



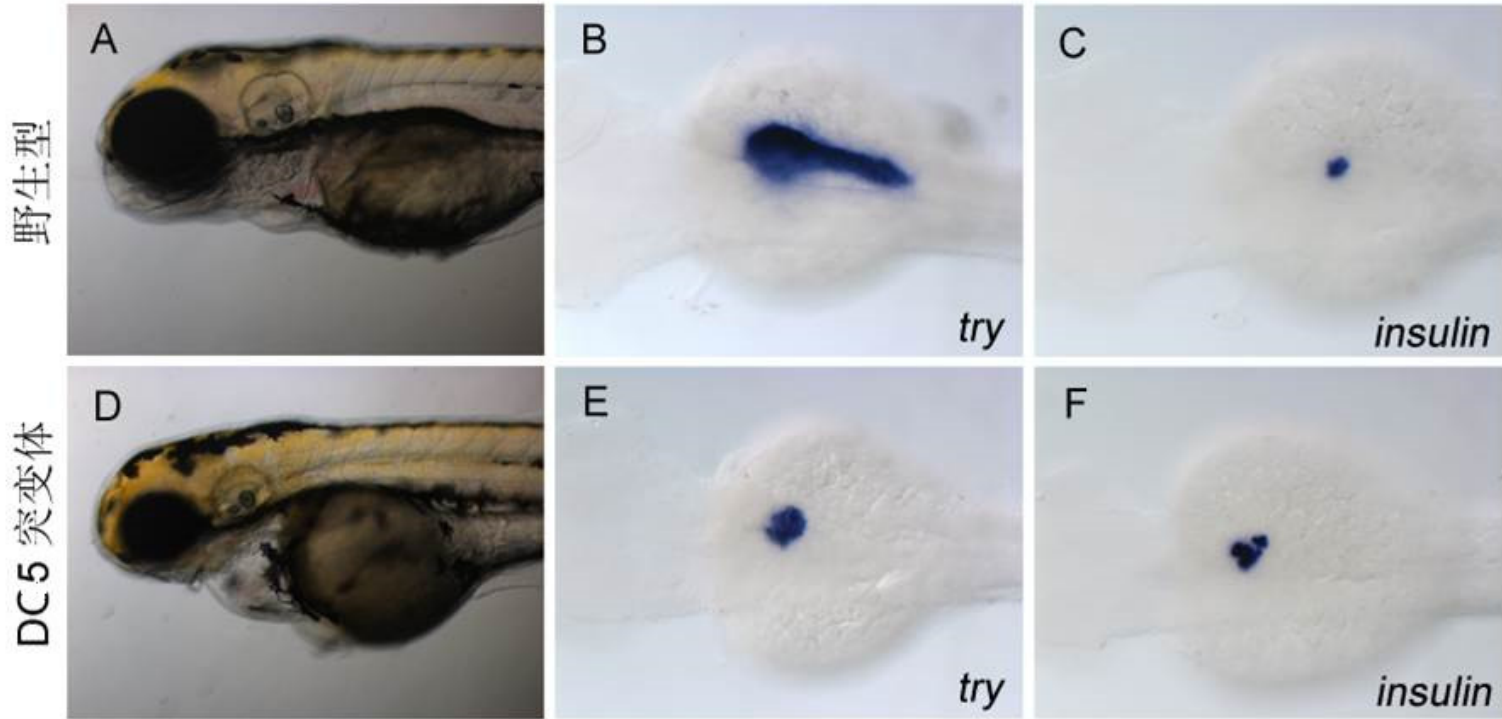
斑马鱼 *nom1* 基因 序列分析及功能预测

G10

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小组成员：冯燕 冯园园 闫冠蓉

nom1 mutants DC5



Summary of gene *nom1*

Gene: nom1 ENSDARG00000060027

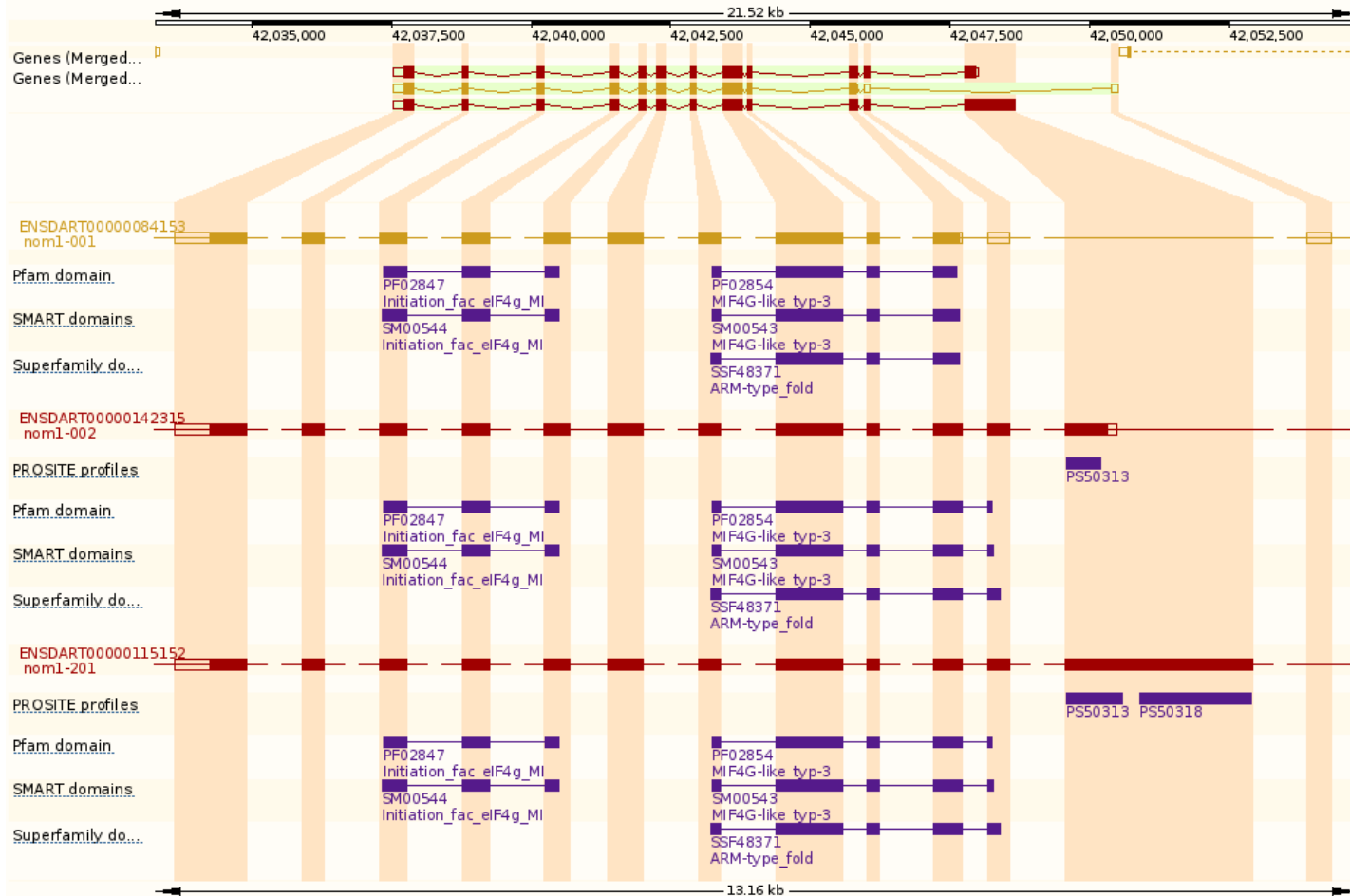
Description nucleolar protein with MIF4G domain 1 [Source:ZFIN;Acc:ZDB-GENE-060503-321]

