



# 鸟嘌呤核苷酸结合蛋白(NOG2)的分析 Analysis of Nucleolar GTP-binding protein 2

郑吕钦 宋婧 王曼柳 王晓彤  
周昕禹 车瑞 朱丹 廖礼铭 朱文苑

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# 故事起源-NOG2蛋白结构的解析

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Letter

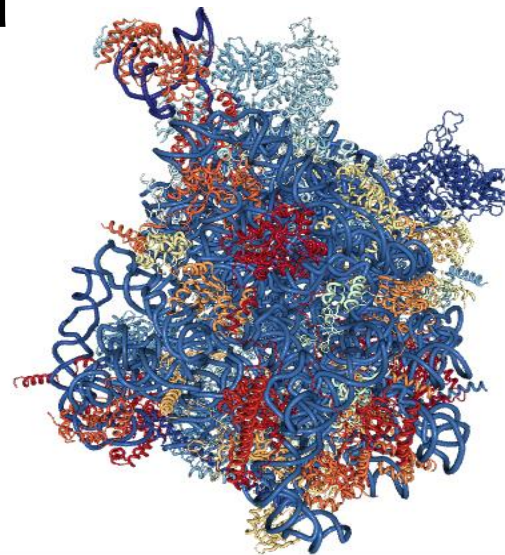
## Diverse roles of assembly factors revealed by structures of late nuclear pre-60S ribosomes

Shan Wu, Beril Tutuncuoğlu, Kaige Yan, Hailey Brown, Yixiao Zhang, Dan Tan, Michael Gamalinda, Yi Yuan, Zhifei Li, Jelena Jakovljevic, Chengying Ma, Jianlin Lei, Meng-Qiu Dong, John L. Woolford & Ning Gao

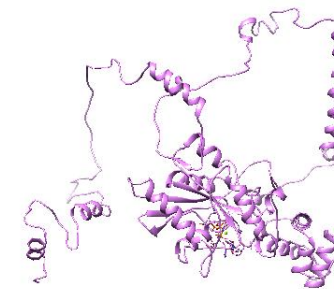
*Nature* 534, 133–137 (02 June 2016)  
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Cryo-electron microscopy Ribosome  
Ribozymes RNA RNA transport



60S ribosomes



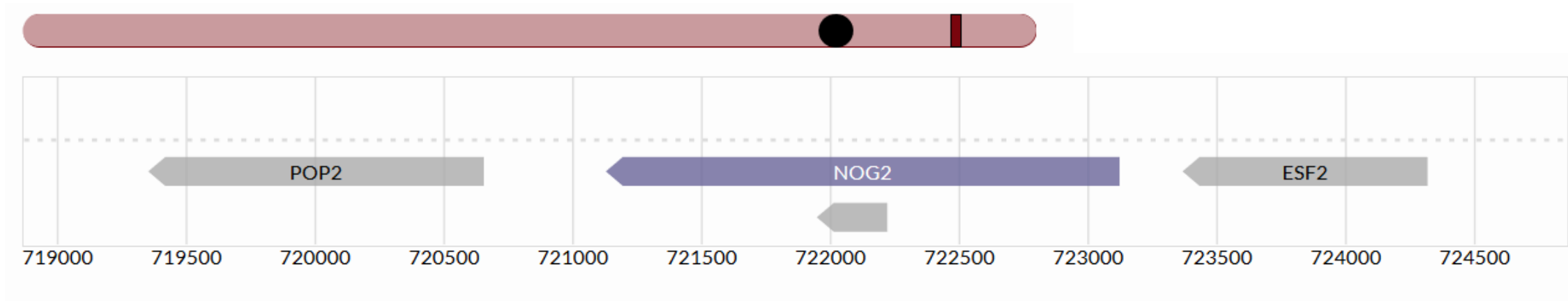
NOG2

- 高宁实验室在2016年解析出酵母核糖体蛋白NOG2结构
- 人源NOG2结构还未解出
- 通过使用生物信息课学到的相关知识初步解读NOG2蛋白的相关信息



# NOG2 基因信息以及氨基酸序列

NOG2 定位在14号染色体的 721120..723112



MGTGKKEKSRRIREGDTKDG NLRVKGENFYRDSKRVKFLNMYTSGKEIRNKKGNLIRAAS  
FQDSTIPDARVQPDRRWF GNTRV ISQDALQHFRSALGETQKDTYQVLLRRNKLPM S LLEE  
KDADESPKARILDTE SYADAFGPKAQRKR PRLAASNLEDLVKATNEDITKYEEKQVLDAT  
LGLMGNQEDKENGWTSAAKEAIFSKGQSKRIWNEL YKVIDSSDVV IHVLDARDPLGTRCK  
SVEEYMKKETPHKHLIYVLNKCDLVPTWVAAA WVKHLSKERPTLAFHASITNSFGKGLI  
QLLRQFSQLHTDRKQISVGFIGYPNTGKSSIINTLRKKKVCQVAPIPGETKVVWQYITLMK  
RIFLIDCPGIVPPSSKDSEEDILFRGVVRVEHVTHPEQYIPGVLKRCQVKHLERTYEISG  
WKDATEFIEILARKQGRLLKGGEPDESGVSKQILNDFNRGKIPWFVLPPEKEGEEKPKKK  
EVEKTA

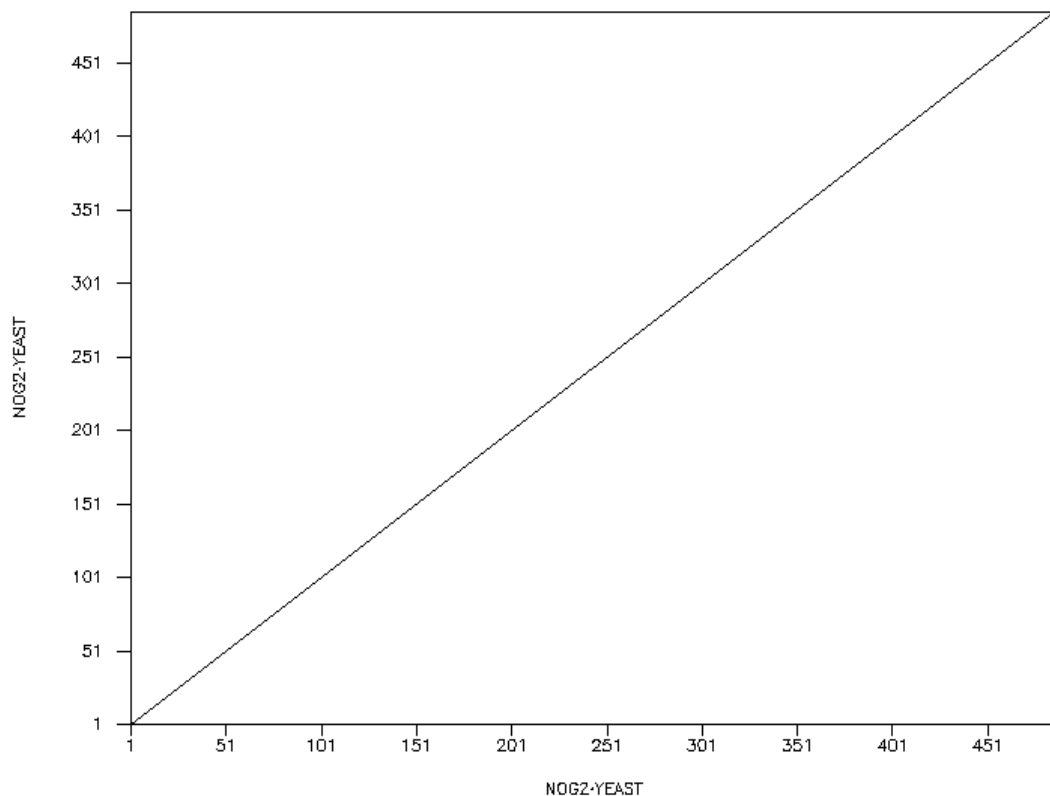
共由486个氨基酸组成，  
55.49KD大小

NOG2p定位在生物体  
内的核仁和核质上



# 运用WebLab进行重复序列分析

Dottup: fasta::1035699:NOG2-YEAST vs fasta::1035700:NOG2...  
Fri 5 Jan 2018 23:36:45



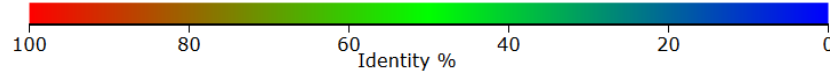
- 【Tool】 WebLab-Dottup
- 【Parameter】 default
- Dottup 是精确匹配，两个序列比对中，word size 内精确匹配时以图上的点表示，匹配程度较高时适用，重复匹配
- DotMatcher 是近似匹配，用给定的计分矩阵对window size 内的序列进行打分，高于threshold 的在图上以点显示，可用于匹配程度不高的两个序列，重复匹配
- DotPath 与Dottup 相似，是word size 内的精确匹配，但不进行重复匹配。

✓该蛋白不含重复序列

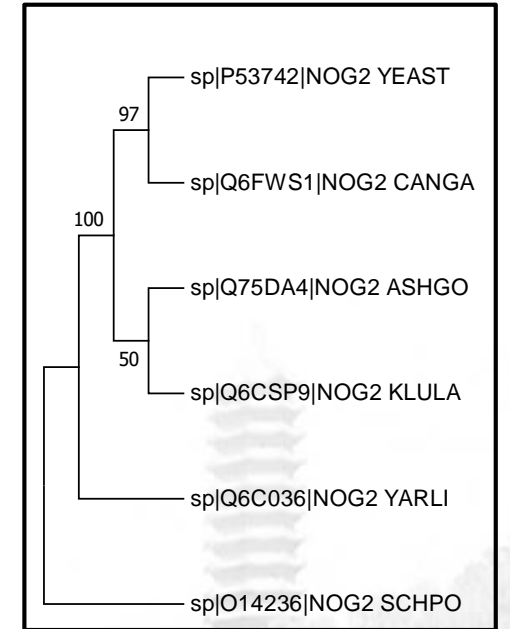


# Blast 酵母NOG2蛋白序列

- 运用UniProt数据库对酵母NOG2进行blast，得到250条相似序列，reviewed 6条如下；
- 其中100%一条是自己，其他均为其他物种的NOG2，说明高度保守；



Entry	Alignment overview	Info	Status
<input type="checkbox"/> Query: sp P53742 NOG2_YEAST B20180109ACFE4208EAF842A78A1B3BA7138A93D996171Q			
<input type="checkbox"/> P53742	NOG2_YEAST - Nucleolar GTP-binding protein 2 - <i>Saccharomyces ce...</i> - View alignment 	E-value: 0.0 Score: 2,533 Ident.: 100.0%	
<input type="checkbox"/> Q6FWS1	NOG2_CANGA - Nucleolar GTP-binding protein 2 - <i>Candida glabrata...</i> - View alignment 	E-value: 0.0 Score: 2,268 Ident.: 88.6%	
<input type="checkbox"/> Q75DA4	NOG2_ASHGO - Nucleolar GTP-binding protein 2 - <i>Ashbya gossypii ...</i> - View alignment 	E-value: 0.0 Score: 2,118 Ident.: 82.4%	
<input type="checkbox"/> Q6CSP9	NOG2_KLULA - Nucleolar GTP-binding protein 2 - <i>Kluyveromyces la...</i> - View alignment 	E-value: 0.0 Score: 2,112 Ident.: 82.0%	
<input type="checkbox"/> Q6C036	NOG2_YARLI - Nucleolar GTP-binding protein 2 - <i>Yarrowia lipolyt...</i> - View alignment 	E-value: 0.0 Score: 1,824 Ident.: 71.9%	
<input type="checkbox"/> O14236	NOG2_SCHPO - Nucleolar GTP-binding protein 2 - <i>Schizosaccharomy...</i> - View alignment 	E-value: 0.0 Score: 1,607 Ident.: 66.4%	

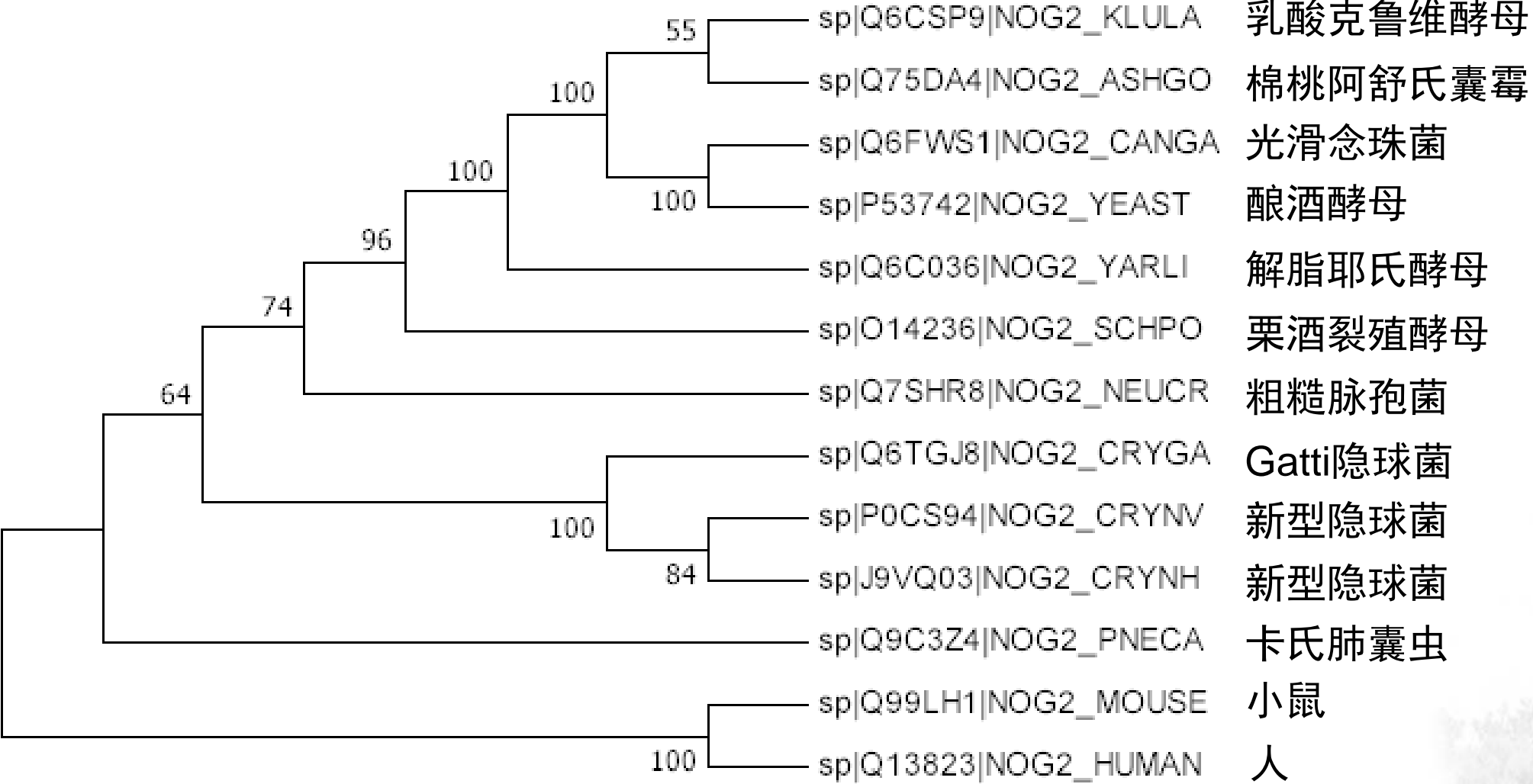


# NOG2家族

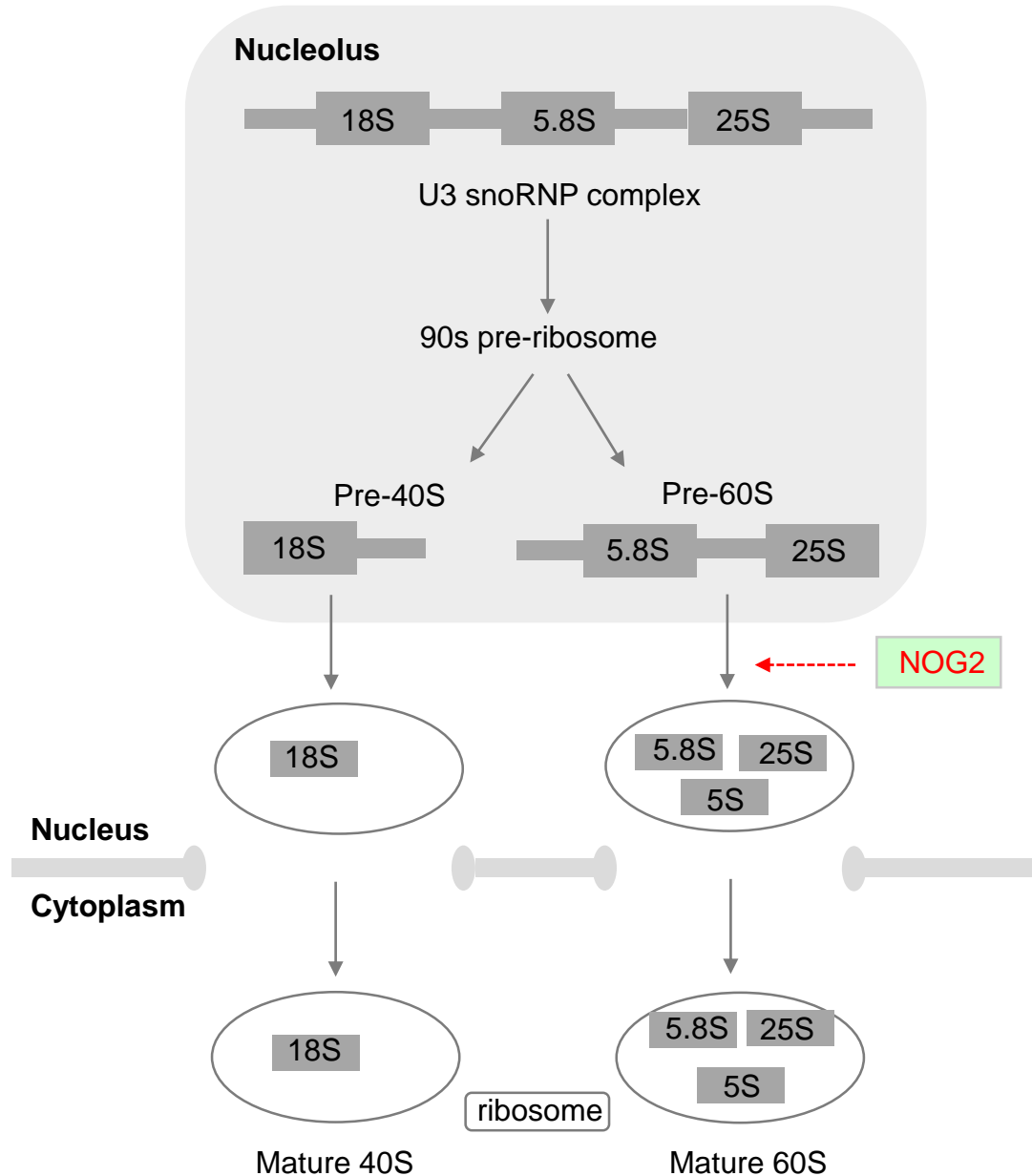
- 酵母NOG2属于TRAFAC class YlqF/YawG GTPase 大家族和NOG2 亚家族
- NOG2亚家族在UniProt数据库里reviewed共有13个成员

编号	物种	uniprot登录号	蛋白长度	Domain	Nucleotide binding位点
NOG2_CRYNV	<i>Cryptococcus neoformans var. grubii</i> 新型隐球菌	P0CS94	693	198-359	308-315; 352-356
NOG2_PNECA	<i>Pneumocystis carinii</i> 卡氏肺囊虫	Q9C3Z4	483	189-350	299-306; 343-347
NOG2_YARLI	<i>Yarrowia lipolytica</i> 解脂耶氏酵母	Q6C036	509	204-365	314-321; 358-362
NOG2_KLULA	<i>Kluyveromyces</i> 乳酸克鲁维酵母	Q6CSP9	513	211-372	321-328; 365-369
NOG2_MOUSE	<i>Mus musculus</i> 鼠	Q99LH1	728	207-368	317-324; 361-365
NOG2_ASHGO	<i>Ashbya gossypii</i> 棉桃阿舒氏囊霉	Q75DA4	502	211-372	321-328; 365-369
NOG2_CRYGA	<i>Cryptococcus gatti</i> Gatti隐球菌	Q6TGJ8	731	223-396	345-352; 389-393
NOG2_CANGA	<i>Candida glabrata</i> 光滑念珠菌	Q6FWS1	494	212-373	322-329; 366-370
NOG2_CRYNH	<i>Cryptococcus neoformans var. grubii</i> serotype A新型隐球菌	J9VQ03	720	225-386	335-342; 379-383
NOG2_HUMAN	<i>Homo sapiens</i> 人	Q13823	731	207-368	317-324; 361-365
NOG2_NEUCR	<i>Neurospora crassa</i> 粗糙脉孢菌	Q7SHR8	619	222-383	332-339; 376-380
NOG2_SCHPO	<i>Schizosaccharomyces pombe</i> 栗酒裂殖酵母	O14236	537	207-368	317-324; 361-365
NOG2_YEAST	<i>Saccaromyces cerevisiae</i> 酿酒酵母	P53742	486	212-373	322-329; 366-370

