Analysis of the sequence, structure and function of Ankyrin G

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PKU 2013 fall G12
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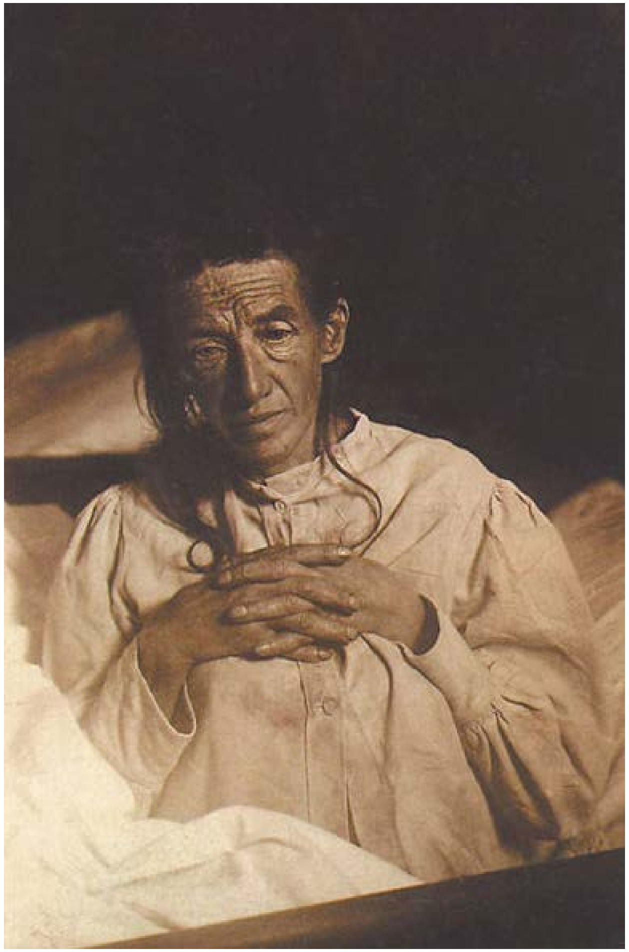
Alzheimer’s disease

