Protein Prediction and Structure Analysis of N-terminal of E3L Protein in SPPV

绵羊痘病毒E3L蛋白N端结构与功能预测和分析

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报告：卢昌

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1. Background

The E3 protein of vaccina virus, the prototypic member of erthopoxviruses, functions as an inhibitior of innate immune signaling and is essential for vaccinia replication in vivo and in many human cell culture systems.

E3L is vary conserved in variola and related viruses and plays a key role in cirumventing the IFN-mediated defense of host cells.(Moss.B, J.L.Shisler. Immunology 101 at poxvirus U: immune evasion genes. Semin Immunol, 2001,13:59-66.)

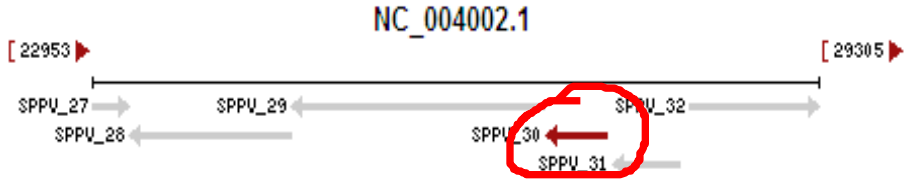
TABLE 1. SPPV and GTPV ORFs

ORF no.[a]	Accession no.[b]	SPPV TU Position	SPPV TU Length[c]	SPPV TU Changes[d] vs. SA	SPPV TU Changes[d] vs. NK	SPPV SA Length	SPPV SA Changes vs. NK	SPPV SA % Id[e] vs. PL	SPPV NK Length	GTPV PL Position	GTPV PL Length	GTPV PL Changes vs. GV	GTPV GV Length	LSDV Length	LSDV % Id vs. SA	LSDV % Id vs. PL	Predicted structure and/or function[f]	MYXV ORF[g]	VACV ORF[h]
001	M28823	589-113		Q/H			H/Q	97		648-172				159	96	99		M003.1	B15R
002	M28823													131				M003.2	
003	M28823	2167-1235	311	+72 aa	+72 aa			97		2056-1337				240	97	99	ER-localized apoptosis regulator	M004	B9R
004														57				M004.1	
005		2243-2746	168			168		92	168	2333-2842				170	93	93	IL-10		
006		3455-2763						95		3551-2859				231	96	96	IL-1R		B16R
007		4545-3481						96		4640-3576				355	98	98			C10L
008		5454-4630		I/N	I/N			94		5530-4706				275	94	95	Interferon-γ receptor	M007	B8R
009														230			α-Amanitin sensitive protein	M139R	N2L
010		6646-6161		V/A				93		6631-6146				162	95	94	LAP/PHD-finger protein	M153R	
011	S78201	7818-6697	374	A/T	A/T	374		92	374	7826-6684				381	92	95	G protein-coupled chemokine receptor		
012	S78201	8557-7925						95		8562-7930				211	95	95	Ankyrin repeat protein	M149R	B4R
013	S78201													341			IL-1R		B16R
014		9918-9652						93		9903-9637				89	96	96	eIF2α-like PKR inhibitor	M156R	K3L
015		10390-9908						94		10375-9893				161	95	96	IL-18 binding protein		
016		10698-10399	100			100		92	100	10683-10396	96		96	89	96	97	EGF-like growth factor	M010L	C11R
017		11219-10692		D/N	D/N			95		11204-10677				176	94	96	Antiapoptotic virulence factor	M011L	
018		11701-11264						99		11683-11246				146	98	97	dUTPase	M012L	F2L
019 (a)		13452-11746						93		13414-11729	562		282	569	95	95	Kelch-like protein	M014L	F3L
(b)													231						
020		14488-13526						97		14444-13482				321	98	98	Ribonucleotide reductase, small subunit	M015L	F4L
021		14767-14531	79	A/S		79	S/A	86	79	14719-14483	79		79	86	81	82		M016L	
022		15148-14840	103			103		85	103	15114-14791	108		108	112	83	87			
023		15557-15342						95		15534-15319				72	97	97		M018L	F8L
024		16286-15639						97		16265-15618				216	98	98		M019L	F9L
025		17607-16267						99		17586-16246				447	98	99	Ser/Thr protein kinase; virus assembly	M020L	F10L
026														302					F11L
027		20390-18474	639	R/K,-N	R/K,-N	640		96	640	20429-18513	639		639	638	97	97	EEV maturation	M021L	F12L
028	AF119594	21509-20400		T/A	G/C,T/A		G/C	98		21548-20439				370	98	99	Palmitylated EEV envelope protein	M022L	F13L
029		22148-21714						99		22187-21753				145	99	100		M024L	F15L
030		22881-22225						96		22919-22263				219	97	97		M025L	F16L
031		22953-23264						95		22994-23305				104	96	95	DNA-binding virion core protein	M026L	F17L
032		24695-23274		K/N	K/N			97		24736-23315				474	97	98	Poly(A) polymerase large subunit PAP$_L$	M027L	E1L
033		[illegible]						[illegible]		[illegible]				[illegible]	[illegible]	[illegible]		[illegible]	[illegible]
034		27444-26914		I/M				97		27530-26955	192		192	177	97	97	dsRNA-binding PKR inhibitor	M029L	E3L
035		[illegible]	[illegible]			[illegible]		[illegible]	[illegible]	[illegible]	[illegible]		[illegible]	[illegible]	[illegible]	[illegible]		[illegible]	[illegible]
036		28087-27506	194	D/E,K/N	D/E,K/N	194		96	194	28150-27548				201	95	97	RNA polymerase subunit RPO30	M030L	E4L
037		29315-31012			S/R		S/R	98		29376-31073				566	99	98		M032R	E6R
038		31025-31819	265			265		99	265	31086-31880	265	N/D	265	266	99	99		M033R	E8R
039		34851-31822		S/L,A/S	S/L,A/S			97		34912-31883				1010	98	98	DNA polymerase	M034L	E9L
040		34885-35169			S/T		S/T	95		34946-35230				95	98	96	IMV redox protein, virus assembly	M035R	E10R
041		35561-35172						92		35622-35233				130	93	97	Virion core protein		E11L
042		37602-35551		H/N	H/N			96		37663-35612				684	97	97		M036L	O1L
043		38652-37711						99		38713-37772				314	99	99	DNA-binding virion core protein	M038L	I1L
044		38874-38662	71			71		97	71	38935-38723	71		71	72	95	95		M039L	I2L
045		39705-38878		V/I	V/I			95		39766-38939				276	96	97	DNA-binding phosphoprotein	M040L	I3L
046		40001-39768						97		40049-39816				78	100	97	IMV membrane protein	M041L	I5L
047		41203-40022						98		41251-40070				394	98	99		M042L	I6L
048		42497-41199						99		42545-41247				433	99	100	Virion core protein	M043L	I7L
049		[illegible]		[illegible]	[illegible]			[illegible]		[illegible]				[illegible]	97	[illegible]	NPH-II, RNA helicase	M044R	I8R
050		46317-44533	595			595		98	595	46365-44581	595		595	596	98	98	Metalloprotease, virion morphogenesis	M045L	G1L
051		46640-47305						98		46688-47353				222	98	100	Putative transcriptional elongation factor	M047R	G2R
052		[illegible]						99		[illegible]				[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
053		47652-47275						98		47700-47323				126	99	99	Glutaredoxin 2, virion morphogenesis	M048L	G4L

Comparison of CaPV genomes and vaccinia virus genomes.(E.R.Tulman, C.L.Afonso, et al. The Genomes of Sheeppox and Goatpox Viruses. Journal of Virology, 2002, 76:6054-6061.)

Genomic context

Sequence: NC_004002.1 (26911..27444, complement)

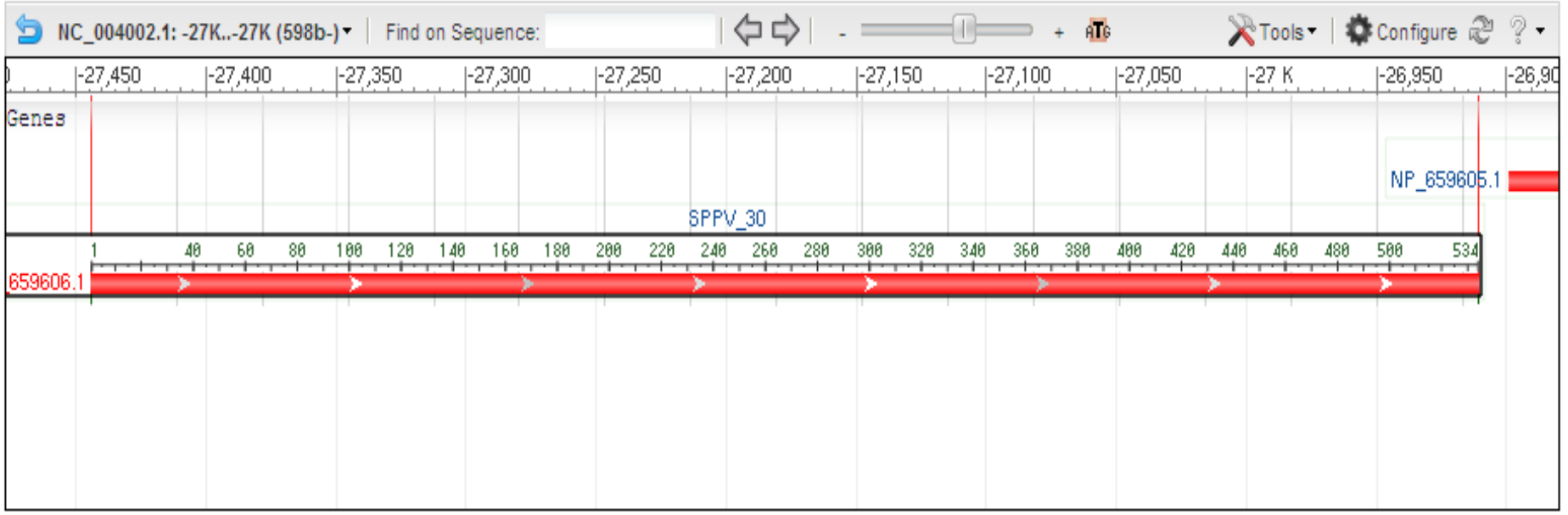


Genomic regions, transcripts, and products

Genomic Sequence NC_004002

Go to reference sequence details

Go to nucleotide Graphics FASTA GenBank



- The E3 protein is composed of a carboxy-terminal dsRNA binding domain and an anmino-terminal Z-DNA binding domain. While wild-type vaccinia virus displays a broad cellular tropism and is highly resistant to effects of interferon(IFN), deletion of E3 results in restricted tropism and sensitivity ro IFNs.

