Report generated by: smandava
Sequence name: inv_arf6
Length: 175 aa
Organism: ()
Description:
Date: Wed Mar 14 09:30:39 CDT 2007

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1. Protein statistics

1.1 Sequence information

Sequence type	Protein
Length	175 aa
Organism	()
Name	inv_arf6
Description	
Modification Date	14-Mar-2007
Weight	20.082 kDa
Isoelectric point	9.22
Aliphatic index	91.886

1.2 Half-life

N-terminal aa	Half-life mammals	Half-life yeast	Half-life E.Coli
Methionine	30 hours	>20 hours	>10 hours

1.3 Extinction coefficient

Conditions	Extinction coefficient at 280nm	Absorption at 280nm 0.1% (=1 g/l)
Non-reduced cysteines	31,840	1.586
Reduced cysteines	31,720	1.58

1.4 Atomic composition

Atom	Count	Frequency
Sulphur (S)	7	0.002
Oxygen (O)	259	0.091
Hydrogen (H)	1,429	0.503
Carbon (C)	898	0.316
Nitrogen (N)	249	0.088

1.5 Count of hydrophobic and hydrophilic residues

Hydrophobicity	Count	Frequency
Hydrophobic (A,F,G,I,L,M,P,V,W)	83	0.474
Hydrophilic (C,N,Q,S,T,Y)	43	0.246
Other	49	0.280

1.6 Count of charged residues

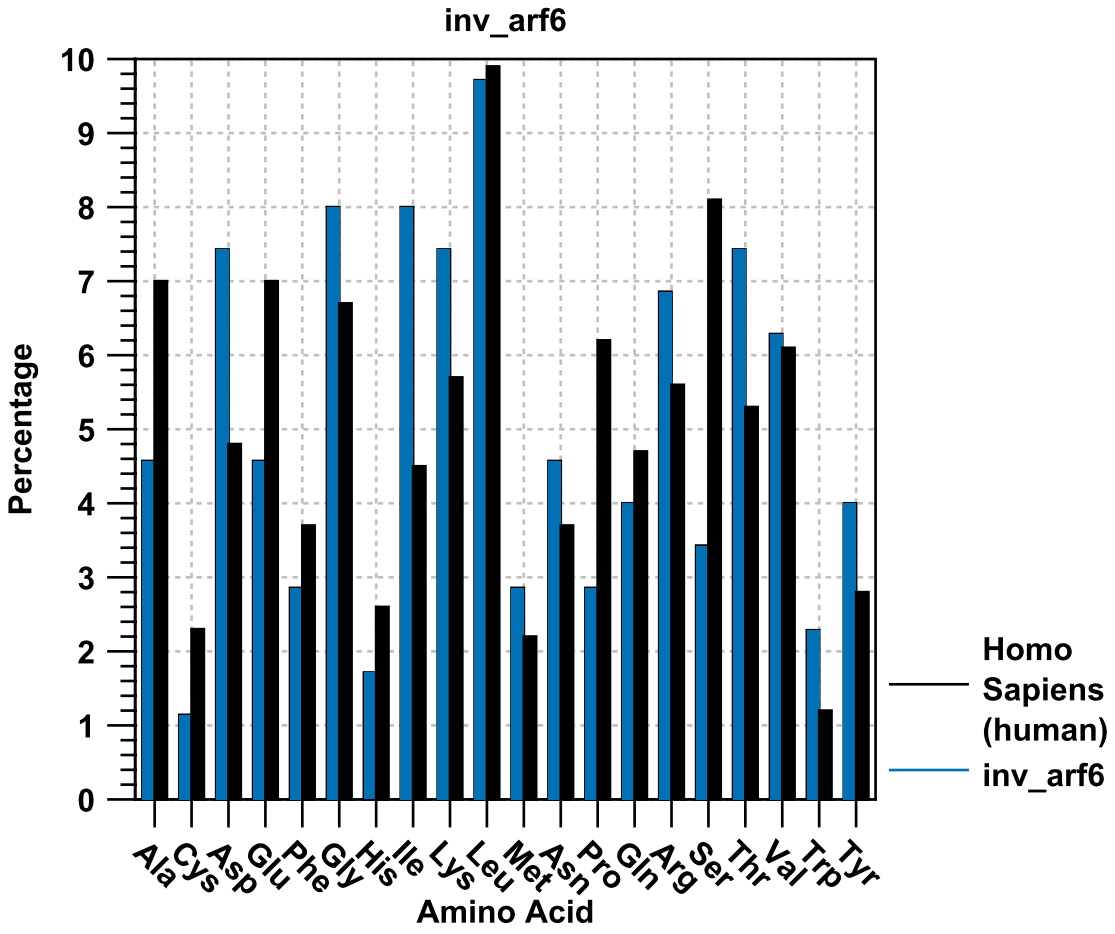
Charge Type	Count	Frequency
Negatively Charged (D & E)	21	0.120
Positively Charged (R & K)	25	0.143
Other	129	0.737

