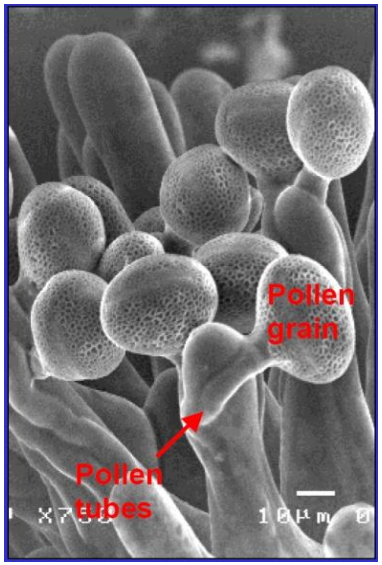
The bioinformatic analysis of CRK in *Arabidopsis thaliana*

2018/06/23

PKU G01-G03

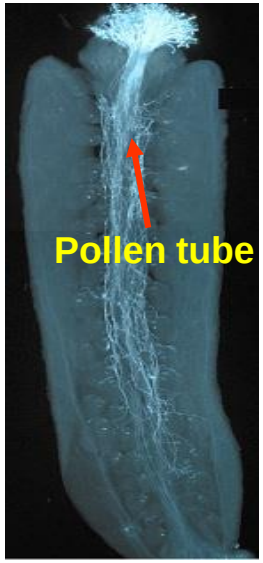
双受精过程

Pollen germination



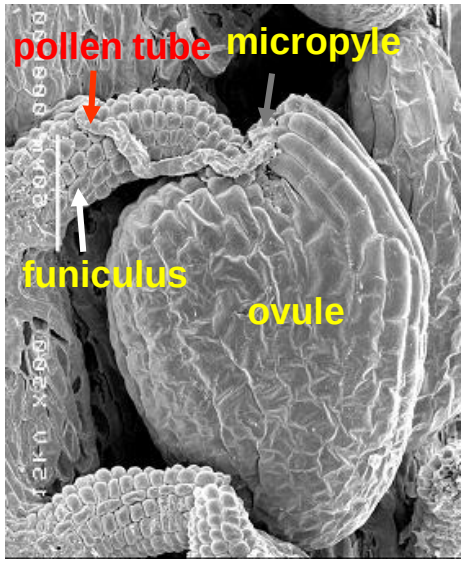
花粉萌发

Pollen tube growth in pistil



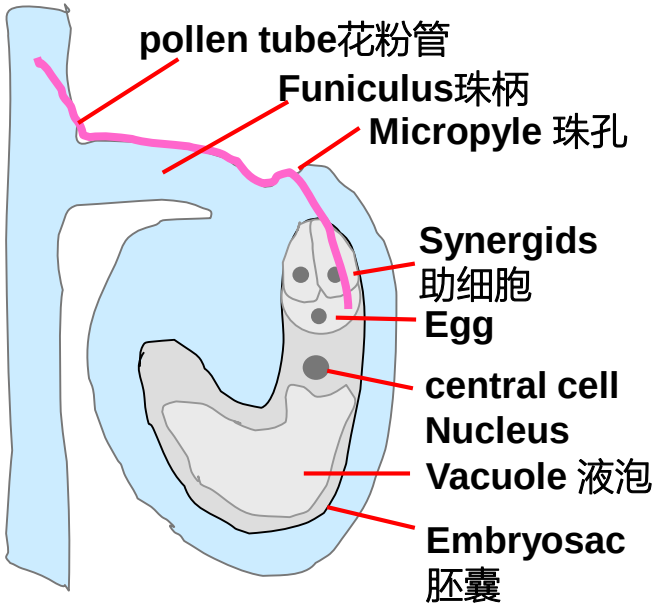
花粉管伸长

Pollen tube attracted to ovule



珠柄导向&珠孔导向

Pollen tube reception and sperm release



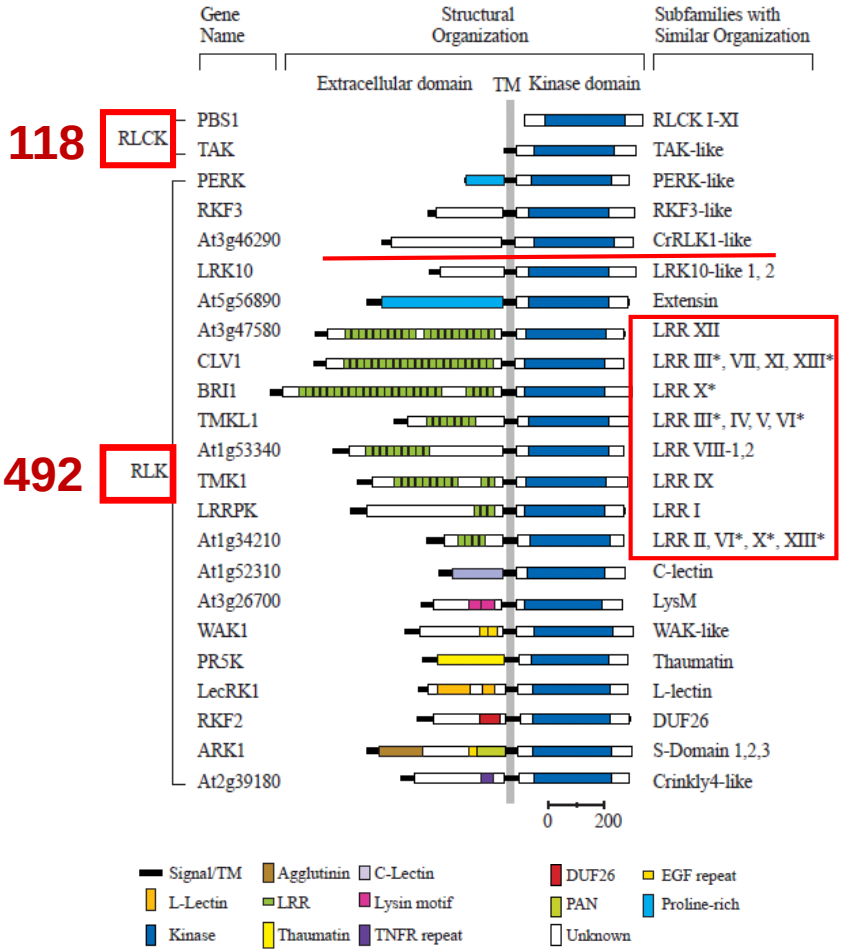
雌雄配子融合

Receptor

信号与受体相互作用

RLKs家族分类

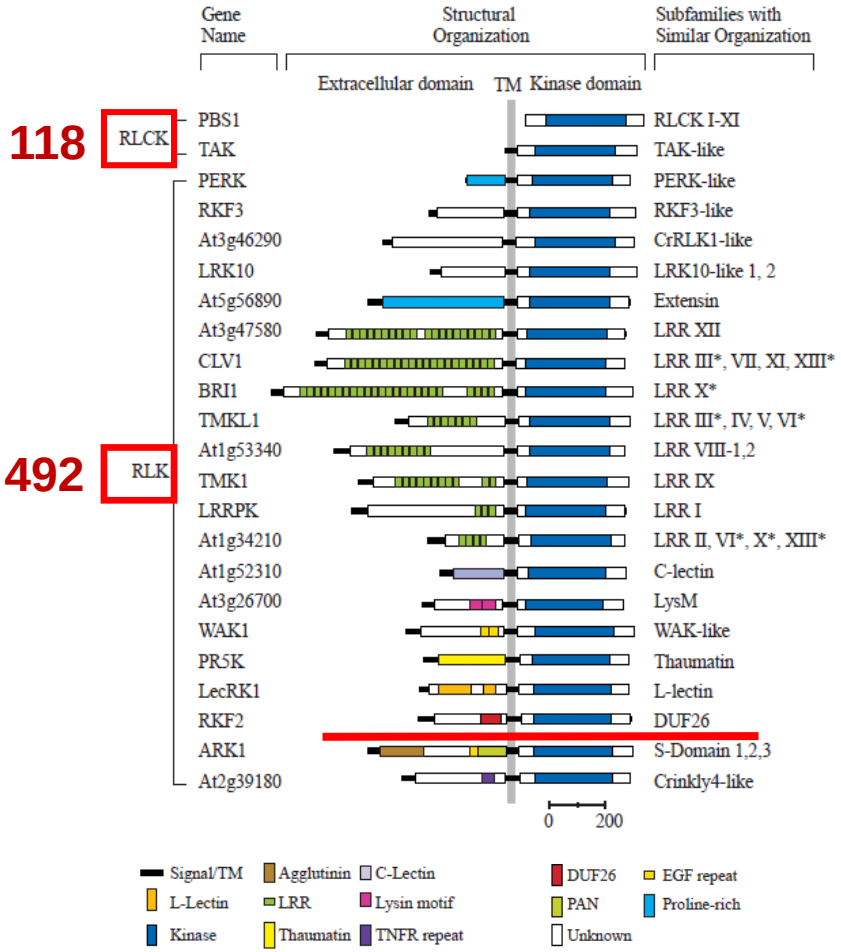
Receptor-like kinase (RLK)
类受体激酶



Shiu *et al., Proceedings of the National Academy of Sciences of the United States of America*, 2001

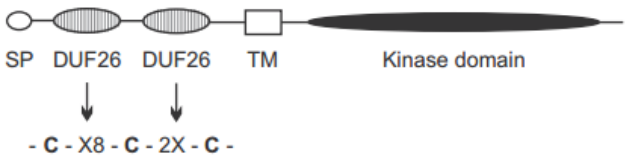
