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# Sequence and function analysis and structure prediction of Human RNA binding protein NOB1

## 人RNA结合蛋白NOB1序列和功能分析以及结构预测

组 别：G09

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报告人：王迪

2015-1-25



# Outline

- ❖ Background
- ❖ Sequence analysis of NOB1
- ❖ Structure prediction of NOB1
- ❖ Function analysis of NOB1
- ❖ Summary
- ❖ Acknowledgement



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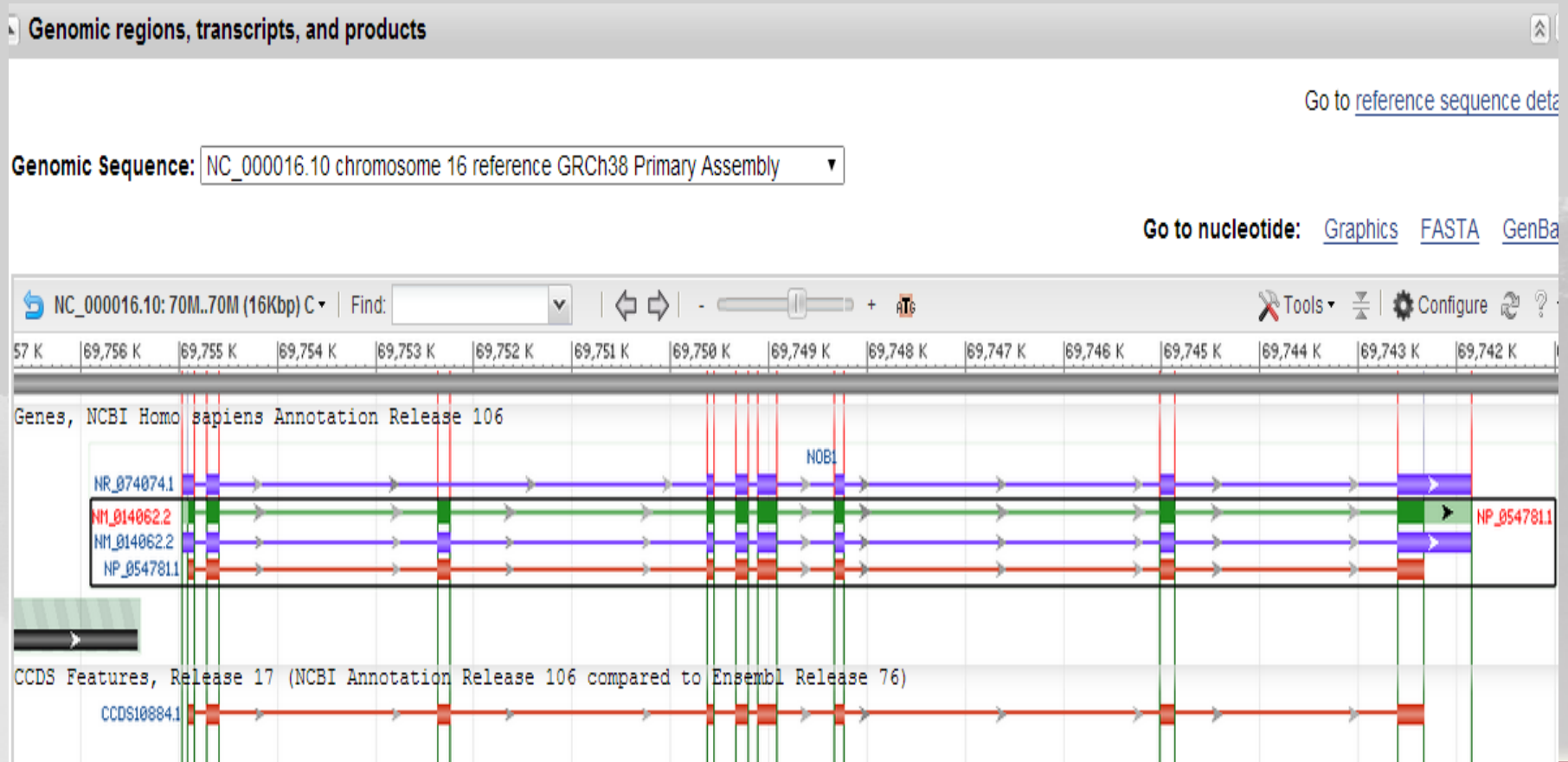
# Background

