C	0.961	40	L	H	0.833	79	K	H	0.636
2	L	C	0.932	41	E	H	0.799	80	G	H	0.498
3	S	C	0.857	42	K	H	0.862	81	H	C	0.539
4	E	H	0.794	43	F	H	0.828	82	H	H	0.876
5	G	H	0.851	44	D	H	0.814	83	E	H	0.930
6	E	H	0.919	45	R	H	0.650	84	A	H	0.937
7	W	H	0.954	46	F	C	0.533	85	E	H	0.965
8	Q	H	0.957	47	K	C	0.714	86	L	H	0.967
9	L	H	0.963	48	H	C	0.838	87	K	H	0.965
10	V	H	0.965	49	L	C	0.883	88	P	H	0.961
11	L	H	0.969	50	K	C	0.877	89	L	H	0.954
12	H	H	0.968	51	T	C	0.771	90	A	H	0.939
13	V	H	0.967	52	E	H	0.618	91	Q	H	0.936
14	W	H	0.956	53	A	H	0.619	92	S	H	0.897
15	A	H	0.929	54	E	H	0.532	93	H	H	0.758
16	K	H	0.858	55	M	C	0.496	94	A	H	0.581
17	V	H	0.672	56	K	C	0.636	95	T	C	0.653
18	E	C	0.543	57	A	C	0.850	96	K	C	0.695
19	A	C	0.801	58	S	C	0.880	97	H	C	0.823
20	D	C	0.878	59	E	H	0.660	98	K	C	0.870
21	V	C	0.655	60	D	H	0.644	99	I	C	0.849
22	A	H	0.569	61	L	H	0.642	100	P	C	0.855
23	G	H	0.578	62	K	H	0.827	101	I	H	0.730
24	H	C	0.604	63	K	H	0.780	102	K	H	0.728
25	G	H	0.826	64	H	H	0.639	103	Y	H	0.837
26	Q	H	0.953	65	G	H	0.744	104	L	H	0.896
27	D	H	0.966	66	V	H	0.874	105	E	H	0.909
28	I	H	0.970	67	T	H	0.919	106	F	H	0.912
29	L	H	0.974	68	V	H	0.938	107	I	H	0.871
30	I	H	0.978	69	L	H	0.958	108	S	H	0.864
31	R	H	0.976	70	T	H	0.959	109	E	H	0.830
32	L	H	0.966	71	A	H	0.960	110	A	H	0.905
33	F	H	0.933	72	L	H	0.962	111	I	H	0.933
34	K	H	0.750	73	G	H	0.961	112	I	H	0.956
35	S	C	0.523	74	A	H	0.964	113	H	H	0.965
36	H	C	0.836	75	I	H	0.961	114	V	H	0.960
37	P	C	0.811	76	L	H	0.933	115	L	H	0.954
38	E	C	0.567	77	K	H	0.878	116	H	H	0.929
39	T	H	0.763	78	K	H	0.727	117	S	H	0.797

118 R	H	0.528	131 M	H	0.966	144 A	H	0.951
119 H	C	0.840	132 N	H	0.966	145 K	H	0.913
120 P	C	0.913	133 K	H	0.965	146 Y	H	0.877
121 G	C	0.888	134 A	H	0.959	147 K	H	0.901
122 D	C	0.835	135 L	H	0.959	148 E	H	0.821
123 F	C	0.888	136 E	H	0.958	149 L	H	0.571
124 G	C	0.908	137 L	H	0.963	150 G	C	0.659
125 A	H	0.881	138 F	H	0.961	151 Y	C	0.834
126 D	H	0.932	139 R	H	0.964	152 Q	C	0.914
127 A	H	0.957	140 K	H	0.960	153 G	C	0.968
128 Q	H	0.970	141 D	H	0.958	154 END		
129 G	H	0.967	142 I	H	0.955			
130 A	H	0.963	143 A	H	0.952			
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GFP Prediction