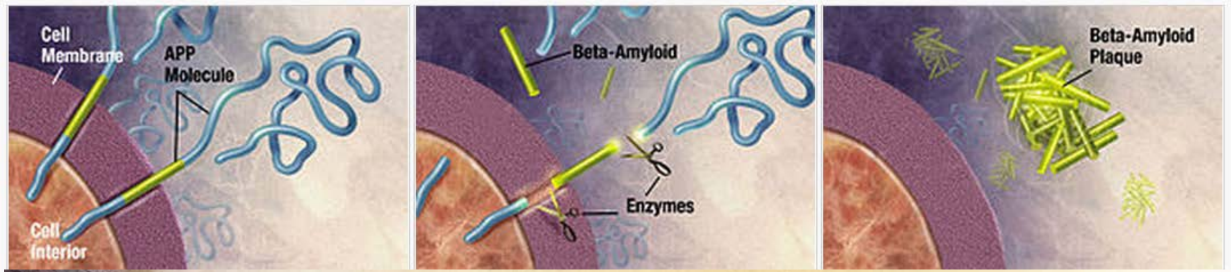


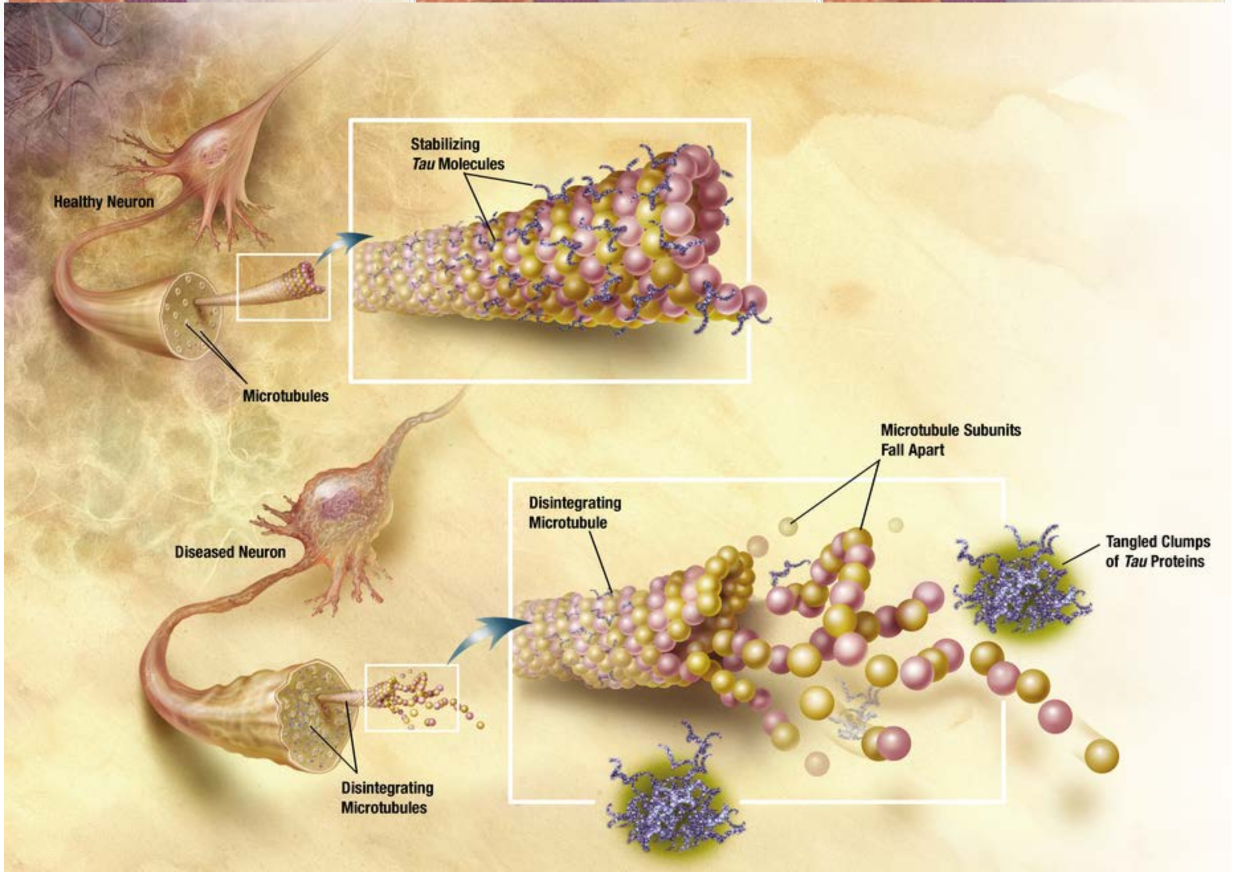
Auguste Deter

Dr. Alois Alzheimer

From wikipedia

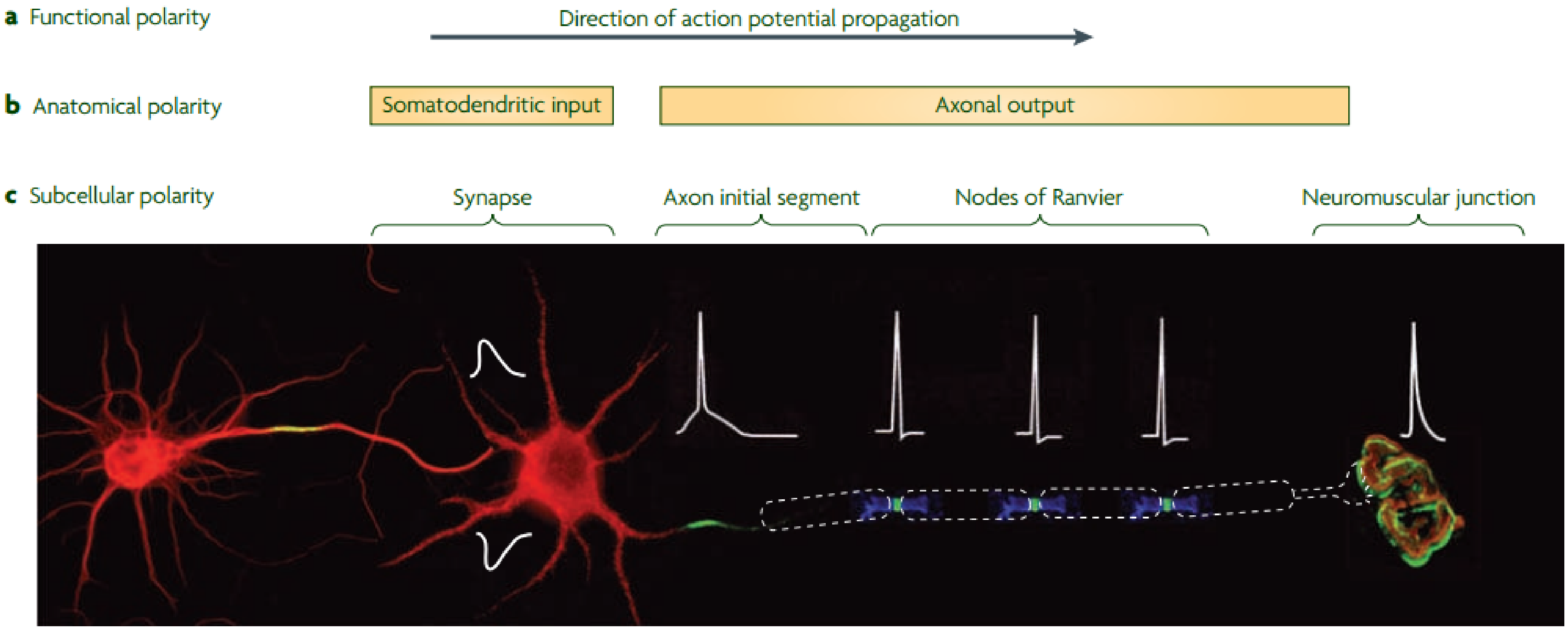
Prevailing Pathology





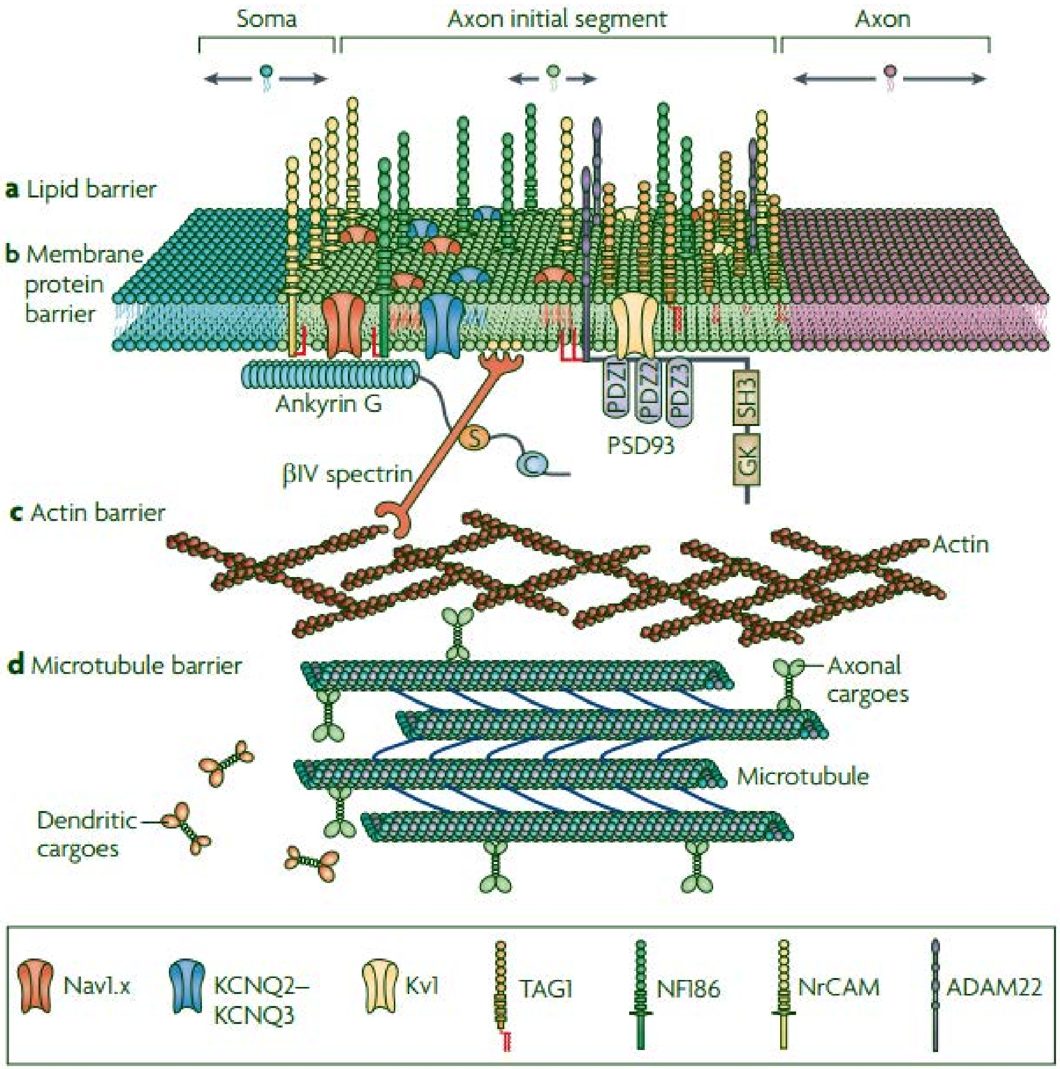
From wikipedia

Axon Initial segment



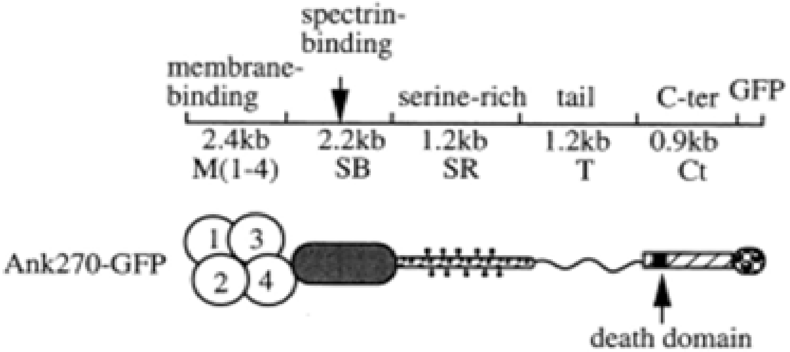
Rasband M N. Nature Reviews Neuroscience, 2010, 11(8): 552-562.

Ankyrin G (ANK3)



Rasband M N. Nature Reviews Neuroscience, 2010, 11(8): 552-562.

Rat Ankyrin G isoform:
190kDa(2622aa) and 270kDa(1762aa)



Zhang X, Bennett V. The Journal of cell biology, 1998, 142(6): 1571-1581.

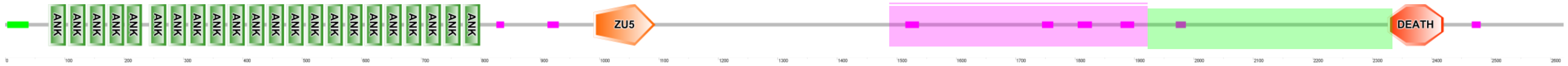
LENGTH	SCORE	IDENTITY	SIMILARITY	GAPS
377	1578.0	328/377 (87.0%)	345/377 (91.5%)	1/377 (0.3%)

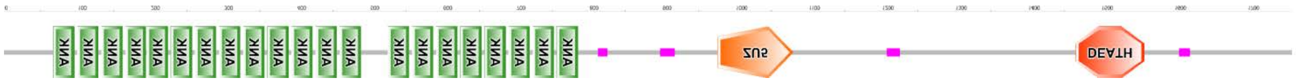
```
M-death      -----------------------------------------------------------TDIRM 5
H-death      -----------------------------------------------------------TDIRM 5