Location [Chromosome 7: 42,037,543-42,050,504](#) reverse strand.

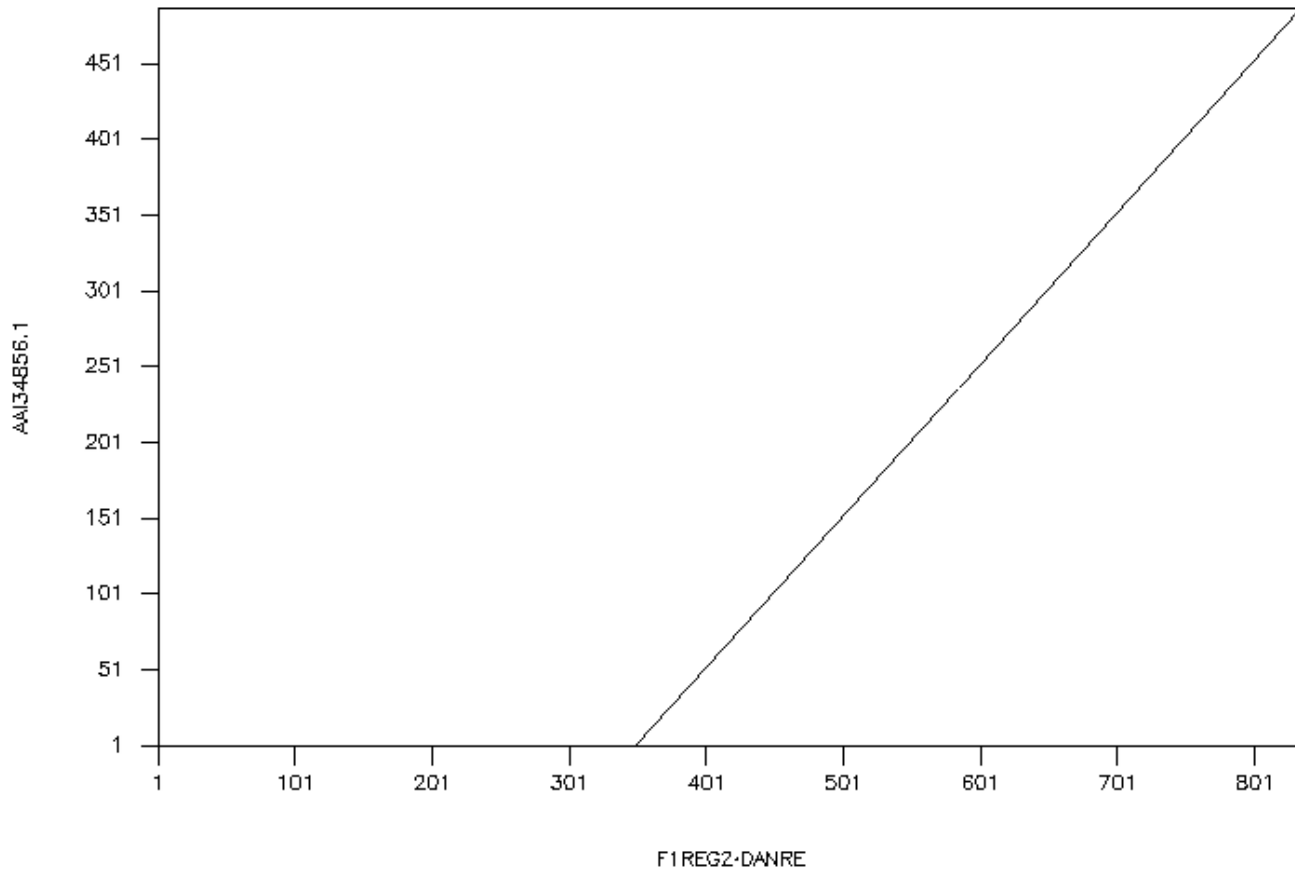
Transcripts This gene has 3 transcripts (splice variants) [Hide transcript table](#)

Show/hide columns		Filter			
Name	Transcript ID	Length (bp)	Protein ID	Length (aa)	Biotype
nom1-201	ENSDART00000115152	2680	ENSDARP00000100654	835	Protein coding
nom1-002	ENSDART00000142315	2017	ENSDARP00000122404	598	Protein coding
nom1-001	ENSDART00000084153	1886	ENSDARP00000078588	487	Protein coding

