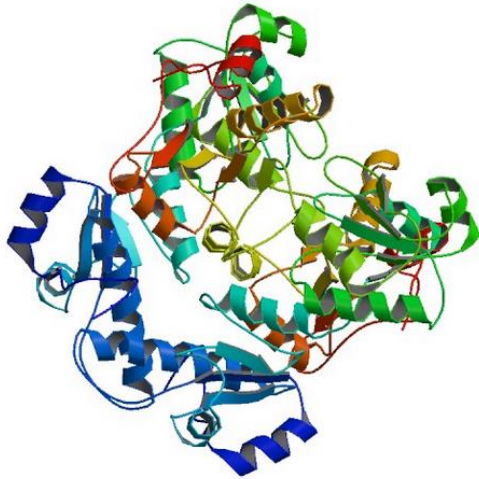


The structure and function analysis of Calsequestrin2(CASQ2)

隐钙素2的结构和功能分析



G03:
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Peixue Xia
Jiechun Yang
Lejiao Ren

2016.12.10

Contents

- **Background**

- **Analysis:**

 - Sequence

 - Secondary Structure

 - physicochemical property

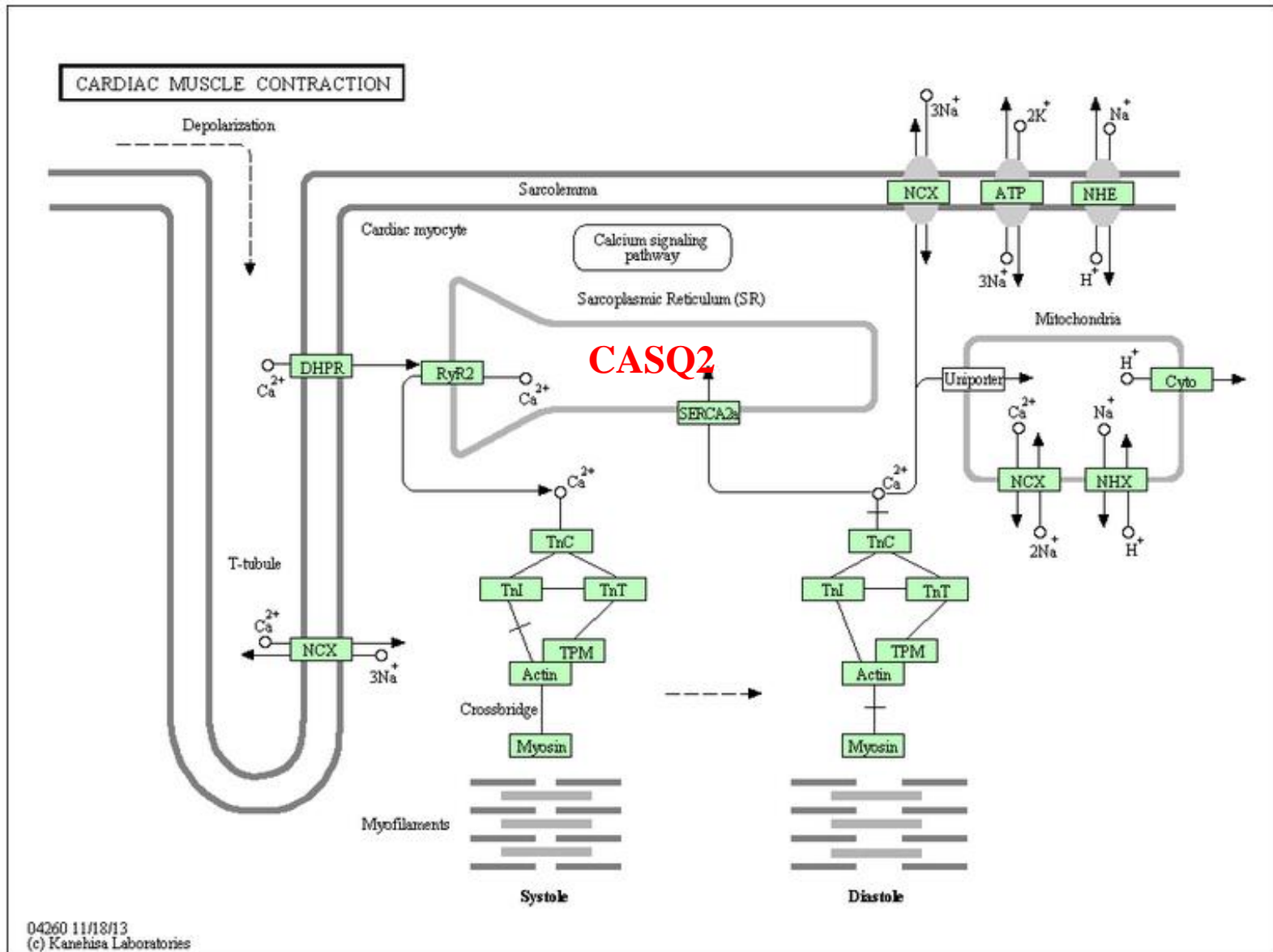
 - 3D Structure

- **Research conclusion**

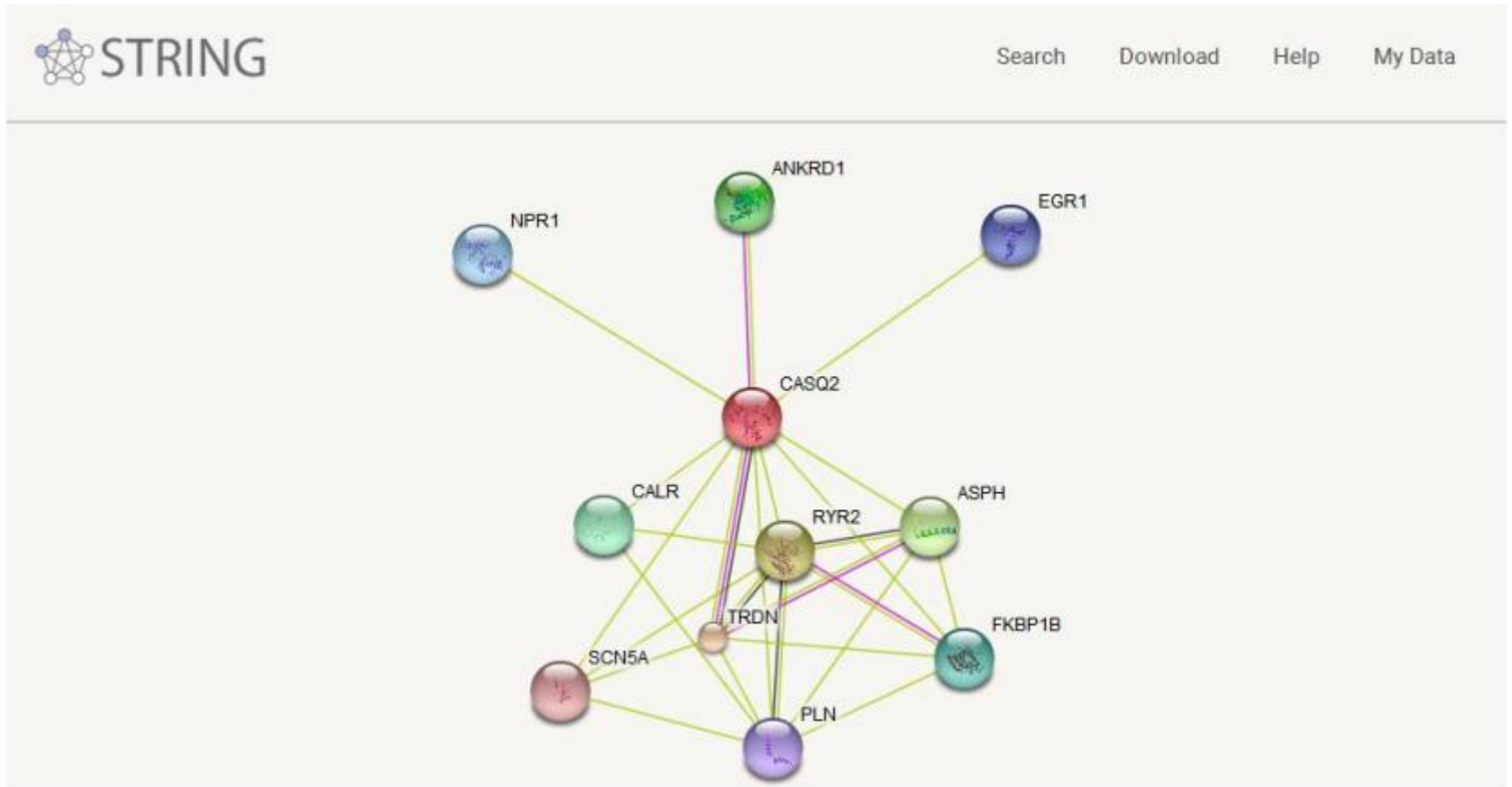
- **Acknowledgement**

Background

Weblab/pathway

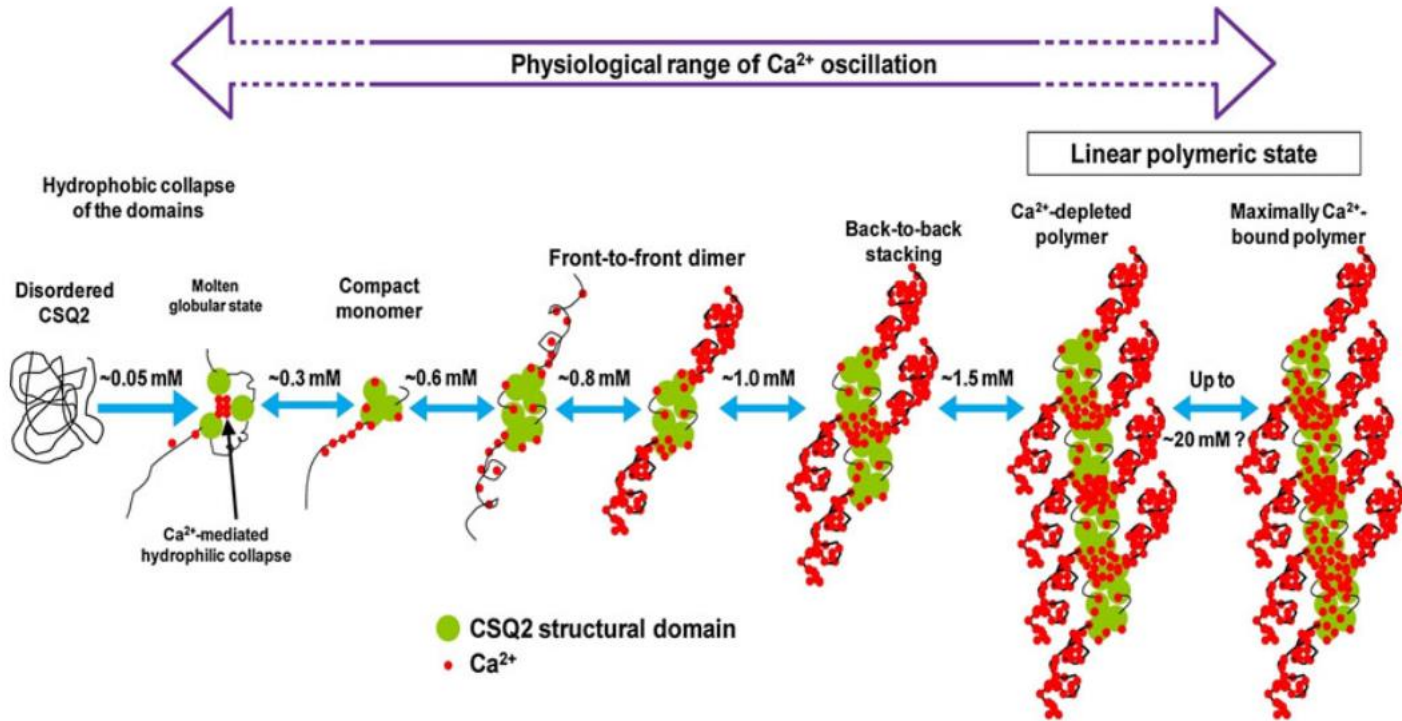


Background



Background

Uniprot/publications



Background

Uniprot/publications

共检索到45篇文献，其中报道的治病突变位点的如下，包括：
D307H/R33Q/L167H/K180R/K206N/F189L

11. **"Calsequestrin mutant D307H exhibits depressed binding to its protein targets and a depressed response to calcium."**
Houle T.D., Ram M.L., Cala S.E.
Cardiovasc. Res. 64:227-233(2004) [PubMed] [Europe PMC] [Abstract]
13. **"Catecholaminergic polymorphic ventricular tachycardia-related mutations R33Q and L167H alter calcium sensitivity of human cardiac calsequestrin."**
Valle G., Galla D., Nori A., Priori S.G., Gyorke S., de Filippis V., Volpe P.
Biochem. J. 413:291-303(2008) [PubMed] [Europe PMC] [Abstract]
