

实用生物信息技术
期末总结交流报告会
**Semester Summary Seminar for
Applied Bioinformatics Course**
2020年12月12日

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小组成员

| 编号 | 姓名 | 研究所 | 导师 | 研究方向 |
|-----|-----|-----|-----|--------------|
| G3A | 候琳琳 | 水稻所 | 高振宇 | 水稻硝态氮利用的遗传机制 |
| G3B | 段影青 | 水稻所 | 胡培松 | 稻米品质 |
| G3C | 朱黎欣 | 水稻所 | 钱前 | 水稻分蘖突变体研究 |
| G3D | 张佳玲 | 作科所 | 侯文胜 | 光周期调控基因作用机制 |

大豆韧皮部伴胞细胞中开花调控基因*GmMRF1*
序列分析

**Sequence Analysis of Flowering Regulator in
Soybean Phloem Companion Cell**

主要内容

1. 背景介绍
2. 大豆MRF1蛋白序列分析
3. 大豆MRF1蛋白结构分析
4. 互作蛋白分析

背景介绍

大豆(*Glycine max* (L.) Merr.)起源于我国，是我国重要的油料作物和高蛋白粮饲兼用作物，种植面积仅次于水稻、玉米和小麦，居第四位。然而多年来，我国大豆生产一直停滞不前，并由于国内主要粮食作物水稻、小麦紧缺，大豆种植面积被逐步取代锐减。大豆总产自 20 世纪 50 年代初期的世界第一位，滑坡到现在的世界第四。

随着国内消费结构升级，大豆需求快速增加，国内大豆产需缺口不断扩大。美国是全球重要的大豆出口国，在世界粮食市场具有充分话语权，我国作为全球目前最大的大豆进口国，而自中美贸易争端开始以来，中美两国在众多贸易领域产生摩擦并不断升级。

但国产大豆仅能满足国内食品加工消费需求，并且国产大豆价格高、产不足需，中国大豆进口量持续攀升，大豆对外依存度居高不下。为实施国家粮食安全战略，积极应对复杂国际贸易环境，促进我国大豆生产恢复发展，提升国产大豆自给水平，从 2019年起中国实施大豆振兴计划，提高大豆产量减少大豆依赖。