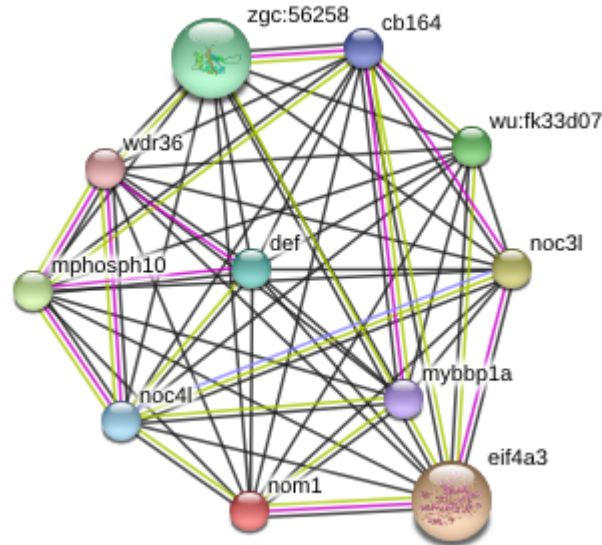
Splice variants



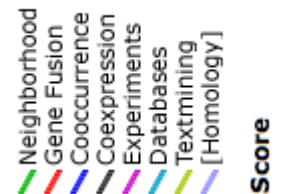
Dottup:Nom1-AA-835 vs .487



String: Functional protein association networks of nom1

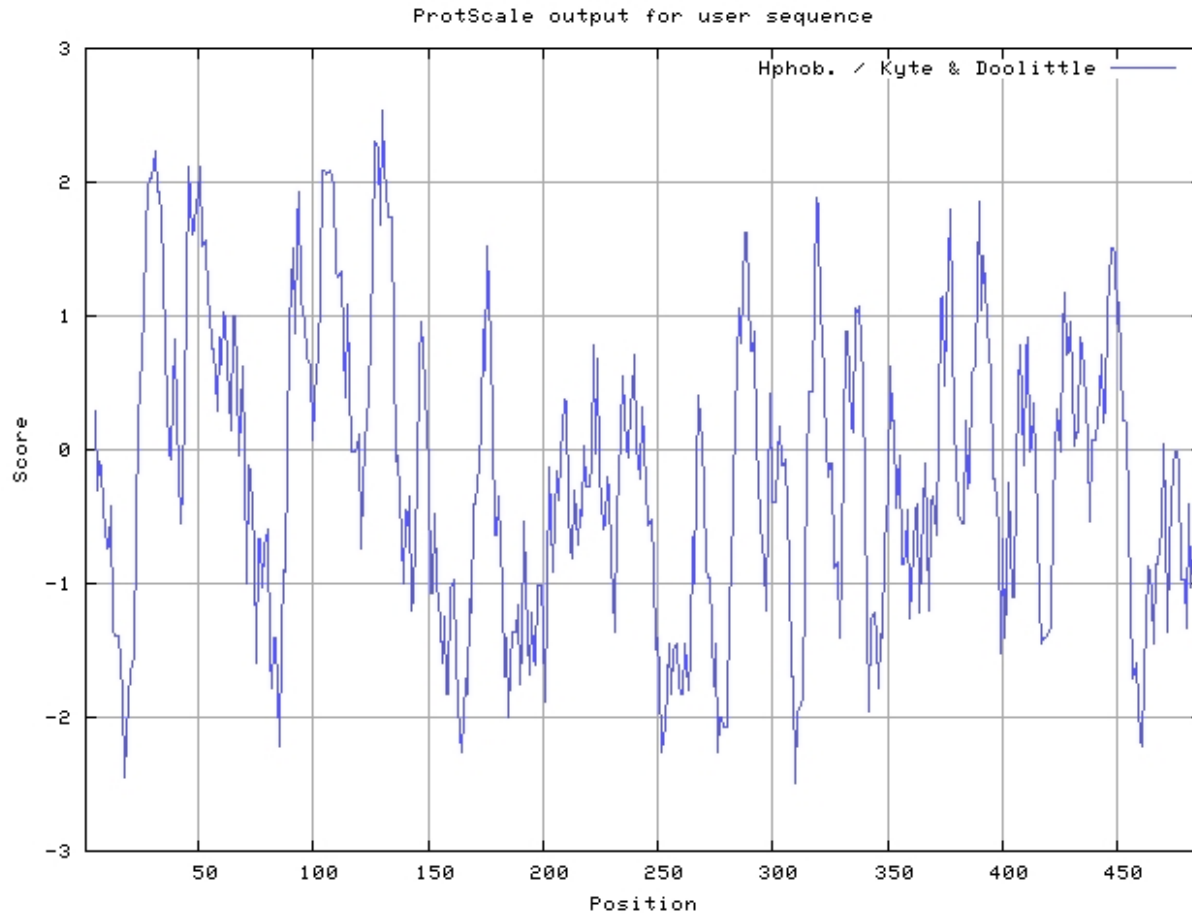


● nom1 nucleolar protein with MIF4G domain 1 (*Danio rerio*)

