



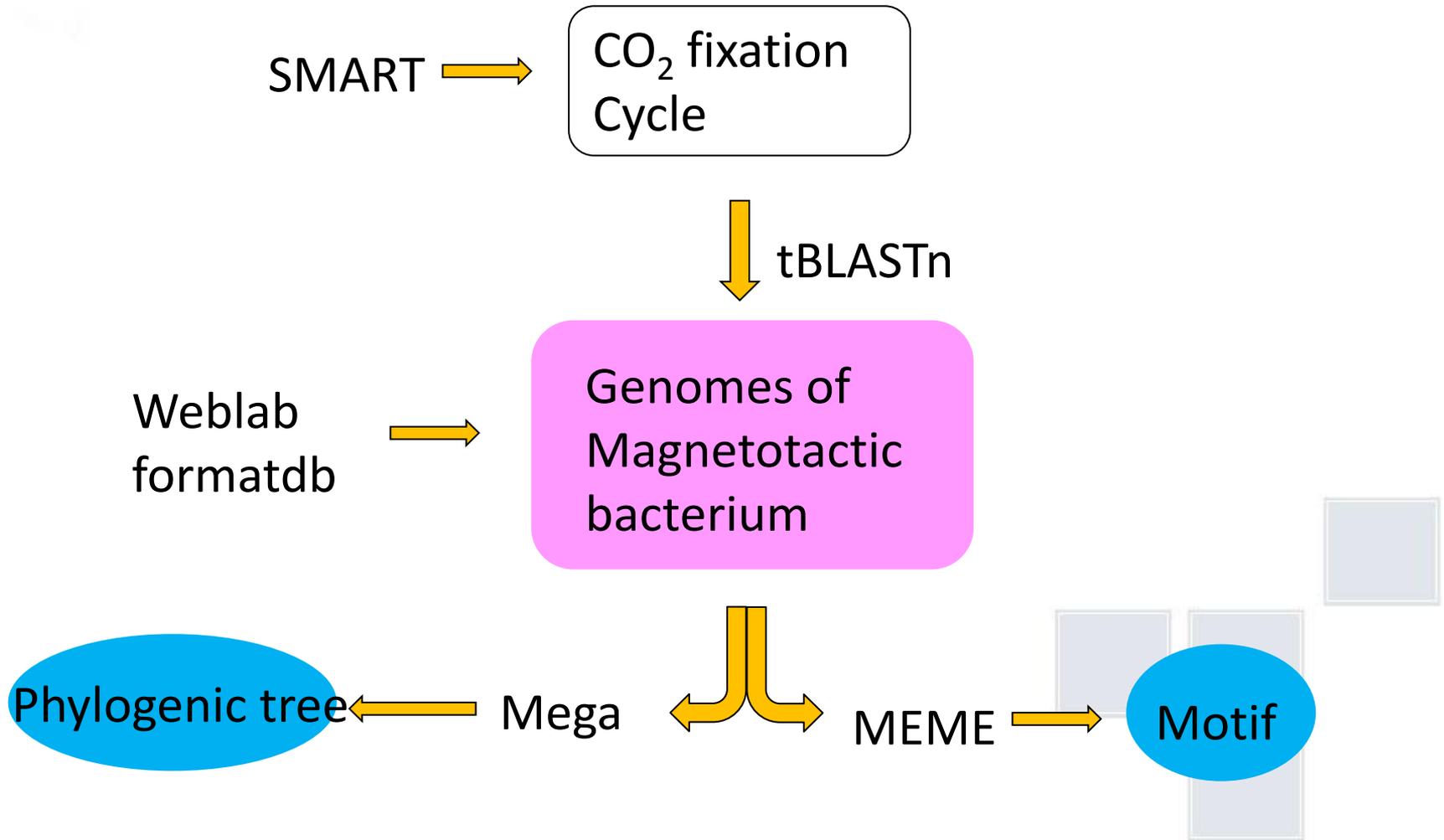
“实用生物信息技术” 课程总结

北大3班



Overview of other group's work-1

——趋磁细菌的化能合成作用初探

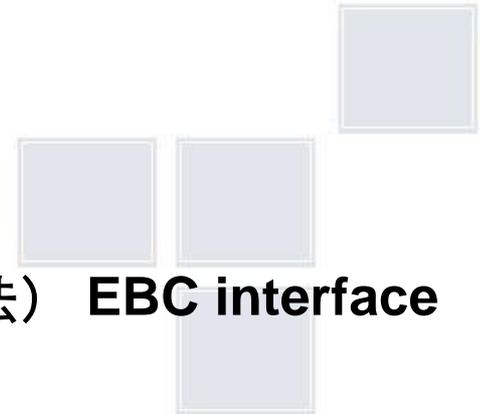




Overview of other group's work-2

——拟南芥Bzip转录因子家族成员At1g06070

- 克隆目的基因片段
- 将目的基因片段跟基因组进行**BLAST**, 得到基因定位
- 预测基因结构, 比较各种软件之间的差异 (**GenScan**、 **Softberry**、 **HMMgene**、 **AUGUSTUS**)
- **tBLAST**, 预测可能功能
- 细胞亚细胞定位 (**TargetP1.1**、 **psort**)
- **motif**预测 (**smart**、 **pfam**、 **interpro scan**、 **MEME**)
- 一级结构分析 (**pepinfo**、 **pepstats**、 **protscale**)
- 二级结构分析 (**Tmap**、 **TMHMM**、 **garnier**)
- 三级结构预测 (**Swiss-model**)
- 系统发育树构建 (邻位相连、 最小进化、 最大简约法) **EBC interface**