背景介绍

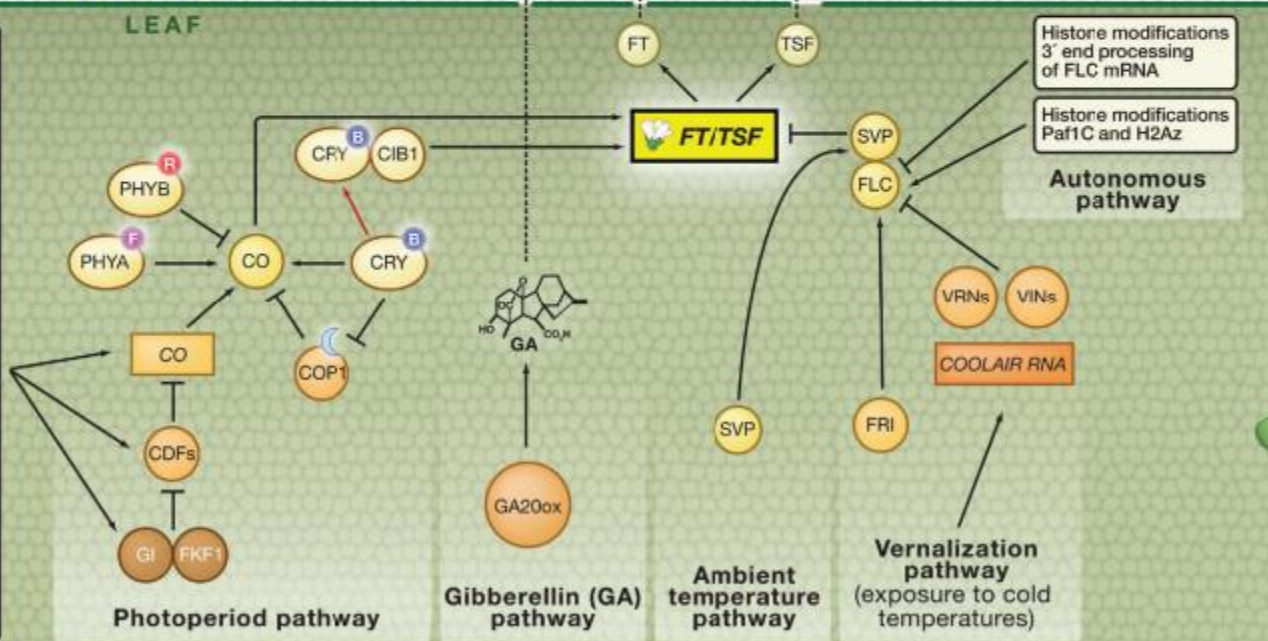
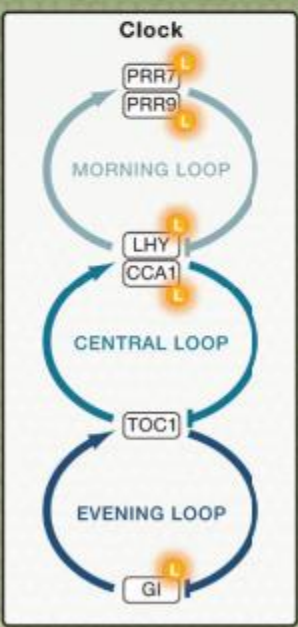
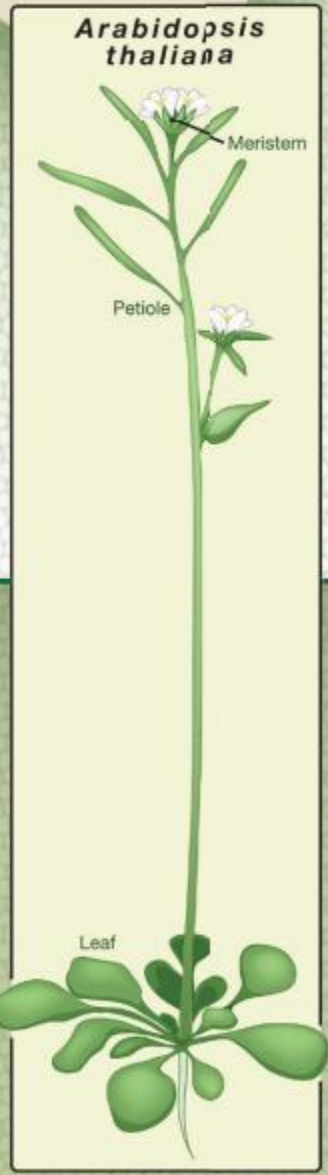
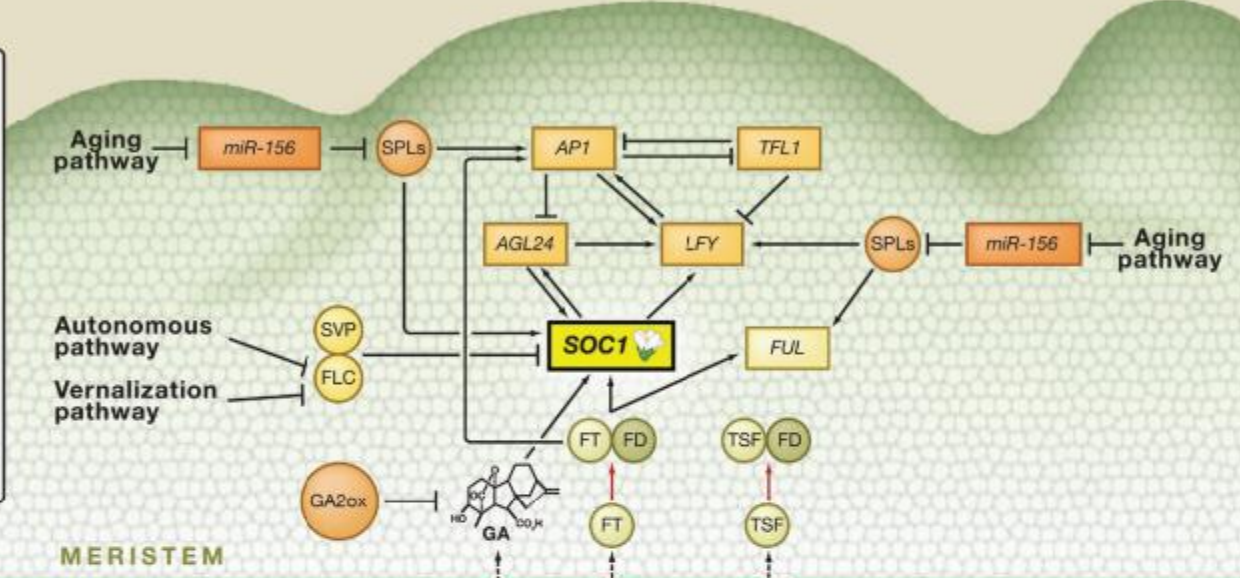
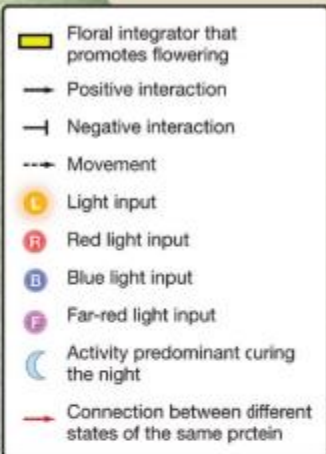
大豆对光周期反应敏感，是典型的短日植物，绝大多数大豆品种只有在日照长度缩短到一定程度后，才能从营养生长转入生殖生长，进而开花结荚。