RLKs家族分类

DUF26 (Domain of Unknown Function 26)
DUF26 功能未知



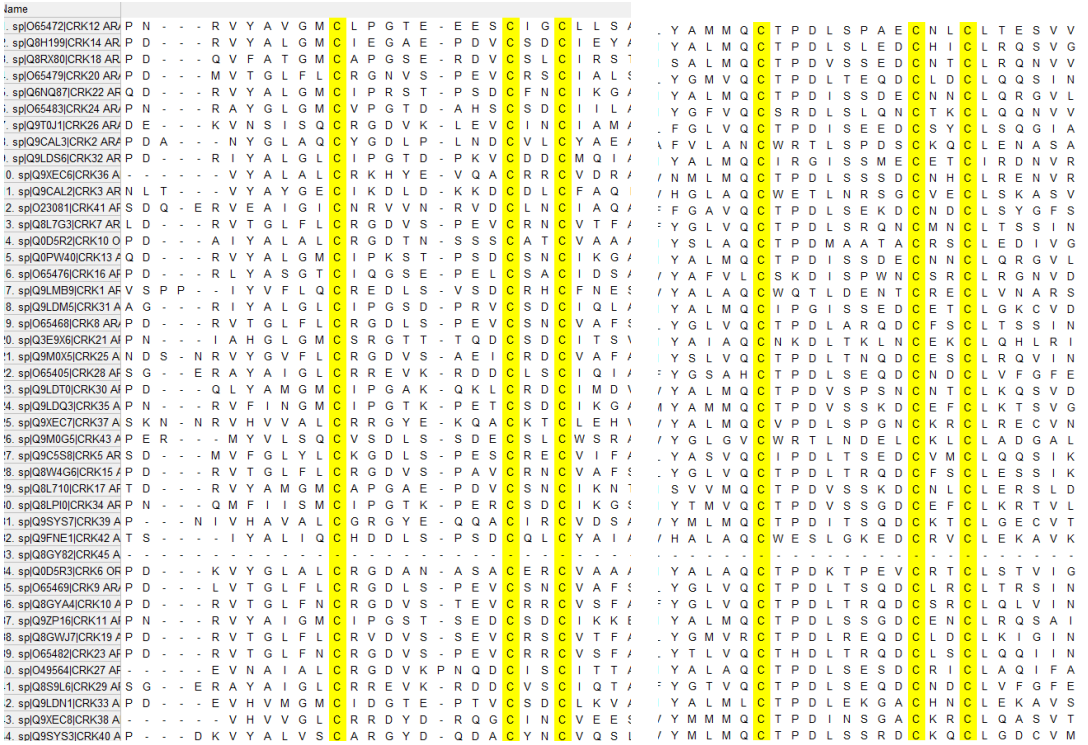
Shiu *et al., Proceedings of the National Academy of Sciences of the United States of America*, 2001

CRKs研究进展



Cysteine-rich Receptor-like Kinases (CRKs)

富含半胱氨酸的类受体激酶



Idänheimo *et al.,* Biochemical & Biophysical ResearchCommunications, 2014

Chen, Plant Physiology, 2001

CRKs研究进展

CRK20

CRK20 modulates host responses to *Pseudomonas syringae* infection.

CRK6 and *CRK7*

CRK6 and *CRK7* protect against apoplastic oxidative stress.

CRK13

CRK13 Enhances resistance to *Pseudomonas syringae.*

CRK45

CRK45 functions in the responses to abscisic acid and abiotic stresses.