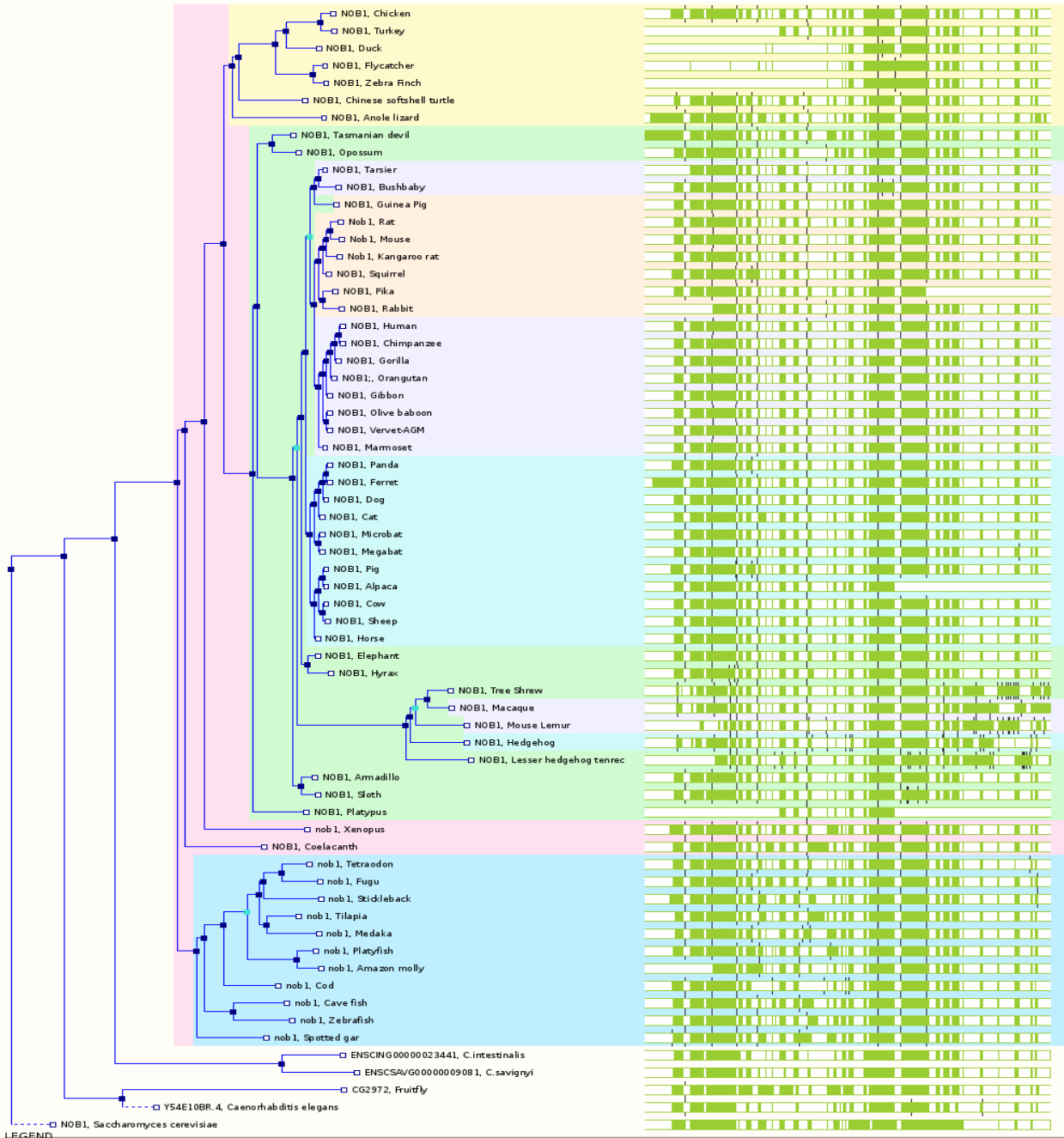




# NOB1 gene

ch16: Exons: 9, Coding exons: 9, Transcript length: 1,734 bps , Translation length: 412 residues





# Gene Tree of NOB1 gene between species

Ensembl:GeneTree  
 ENSGT003900000  
 15857

**LEGEND**

<b>Branch Length</b>	<b>Nodes</b>	<b>Genes</b>	<b>Collapsed nodes</b>	<b>Collapsed Alignments</b>	<b>Expanded Alignments</b>
— x1 branch length	□ gene node	Gene ID gene of interest	◀ collapsed sub-tree	◻ 0 - 33% aligned seq	◻ gap
- - - x10 branch length	■ speciation node	Gene ID within-sp. paralog	▶ collapsed (this gene)	◻ 33 - 66% aligned seq	◻ aligned seq
- - - x100 branch length	■ duplication node		▶ collapsed (paralog)	◻ 66 - 100% aligned seq	
	■ ambiguous node		(x10 branch length)		
	■ gene split event		(x100 branch length)		