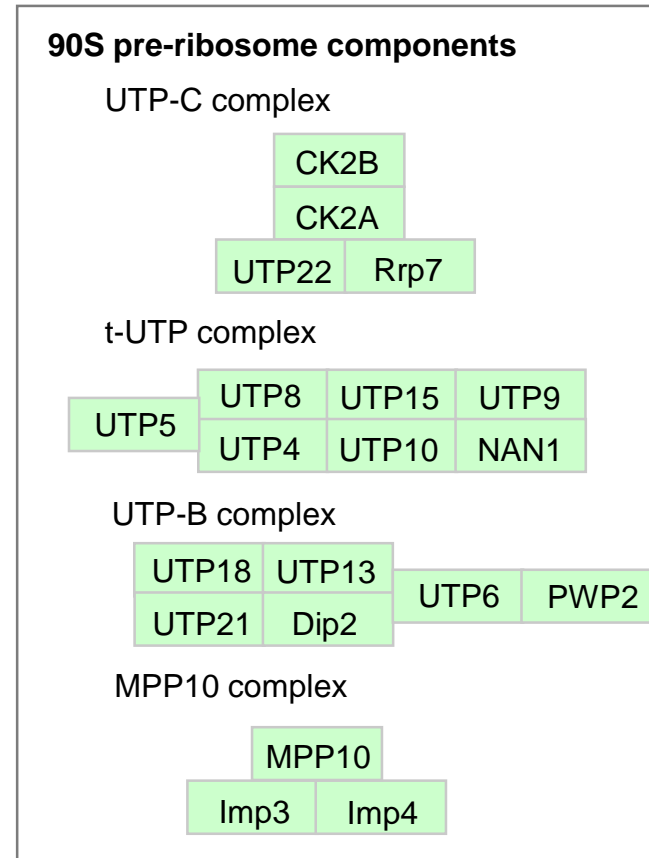
# 最优化后的NOG2建树



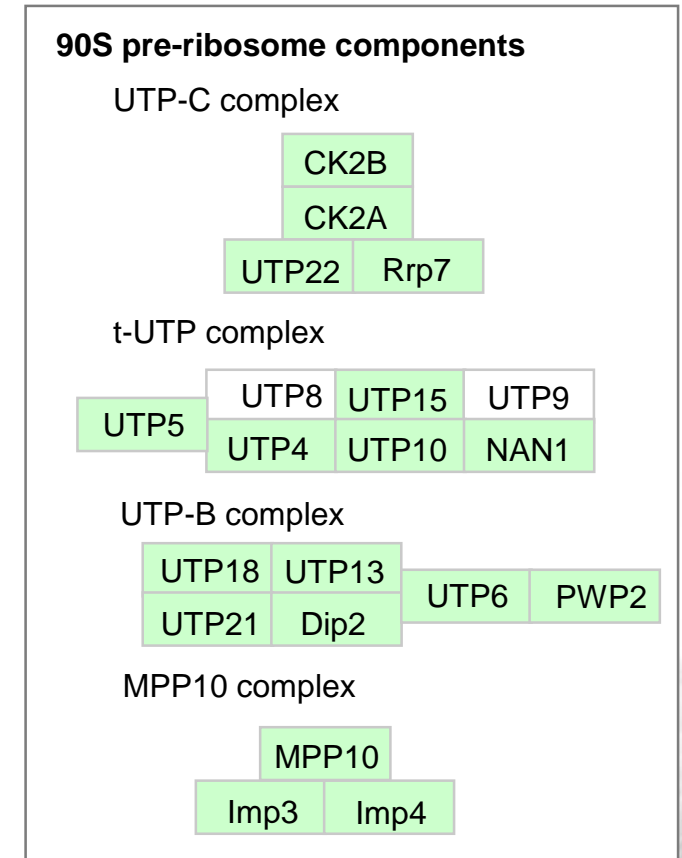
# KEGG 通路—核糖体生物机理



## Yeast NOG2



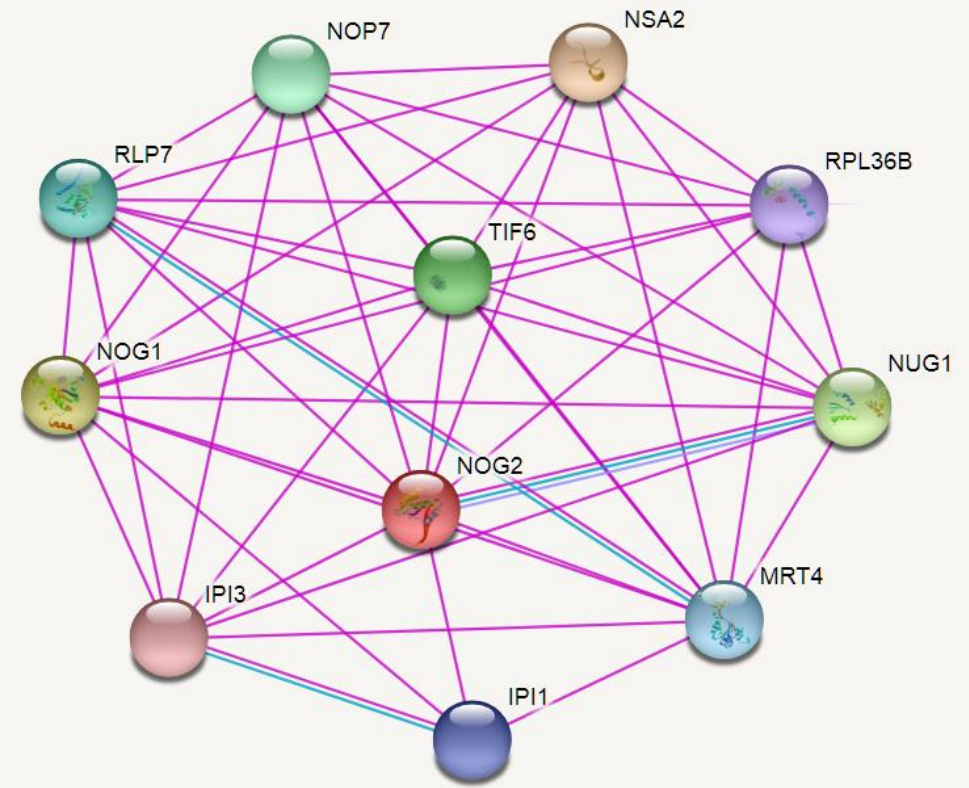
## Human NOG2



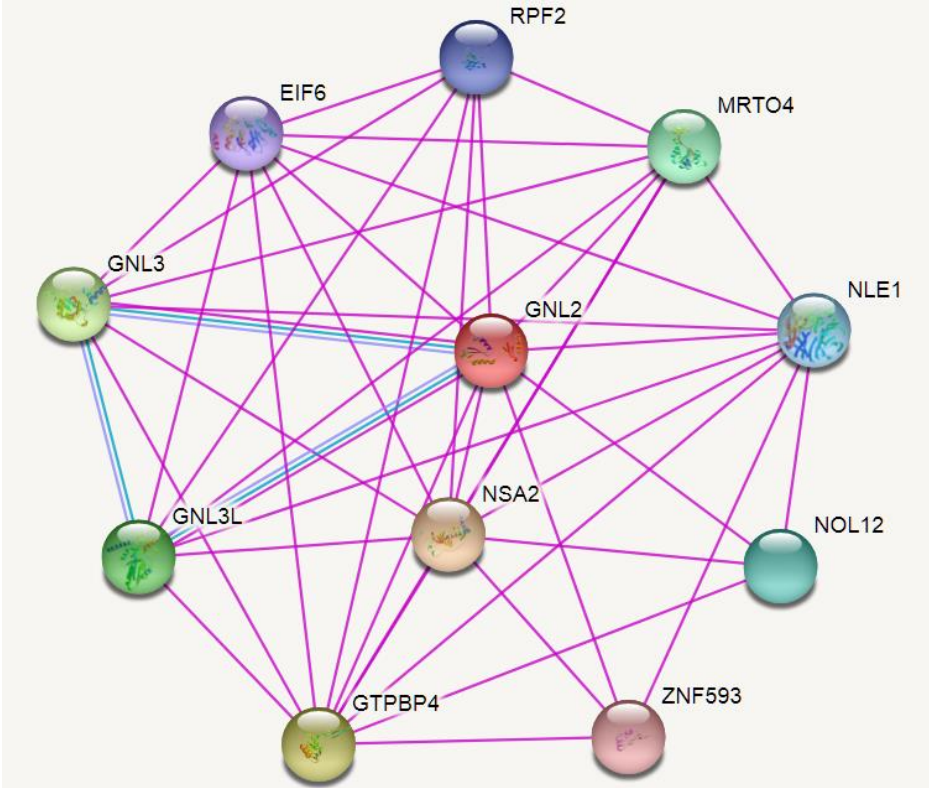


# 蛋白相互作用信息

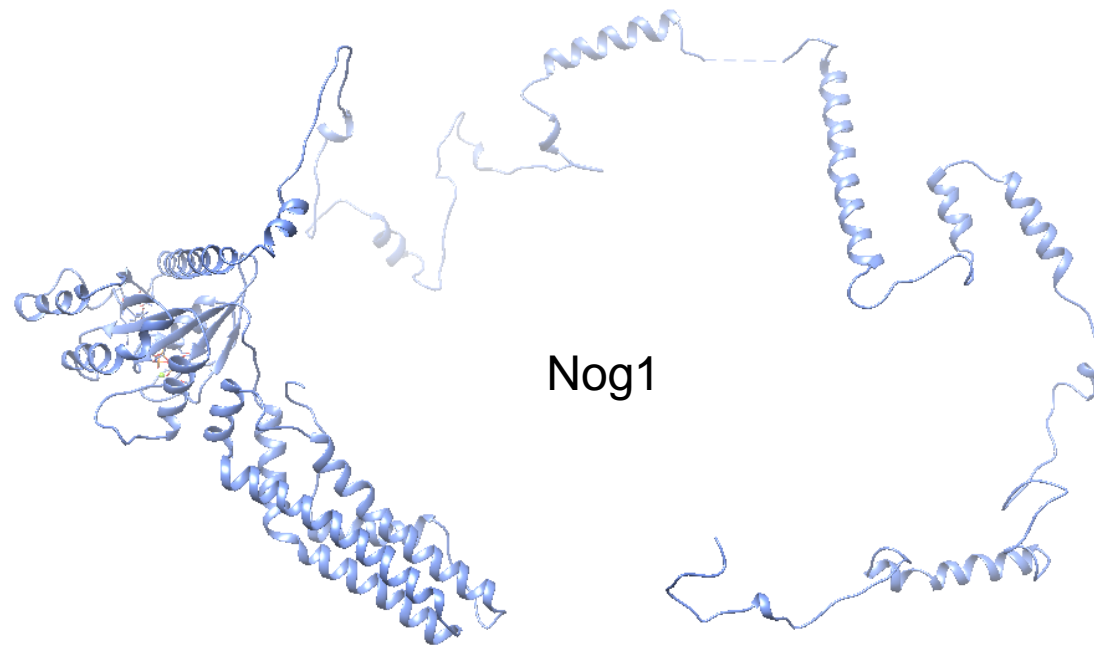
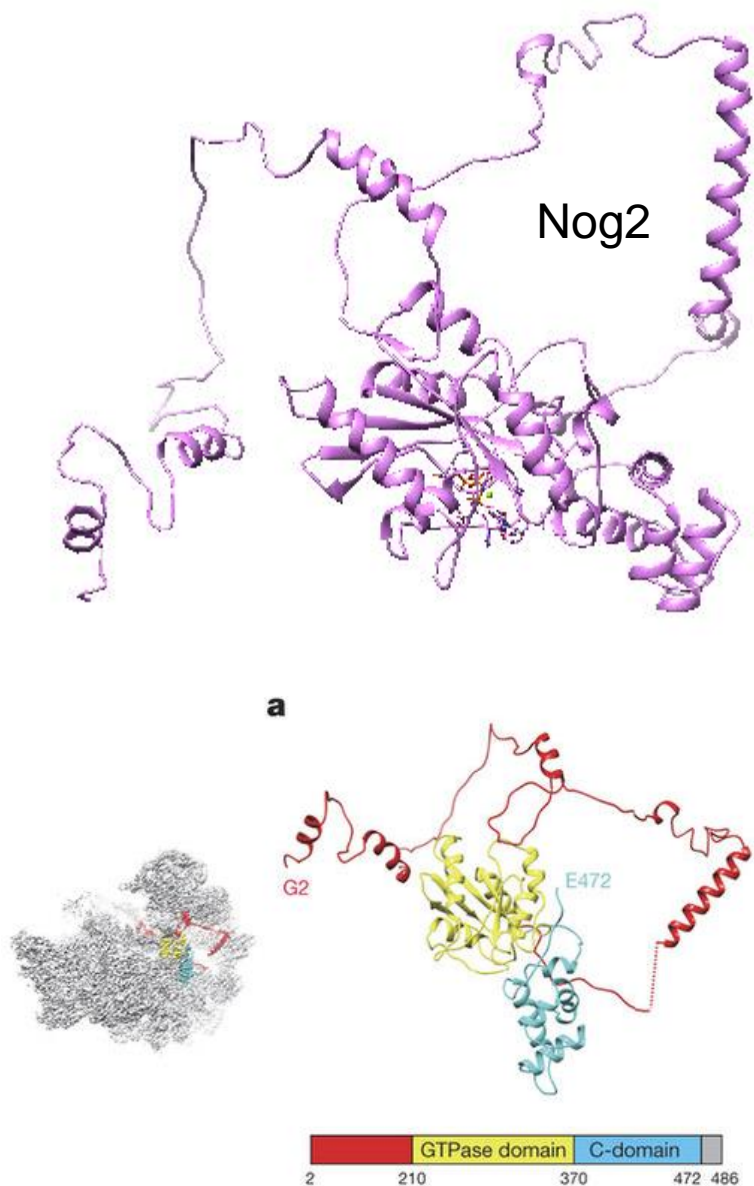
## Yeast NOG2



## Human NOG2

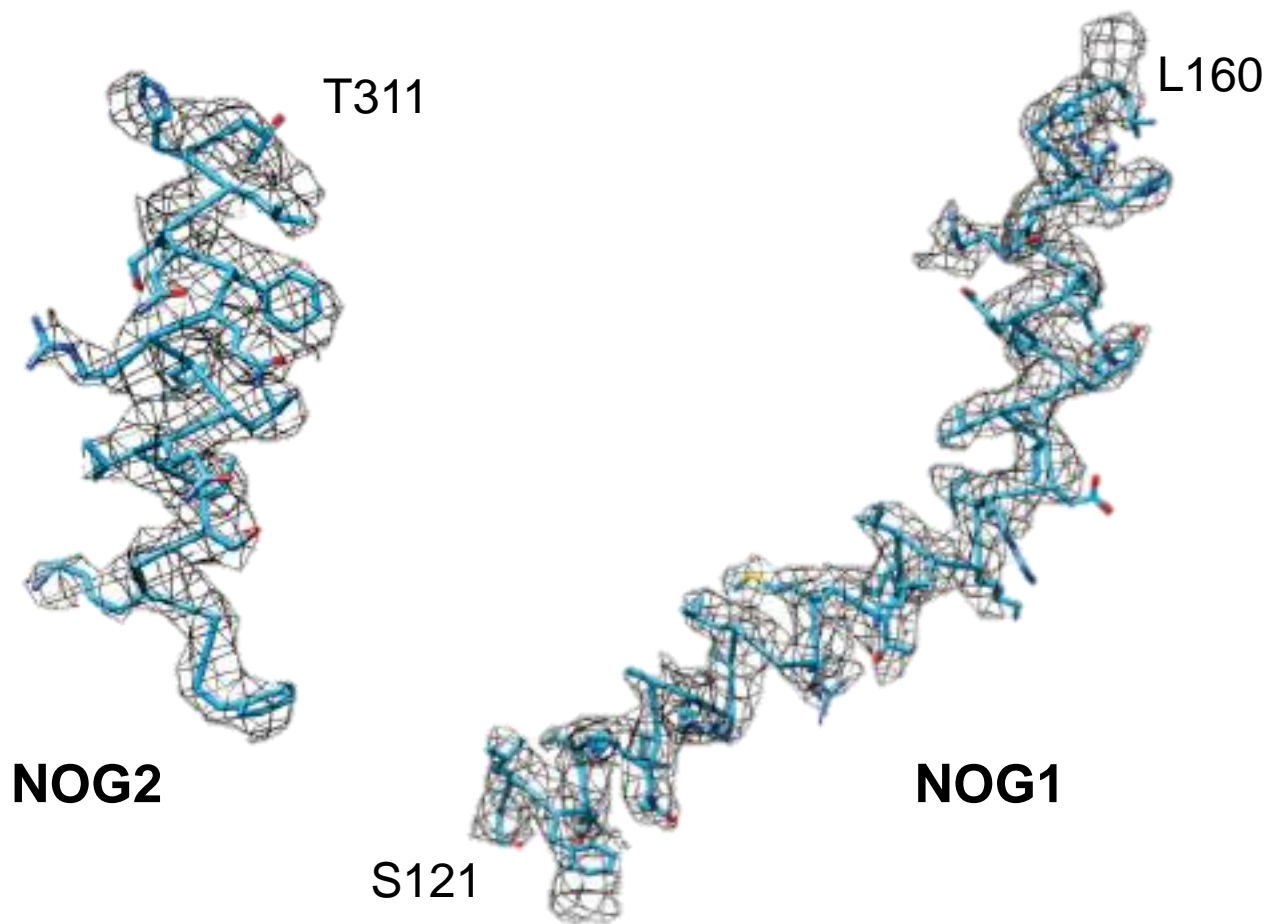


# 原子模型组装结构-NOG2



- NOG2主要结构域可分为三大部分，GTPase结构域，羧基（C）-末端结构域与多螺旋连接结构域。

# 酵母NOG2-冷冻电镜密度图



- 通过碱基互补配对原则搭建模型

- NOG2是一种重要的GTP酶，
- 与Nog1一同作为中枢蛋白与多个远处的装配因子和功能性核糖体RNA元件相互作用。



# 酵母NOG2和人NOG2序列比对

54.78%  
57.81%

Target	MVKPKYKGRSTINPSKASTNPDRVQAGGQNM-RDRATIRRLNMYRQ-KERRNSRGKIIKPLQYQ-STVASGTVARVEPNIKWFG	82
3jct.1.c	--KKEKSRRIREGD--TKDGNLRVKG--ENFY-RDSKRVKFLNMYTSGKEIRNKKGNLIRAASFQ-DSTIPD--ARVQPD RRWFG	79
3jct.1.c	-----GENFYRDSKRVKFLNMYTSGKEIRNKKGNLIRAASFQDSTIPD--ARVQPD RRWFG	79
Target	NTRVIKQSSSLQKFQEEMDTVMKDPYKVVVKQSKLPMSLLHDIRPHNLKVHILDIESFETTFGPKSQRKRPNLFASDMQSLIENA	167
3jct.1.c	NTRVISQDALQHFRSALGETQKDTYQVLLRRNKLPMSSLLEEKDADESPKARILDIESYADAFGPKAQRKRPRLAASNLEDLVKAT	164
3jct.1.c	NTRVISQDALQHFRSALGETQKDTYQVLLRRNKLPMSSLLEEKDADESPKARILDIESYADAFGPKAQRKRPRLAASNLEDLVKAT	164
Target	EMSTESYDQGKDRDL-----VT-----EDTGVRNAEQEEIYKKGQSKRIWGELYKVIDSSDVVVQVLDARDPMGTRSPH	236
3jct.1.c	NEDITKYEEKQVLDATLGLMGNQED-----KENGWTSAAKEAIFSKGQSKRIWNELYKVIDSSDVVIHVLDARDPLGTRCKS	241
3jct.1.c	NEDITKYEEKQVLD-----TLGLMGNQEDKENGWTSAAKEAIFSKGQSKRIWNELYKVIDSSDVVIHVLDARDPLGTRCKS	241
Target	IETYLKKEKPKWHLIFVLNKC DLVPTWATKRVAVLSQDYPTLAFHASLTNPFPGKAFIQLLRQFGKLHTDKKQISVGFYGPNT	321
3jct.1.c	VEEYMKKETPHKHLIYVLNKC DLVPTWAAA VVKHLSKERPTLAFHASITNSFGKGS LIQLLRQFSQLHTDRKQISVGFYGPNT	326
3jct.1.c	VEEYMKKETPHKHLIYVLNKC DLVPTWAAA VVKHLSKERPTLAFHASITNSFGKGS LIQLLRQFSQLHTDRKQISVGFYGPNT	326
Target	GKSSVINTLRSKKVCNVAPIAGETKVVQYITLMRRIFLIDCPGVVYP-SE-DSETDIVLKGVVQVEKIKSPEDHIGAVLERAKPE	404
3jct.1.c	GKSSIINTLRKKKVCQVAPIPGETKVVQYITLMKRIFLIDCPGIVPP-SSKDSEEDILFRGVVVRVEHVTHPEQYIPGVLRQCQVK	410
3jct.1.c	GKSSIINTLRKKKVCQVAPIPGETKVVQYITLMKRIFLIDCPGIVPPSSK-DSEEDILFRGVVVRVEHVTHPEQYIPGVLRQCQVK	410
Target	YISKTYKIDSWENAEDFLEKLA FRTGKLLKGGE PDLQTVGKMVLNDWQRGRIPFFVKPPNAEPLVAPQLLPSSSLEVVEAAQNN	489
3jct.1.c	HLERTYEISGWKDATEFIEILARKQGRLLKGGE PDES <sup>G</sup> VS <sup>K</sup> QILNDFNRGKIPWFVLPPEKEGE-----	474
3jct.1.c	HLERTYEISGWKDATEFIEILARKQGRLLKGGE PDES <sup>G</sup> VS <sup>K</sup> QILNDFNRGKIPWFV-----	466
Target	PGEEVTETAGEGSESIKEETEENSHCDANTEMQQILTRVRQNFQKINVVPPQFSGDDLVPVEVSDLEEELESFSDEEEEEEQEQQR	574
3jct.1.c	-----	
3jct.1.c	-----	
Target	DDAEESSEPEEENVGNDTKAVIKALDEKIAKYQKFLDKAKAKKFSAVRISKGLSEKIFAKPEEQRTLEEDVDDRAPS <sup>K</sup> KGK <sup>K</sup> R	659
3jct.1.c	-----	
3jct.1.c	-----	
Target	KAQREEEQEHSNKAPRALTSKERRRAVRQQRPKKVGVRYYETHNVKNNRNKKKINDSEGQKHKKR <sup>K</sup> KFR <sup>K</sup> Q <sup>K</sup>	731
3jct.1.c	-----	
3jct.1.c	-----	