CRKs 在拟南芥抗病、抗逆、细胞凋亡等过程中起作用。

Acharya *et al.,* Plant Journal for Cell & Molecular Biology, 2010
Ederli *et al.,* Journal of Plant Physiology, 2011
Zhang *et al.,* Plant Physiology & Biochemistry, 2013
Idänheimo *et al.,* Biochemical & Biophysical ResearchCommunications, 2014

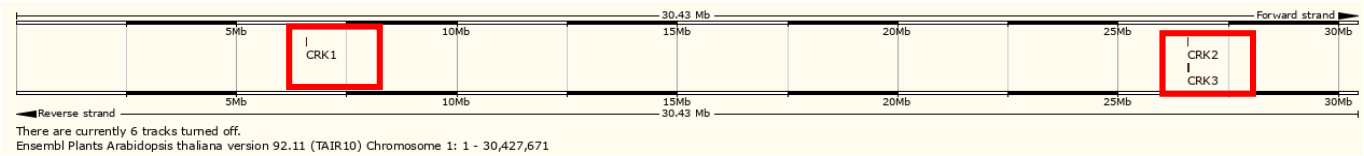
*Arabidopsis thaliana*中的CRK基因

No.	Entry	Gene_id	Gene_name	Chromosome	No.	Entry	Gene_id	Gene_name	Chromosome
1	Q9LMB9	At1g19090	CRK1	1	23	Q9C5S9	At4g23140	CRK6	4
2	Q9CAL3	At1g70520	CRK2	1	24	Q8L7G3	At4g23150	CRK7	4
3	Q9CAL2	At1g70530	CRK3	1	25	O65468	At4g23160	CRK8	4
4	Q9LZU4	At3g45860	CRK4	3	26	O45469	At4g23170	CRK9	4
5	O23081	At4g00970	CRK41	4	27	Q8GYA4	At4g23180	CRK10	4
6	Q9XEC6	At4g04490	CRK36	4	28	Q9ZP16	At4g23190	CRK11	4
7	Q9XEC7	At4g04500	CRK37	4	29	O65472	At4g23200	CRK12	4
8	Q9XEC8	At4g04510	CRK38	4	30	Q0PW40	At4g23210	CRK13	4
9	Q9SYS7	At4g04540	CRK39	4	31	Q8H199	At4g23220	CRK14	4
10	Q9SYS3	At4g04570	CRK40	4	32	Q8W4G6	At4g23230	CRK15	4
11	Q9M0X5	At4g05200	CRK25	4	33	O65476	At4g23240	CRK16	4
12	Q9LDT0	At4g11460	CRK30	4	34	Q8L710	At4g23250	CRK17	4
13	Q9LDM5	At4g11470	CRK31	4	35	Q8RX80	At4g23260	CRK18	4
14	Q9LDS6	At4g11480	CRK32	4	36	Q8GWJ7	At4g23270	CRK19	4
15	Q9LDN1	At4g11490	CRK33	4	37	O65479	At4g23280	CRK20	4
16	Q8LPI0	At4g11521	CRK34	4	38	Q3E9X6	At4g23290	CRK21	4
17	Q9LDQ3	At4g11530	CRK35	4	39	Q6NQ87	At4g23300	CRK22	4
18	Q8GY82	At4g11890	CRK45	4	40	O65482	At4g23310	CRK23	4
19	O49564	At4g21230	CRK27	4	41	O65483	At4g23320	CRK24	4
20	O65405	At4g21400	CRK28	4	42	Q9M0G5	At4g28670	CRK43	4
21	Q8S9L6	At4g21410	CRK29	4	43	Q9T0J1	At4g38830	CRK26	4
22	Q9C5S8	At4g23130	CRK5	4	44	Q9FNE1	At5g40380	CRK42	5