Overview of other group's work-5

——克隆的牛SOX9基因的验证

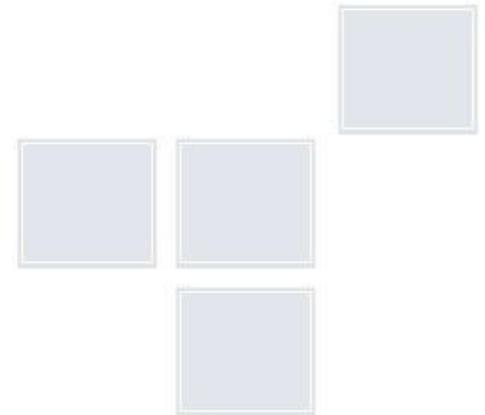
- 结构域分析 (SMART)
- 跨膜区预测 (TMHMM、SUSUI)
- 信号肽 (signal peptide)
- 亚细胞定位 (TargetP、 Softberry-Protcomp)
- O-连接糖基化预测 (NetOGlyc 3.1 Server)
- N-连接糖基化预测 (NetCGlyc 1.0 Server)
- 二硫键分析 (SCRATCH Protein Predictor)
- 磷酸化位点预测 (CBS-NetPhos2.0 Server)
- 二级结构预测 (PBIL LYON-GERLAND、Garnier)
- 三级结构预测 (The Protein Model Portal)



Overview of other group's work-G7

——Rip3在代谢综合症中的作用分析

- Rip3的基本信息查找
- UCSC, ATLAS, EBI microarray database寻找Rip3是否与代谢综合征相关
- KEGG 数据库预测Rip3可能的信号通路
- 不同种属间, Rip3的保守性分析





Overview of other group's work-G8

——猪流感病毒外膜蛋白GP5的分析

■ 一级结构分析

抗原表位预测

糖基化位点预测 (**NetOGlyc 31 Server**)

理化性质分析 (**Protparam**)

亲疏水性分析 (**ProtScale**)

信号肽预测 (**signalP-HMM**)

■ 二级结构预测

跨膜区预测 (**TMHMM、TMPred、SOSUI、TMAP**)

PHD、PROF、PSIPRED三种二级结构预测软件比较

■ 构建不同毒株GP5蛋白的系统进化树



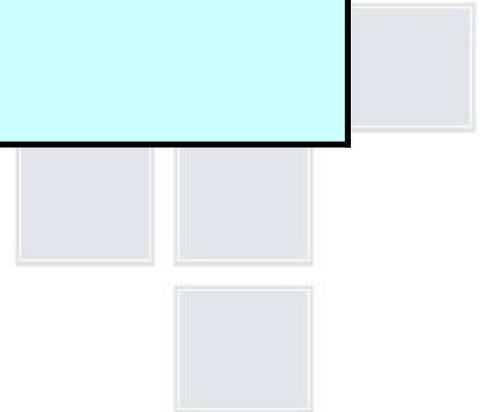
EFTUD2生物信息分析

小组成员：雷蕾、李萌、蒋蓓蓓、黄章泷

2010.06.13

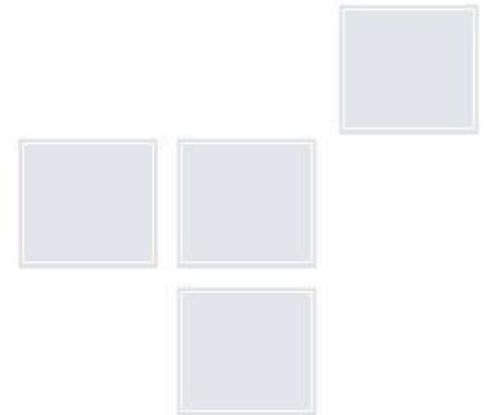


组员	分工
李萌	基本信息搜索及分析、系统发育树构建
蒋蓓蓓	结构域分析
黄章泷	3D结构分析
雷蕾	背景





- 研究背景
- 同源基因搜索及亲缘关系分析
- **EFTUD2**基本信息分析及结构域分析
- **EFTUD2** 3D结构预测
- 斑马鱼突变体与野生型**EFTUD2**结构比较