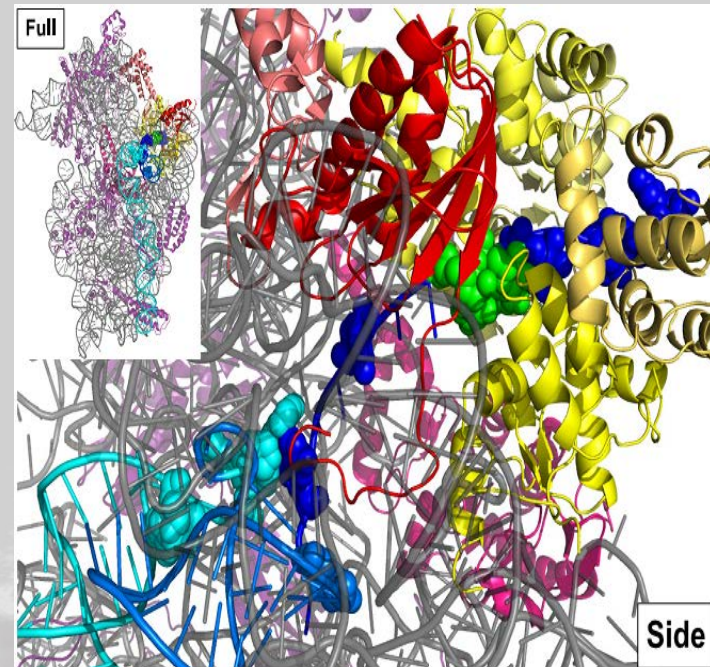
# Introduction to NOB1

NOB1 : RNA-binding protein

UniProt :

>>Function : **May** play a role in mRNA degradation during the synthesis of ribosome.

In yeast , it has a role in processing 20S pre-rRNA into the mature 18S rRNA , where it is required for cleavage at the 3' end of the mature 18S rRNA (D-site).

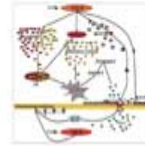


**Model for the interaction of Nob1's PIN domains with preribosomes**



Gene silencing of NOB1 by lentivirus suppresses growth and migration of human osteosarcoma cells

Open Access



6(10): 2137-2144.  
2013.

PMCID: PMC

Authors: Bingpeng Chen, Jingjing Liu, Dankai Wu, Yanguo Qin, Chuangang Peng, Chen Jincheng Wang

Influence of NOB1 expression in breast infiltrating ductal

Downregulation of NOB1 suppresses the proliferation and tumor growth of non-small cell lung cancer in vitro and in vivo



Jin-Feng Zhang, Lin Fang



Authors: Yang Li, Chengyuan Ma, Ming Qian, Zhongmei Wen, Hongyu Jing, Donghua



Suppresses the

verdrückt die Zellproliferation

Thieme

Year

Y. Liu, H. Huang, B. Yuan, L. Y. Zhuang, T. P. Luo, Q. Zhang



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## Goal

Explore the mechanism in the term of structure biology

Use bioinformatic methods to give us information about NOB1's properties , purification and structure.

**Half day on the Web, saves you half month in the lab!**





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# Sequence analysis of NOB1



# NOB1 protein sequence

>sp|Q9ULX3|NOB1\_HUMAN RNA-binding protein NOB1 OS=Homo sapiens GN=NOB1 PE=1 SV=1

MAPVEHVADAGAFRLRHAALQDIGKNIYTIREVVTEIRDKATRRRLAVLPYE  
 LRFKEPLPEYVRLVTEFSKKTGDYPSLSATDIQVLALTYQLEAEFVGVSHL  
 KQEPQKVKVSSSIQHPETPLHISGFHLPYKPKPPQETEKGHSACEPENLEF  
 SSFMFWRNPLPNIDHELQELLIDRGEDVPSEEEEEEEENGFEEDRKDDSDDD  
 GGGWITPSNIKQIQQELEQCDVPEDVRVGCLTTDFAMQNVLLQMGLHVLA  
 VNGMLIREARSYILRCHGCFKTTSDMSRVFCSHCGNKTLLKVSVTVSDDG  
 TLHMHFSRNPKVLNPRGLRYSLPTPKGGKYAINPHLTEDQRFPQLRLSQK  
 ARQKTNVFAPDYIAGVSPFVENDISSRSATLQVRDSTLGAGRRRLNPNAS  
 RKKFVKKR

## Q9ULX3 - NOB1\_HUMAN

Protein	RNA-binding protein NOB1
Gene	NOB1
Organism	<i>Homo sapiens (Human)</i>
Status	Reviewed -  - Experimental evidence at protein level <sup>1</sup>

**Length:** 412  
**Mass (Da):** 46,675  
**Last modified:** May 1, 2000 - v1  
**Checksum:**<sup>i</sup> 369680A6DCFC7CB0