1.7 Amino acid distribution table

Amino acid	Count	Frequency	Freq. in Homo Sapiens (human)
Alanine (A)	8	0.046	0.070
Cysteine (C)	2	0.011	0.023
Aspartic Acid (D)	13	0.074	0.048
Glutamic Acid (E)	8	0.046	0.070
Phenylalanine (F)	5	0.029	0.037
Glycine (G)	14	0.080	0.067
Histidine (H)	3	0.017	0.026
Isoleucine (I)	14	0.080	0.045
Lysine (K)	13	0.074	0.057
Leucine (L)	17	0.097	0.099
Methionine (M)	5	0.029	0.022
Asparagine (N)	8	0.046	0.037
Proline (P)	5	0.029	0.062
Glutamine (Q)	7	0.040	0.047
Arginine (R)	12	0.069	0.056

Amino acid	Count	Frequency	Freq. in Homo Sapiens (human)
Serine (S)	6	0.034	0.081
Threonine (T)	13	0.074	0.053
Valine (V)	11	0.063	0.061
Tryptophan (W)	4	0.023	0.012
Tyrosine (Y)	7	0.040	0.028

1.8 Amino acid distribution histogram



1.9 Annotation table

No features assigned

1.10 Counts of di-peptides

1.pos\2.pos	Ala	Cys	Asp	Glu
Ala	1	0	1	0
Cys	2	0	0	0
Asp	3	1	0	1
Glu	1	0	0	0
Phe	1	0	0	0
Gly	0	0	1	0
His	0	0	0	1
Ile	0	0	1	0
Lys	0	0	0	1
Leu	0	0	1	0
Met	0	0	0	0
Asn	0	0	1	0
Pro	0	0	1	0
Gln	0	0	2	2
Arg	0	0	3	1
Ser	0	1	0	0
Thr	0	0	0	0
Val	0	0	1	1
Trp	0	0	1	0
Tyr	0	0	0	1

Phe	Gly	His	Ile	Lys
0	1	0	1	0
0	0	0	0	0
0	1	0	0	1
0	1	0	1	1
0	1	0	0	0
1	1	0	0	2
0	0	0	0	0
3	0	0	2	0
1	0	0	2	0

Phe	Gly	His	Ile	Lys
0	3	1	2	1
0	1	0	0	1
0	0	0	0	2
0	0	1	0	0
0	1	0	0	0
0	0	1	4	0
0	1	0	0	1
0	1	0	2	0
0	2	0	0	1
0	0	0	0	0
0	0	0	0	3

Leu	Met	Asn	Pro	Gln
0	1	1	0	0
0	0	0	0	0
1	0	0	0	0
1	2	0	0	0
0	0	2	0	0
5	0	1	0	2
0	0	0	0	0
3	0	1	1	1
3	0	1	1	1
0	1	0	1	0
1	0	0	0	0
0	0	0	0	0
1	0	0	0	0
0	0	0	1	0
0	0	1	1	1
0	0	1	0	0
0	0	0	0	1
1	0	0	0	1
1	0	0	0	0