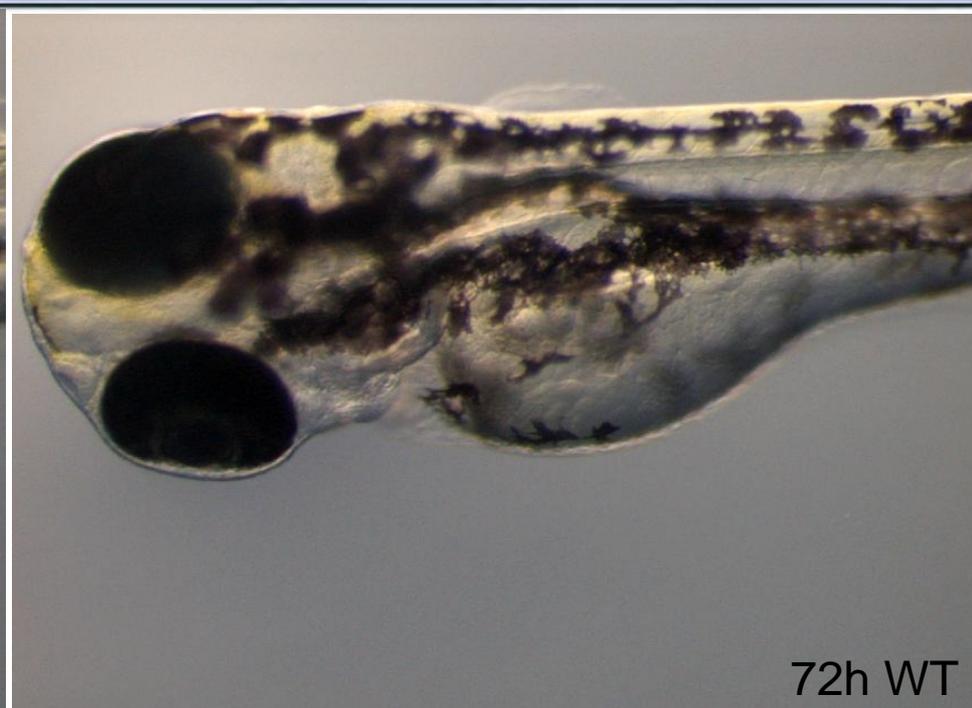


- 心血管疾病是威胁人类健康的最常见疾病，其发病率在我国也居于首位。
- 斑马鱼是研究心血管发育及相关疾病的重要模式生物。





72h MT

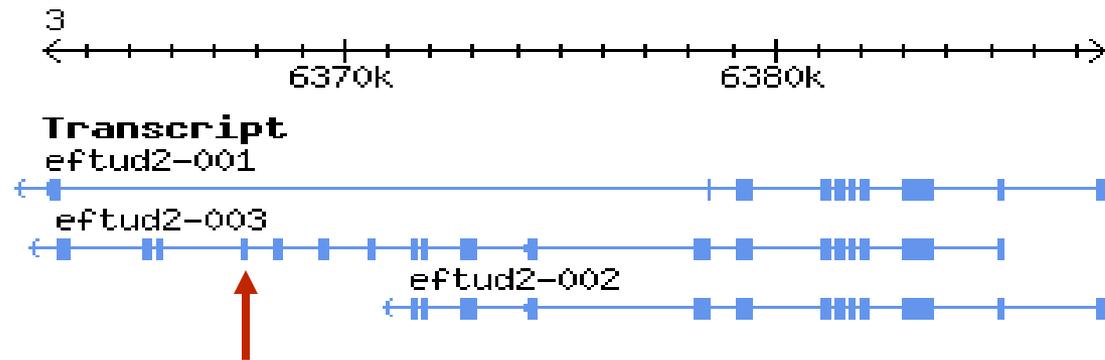


72h WT

定位克隆：*eftud2* (*elongation factor Tu GTP binding domain containing 2*) 发生突变，其mRNA第2413位由C变成T，形成终止子 (TAA)



斑马鱼EFTUD2生物信息



Protein attributes Hide

Sequence length	973 AA.
Sequence status	Complete.
Protein existence	Evidence at transcript level.

88 MOUSE EF2
95 RAT EF2
99 BOVIN EF2
65 HUMAN EF2
100 CHICK EF2

Mammals

zibrafish EFTUD 2

CHICK EFTUD 2

100

Pongo abelii EFTUD 2

99

HUMAN EFTUD 2

97

MOUSE EFTUD 2

69

BOVIN EFTUD 2

y protein 1

CHICK EFTUD 2

100

Pongo abelii EFTUD 2

99

HUMAN EFTUD 2

97

MOUSE EFTUD 2

69

BOVIN EFTUD 2

Mammals

Aquifex aeolicus EFG

100

AQUPY EFG

75

69

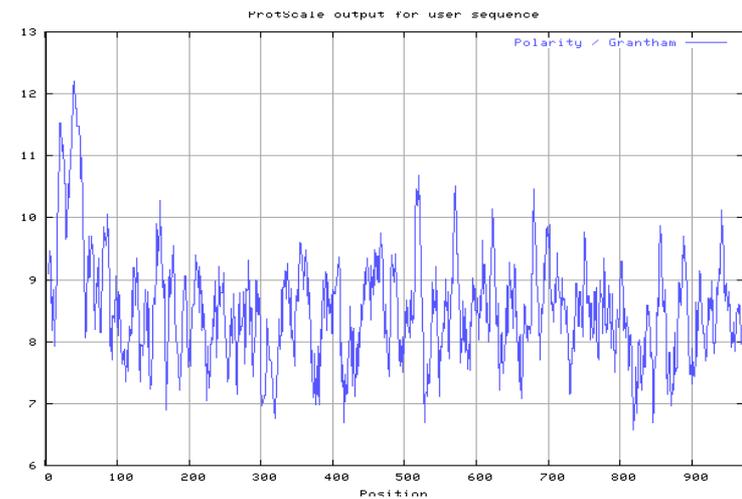
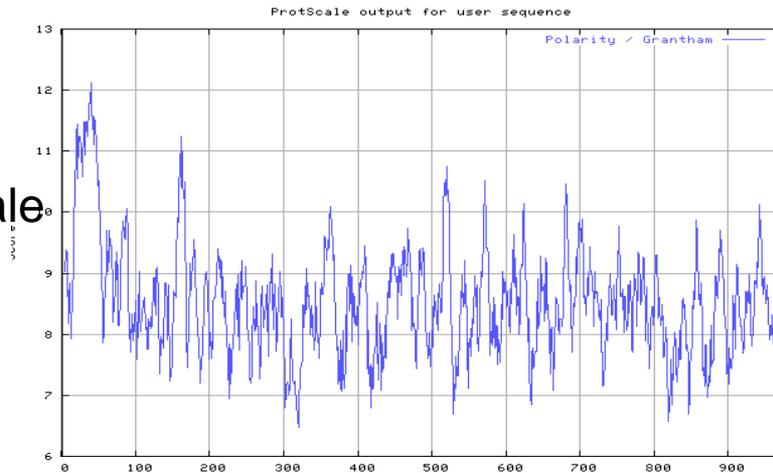
斑马鱼与人的EFTUD2比对



needle

LENGTH	SCORE	IDENTITY	SIMILARITY	GAPS
974	4724.5	892/974 (91.6%)	937/974 (96.2%)	3/974 (0.3%)