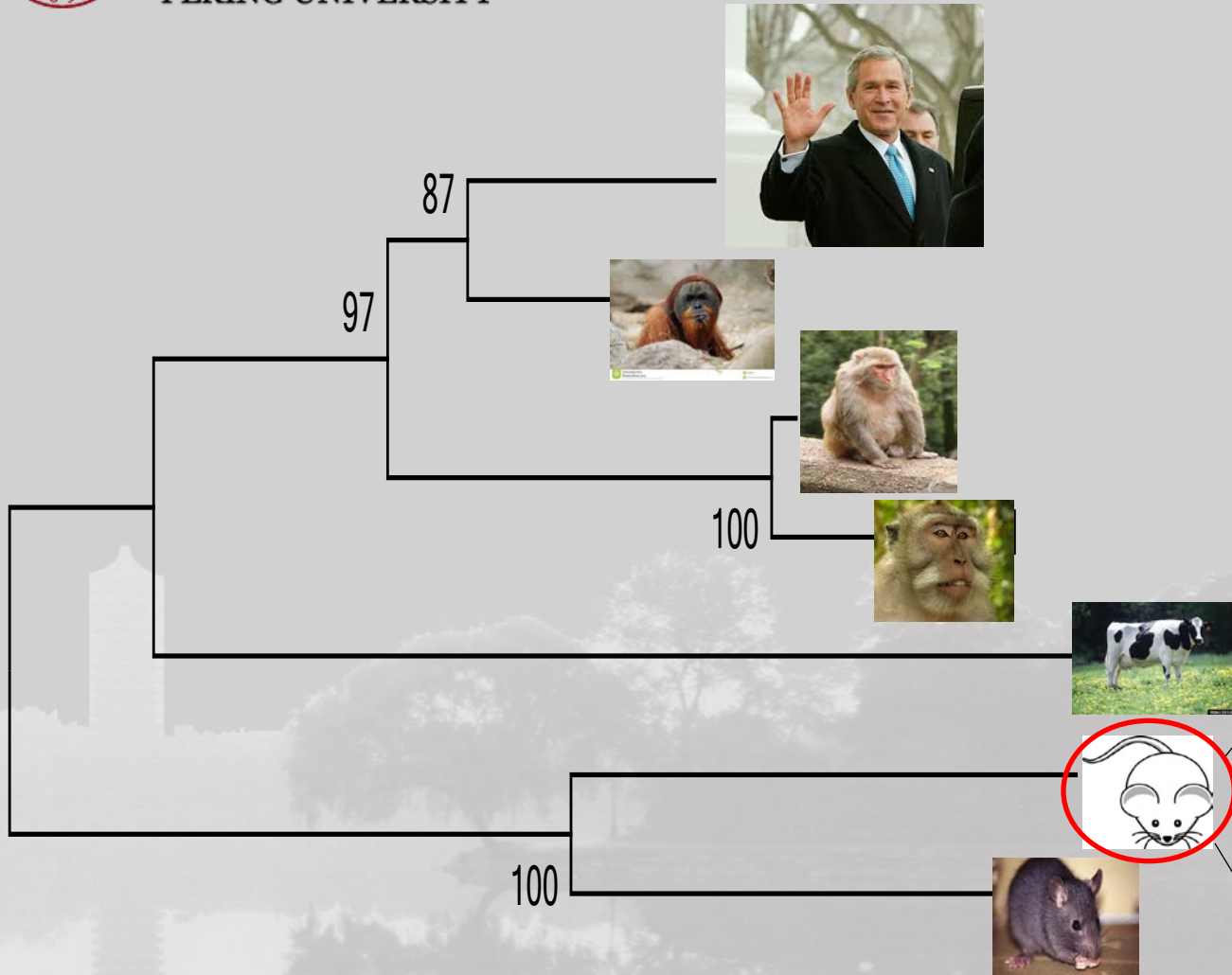
# protein sequence alignment

NO	Accession	Name	Species	Total score	Query cover	E value	Ident
1	NP_054781.1	hNOB1	<i>Homo sapiens</i>	631	100%	0.0	100%
2	NP_001245126.1	mmNOB1	<i>Macaca mulatta</i>	616	100%	0.0	96%
3	NP_001270471.1	mfNOB1	<i>Macaca fascicularis</i>	614	100%	0.0	96%
4	NP_001127354.1	pNOB1	<i>Pongo abelii</i>	614	100%	0.0	97%
5	NP_898906.1	bNOB1	<i>Bos taurus</i>	601	100%	0.0	90%
6	NP_080553.1	mNOB1	<i>Mus musculus</i>	594	100%	0.0	87%
7	NP_954517.1	rNOB1	<i>Rattus norvegicus</i>	593	100%	0.0	88%



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# Phylogenetic tree



Mouse NOB1 CTD  
(PDB ID: 2CON)

0.01

MEGA 6.0



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# Structure prediction





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# Secondary structure and disorder prediction