16. **"A missense mutation in the CASQ2 gene is associated with autosomal-recessive catecholamine-induced polymorphic ventricular tachycardia."**
Eldar M., Pras E., Lahat H.
Trends Cardiovasc. Med. 13:148-151(2003) [PubMed] [Europe PMC] [Abstract]
22. **"[A Novel mutation of F189L in CASQ2 in families with catecholaminergic polymorphic ventricular tachycardia]."**
Liu Q.Q., Oberti C., Zhang X.Q., Ke T., Zhang T., Scheinman M., Hu D.Y., Wang Q.K.
Zhonghua Yi Xue Yi Chuan Xue Za Zhi 25:334-337(2008) [PubMed] [Europe PMC] [Abstract]
29. **"The human CASQ2 mutation K206N is associated with hyperglycosylation and altered cellular calcium handling."**
Kirchhefer U., Wehrmeister D., Postma A.V., Pohlentz G., Mormann M., Kucerova D., Muller F.U., Schmitz W., Schulze-Bahr E., Wilde A.A., Neumann J.
J. Mol. Cell. Cardiol. 49:95-105(2010) [PubMed] [Europe PMC] [Abstract]
34. **"Cardiomyocytes generated from CPVTD307H patients are arrhythmogenic in response to beta-adrenergic stimulation."**
Novak A., Barad L., Zeevi-Levin N., Shick R., Shtrichman R., Lorber A., Itskovitz-Eldor J., Binah O.
J. Cell. Mol. Med. 16:468-482(2012) [PubMed] [Europe PMC] [Abstract]

