

泛素-蛋白酶体相关调节因子CSN5B序列及结构分析

第13组

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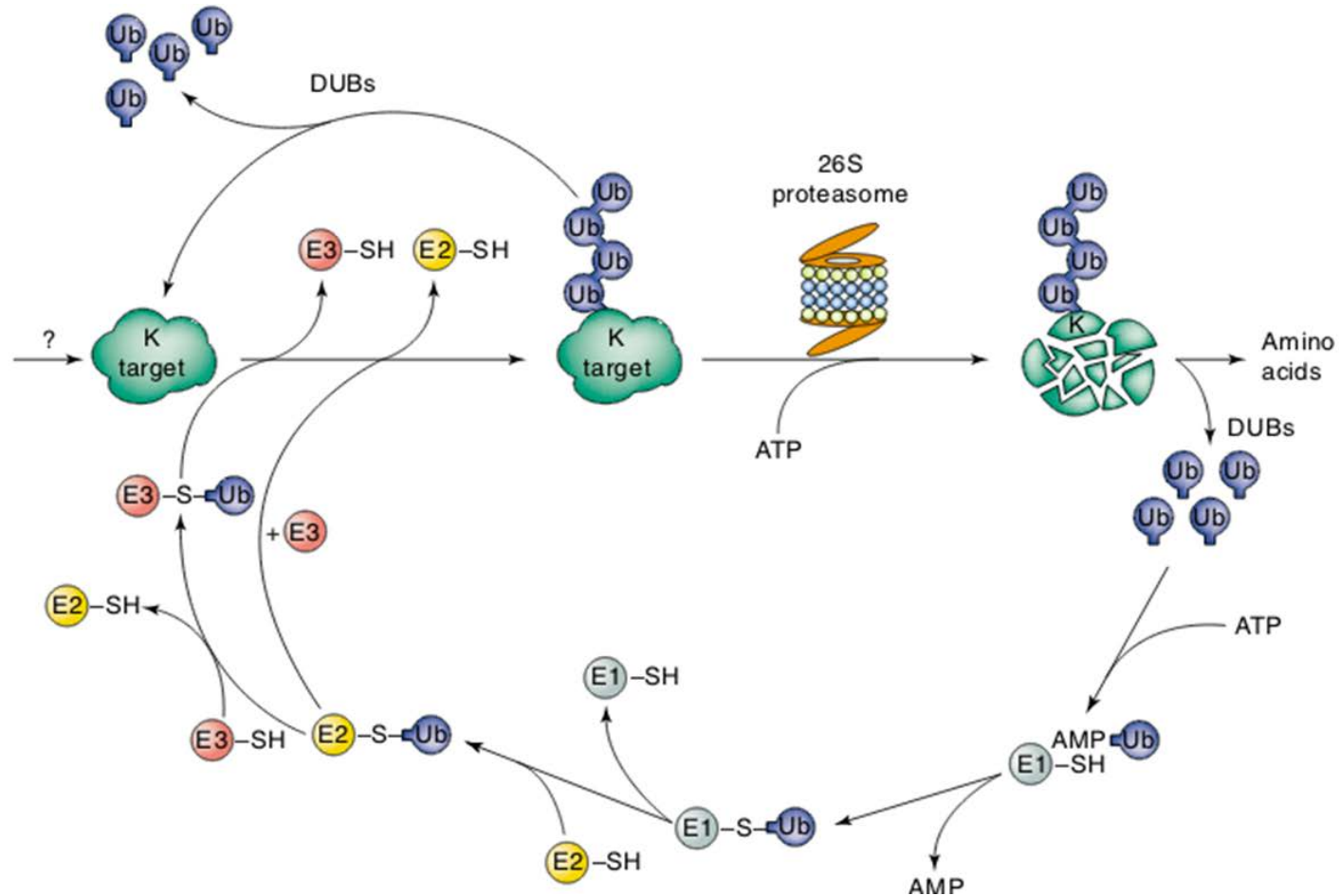
CSN5B蛋白的背景

CSN5B是泛素-蛋白酶体相关调节因子。

CSN: COP9 signalosome complex

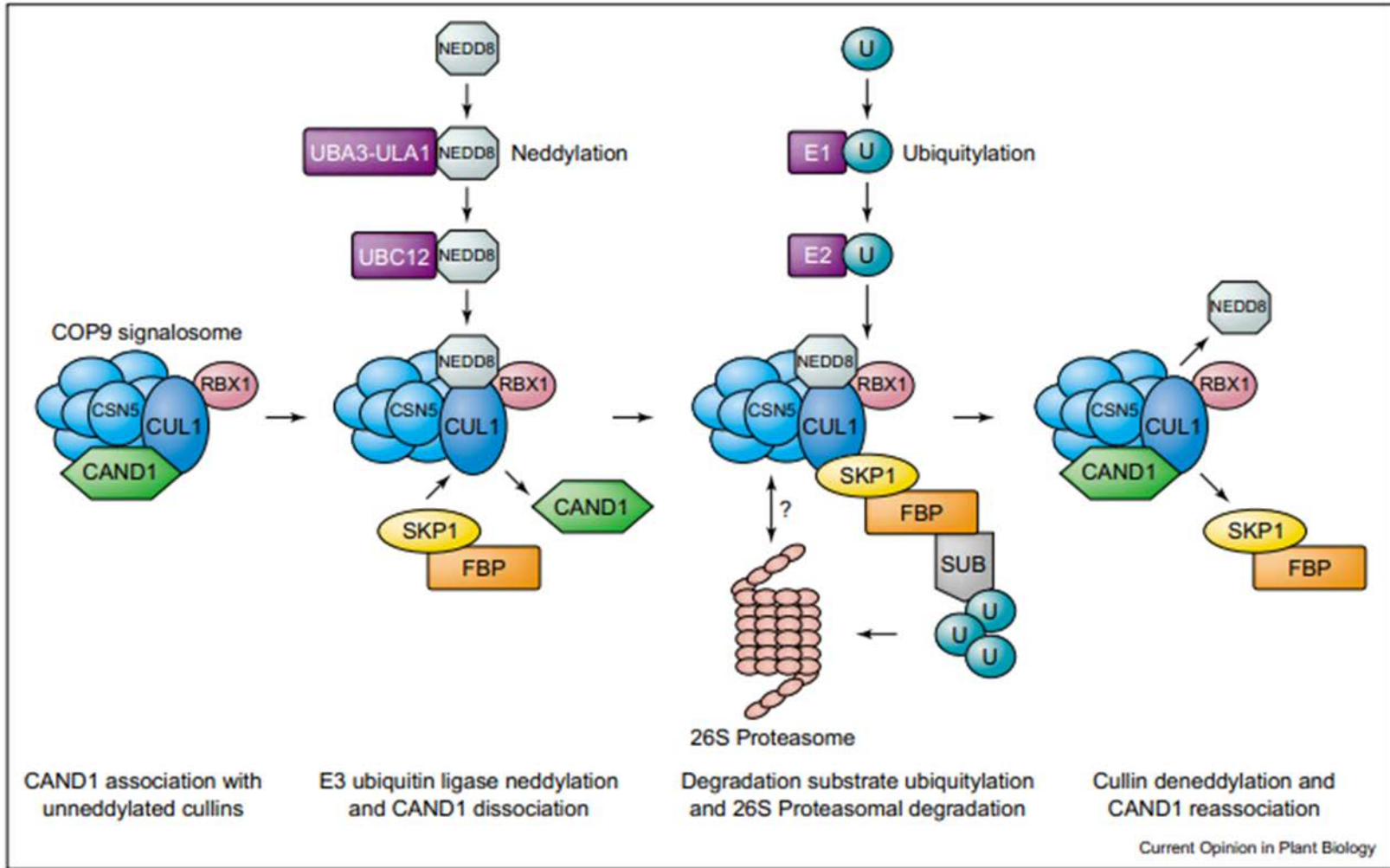
泛素-蛋白酶体系统（ubiquitin-proteasome system, UPS）是细胞内蛋白质降解的主要途径，参与细胞内80%以上蛋白质的降解。