1 M	C	0.964	41 K	E	0.542	81 F	H	0.490
2 S	C	0.930	42 L	E	0.773	82 F	H	0.501
3 K	C	0.898	43 T	E	0.920	83 K	H	0.463
4 G	C	0.808	44 L	E	0.956	84 S	C	0.419
5 E	C	0.558	45 K	E	0.959	85 A	C	0.639
6 E	C	0.415	46 F	E	0.956	86 M	C	0.849
7 L	E	0.432	47 I	E	0.951	87 P	C	0.874
8 F	E	0.539	48 C	E	0.904	88 E	C	0.854
9 T	E	0.554	49 T	E	0.624	89 G	C	0.832
10 G	E	0.582	50 T	C	0.705	90 Y	C	0.723
11 V	E	0.769	51 G	C	0.868	91 V	E	0.522
12 V	E	0.875	52 K	C	0.889	92 Q	E	0.742
13 P	E	0.903	53 L	C	0.854	93 E	E	0.786
14 I	E	0.948	54 P	C	0.848	94 R	E	0.833
15 L	E	0.954	55 V	C	0.862	95 T	E	0.926
16 V	E	0.949	56 P	C	0.833	96 I	E	0.936
17 E	E	0.921	57 W	C	0.687	97 F	E	0.928
18 L	E	0.836	58 P	C	0.522	98 F	E	0.865
19 D	E	0.643	59 T	C	0.405	99 K	E	0.645
20 G	E	0.514	60 L	E	0.493	100 D	C	0.837
21 D	C	0.496	61 V	E	0.505	101 D	C	0.887
22 V	C	0.540	62 T	E	0.486	102 G	C	0.716
23 N	C	0.698	63 T	E	0.511	103 N	E	0.698
24 G	C	0.659	64 F	E	0.592	104 Y	E	0.870
25 H	E	0.612	65 X	E	0.593	105 K	E	0.922
26 K	E	0.863	66 V	E	0.595	106 T	E	0.918
27 F	E	0.943	67 Q	E	0.658	107 R	E	0.893
28 S	E	0.959	68 C	E	0.664	108 A	E	0.825
29 V	E	0.947	69 F	E	0.643	109 E	E	0.886
30 S	E	0.869	70 S	E	0.551	110 V	E	0.927
31 G	E	0.696	71 R	C	0.506	111 K	E	0.917
32 E	E	0.566	72 Y	C	0.762	112 F	E	0.852
33 G	C	0.609	73 P	C	0.827	113 E	E	0.637
34 E	C	0.780	74 D	C	0.740	114 G	C	0.783
35 G	C	0.870	75 H	C	0.705	115 D	C	0.728
36 D	C	0.858	76 M	C	0.711	116 T	E	0.795
37 A	C	0.812	77 K	C	0.738	117 L	E	0.920
38 T	C	0.732	78 R	C	0.616	118 V	E	0.956
39 Y	C	0.615	79 H	C	0.577	119 N	E	0.971
40 G	C	0.618	80 D	C	0.499	120 R	E	0.962

121 I	E	0.942	160 K	E	0.842	199 L	E	0.676