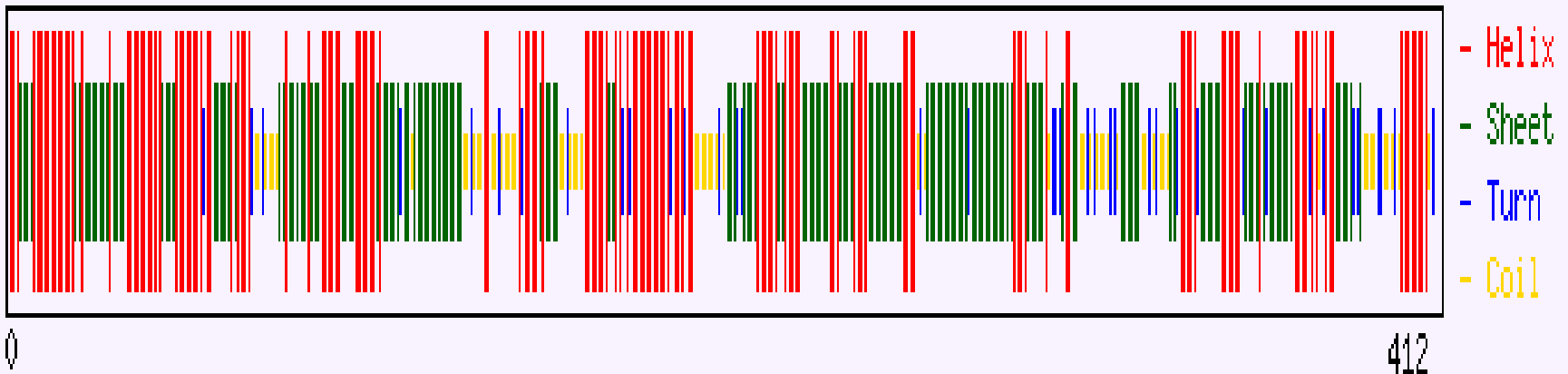


## CFSSP: Chou & Fasman Secondary Structure Prediction Server

[Home](#)[Blog](#)[Forum](#)[Tools](#)[Academic](#)[Contact](#)[Mail](#)

Name of the sequence is *sp|Q9ULX3|NOB1\_HUMAN RNA-binding protein NOB1 OS=Homo sapiens GN=NOB1 PE=1 SV=1*.

Sequence consists of 412 amino acids.



Total Residues: H: 249 E: 249 T: 59

Percent: H: 60.4 E: 60.4 T: 14.3



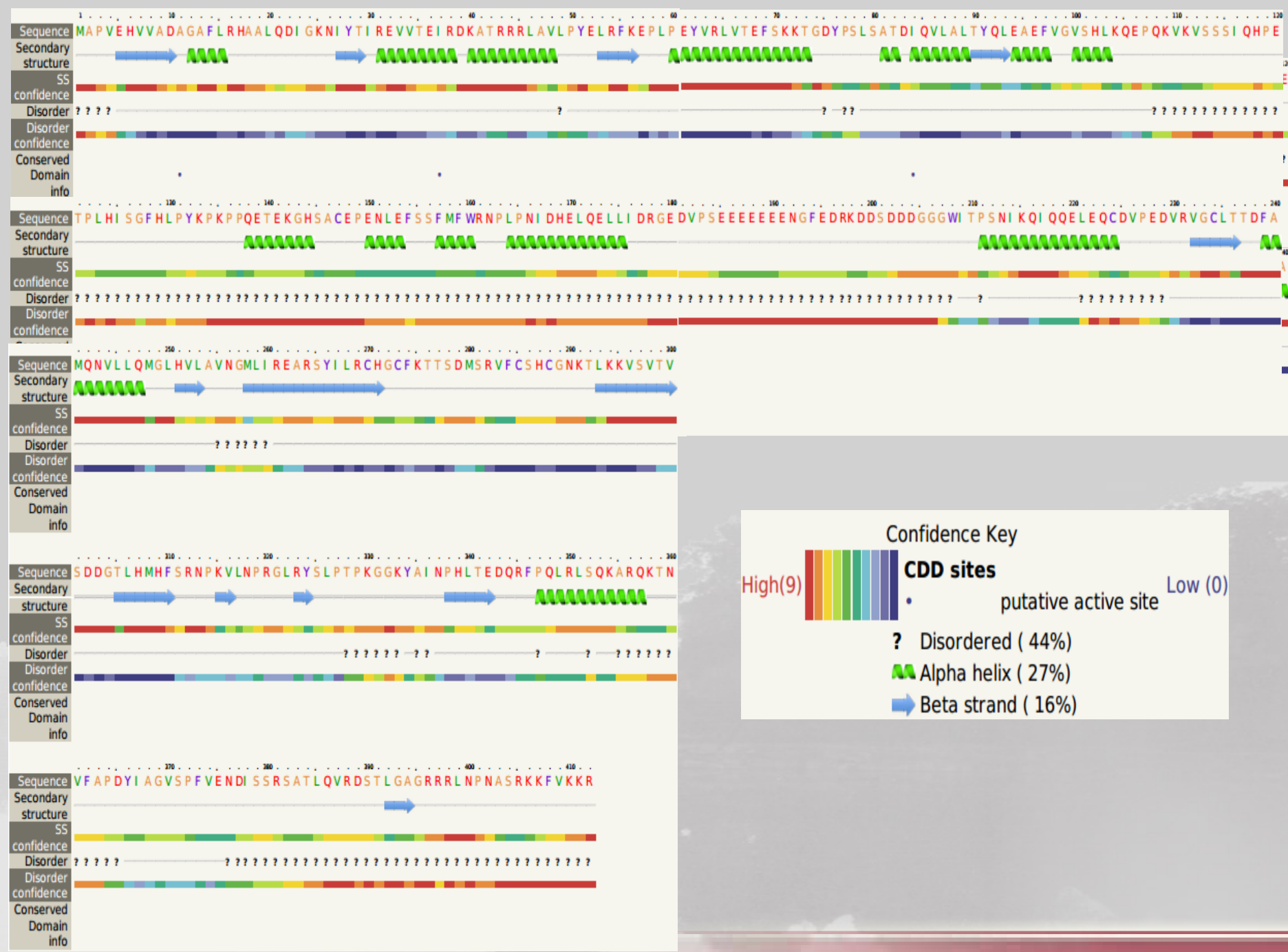
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# Secondary structure and disorder prediction