人的NOG2蛋白在C端多200bp的序列



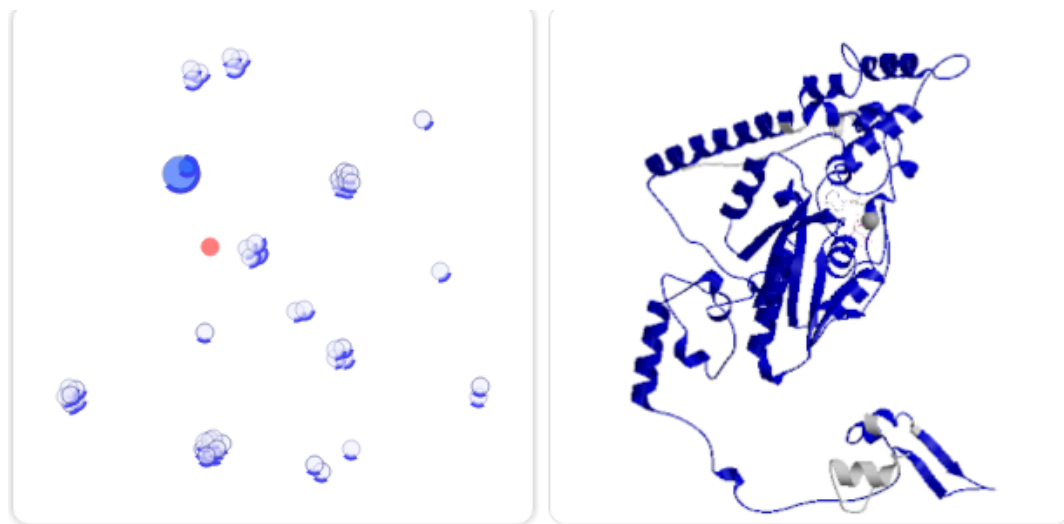
# 人源NOG2蛋白预测模板

Templates		Quaternary Structure	Sequence Similarity	Alignment of Selected Templates	More ▾	
◆ Name ◆	Title	◆ Coverage ◆	◆ Identity ◆	◆ Method ◆	◆ Oligo State ◆	Ligands
<input checked="" type="checkbox"/> <input checked="" type="checkbox"/> <input checked="" type="checkbox"/> <b>3jct.1.c</b>	Nucleolar GTP-binding protein 2		54.78	EM	hetero-54-mer $\Delta$	2 x GTP , 4 x ZN 2 x MG
<input checked="" type="checkbox"/> <input checked="" type="checkbox"/> <b>3jct.1.c</b>	Nucleolar GTP-binding protein 2		57.81	EM	hetero-54-mer $\Delta$	2 x GTP , 4 x ZN 2 x MG
<input type="checkbox"/> <b>3cnn.1.A</b>	Putative uncharacterized protein		34.51	X-ray, 2.3Å	monomer ✓	1 x GTP
<input type="checkbox"/> <b>3cno.1.A</b>	Putative uncharacterized protein		34.51	X-ray, 2.3Å	monomer ✓	1 x GDP
<input type="checkbox"/> <b>3cni.1.A</b>	Putative uncharacterized protein		34.51	X-ray, 2.0Å	monomer ✓	1 x GNP
<input type="checkbox"/> <b>3cno.1.A</b>	Putative uncharacterized protein		25.63	X-ray, 2.3Å	monomer ✓	1 x GDP
<input type="checkbox"/> <b>3cni.1.A</b>	Putative uncharacterized protein		25.63	X-ray, 2.0Å	monomer ✓	1 x GNP
<input type="checkbox"/> <b>3cnn.1.A</b>	Putative uncharacterized protein		25.63	X-ray, 2.3Å	monomer ✓	1 x GTP
<input type="checkbox"/> <b>2rcn.1.A</b>	Probable GTPase engC		19.52	X-ray, 2.2Å	monomer ✓	1 x GDP , 1 x ZN 1 x MG
<input type="checkbox"/> <b>5uz4.1.U</b>	Small ribosomal subunit biogenesis GTPase RsgA		20.00	EM	hetero-20-mer $\Delta$	1 x GGM , 1 x ZN 
<input type="checkbox"/> <input checked="" type="checkbox"/> <b>5no2.1.S</b>	Small ribosomal subunit biogenesis GTPase RsgA		20.00	EM	hetero-18-mer $\Delta$	6 x MG , 1 x ZN , 1 x GNP
<input type="checkbox"/> <b>2ykr.1.V</b>	PUTATIVE RIBOSOME BIOGENESIS GTPASE RSGA		19.05	EM, 9.8Å	hetero-21-mer $\Delta$	None

## 60S ribosomal protein L4-A



# 基于酵母NOG2预测人NOG2结构



SMTL ID **3jct.1.c**

Title Nucleolar GTP-binding protein 2

Coverage

Identity 57.81

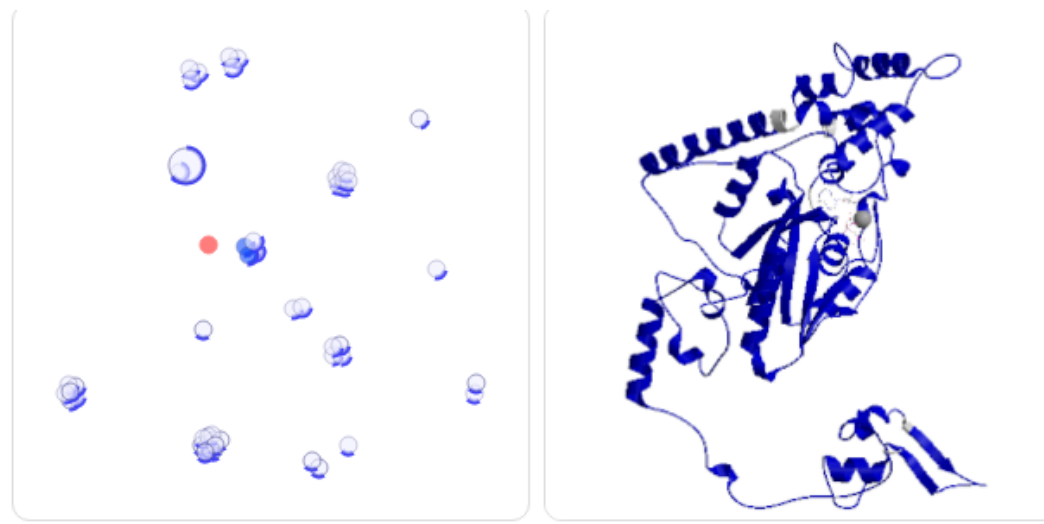
Similarity 0.47

Ligands 2 x GTP4 x ZN2 x MG

Method EM 0.00Å

Oligo State monomer

Found By BLAST



SMTL ID **3jct.1.c**

Title Nucleolar GTP-binding protein 2

Coverage

Identity 54.78

Similarity 0.46

Ligands 2 x GTP4 x ZN2 x MG

Method EM 0.00Å

Oligo State monomer

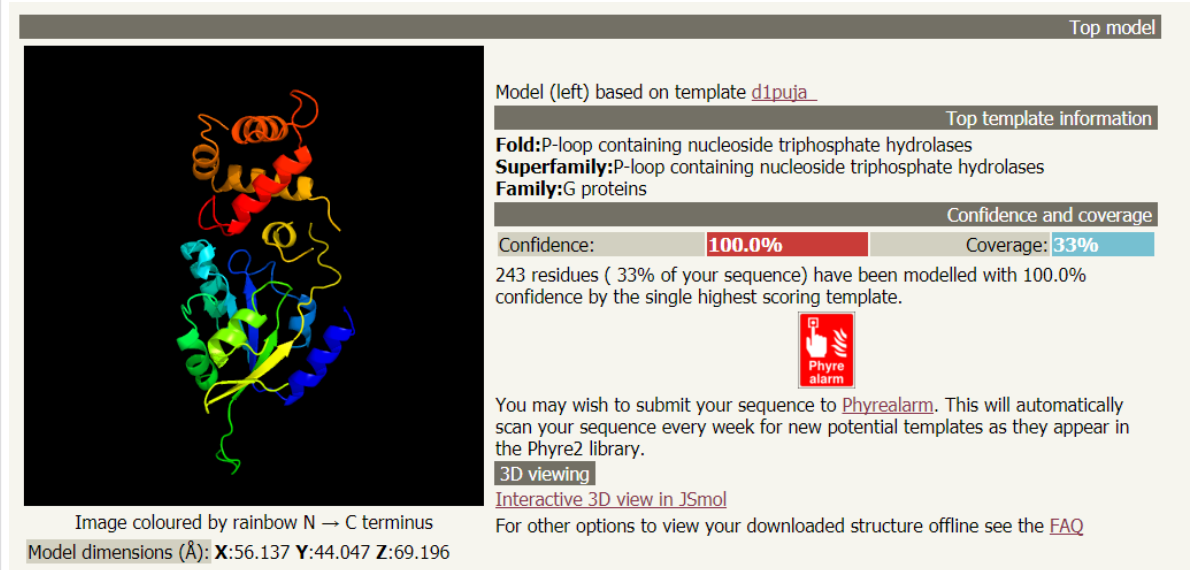
Found By HHblits



# NOG2\_Human结构预测

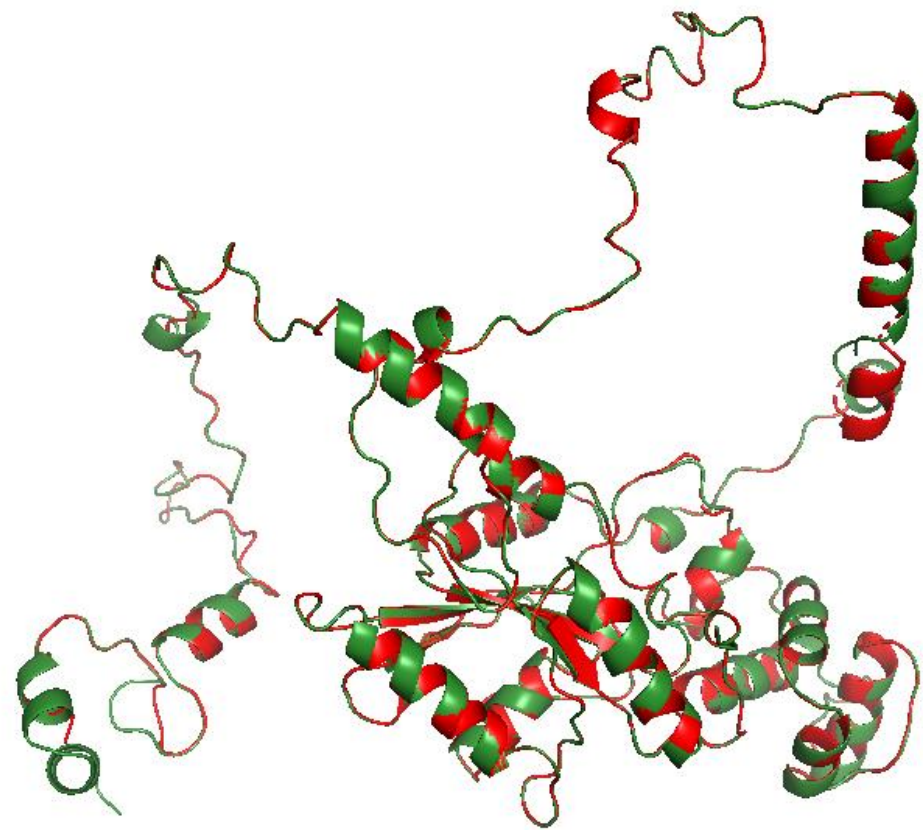
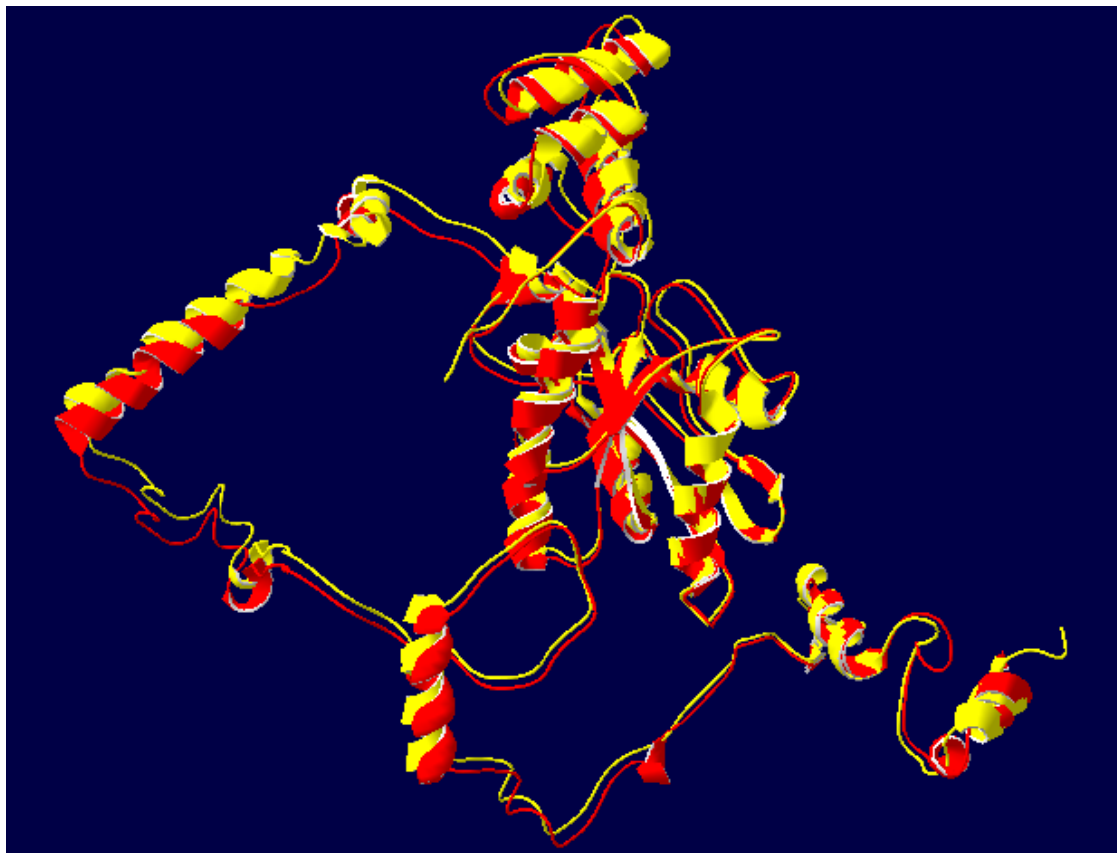