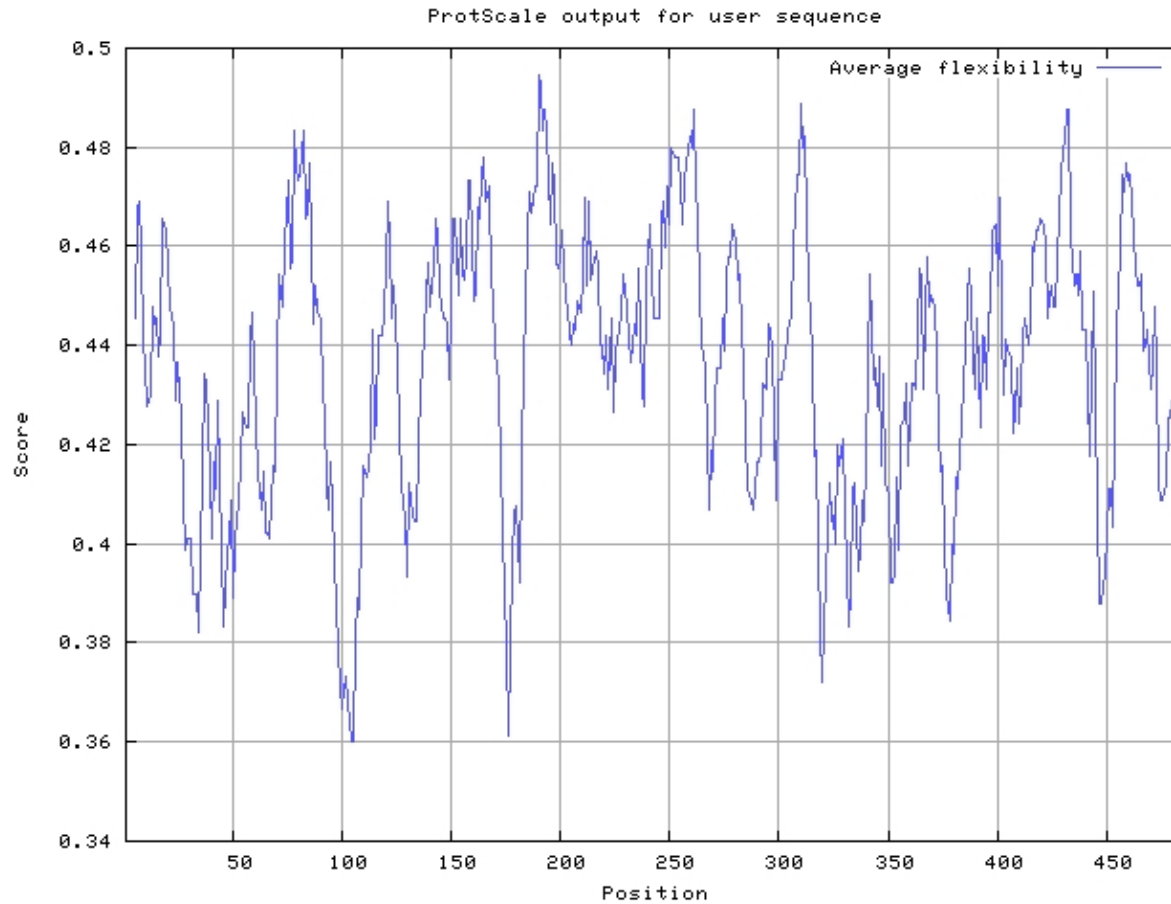


Protein	Description	Neighborhood	Gene Fusion	Cooccurrence	Coexpression	Experiments	Databases	Textmining	[Homology]	Score
eif4a3	Eukaryotic initiation factor 4A-III (EC 3.6.1.-)(Eukaryotic translation initiation factor 4A is [...]) (406 aa)				●	●			●	0.864
noc3l	Nucleolar complex protein 3 homolog (NOC3 protein homolog)(NOC3-like protein)(Nucleolar complex [...]) (800 aa)				●					0.819
mphosph10	M-phase phosphoprotein 10 (U3 small nucleolar ribonucleoprotein) (695 aa)				●					0.806
wu:fk33d07	Novel protein (533 aa)				●					0.789
zgc:56258	RNA binding motif protein 28 (856 aa)				●					0.789
def	Digestive organ expansion factor ; Regulates the p53 pathway to control the expansion growth of [...]) (753 aa)				●					0.781
noc4l	Nucleolar complex protein 4 homolog (NOC4 protein homolog)(NOC4-like protein)(Nucleolar complex [...]) (528 aa)				●				●	0.771
cb164	Si-dkey-91i17.1 protein Fragment (676 aa)				●					0.762
mybbp1a	Myb-binding protein 1A-like protein ; May activate or repress transcription via interactions wi [...]) (1140 aa)				●				●	0.753
wdr36	WD repeat domain 36 (896 aa)				●					0.752

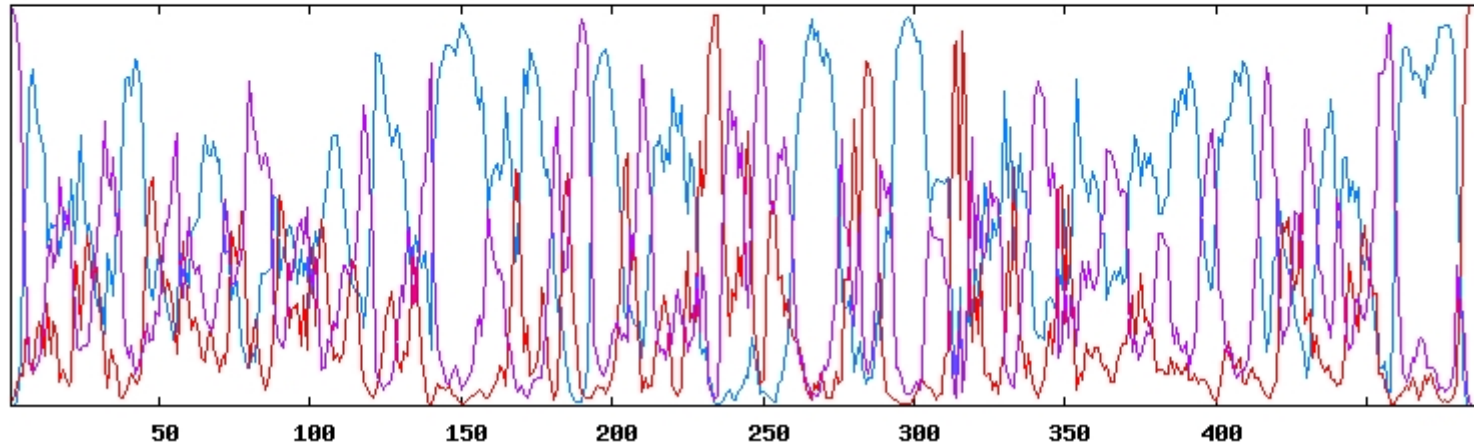
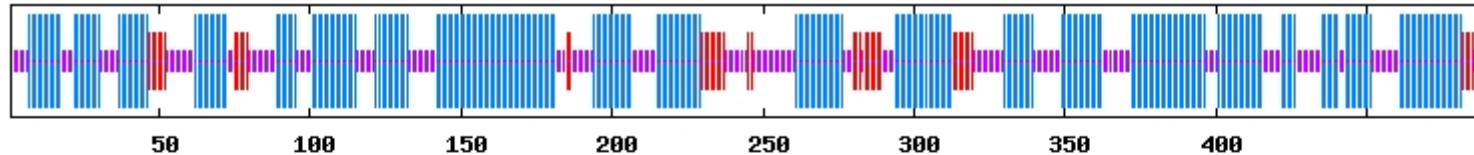
Hydrophily & Hydrophobic Analysis