Leu	Met	Asn	Pro	Gln
0	0	0	0	0

Arg	Ser	Thr	Val	Trp
1	0	1	0	0
0	0	0	0	0
4	0	0	1	0
0	0	1	0	0
0	0	0	1	0
0	0	1	0	0
1	0	0	0	0
2	0	0	0	0
0	1	1	1	0
0	1	3	0	1
2	0	0	0	0
0	0	0	3	1
0	1	1	0	0
0	1	0	0	0
0	0	0	0	0
0	0	0	1	0
1	2	2	2	1
0	0	2	1	1
1	0	0	0	0
0	0	1	1	0

Tyr
0
0
0
0
0
0
1
0
0

Tyr
2
0
1
0
0
0
0
1
0
1
1

1.11 Frequency of di-peptides

1.pos\2.pos	Ala	Cys	Asp	Glu
Ala	0.006	0.000	0.006	0.000
Cys	0.011	0.000	0.000	0.000
Asp	0.017	0.006	0.000	0.006
Glu	0.006	0.000	0.000	0.000
Phe	0.006	0.000	0.000	0.000
Gly	0.000	0.000	0.006	0.000
His	0.000	0.000	0.000	0.006
Ile	0.000	0.000	0.006	0.000
Lys	0.000	0.000	0.000	0.006
Leu	0.000	0.000	0.006	0.000
Met	0.000	0.000	0.000	0.000
Asn	0.000	0.000	0.006	0.000
Pro	0.000	0.000	0.006	0.000
Gln	0.000	0.000	0.011	0.011
Arg	0.000	0.000	0.017	0.006
Ser	0.000	0.006	0.000	0.000
Thr	0.000	0.000	0.000	0.000
Val	0.000	0.000	0.006	0.006

1.pos\2.pos	Ala	Cys	Asp	Glu
Trp	0.000	0.000	0.006	0.000
Tyr	0.000	0.000	0.000	0.006

Phe	Gly	His	Ile	Lys
0.000	0.006	0.000	0.006	0.000
0.000	0.000	0.000	0.000	0.000
0.000	0.006	0.000	0.000	0.006
0.000	0.006	0.000	0.006	0.006
0.000	0.006	0.000	0.000	0.000
0.006	0.006	0.000	0.000	0.011
0.000	0.000	0.000	0.000	0.000
0.017	0.000	0.000	0.011	0.000
0.006	0.000	0.000	0.011	0.000
0.000	0.017	0.006	0.011	0.006
0.000	0.006	0.000	0.000	0.006
0.000	0.000	0.000	0.000	0.011
0.000	0.000	0.006	0.000	0.000
0.000	0.006	0.000	0.000	0.000
0.000	0.000	0.006	0.023	0.000
0.000	0.006	0.000	0.000	0.006
0.000	0.006	0.000	0.011	0.000
0.000	0.011	0.000	0.000	0.006
0.000	0.000	0.000	0.000	0.000
0.000	0.000	0.000	0.000	0.017

Leu	Met	Asn	Pro	Gln
0.000	0.006	0.006	0.000	0.000
0.000	0.000	0.000	0.000	0.000
0.006	0.000	0.000	0.000	0.000
0.006	0.011	0.000	0.000	0.000
0.000	0.000	0.011	0.000	0.000
0.029	0.000	0.006	0.000	0.011
0.000	0.000	0.000	0.000	0.000
0.017	0.000	0.006	0.006	0.006