通过 Swiss-Model 对NOG2\_Human蛋白进行结构模拟后，选取最优结果，与已测定结构的NOG2\_Yeast蛋白进行结构比对。



通过 Phyre2 对NOG2\_Human蛋白进行结构模拟后，选取最优结果，与已测定结构的NOG2\_Yeast蛋白进行结构比对。

# 人和酵母NOG2结构比对

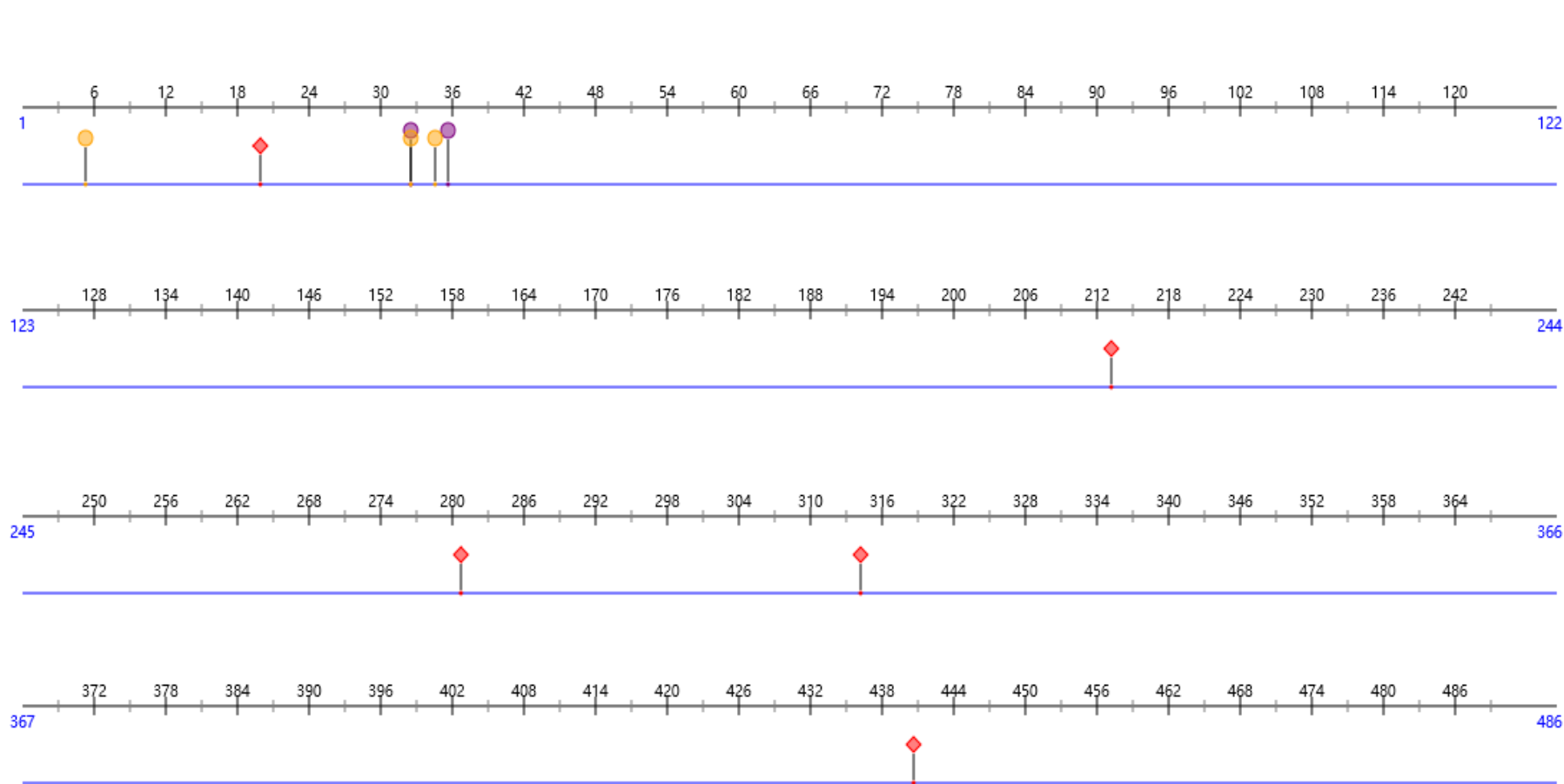


红色：预测的人NOG2结构  
绿色、黄色：酵母的NOG2结构





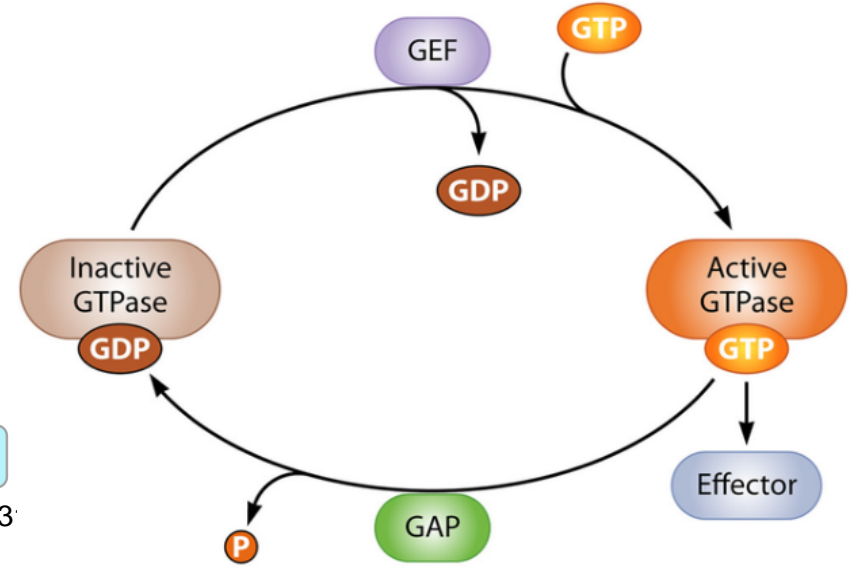
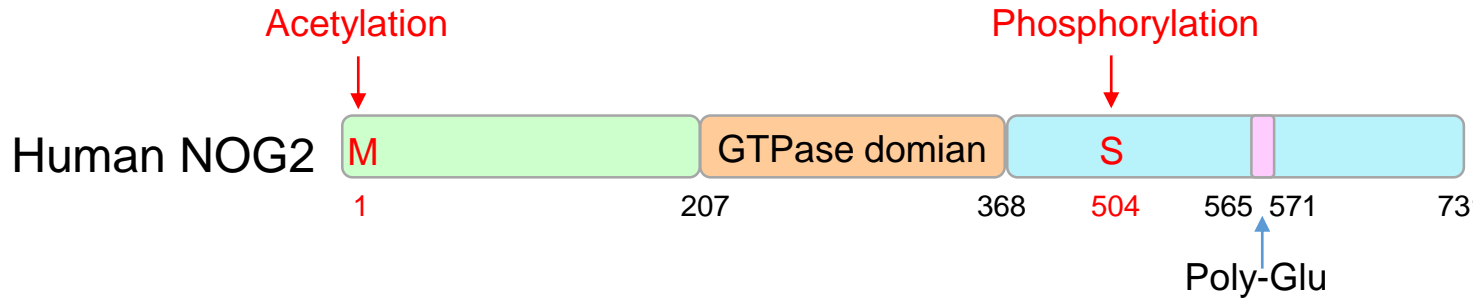
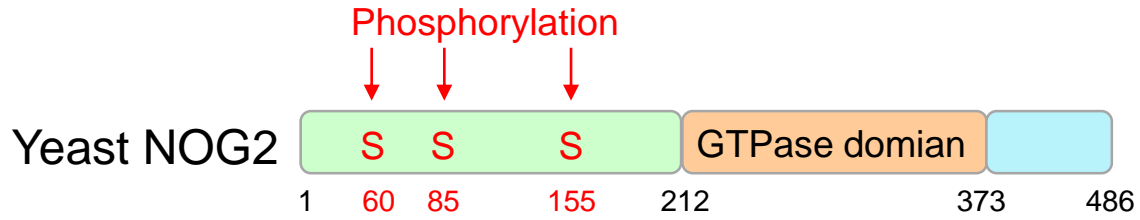
# 酵母NOG2 蛋白-蛋白，蛋白-核酸作用位点



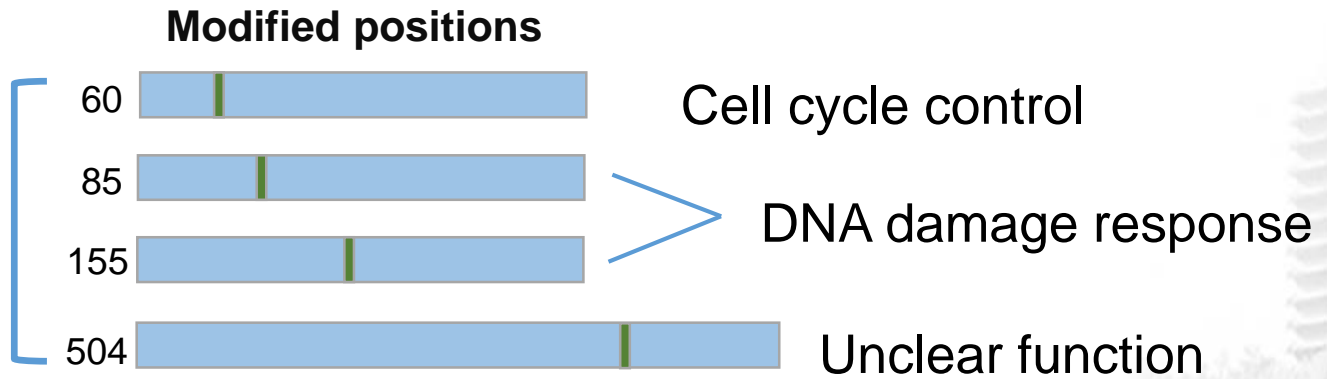
- DNA-binding region
- RNA-binding region
- ◆ Protein binding region



# 蛋白结构域和修饰位点



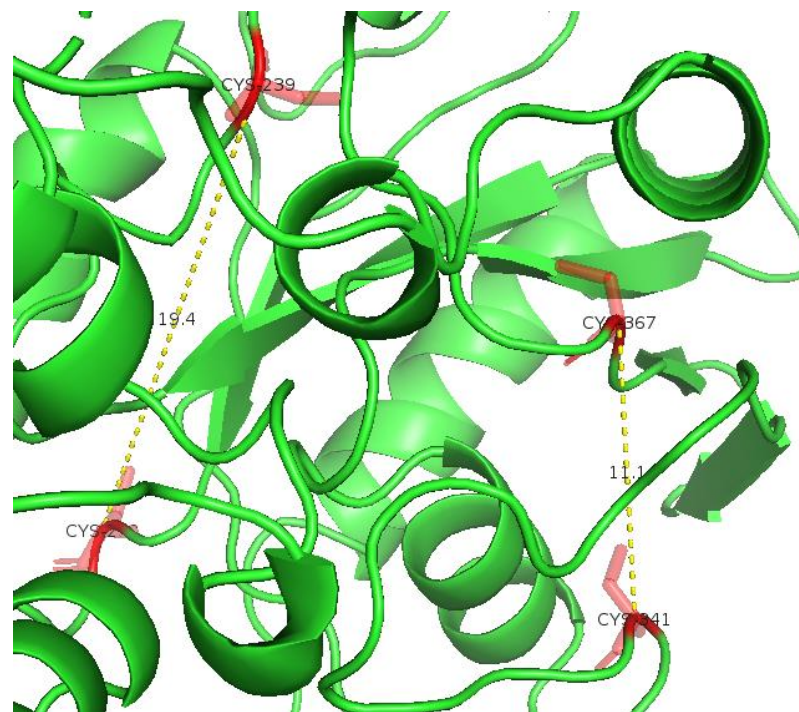
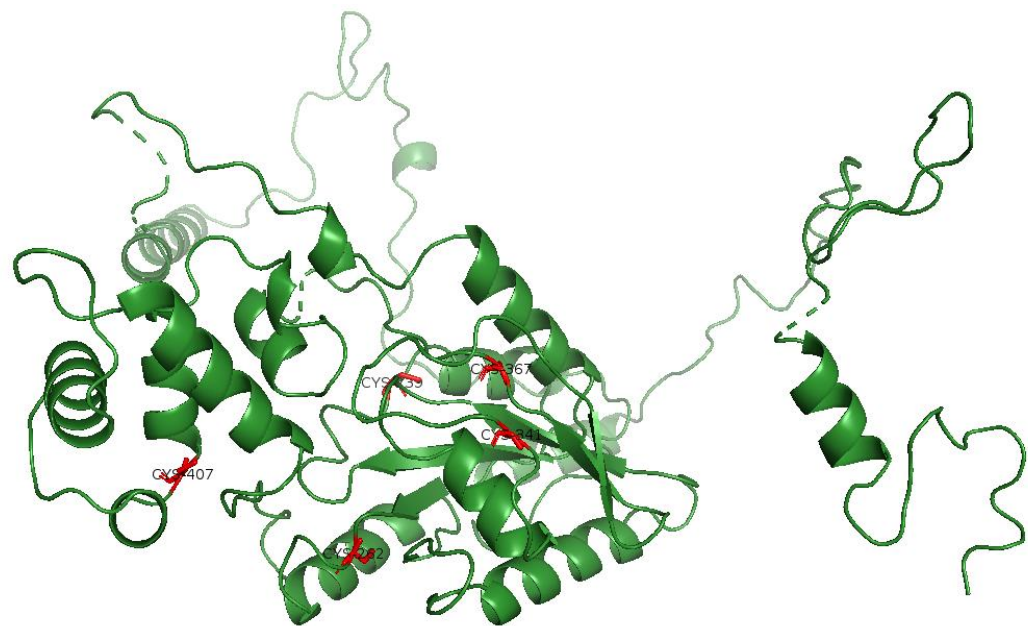
## Phosphoproteome analysis



## N-terminal acetylome analysis



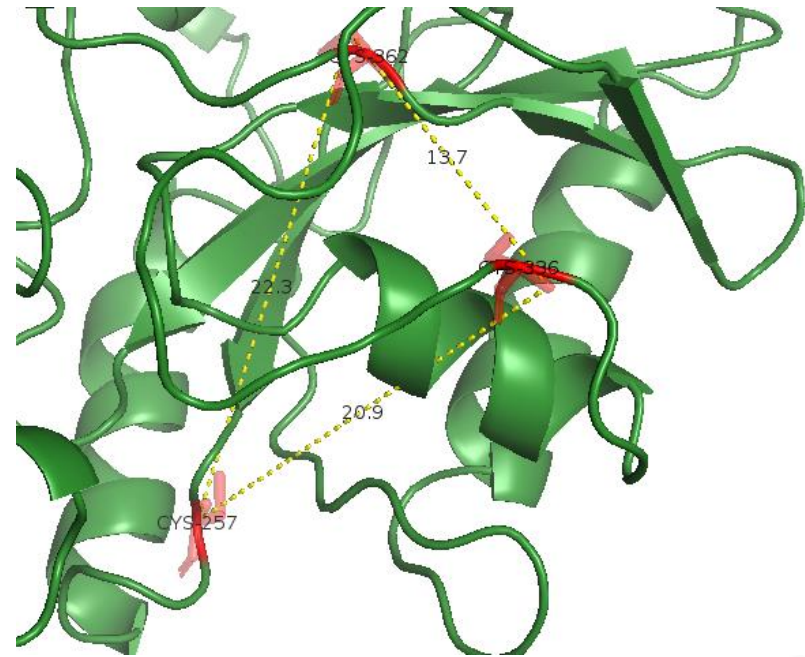
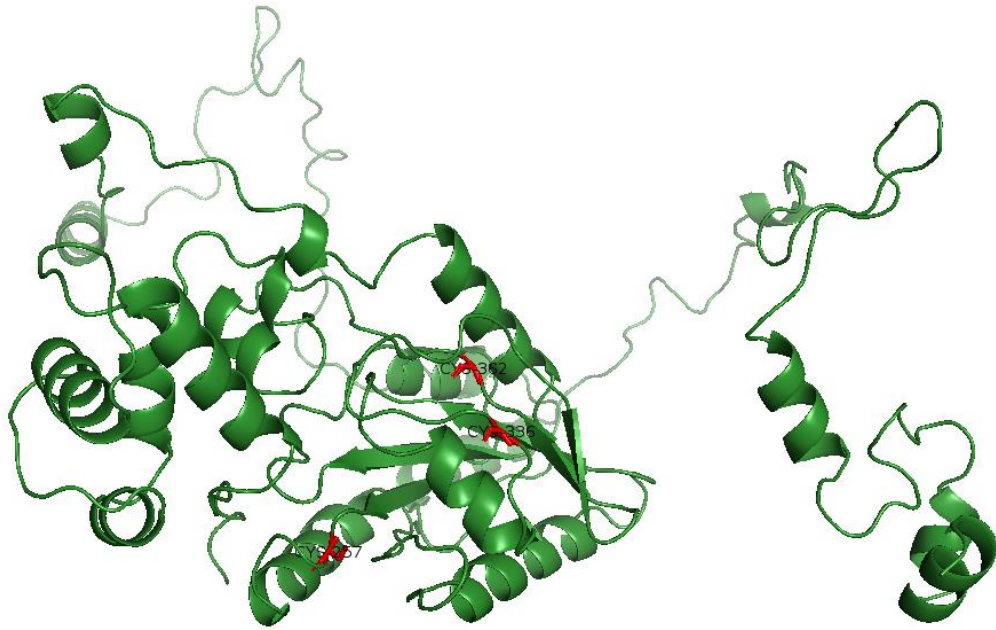
# 酵母NOG2二硫键分析



- NOG2\_Yeast
- 有五个Cys残基，分别为Cys239， Cys262， Cys341， Cys367， Cys407



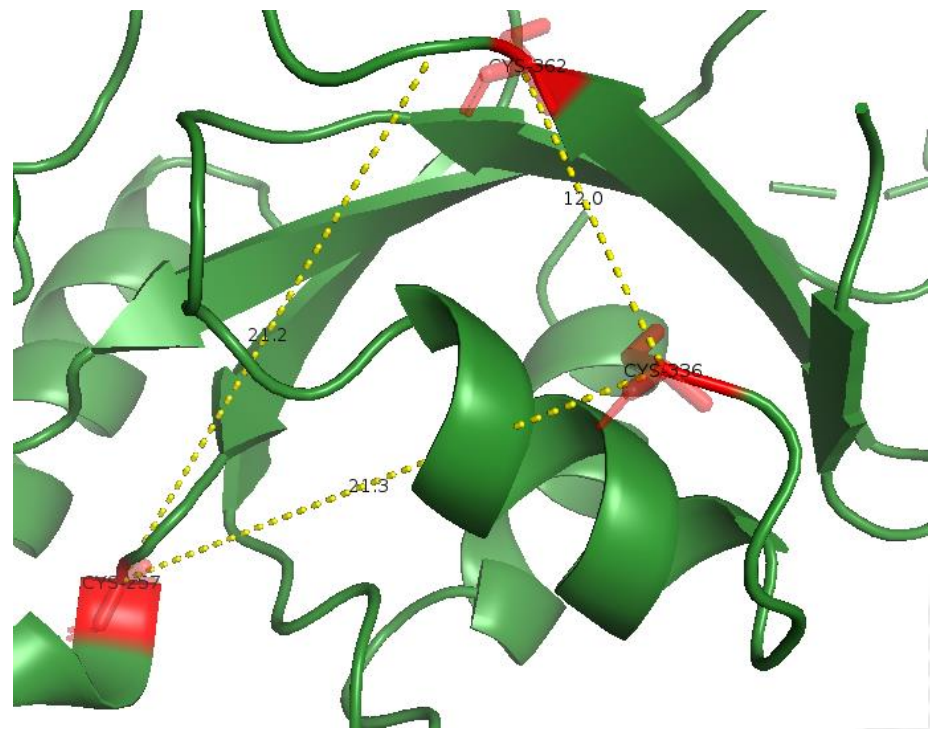
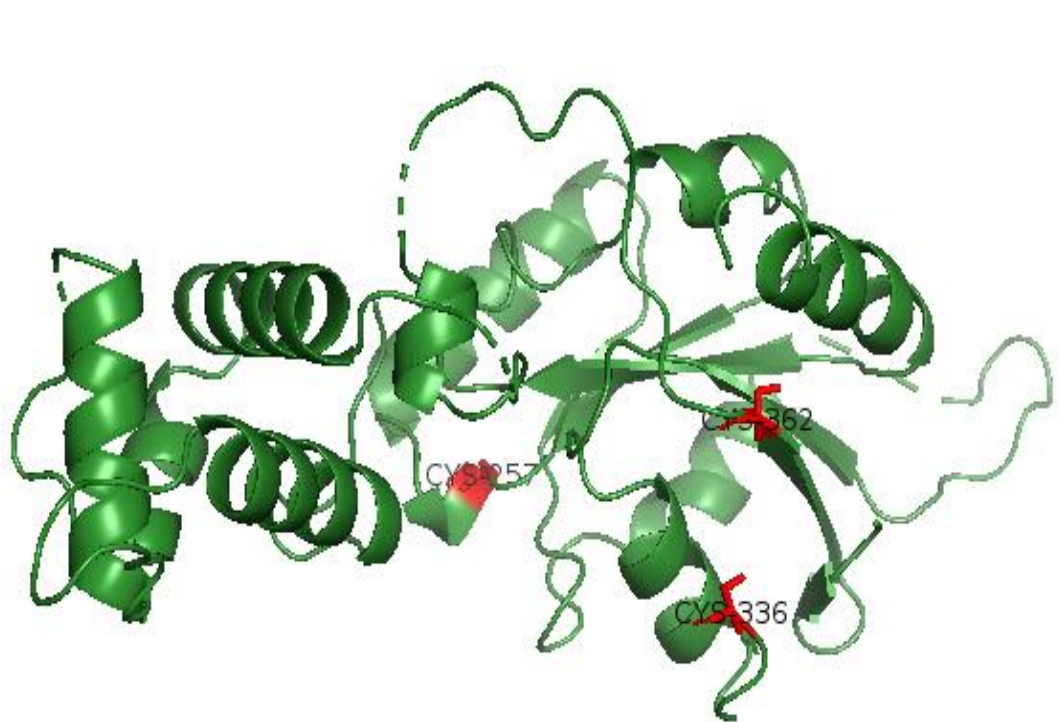
# Swiss-Model预测的人NOG2二硫键分析



- NOG2\_Human Swiss-Model
- 有三个Cys残基，分别为Cys257， Cys336， Cys362



# Phyre2预测的人NOG2二硫键分析

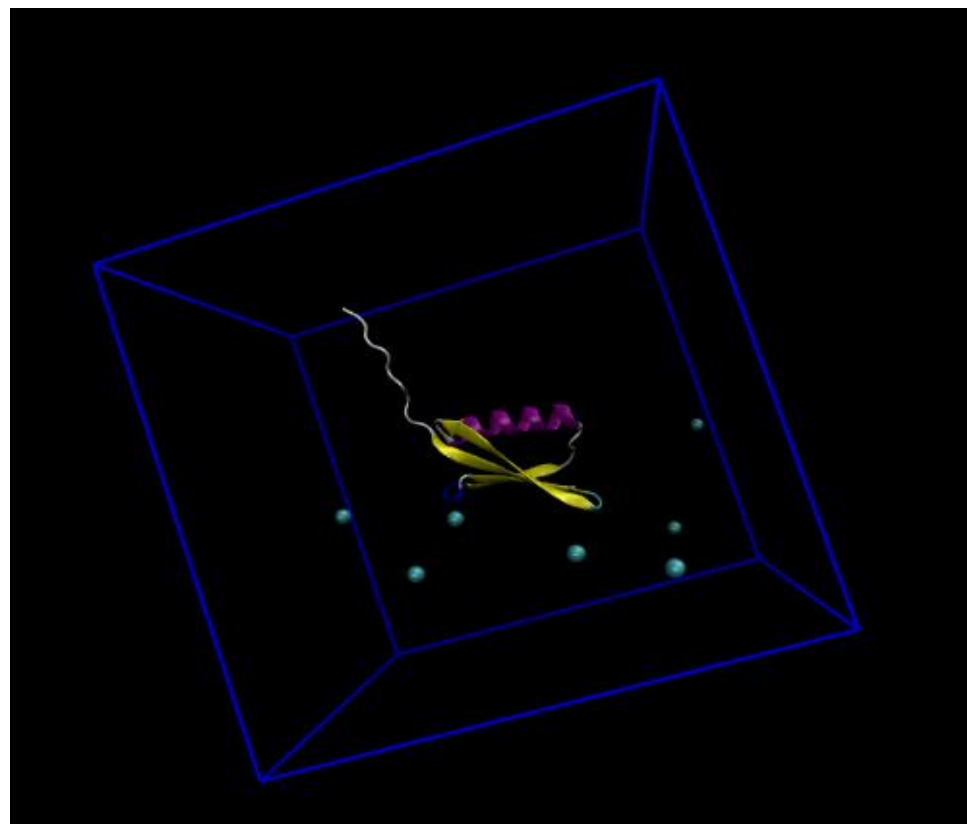
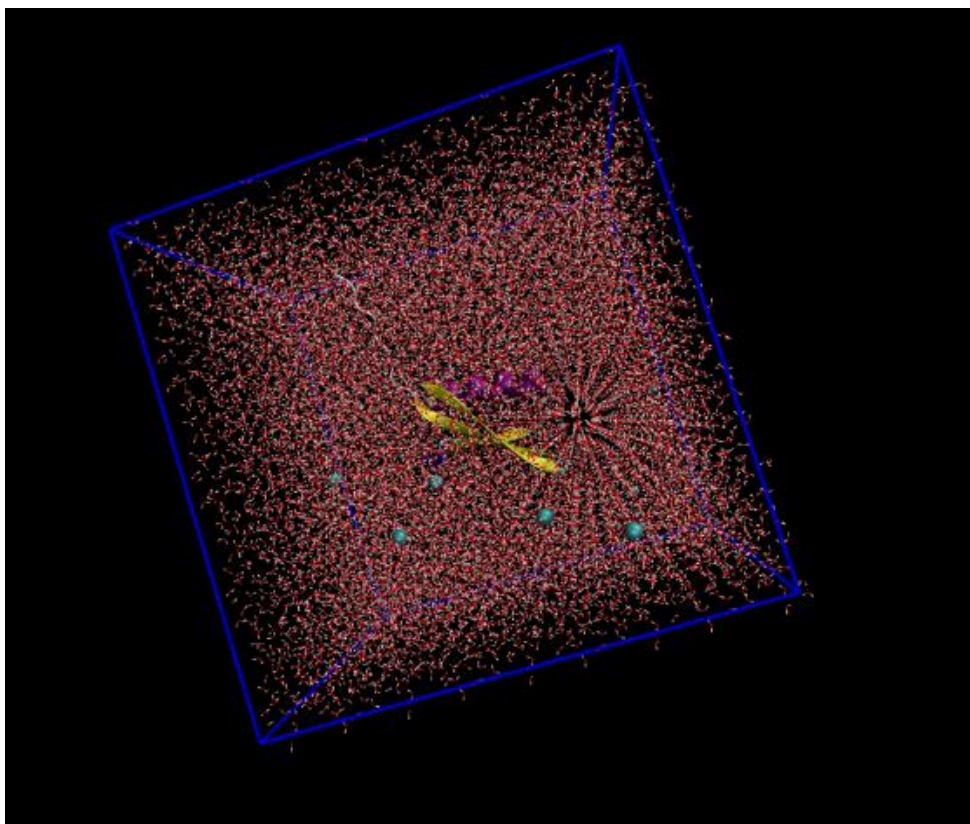