大豆的这种光周期反应特性，造成大豆品种北移种植时，因生长季日照加长，往往表现为晚花晚熟、生长期延长，甚至不能开花或正常成熟；南移种植时，则因生长季日照缩短，一般表现为过早开花、生长期缩短，产量降低甚至不能正常生长。大豆开花期和成熟期因受种植区域生长季日照长度的影响严重，导致大豆品种适宜种植区域普遍比较狭小。

因而研究大豆光周期反应特性以提高大豆品种区域适应性增加种植面积对大豆增产具有重要意义。

SnapShot: Control of Flowering in *Arabidopsis*

Fabio Fomara, Amaury de Montaigu, and George Coupland
 Max Planck Institute for Plant Breeding Research, Köln 50829, Germany





Phloem companion cell-specific transcriptomic and epigenomic analyses identify *MRF1*, a novel regulator of flowering

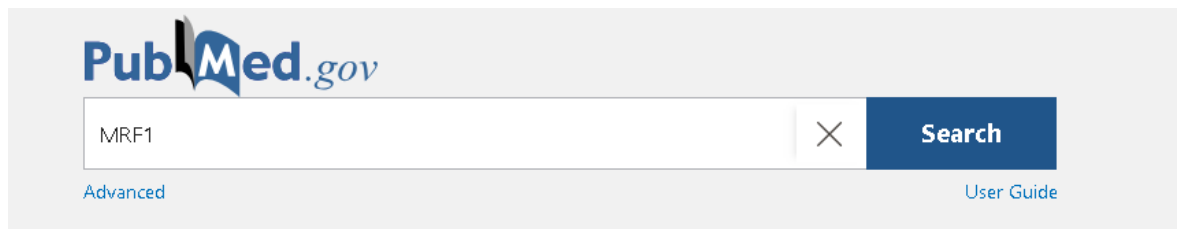
Yuan You, Aneta Sawikowska, Joanne E Lee, Ruben Maximilian Benstein, Manuela Neumann, Paweł Krajewski, Markus Schmid

Published January 2019. DOI: <https://doi.org/10.1105/tpc.17.00714>

研究利用 INTACT (Isolation of Nuclei TAgged in specific Cell Types) 和高通量测序研究了不同光周期条件下拟南芥韧皮部伴胞中转录组和表观基因组的动态变化。该研究发现，在韧皮部伴胞中 H3K4 甲基化水平与一些在伴胞中发挥重要功能的基因表达是正相关的，这些基因参与代谢调节，生物节律，发育和表观遗传修饰。