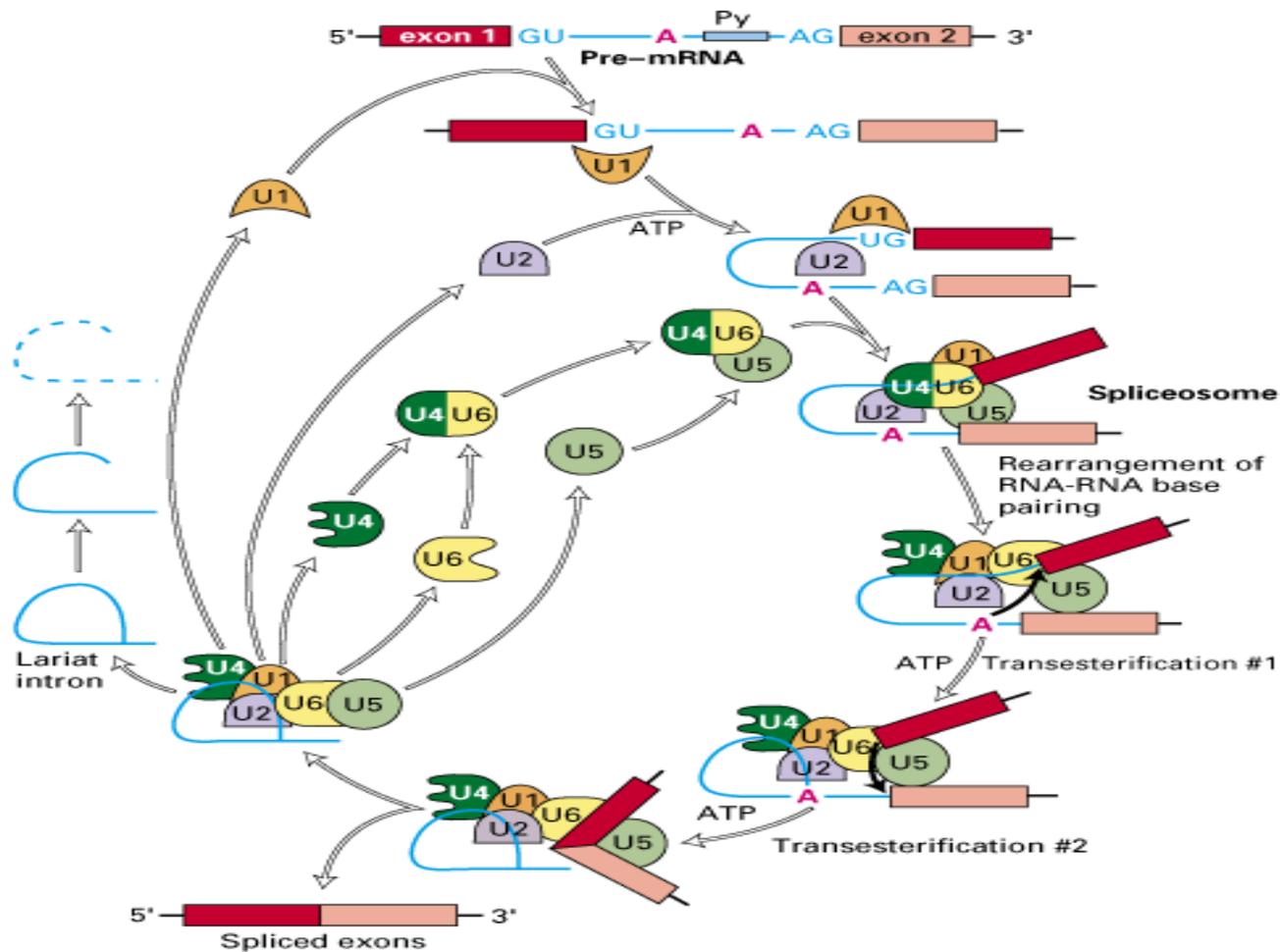
ProtScale



- **Zebrafish EFTUD2:**
- **Number of amino acids: 973 Molecular weight: 109288.3 Theoretical pI: 4.7**
- **Total number of negatively charged residues (Asp + Glu): 159**
- **Total number of positively charged residues (Arg + Lys): 97**

- **Human EFTUD2:**
- **Number of amino acids: 972 Molecular weight: 109435.7 Theoretical pI: 4.84**
- **Total number of negatively charged residues (Asp + Glu): 156**
- **Total number of positively charged residues (Arg + Lys): 100**

- Component of the U5 snRNP complex required for pre-mRNA splicing



Signaling pathways

- Biochemical and Signaling Pathways

Reactome (by CSHL, EBI, and GO)

Protein Q15029 ([Reactome details](#)) participates in the following event(s):

- [75083](#) ATAC spliceosome mediated 3' splice site cleavage, exon ligation
- [72143](#) Lariat Formation and 5'-Splice Site Cleavage
- [72139](#) Formation of the active Spliceosomal C complex
- [72130](#) Formation of an intermediate Spliceosomal C complex
- [72127](#) Formation of the Spliceosomal B Complex
- [72160](#) Cleavage at the 3'-Splice Site and Exon Ligation
- [75081](#) Formation of AT-AC B Complex
- [75082](#) ATAC spliceosome mediated Lariat formation, 5' splice site cleavage
- [75079](#) Formation of AT-AC C complex
- [156661](#) Formation of Exon Junction Complex
- [72165](#) mRNA Splicing - Minor Pathway
- [72163](#) mRNA Splicing - Major Pathway
- [72172](#) mRNA Splicing
- [72203](#) Processing of Capped Intron-Containing Pre-mRNA
- [76043](#) Elongation of Intron-Containing Transcripts and co-transcriptional mRNA splicing
- [112295](#) Elongation and Processing of Capped Transcripts
- [75983](#) Formation and Maturation of mRNA Transcript
- [74160](#) Gene Expression