- NOG2\_Human Phyre2
- 有三个Cys残基，分别为Cys257， Cys336， Cys362



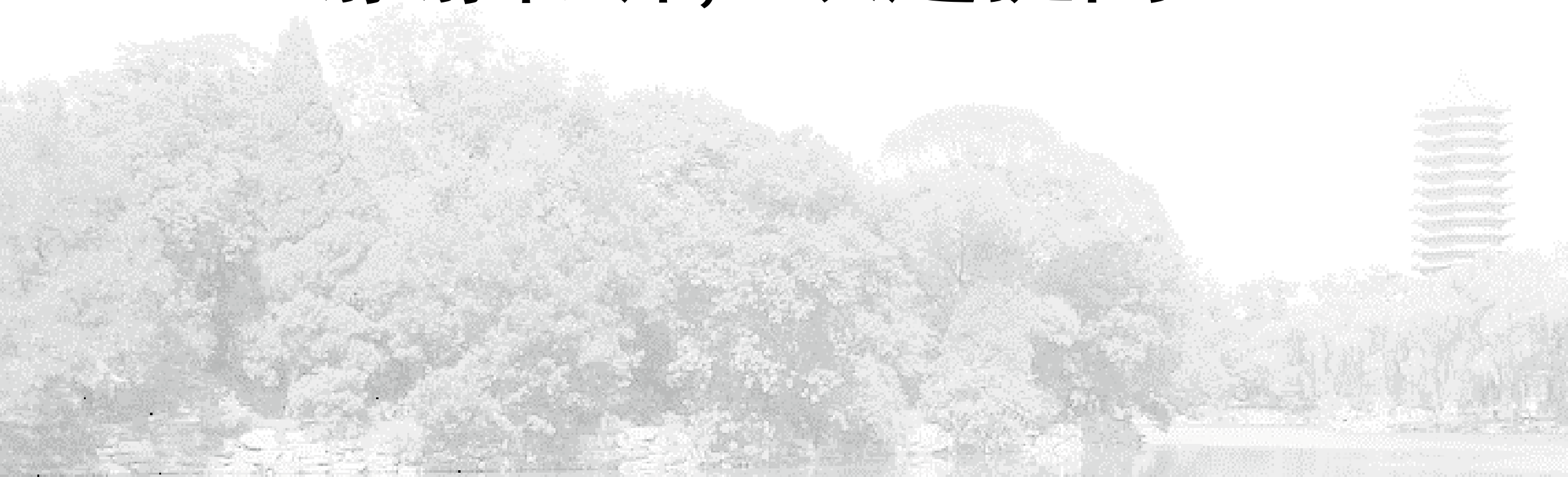
# 场环境下的NOG2

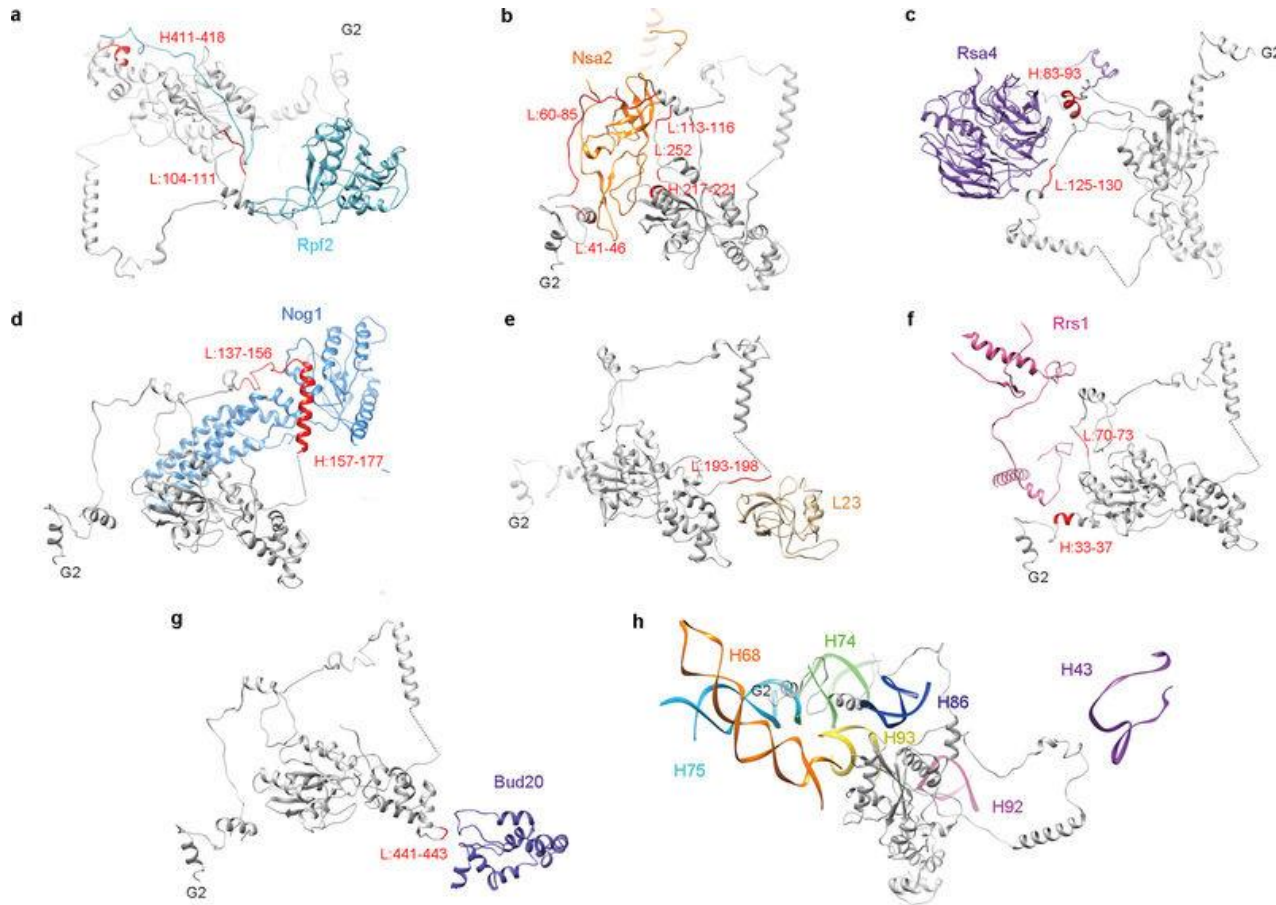
- 对NOG2部分结构域进行水环境模拟，由于生命体系中不存在净电荷，所以必须往体系中添加了7个钠离子，以保证总电荷为零。
- 左图水分子可视化，右图忽略水分子看到蛋白和加入的离子条件





谢谢聆听，欢迎提问！





“

Nog2 binds at the centre of the pre-60S particle, via interaction of its GTPase domain and carboxy (C)-terminal domain with a multi-helical junction , making extensive contacts with H93, H62, H64, H67, H69 and H71 of 25S ribosomal RNA (rRNA), and Bud20. This interaction stabilizes H69 and H71 in a nearly 180° -flipped position compared with their mature forms<sup>17</sup>. In addition, the C-terminal extended loop of Rpf2 (residues 275–300) is inserted into the interface of Nog2–GTPase domain–C-terminal domain and H69–H71 , also contributing to the displacement of H69–H71.

”

Gao N *et al. Nature*. 534, 133–137 (2016)





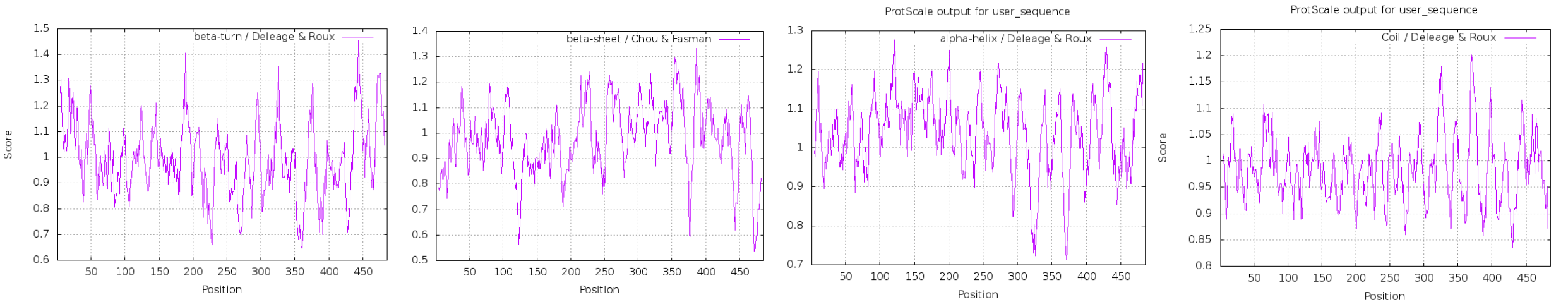
# 引物设计 (NM\_001183230.1)

- 【Tool】 WebLab-Eprimer32
- 【Database】 default
- 【Product size range】 1400-2000

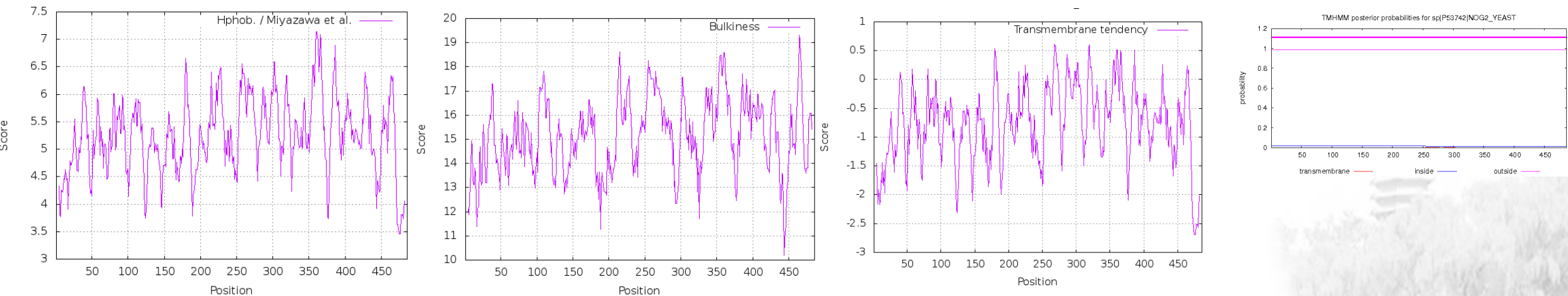
#		Start	Len	Tm	GC%	Sequence
1	PRODUCT SIZE: 1400					
	FORWARD PRIMER	28	26	58.27	46.15	AGACGTATTCGTGAAGGTGACACCAA
	REVERSE PRIMER	1402	26	57.17	46.15	TTTTCTTCCCCTTCCTTTTCAGGTGG
2	PRODUCT SIZE: 1400					
	FORWARD PRIMER	28	26	58.27	46.15	AGACGTATTCGTGAAGGTGACACCAA
	REVERSE PRIMER	1401	27	58.12	44.44	TTTTCTTCCCCTTCCTTTTCAGGTGGA
3	PRODUCT SIZE: 1400					
	FORWARD PRIMER	29	25	57.33	48.00	GACGTATTCGTGAAGGTGACACCAA
	REVERSE PRIMER	1402	27	57.50	44.44	TTTTCTTCCCCTTCCTTTTCAGGTGG



# NOG2蛋白的二维结构分析



$\beta$ -sheet/ $\beta$ -turn/ $\alpha$ -helix/coil

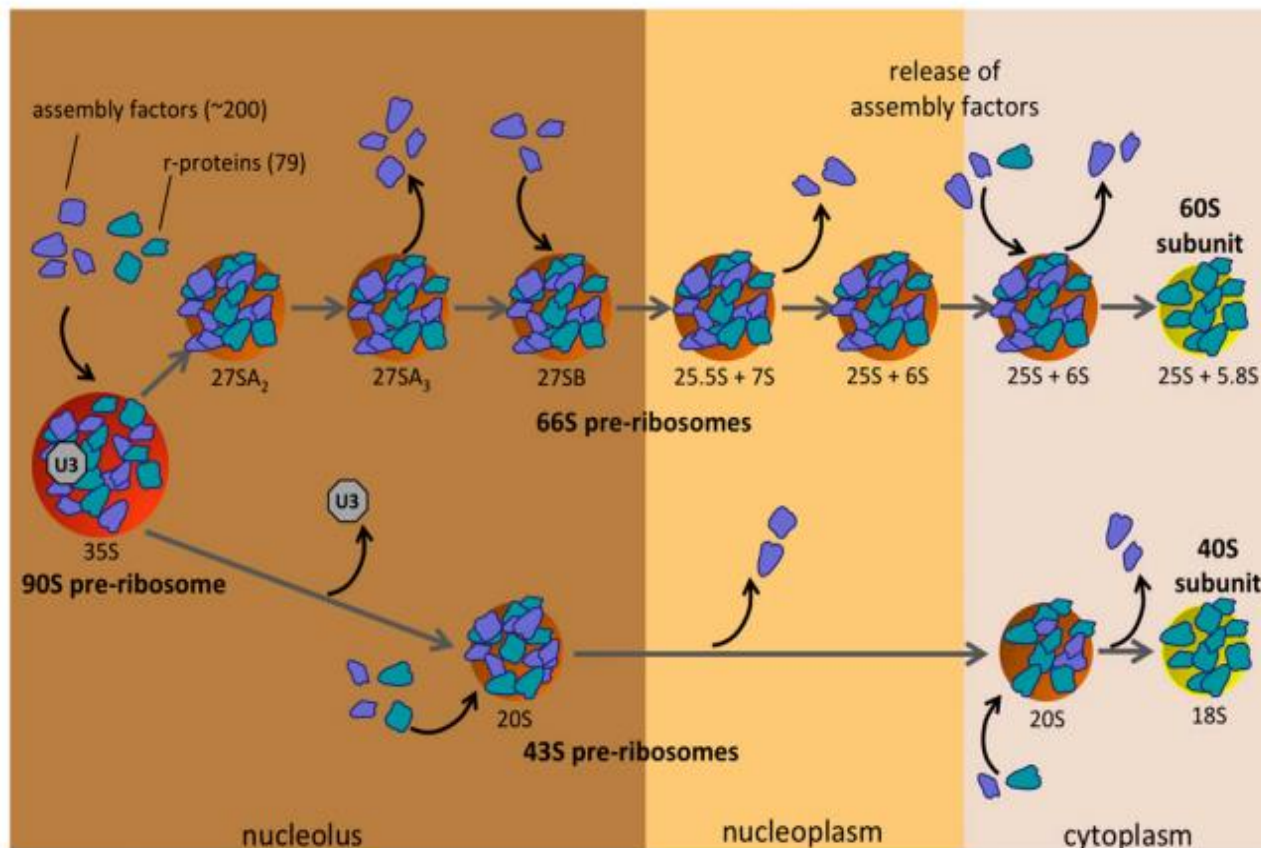


亲水/疏水，空间位阻和跨膜结构预测20



# 背景-40s/60s 核糖体小体的通路

PMC  Search  
Create alert Journal List Advanced



Send to: Filter your results:

All (117)

[NIH grants \(54\)](#)

Embargoed (0)

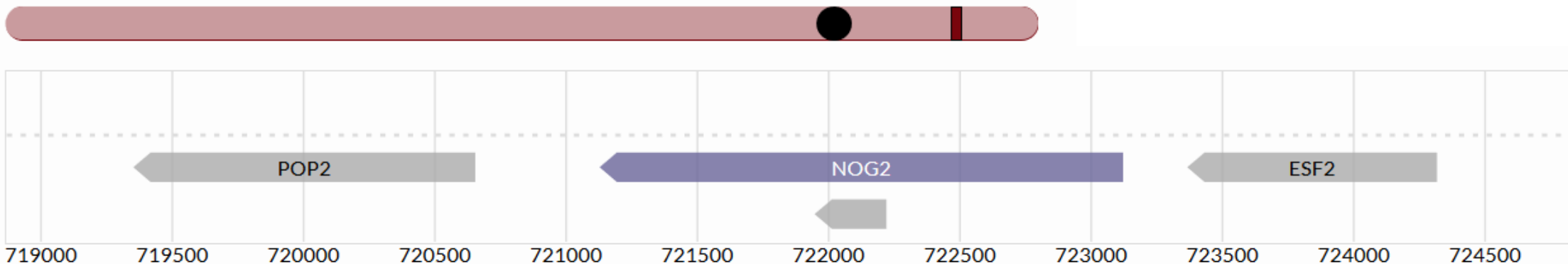
1 of 6 Next > Last >>

- PMC检索NOG2共有117篇相关文献
- 该蛋白与60S亚基装配过程息息相关
- 图示为生物体中核糖体前体的装配过程

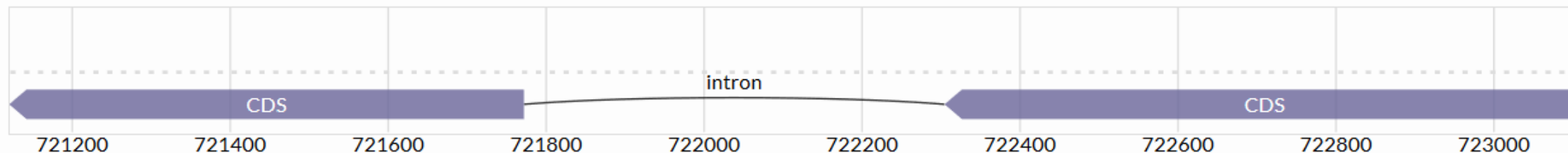


# NOG2 基因信息

NOG2 定位在14号染色体的 721120..723112



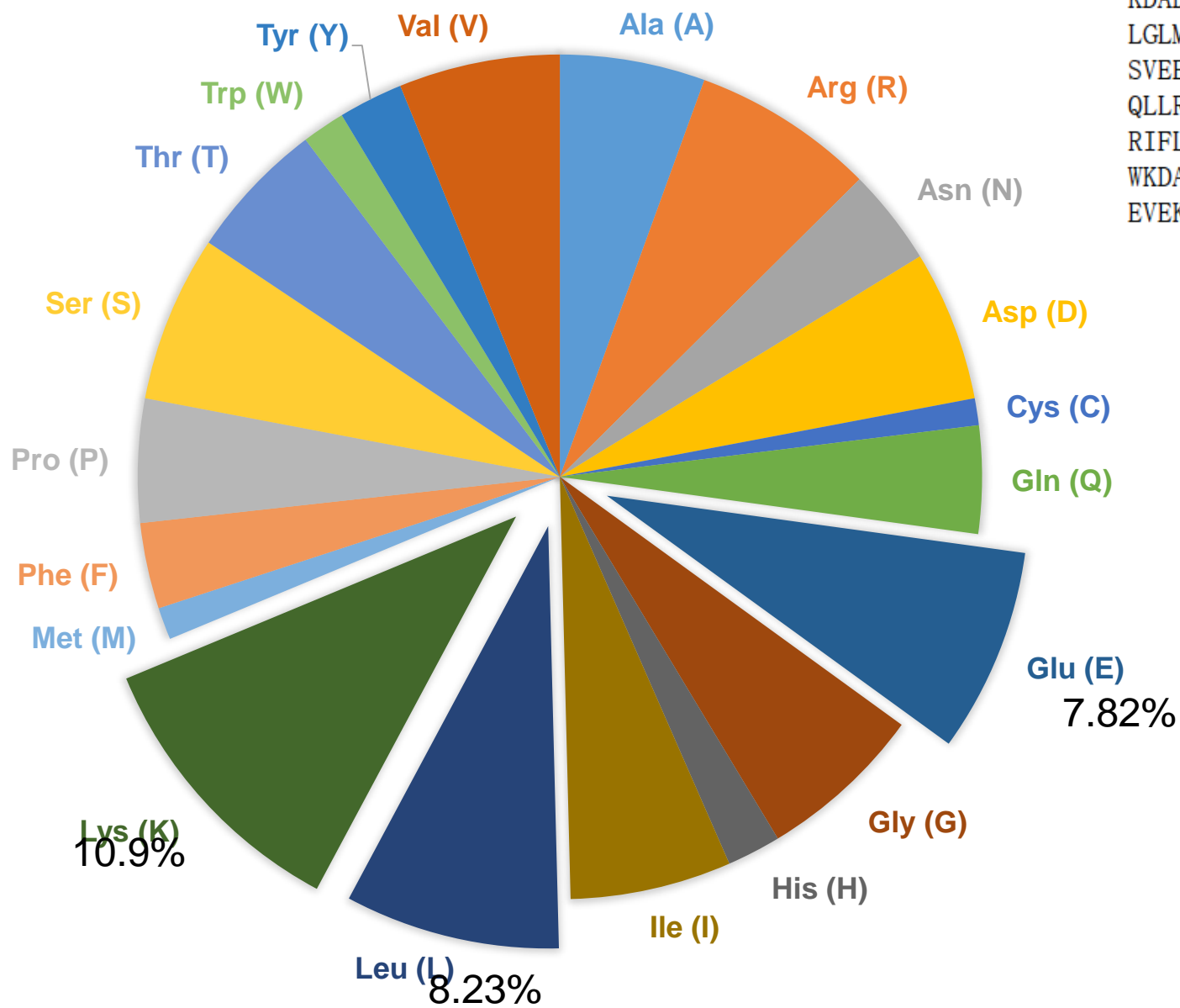
NOG2 基因信息:



Feature	Relative Coordinates	Coordinates	Coord. Version	Seq. Version
CDS	1..810	chrXIV:723112..722303	2011-02-03	1997-01-28
intron	811..1342	chrXIV:722302..721771	2011-02-03	2011-02-03
CDS	1343..1993	chrXIV:721770..721120	2011-02-03	1997-01-28



# 酵母NOG2氨基酸序列



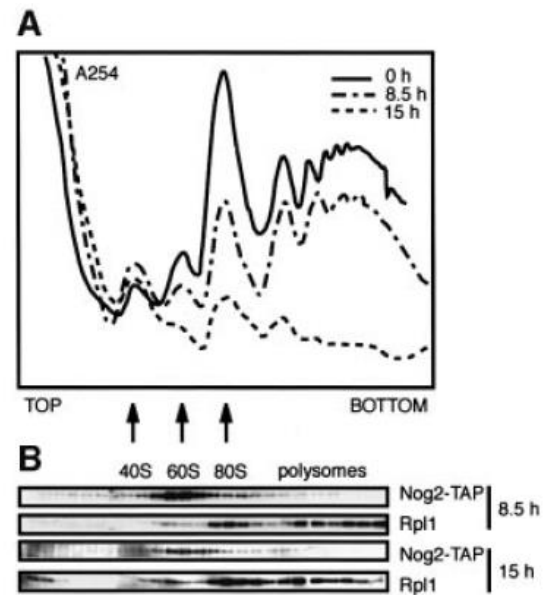
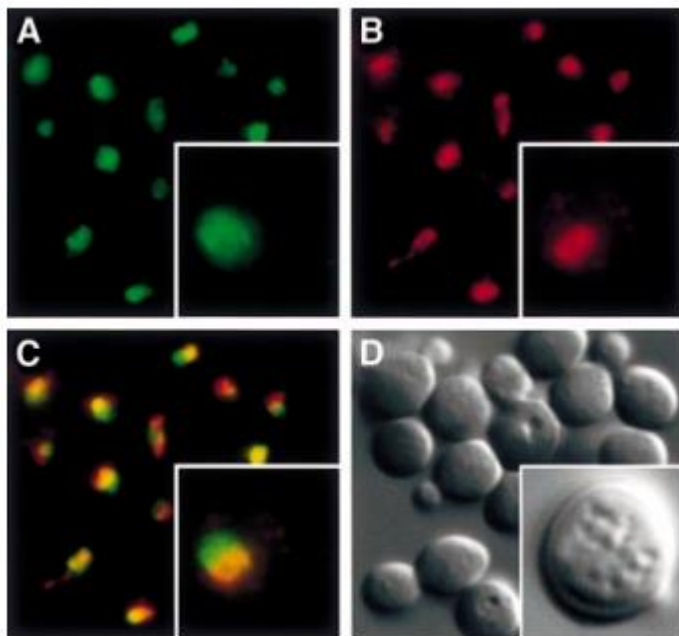
MGTGKKEKSRRIREGDTKDG NLRVKGENFYRDSKRVKFLNMYTSGKEIRNKKGNLIRAAS  
FQDSTIPDARVQPDRRWFGNTRVVISQDALQHFRSALGETQKDTYQVLLRRNKLPM S LLEE  
KDADESPKARILDTESYADAFGPKAQRKRPRLAASNLEDLVKATNEDITKYEEKQVLDAT  
LGLMGNQEDKENGWTSAAKEAIFSKGQSKRIWNELYKVIDSSDVVIHVLDARDPLGTRCK  
SVEEYMKKETPHKHLIYV LNKCDLVPTWVAAAWVKHLSKERPTLAFHASITNSFGKGS LI  
QLLRQFSQLHTDRKQISVGF IGY PNTGKSSIINTLRKKKVCQVAPIPGETKVVQYITLMK  
RIFLIDCPGIVPPSSKDSEEDILFRGVVRVEHVTHPEQYIPGV LKRCQVKHLERTYEISG  
WKDATEFIEILARKQGRL LKGGEPDES GVS KQILNDFNRGKIPWFVLPPEKEGEEKPKKK  
EVEKTA

共由486个氨基酸组成，  
55.49KD大小

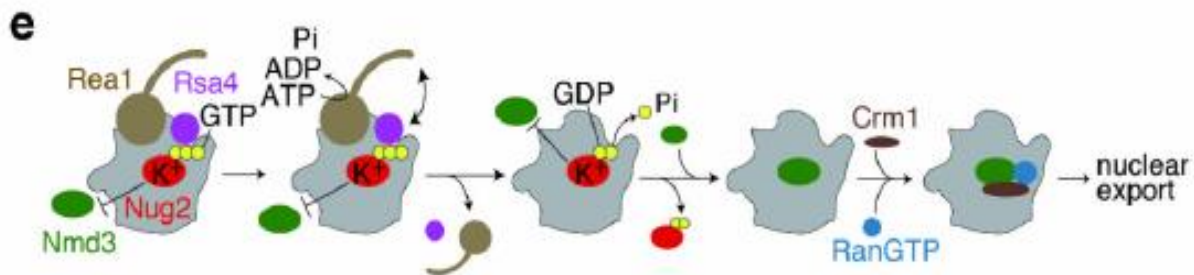


# 背景-NOG2, 一个重要的GTP酶

- NOG2p定位在生物体内的核仁和核质上



Saveanu C, et al. EMBO J. 2001; 20:6475–6484.

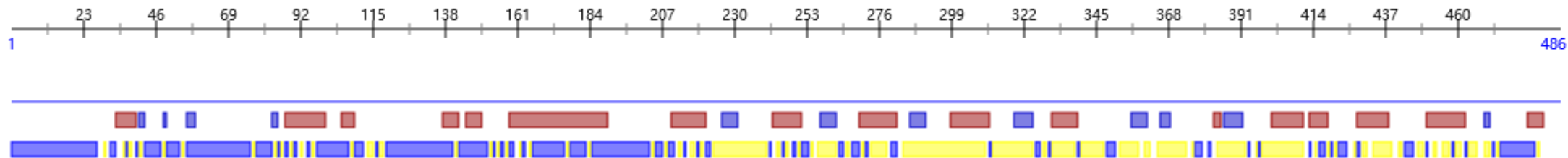


Model of pre-60S subunit maturation starting from the Rix1-particle with final Nmd3-Crm1-RanGTP recruitment

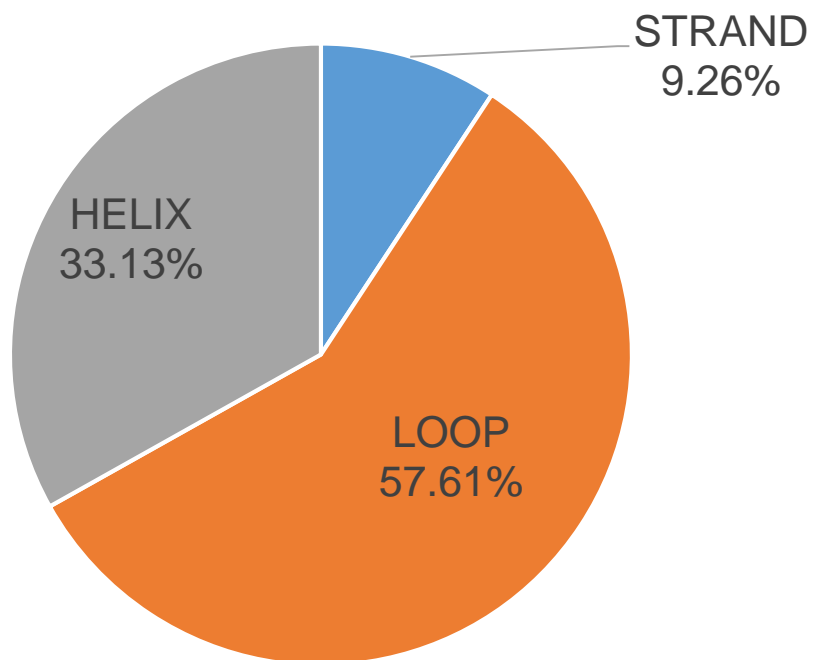
Matsuo Y, et al. Nature. 2014; 505:112–116.



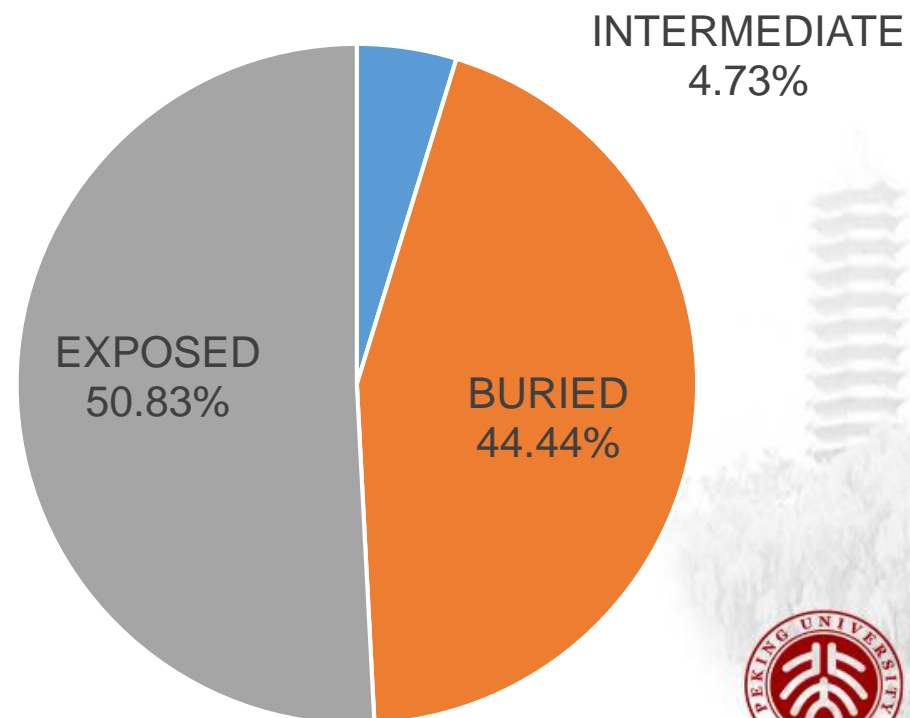
# 酵母NOG2 二级结构信息



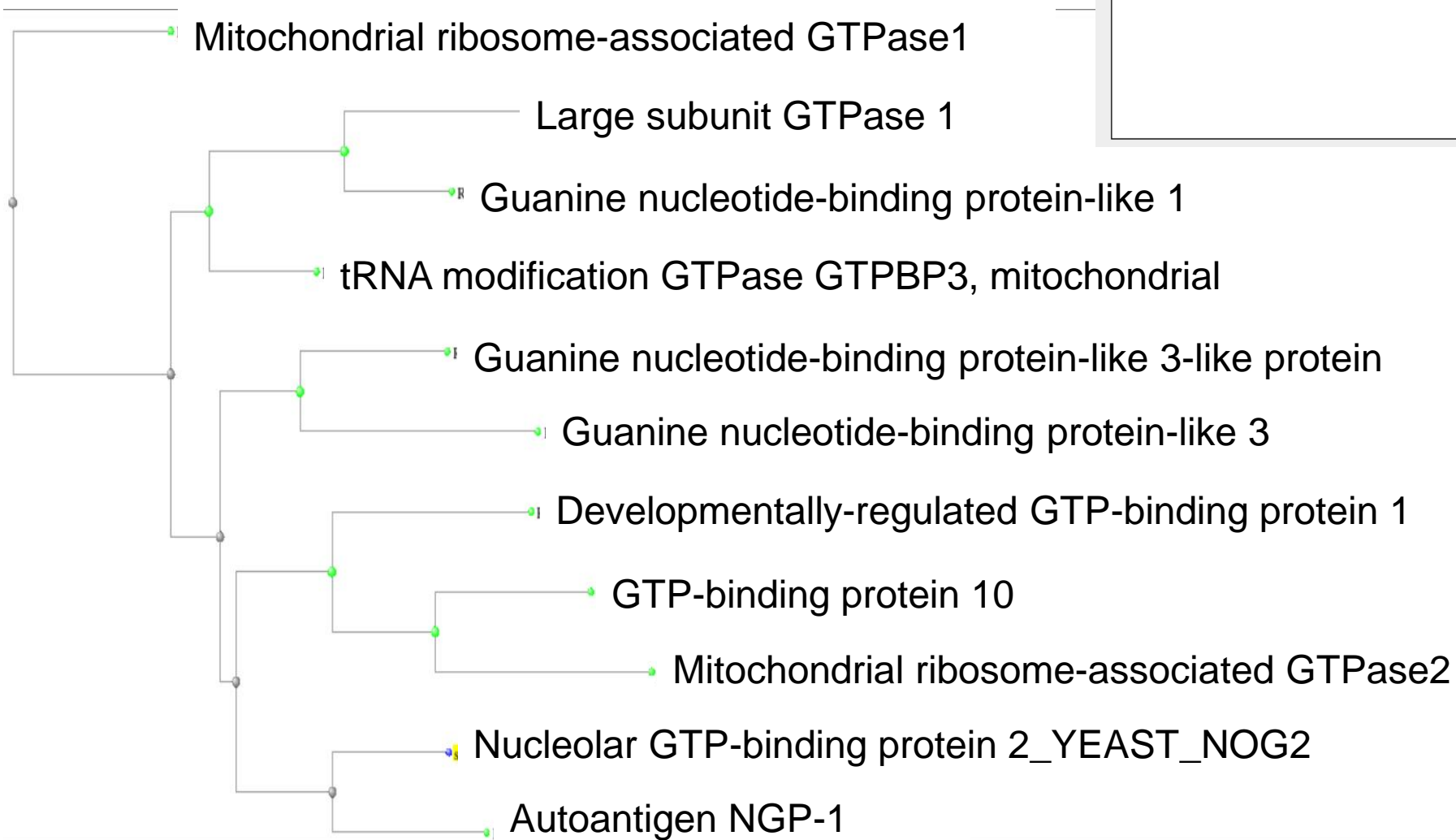
二级结构组成



Solvent Accessibility

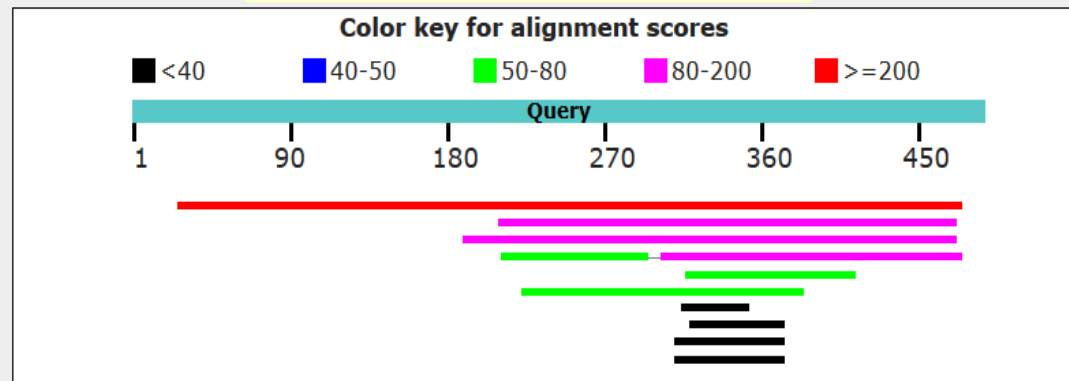


# Blast 酵母NOG2蛋白序列-1



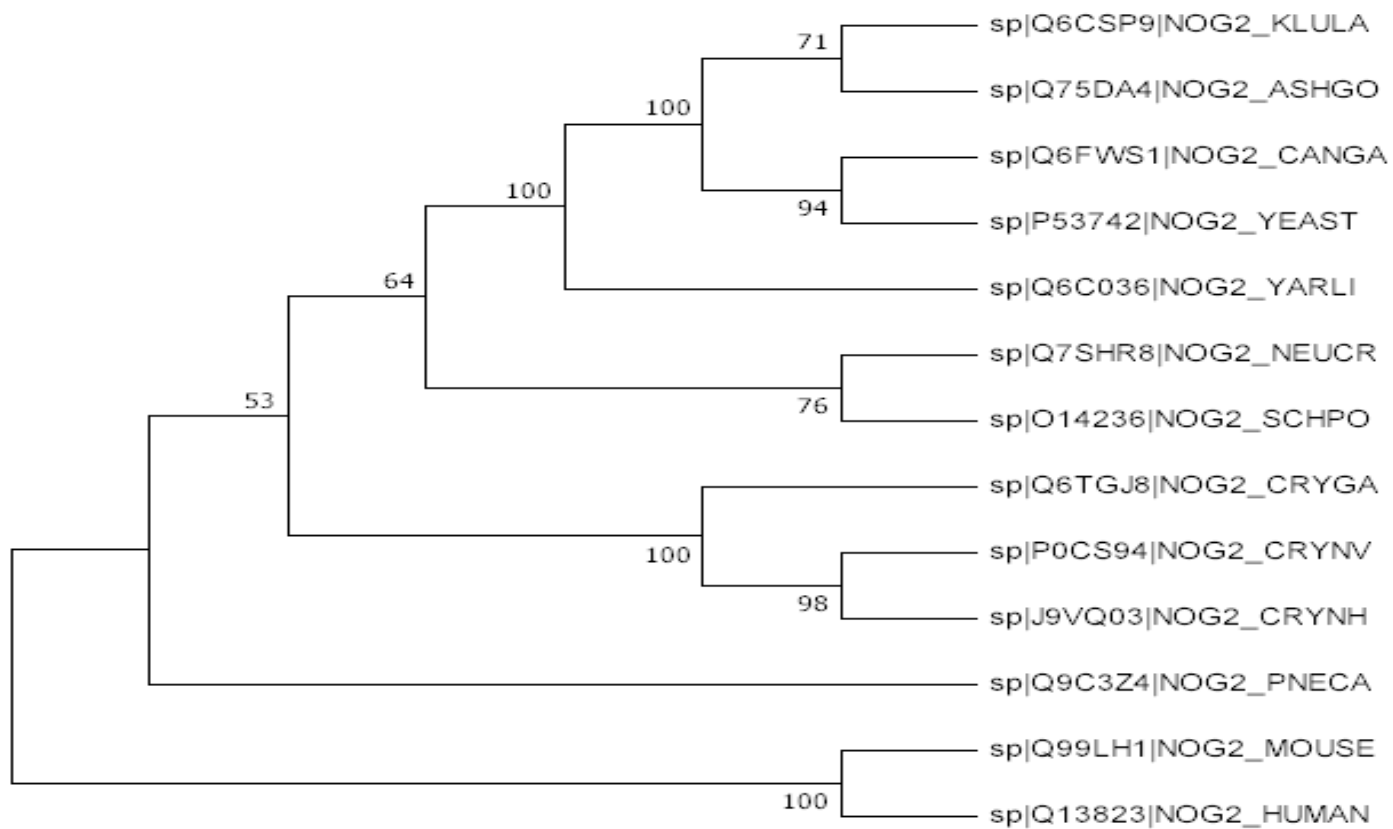
Distribution of the top 11 Blast Hits on 10 subject sequences