Highlight

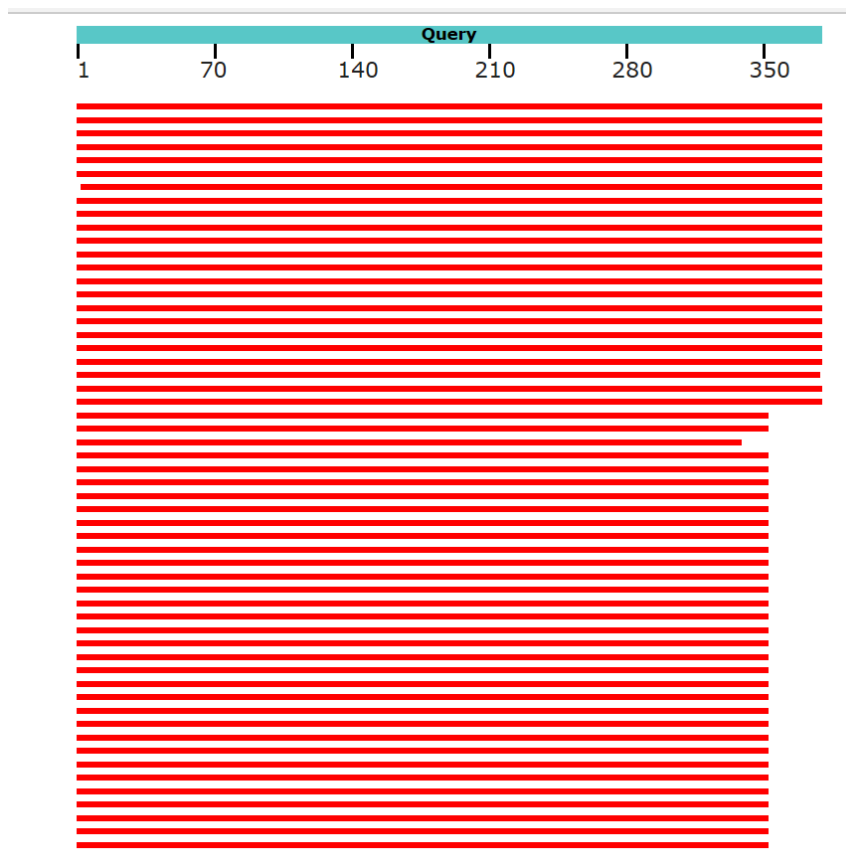
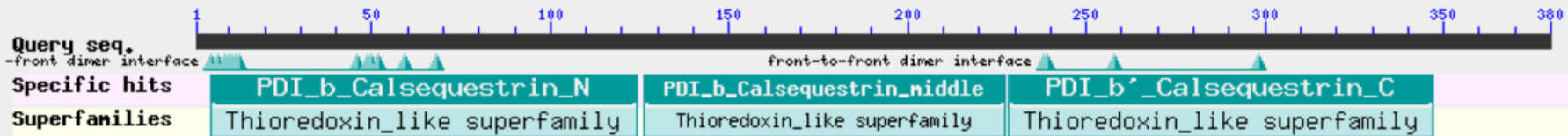
Annotation

- Glycosylation
- Region
- Helix
- Compositional bias
- Natural variant
- Chain
- Mutagenesis
- Beta strand
- Signal peptide
- Non-terminal residue

O14958	CASQ2_HUMAN	1	MKRTHLFIVGIYFLSSCRAEE
O09161	CASQ2_MOUSE	1	MKRIYLLMVGIVYLLSLSGAEE
P51868	CASQ2_RAT	1	MKRIYLLVVGLYLLSFSRAEE
P12637	CASQ2_CANLF	1	MKRTHLFIAGLYLLASCRAEE
P31235	CASQ2_RABIT	1	MKRAHLFVVGIVYLLSSCRAEE
P19204	CASQ2_CHICK	1	MKATCWILAGFCLLFCCKAEE
Q5RAN9	CASQ2_PONAB	1	MKRTHLFIVGVYVLSSCRAEE
O18934	CASQ2_PIG	1	-----
O14958	CASQ2_HUMAN	61	SSDKVTQKQFQLKEIVLELVA
O09161	CASQ2_MOUSE	61	SSDKVSQKQFQLKEIVLELVA
P51868	CASQ2_RAT	61	SSDKVAQKQFQLKEIVLELVA
P12637	CASQ2_CANLF	61	SSDKVAQKQFQLKEIVLELVA
P31235	CASQ2_RABIT	61	SADKVAQKQFQLKEIVLELVA
P19204	CASQ2_CHICK	61	SSDRVSQKQFQMTMVLELAA
Q5RAN9	CASQ2_PONAB	61	SSDKVAQKQFQLKEIVLELVA
O18934	CASQ2_PIG	1	-----
O14958	CASQ2_HUMAN	121	RTIEFDGEFAADVLVLEFLLDI

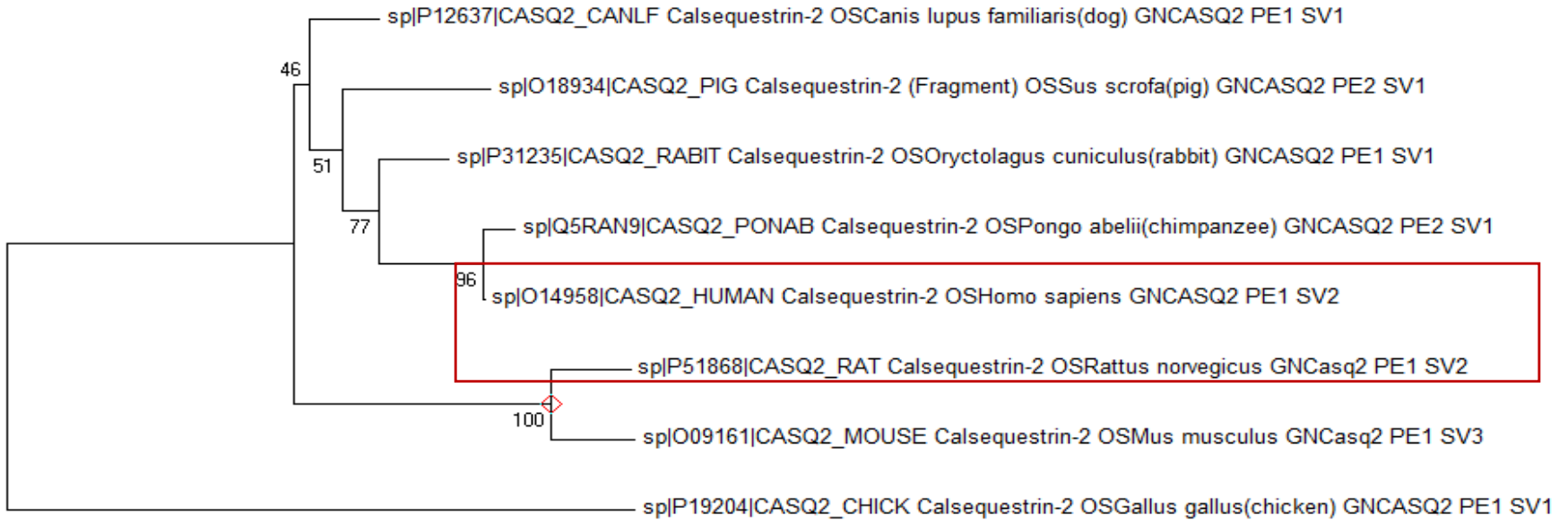
Sequence

Putative conserved domains have been detected, click on the image below for detailed results.