- The ability to bind Z-DNA is essential for E3L activity. A replacement of the N-terminal domain of E3L with a domain defective in Z-DNA binding results in a less pathogenic or nonpathogenic virus.

- Z-DNA-forming sequences found near the transcription start site can flip into the Z-conformation in some actively transcribing genes , and E3L may bind to the Z-DNA segment of such genes.

2.Basic protein information

```
LOCUS       NP_659606                177 aa            linear   VRL 26-MAR-2010
DEFINITION  dsRNA-binding PKR inhibitor [Sheeppox virus].
ACCESSION   NP_659606
VERSION     NP_659606.1  GI:21492487
DBLINK      Project: 14196
DBSOURCE    REFSEQ: accession NC_004002.1
KEYWORDS    .
SOURCE      Sheeppox virus
  ORGANISM  Sheeppox virus
            Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
            Capripoxvirus.
REFERENCE   1  (residues 1 to 177)
  AUTHORS   Tulman,E.R., Afonso,C.L., Lu,Z., Zsak,L., Sur,J.H., Sandybaev,N.T.,
            Kerembekova,U.Z., Zaitsev,V.L., Kutish,G.F. and Rock,D.L.
  TITLE     The genomes of sheeppox and goatpox viruses
  JOURNAL   J. Virol. 76 (12), 6054-6061 (2002)
   PUBMED   12021338
REFERENCE   2  (residues 1 to 177)
  CONSRTM   NCBI Genome Project
  TITLE     Direct Submission
  JOURNAL   Submitted (14-JUN-2002) National Center for Biotechnology
            Information, NIH, Bethesda, MD 20894, USA
REFERENCE   3  (residues 1 to 177)
  AUTHORS   Tulman,E.R., Afonso,C.L., Lu,Z., Zsak,L., Sur,J.-H.,
            Sandybaev,N.T., Kerembekova,U.Z., Zaitsev,V.L., Kutish,G.F. and
            Rock,D.L.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-JAN-2002) African Swine Fever Research, Plum Island
            Animal Disease Center, U.S. Dept. Agriculture, Agricultural
            Research Service, P.O. Box 848, Greenport, NY 11944-0848, USA
COMMENT     PROVISIONAL REFSEQ: This record has not yet been subject to final
            NCBI review. The reference sequence was derived from SPPV_30.
            Method: conceptual translation.
FEATURES             Location/Qualifiers
     source          1..177
                     /organism="Sheeppox virus"
```

Run BLAST

Identify Conserved Domains

Highlight Sequence Features

Find in this Sequence

Articles about the SPPV_30 gene

The genomes of sheeppox and goatpox viruses. [J Virol. 2002]

See all...

Protein clusters for NP_659606.1

Double-strand RNA-binding protein - double-strand RNA-binding protein; has adenosine deaminase activity (converts adenosines to

Total proteins: 18

Total genera: 6

Conserved in: Chordopoxvirinae

More about the gene SPPV_30

SPPV_30 gene

Also Known As: SPPV_30

Related information

BLink

Related Sequences

BioProject

CDD Search Results

Protein 1..177
/product="double-strand RNA-binding protein"
/calculated_mol_wt=20401

Region 1..177
/region_name="PHA03103"
/note="double-strand RNA-binding protein; Provisional"
/db_xref="CDD:177529"

Region <33..66
/region_name="z-alpha"
/note="adenosine deaminase z-alpha domain; cl02659"
/db_xref="CDD:207691"

Region 104..169
/region_name="DSRM"
/note="Double-stranded RNA binding motif. Binding is not sequence specific but is highly specific for double stranded RNA. Found in a variety of proteins including dsRNA dependent protein kinase PKR, RNA helicases, Drosophila staufen protein, E. coli RNase III; cd00048"
/db_xref="CDD:28930"

Site order(104,110..111,152..155,158)
/site_type="other"
/note="dsRNA binding site [nucleotide binding]"
/db_xref="CDD:28930"

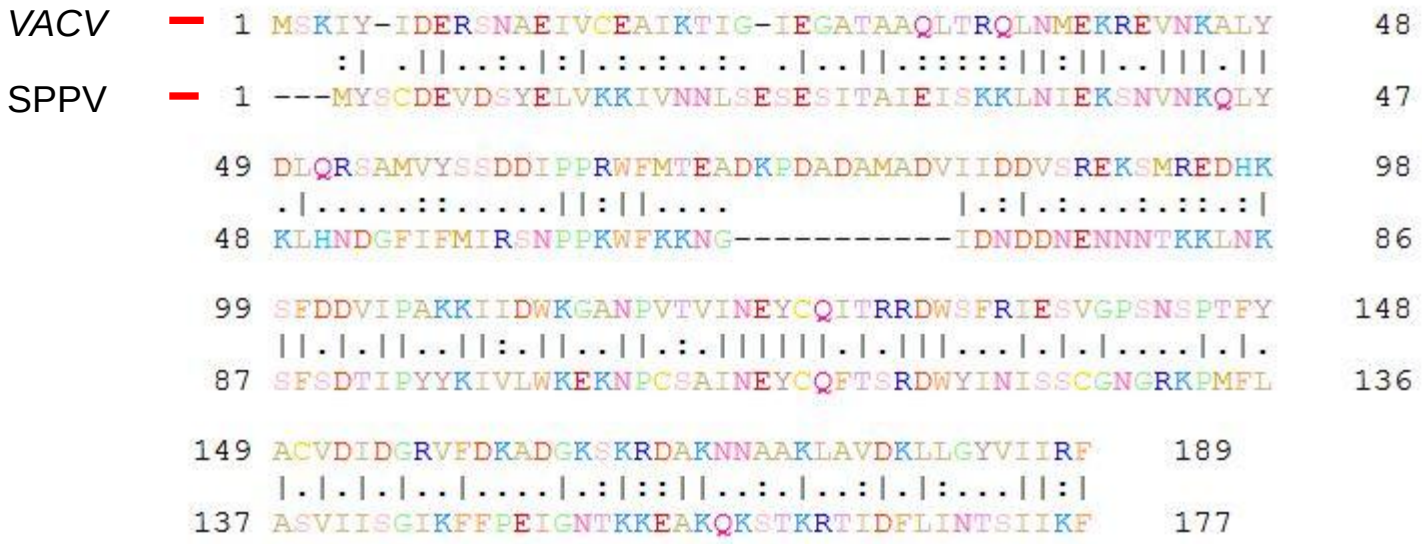
CDS 1..177
/locus_tag="SPPV_30"
/coded_by="complement(NC_004002.1:26911..27444)"
/note="double-strand RNA-binding protein; has adenosine deaminase activity (converts adenosines to inosines); involved in viral immune evasion, The poxviridae are enveloped unsegmented dsDNA viruses; unlike many dsDNA viruses that replicate in the host nucleus poxviruses encode their own replication machinery and therefore replicate in the cytoplasm; viral genes are expressed in a bi-phasic manner with early genes genes encoding non-structural proteins involved in genome replication and late genes encoding the viral structural proteins"
/db_xref="GeneID:944663"

Protein Clusters
PubMed
PubMed (RefSeq)
PubMed (Weighted)
Related Structures (List)
Related Structures (Summary)
Taxonomy

Alignment of E3l in SPPV and VACV

Pairwise Alignment Result

LENGTH	SCORE	IDENTITY	SIMILARITY	GAPS
191	297.0	66/191 (34.6%)	96/191 (50.3%)	16/191 (8.4%)



PEPSTATS of dsRNA-binding from 1 to 177

Molecular weight = 20532.49 Residues = 177

Average Residue Weight = 116.003 Charge = 8.5

Isoelectric Point = 9.6391

A280 Molar Extinction Coefficient = 26030

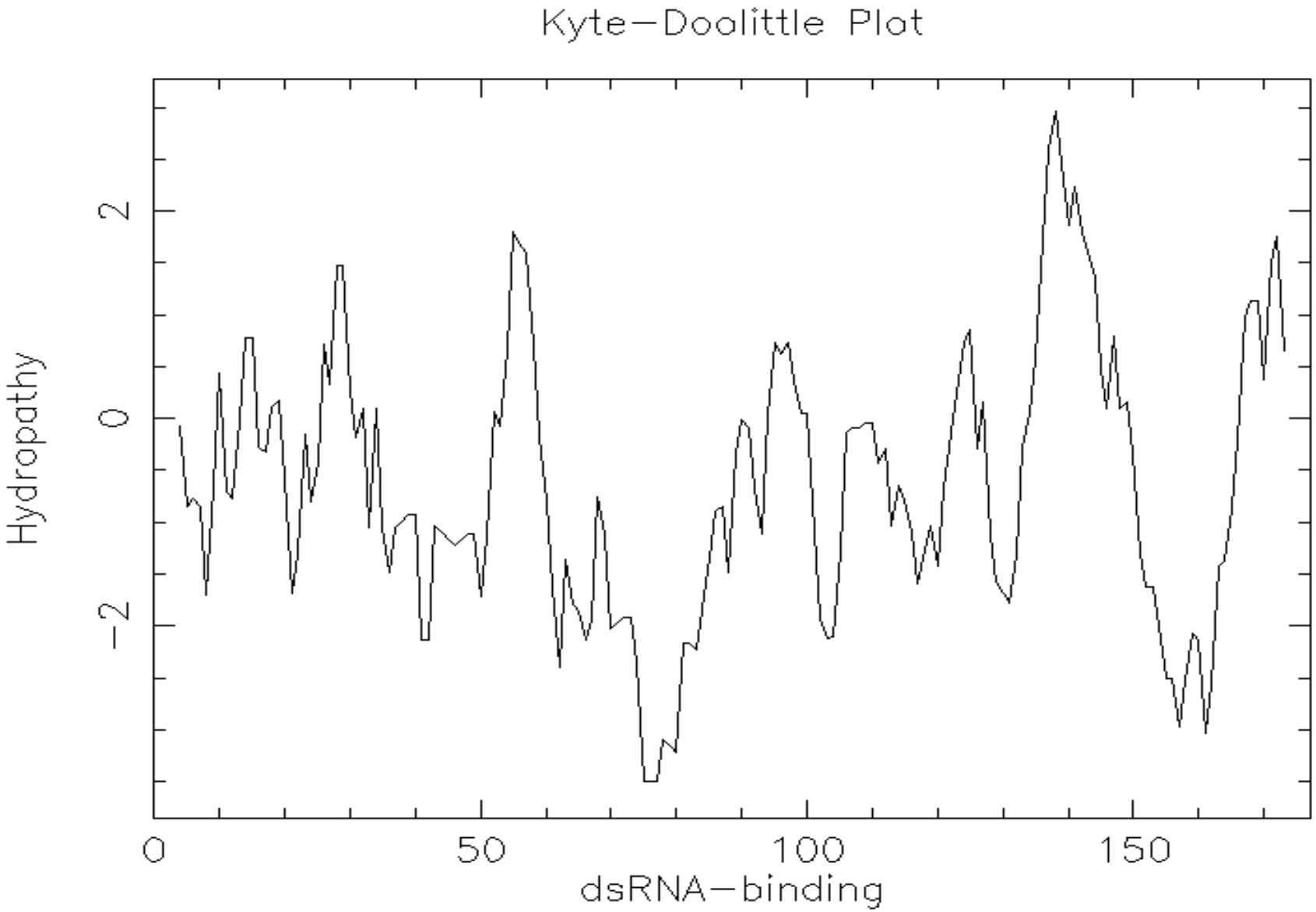
A280 Extinction Coefficient 1mg/ml = 1.27