CSN5B蛋白的背景



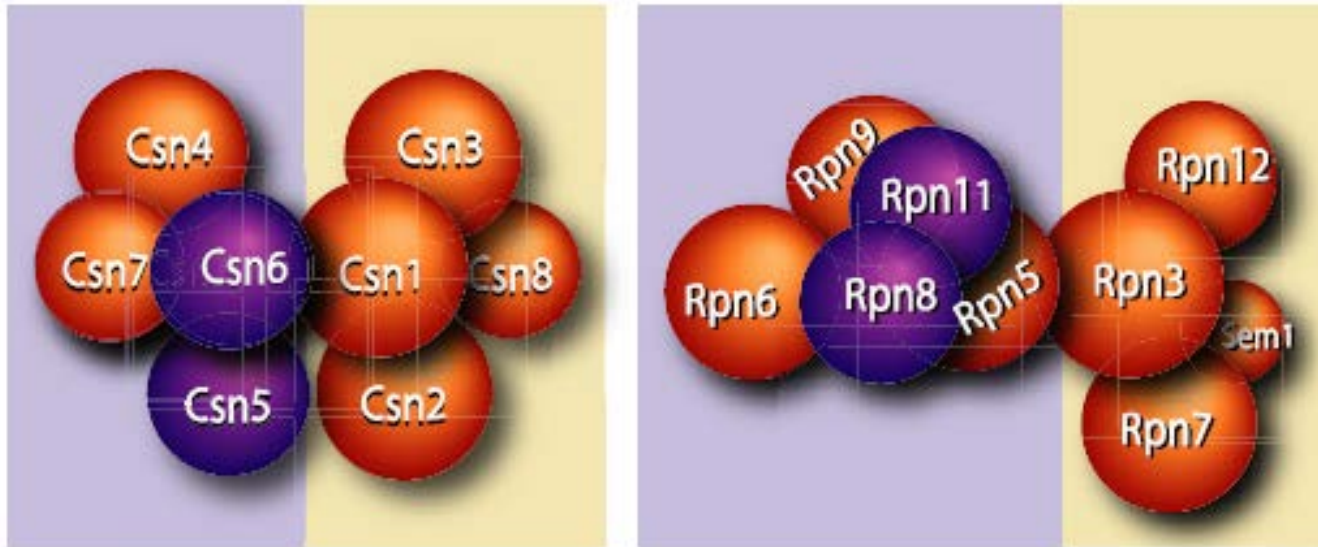
Vierstra R.D. et al., Trends in Plant Science, 2003, 8: 135-142