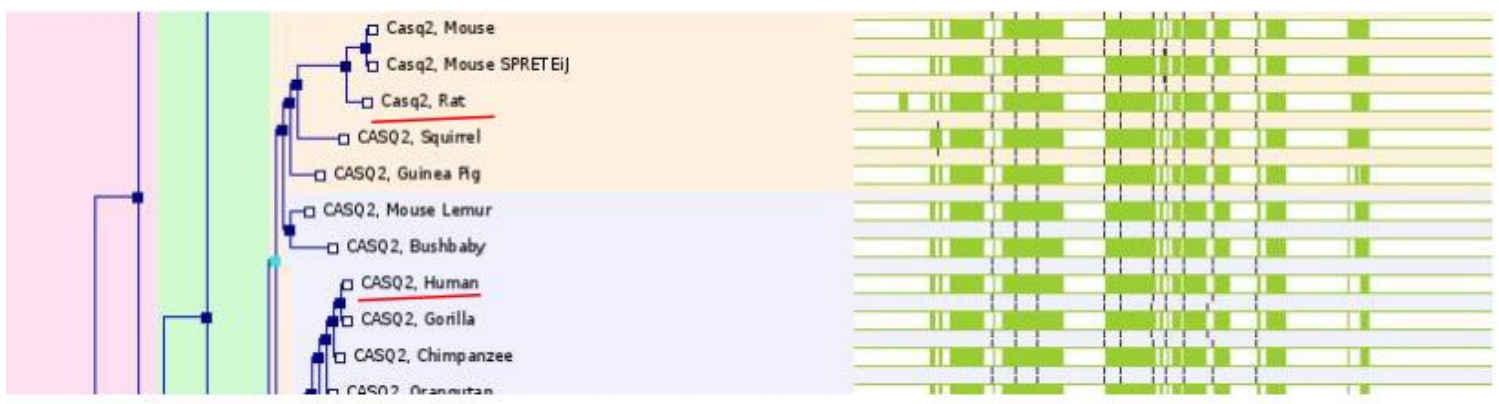
<input type="checkbox"/>	calsequestrin-2 precursor (Homo sapiens)	753	753	100%	0.0	100%	NP_001223.2
<input type="checkbox"/>	Calsequestrin 2 (cardiac muscle) (Rattus norvegicus)	676	676	92%	0.0	94%	AAH72547.1

MEGA:进化树分析

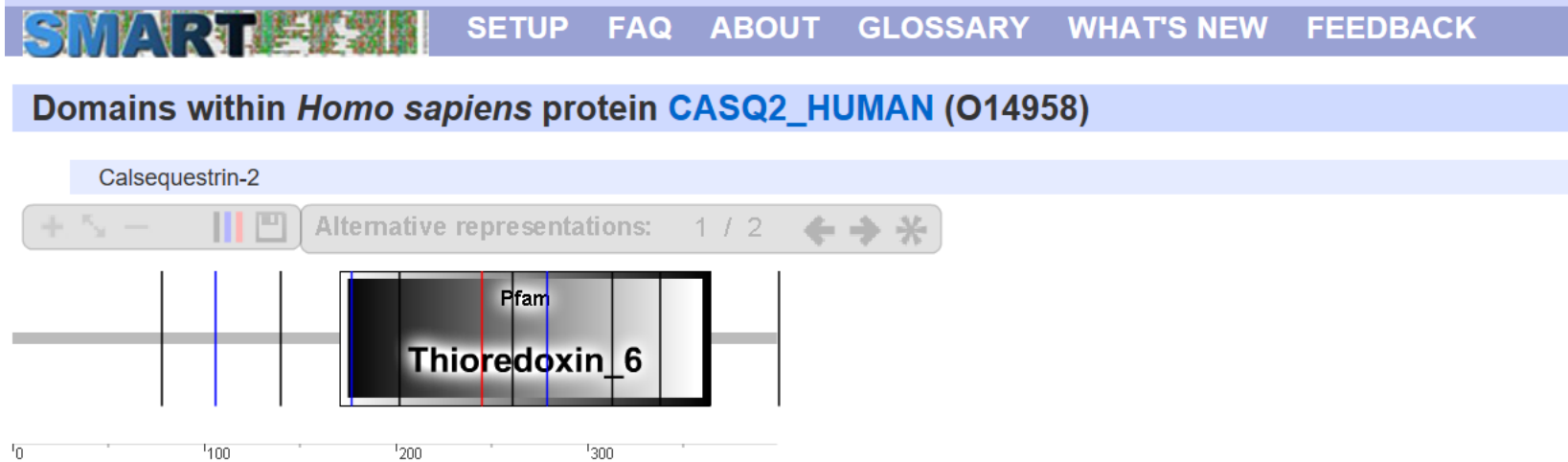


0.020

Genetree



Secondary structure analysis



Confidently predicted domains, repeats, motifs and features:

Name	Start ▲	End	E-value
Pfam:Calsequestrin	2	382	1.3e-235
Pfam:Thioredoxin_6	171	364	8.9e-22