Improbability of expression in inclusion bodies = 0.911

Residue	Number	Mole%	DayhoffStat
A = Ala	4	2.260	0.263
B = Asx	0	0.000	0.000
C = Cys	4	2.260	0.779
D = Asp	9	5.085	0.924
E = Glu	11	6.215	1.036
F = Phe	10	5.650	1.569
G = Gly	6	3.390	0.404
H = His	1	0.565	0.282
I = Ile	21	11.864	2.637
J = ---	0	0.000	0.000
K = Lys	24	13.559	2.054
L = Leu	9	5.085	0.687
M = Met	3	1.695	0.997
N = Asn	20	11.299	2.628
O = ---	0	0.000	0.000
P = Pro	6	3.390	0.652
Q = Gln	3	1.695	0.435
R = Arg	4	2.260	0.461
S = Ser	18	10.169	1.453
T = Thr	8	4.520	0.741
U = ---	0	0.000	0.000
V = Val	6	3.390	0.514
W = Trp	3	1.695	1.304
X = Xaa	0	0.000	0.000
Y = Tyr	7	3.955	1.163
Z = Glx	0	0.000	0.000

Property	Residues	Number	Mole%	
Tiny	(A+C+G+S+T)	40		22.599
Small	(A+B+C+D+G+N+P+S+T+V)	81	45.763	
Aliphatic	(A+I+L+V)	40	22.599	
Aromatic	(F+H+W+Y)	21	11.864	
Non-polar	(A+C+F+G+I+L+M+P+V+W+Y)	79	44.633	
Polar	(D+E+H+K+N+Q+R+S+T+Z)	98	55.367	
Charged	(B+D+E+H+K+R+Z)	49		27.684
Basic	(H+K+R)	29		16.384
Acidic	(B+D+E+Z)	20	11.299	

hydropathy


Kyte–Doolittle Plot
Hydropathy
2
0
-2
0
50
100
150
dsRNA–binding

Averaae flexibility

ProtScale

User-provided sequence:

```
         10         20         30         40         50         60
MYSCDEVDSY ELVKKIVNNL SESESITAIE ISKKLNIEKS NVNKQLYKLH NDGFIFMIRS

         70         80         90        100        110        120
NPPKWFKKNG IDNDDNENNN TKKLNKSFSD TIPYYKIVLW KEKNPCSAIN EYCQFTSRDW

        130        140        150        160        170
YINISSCGNG RKPMFLASVI ISGIKFFPEI GNTKKEAKQK STKRTIDFLI NTSIIKF
```

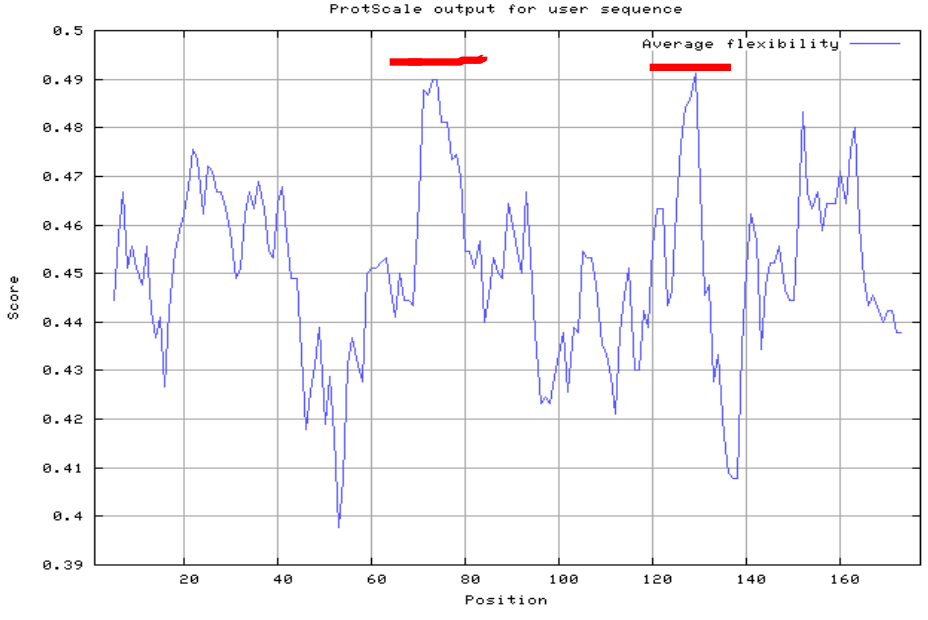
SEQUENCE LENGTH: 177

Using the scale **Average flexibility**, the individual values for the 20 amino acids are:

```
Ala:  0.360  Arg:  0.530  Asn:  0.460  Asp:  0.510  Cys:  0.350  Gln:  0.490
Glu:  0.500  Gly:  0.540  His:  0.320  Ile:  0.460  Leu:  0.370  Lys:  0.470
Met:  0.300  Phe:  0.310  Pro:  0.510  Ser:  0.510  Thr:  0.440  Trp:  0.310
Tyr:  0.420  Val:  0.390  :  0.485  :  0.495  :  0.428
```

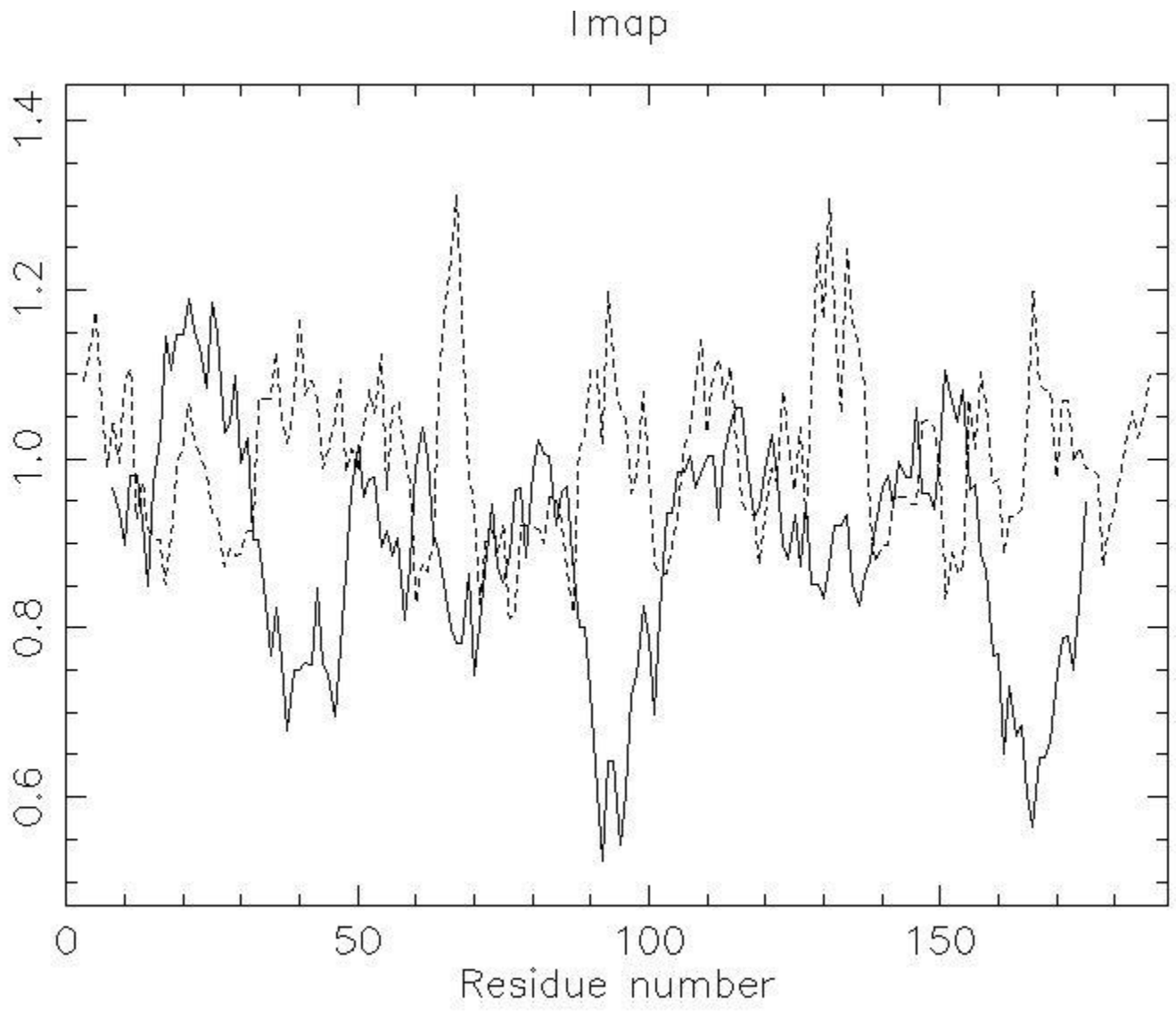
Weights for window positions 1,..,9, using **linear weight variation model**:

```
   1     2     3     4     5     6     7     8     9
1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00
edge                    center                edge
```