CSN 通过 NEDD 化修饰调节 E3



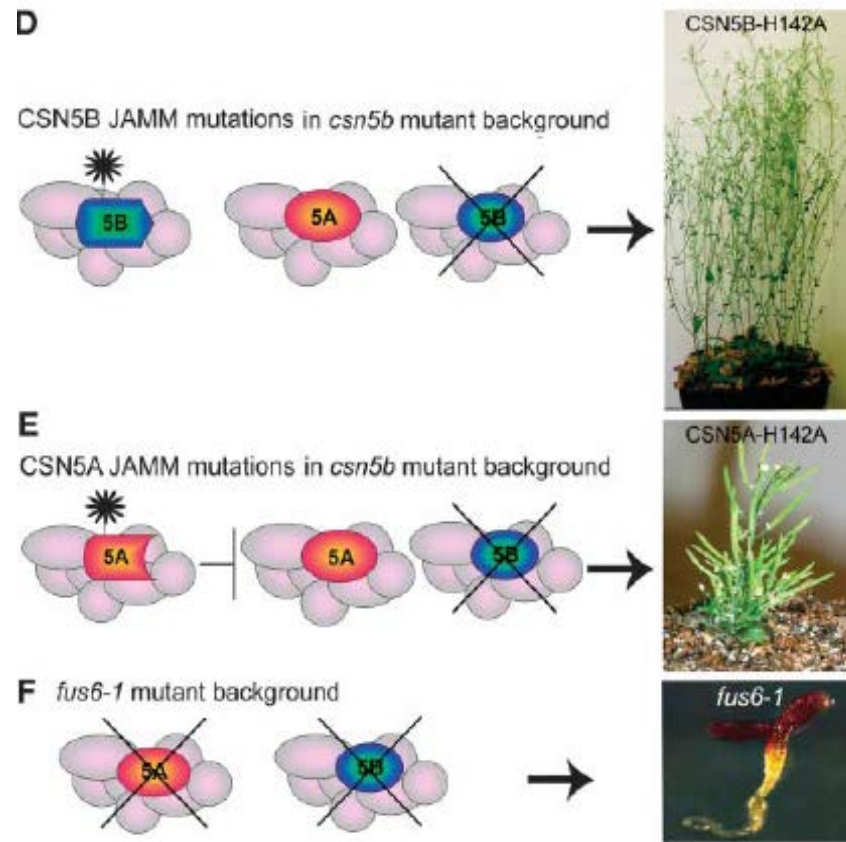
CSN 类似 26S 蛋白酶体的19S盖子

CSN由8个亚基构成，第五个亚基CSN5有两个同源蛋白，分别为CSN5A和CSN5B



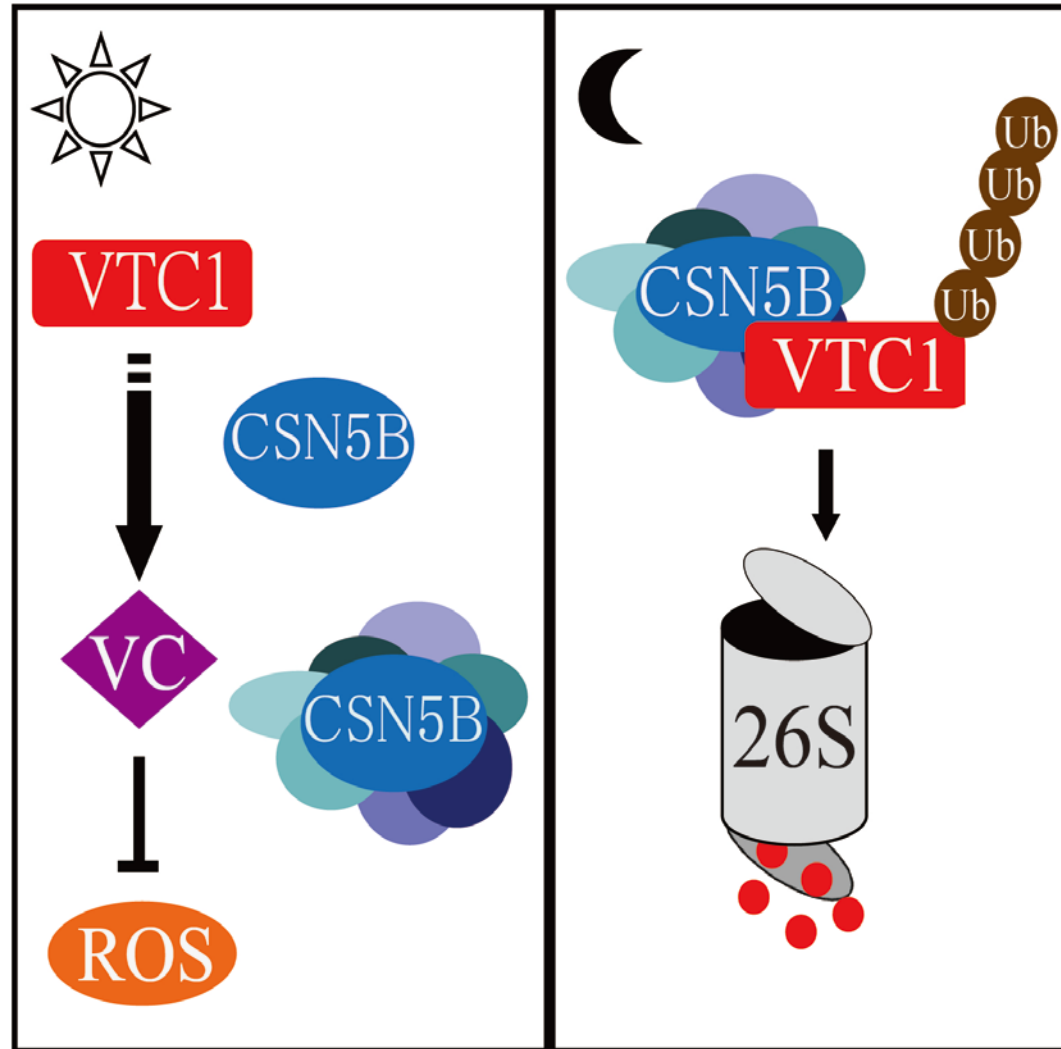
CSN5A与CSN5B

CSN5A 目前功能已知 CSN5B通过与拟南芥合成酶VTC1互作偶联 CSN 复合体相互作用参与光调控植物抗坏血酸的生物合成



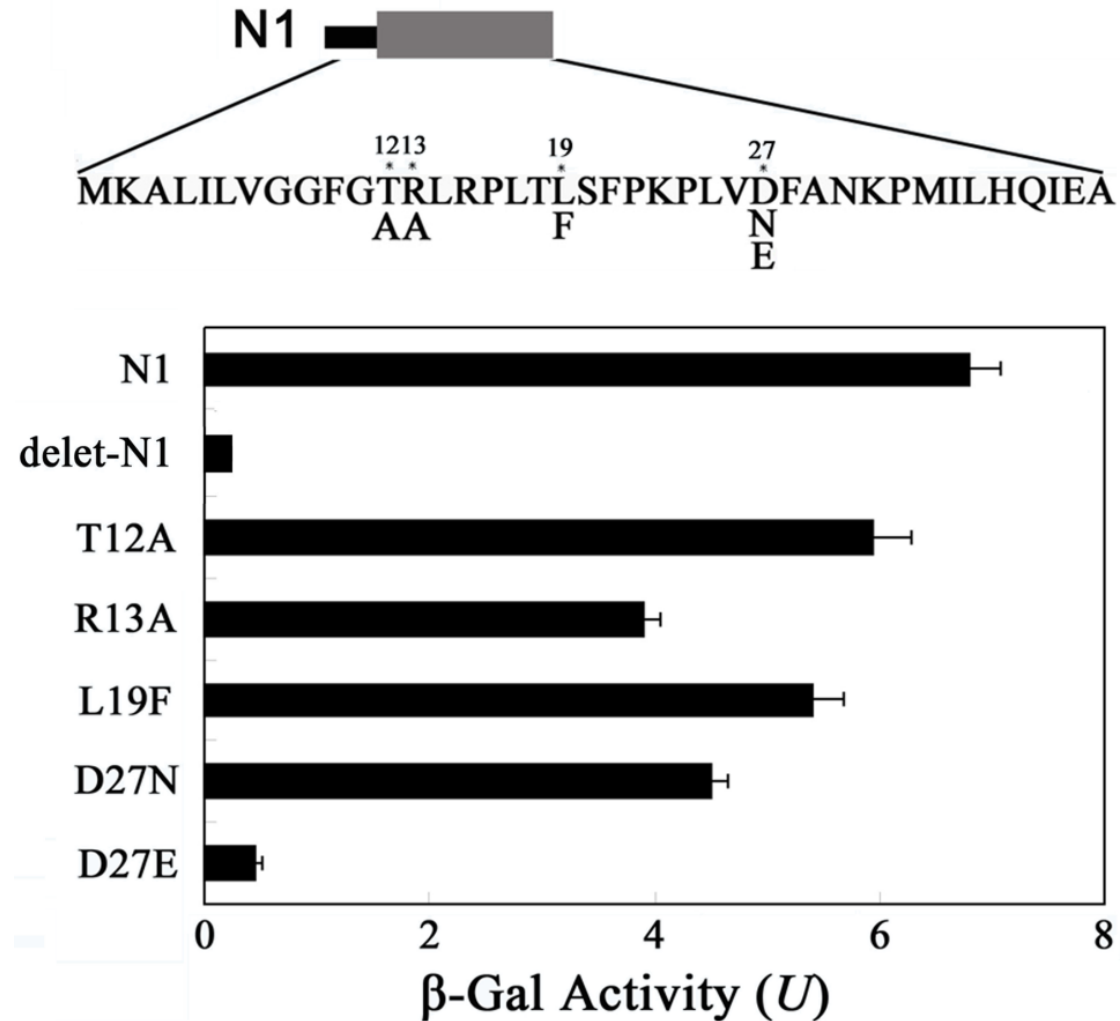
CSN5B 通过与 VTC1 互作调控 VC 合成

CSN5B 促进
VTC1 在暗中
泛素化并进
入 26S 蛋白酶
体途径降解








VTC1 通过与 CSN5B 互作偶联 CSN 复合体

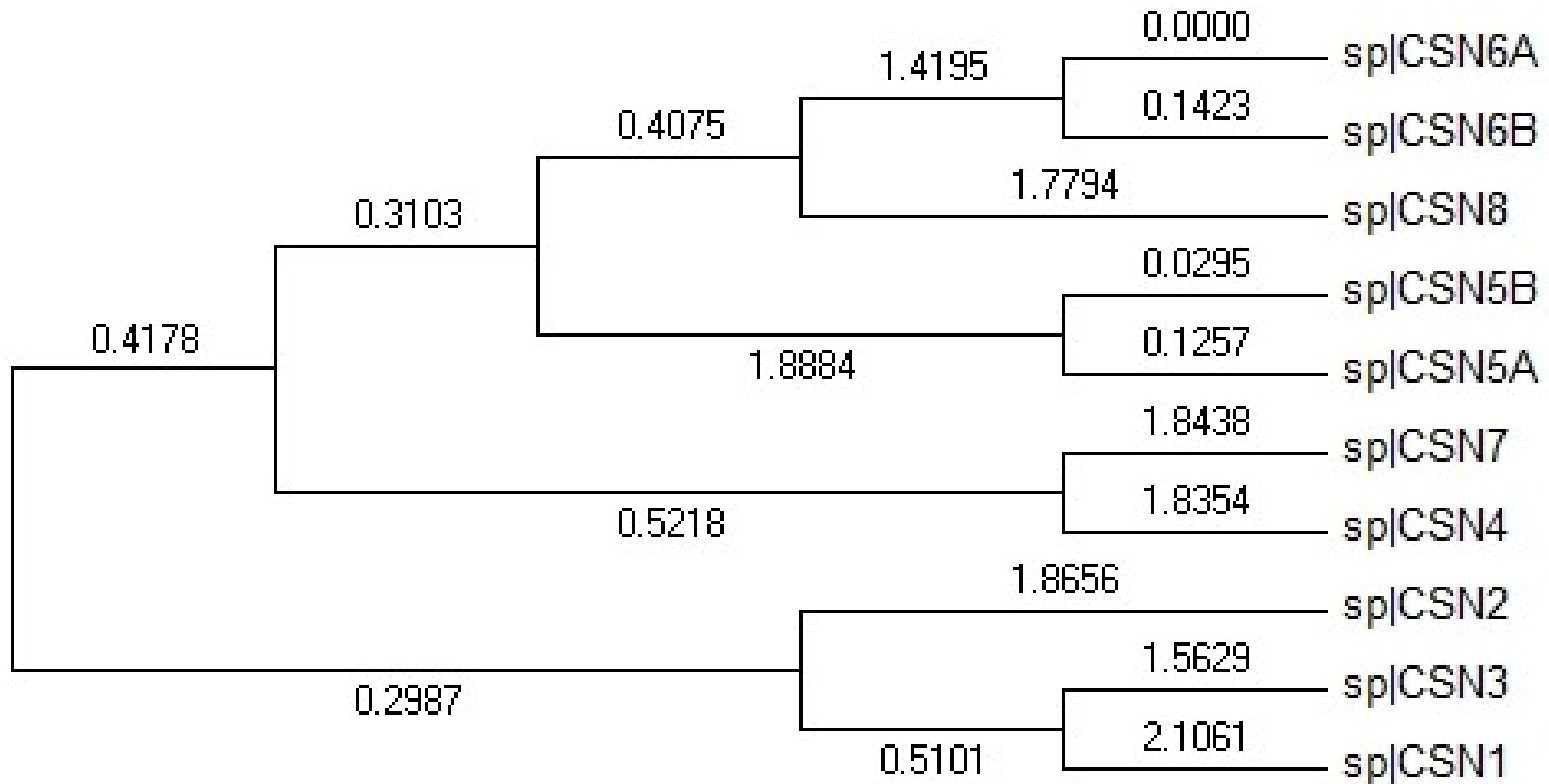
D27 是 VTC1-CSN5B 互作的关键氨基酸



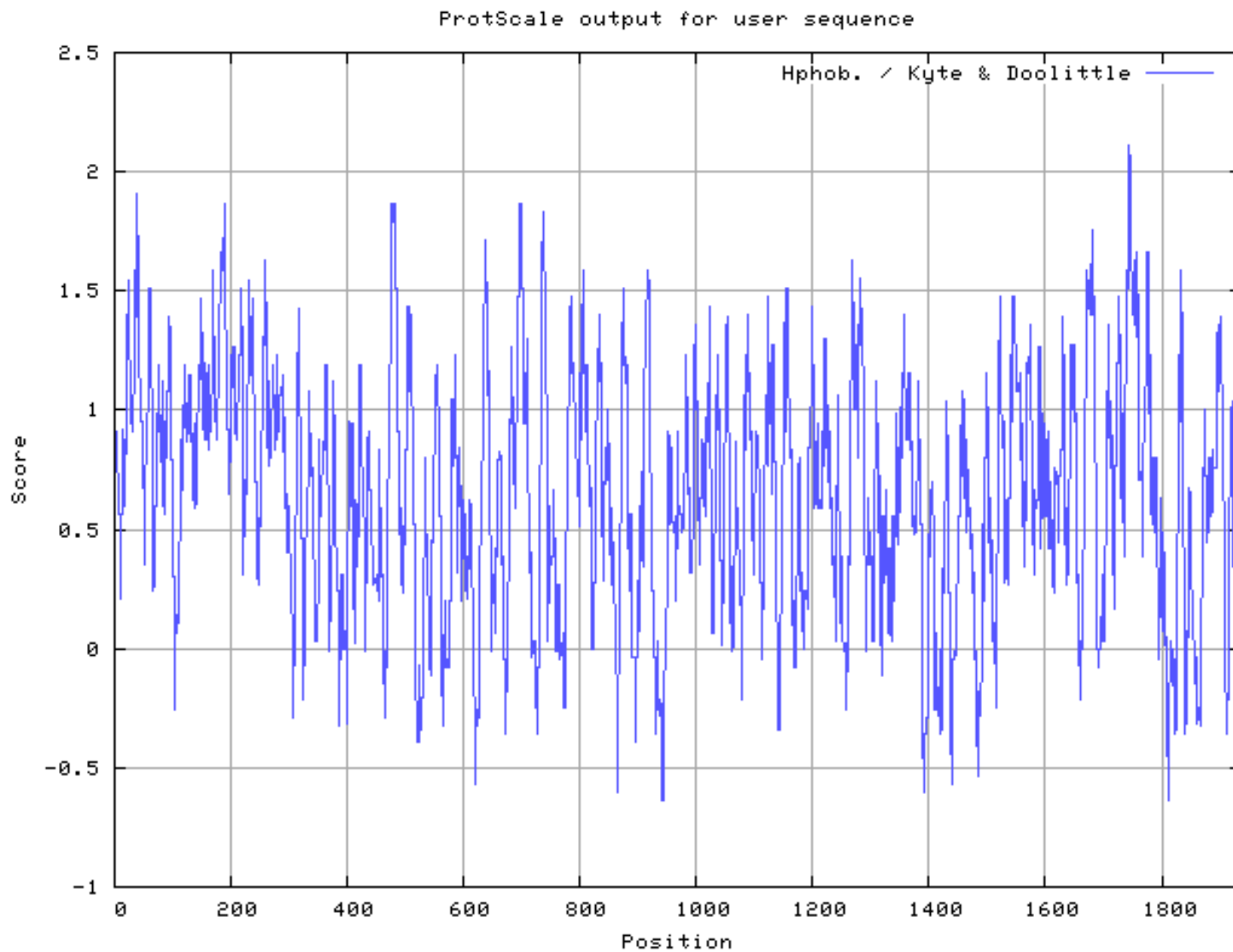
tair

Locus 	Description 	Gene Model(s) 	Other Names 	Keywords 
1 <input type="checkbox"/> AT1G22920	AJH1 encodes a protein similar to JAB1, a specific mammalian coactivator of AP-1 transcription. Encodes a subunit of the COP9....	AT1G22920.1	AJH1 ARABIDOPSIS JAB1 HOMOLOG 1 COP9 SIGNALOSOME 5A CSN5A	cullin deneddylation, negative regulation of photomorphogenesis, nucleus, photomorphogenesis, positive regulation of G2/M transition of mitotic cell cycle, protein binding, protein deneddylation, regulation of defense response, response to auxin stimulus, signalosome, signalosome assembly, specification of floral organ identity
2 <input type="checkbox"/> AT1G71230	Encodes a subunit of the COP9 complex, similar to JAB1, a specific mammalian coactivator of AP-1 transcription. Involved in	AT1G71230.1	AJH2 COP9-SIGNALOSOME 5B CSN5 CSN5B	DNA-dependent, cullin deneddylation, histone methylation, negative regulation of photomorphogenesis, nucleus, photomorphogenesis, positive regulation of G2/M transition of mitotic cell cycle, positive regulation of protein catabolic process, positive regulation of transcription, positive regulation of transcription, DNA-dependent, protein binding, protein deneddylation, protein deubiquitination, protein ubiquitination, regulation of L-ascorbic acid biosynthetic process, response to auxin stimulus, signalosome, signalosome assembly