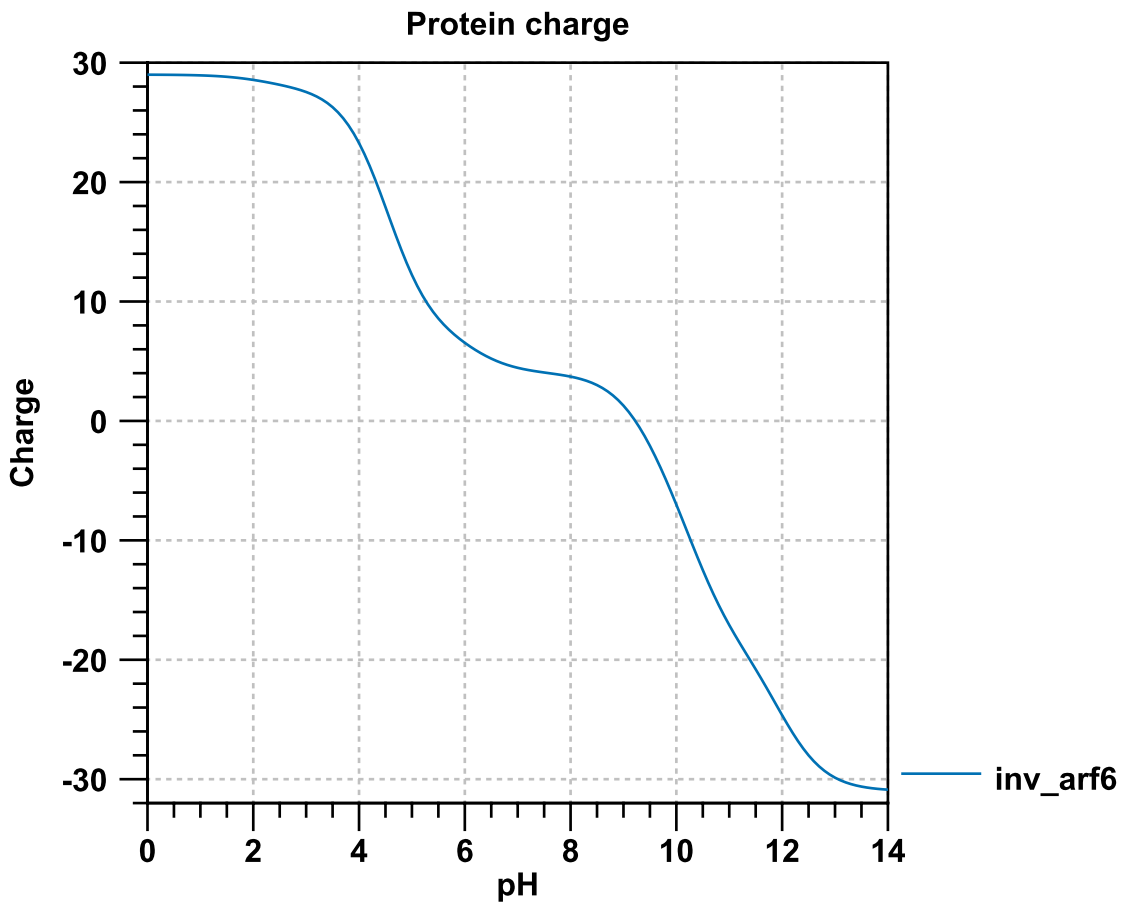
Leu	Met	Asn	Pro	Gln
0.017	0.000	0.006	0.006	0.006
0.000	0.006	0.000	0.006	0.000
0.006	0.000	0.000	0.000	0.000
0.000	0.000	0.000	0.000	0.000
0.006	0.000	0.000	0.000	0.000
0.000	0.000	0.000	0.006	0.000
0.000	0.000	0.006	0.006	0.006
0.000	0.000	0.006	0.000	0.000
0.000	0.000	0.000	0.000	0.006
0.006	0.000	0.000	0.000	0.006
0.006	0.000	0.000	0.000	0.000
0.000	0.000	0.000	0.000	0.000

Arg	Ser	Thr	Val	Trp
0.006	0.000	0.006	0.000	0.000
0.000	0.000	0.000	0.000	0.000
0.023	0.000	0.000	0.006	0.000
0.000	0.000	0.006	0.000	0.000
0.000	0.000	0.000	0.006	0.000
0.000	0.000	0.006	0.000	0.000
0.006	0.000	0.000	0.000	0.000
0.011	0.000	0.000	0.000	0.000
0.000	0.006	0.006	0.006	0.000
0.000	0.006	0.017	0.000	0.006
0.011	0.000	0.000	0.000	0.000
0.000	0.000	0.000	0.017	0.006
0.000	0.006	0.006	0.000	0.000
0.000	0.006	0.000	0.000	0.000
0.000	0.000	0.000	0.000	0.000
0.000	0.000	0.000	0.006	0.000
0.006	0.011	0.011	0.011	0.006
0.000	0.000	0.011	0.006	0.006
0.006	0.000	0.000	0.000	0.000