Secondary structure analysis

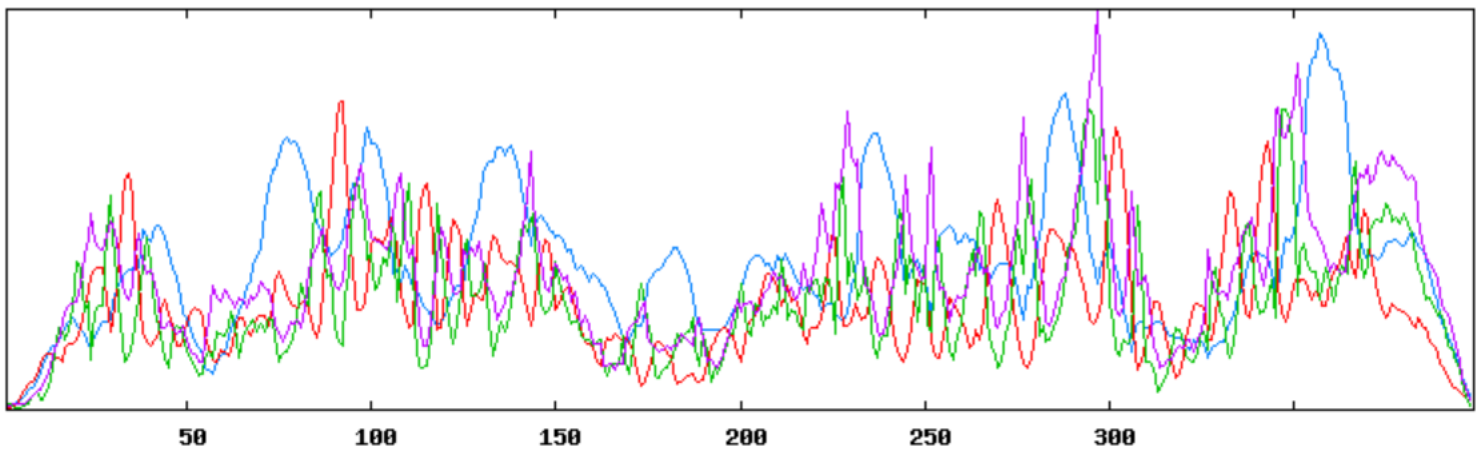
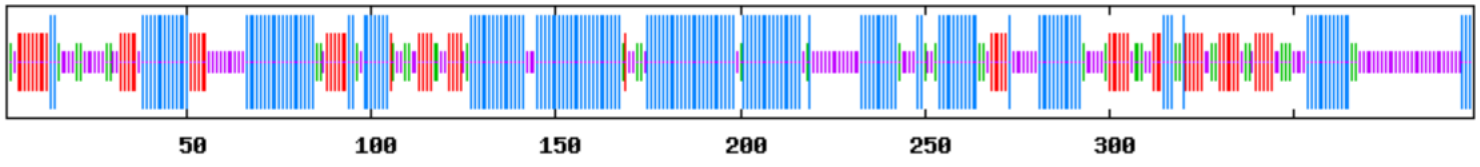
Expasy.org

```

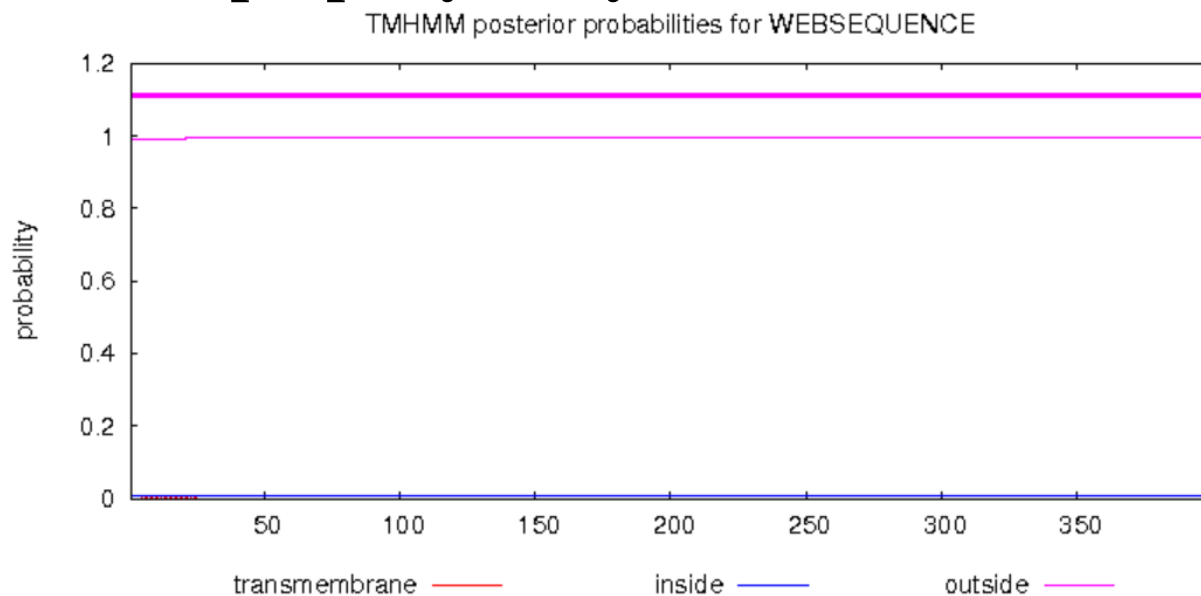
      10      20      30      40      50      60      70
      |      |      |      |      |      |      |
MKRTHLFIVGIYFLSSCRAEEGLNFPTYDGKDRVSVLSEKNFKQLKKYDLLCLYHEPVSSDKVTQKQF
httceeeeeeeehhtccccccttcccccttceeeeeehhhhhhhhhhhhhheeeecccccccchhhh
QLKEIVLELVAQVLEHKAIGFVMDAKKEAKLAKKLGDFDEEGSLYILKGDRTIEFDGEFAADVLEFLLD
hhhhhhhhhhhhhhhttcceeeeeehhtchhhhhhhhtcccttceeeettceeeecthhhhhhhhhhhh
LIEDPVEIISSKLEVQAFERIEDYIKLIGFFKSEDSEYYKAFEEAAEHFQPYIKFFATFDKGVAKKLSLK
hhccchhhhhhhhhhhhhhhhhhhhhhteccttchhhhhhhhhhhhhhhhhhhhhcthhhhhhhhhh
MNEVDFYEPFMDPEIAIPNKPYTEELVEFVKEHQRPTRLRLRPEEMFETWEDDLNGIHIVAFAEKSDPD
hhhhhhhhcthccccccccccccchhhhhhhhhhtcccchtccthhhhhhhhhhhhhttcceeeehcccccc
GYEFLEILKQVARDNTDNPDLISLWIDPDDFPLLVAYWEKTFKIDLFRPQIGVVNVTADADSVWMEIPDDD
chhhhhhhhhhhhtcccccteeeeectttceeehhthteeeecctteeeeeecttceeeeccttt
DLPTAEELDWIEDVLSGKINTEDDDEDDDDDDNSDEEDNDDSDDDDE
ccccchhhhhhhhhhhhtccccccccccccccccccccccccccccchhh
  
```

SOPMA :

Alpha helix	(Hh) :	178 is	44.61%
3 ₁₀ helix	(Gg) :	0 is	0.00%
Pi helix	(Ii) :	0 is	0.00%
Beta bridge	(Bb) :	0 is	0.00%
Extended strand	(Ee) :	65 is	16.29%
Beta turn	(Tt) :	42 is	10.53%
Bend region	(Ss) :	0 is	0.00%
Random coil	(Cc) :	114 is	28.57%
Ambiguous states (?)	:	0 is	0.00%
Other states	:	0 is	0.00%