该研究进一步鉴定了韧皮部伴胞中的 *MRF1* (MORN-MOTIF REPEAT PROTEIN REGULATING FLOWERING 1) 基因，其表达受光周期强烈诱导。*mrf1* 突变后拟南芥开花延迟，而过表达 *MRF1* 则促进开花。

主要内容



Similar articles

FE, a phloem-specific Myb-related protein, promotes flowering through transcriptional activation of FLOWERING LOCUS T and FLOWERING LOCUS T INTERACTING PROTEIN 1.

Abe M, Kaya H, Watanabe-Taneda A, Shibuta M, Yamaguchi A, Sakamoto T, Kurata T, Ausin I, Araki T, Alonso-Blanco C.

Plant J. 2015 Sep;83(6):1059-68. doi: 10.1111/tpj.12951.

PMID: 26239308

Export of FT protein from phloem companion cells is sufficient for floral induction in Arabidopsis.

Mathieu J, Warthmann N, Küttner F, Schmid M.

Curr Biol. 2007 Jun 19;17(12):1055-60. doi: 10.1016/j.cub.2007.05.009. Epub 2007 May 31.

PMID: 17540570

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Abstract

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相关信息

Gene : AT1G21920 *A. thaliana*

DB identifier

AT1G21920

Secondary Identifier

Brief Description

Histone H3 K4-specific methyltransferase SET7/9 family protein

TAIR Computational Description

Histone H3 K4-specific methyltransferase SET7/9 family protein;(source:Araport11)



1. 序列分析

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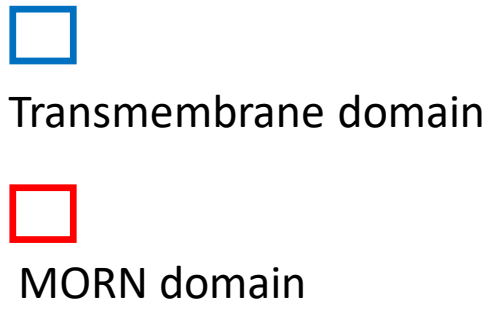
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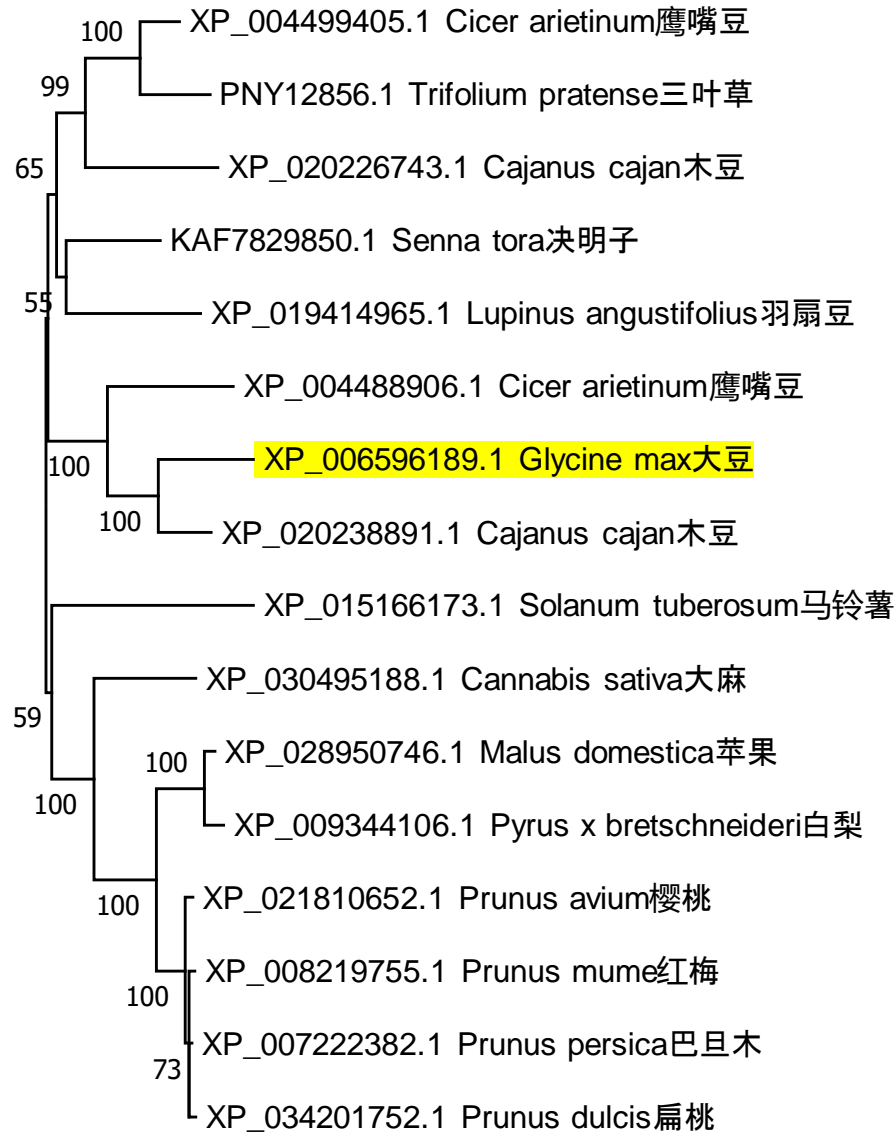
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系统发育树