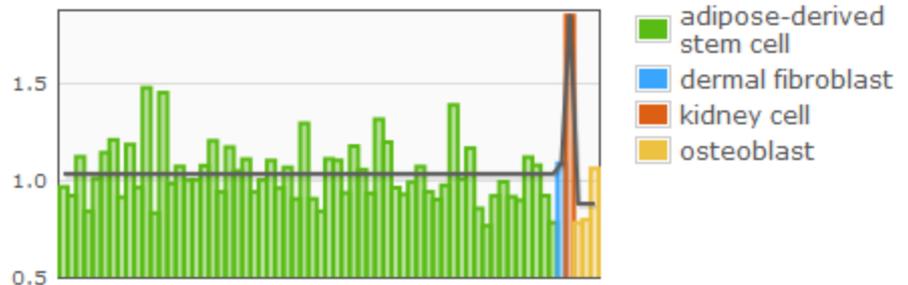
Tissue distribution



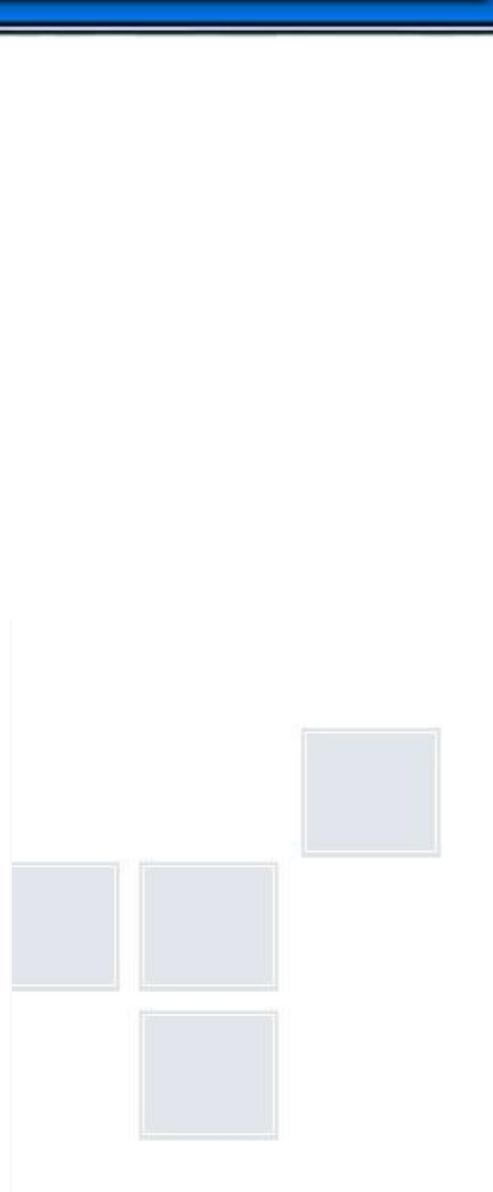
E-MEXP-1216: Transcription profiling of human adipose derived stem cells before induction and at two time points after induction of differentiation

Experimental Factors

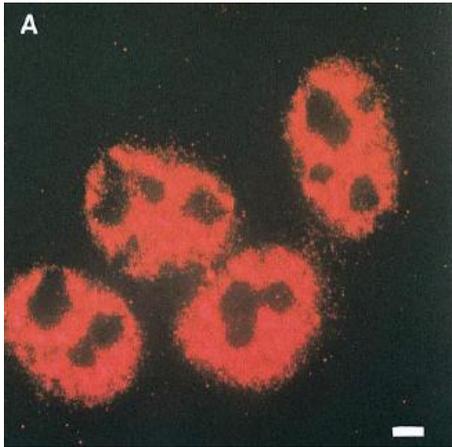
- Time
- Cell Type
- Individual



Show expression profile / experiment details

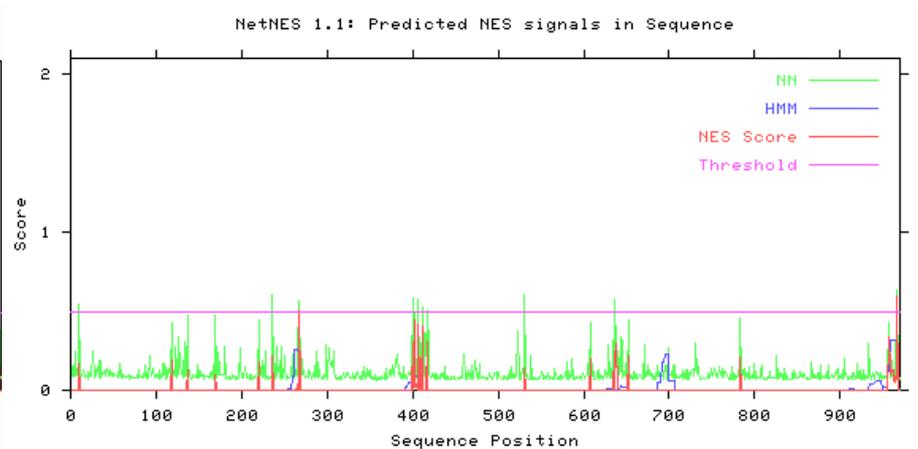
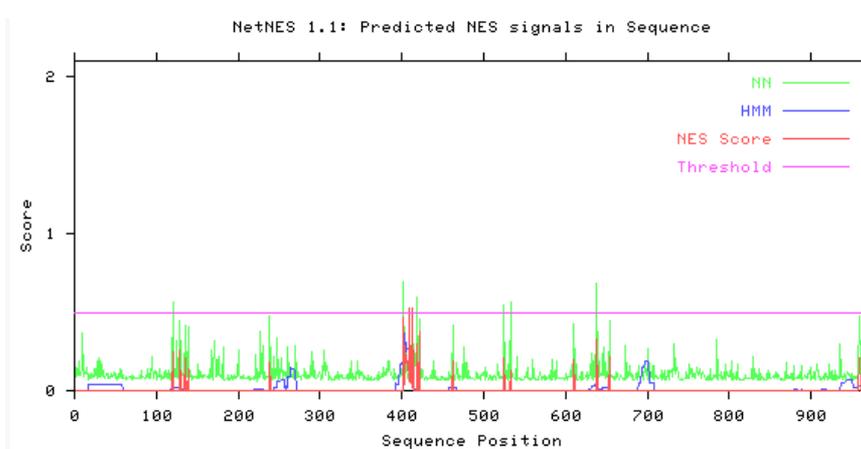