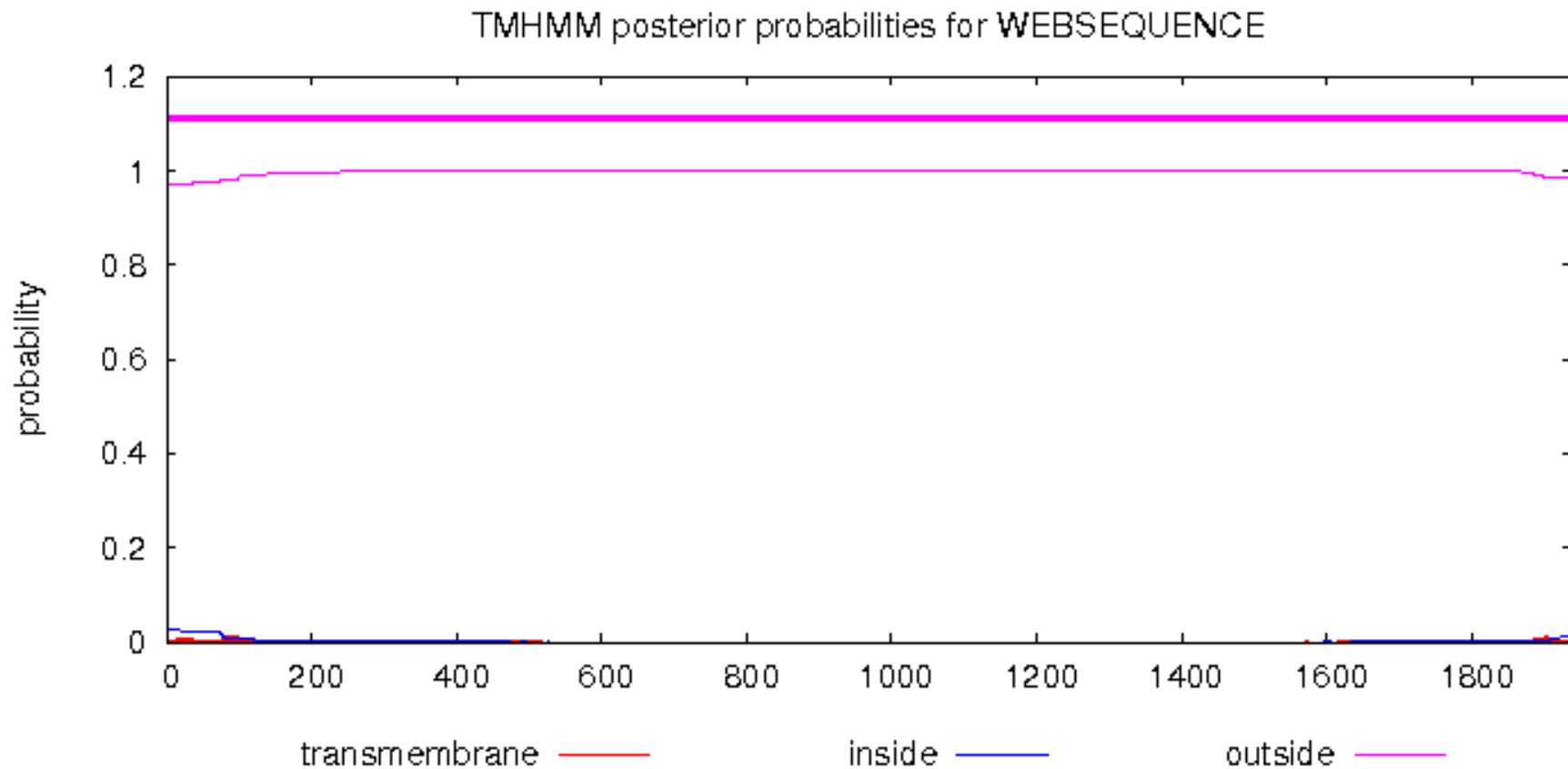
CSN5B的系统发育树



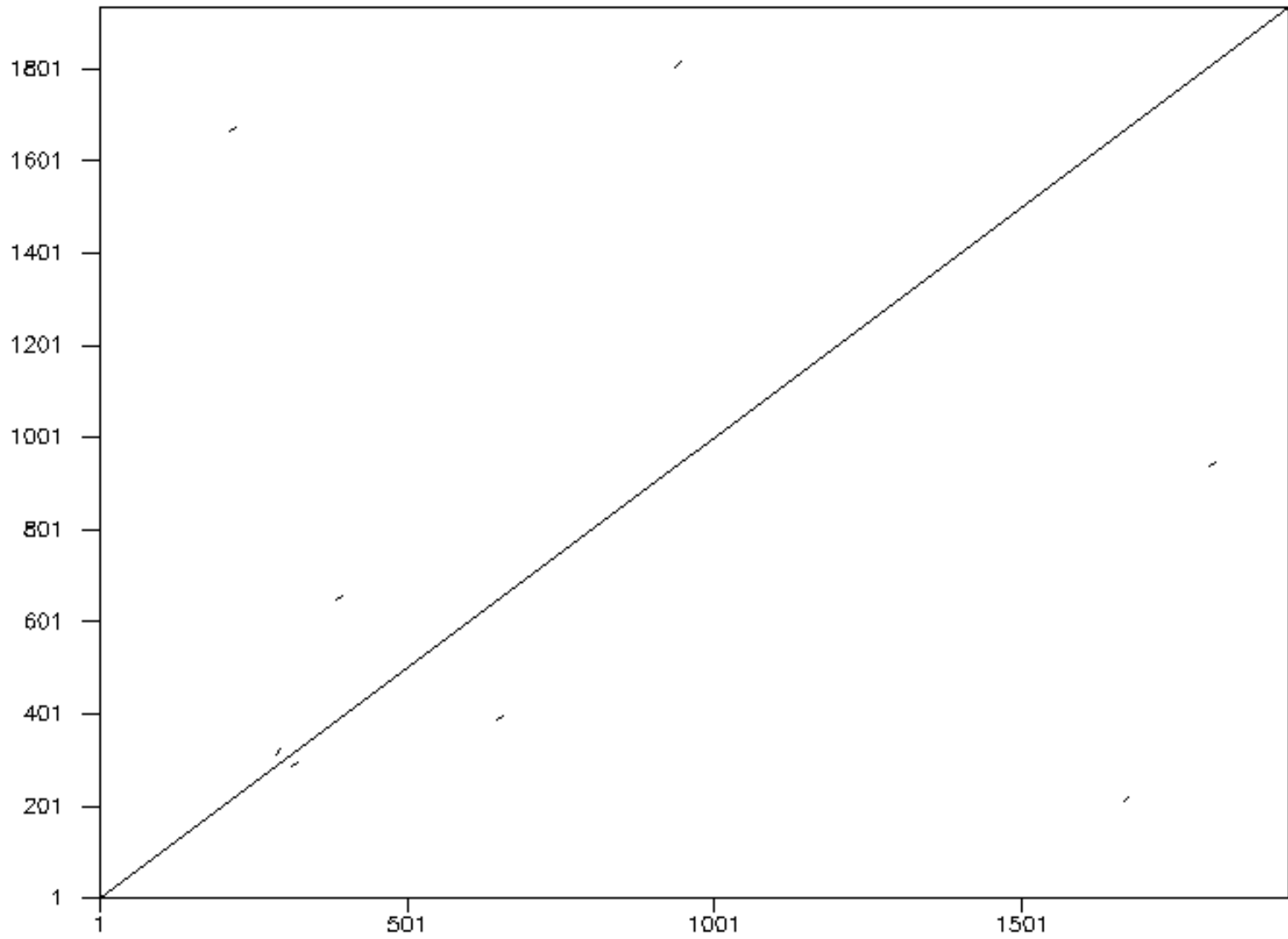
疏水性分析 CSN5B



跨膜区域

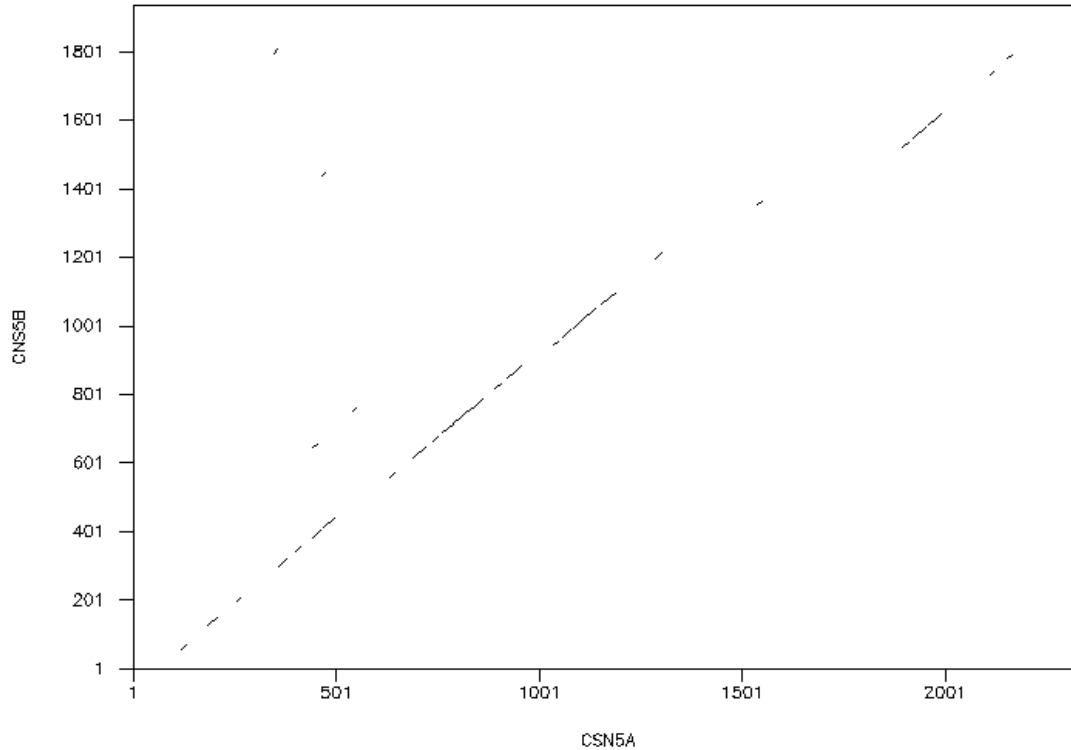


Property	Residues	Number	Mole%	
Tiny	(A+C+G+S+T)		1089	100.000
Small	(A+B+C+D+G+N+P+S+T+V)	1089		100.000
Aliphatic	(A+I+L+V)	283	25.987	
Aromatic	(F+H+W+Y)	0	0.000	
Non-polar	(A+C+F+G+I+L+M+P+V+W+Y)	804		73.829
Polar	(D+E+H+K+N+Q+R+S+T+Z)	285		26.171
Charged	(B+D+E+H+K+R+Z)		0	0.000
Basic	(H+K+R)		0	0.000
Acidic	(B+D+E+Z)	0		0.000