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0.020

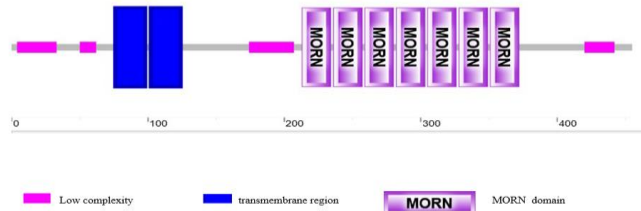
启动子作用元件预测

| 顺式作用元件 | 功能 | 数量 |
|-------------|---------------|----|
| G-box | 参与光反应 | 5 |
| Box 4 | 参与光反应 | 7 |
| TCT-motif | 光响应元件的一部分 | 2 |
| GARE-motif | 响应赤霉素 | 1 |
| MSA-like | 参与细胞周期调节 | 1 |
| TGACG-motif | 参与MeJA反应 | 2 |
| CGTCA-motif | 参与MeJA反应 | 2 |
| TCA-element | 参与水杨酸反应 | 1 |
| MBS | MYB结合位点参与干旱诱导 | 1 |
| ABRE | 参与脱落酸反应 | 3 |

2. MRF1蛋白结构

结构域预测

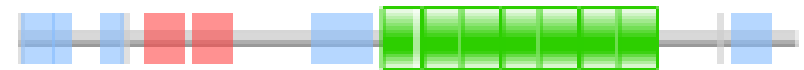
SMART



Confidently predicted domains, repeats, motifs and features:

| Name | Start ▲ | End | E-value |
|----------------------|---------|-----|------------|
| low complexity | 4 | 33 | N/A |
| low complexity | 50 | 62 | N/A |
| transmembrane region | 76 | 98 | N/A |
| transmembrane region | 102 | 124 | N/A |
| low complexity | 174 | 207 | N/A |
| MORN | 213 | 234 | 0.0361 |
| MORN | 236 | 257 | 0.0193 |
| MORN | 259 | 280 | 0.0889 |
| MORN | 282 | 303 | 0.0337 |
| MORN | 305 | 326 | 0.000132 |
| MORN | 328 | 349 | 0.00000767 |
| MORN | 351 | 372 | 0.0137 |
| low complexity | 420 | 442 | N/A |