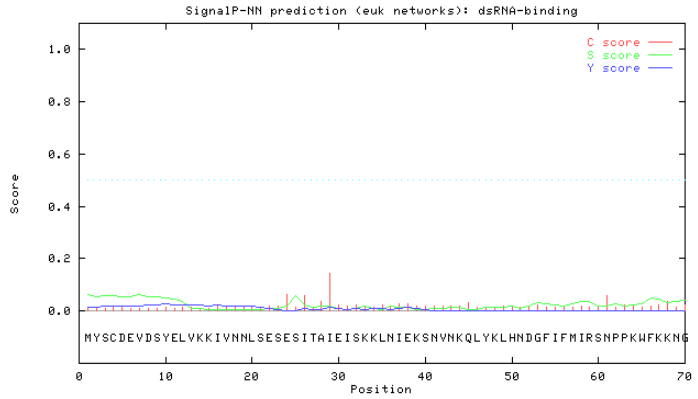
```
#
# Please cite:
# Garnier, Osguthorpe and Robson (1978) J. Mol. Biol. 120:97-120
#
#
#=====================================
          .   10    .   20    .   30    .   40    .   50
     MYSCDEVDSYELVKKIVNNLSESESITAIEISKKLNIEKSNVNKQLYKLH
helix      HHHHHHHHHH       HHHHHHHHHHHHHHHHH HHHHH
sheet E EE           EE                        EEEE
turns  T  T                              T
 coil                CCCCC                        C
          .   60    .   70    .   80    .   90    .  100
     NDGFIFMIRSNPPKWFKKNGIDNDDNENNNTKKLNKSFSDTIPYYKIVLW
helix                              HHHHH             H
sheet    EEEEE      EE                EE   EE  EEEEE
turns TTT     T   TTT  TTT      TT      T  TTT  TT
 coil          CCC        CCCCCC       C
          .  110    .  120    .  130    .  140    .  150
     KEKNPCSAINEYCQFTSRDWYINISSCGNGRKPMFLASVIISGIKFFPEI
helix H                                   HH         H
sheet         EE          EE        EEEEE  EEE   EEE
turns  TT TTTTT  TTTTTTTTTTT  TTTTTT           T     T
 coil    C                        CC          CC
          .  160    .  170
     GNTKKEAKQKSTKRTIDFLINTSIIKF
helix  HHHHHHHHHH
sheet             EEEEEEE    EEE
turns T          TT
 coil                   CCCC
#-------------------------------------
#
# Residue totals: H: 52   E: 50   T: 50   C: 25
#        percent: H: 32.3 E: 31.1 T: 31.1 C: 15.5
#
#-------------------------------------
#-------------------------------------
# Total_sequences: 1
# Total_hitcount: 52
#-------------------------------------
```

Trans membrane



SignalP predictions

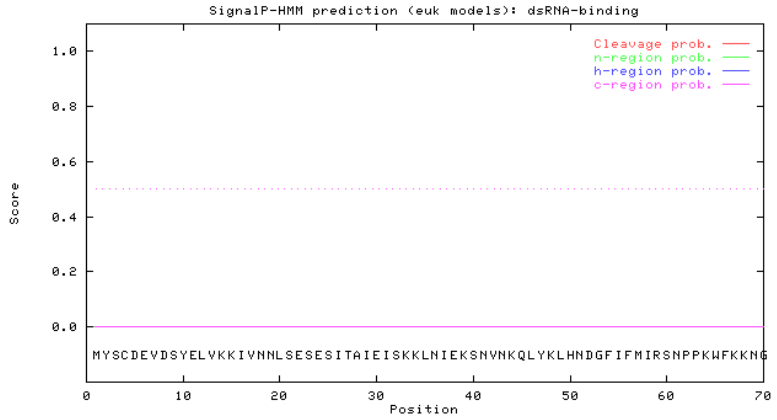
SignalP-NN result:



data

```
>dsRNA-binding          length = 70
# Measure  Position  Value  Cutoff  signal peptide?
  max. C     29       0.146   0.33   NO
  max. Y     10       0.026   0.32   NO
  max. S      1       0.063   0.82   NO
  mean S     1-9      0.057   0.47   NO
```

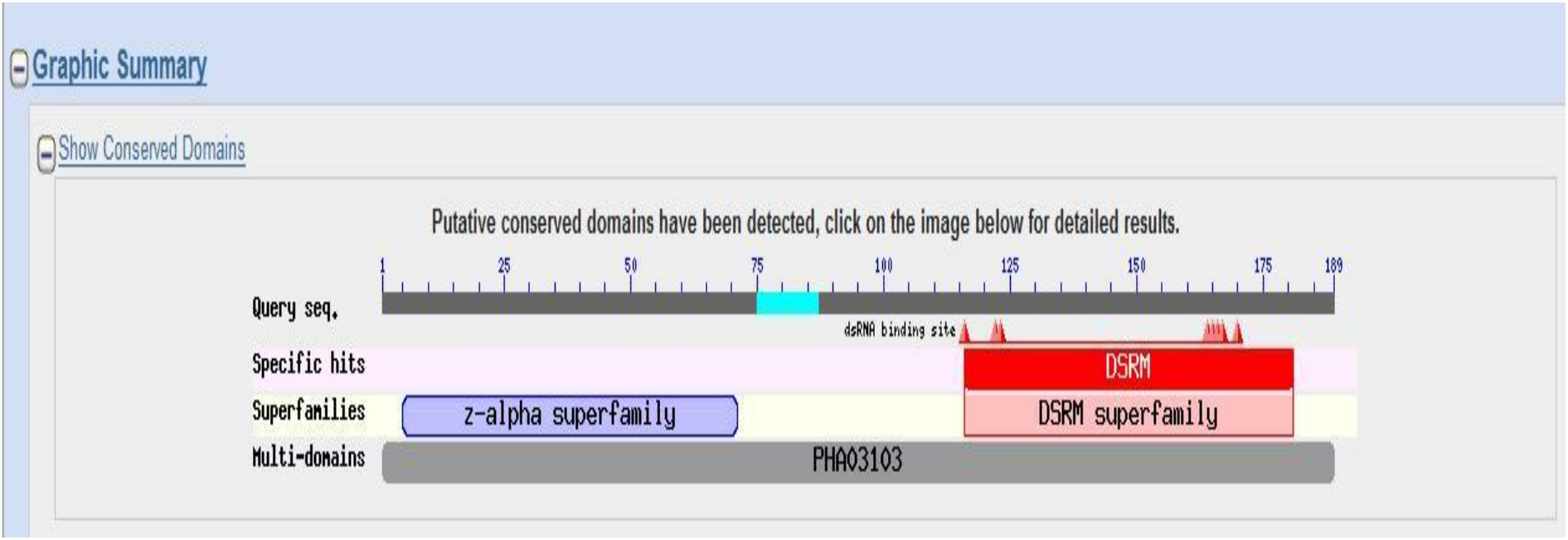
SignalP-HMM result:



data

```
>dsRNA-binding
Prediction: Non-secretory protein
Signal peptide probability: 0.000
Signal anchor probability: 0.000
Max cleavage site probability: 0.000 between pos. -1 and  0
```

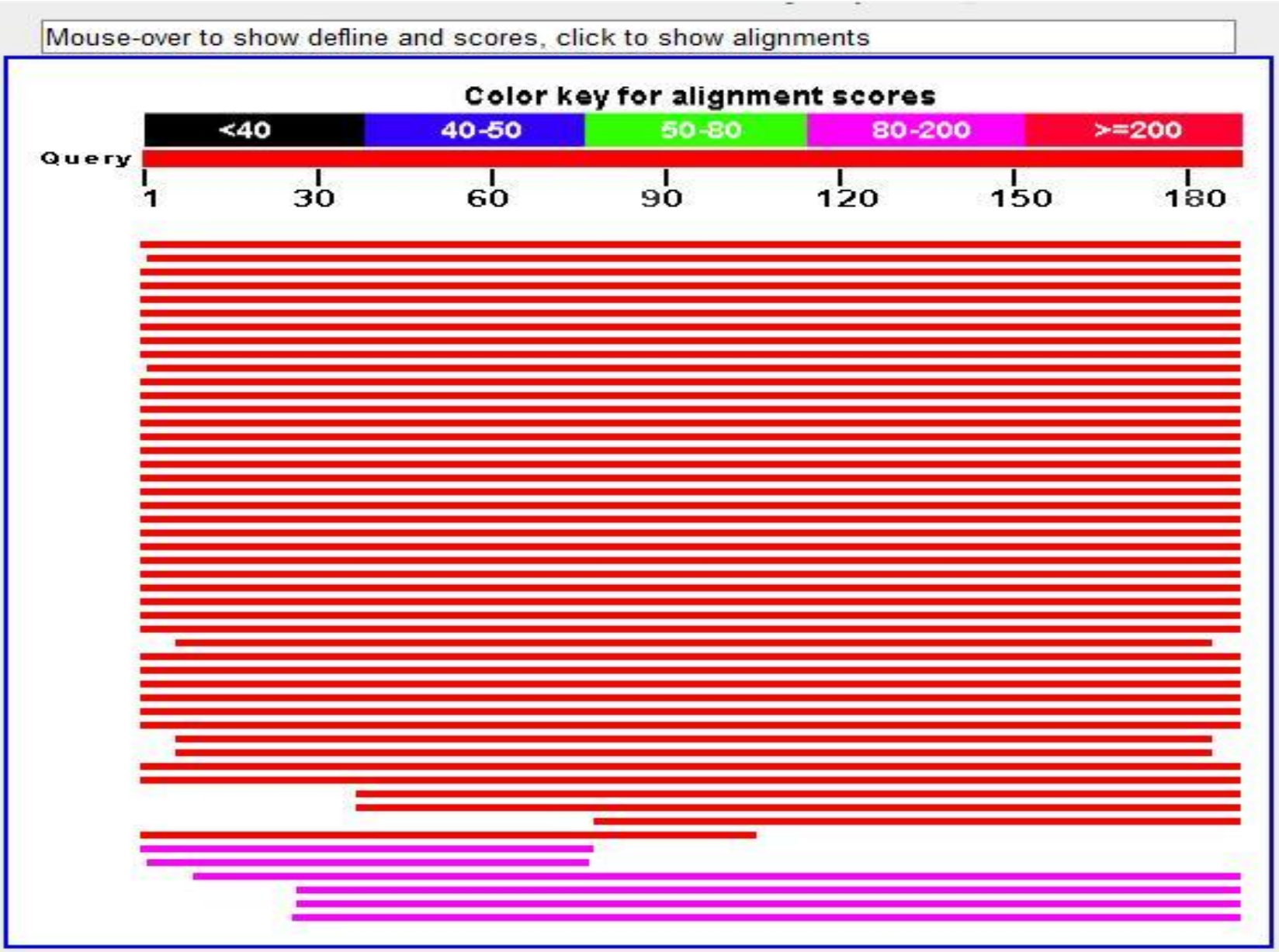
Using BLAST to search the similary sequence of E3L in the protein database.