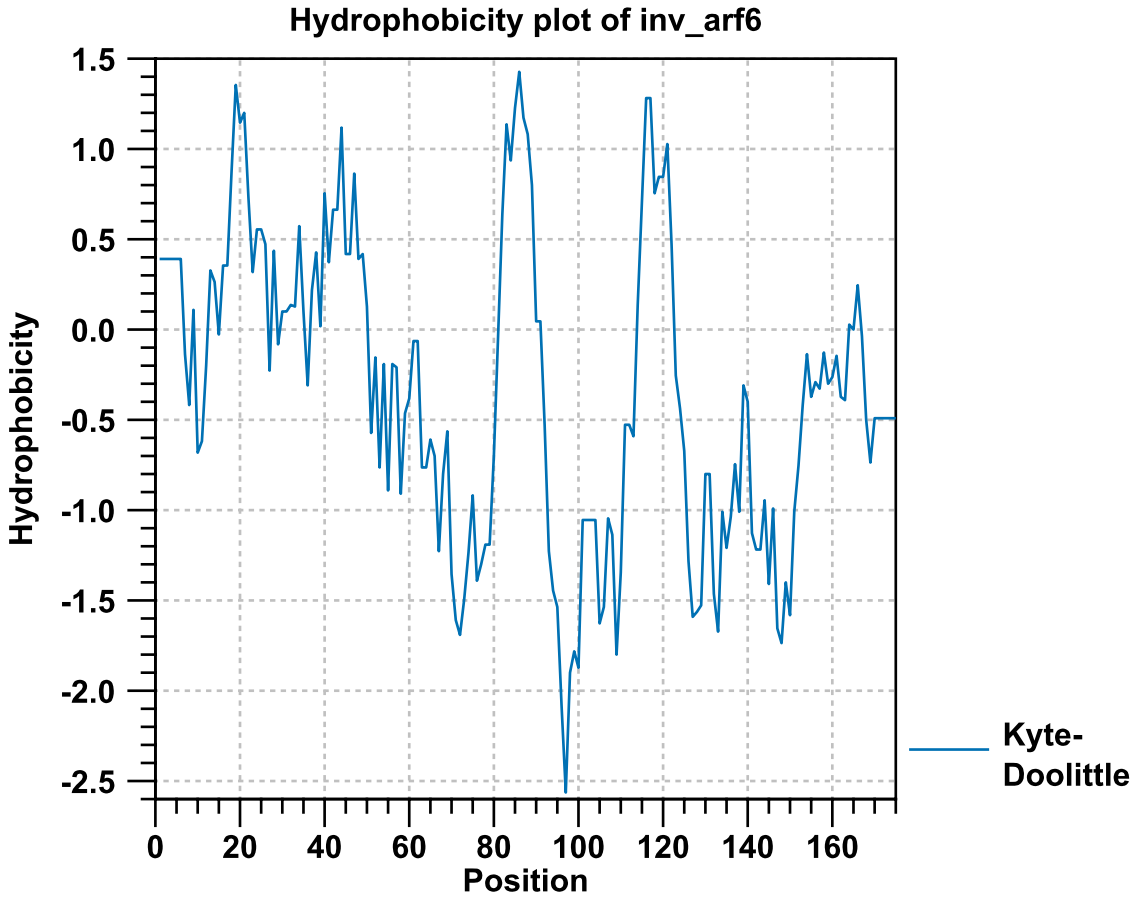
Arg	Ser	Thr	Val	Trp
0.000	0.000	0.006	0.006	0.000

Tyr
0.000
0.000
0.000
0.000
0.000
0.000
0.006
0.000
0.000
0.011
0.000
0.006
0.000
0.000
0.000
0.000
0.006
0.000
0.006
0.006