RAT-270kDa   LAGLFEMKSAMSPDVAKSAAETSAQHAEKDNQMKPKLERIIEVHIEKGPQSPCERTDIRM 2340
                                                                        *****

M-death      AIVADHLGLSWTELARELNFSVDEINQIRVENPNSLISQSFMLLKKWVTRDGKNATTDAL 65
H-death      AIVADHLGLSWTELARELNFSVDEINQIRVENPNSLISQSFMLLKKWVTRDGKNATTDAL 65
RAT-270kDa   AIVADHLGLSWTELARELNFSVDEINQIRVENPNSLISQSFMLLKKWVTRDGKNATTDAL 2400
             ************************************************************

M-death      TSVLTKINRIDIVTLLEGPI---------------------------------------- 85
H-death      TSVLTKINRIDIVTLLEGPI---------------------------------------- 85
RAT-270kDa   TSVLTKINRIDIVTLLEGPIFDYGNISGTRSFADENNVFHDPVDGWQNETPSGSLESPAQ 2460
             ********************
```

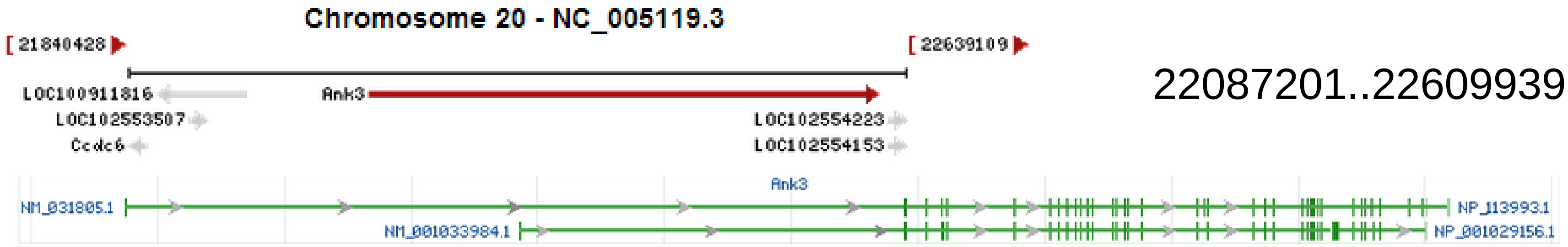
Ankyrin repeat(33aa) ZU5 domain serine-rich domain tail death domain(85aa)





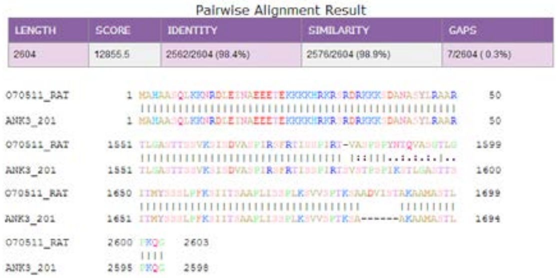
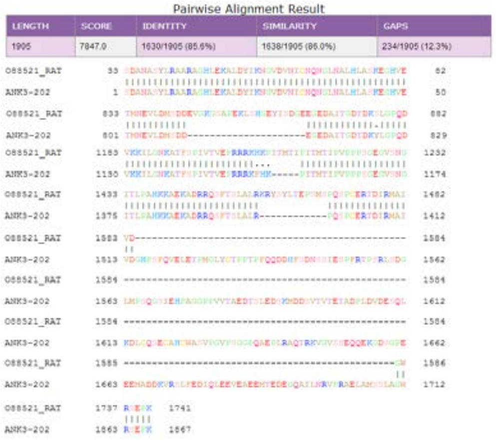
270 kDa Ankyrin G: AIS and node of Ranvier