Physicochemical property analysis



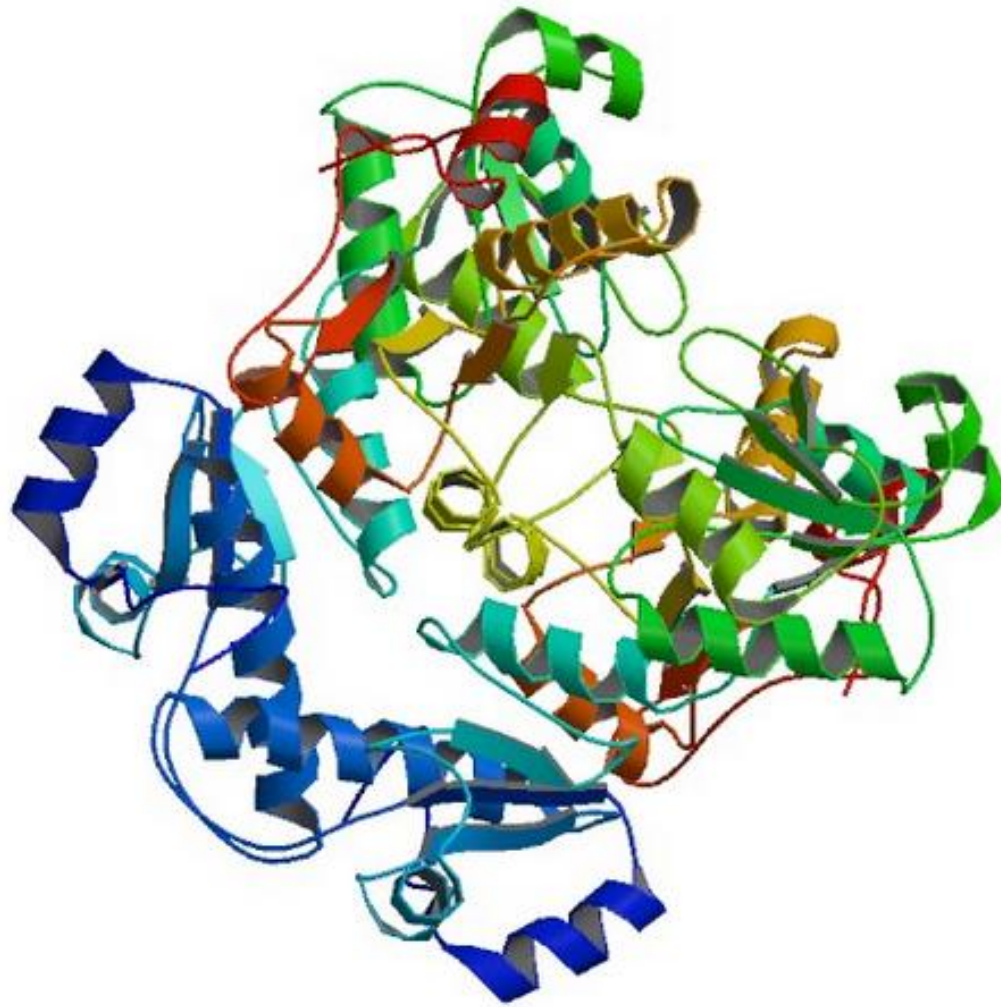
Theoretical pI/Mw (average) for the user-entered sequence:

```
      10      20      30      40      50      60
MKRTHLFIVG IYFLSSCRAE EGLNFPTYDG KDRVVSLSEK NFKQVLKKYD LLCLYYHEPV
      70      80      90     100     110     120
SSDKVTQKQF QLKEIVLELV AQVLEHKAIG FVMVDAKKEA KLAKKLGFD EGSLYILKGD
      130     140     150     160     170     180
RTIEFDGEFA ADLVEFLLD LIEDPVEIIS SKLEVQAFER IEDYIKLIGF FKSEDSEYYK
      190     200     210     220     230     240
AFEEAAEHFQ PYIKFFATFD KGVAKKLSLK MNEVDFYEPF MDEFIAIPNK PYTEEELVEF
      250     260     270     280     290     300
VKEHQRPCLR RLRPEEMFET WEDDLNGIHI VAFAEKSDPD GYEFLEILKQ VARDNTDNPD
      310     320     330     340     350     360
LSILWIDPDD FPLLVAYWEK TFKIDLFRPQ IGVVNVTDAD SVWMEIPDD DLPTAEELED
      370     380     390
WIEDVLSGKI NTEDDDEDDD DDDNSDEEDN DDSDDDDDE
```

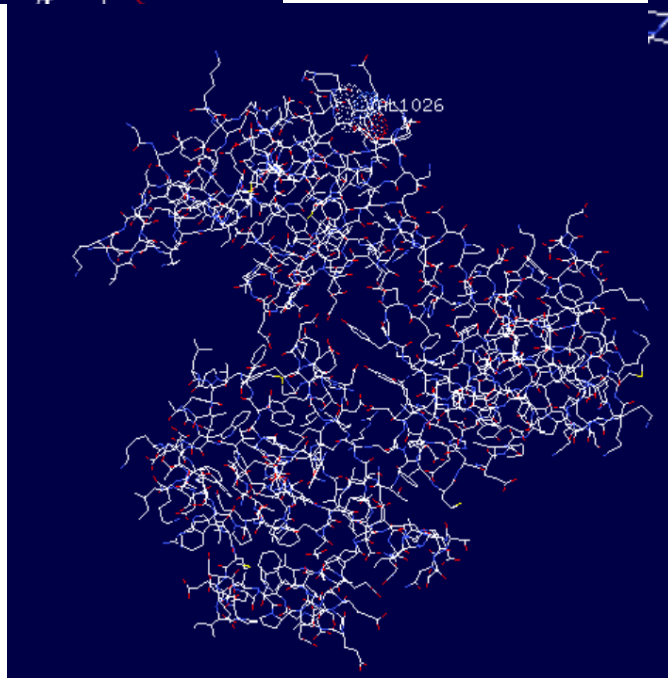
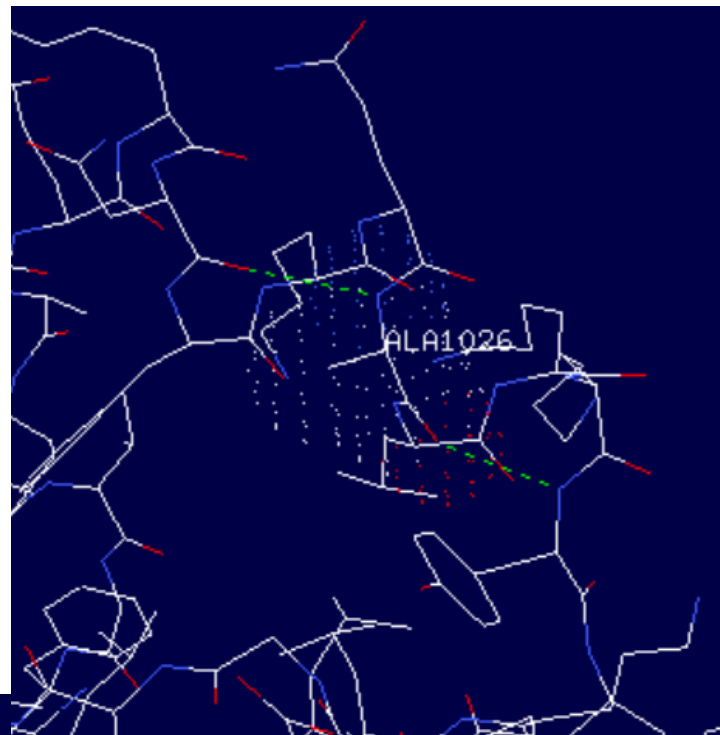
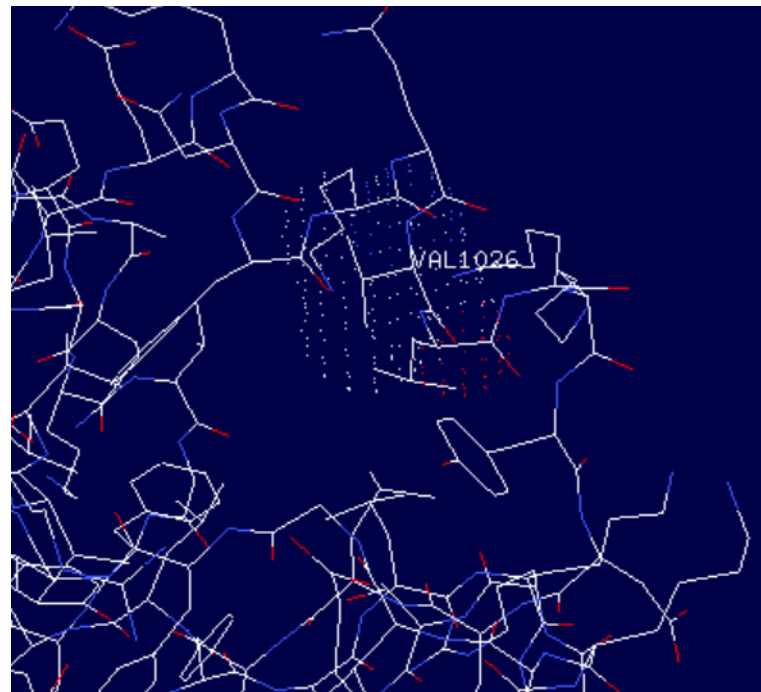
Theoretical pI/Mw: 4.21 / 46435.79