2. Electrical charge as a function of pH



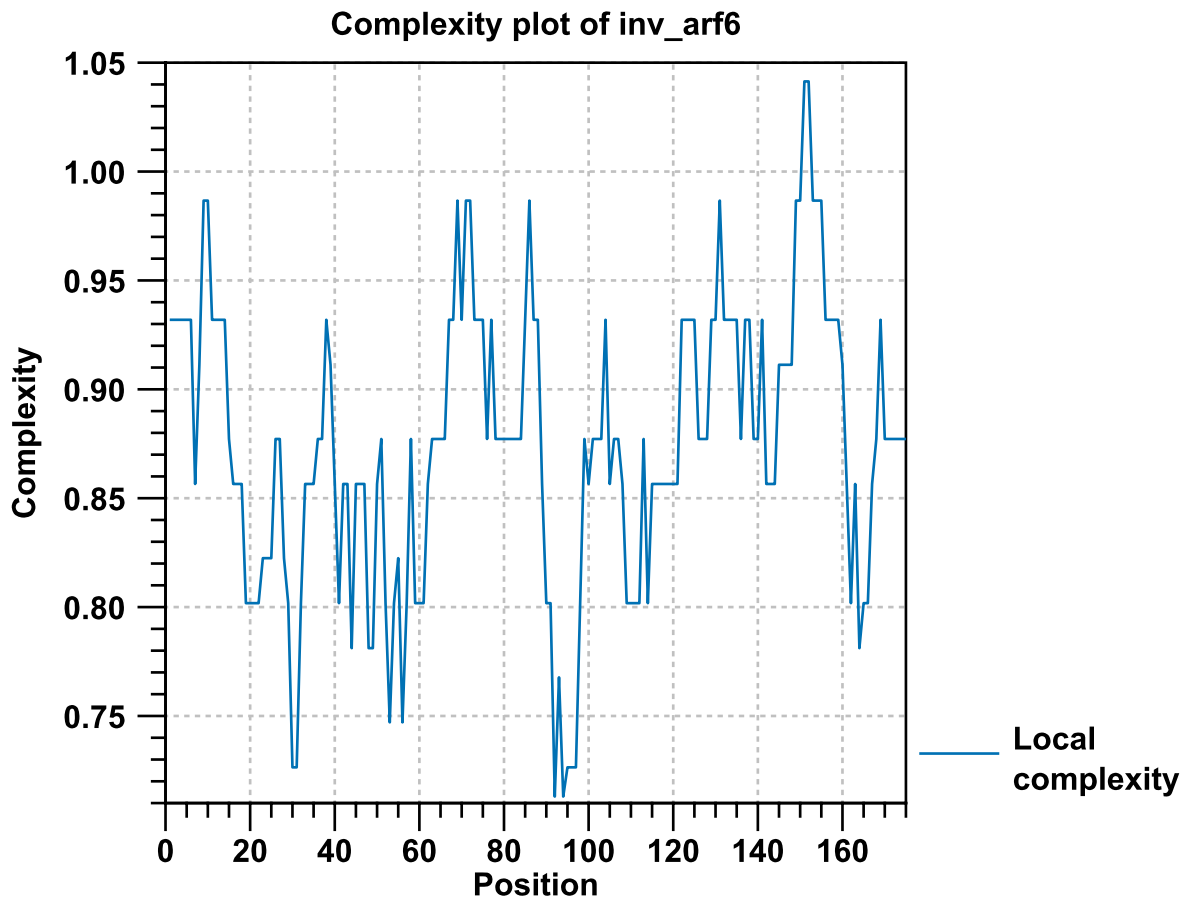
3. Plot of local Hydropathy



Kyte-Doolittle scale:
Kyte-Doolittle hydropathy plots provide information about the possible structure of a protein, and can identify features such as transmembrane or surface regions.For surface region discovery in a globular protein, a window size of 9 is considered optimal ,marked negative dips in the graph indicate possible surface regions.A region size of 19 is consiered optimal for the discovery of transmembrane regions whcich can be identified by peaks above a value of 1.8.