Dottup: fasta::7051:CSN5A vs fasta::7052:CNS5B

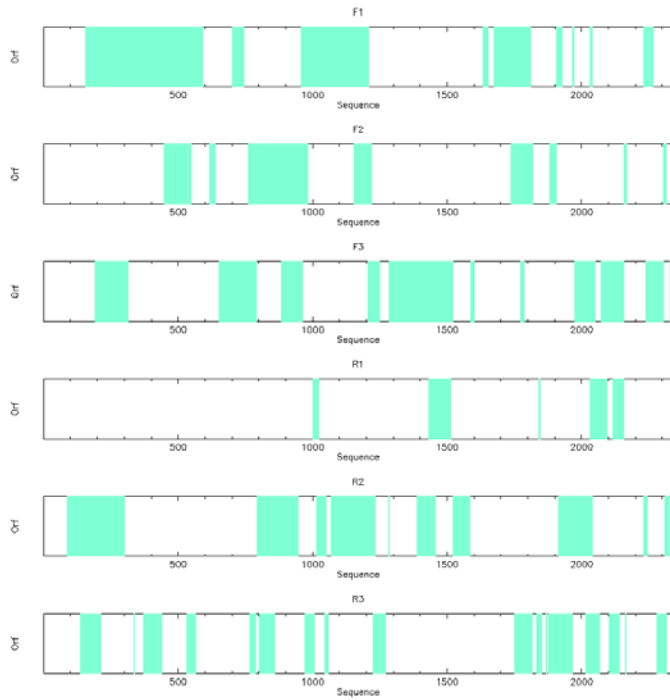
Sat 11 Jan 2014 17:05:29



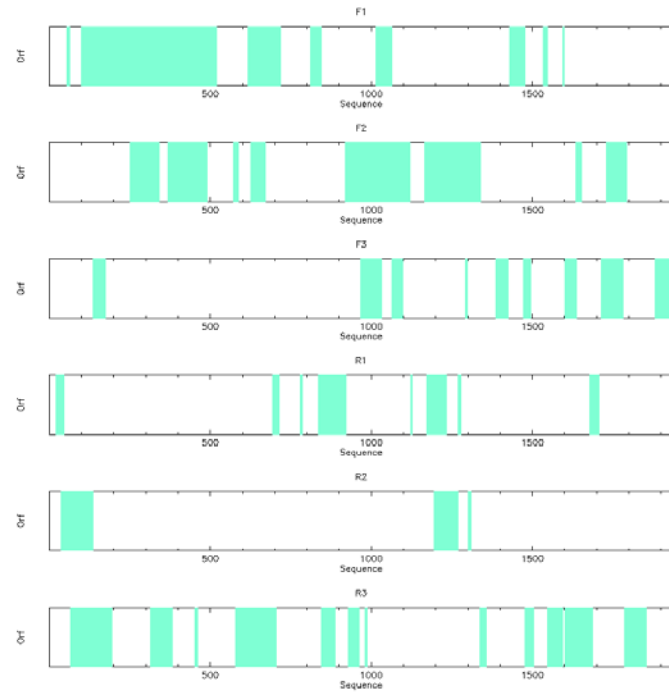
从图中看出，CSN5A与
CNS5B两条序列重叠区较大，
相似度较高。

dottup是以点阵图来分析序列的相似性，能够在全局直观的反映两条或多条序列的相似程度

Plotorf分析



CSN5A



CSN5B

Plotorf 以图形结果來显示核酸序列的 orf 位置，分析结果图形显示，两个序列中，均在第一个frame (F1) 之约150—590 bp 位置可能具有一个 ORF，但真正在第几个碱基的位置，需要用Getorf分析

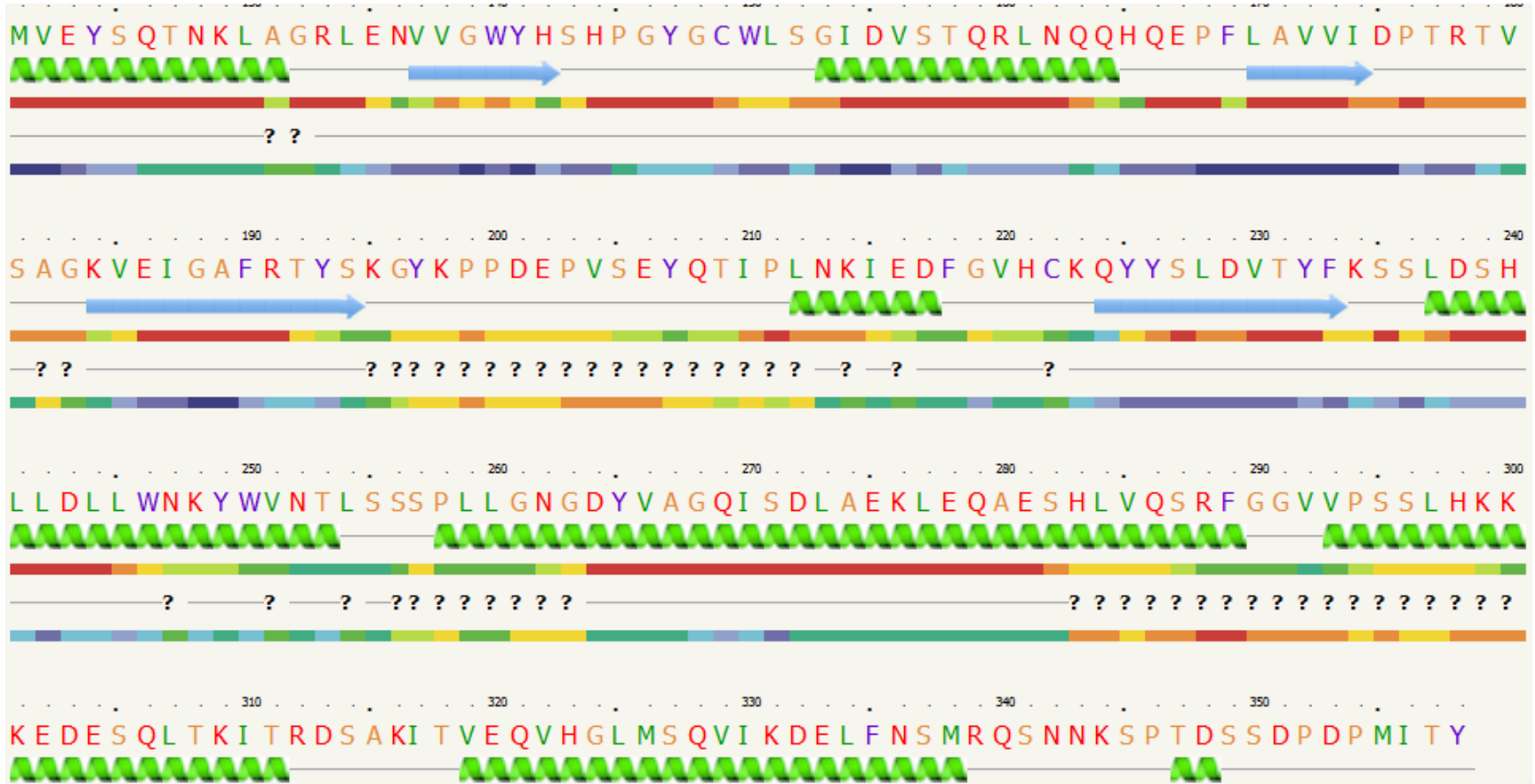
Getorf分析

```
>CSN5A_1 [157 - 591]
ATGGAAGGTTTCCTCGTCAGCCATCGCGAGGGAAGACATGGGAGCTAGAGAACAACATTCTC
CCAGTGGAACCAACCGATTACGCTCCGACAGTATATTCCACTACGACGACGCTTCACAA
GCCAAAATCCAGCAGGAGAAGCCATGGGCCTCCGATCCTAACTACTTCAAGCGCGTTCAC
ATCTCAGCCCTTGCTCTTCTCAAGATGGTGGTTCACGCTCGCTCCGGTGGCACAATCGAG
ATCATGGGTCTTATGCAGGGTAAAACCGAGGGTGATACAATCATCGTTATGGATGCTTTT
GCTTTGCCTGTTGAAGGTAAGGTAAGGTTAATGCTCAGTCTGATGCCTATGAGTAT
ATGGTTGAATACTCTCAGACCAGCAAGCTGGTAAGATATCTCTTATTCATCTCTCGCTGT
AGCTCCTTGTTAAT
```