Uniprot+Ensembl

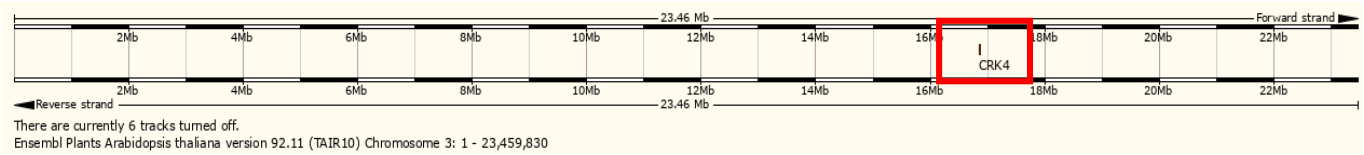
44 CRK Genes in *Arabidopsis thaliana*

Chr 1



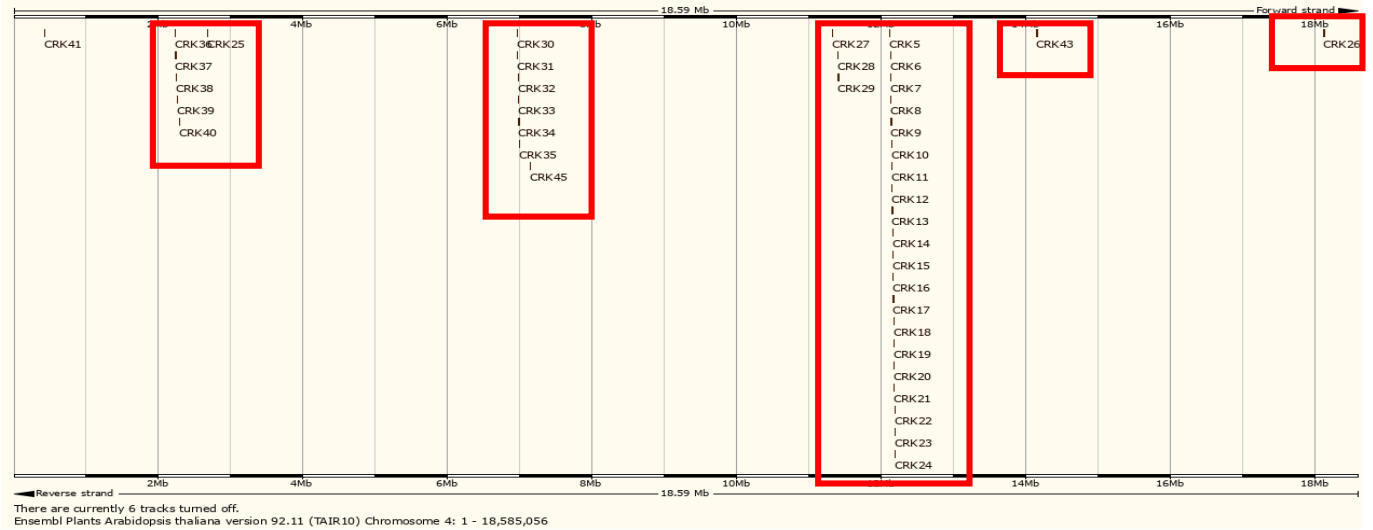
3个

Chr 3



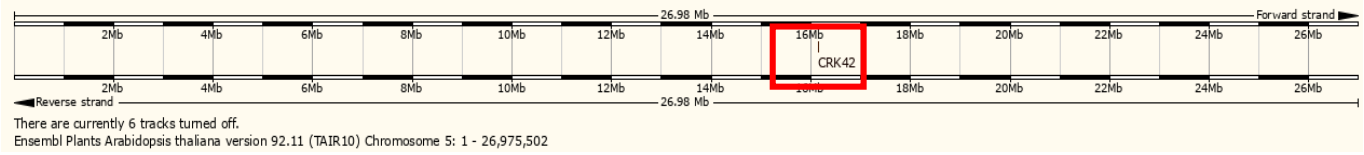
1个

Chr 4



39个

Chr 5



1个

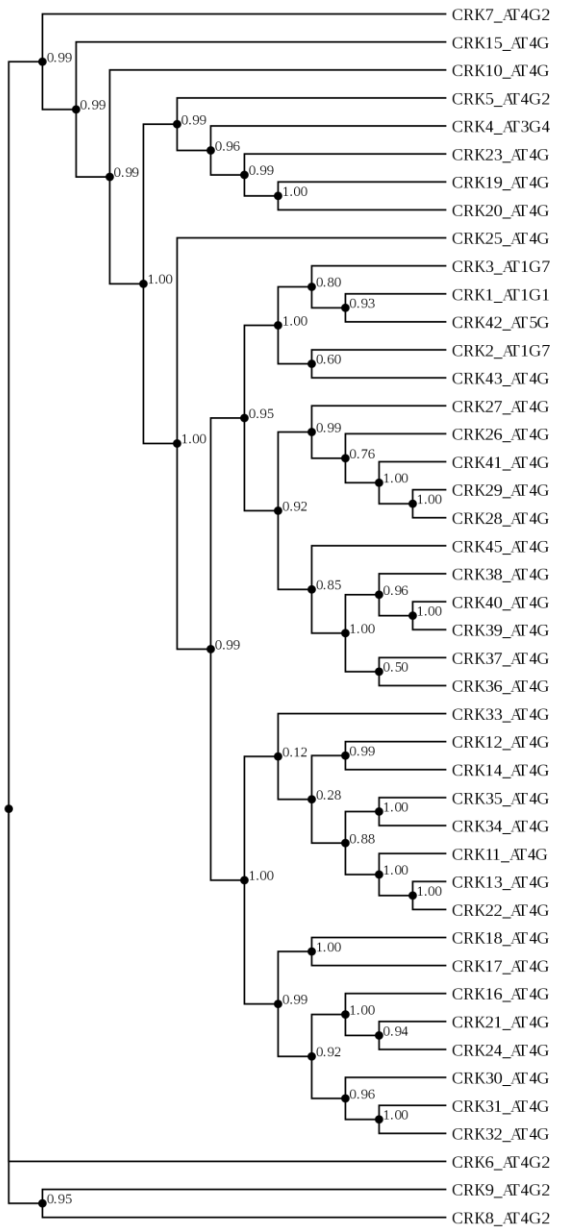
大多CRK定位在4号染色体上.

Ensembl

CRKs进化树分析

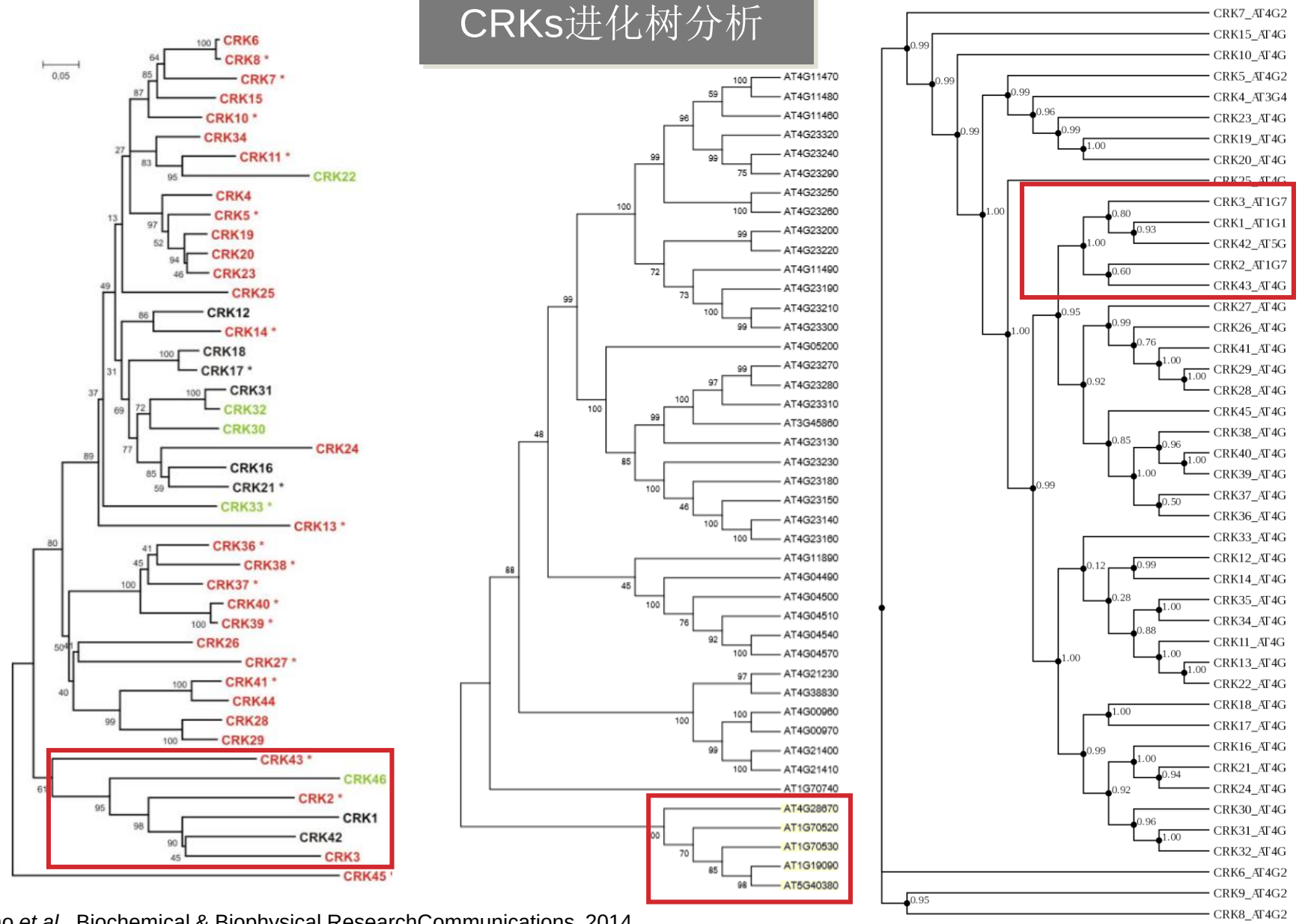
PhyML 3.0: new algorithms, methods and utilities

Please cite:
"New Algorithms and Methods to Estimate Maximum-Likelihood Phylogenies: Assessing the Performance of PhyML 3.0."
Guindon S., Dufayard J.F., Lefort V., Anisimova M., Hordijk W., Gascuel O.
Systematic Biology, 59(3):307-21, 2010.