Mouse over to see the title, click to show alignments





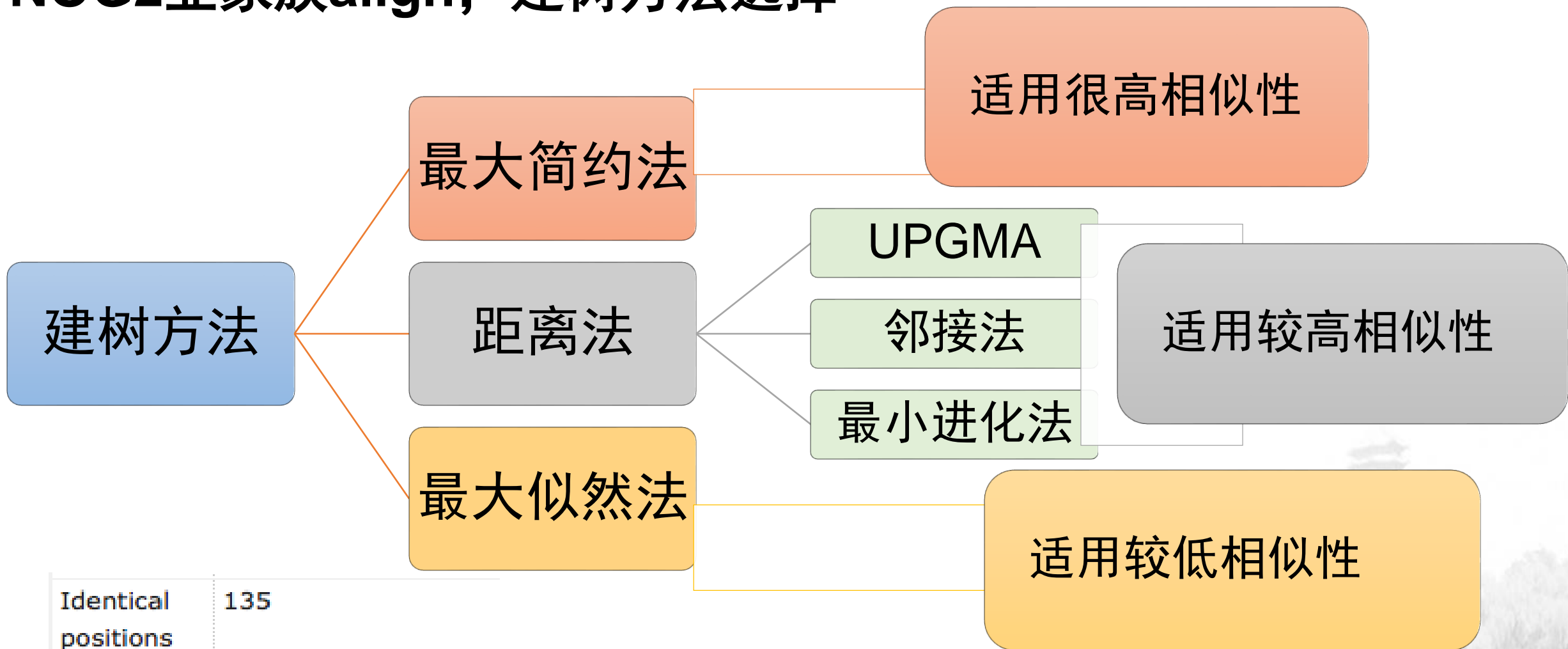
# 建树



最小进化法  
(Minimum Evolution Tree)



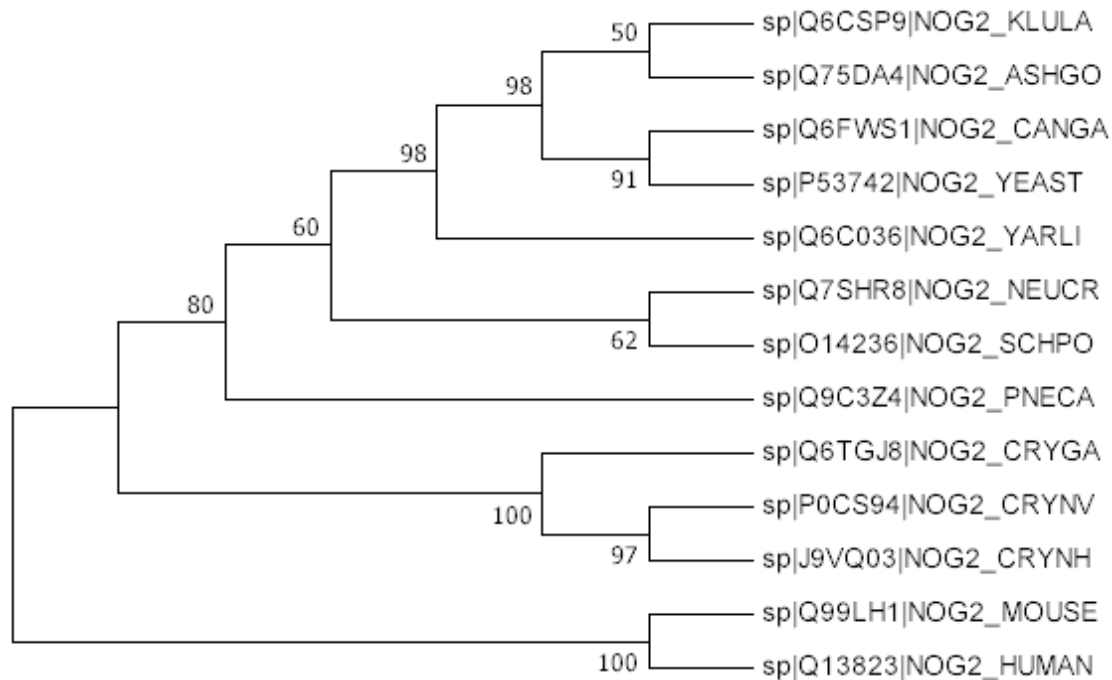
# NOG2亚家族align, 建树方法选择



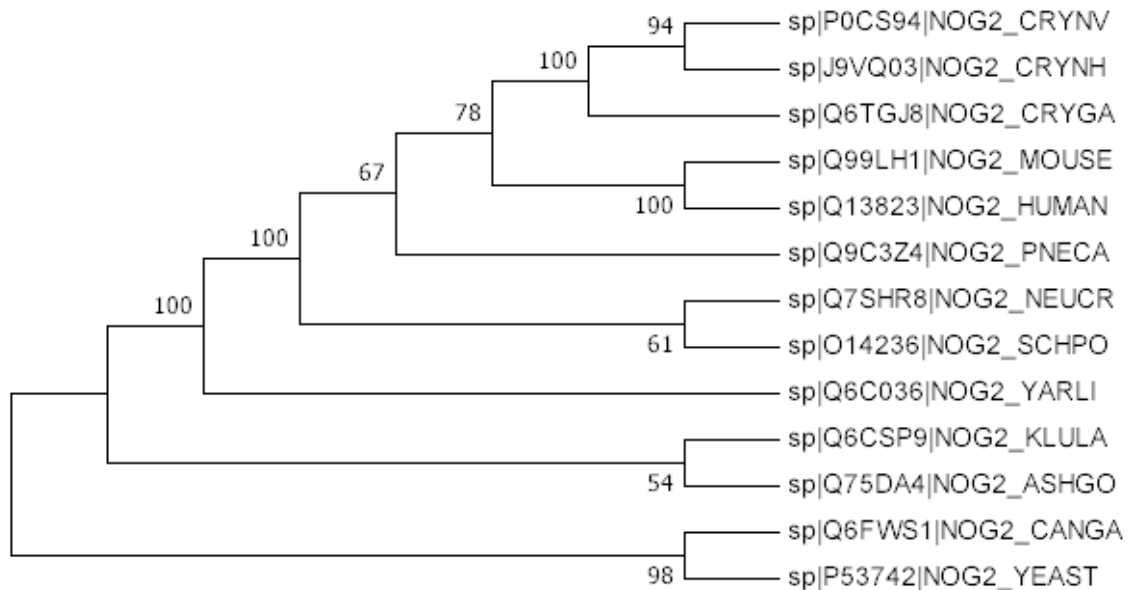
Identical positions	135
Identity	16.896%
Similar positions	124



# 建树



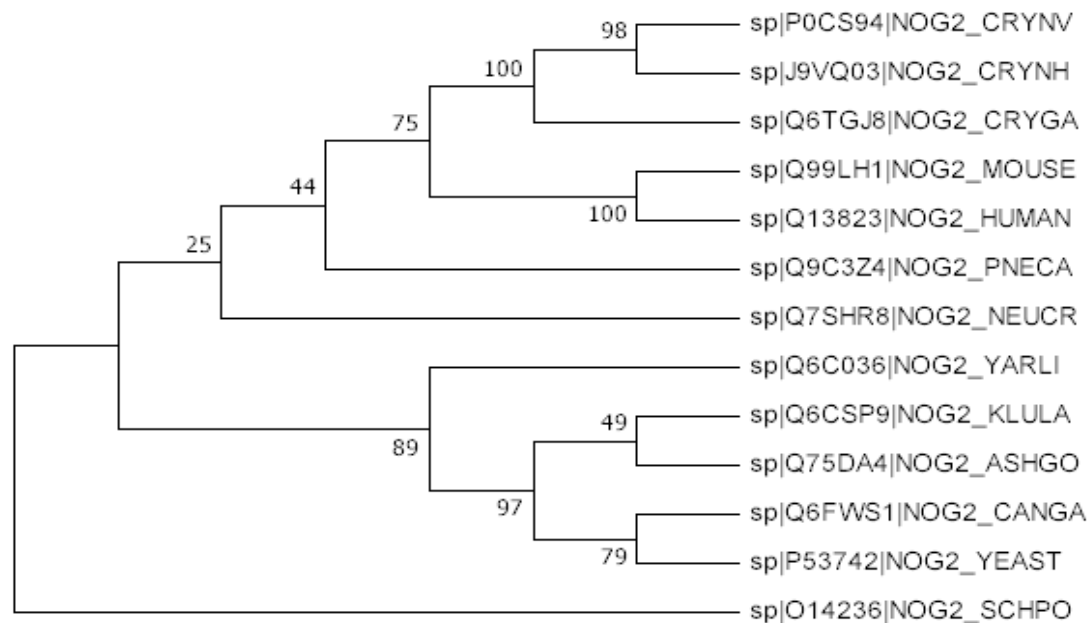
最大似然法  
(Maximum Likelihood Tree)



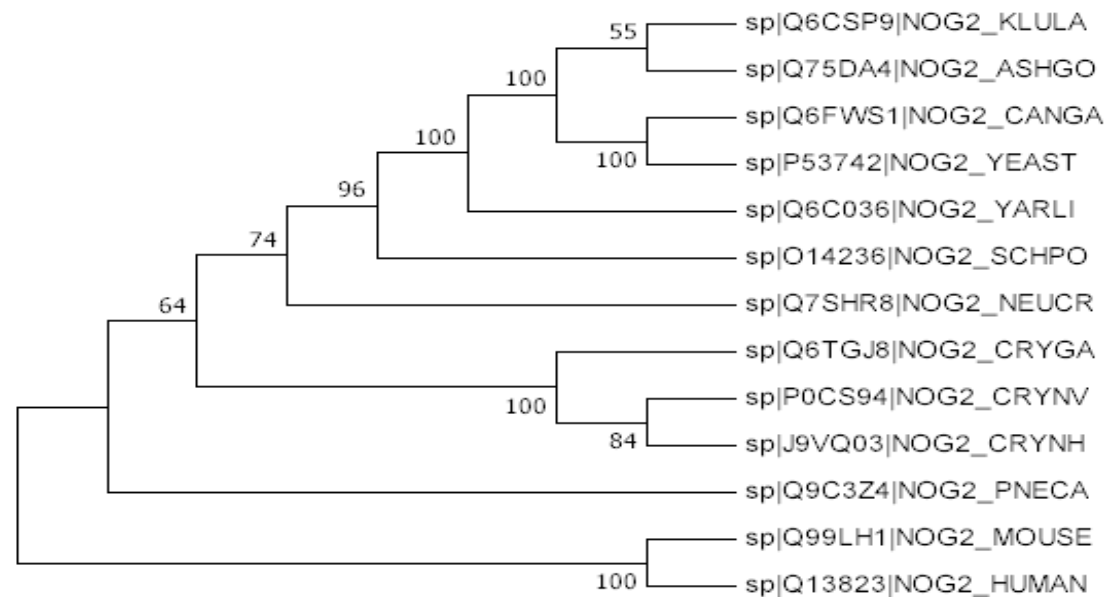
邻接法  
(Neighbor-joining Tree)



# 建树



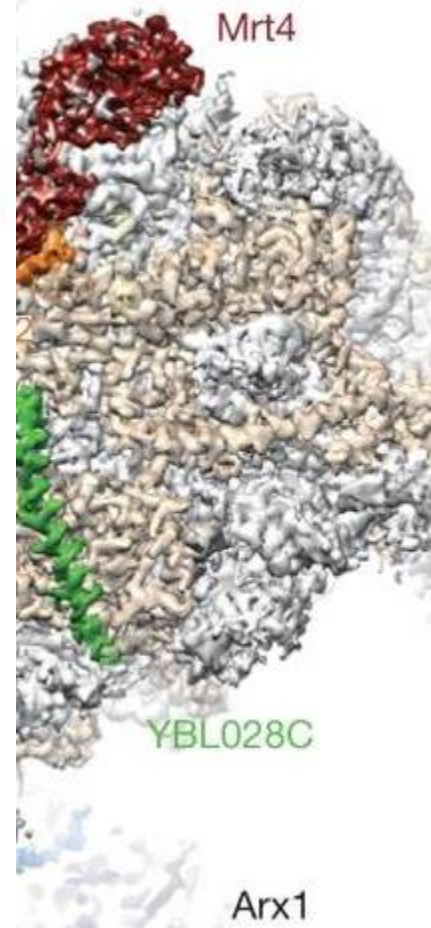
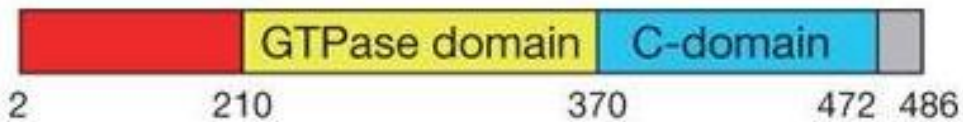
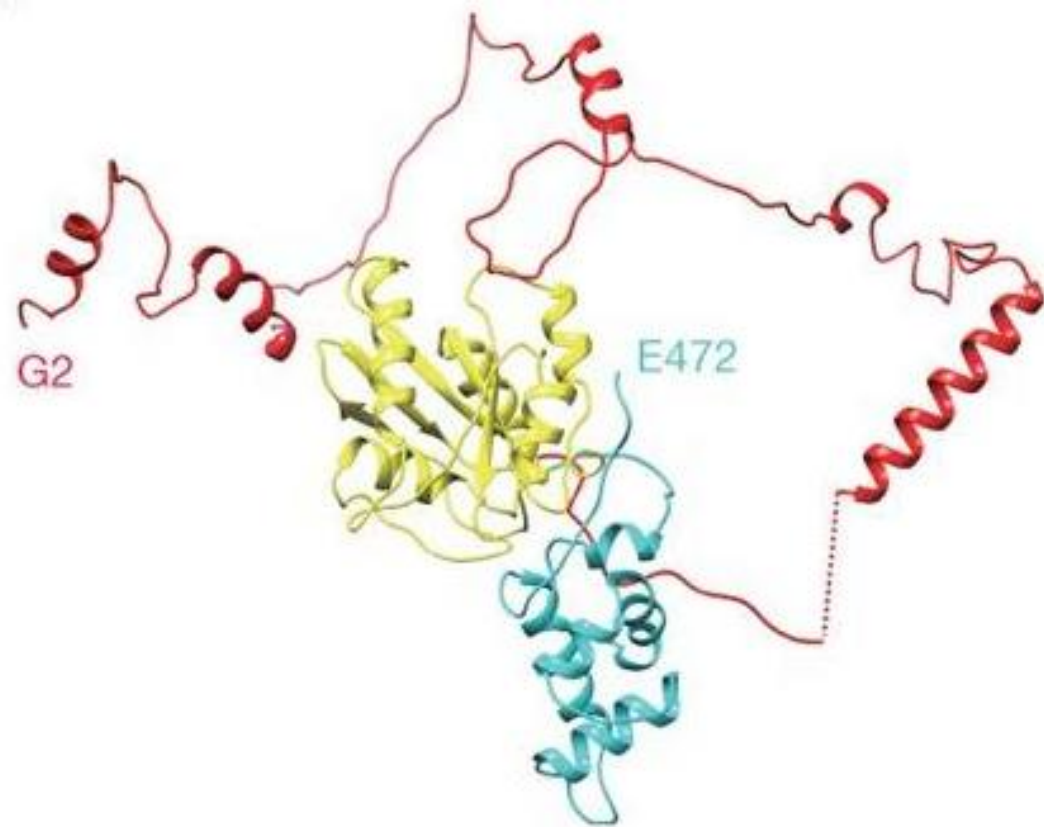
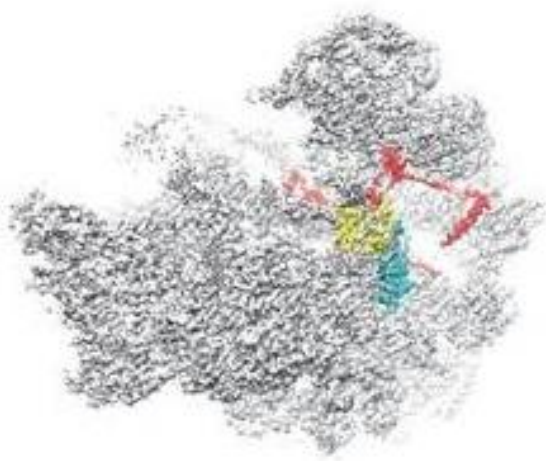
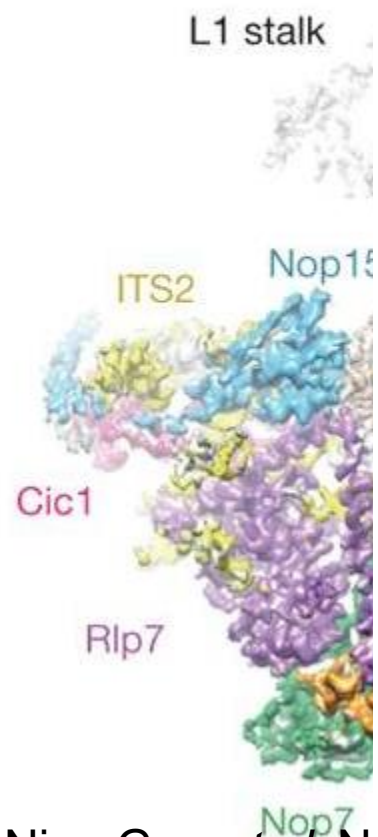
最大简约法  
(Maximum Parsimony Tree)



UPGMA法



# NOG2结构解析



Ning Gao *et al.* Nature. 2016 Jun 2; 534(7605): 133–137.