用PredictNLS 预测该蛋白质是否有核定位与核输出信号



已有结果表明，人的EFTUD2定位在核内。

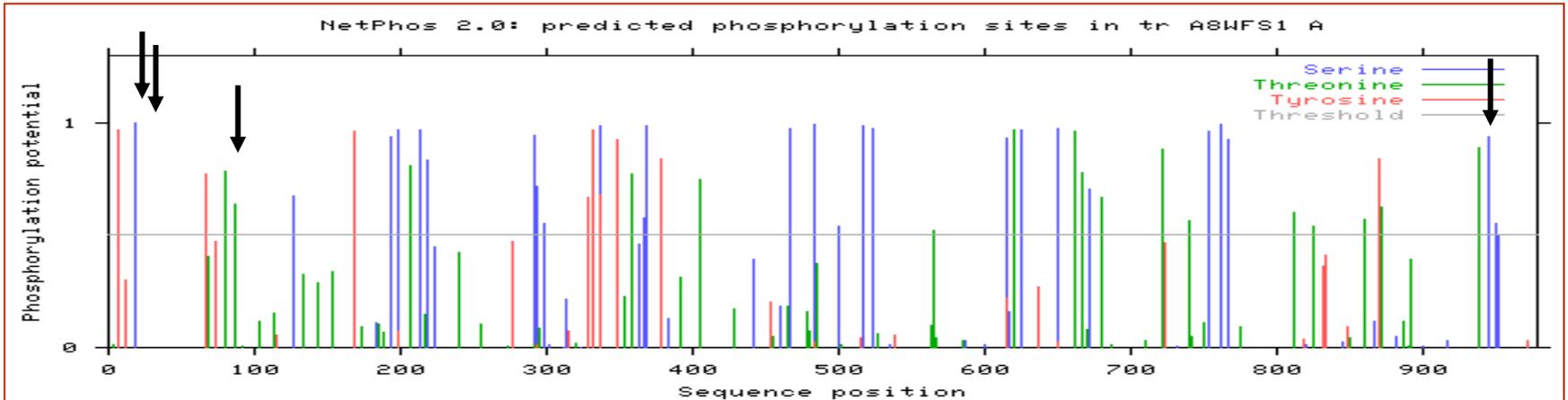
Fabrizio, *et, al.* EMBO, 1997



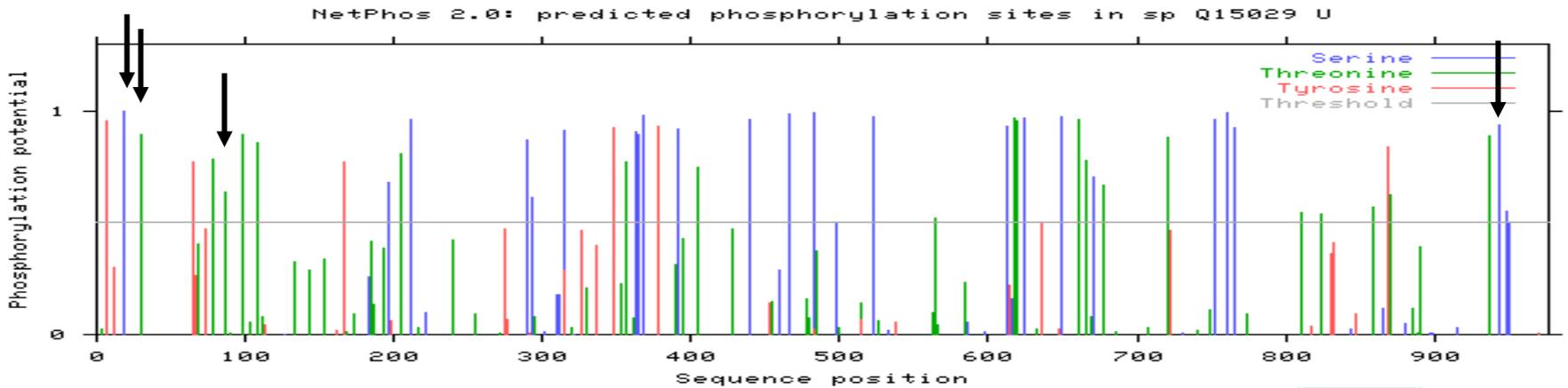
分析结果表明，该蛋白质既没有核定位信号也没有核输出信号。

NetPhos 分析磷酸化位点

斑马鱼



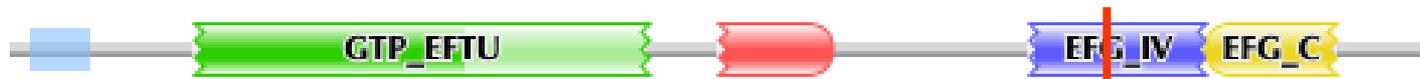
人





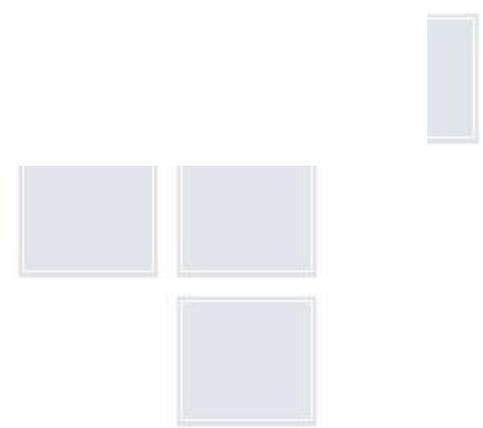
Pfam domains

This image shows the arrangement of the Pfam domains that we found on this sequ entry. The table below gives the domain boundaries for each of the domains.



Source	Domain	Start ^	End
low_complexity		16	55
Pfam A	GTP_EFTU	128	441
Pfam A	GTP_EFTU_D2	490	567
Pfam A	EFG_IV	704	825
Pfam A	EFG_C	827	916