<http://web.expasy.org/compute>
<http://www.cbs.dtu.dk/services/TMHMM/>

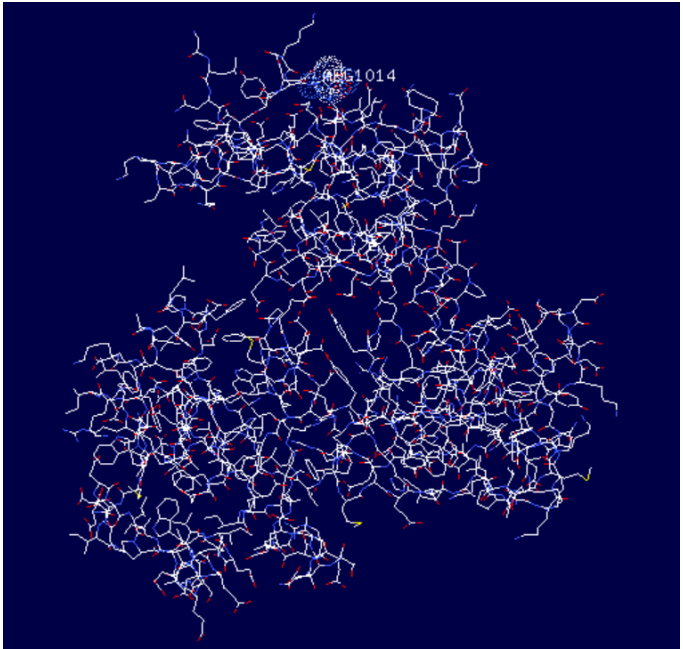
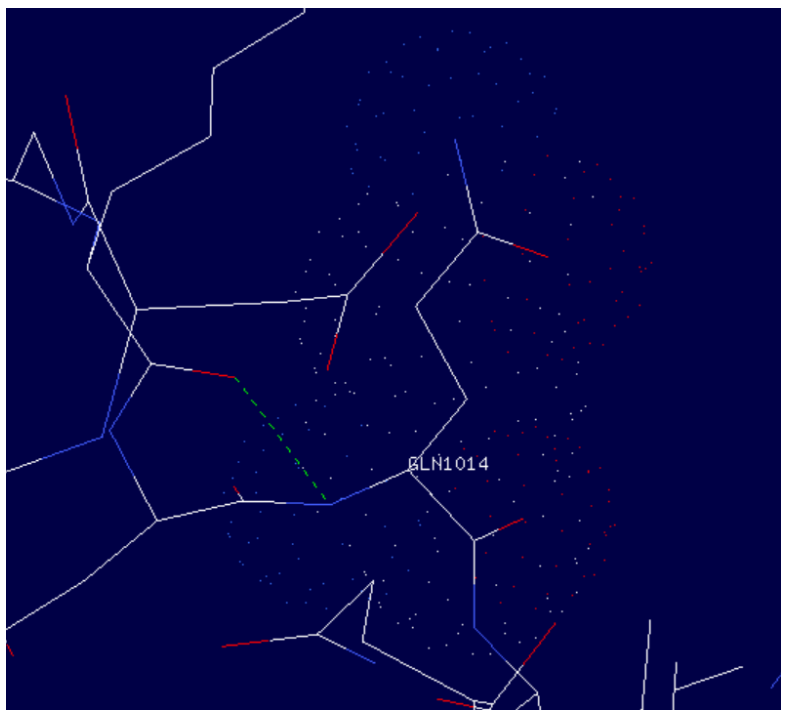
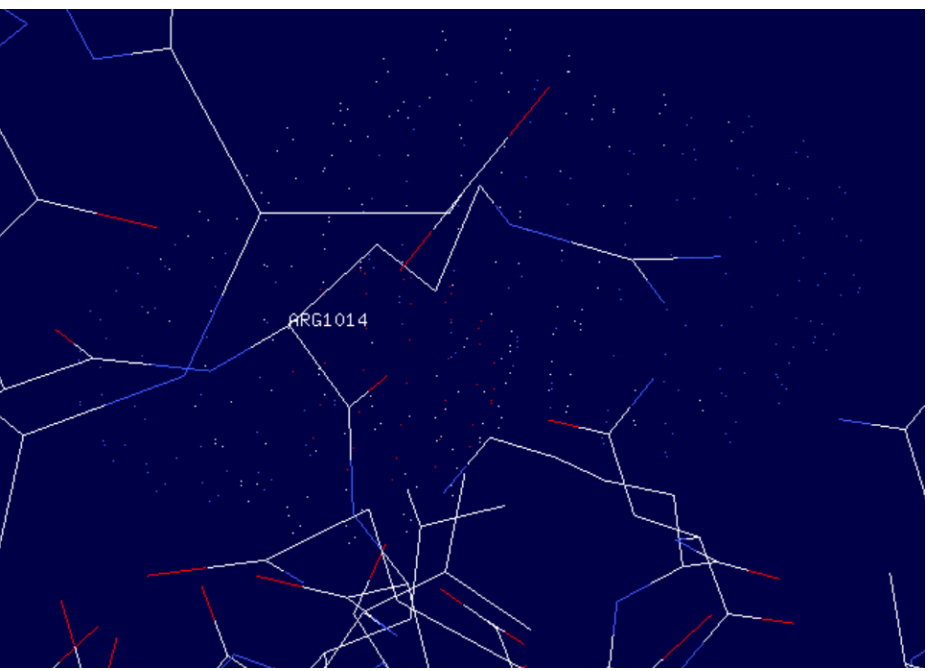
3D Structure