# 同源建模算法比较

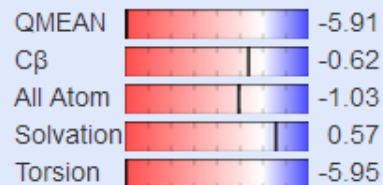
Oligo-State Ligands

Monomer None

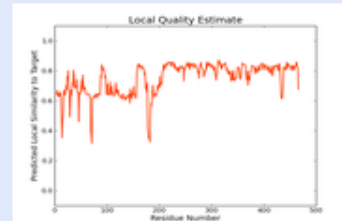
GMQE QMEAN

0.51 -5.91

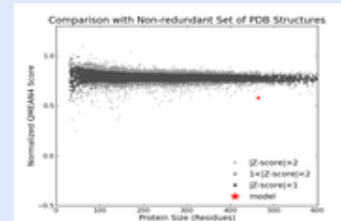
Global Quality Estimate



Local Quality Estimate



Comparison



Template Seq Identity Coverage

3jct.1.c 54.78%

Description

Nucleolar GTP-binding protein 2

Biounit Oligo State	Method	Seq Similarity	Range	Coverage
hetero-54-mer	EM	0.46	3 - 466	0.63

Ligand	Added to Model	Description
GTP	X - Binding site not conserved.	GUANOSINE-5'-TRIPHOSPHATE
GTP	X - Binding site not conserved.	GUANOSINE-5'-TRIPHOSPHATE
MG	X - Binding site not conserved.	MAGNESIUM ION
MG	X - Binding site not conserved.	MAGNESIUM ION
ZN	X - Binding site not conserved.	ZINC ION
ZN	X - Binding site not conserved.	ZINC ION
ZN	X - Binding site not conserved.	ZINC ION
ZN	X - Binding site not conserved.	ZINC ION

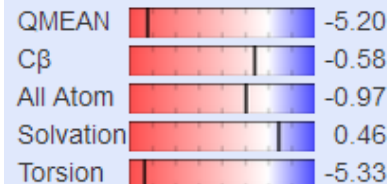
Oligo-State Ligands

Monomer None

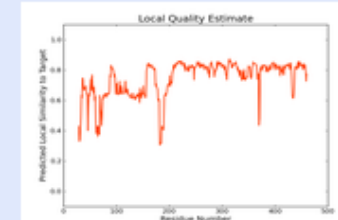
GMQE QMEAN

0.48 -5.20

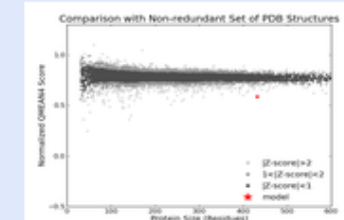
Global Quality Estimate



Local Quality Estimate



Comparison



Template Seq Identity Coverage

3jct.1.c 57.81%

Description

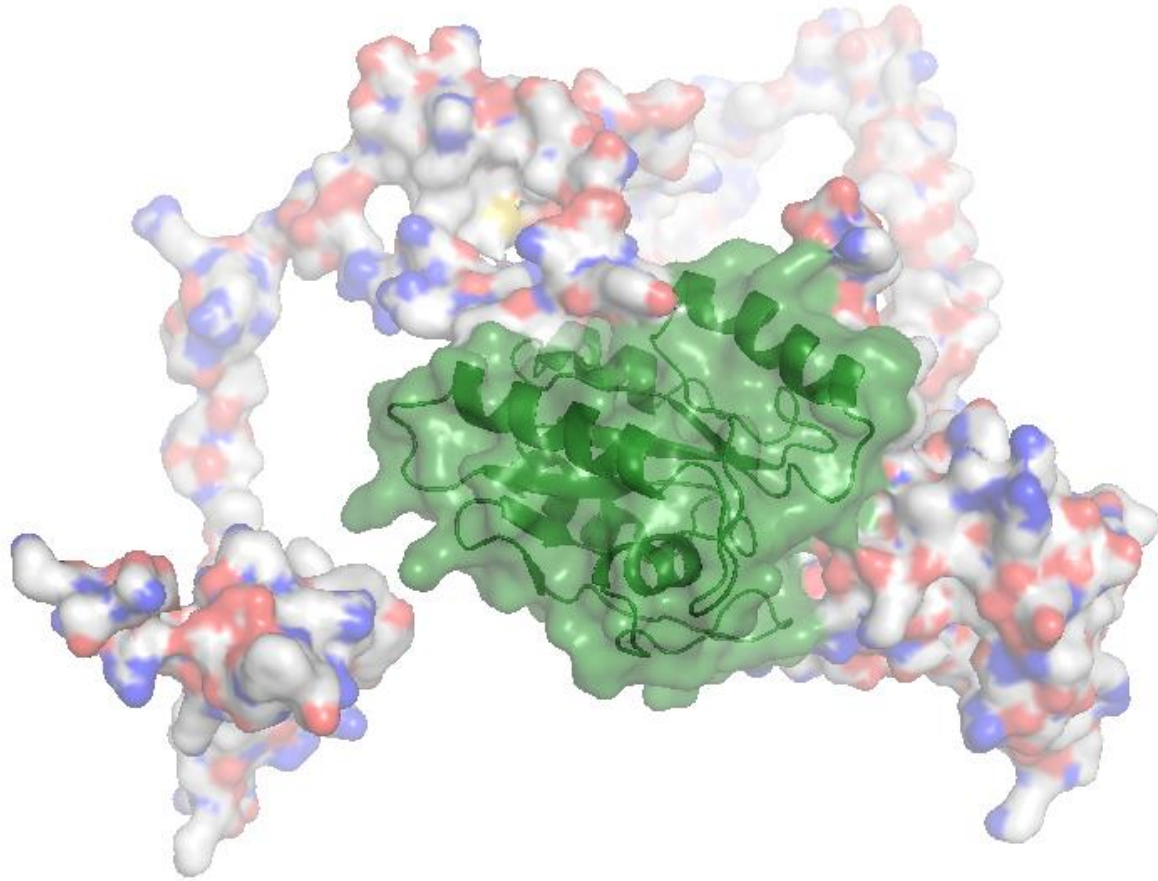
Nucleolar GTP-binding protein 2

Biounit Oligo State	Method	Seq Similarity	Range	Coverage
hetero-54-mer	EM	0.47	29 - 460	0.59

Ligand	Added to Model	Description
GTP	X - Binding site not conserved.	GUANOSINE-5'-TRIPHOSPHATE
GTP	X - Binding site not conserved.	GUANOSINE-5'-TRIPHOSPHATE
MG	X - Binding site not conserved.	MAGNESIUM ION
MG	X - Binding site not conserved.	MAGNESIUM ION
ZN	X - Binding site not conserved.	ZINC ION
ZN	X - Binding site not conserved.	ZINC ION
ZN	X - Binding site not conserved.	ZINC ION
ZN	X - Binding site not conserved.	ZINC ION



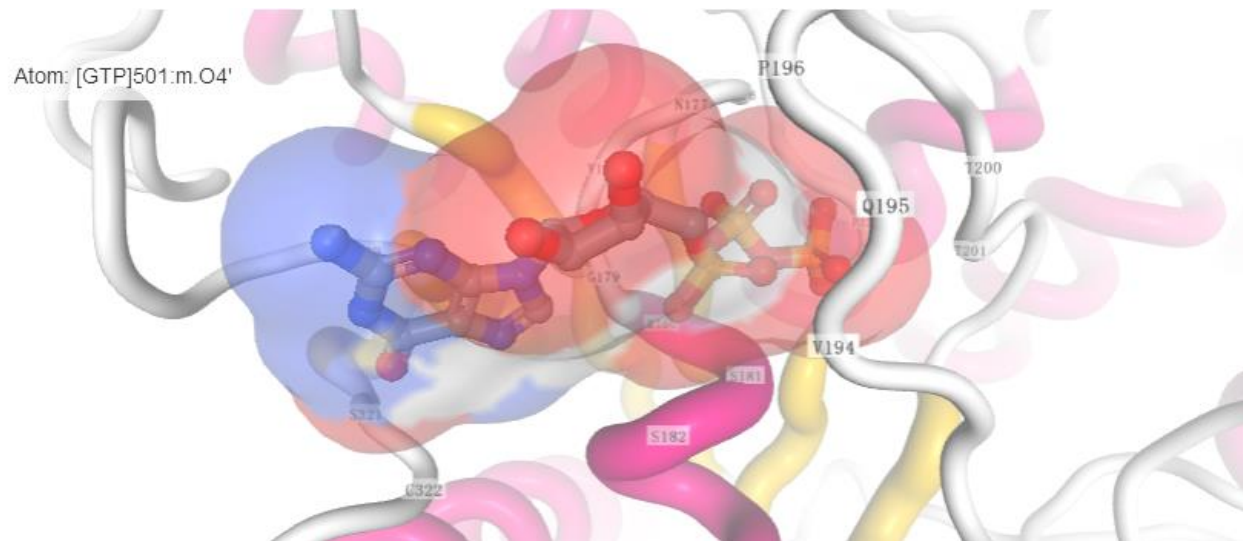
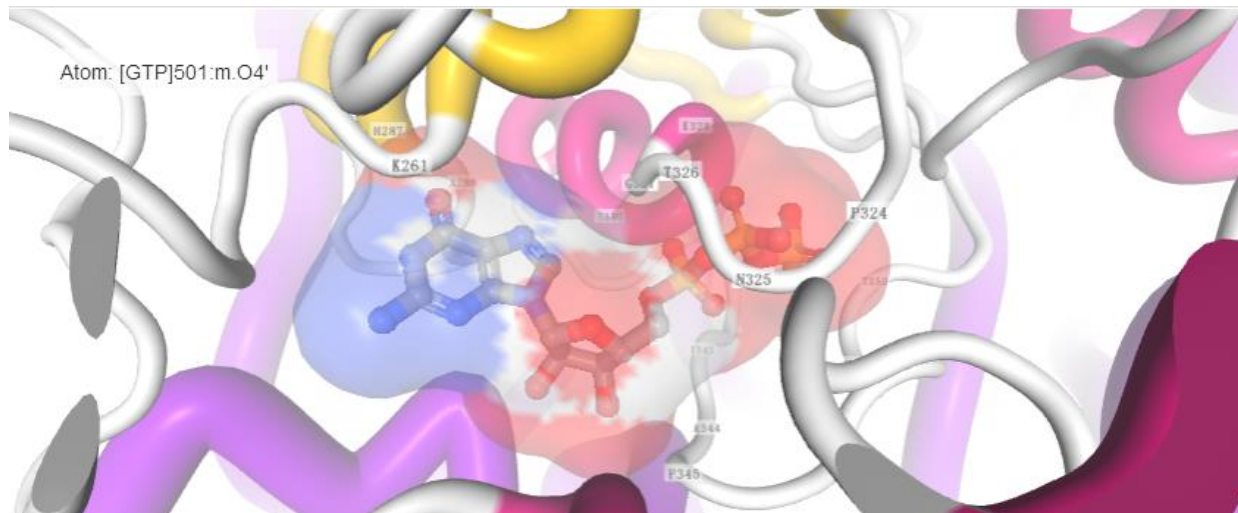
# 酵母NOG2的GTP结合位点（绿）



- NOG2蛋白的GTPase结构域为其功能结构域
- NOG2蛋白的GTPase结构域需要有互作蛋白才能行使其功能



# NOG2蛋白在60S ribosomal中的重要性

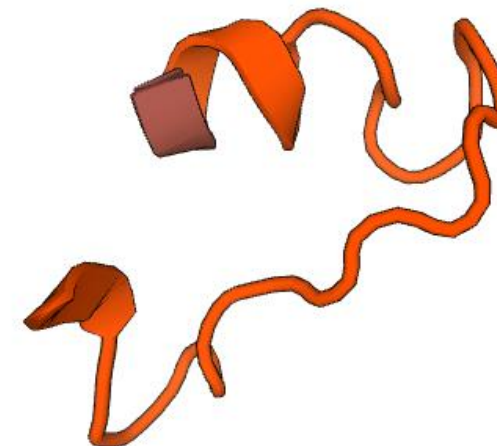
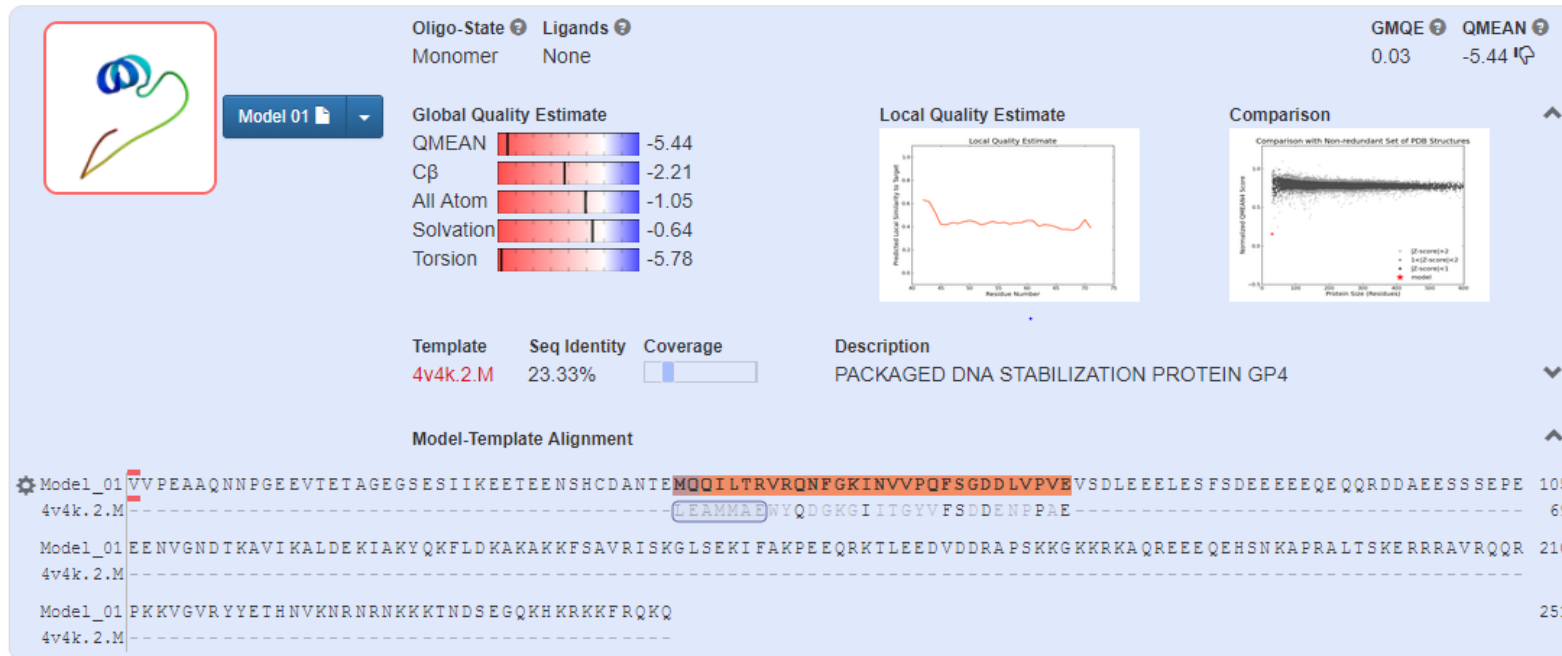


GTP结合位点!!!  
NOG1, NOG2





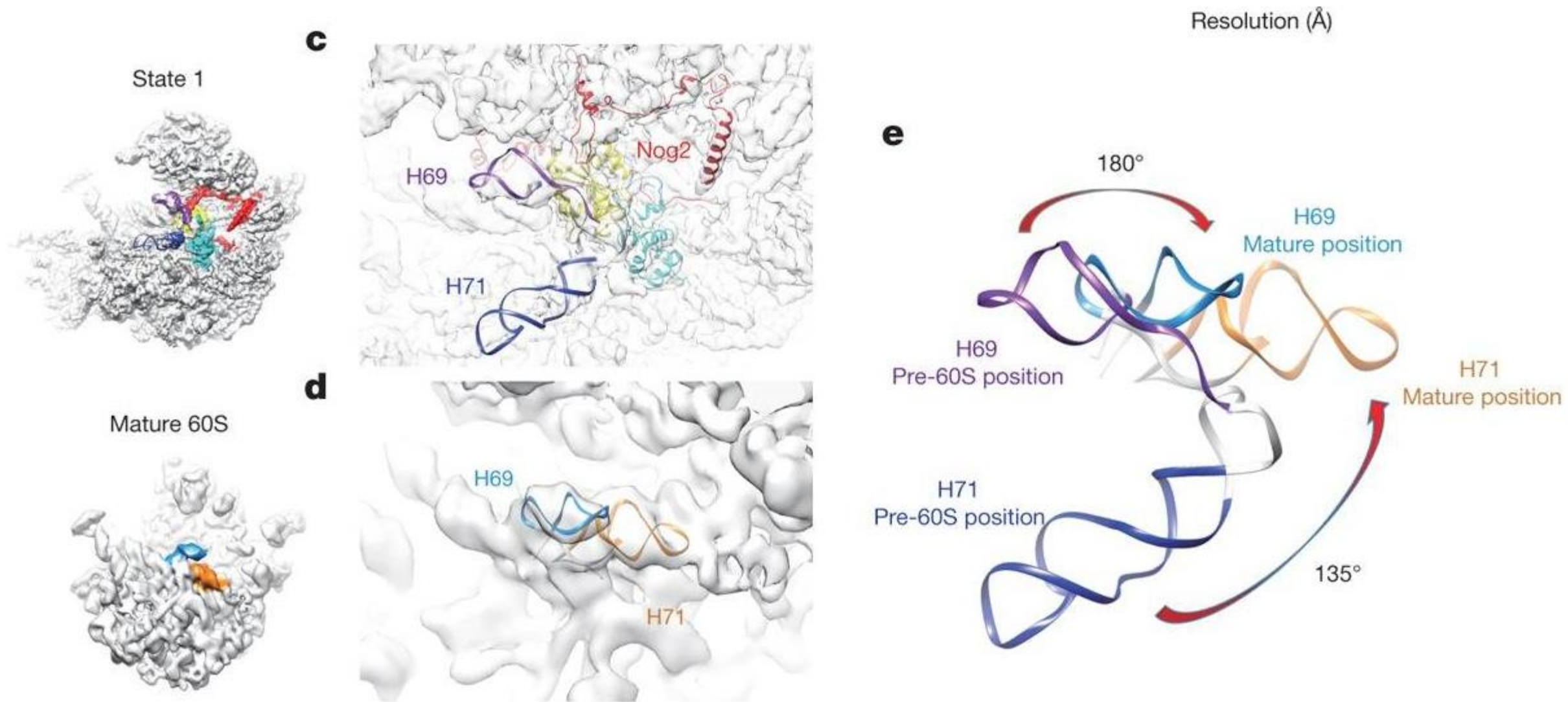
# Swiss Model预测的人NOG2部分序列



- 从序列比对情况来看，NOG2\_Human蛋白C'端多了一个结构域，长度约200个氨基酸。
- 对这200个氨基酸进行单独 Swiss-Model结构模拟后，结果如图。

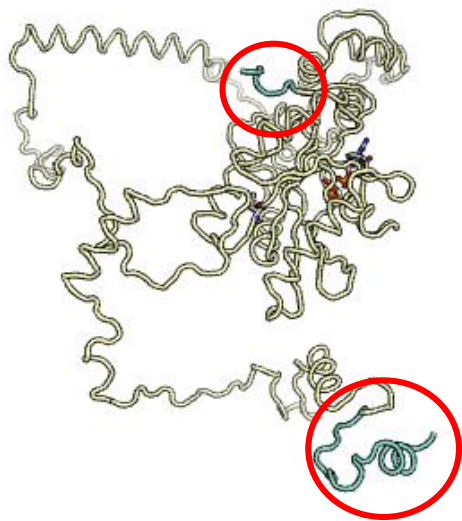


# 蛋白结构揭示互作机理

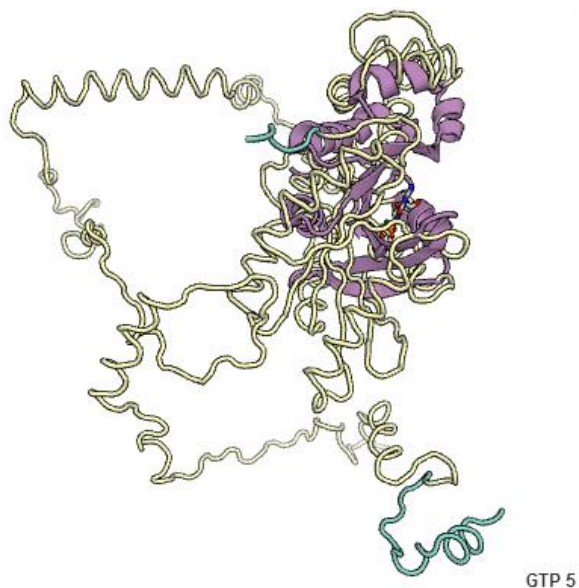
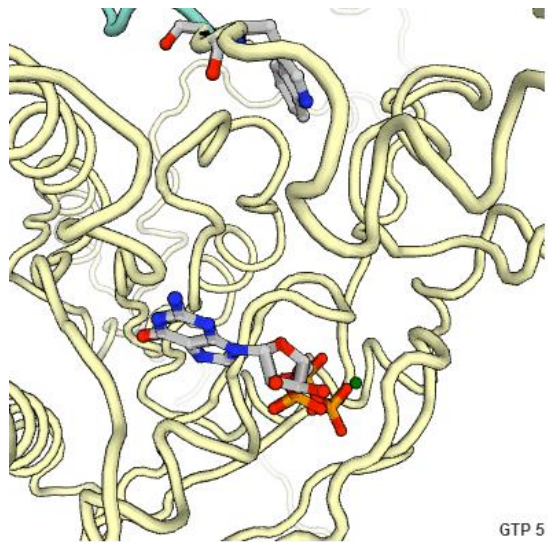


# NOG2\_Human预测结构图

54.78%



57.81%



- 多次预测结果显示出不同信息
- 下图表征GTP结合位点