Rat Ankyrin G Gene



22087201..22609939

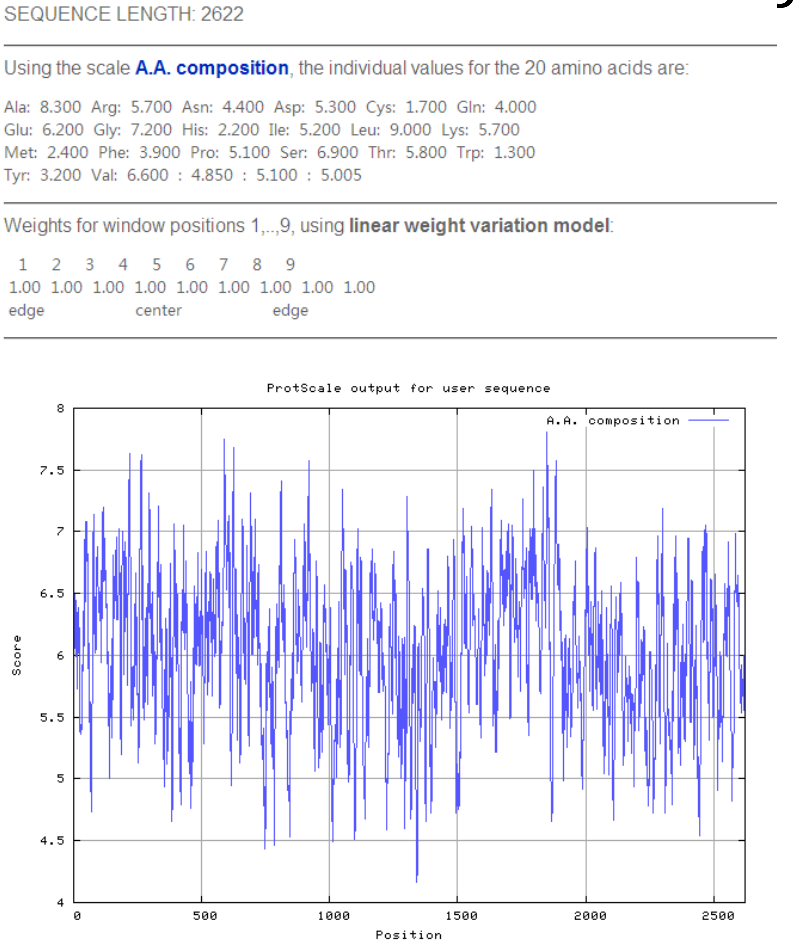
ENSEMBL： Ank3 ENSRNOG00000024011   Chromosome 20: 22,243,056-22,609,934，366878bp

	RAT ANK3 variant1	RAT ANK3 variant2
NCBI	2622aa	1762aa
ENSEMBL	2598aa	1964aa
Protein Alignment	98.4%，0.3%	86.0%，12.3%
	 Pairwise Alignment Result LENGTH: 2604 SCORE: 12855.5 IDENTITY: 2562/2604 (98.4%) SIMILARITY: 2576/2604 (98.9%) GAPS: 7/2604 (0.3%)	 Pairwise Alignment Result LENGTH: 1905 SCORE: 7847.0 IDENTITY: 1630/1905 (85.6%) SIMILARITY: 1638/1905 (86.0%) GAPS: 234/1905 (12.3%)

AnkyrinG的功能分析

氨基酸组成分析 A.A.comp.in swiss-prot

疏水性和亲水性分析 Hphob. / Kyte & Doolittle



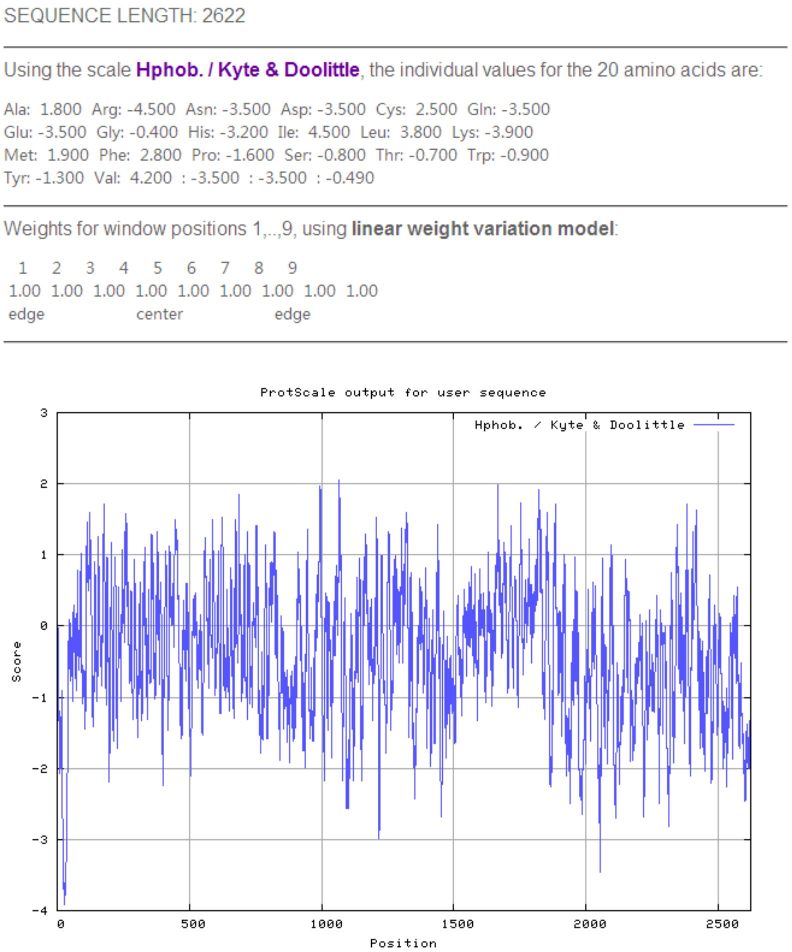
SEQUENCE LENGTH: 2622

Using the scale **A.A. composition**, the individual values for the 20 amino acids are:

Ala: 8.300 Arg: 5.700 Asn: 4.400 Asp: 5.300 Cys: 1.700 Gln: 4.000
Glu: 6.200 Gly: 7.200 His: 2.200 Ile: 5.200 Leu: 9.000 Lys: 5.700
Met: 2.400 Phe: 3.900 Pro: 5.100 Ser: 6.900 Thr: 5.800 Trp: 1.300
Tyr: 3.200 Val: 6.600 : 4.850 : 5.100 : 5.005