Mutation site





3D Modeling-SWISS MODEL

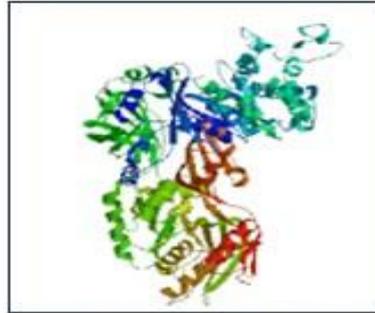
Select a template

Alignment

Modeling log

evaluation

Model Details: ? Segment 1

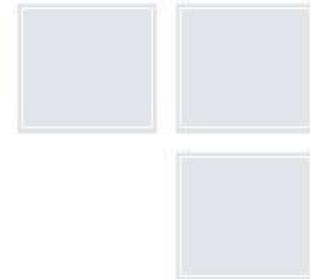


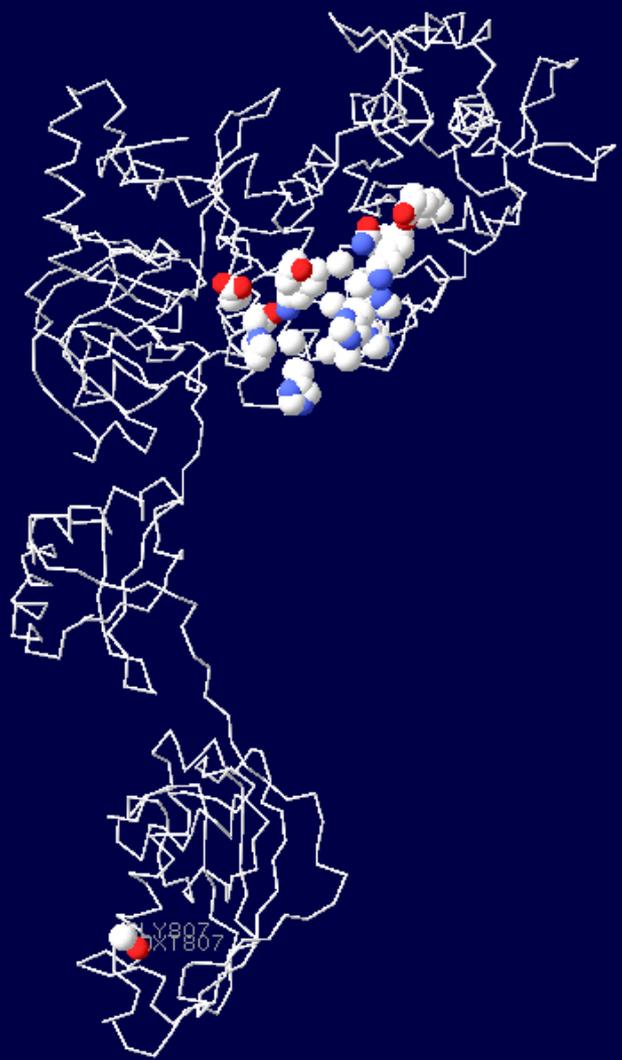
Model info:

modelled residue range: 113 to 956
based on template **2e1rA** (3.15 Å)
Sequence Identity [%]: 34.727
Evalue: 0.00e-1

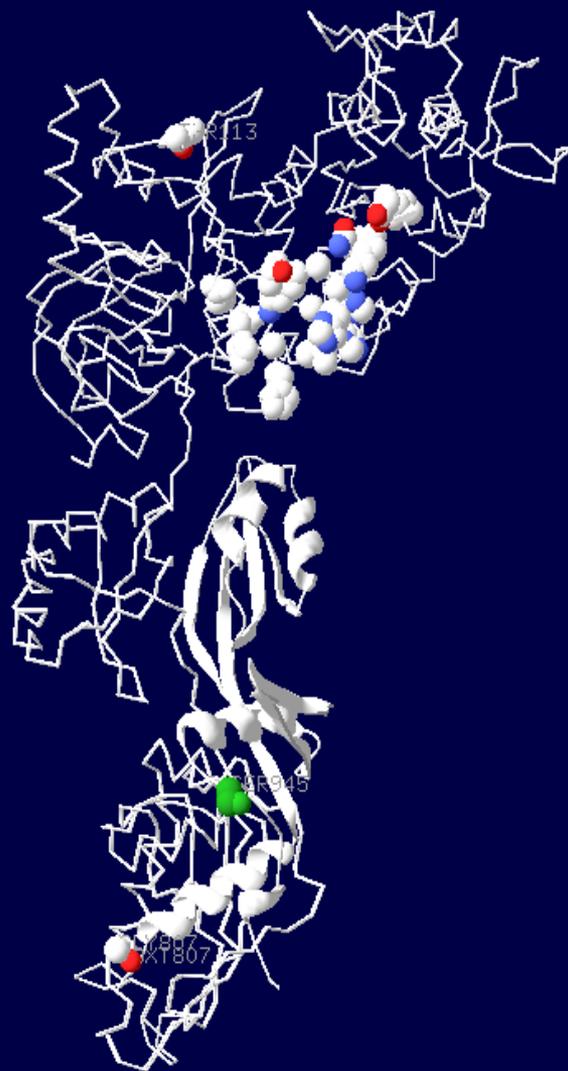
display model: as pdb - as DeepView project