Hardness&Flexibility Analysis



Secondary structure prediction

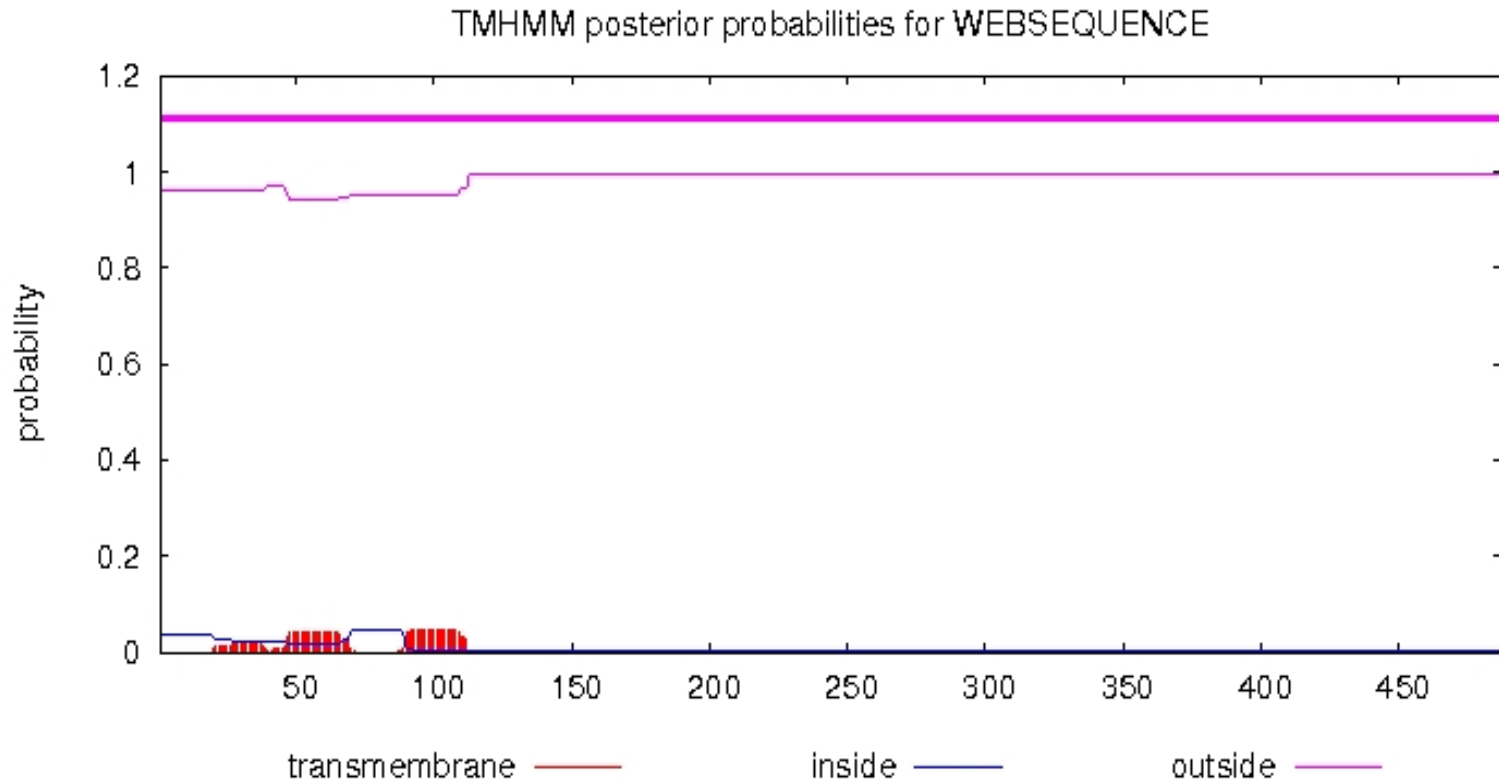


Sequence length : 487

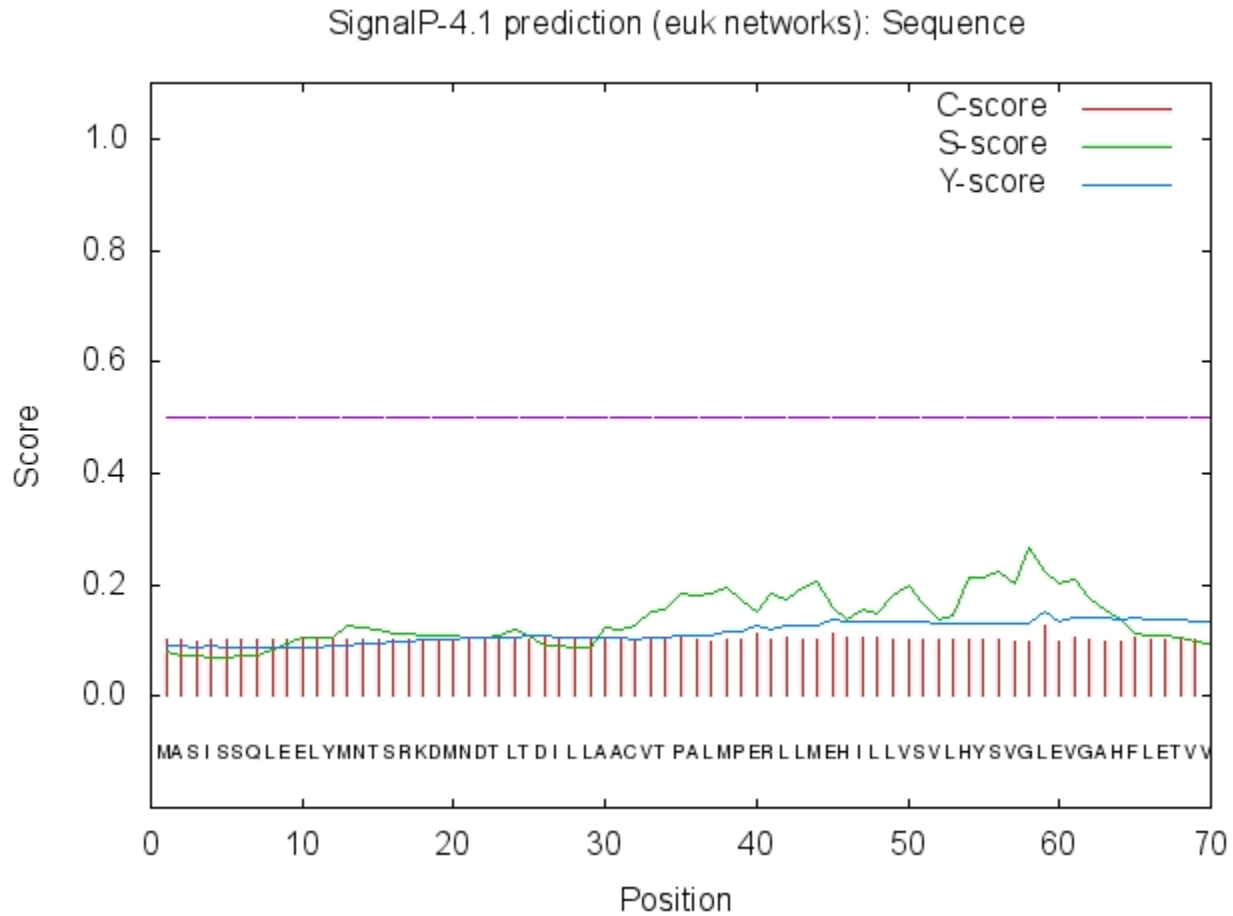
GOR4 :

Alpha helix	(Hh)	:	282	is	57.91%
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)	:	43	is	8.83%
Beta turn	(Tt)	:	0	is	0.00%
Bend region	(Ss)	:	0	is	0.00%
Random coil	(Cc)	:	162	is	33.26%
Ambiguous states (?)		:	0	is	0.00%
Other states		:	0	is	0.00%