The result shows that there exist sequences when align conserved domain using blastp. From the above image we can see E3L protein consists of two superfamilies, z-alpha superfamily and DSRM

superfamily

Distribution of 50 Blast Hits on the Query Sequence



Tree

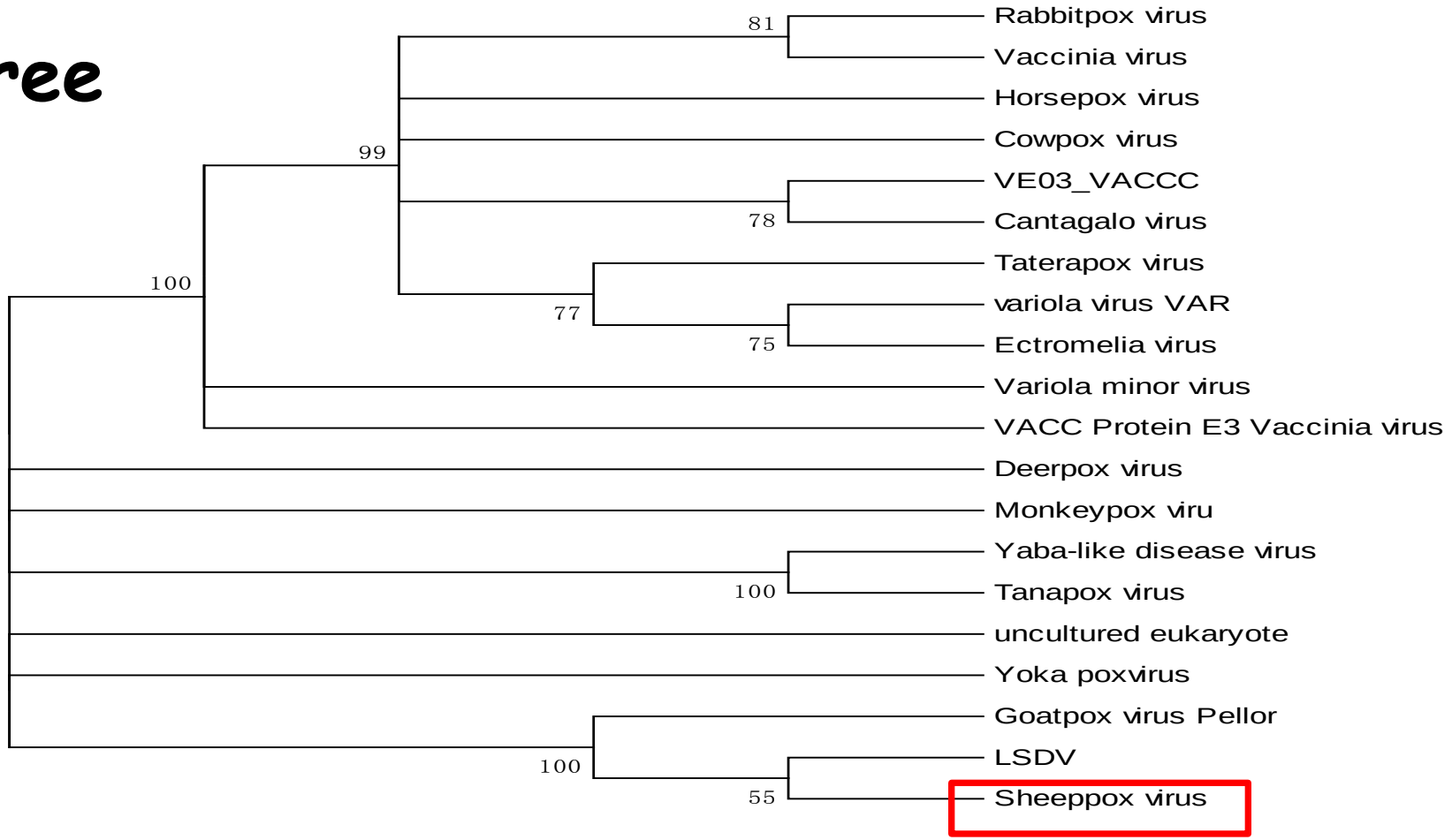


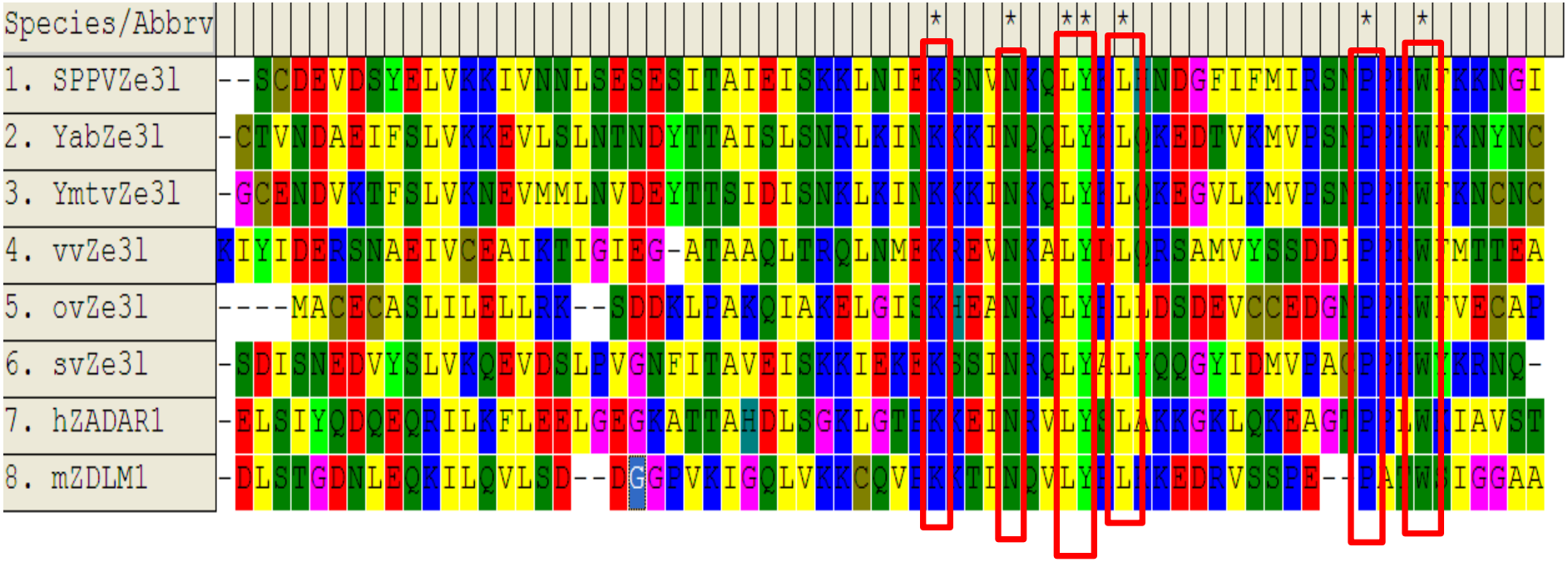
Figure. Evolutionary relationships of taxa

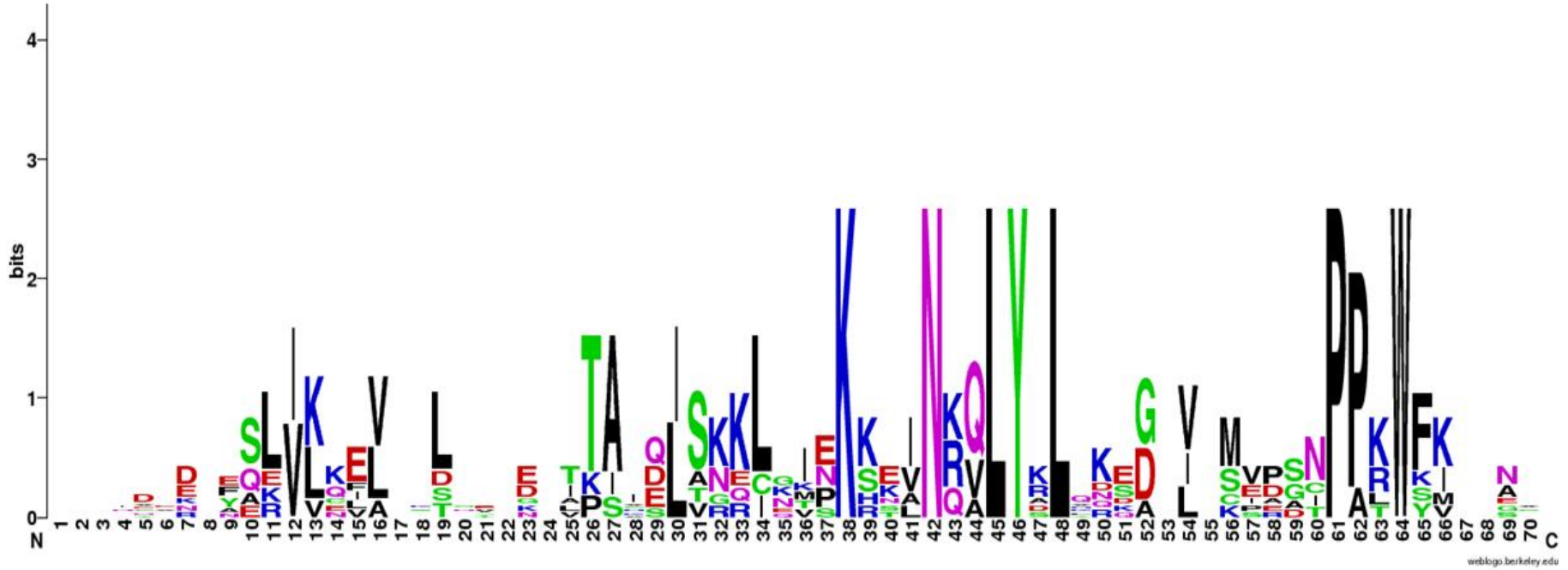
The evolutionary history was inferred using the Neighbor-Joining method . The percentage of replicate trees in which the associated taxa clustered together in the bootstrap test are shown next to the branches . The evolutionary distances were computed using the Poisson correction method and are in the units of the number of amino acid substitutions per site. The analysis involved 20 amino acid sequences. All positions containing gaps and missing data were eliminated. Evolutionary analyses were conducted in MEGA5 .