Pfam



| Source | Domain | Start | End |
|----------------|----------------------|-------|-----|
| disorder | n/a | 1 | 11 |
| low_complexity | n/a | 3 | 21 |
| disorder | n/a | 15 | 21 |
| low_complexity | n/a | 17 | 32 |
| disorder | n/a | 24 | 25 |
| disorder | n/a | 48 | 66 |
| low_complexity | n/a | 49 | 61 |
| transmembrane | n/a | 76 | 97 |
| transmembrane | n/a | 103 | 124 |
| low_complexity | n/a | 109 | 118 |
| low_complexity | n/a | 173 | 206 |
| disorder | n/a | 174 | 181 |
| Pfam | MORN | 215 | 237 |
| Pfam | MORN | 238 | 260 |
| Pfam | MORN | 261 | 283 |
| Pfam | MORN | 284 | 306 |
| Pfam | MORN | 307 | 329 |
| Pfam | MORN | 330 | 352 |
| Pfam | MORN | 353 | 375 |
| disorder | n/a | 411 | 412 |
| low_complexity | n/a | 419 | 441 |

3D结构分析

Phyre2

| | |
|---------------|---|
| Email | I503986256@163.com |
| Description | GmMRF1 |
| Date | Fri Dec 11 13:30:13 GMT 2020 |
| Unique Job ID | fab2407a630fea6d |
| Sequence | MEAQKKTQTQ ... Download FASTA |
| Job Type | normal |
| Job Expiry | |

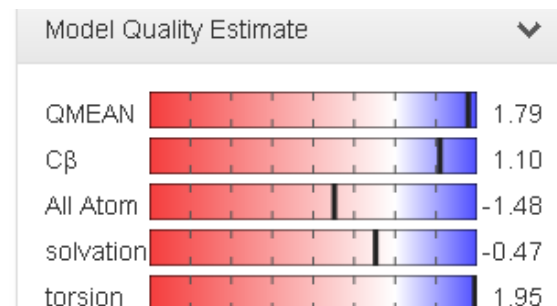
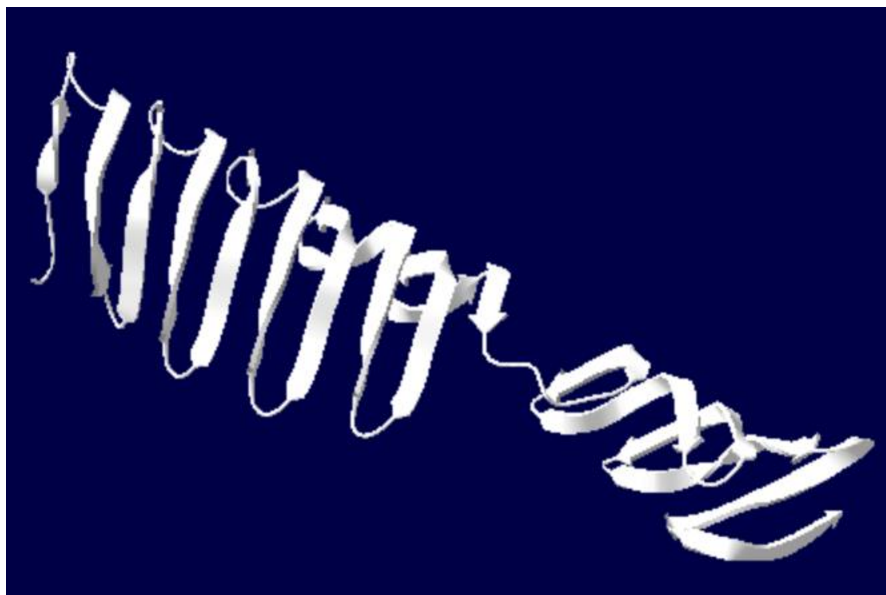
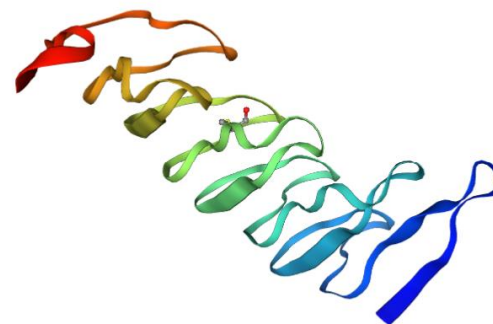
BIOZENTRUM
University of Basel
The Center for Molecular Life Sciences