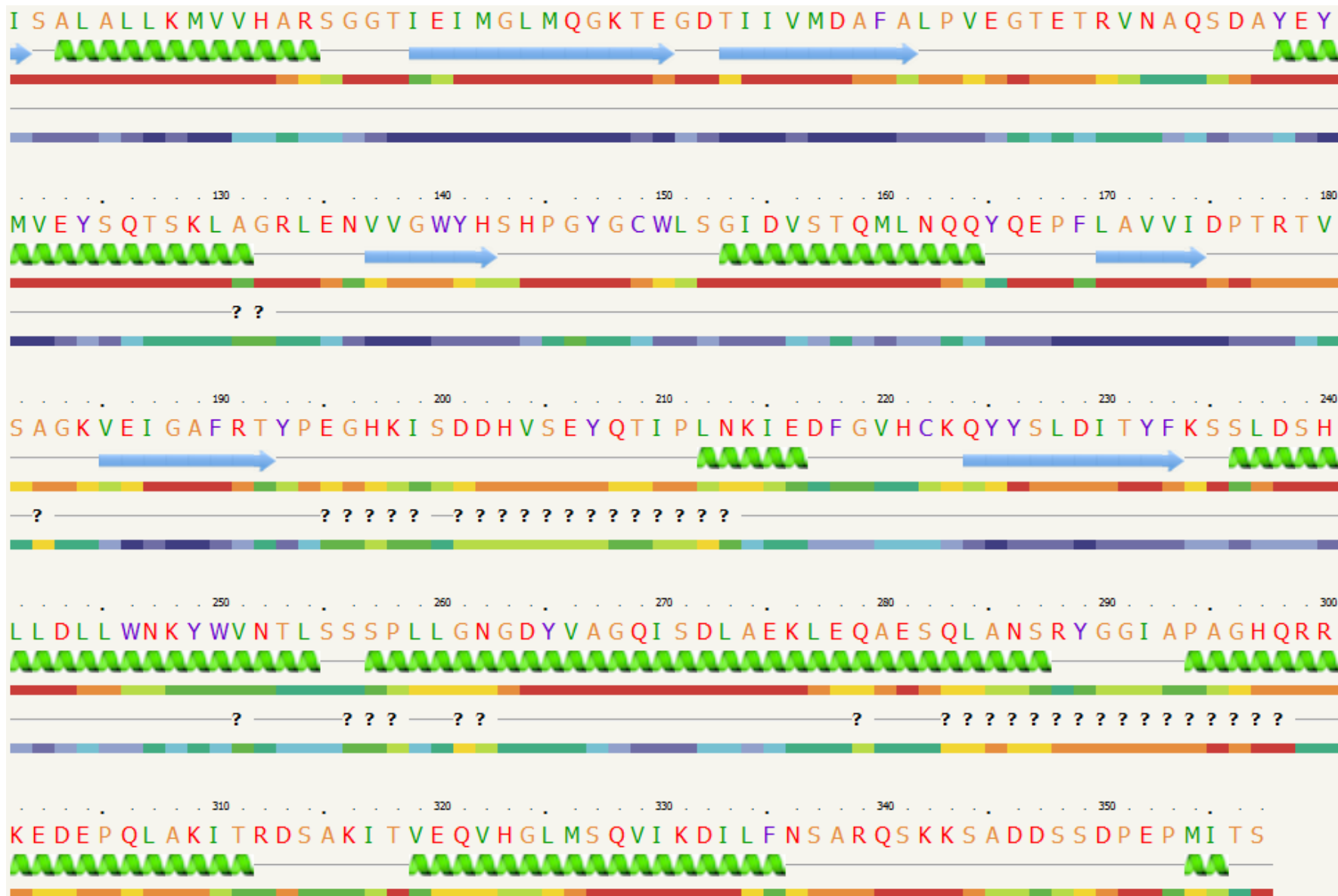
```
>CNS5B_1 [100 - 519]
ATGGAGGGTTCGTCGTCGACGATAGCAAGGAAGACATGGGAACTAGAGAACAGCATTCTA
ACAGTAGACTCACCTGATTCAACCTCCGACAACATCTTCTACTACGACGATACTTCACAG
ACTAGGTTCCAGCAAGAGAAACCGTGGGAGAATGATCCTCACTACTTTAAACGAGTCAAG
ATCTCAGCGCTCGCTCTTCTTAAGATGGTGGTTCACGCTCGCTCTGGTGGTACAATTGAA
ATAATGGGTCTTATGCAAGGTAAGACCGATGGTGATACTATCATTGTTATGGATGCTTTT
GCTTTACCAGTGAAGGTAAGGTAAGGTTAATGCTCAGGATGATGCTTATGAGTAC
ATGGTTGAGTATTCACAGACCAACAAGCTCGTAAGTGAGATTCAAGAACTTCAAAGTTT
```

由序列的 6 个 frames 之中分析完成后，在显示的结果中均有一条最长（第一条），如图所示，CSN5A为157—591，CSN5B为100—519，与plotorf预测结果基本一致。

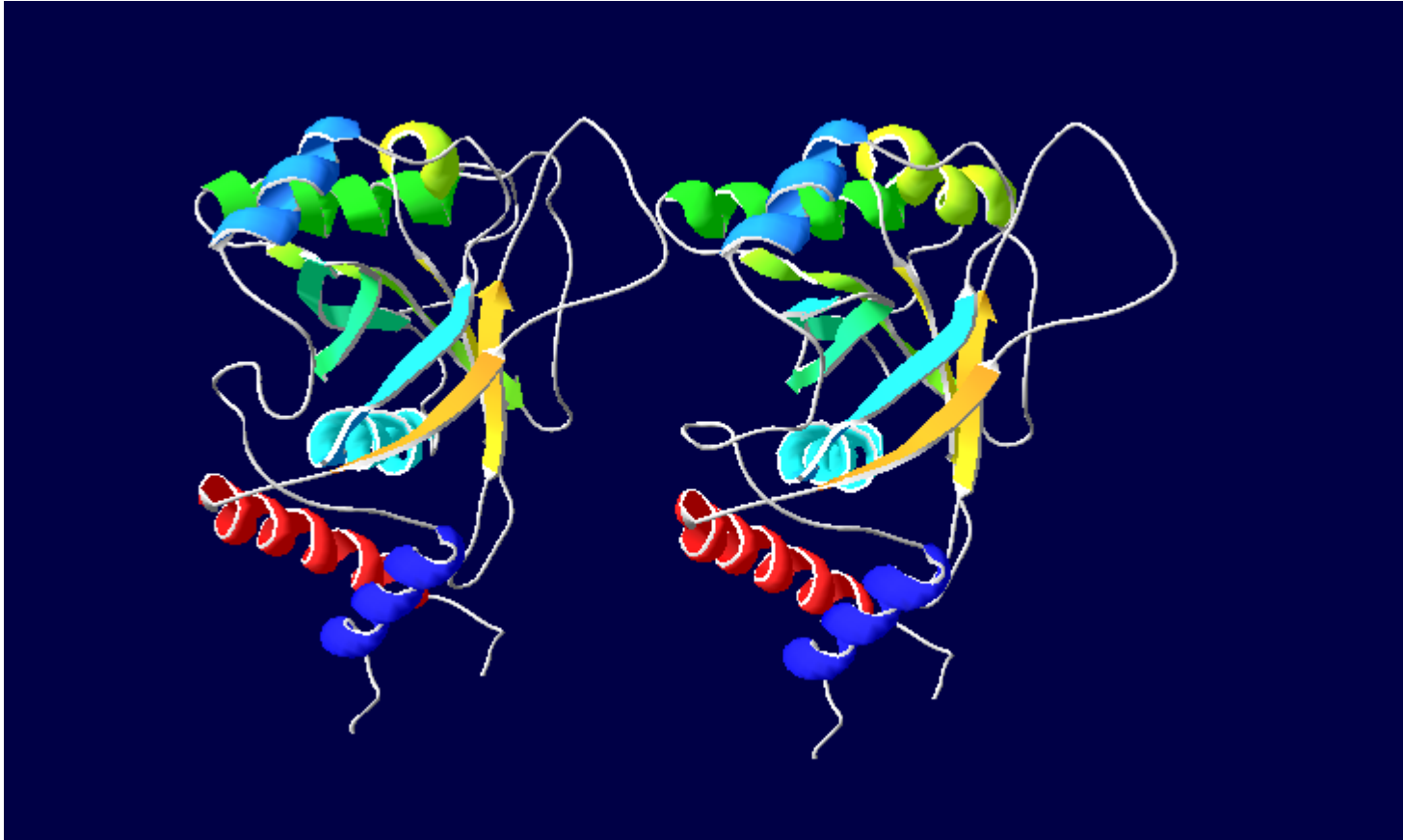
CSN5A



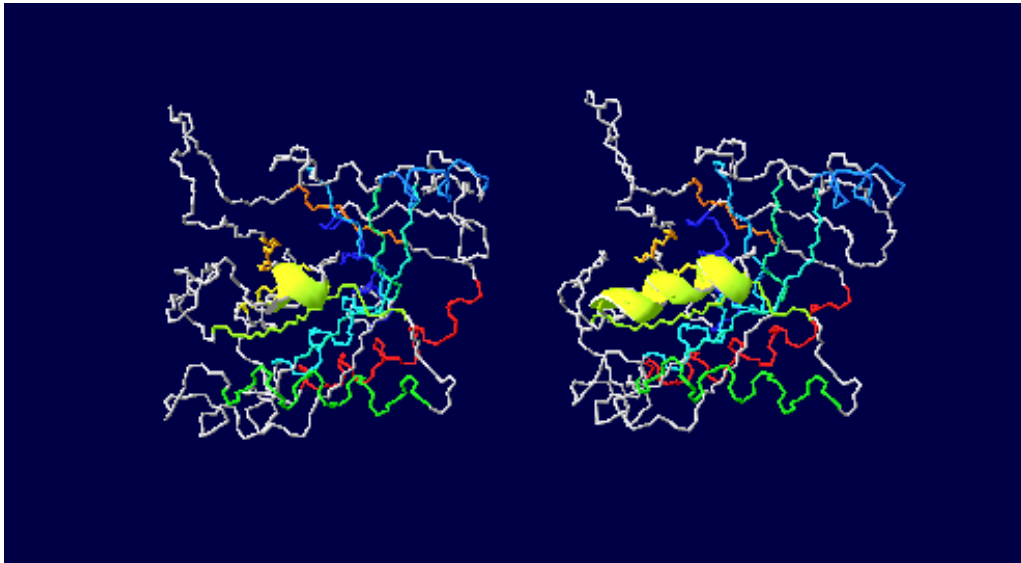
CSN5B



Swiss-PDB 分析



α 螺旋和 β 折叠的数目和区域几乎完全一样



h VAL156	v	
h SER157	v	
h THR158	v	
h GLN159	v	
h ARG160	v	
h LEU161	v	
h ASN162	v	h ASN162
h GLN163	v	h GLN163
h GLN164	v	h GLN164
h HIS165	v	h TYR165
h GLN166	v	h GLN166
		GLN167