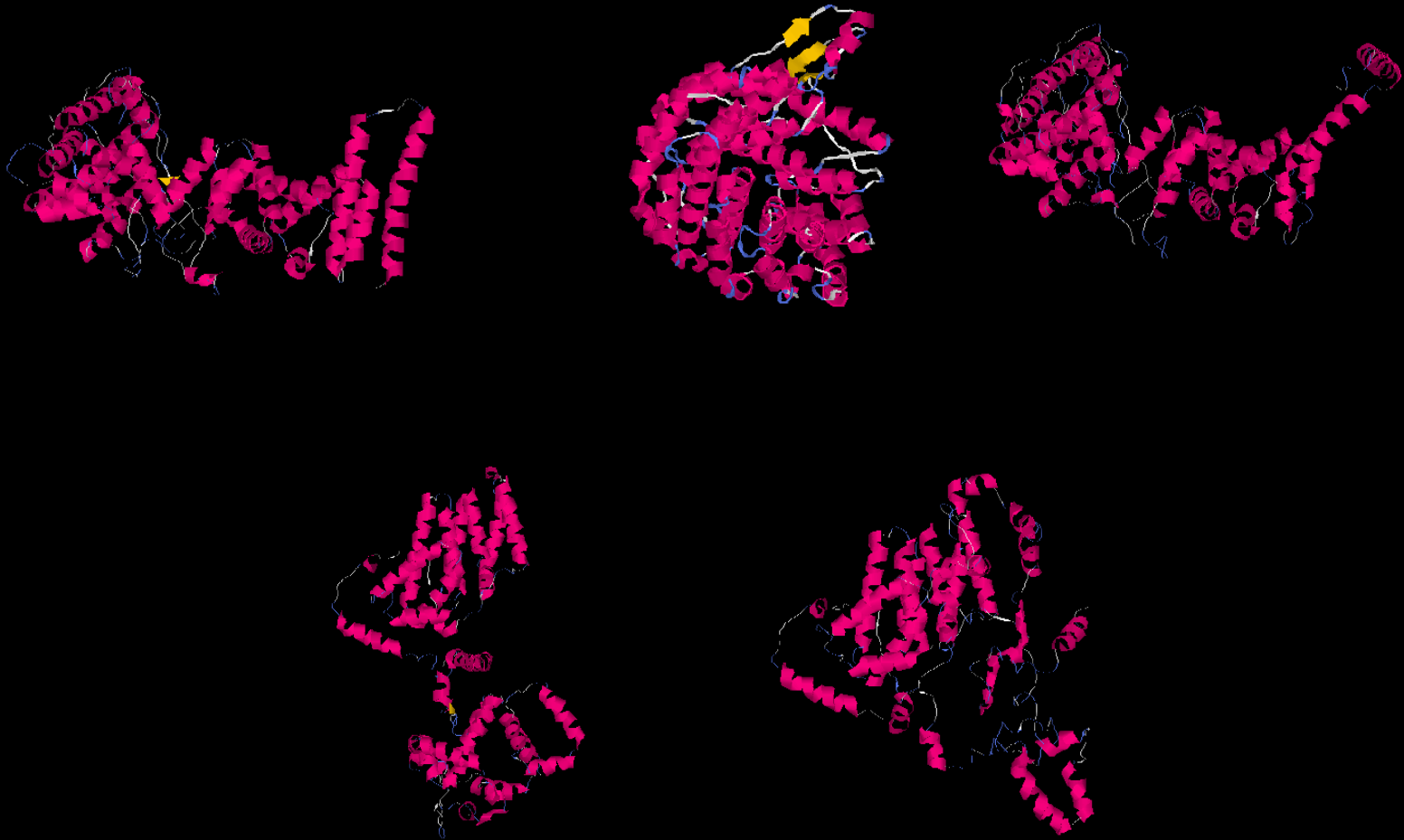
TMHMM



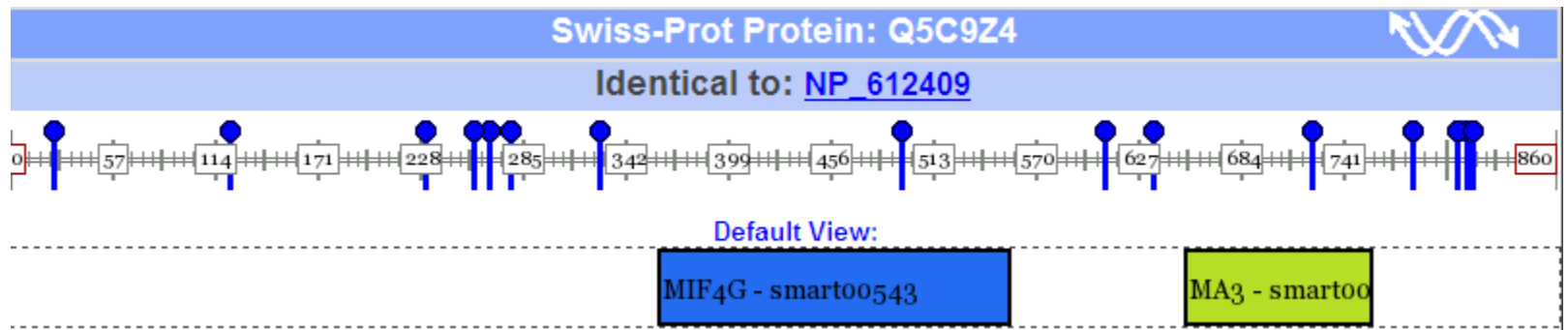
Signal IP Prediction



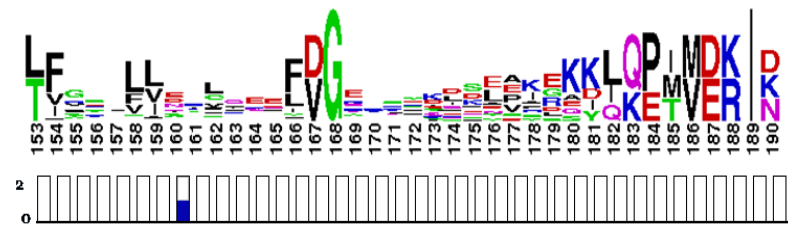
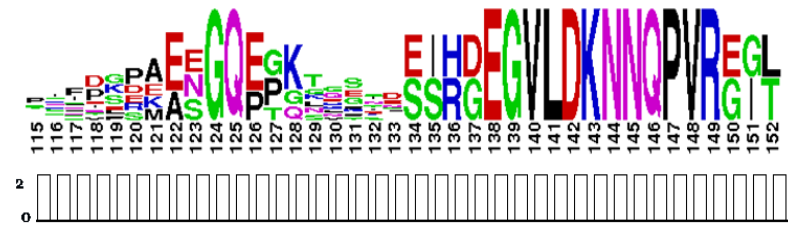
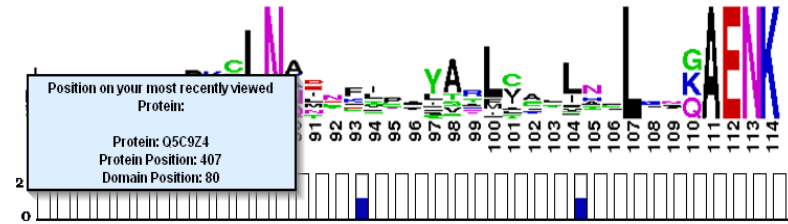