# Phyre<sup>2</sup>

Email	[REDACTED]
Description	NOB1_3D_
Date	Sat Jan 17 02:11:39 GMT 2015
Unique Job ID	3dcc997cd47732b1
Sequence	MAPVEHWAD ... <a href="#">Download FASTA</a>
Job Expiry	30 days





### Confidence Key

High(9) Low (0)

**CDD sites**

putative active site

- ? Disordered ( 44%)
- AA Alpha helix ( 27%)
- ➔ Beta strand ( 16%)



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# 3D structure prediction



Model 01

Oligo-State	Ligands	GMQE <sup>2</sup>	QMEAN4 <sup>2</sup>
MONOMER	None	0.20	-5.09

Template	Seq Identity	Coverage	Description
2lcq.1.A	29.05%		Putative toxin VapC6

Model-Template Alignment



Model 02

Oligo-State	Ligands	GMQE <sup>2</sup>	QMEAN4 <sup>2</sup>
MONOMER	None	0.10	-4.24

Template	Seq Identity	Coverage	Description
2lcq.1.A	36.47%		Putative toxin VapC6

Model-Template Alignment



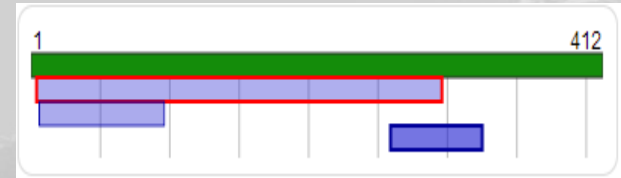
Model 03

Oligo-State	Ligands	GMQE <sup>2</sup>	QMEAN4 <sup>2</sup>
MONOMER	None	0.10	-2.71

Template	Seq Identity	Coverage	Description
2con.1.A	92.42%		nin one binding protein

Model-Template Alignment





## 2lcq: Solution structure of the endonuclease Nob1 from *P.horikoshii*

↑ **Molecular Description**

**Classification:** Metal Binding Protein [↗](#)

**Structure Weight:** 18397.98 [i](#)

**Molecule:** Putative toxin VapC6

**Polymer:** 1    **Type:** protein    **Length:** 165

**Chains:** A

**EC#:** 3.1 [↗](#) [EC](#)

**Organism:** *Pyrococcus horikoshii* OT3 [↗](#)

**Gene Names:** nob1 vapC6 PH0709

**UniProtKB:** [Protein Feature View](#) | [Search PDB](#) [↗](#) | [O58440](#) [↗](#)

The diagram illustrates the protein structure and associated motifs for Nob1. It features a vertical axis on the left with labels: UniProtKB (O58440), Molec. Processing (Endoribonuclease Nob1), Motif (PINc, Fle, Zinc ribbon), E.C. (Endoribonuclease Nob1), UP Sites, Secstruc, and PDB (2LCQ.A). The main structure is shown as a horizontal bar with a grey top section and a blue bottom section. A green bar represents the protein sequence, with a yellow box labeled 'PINc' and a green box labeled 'Fle'. A red bar represents the zinc ribbon motif. Blue dots indicate UP sites. The PDB entry 2LCQ.A is shown at the bottom.



## 2con: Solution Structure of a Zn-ribbon module in Mouse cDNA

† Molecular Description

**Classification:** Ribosome

**Structure Weight:** 8641.16

**Molecule:** nin one binding protein

**Polymer:** 1    **Type:** protein    **Length:** 79

**Chains:** A

**Fragment:** Zn-ribbon module

**Organism:** Mus musculus

**Gene Name:** Nob1

**UniProtKB:** [Protein Feature View](#) | [Search PDB](#) | Q8BW10

The diagram illustrates the protein structure and associated motifs. It features a horizontal bar representing the protein sequence, with a grey bar above it and a green bar below it. The green bar is labeled 'RNA-binding protein NOB1' and contains a 'PINc' motif. Below the green bar, a 'Po' motif is indicated. The 'UP Sites' are shown as blue dots on the green bar. The 'Secstruc' is shown as a blue bar at the bottom. The 'PDB' entry '2CON.A' is also indicated. The UniProtKB entry 'Q8BW10' is shown on the left side of the diagram.