download model: as - as Deepview project - as text

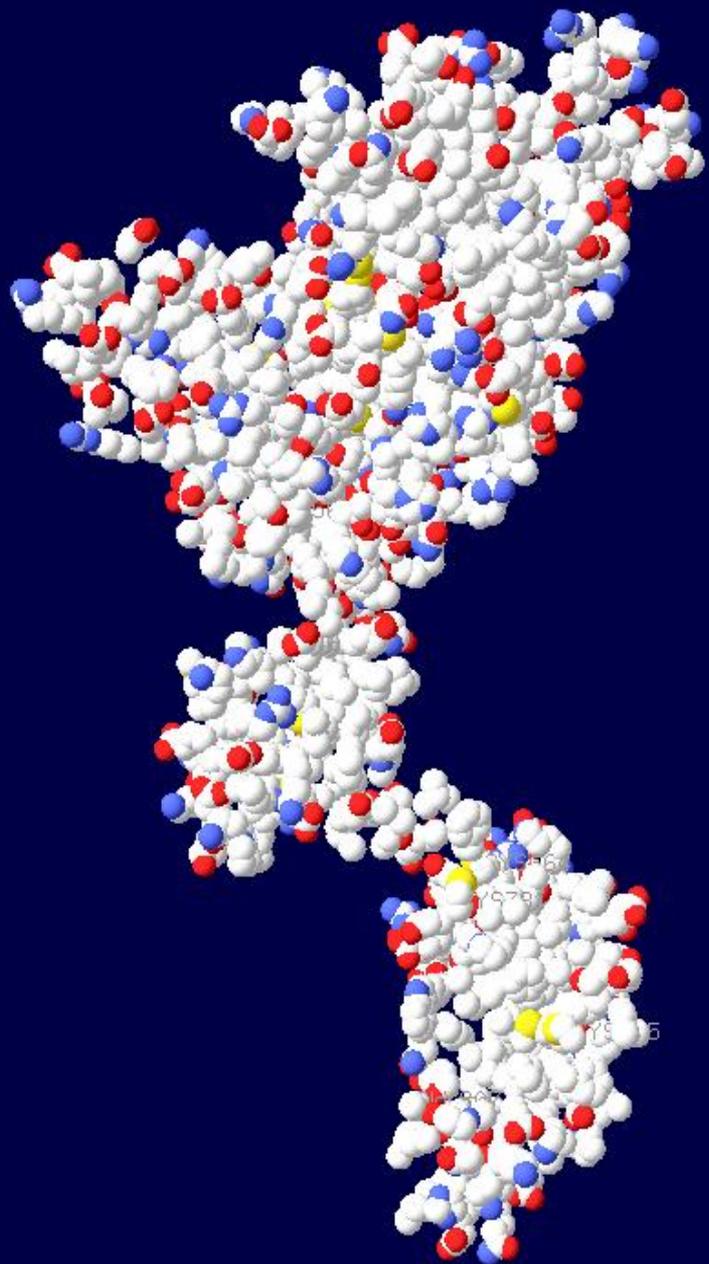




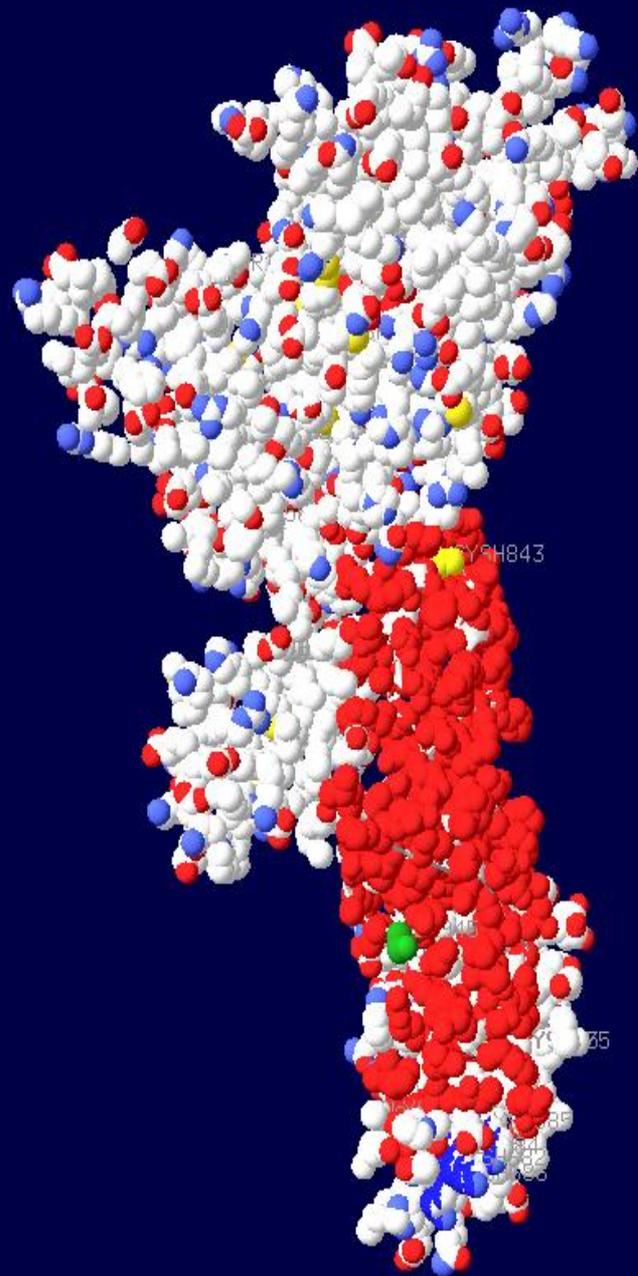
MT



WT

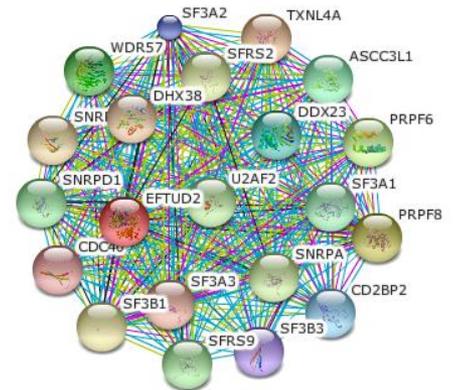


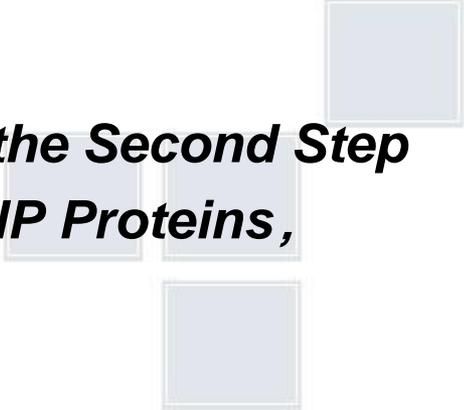
MT



WT

- **EFTUD2**是一种高度保守的蛋白
- **EFTUD2**没有核定位序列，可能通过其他蛋白的相互作用入核
- 斑马鱼中缺少的四个重要磷酸化位点之一，表明其调控方式可能与人的不同。
- **EFTUD2 C端**一段序列的缺失可能导致蛋白结构的改变，进而影响**GTP**的结合；缺失的氨基酸片段在蛋白表面，可能影响它与其他蛋白的相互作用。



- 
- <http://swissmodel.expasy.org/>
 - <http://zfin.org/>
 - <http://www.cbs.dtu.dk/services/NetPhos/>
 - <http://www.uniprot.org/uniprot/Q15029>
 - <http://weblab.cbi.pku.edu.cn/program>
 - <http://www.expasy.org/>
 - ***Fabrizio, An evolutionarily conserved U5 snRNP-specific protein is a GTP-binding factor closely related to the ribosomal translocase EF-2, EMBO, 1997***
 - ***Shi, PP1/PP2A Phosphatases Are Required for the Second Step of Pre-mRNA Splicing and Target Specific snRNP Proteins, Molecular Cell, 2006***
- 



Thank you!