122 E	E	0.923	161 V	E	0.913	200 S	E	0.669
123 L	E	0.832	162 N	E	0.931	201 T	E	0.665
124 K	E	0.592	163 F	E	0.929	202 Q	E	0.688
125 G	C	0.577	164 K	E	0.928	203 S	E	0.693
126 I	C	0.705	165 I	E	0.920	204 A	E	0.625
127 D	C	0.821	166 R	E	0.899	205 L	E	0.468
128 F	C	0.878	167 H	E	0.786	206 S	C	0.602
129 K	C	0.878	168 N	E	0.541	207 K	C	0.762
130 E	C	0.855	169 I	C	0.675	208 D	C	0.870
131 D	C	0.854	170 E	C	0.750	209 P	C	0.881
132 G	C	0.840	171 D	C	0.796	210 N	C	0.857
133 N	C	0.738	172 G	C	0.818	211 E	C	0.825
134 I	C	0.533	173 S	C	0.700	212 K	C	0.785
135 L	E	0.507	174 V	E	0.610	213 R	C	0.709
136 G	E	0.520	175 Q	E	0.778	214 D	C	0.496
137 H	E	0.559	176 L	E	0.795	215 H	E	0.636
138 K	E	0.627	177 A	E	0.740	216 M	E	0.776
139 L	E	0.606	178 D	E	0.628	217 V	E	0.773
140 E	E	0.666	179 H	E	0.494	218 L	E	0.550
141 Y	E	0.688	180 Y	E	0.476	219 L	H	0.494
142 N	E	0.505	181 Q	E	0.446	220 E	H	0.612
143 Y	C	0.653	182 Q	C	0.516	221 F	H	0.666
144 N	C	0.765	183 N	C	0.750	222 V	H	0.747
145 S	C	0.687	184 T	C	0.845	223 T	H	0.795
146 H	E	0.521	185 P	C	0.829	224 A	H	0.697
147 N	E	0.780	186 I	C	0.826	225 A	C	0.532
148 V	E	0.920	187 G	C	0.854	226 G	C	0.789
149 Y	E	0.947	188 D	C	0.876	227 I	C	0.794
150 I	E	0.911	189 G	C	0.877	228 T	C	0.768
151 M	E	0.709	190 P	C	0.791	229 H	C	0.847
152 A	C	0.494	191 V	C	0.598	230 G	C	0.878
153 D	C	0.734	192 L	C	0.529	231 M	C	0.771
154 K	C	0.770	193 L	C	0.630	232 D	C	0.508
155 Q	C	0.807	194 P	C	0.751	233 E	C	0.477
156 K	C	0.809	195 D	C	0.801	234 L	C	0.494
157 N	C	0.811	196 N	C	0.724	235 Y	C	0.562
158 G	C	0.687	197 H	C	0.538	236 K	C	0.930
159 I	E	0.541	198 Y	E	0.628			