Preliminary results

CRKs进化树分析



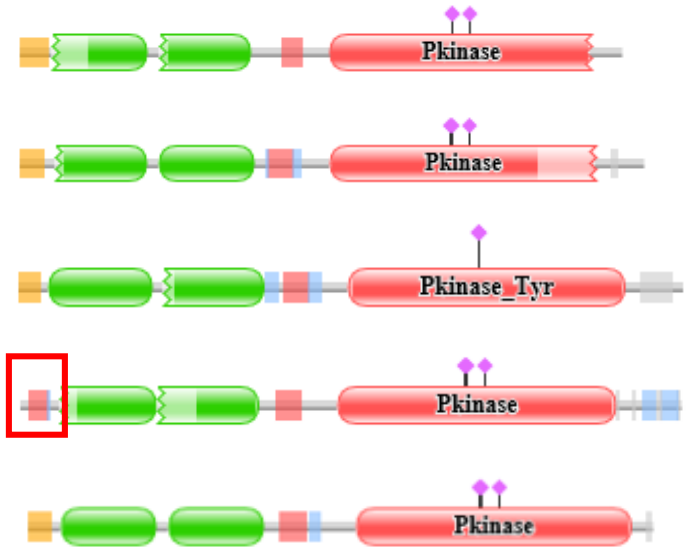
Idänheimo *et al.,* Biochemical & Biophysical ResearchCommunications, 2014

5 个CRK 基因及其不同剪接体

Gene ID	Gene Name	Location	Transcripts ID	Transcripts Length(bp)	Protein Length(aa)	Biotype
AT1G19090	CRK1,RKF2	Chromosome 1	AT1G19090.1	2509	NA	Nontranslating CDS
AT1G70520	CRK2	Chromosome 1	AT1G70520.1	2403	649	Protein coding
AT1G70530	CRK3	Chromosome 1	AT1G70530.3	2720	488	Protein coding
			AT1G70530.2	2699	538	Protein coding
			AT1G70530.1	2697	646	Protein coding
AT5G40380	CRK42	Chromosome 5	AT5G40380.1	2694	651	Protein coding
			AT5G40380.2	2569	556	Protein coding
			AT5G40380.3	1820	480	Protein coding
AT4G28670	CRK43	Chromosome 4	AT4G28670.1	1878	625	Protein coding

Ensembl

蛋白结构预测



CRK1 615aa

CRK2 649aa

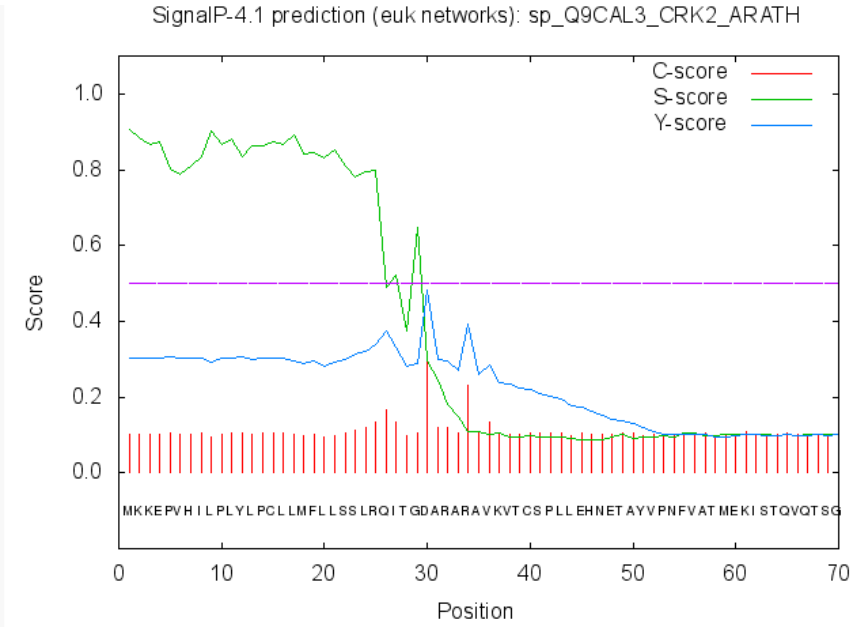
CRK3 646aa

CRK42 651aa

CRK43 625aa

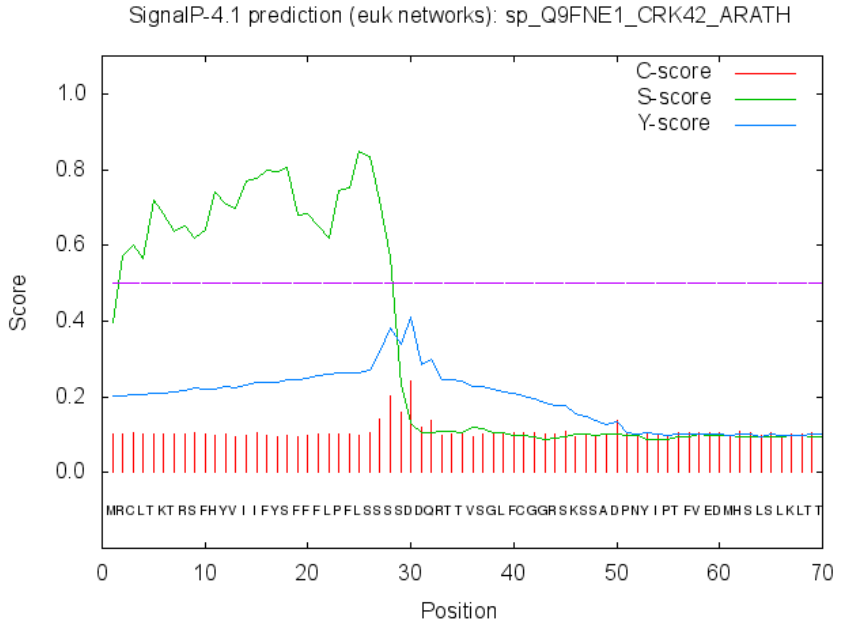
Pfam

CRK2&CRK42信号肽预测



# Measure	Position	Value	Cutoff	signal peptide?
max. C	30	0.295		
max. Y	30	0.481		
max. S	1	0.907		
mean S	1-29	0.800		
D	1-29	0.653	0.450	YES