SWISS-MODEL

```

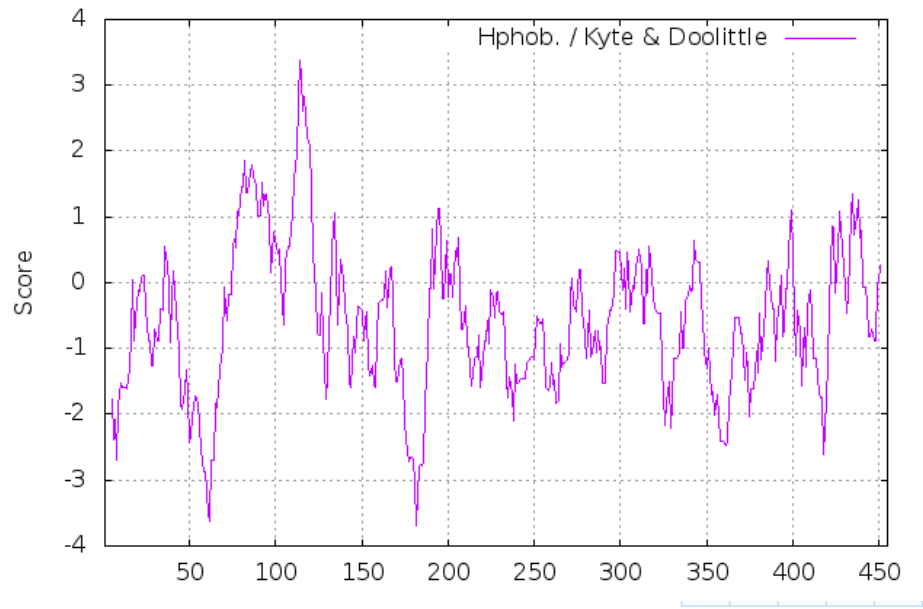
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991 UniRef50_IP1001BCAB80
992 UniRef50_Q5DWB1
993 UniRef50_Q7P244
994 UniRef50_Q1VF01
995 UniRef50_A2TUF3
996 UniRef50_C3WL08
997 UniRef50_A0D1Y7
998 UniRef50_IP1001BCAB7C
999 UniRef50_Q22HF6
000 UniRef50_A9DKQ2
consensus/100%
consensus/90%
consensus/80%