3. Sequence analysis of Za family and SPPVZae31

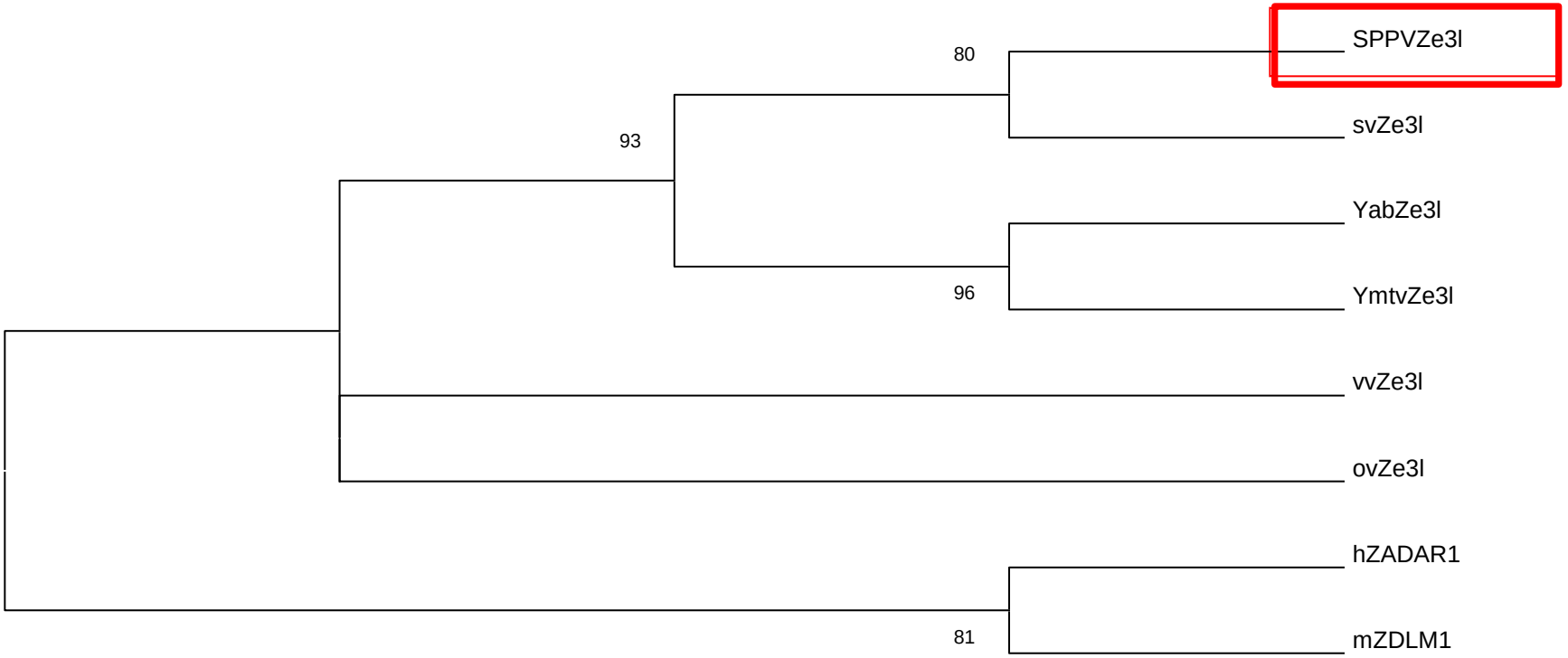
- >SPPVZae3l
- SCDEVDSYELVKKIVNNLSESESITAIEISKKLNIEKSNVNKQLYKLHNDG FIFMIRSNPPKWFKKNGI
- >YabZae3l
- CTVNDAEIFSLVKKEVLSLNTNDYTTAISLSNRLKINKKKINQQLYKLQKE DTVKMVPSNPPKWFKNYNC
- >YmtvZae3l
- GCENDVKTFSLVKNEVMMLNVDEYTTSIDISNKLKINKKKINKQLYKLQK EGVLKMVPSNPPKWFKNCNC
- >vvZae3l
- KIYIDERSNAEIVCEAIKTIGIEGATAAQLTRQLNMEKREVNKALYDLQR SAMVYSSDDIPPRWFMTTEA
- >ovZae3l
- MACECASLILELLRKSDDKLPAKQIAKELGISKHEANRQLYRLLDSDEVCCE DGNPPRWFVECAP
- >svZae3l
- SDISNEDVYSLVKQEVDSLPVGNFITAVEISKKIEKEKSSINRQLYALYQQ GYIDMVPACPPKWYK-RNQ
- >hZaADAR1
- ELSIYQDQEQRILKFLEELGEGKATTAHDLSGKLGTPKKEINRVLYSLAKKG KLQKEAGTPPLWKIAVST
- >mZaDLM1
- DLSTGDNLEQKILQVLSDDGGPVKIGQLVKKCQVPKKTLNQVLYRLKKEDR VSSPEPATWSIGGAA

Multiple Sequence Alignment





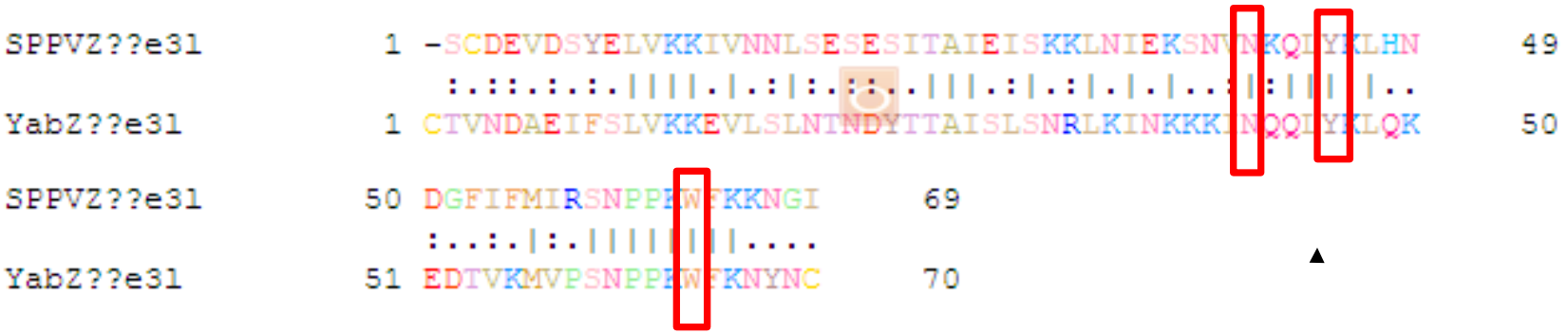
The Z-DNA binding domain of the Za family.(Used WebLogo. http://weblogo.berkeley.edu/)



The Za family evolutionary history was inferred using the Neighbor-Joining method. The bootsrap consensus tree inferred 500 replicates is taken to represent the evolutionary history of the Za family analyed. The percentage of replicate trees in which the associated taxa clustered together in the bootstrap test (500 replicates) are shown next to the branches . The tree is drawn to scale, with branch lengths in the same units as those of the evolutionary distances used to infer the phylogenetic tree. The evolutionary distances were computed using the Poisson correction method and are in the units of the number of amino acid substitutions per site. The analysis involved 8 amino acid sequences. All positions containing gaps and missing data were eliminated. There were a total of 61 positions in the final dataset. Evolutionary analyses were conducted in MEGA5.

Pairwise Alignment Result

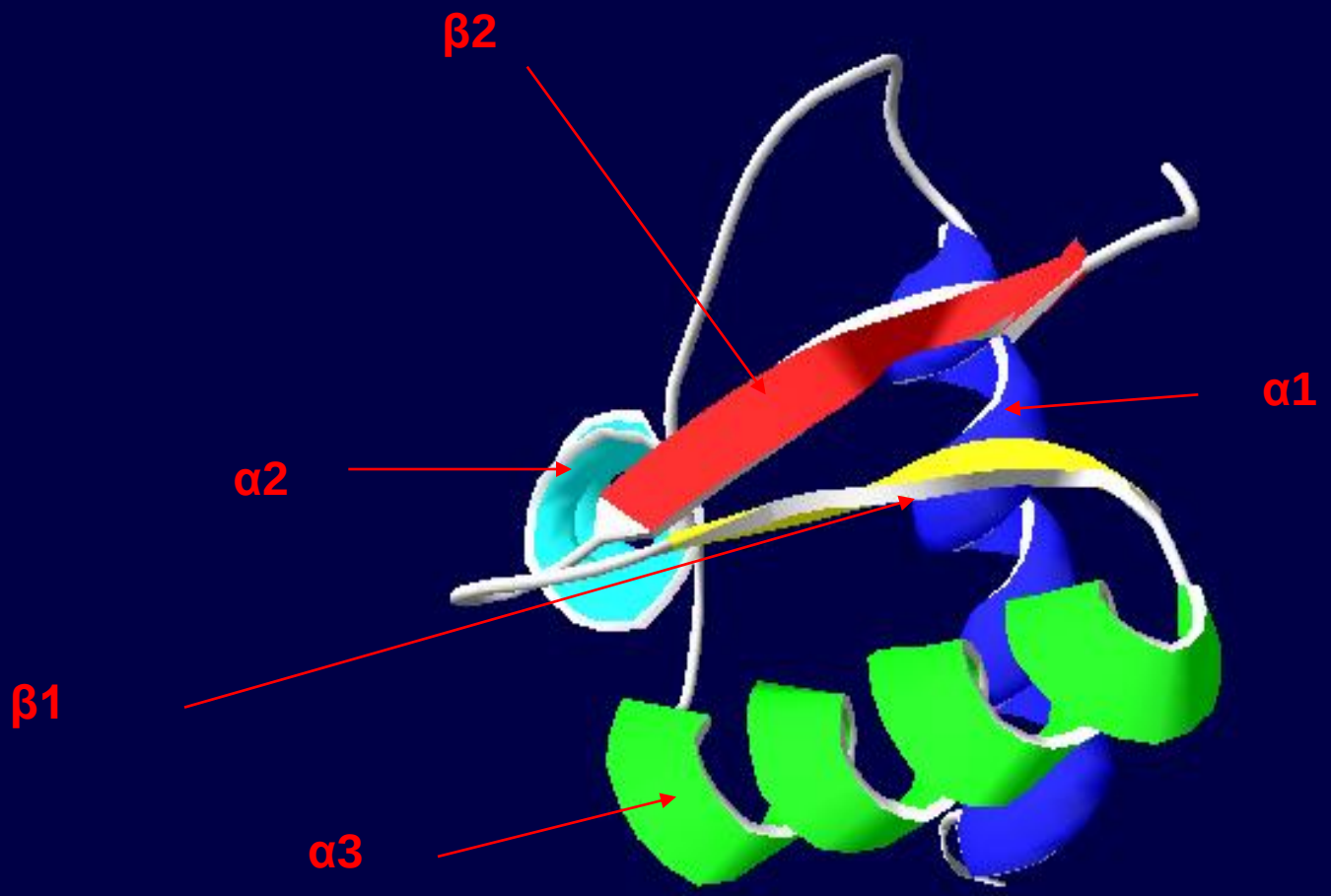
LENGTH	SCORE	IDENTITY	SIMILARITY	GAPS
70	149.0	28/70 (40.0%)	44/70 (62.9%)	1/70 (1.4%)