Yeast eIF6 prediction

1	M	C	0.914	15	V	E	0.959	29	G	C	0.818
2	A	C	0.403	16	F	E	0.957	30	G	C	0.882
3	T	E	0.510	17	S	E	0.920	31	S	C	0.887
4	R	E	0.588	18	K	E	0.832	32	E	C	0.721
5	T	E	0.617	19	L	E	0.603	33	N	C	0.626
6	Q	E	0.629	20	T	C	0.776	34	F	H	0.649
7	F	E	0.559	21	N	C	0.766	35	Y	H	0.779
8	E	C	0.628	22	T	E	0.672	36	S	H	0.782
9	N	C	0.834	23	Y	E	0.895	37	A	H	0.827
10	S	C	0.837	24	C	E	0.946	38	F	H	0.796
11	N	C	0.704	25	L	E	0.960	39	E	H	0.816
12	E	E	0.695	26	V	E	0.945	40	A	H	0.816
13	I	E	0.891	27	A	E	0.775	41	E	H	0.744
14	G	E	0.943	28	V	C	0.592	42	L	C	0.461

43	G	C	0.855	100	R	H	0.539	157	Q	C	0.892
44	D	C	0.859	101	L	H	0.567	158	G	C	0.855
45	A	C	0.807	102	S	H	0.522	159	G	E	0.526
46	I	C	0.645	103	A	C	0.491	160	L	E	0.789
47	P	E	0.645	104	L	C	0.804	161	V	E	0.821
48	I	E	0.879	105	G	C	0.863	162	H	E	0.523
49	V	E	0.931	106	N	C	0.657	163	P	C	0.772
50	H	E	0.928	107	V	E	0.835	164	Q	C	0.823
51	T	E	0.914	108	I	E	0.940	165	T	C	0.842
52	T	E	0.854	109	C	E	0.936	166	S	C	0.893
53	I	E	0.729	110	C	E	0.828	167	V	H	0.796
54	A	C	0.663	111	N	C	0.602	168	Q	H	0.818
55	G	C	0.739	112	D	C	0.863	169	D	H	0.829
56	T	E	0.609	113	Y	C	0.767	170	Q	H	0.887
57	R	E	0.867	114	V	E	0.736	171	E	H	0.897
58	I	E	0.929	115	A	E	0.889	172	E	H	0.915
59	I	E	0.948	116	L	E	0.914	173	L	H	0.849
60	G	E	0.947	117	V	E	0.830	174	S	H	0.831
61	R	E	0.943	118	H	C	0.498	175	S	H	0.755
62	M	E	0.920	119	P	C	0.749	176	L	H	0.473
63	T	E	0.838	120	D	C	0.871	177	L	C	0.575
64	A	E	0.544	121	I	C	0.882	178	Q	C	0.631
65	G	C	0.821	122	D	C	0.872	179	V	E	0.620
66	N	C	0.887	123	R	H	0.728	180	P	E	0.839
67	R	C	0.837	124	E	H	0.807	181	L	E	0.907
68	R	C	0.610	125	T	H	0.832	182	V	E	0.891
69	G	E	0.600	126	E	H	0.872	183	A	E	0.716
70	L	E	0.761	127	E	H	0.879	184	G	C	0.486
71	L	E	0.789	128	L	H	0.874	185	T	E	0.556
72	V	E	0.621	129	I	H	0.824	186	V	E	0.674
73	P	C	0.658	130	S	H	0.801	187	N	E	0.591
74	T	C	0.765	131	D	H	0.554	188	R	C	0.595
75	Q	C	0.838	132	V	C	0.645	189	G	C	0.722
76	T	C	0.885	133	L	C	0.736	190	S	C	0.531
77	T	C	0.796	134	G	C	0.638	191	S	E	0.701
78	D	H	0.776	135	V	E	0.841	192	V	E	0.848
79	Q	H	0.828	136	E	E	0.935	193	V	E	0.835
80	E	H	0.853	137	V	E	0.943	194	G	E	0.664
81	L	H	0.895	138	F	E	0.917	195	A	E	0.569
82	Q	H	0.906	139	R	E	0.736	196	G	E	0.634
83	H	H	0.868	140	Q	E	0.563	197	M	E	0.750
84	L	H	0.821	141	T	E	0.586	198	V	E	0.846
85	R	H	0.759	142	I	E	0.639	199	V	E	0.825
86	N	H	0.536	143	S	E	0.624	200	N	C	0.547
87	S	C	0.557	144	G	E	0.696	201	D	C	0.805
88	L	C	0.861	145	N	E	0.822	202	Y	C	0.699
89	P	C	0.903	146	I	E	0.894	203	L	E	0.647
90	D	C	0.894	147	L	E	0.900	204	A	E	0.826
91	S	C	0.782	148	V	E	0.876	205	V	E	0.890
92	V	E	0.690	149	G	E	0.843	206	T	E	0.803
93	K	E	0.923	150	S	E	0.848	207	G	E	0.520
94	I	E	0.956	151	Y	E	0.911	208	L	C	0.677
95	Q	E	0.955	152	C	E	0.938	209	D	C	0.830
96	R	E	0.887	153	S	E	0.934	210	T	C	0.876
97	V	E	0.631	154	L	E	0.898	211	T	C	0.898
98	E	C	0.455	155	S	E	0.686	212	A	C	0.855
99	E	C	0.472	156	N	C	0.740	213	P	C	0.612

214 E	H	0.446	218 I	H	0.499	222 F	E	0.452
215 L	H	0.569	219 E	E	0.528	223 R	C	0.698
216 S	H	0.538	220 S	E	0.460	224 L	C	0.938
217 V	H	0.538	221 I	E	0.470			