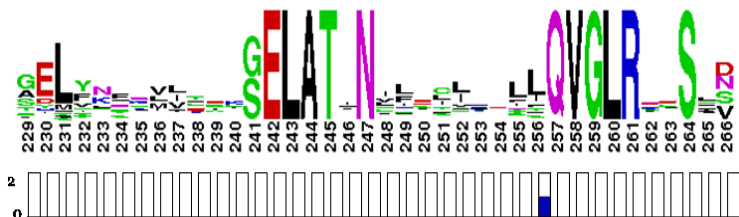
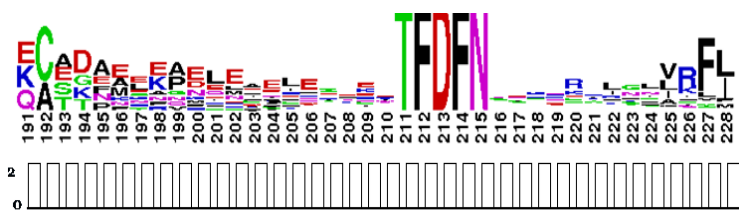
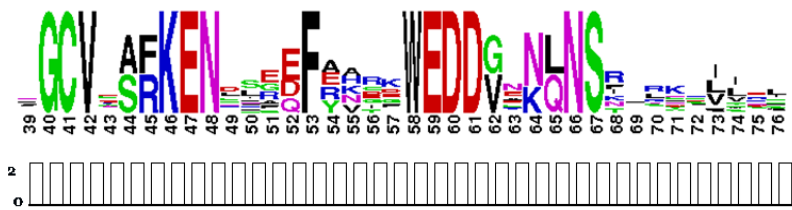
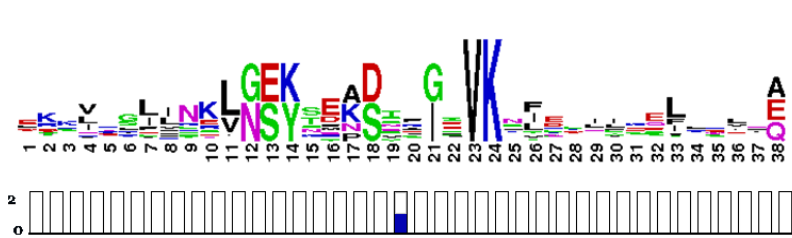
ITESSER: Protein Structure Prediction