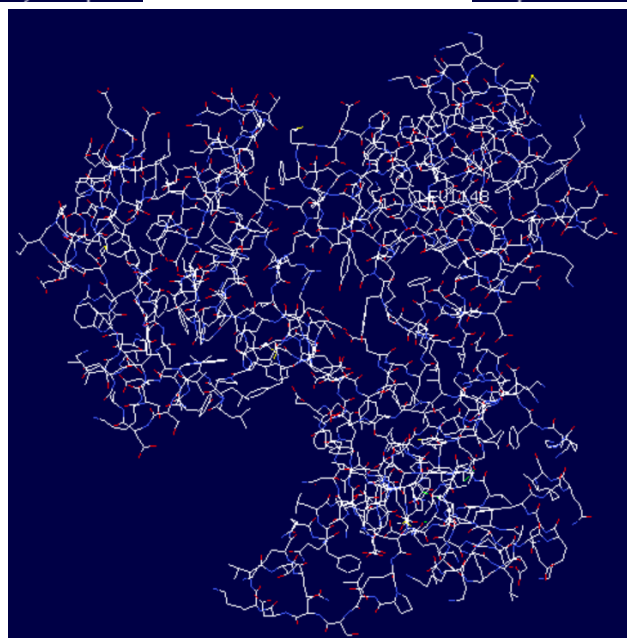
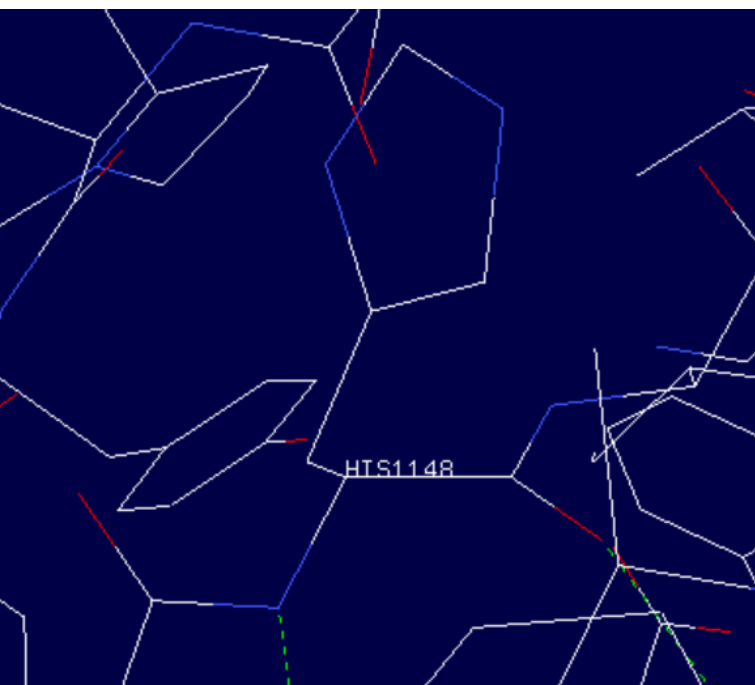
V47A



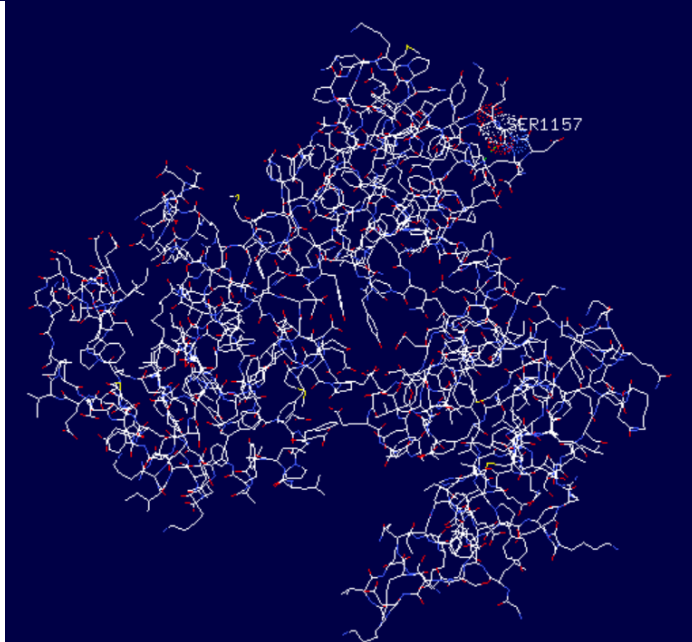
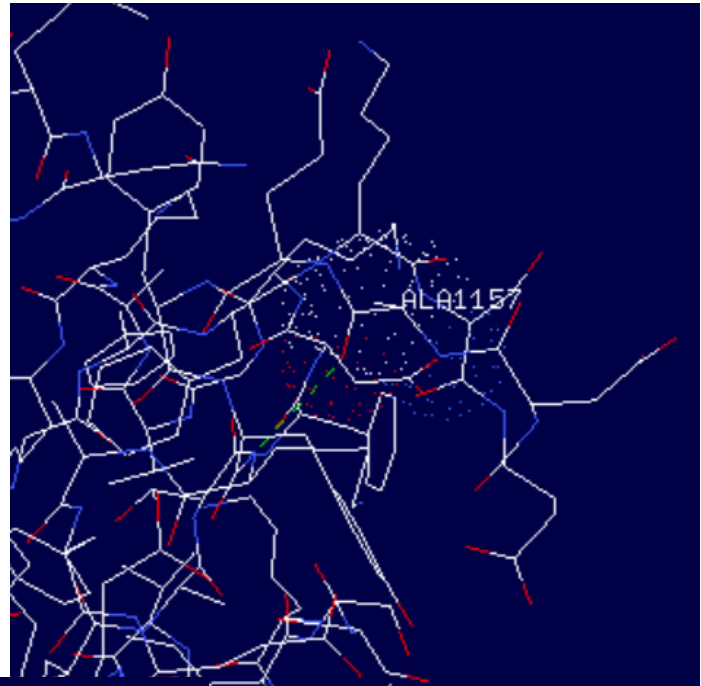
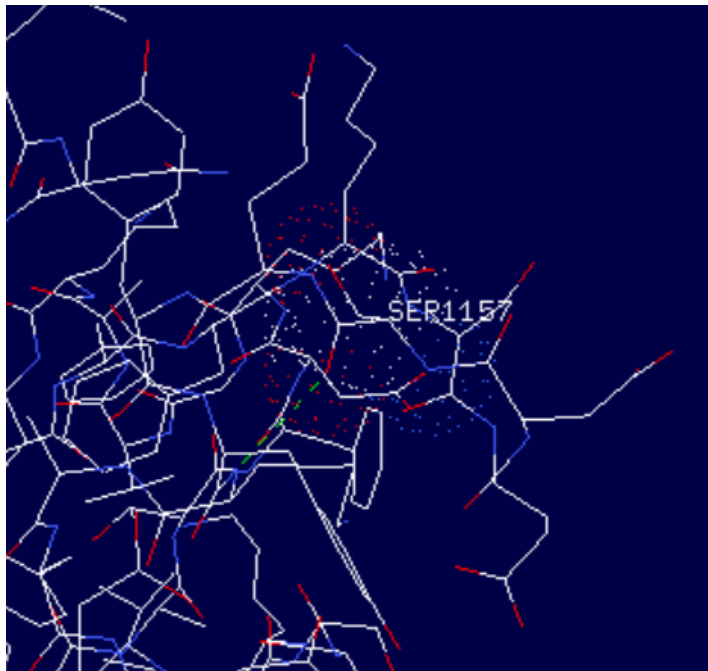
R33Q



L167H



S176A



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Professor Luo
Shiqiang Wang
Xuexin Fan
Peixue Xia
Jiechun Yang
Lejiao Ren

Thanks!