```

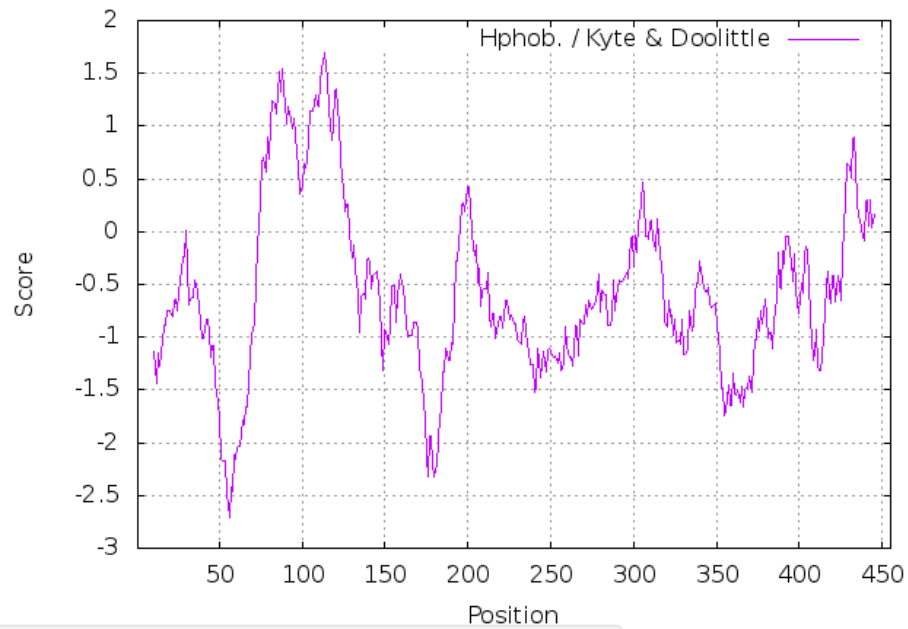


二级结构为贝塔折叠，共两个亚基

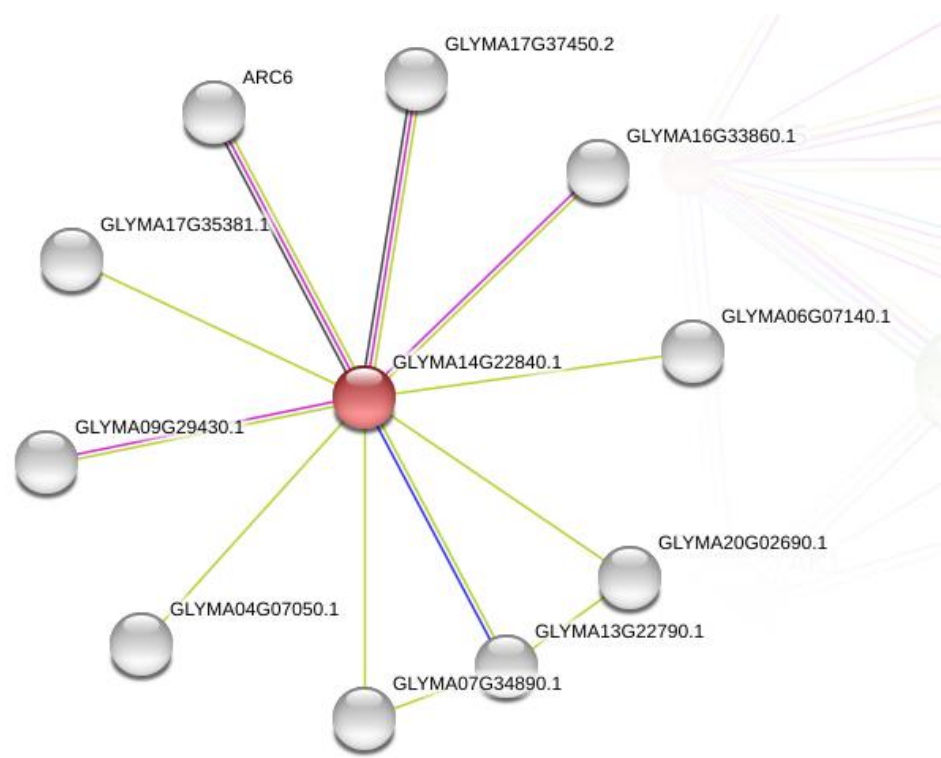
ProtScale output for user_sequence



ProtScale output for user_sequence



4. MRF1 互作蛋白预测



Predicted Functional Partners:

| | NetE | Gen | Coo | Coe | Exp | Data | Text | fHor | Score |
|---|------|-----|-----|-----|-----|------|------|------|-------|
| ● GLYMA07G34890.1 <i>Uncharacterized protein</i> | | | | | | | ● | | 0.681 |
| ● GLYMA20G02690.1 <i>Uncharacterized protein</i> | | | | | | | ● | | 0.681 |
| ● ARC6 <i>Uncharacterized protein</i> | | | | ● | ● | | ● | | 0.652 |
| ● GLYMA17G37450.2 <i>Uncharacterized protein</i> | | | | ● | ● | | ● | | 0.652 |
| ● GLYMA09G29430.1 <i>Uncharacterized protein</i> | | | | | ● | | ● | | 0.553 |
| ● GLYMA16G33860.1 <i>Uncharacterized protein</i> | | | | | ● | | ● | | 0.553 |
| ● GLYMA04G07050.1 <i>Uncharacterized protein</i> | | | | | | | ● | | 0.544 |
| ● GLYMA06G07140.1 <i>Uncharacterized protein</i> | | | | | | | ● | | 0.544 |
| ● GLYMA17G35381.1 <i>Uncharacterized protein</i> | | | | | | | ● | | 0.544 |
| ● GLYMA10G34510.2 <i>Uncharacterized protein; Belongs to the protein-tyrosine phosphatase family. Non-receptor class myotubula...</i> | | | | | | | ● | | 0.540 |

参考文献

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