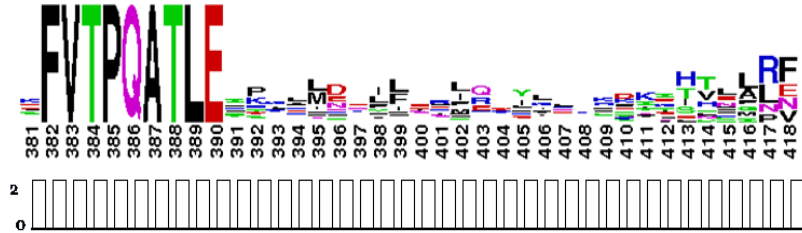
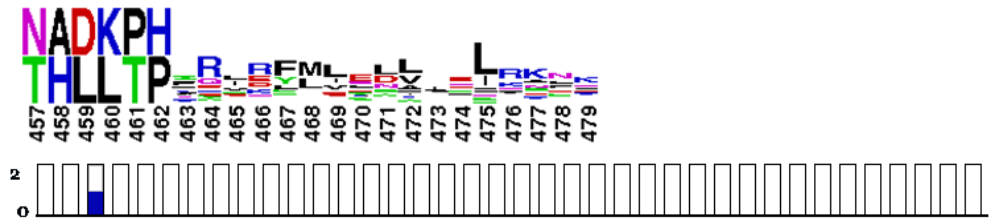
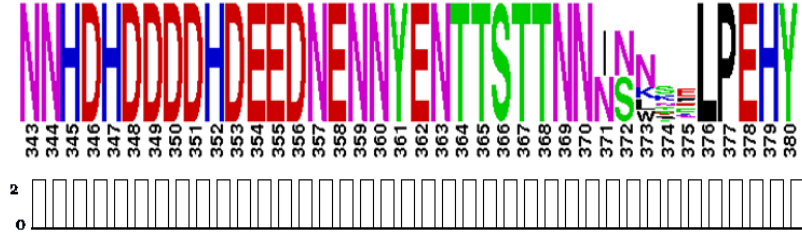
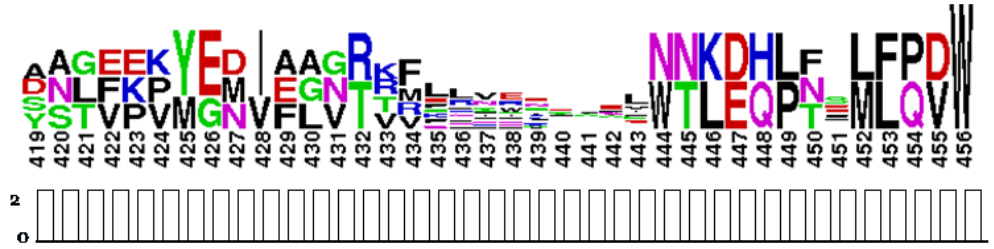
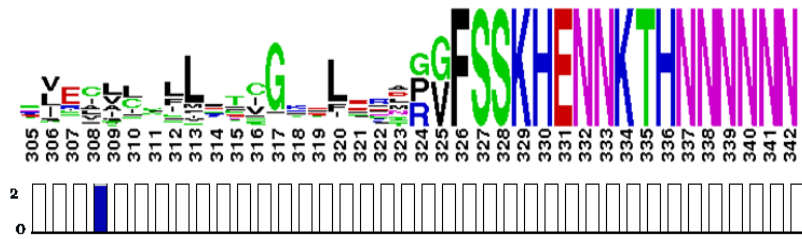
Reference: Human *nom1* gene



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Breast and female reproductive system		
N/A	Breast	
N/A	Vagina	
Not available	Cervix, uterine	
	Uterus	
N/A	Fallopian tube	
	Ovary	
	Placenta	
Skin and soft tissues		
	Adipose tissue	
	Skin	
N/A	Skeletal muscle	
N/A	Smooth muscle	
N/A	Soft tissue	
Blood and immune system (Hematopoietic)		
	Bone marrow	
	Lymph node	
N/A	Tonsil	
	Spleen	
Central nervous system (Brain)		
	Cerebral cortex	
N/A	Hippocampus	
N/A	Lateral ventricle	
N/A	Cerebellum	
Endocrine glands		
	Thyroid gland	
N/A	Parathyroid gland	N/A
	Adrenal gland	
Respiratory system (Lung)		
N/A	Nasopharynx	
N/A	Bronchus	
	Lung	

Needleman Sequence Alignment

Pairwise Alignment Result

LENGTH	SCORE	IDENTITY	SIMILARITY	GAPS
863	1704.0	327/863 (37.9%)	400/863 (46.3%)	379/863 (43.9%)

nom1_human 860Aa
nom1_zebrafish 487Aa

Pairwise Alignment Result

LENGTH	SCORE	IDENTITY	SIMILARITY	GAPS
674	1750.5	335/674 (49.7%)	411/674 (61.0%)	191/674 (28.3%)

nom1_Alligator 670Aa
nom1_zebrafish 487Aa

Pairwise Alignment Result

LENGTH	SCORE	IDENTITY	SIMILARITY	GAPS
488	1750.5	335/488 (68.6%)	411/488 (84.2%)	5/488 (1.0%)

nom1_Alligator 187-670Aa
nom1_zebrafish 487Aa

Pairwise Alignment Result

LENGTH	SCORE	IDENTITY	SIMILARITY	GAPS
1324	1596.5	318/1324 (24.0%)	386/1324 (29.2%)	849/1324 (64.1%)

*nom1_Bosmutus*1312Aa
nom1_Zebrafish 487Aa

Pairwise Alignment Result

LENGTH	SCORE	IDENTITY	SIMILARITY	GAPS
488	1596.5	318/488 (65.2%)	386/488 (79.1%)	13/488 (2.7%)

*nom1_Bosmutus*837-1312Aa
nom1_Zebrafish 487Aa

Thank you for your attention!