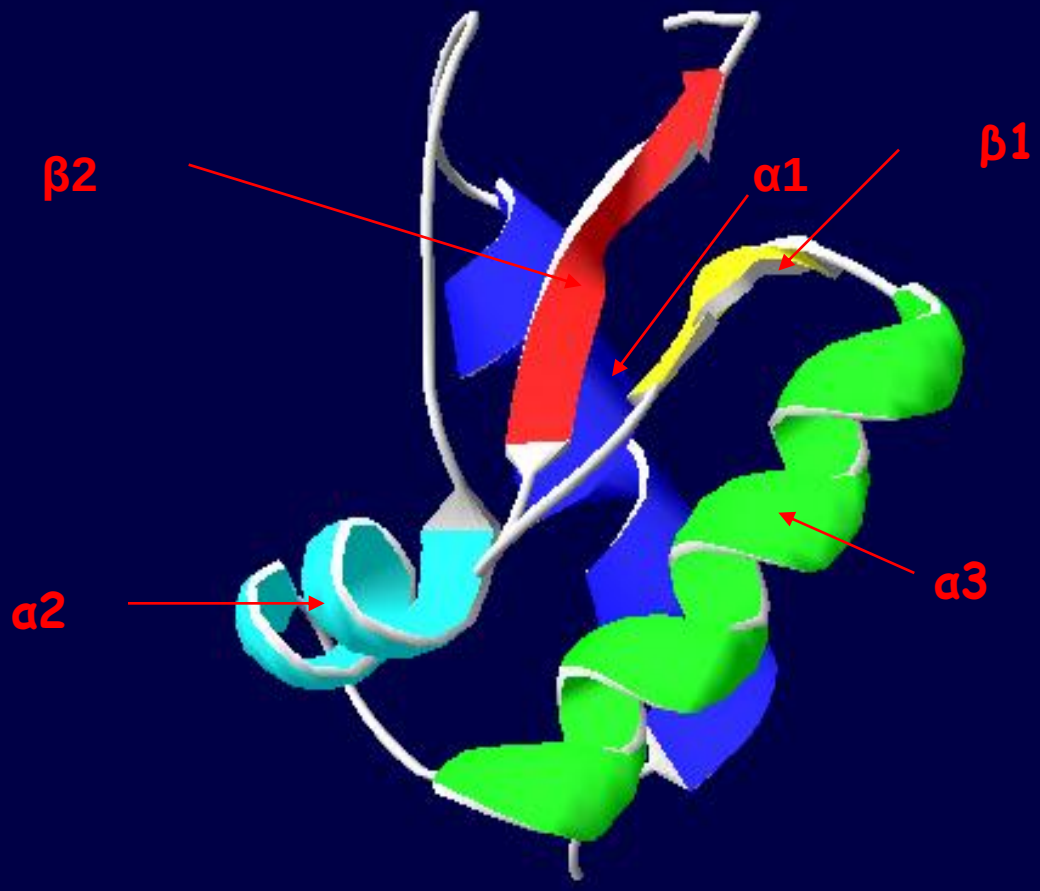
Sequence Alignment result of SPPVZae3l and YabZae3l.

4. 3D structure analysis of SPPVZae3l

- The predicted structure of sppvZaE3L suggests that it may belongs to the Za family of helix-turn-helix (HTH),winged-helix Z-DNA-binding protein. It has an α/β architecture, consisting of two β-strands and three α-helices, although there are three β-strands in YabZaE3L- and vvZaE3L. The three α-helices (α1,α2, α3) form a core domain, which is flanked by a β-sheet of two antiparallel strands (β1 and β2). α2 and α3 form an HTH motif and two antiparallel β-strands form the wing. (Sung Chul Ha, Neratur K.Lokanath, et al. A poxvirus protein forms a complex with left-handed Z-DNA: Crystal structure od a Yatapoxvirus Za bound to DNA [J]. PANS, 2004, 40: 14367-14372.)

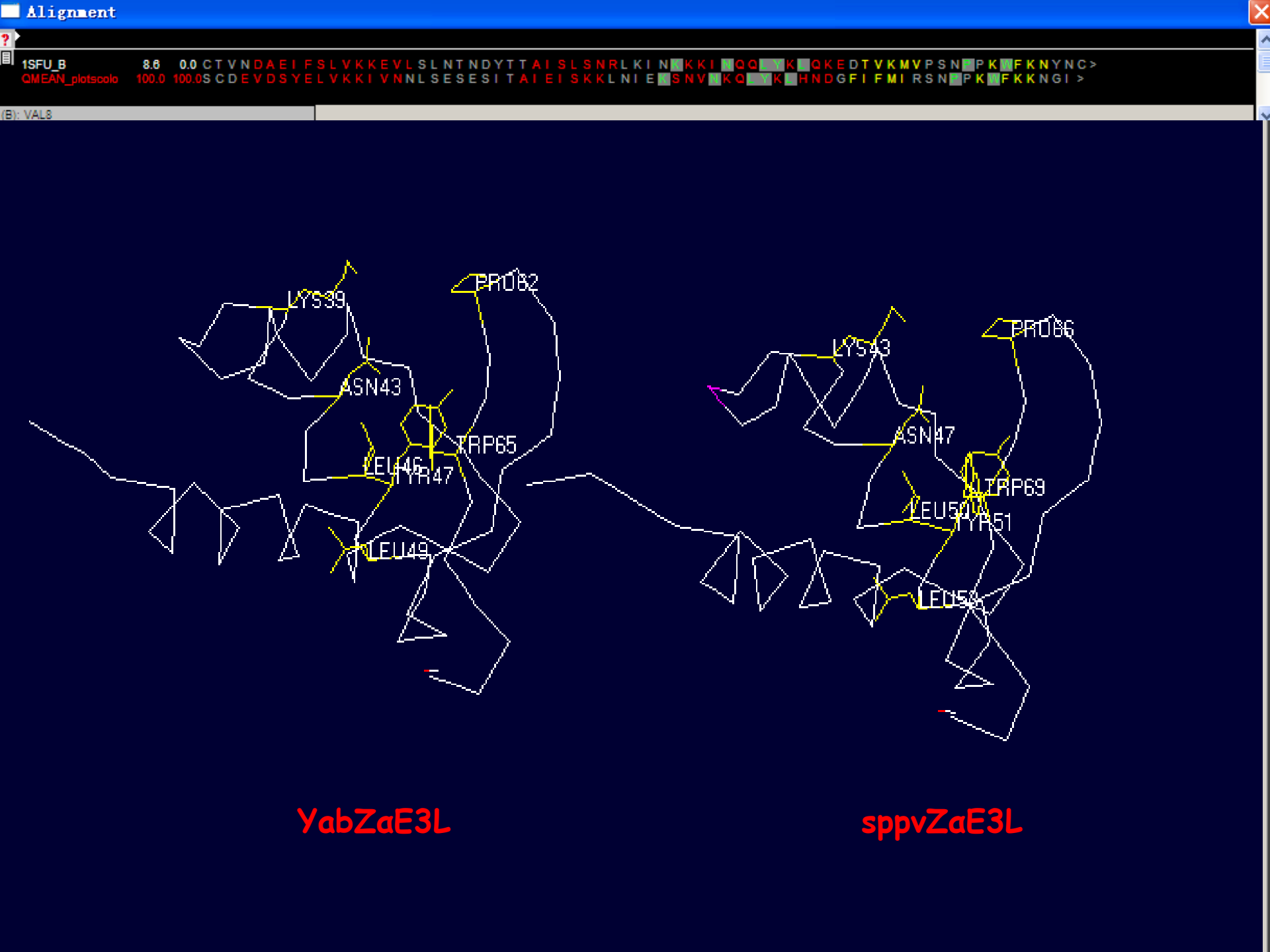


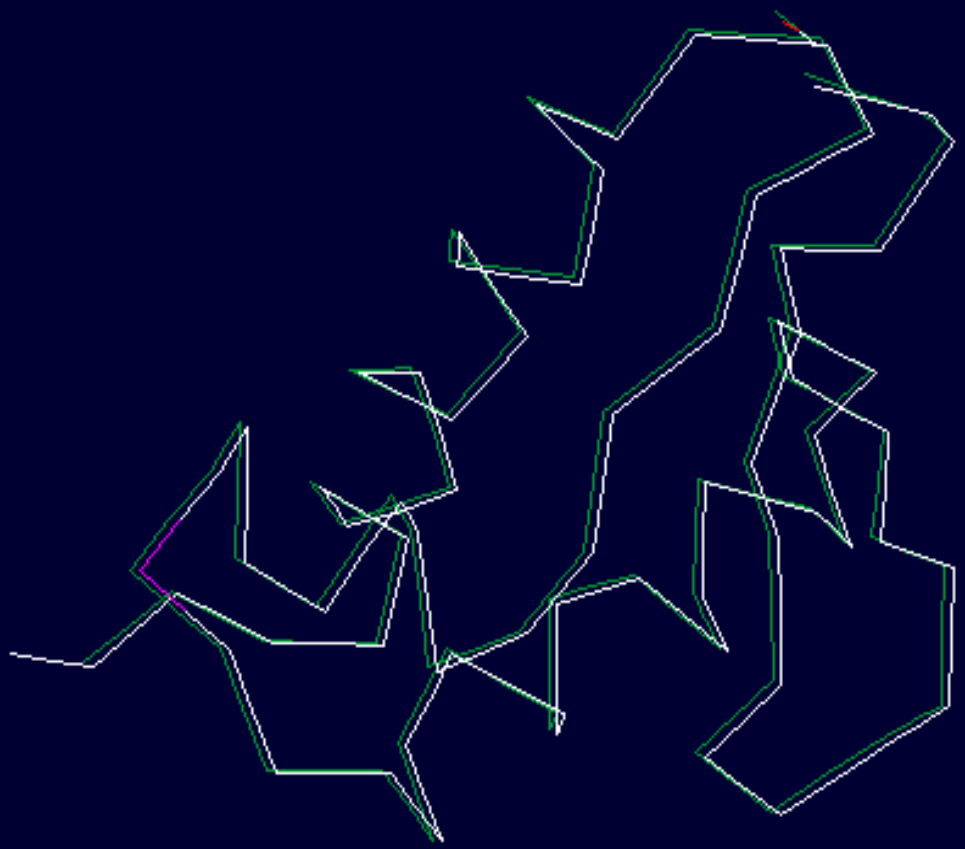
The 3D structure of YabZae3l.