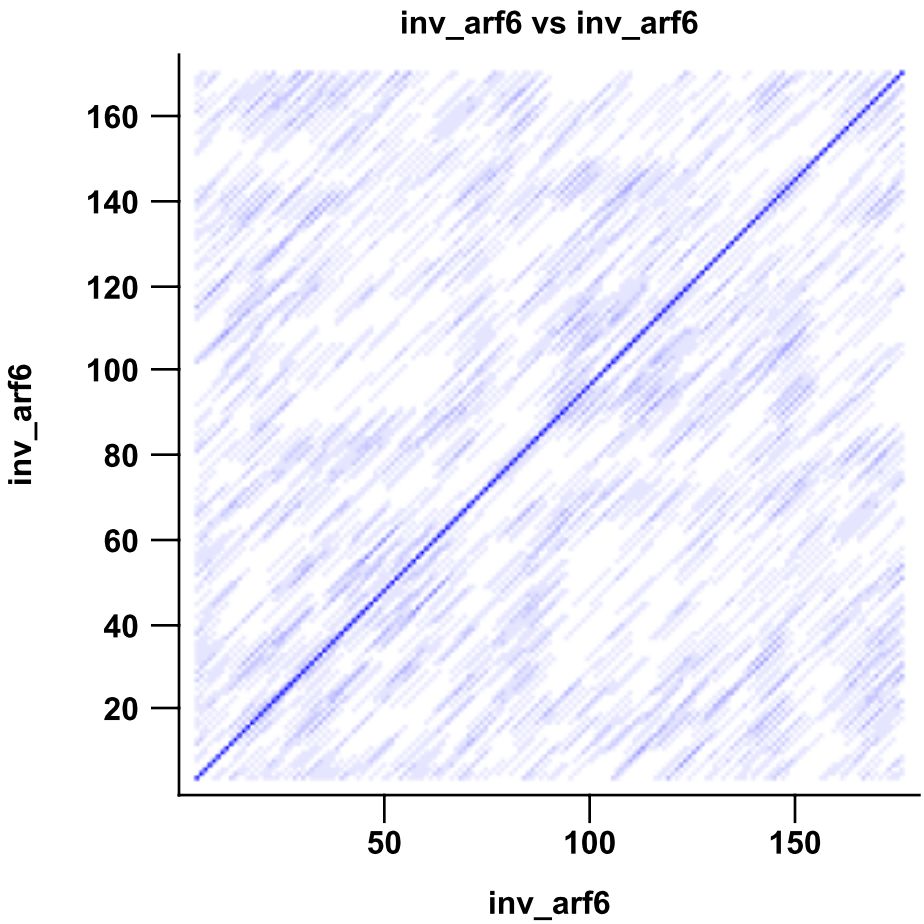
Kyte, J. and Doolittle, R. (1982).A simple method for displaying the hydropathic character of a protein. J. Mol. Biol. 157: 105-132.

4. Plot of local sequence complexity



Y-axis shows the K2 measure of local sequence complexity, as defined in (Wootton and Federhen, 1993, Computers Chem., Vol. 17, pp. 149-163)

5. Dot plot of the sequence against itself



6. Secondary structure

Type	Region
Beta strand	4..8
Beta strand	14..19
Beta strand	27..34
Beta strand	38..42
Beta strand	45

Type	Region
Beta strand	47..55
Beta strand	57..62
Beta strand	75..78
Beta strand	84..89
Alpha helix	93..120
Alpha helix	133..138
Beta strand	144
Beta strand	150..151
Alpha helix	166..167
Beta strand	168..169

7. Pfam result

Domains found with the full model:

Name	Region	E-Value
Ras	15..175	5.1E-8
GTP_EFTU	11..174	0.016
Homeobox	102..148	0.43

8. Signal peptide prediction (SignalP)

Signal peptide found in the region 1..25

9. Transmembrane helix prediction (TMHMM)

No transmembrane helices found