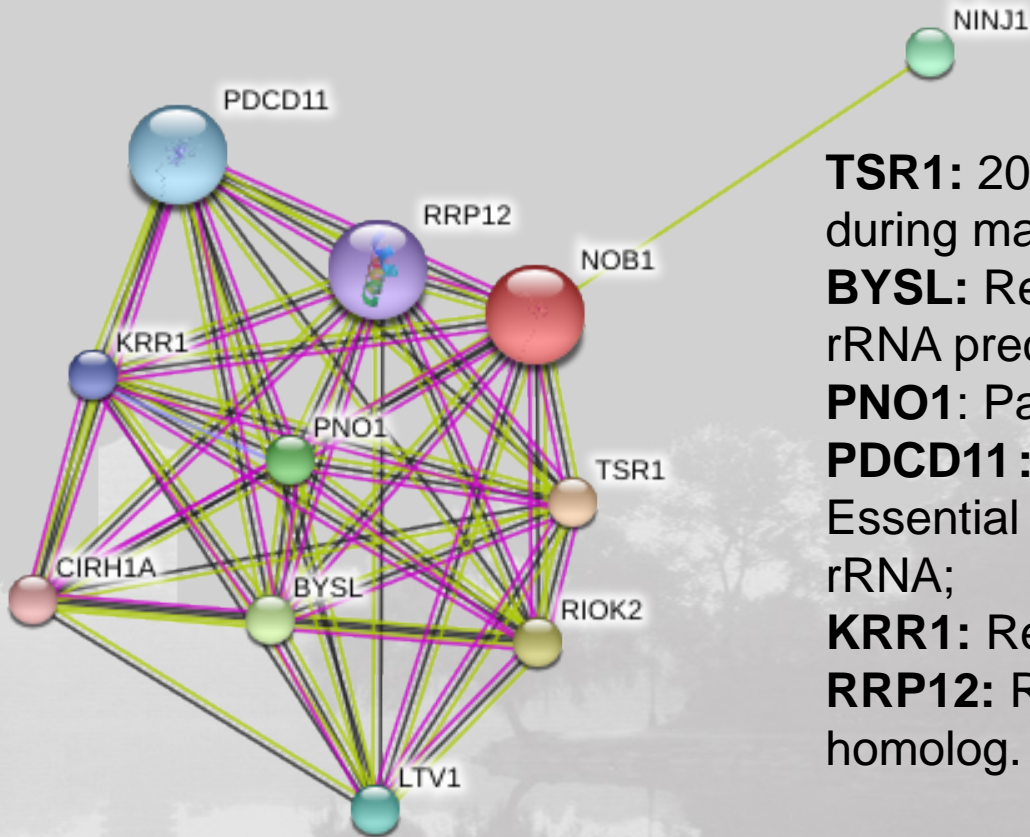


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# function analysis



# Protein interaction of NOB1 in STRING database



**TSR1:** 20S rRNA accumulation, Required during maturation of the 40S rib;

**BYSL:** Required for processing of 20S pre-rRNA precursor and biogenesis of 40S rib;

**PNO1:** Partner of NOB1 homolog;

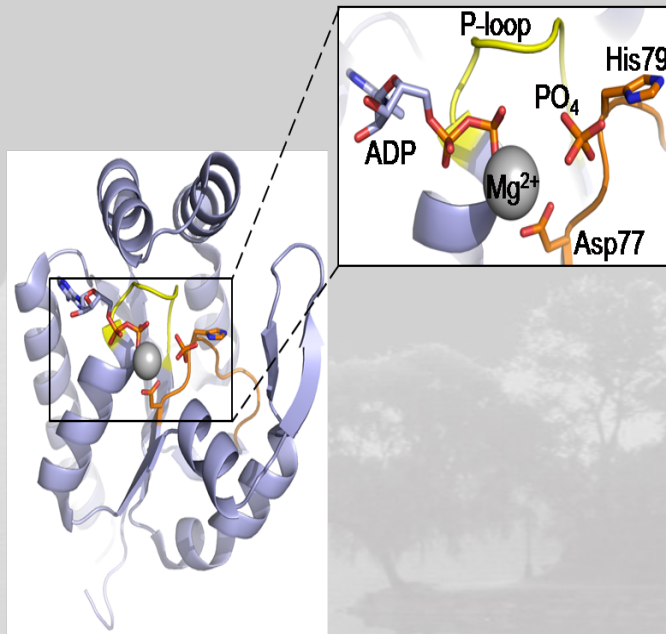
**PDCD11:** Programmed cell death 11; Essential for the generation of mature 18S rRNA;

**KRR1:** Required for 40S ribosome biogenesis

**RRP12:** Ribosomal RNA processing 12 homolog.

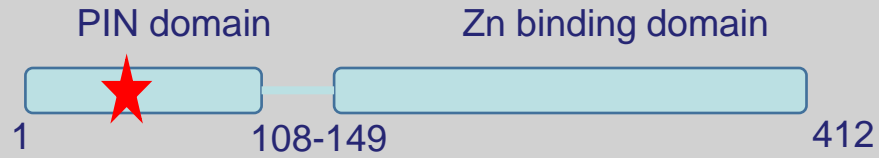


## Another important protein : hCINAP



- A novel protein that has two enzyme activities:  
adenylate kinase and ATPase
- In our previous study , hCINAP also plays an important role in the cleavage and maturation of 18S rRNA .