CRK2

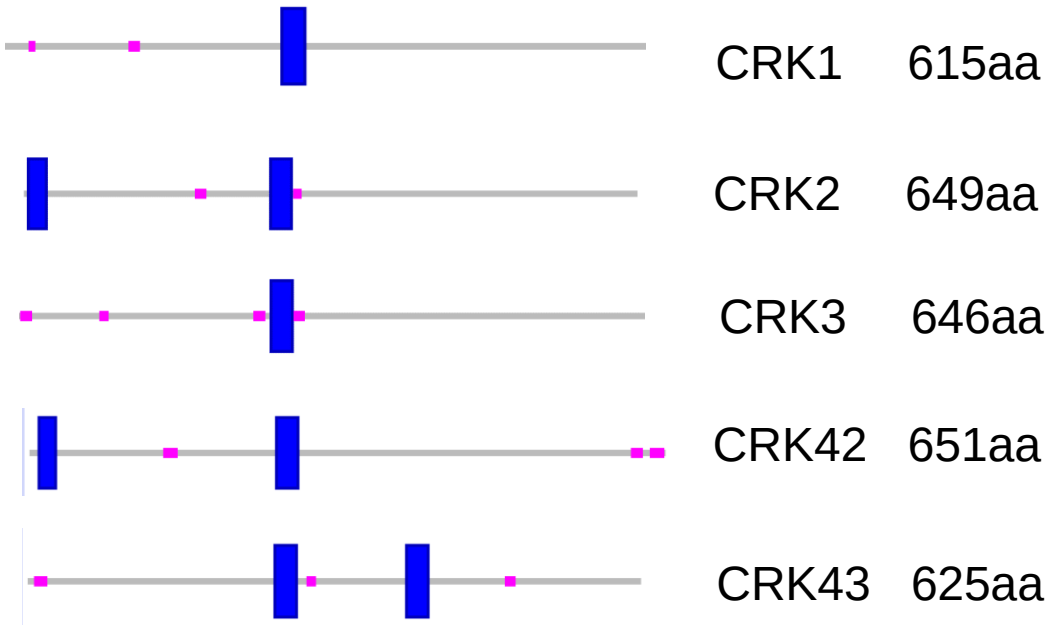


# Measure	Position	Value	Cutoff	signal peptide?
max. C	30	0.243		
max. Y	30	0.412		
max. S	25	0.848		
mean S	1-29	0.673		
D	1-29	0.553	0.450	YES

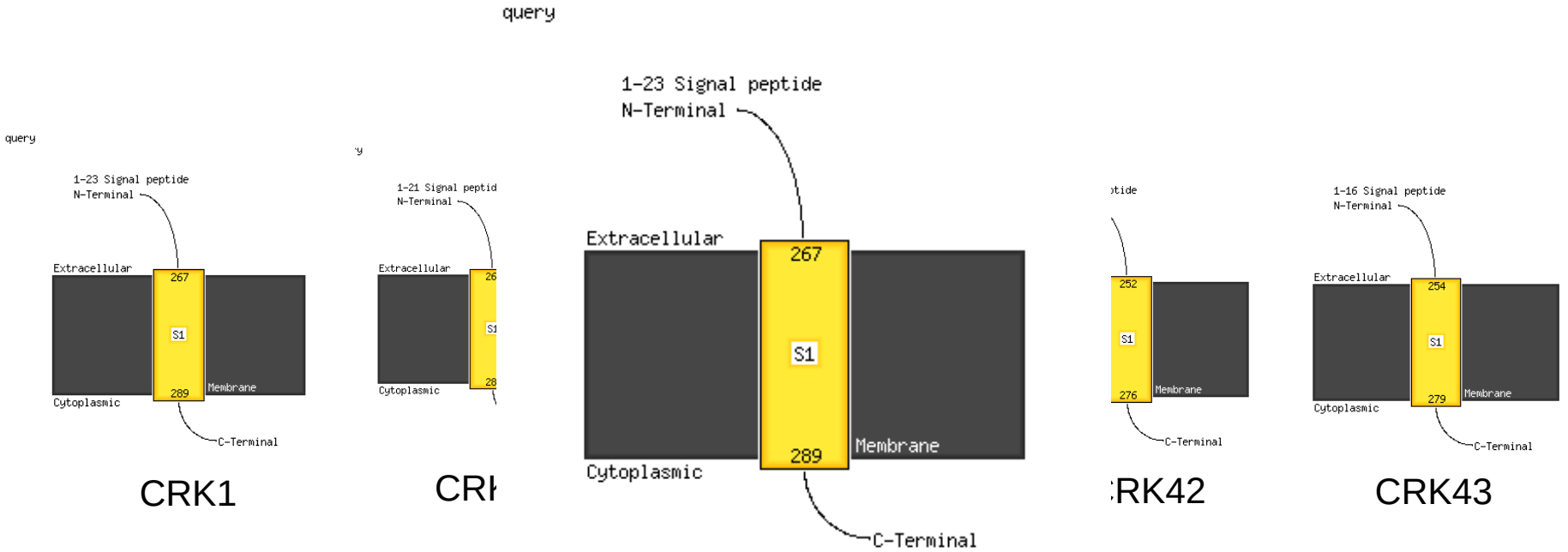
CRK42

被预测为有信号肽区域，但分值较低.

跨膜域预测


CRK1 615aa
CRK2 649aa
CRK3 646aa
CRK42 651aa
CRK43 625aa
跨膜域
低复杂度域

跨膜域预测



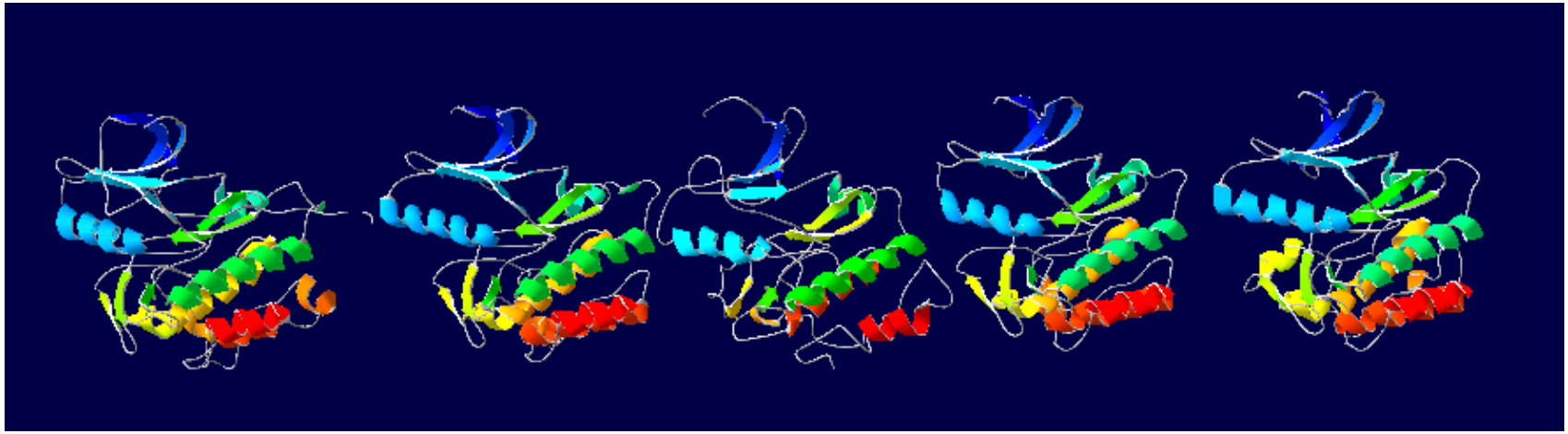
CRK1

Phyre2

3D结构

Protein	Precision	Coverage	Top Template PDB ID	Template binding small molecules
CRK43	100%	43%	2FO0	Yes
CRK2	100%	39%	2FO0	Yes
CRK3	100%	40%	5EBZ	Yes
CRK1	100%	39%	2FO0	Yes
CRK42	100%	39%	2FO0	Yes