Procaspase-7 Prediction

S	C	0.964	A	H	0.938	G	C	0.870
I	C	0.931	L	H	0.957	E	C	0.873
K	C	0.889	F	H	0.964	E	C	0.752
T	C	0.866	K	H	0.967	N	C	0.492
T	C	0.875	C	H	0.951	V	E	0.663
R	C	0.873	F	H	0.938	I	E	0.800
D	C	0.894	R	H	0.897	Y	E	0.740
R	C	0.865	S	H	0.726	G	C	0.495
V	C	0.820	L	C	0.688	K	C	0.809
P	C	0.634	G	C	0.861	D	C	0.855
T	H	0.447	F	C	0.745	G	C	0.832
Y	H	0.435	D	E	0.702	V	C	0.774
Q	E	0.451	V	E	0.914	T	C	0.671
Y	E	0.481	I	E	0.927	P	C	0.694
N	H	0.372	V	E	0.829	I	H	0.633
M	C	0.584	Y	C	0.486	K	H	0.763
N	C	0.761	N	C	0.725	D	H	0.793
F	C	0.816	D	C	0.860	L	H	0.883
E	C	0.841	C	C	0.879	T	H	0.888
K	C	0.855	S	C	0.866	A	H	0.840
L	C	0.798	C	H	0.862	H	H	0.716
G	E	0.551	A	H	0.909	F	C	0.487
K	E	0.869	K	H	0.941	R	C	0.792
C	E	0.947	M	H	0.958	G	C	0.844
I	E	0.952	Q	H	0.964	D	C	0.826
I	E	0.940	D	H	0.966	R	C	0.800
I	E	0.864	L	H	0.959	C	C	0.784
N	E	0.582	L	H	0.950	K	C	0.513
N	C	0.679	K	H	0.936	T	C	0.482
K	C	0.746	K	H	0.907	L	C	0.514
N	C	0.682	A	H	0.822	L	C	0.641
F	C	0.646	S	H	0.620	E	C	0.819
D	C	0.678	E	C	0.511	K	C	0.897
K	C	0.639	E	H	0.513	P	C	0.890
V	C	0.645	D	C	0.642	K	C	0.590
T	C	0.784	H	C	0.828	L	E	0.888
G	C	0.861	T	C	0.881	F	E	0.944
M	C	0.883	N	C	0.897	F	E	0.954
G	C	0.825	A	C	0.885	I	E	0.944
V	C	0.737	A	C	0.806	Q	E	0.894
R	C	0.746	C	E	0.607	A	E	0.704
N	C	0.824	F	E	0.882	A	C	0.539
G	C	0.851	A	E	0.940	R	C	0.764
T	C	0.836	C	E	0.950	G	C	0.849
D	C	0.770	I	E	0.938	T	C	0.857
K	C	0.725	L	E	0.909	E	C	0.882
D	C	0.705	L	E	0.818	L	C	0.881
A	H	0.859	S	E	0.541	D	C	0.870
E	H	0.924	H	C	0.757	D	C	0.827

G	C	0.690	E	H	0.756	H	C	0.801
I	C	0.510	H	C	0.514	H	C	0.833
Q	E	0.570	G	C	0.775	H	C	0.891
A	E	0.501	K	C	0.873	H	C	0.95
D	C	0.658	D	C	0.813			
S	C	0.839	L	C	0.691			
G	C	0.896	E	C	0.649			
P	C	0.898	I	H	0.859			
I	C	0.906	M	H	0.924			
N	C	0.916	Q	H	0.947			
D	C	0.889	I	H	0.955			
T	C	0.862	L	H	0.958			
D	C	0.834	T	H	0.957			
A	C	0.853	R	H	0.937			
N	C	0.871	V	H	0.867			
P	C	0.841	N	H	0.721			
R	C	0.758	D	H	0.672			
Y	C	0.690	R	H	0.676			
K	C	0.669	V	H	0.617			
I	C	0.667	A	H	0.515			
P	C	0.716	R	C	0.395			
V	C	0.759	H	C	0.518			
E	C	0.764	F	C	0.584			
A	C	0.712	E	C	0.673			
D	C	0.537	S	C	0.787			
F	E	0.800	Q	C	0.862			
L	E	0.903	S	C	0.885			
F	E	0.916	D	C	0.898			
A	E	0.902	D	C	0.884			
Y	E	0.840	P	C	0.874			
S	E	0.663	H	C	0.799			
T	C	0.589	F	C	0.581			
V	C	0.813	H	C	0.563			
P	C	0.823	E	C	0.589			
G	C	0.639	K	C	0.610			
Y	E	0.614	K	C	0.669			
Y	E	0.663	Q	C	0.784			
S	E	0.550	I	C	0.854			
W	C	0.471	P	C	0.813			
R	C	0.548	C	C	0.596			
S	C	0.699	V	H	0.496			
P	C	0.819	V	H	0.520			
G	C	0.882	S	H	0.553			
R	C	0.886	M	H	0.489			
G	C	0.753	L	H	0.460			
S	E	0.565	T	H	0.410			
W	E	0.792	K	H	0.462			
F	E	0.744	E	H	0.520			
V	H	0.526	L	H	0.490			
Q	H	0.862	Y	H	0.453			
A	H	0.919	F	H	0.378			
L	H	0.940	S	C	0.607			
C	H	0.952	Q	C	0.664			
S	H	0.958	L	C	0.673			
I	H	0.952	E	C	0.708			
L	H	0.925	H	C	0.783			
E	H	0.880	H	C	0.811			