### Structure of hCINAP

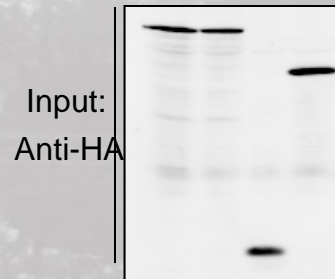
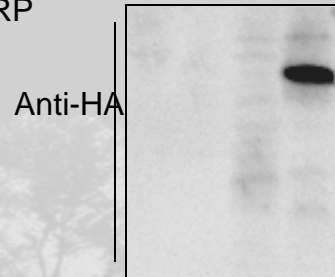


# Interaction between NOB1 and hCINAP

Flag-hCINAP      +      +      +      +

HA-Nob1  
120-412      —      +      +      1-114

Ig      IP: anti-Flag



(By BDM)

hCINAP can interact with NOB1 at its C terminal domain .



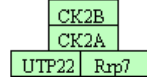
# RIBOSOME BIOGENESIS IN EUKARYOTES

## Ribosomal RNAs

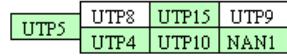


## 90S pre-ribosome components

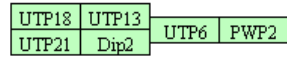
### UTP-C complex



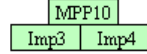
### t-UTP complex



### UTP-B complex

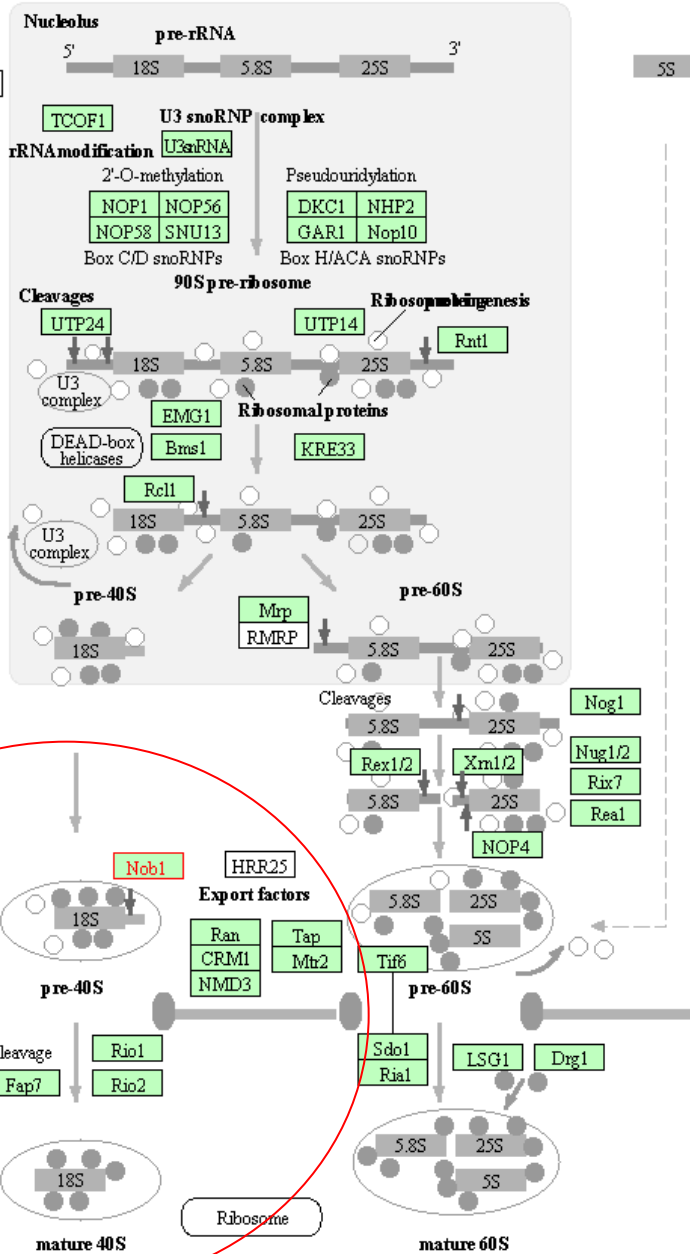


### MPP10 complex



Pol I

Pol III



Pathway involving NOB1 in KEGG database

KEGG:  
hsa: 28987



## Summary

- The NOB1 is very conserved across species;
- Human NOB1 protein may have two potential functional domain according to solved structures in PDB;
- NOB1 have significant effect during ribosome biogenesis.



# Acknowledgement:

- Prof. LUO jingchu
- Yang yongfeng, Liang kai, Sun xin
- Prof. ZHENG xiaofeng
- Prof. XIAO junyu
- Prof. LUO shujin
- Prof. LU jian



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*Thank you for  
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&  
Happy Holiday*