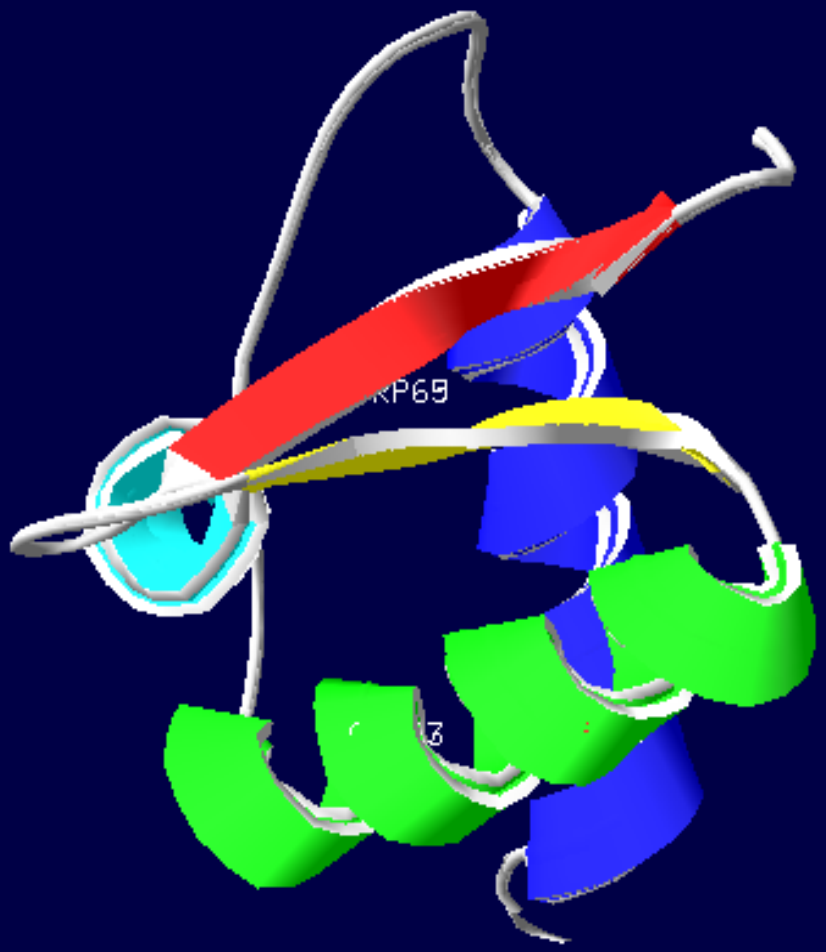
The 3D structure of SPPVZae3l.

- The interaction between members of the Za family and Z-DNA is made up of residues in the α3 helix and the "wing". Three residues, Asn-47, Tyr-51, and Trp-69 as numbered in YabZaE3L-, central to interaction with Z-DNA, are completely conserved with Za family. We can find those three residues (Asn-43, Tyr-47, Trp-65) in sppvZaE3L at the relative positions by these two sequences alignment.


Alignment
1SFU_B 8.6 0.0 CTVNDAEIFSLVKKEVLSLNTNDYTTAISLSNRLKINKKINQQLYKLQKEDTVKMVPSNPKWFKNYNC>
QMEAN_plotscolo 100.0 100.0SCDEVDSYELVKKIVNNLSESESITAIEISKKLNIEKSNVNKQLYKLHNDGFIFMIRSNPKWFKKNGI>
(B): VAL8
LYS39
PRO62
ASN43
TRP65
LEU46
TYR47
LEU49
LYS43
PRO66
ASN47
TRP69
LEU50
TYR51
LEU53
YabZaE3L
sppvZaE3L

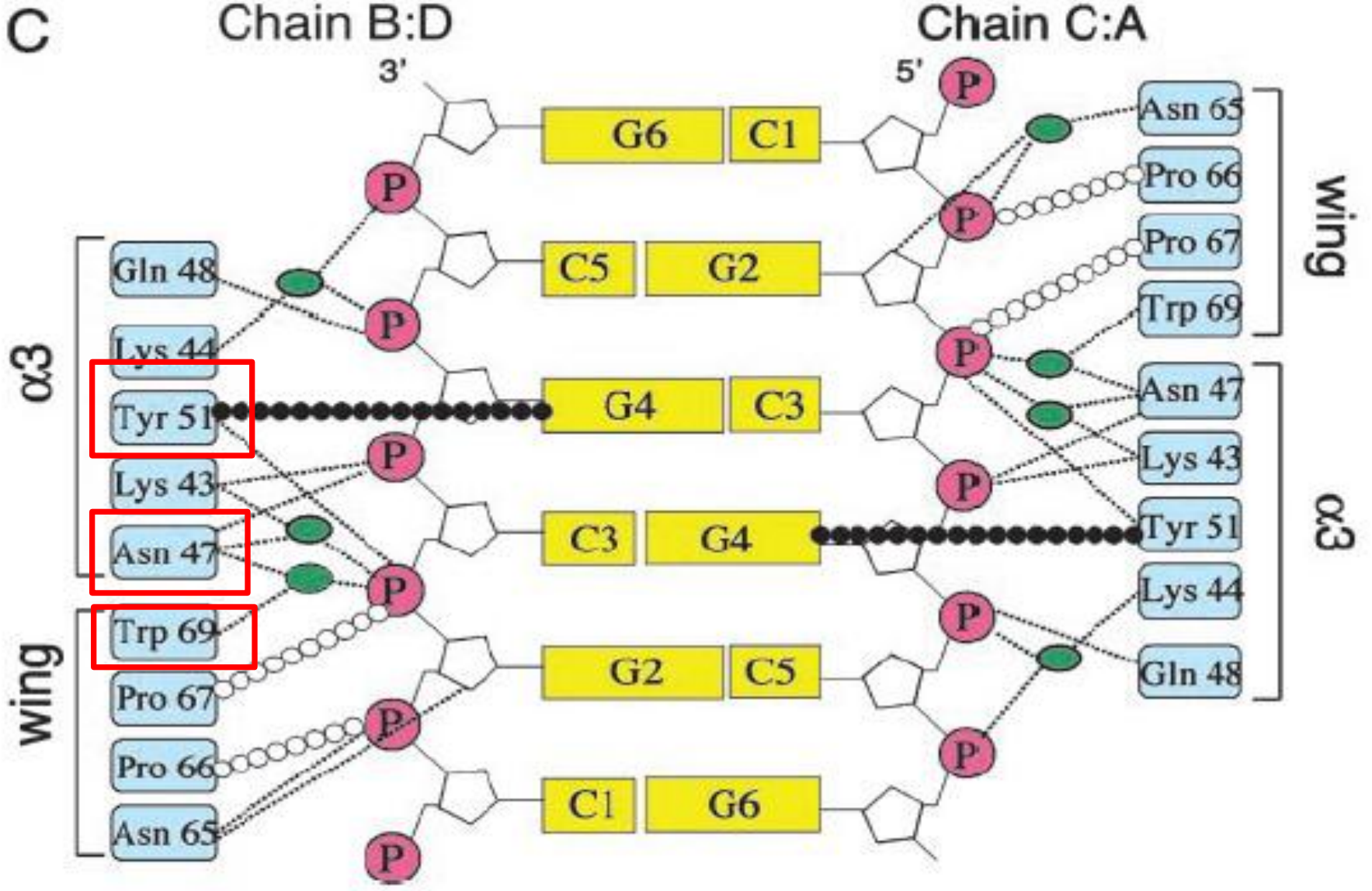


The carbon alpha (CA) fit of SPPVZae3l and YabZae3l. SPPVZae3l is shown by green line. YabZae3l is shown by white line. RMS (CA)=0.06A.



The picture of fit molecule. RMS=0.

- Asn-47 and Trp-69 make water-mediated hydrogen bonds to the phosphate backbone and Tyr-51 makes a direct hydrogen bond to a phosphate in the DNA backbone in YabZaE3L. Asn-43 and Trp-65 may make water-mediated hydrogen bonds to the phosphate backbone and Tyr-47 may makes a direct hydrogen bond to a phosphate in the DNA backbone in sppvZaE3L.



Sung Chul Ha, Neratur K.Lokanath, et al. A poxvirus protein forms a complex with left-handed Z-DNA: Crystal structure od a Yatapoxvirus Za bound to DNA [J]. PANS, 2004, 40: 14367-14372.

5. Conlusion

- The E3 protein in SPPV might be composed of a Za domain and a DSRM domain. There are three α-helices (α1,α2, α3) and two antiparallel strands (β1 and β2). α2 and α3 form an HTH motif and two antiparallel β-strands form the wing. There are also three conserved residues , Asn, Tyr andTrp in sppvZaE3L.

- The sppvZaE3L might play an important role in the pathogenicity of SPPV. This result may allow the design of a class of antiviral agents against SPPV.

Acknowlege

- Thank you for Pro. Luo!
- Thank you for the efforts of all group members!