图中标记的 α 螺旋差别较大，对应的序列CNS5A有11个，CNS5B有5个。

SER THR 磷酸化位点 ARG精氨酸

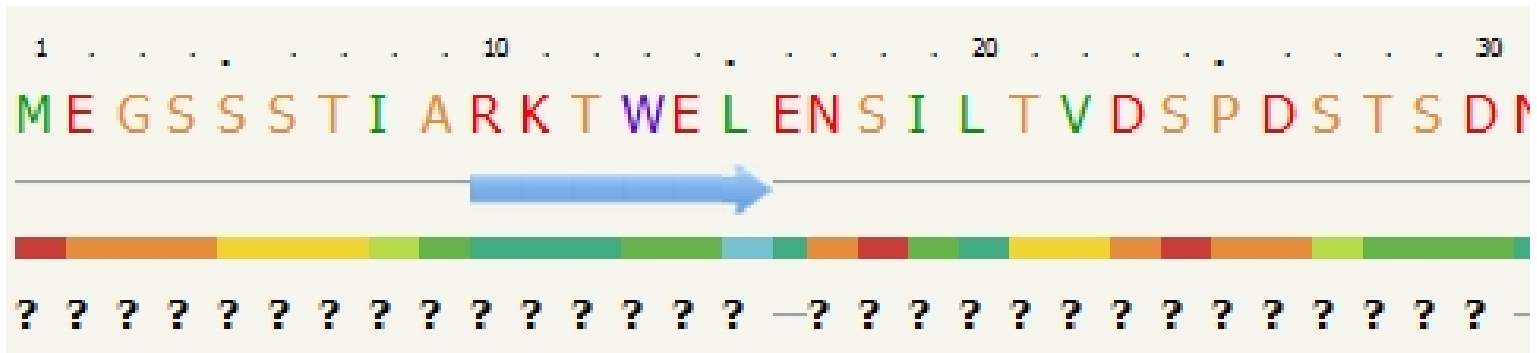
CSN5A和CSN5B序列对比

LENGTH	SCORE	IDENTITY	SIMILARITY	GAPS
358	1589.0	306/358 (85.5%)	326/358 (91.1%)	1/358 (0.3%)

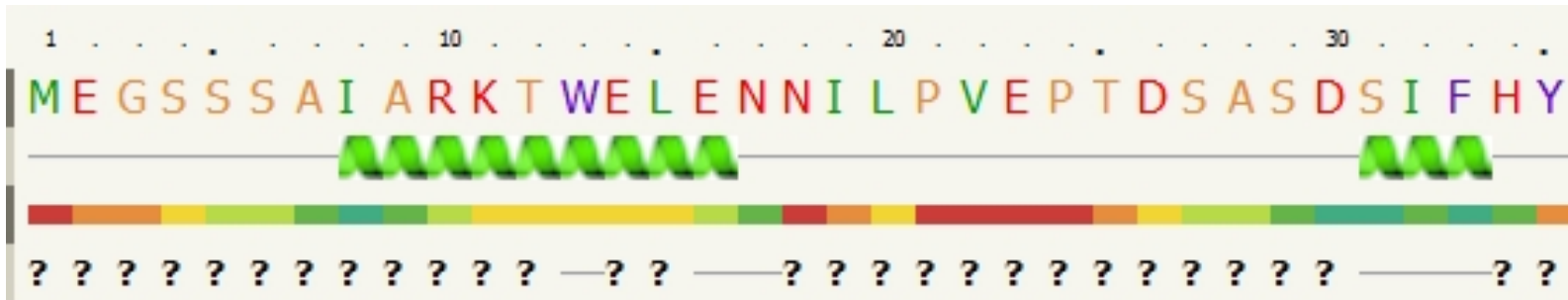
```

1 MEGSSSAIARKTWELENNILPVEPTDSASDSIFHYDDASQAKIQQEKPPWA      50
  |||||.|||||||:|.|:..|.||:|:|.|.|.:.|||||.
1 MEGSSSTIARKTWELENSILTVDSPDSTSDNIFYDDTSQIRFQQEKPPWE      50

51 SDPNYFKRVHISALALLKMVVHARSGGTIEIMGLMQKTEGDTIIVMDAF      100
  :|:|||||.|||||||:|||||||:|||||||
51 NDPHYFKRVKISALALLKMVVHARSGGTIEIMGLMQKTDGDTIIVMDAF      100
  
```

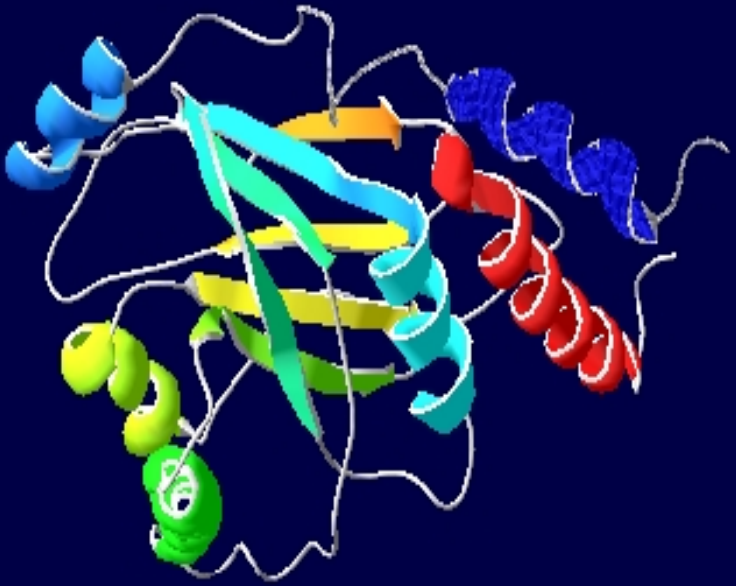


CSN5A

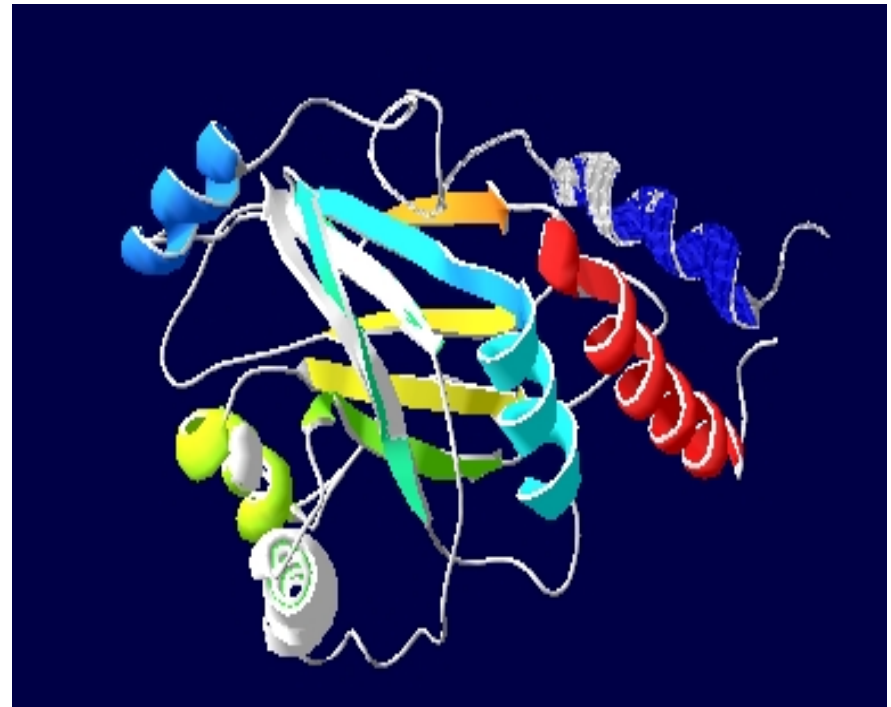


CSN5B

CSN5B蛋白



CSN5A



CSN5B+CSN5A

谢谢

感谢罗老师认真负责的指导和小组成员的意见
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