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



SEQUENCE LENGTH: 2622

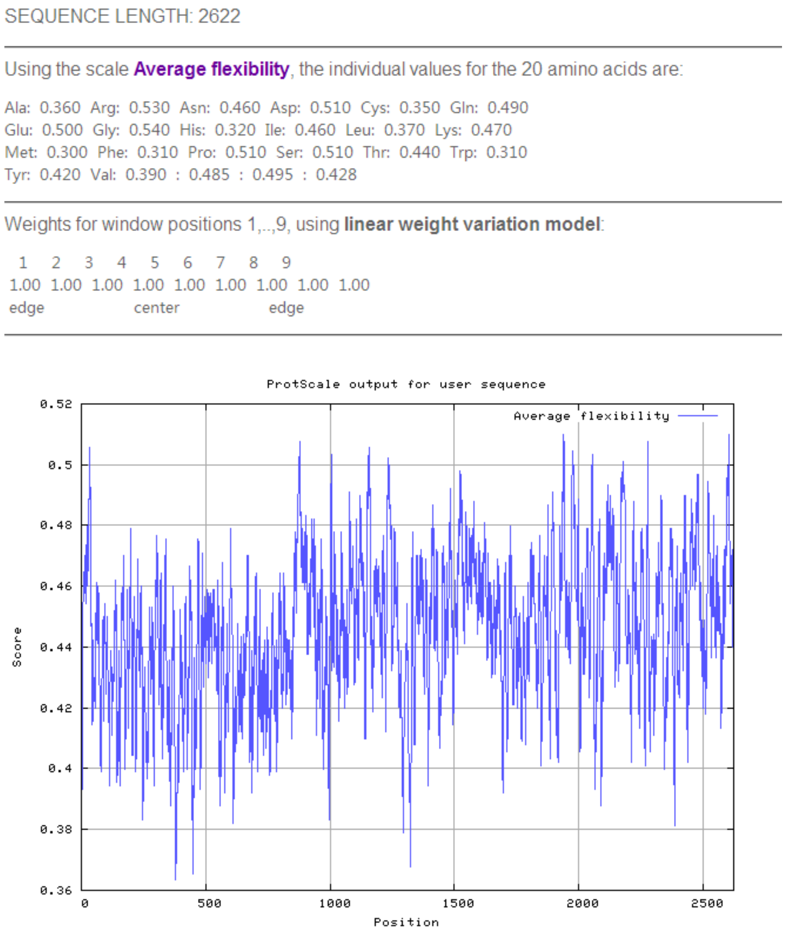
Using the scale **Hphob. / Kyte & Doolittle**, the individual values for the 20 amino acids are:

Ala: 1.800 Arg: -4.500 Asn: -3.500 Asp: -3.500 Cys: 2.500 Gln: -3.500
Glu: -3.500 Gly: -0.400 His: -3.200 Ile: 4.500 Leu: 3.800 Lys: -3.900
Met: 1.900 Phe: 2.800 Pro: -1.600 Ser: -0.800 Thr: -0.700 Trp: -0.900
Tyr: -1.300 Val: 4.200 : -3.500 : -3.500 : -0.490

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

柔性与刚性
（Average flexibility）



SEQUENCE LENGTH: 2622

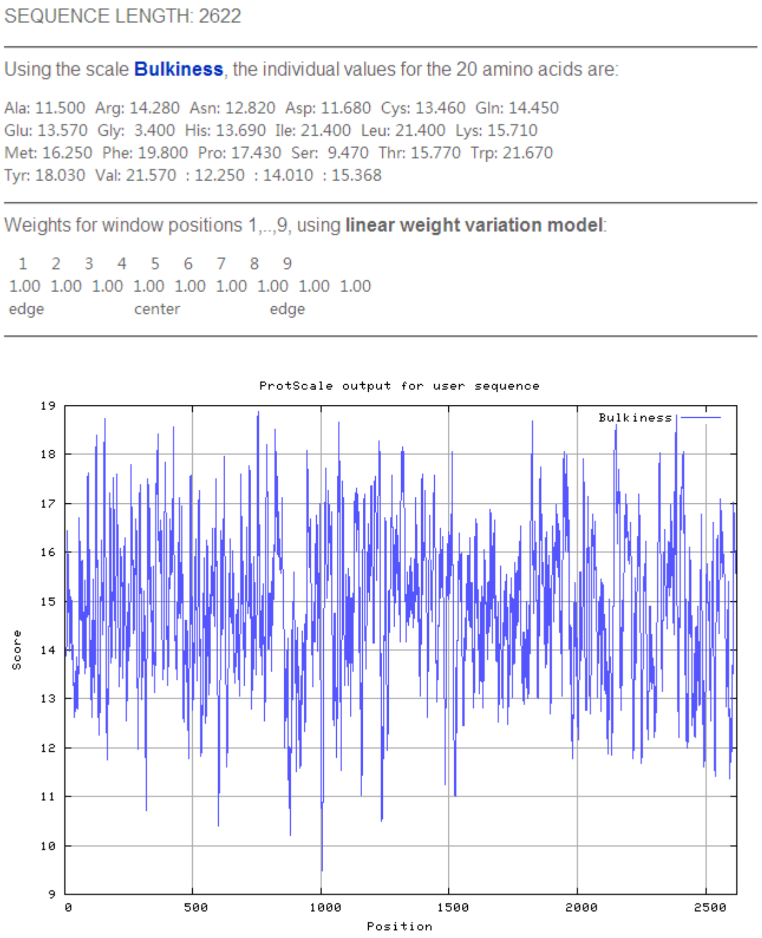
Using the scale **Average flexibility**, the individual values for the 20 amino acids are:

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

空间位阻
（Bulkiness）



SEQUENCE LENGTH: 2622

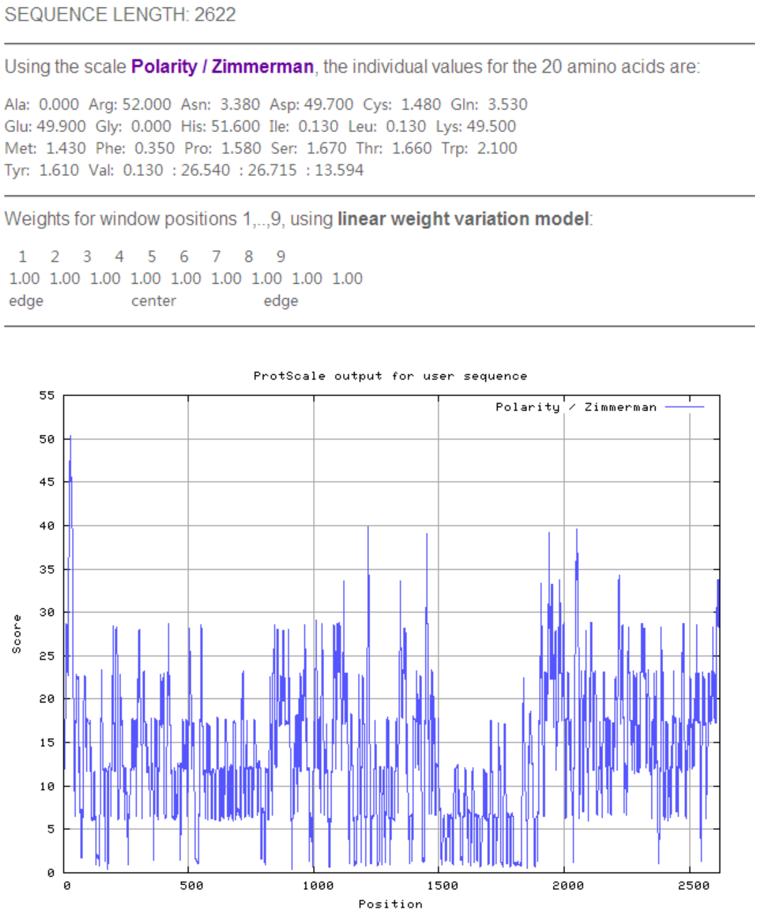
Using the scale **Bulkiness**, the individual values for the 20 amino acids are:

Ala: 11.500 Arg: 14.280 Asn: 12.820 Asp: 11.680 Cys: 13.460 Gln: 14.450
Glu: 13.570 Gly: 3.400 His: 13.690 Ile: 21.400 Leu: 21.400 Lys: 15.710
Met: 16.250 Phe: 19.800 Pro: 17.430 Ser: 9.470 Thr: 15.770 Trp: 21.670
Tyr: 18.030 Val: 21.570 : 12.250 : 14.010 : 15.368

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

溶剂可及性
Polarity / Zimmerman



SEQUENCE LENGTH: 2622

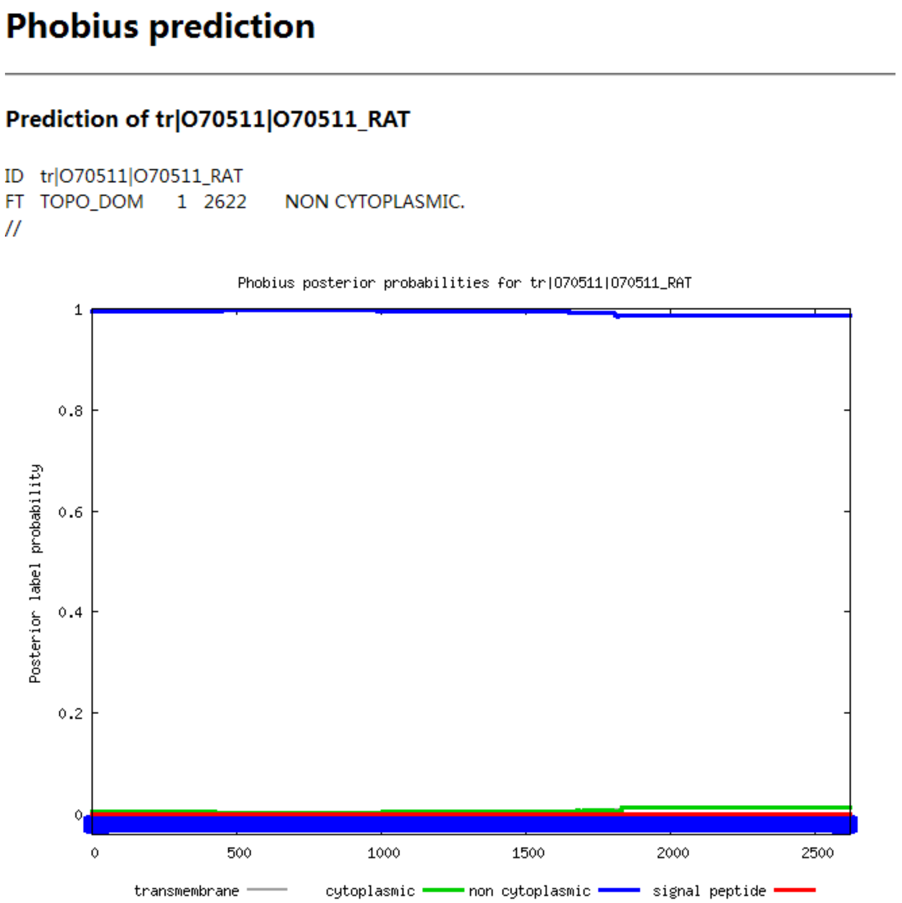
Using the scale **Polarity / Zimmerman**, the individual values for the 20 amino acids are:

Ala: 0.000 Arg: 52.000 Asn: 3.380 Asp: 49.700 Cys: 1.480 Gln: 3.530
Glu: 49.900 Gly: 0.000 His: 51.600 Ile: 0.130 Leu: 0.130 Lys: 49.500
Met: 1.430 Phe: 0.350 Pro: 1.580 Ser: 1.670 Thr: 1.660 Trp: 2.100
Tyr: 1.610 Val: 0.130 : 26.540 : 26.715 : 13.594

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

跨膜结构预测
Phobius prediction

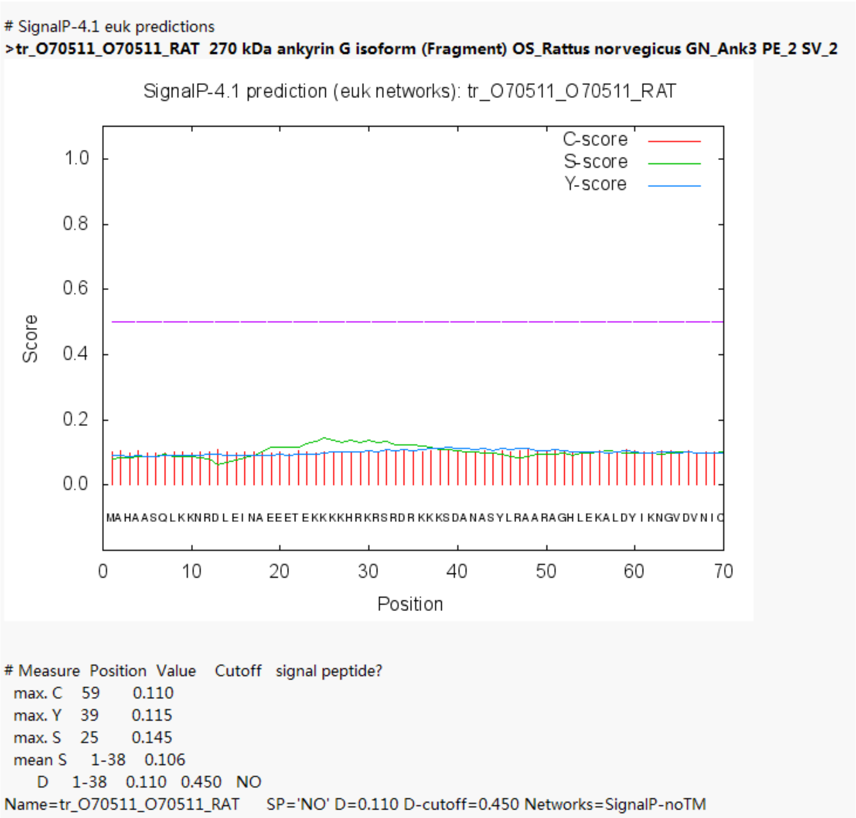


Phobius prediction

Prediction of tr|O70511|O70511_RAT

```
ID   tr|O70511|O70511_RAT
FT   TOPO_DOM     1   2622       NON CYTOPLASMIC.
//
```