3D结构

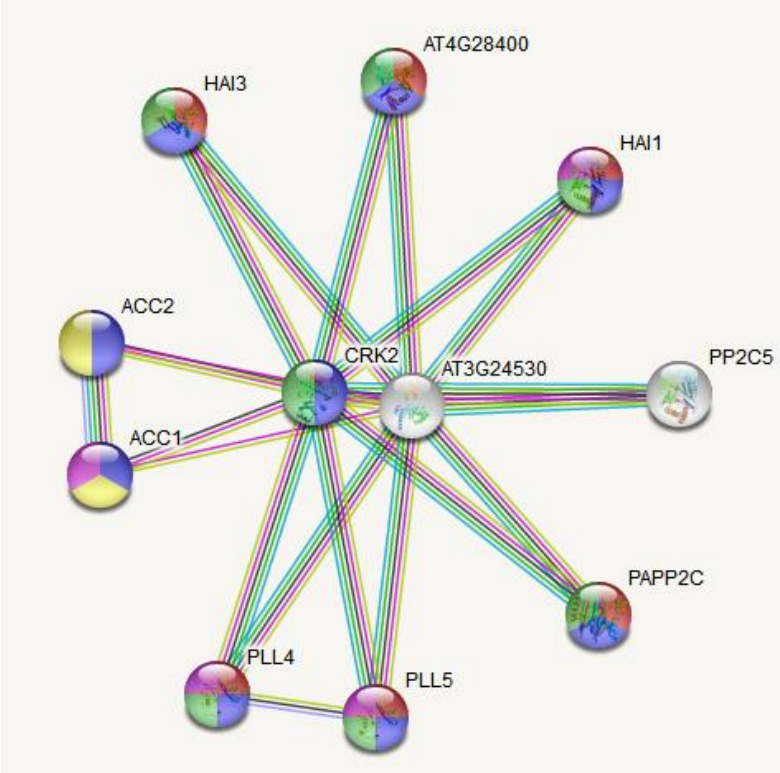


CRK1 CRK2 CRK3 CRK42 CRK43

	CRK1	CRK2	CRK3	CRK42	CRK43
CRK1	-				
CRK2	2.62	-			
CRK3	5.15	3.69	-		
CRK42	3.05	1.53	4.02	-	
CRK43	3.73	2.56	4.53	3.38	-

Phyre2

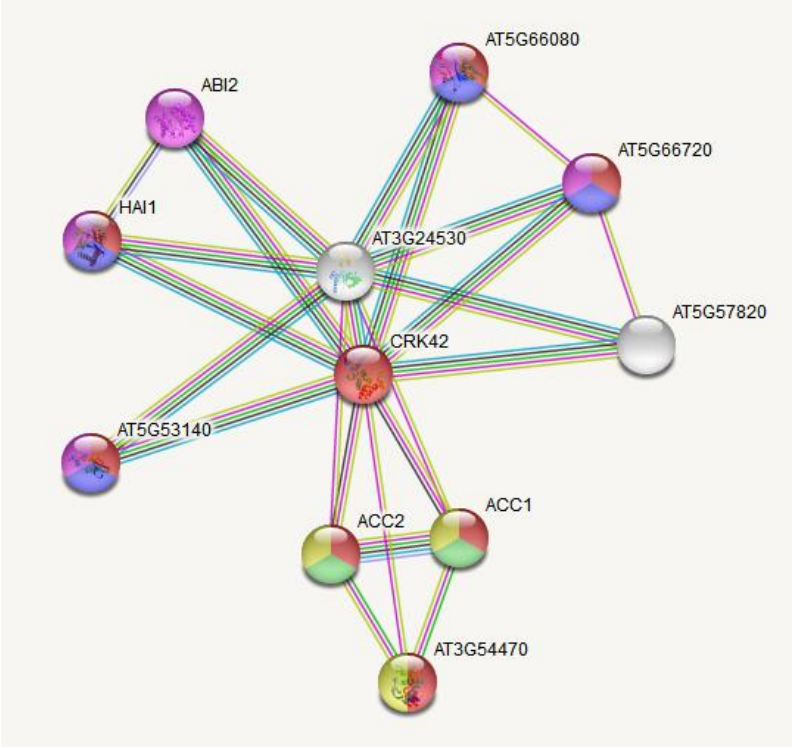
CRK2互作蛋白分析



Biological Process (GO)			
pathway ID	*pathway description*	*count in gene set*	*false discovery rate*
GO:0006470	protein dephosphorylation	6	1.83e-08
GO:0006796	phosphate-containing compound metabolic process	9	2.28e-07
GO:0006464	cellular protein modification process	7	0.000903
GO:2001295	malonyl-CoA biosynthetic process	2	0.000998
GO:0048367	shoot system development	4	0.0108
			(more ...)