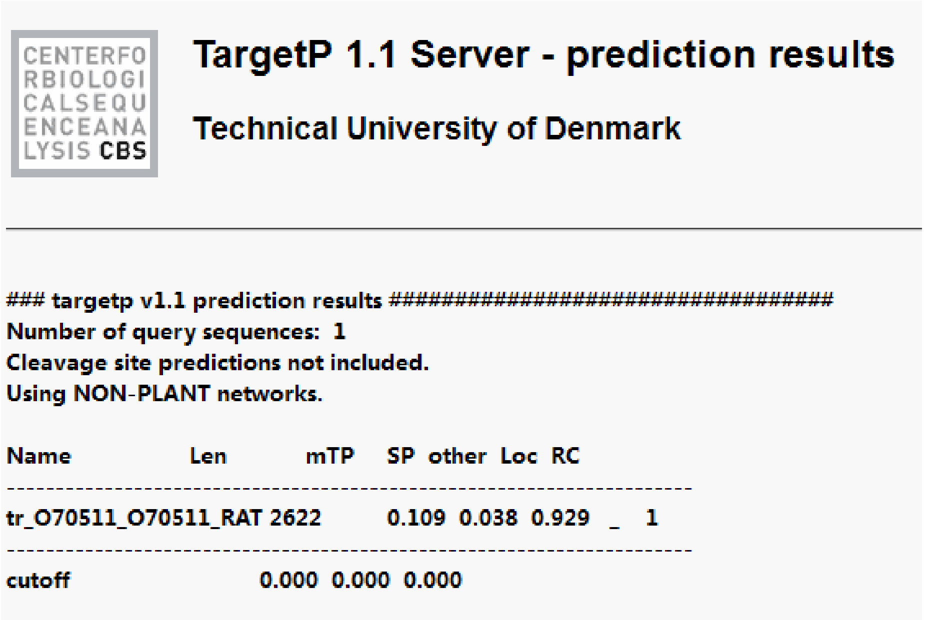
信号肽预测
SignalP



```
# SignalP-4.1 euk predictions
>tr_O70511_O70511_RAT  270 kDa ankyrin G isoform (Fragment) OS_Rattus norvegicus GN_Ank3 PE_2 SV_2
```

```
# Measure  Position  Value    Cutoff   signal peptide?
  max. C    59       0.110
  max. Y    39       0.115
  max. S    25       0.145
  mean S     1-38    0.106
       D    1-38    0.110   0.450   NO
Name=tr_O70511_O70511_RAT     SP='NO' D=0.110 D-cutoff=0.450 Networks=SignalP-noTM
```

亚细胞定位
TargetP



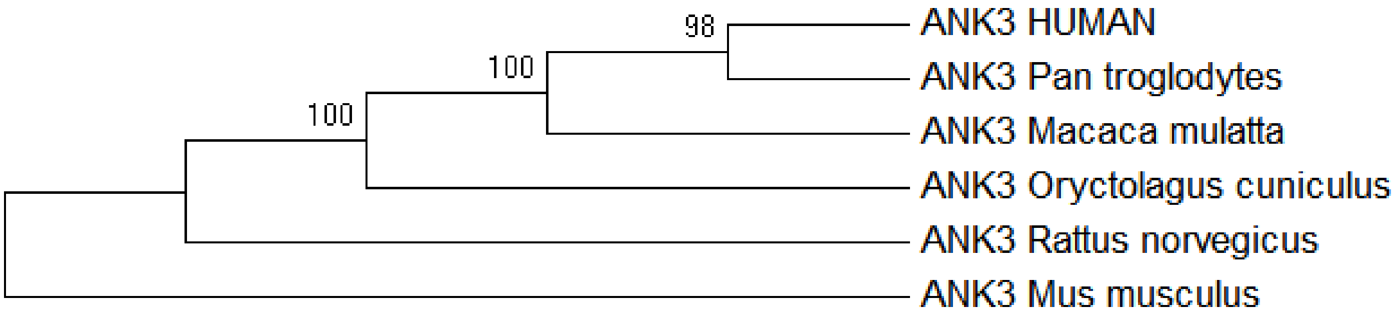
TargetP 1.1 Server - prediction results

Technical University of Denmark

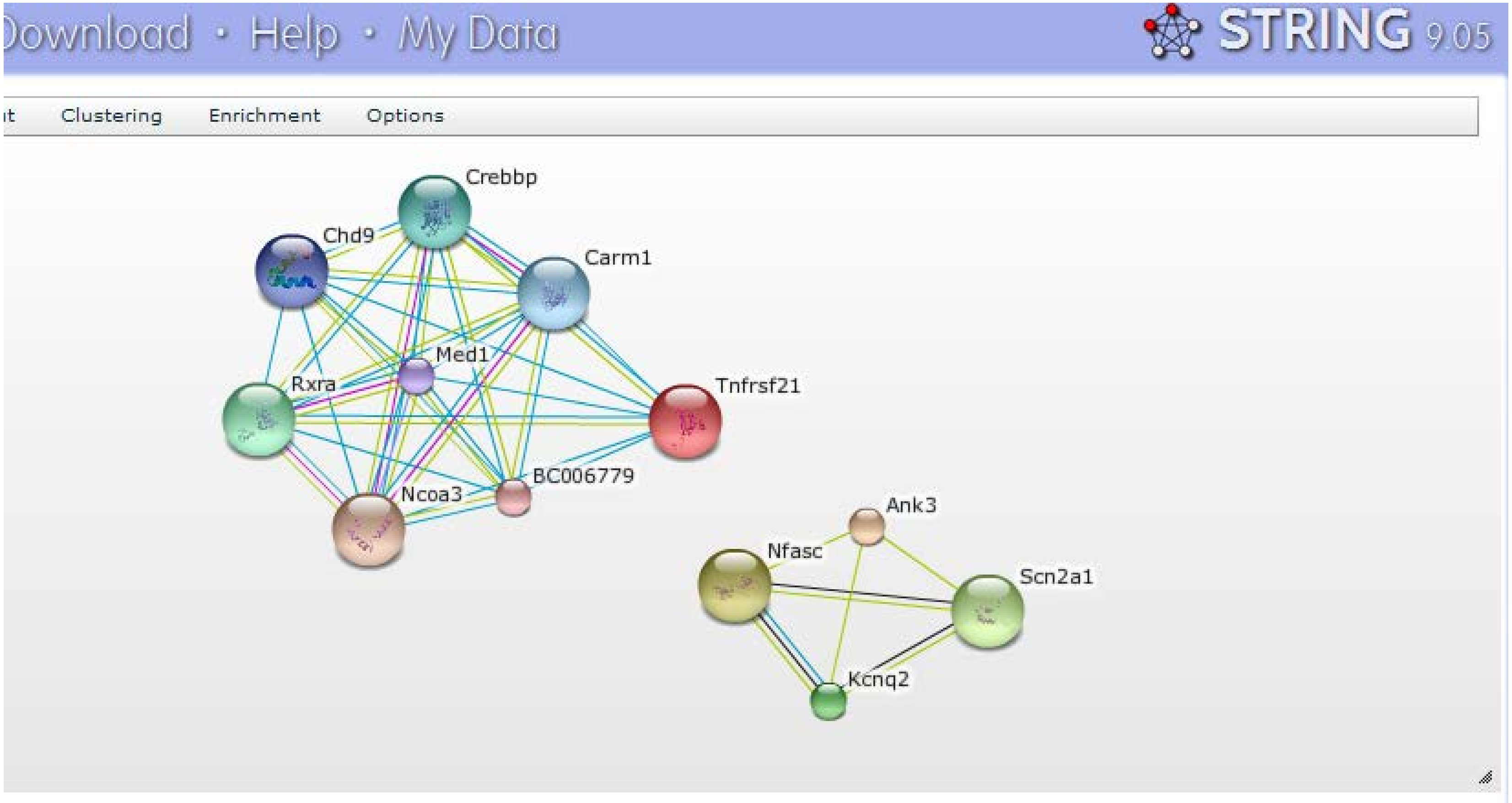
```
### targetp v1.1 prediction results ##################################
Number of query sequences:  1
Cleavage site predictions not included.
Using NON-PLANT networks.

Name                   Len          mTP     SP  other  Loc  RC
----------------------------------------------------------------------
tr_O70511_O70511_RAT 2622          0.109  0.038  0.929  _    1
----------------------------------------------------------------------
cutoff                            0.000  0.000  0.000
```

ANK3：evolution



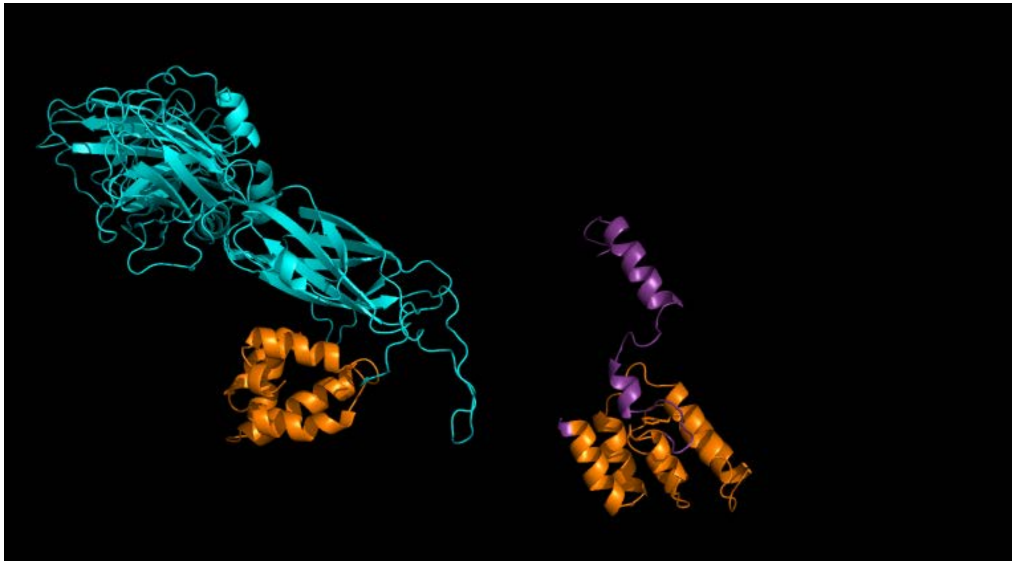
与Dr6之间的相互作用—death结构域



说明

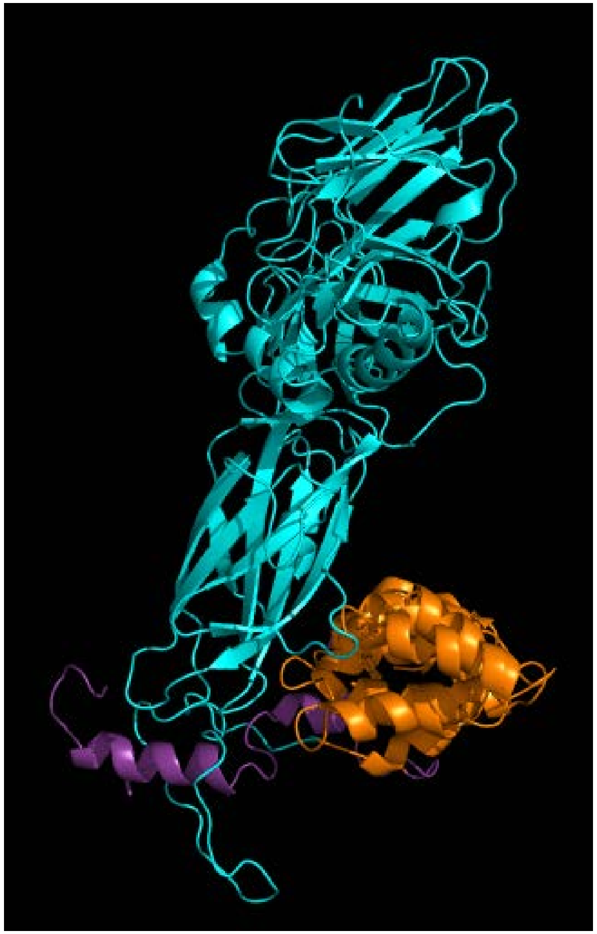
- 看AnkyrinG与DR6的相互作用，但是通过String预测的（不管是基因名称或者是序列）都不能够显示二者存在明显的相关性。可能的原因是所用的含有death domain的大鼠的270KD 的AnkyrinG由于才刚录入，在其他网站（如String中）暂时不能搜索到，所用的是不含有death domain的结构的蛋白，所以无相关性，也可能是其他原因。

Death domain structure prediction



Ank3-mouse
Model: 983-1551
death domain： 1478-1562

Tnfrsf21
Model: 377-500
death domain：415-498



merge