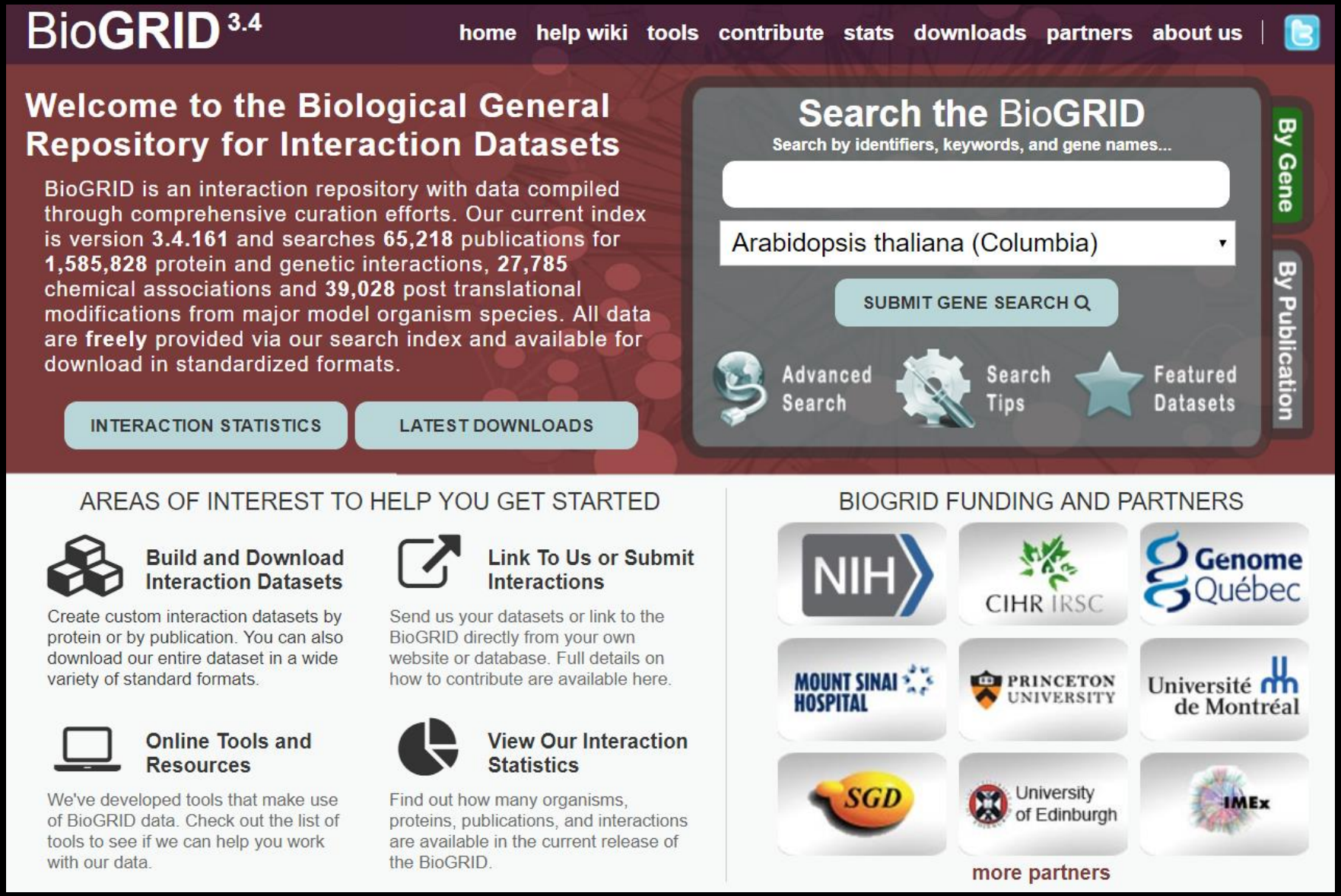
String

CRK42互作蛋白分析



Biological Process (GO)			
pathway ID	*pathway description*	*count in gene set*	*false discovery rate*
GO:0006796	phosphate-containing compound metabolic process	8	2.43e-05
GO:0006470	protein dephosphorylation	4	0.000221
GO:2001295	malonyl-CoA biosynthetic process	2	0.00141
GO:0042455	ribonucleoside biosynthetic process	3	0.00318
GO:0009260	ribonucleotide biosynthetic process	3	0.00334
			(more ...)

String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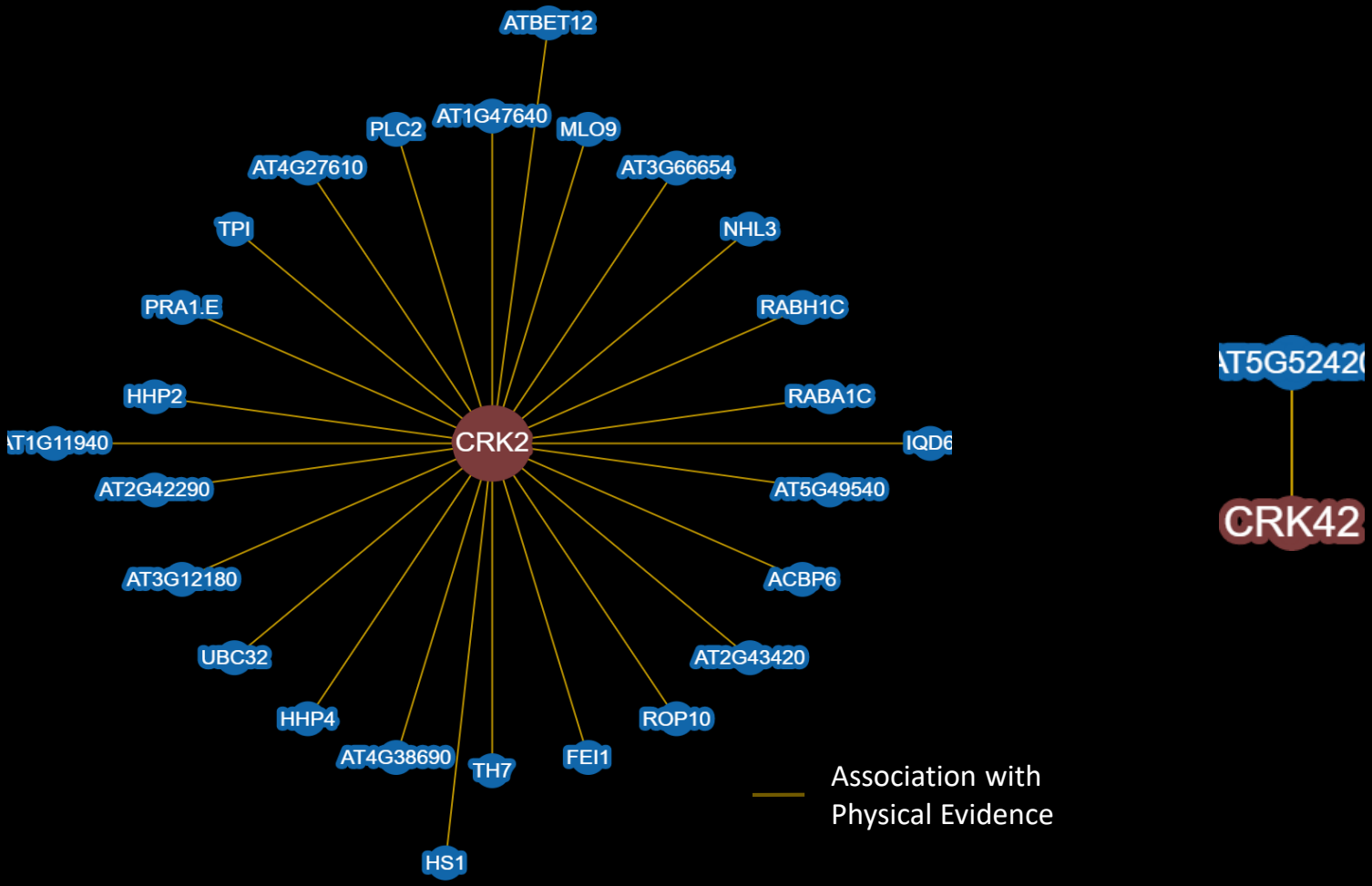
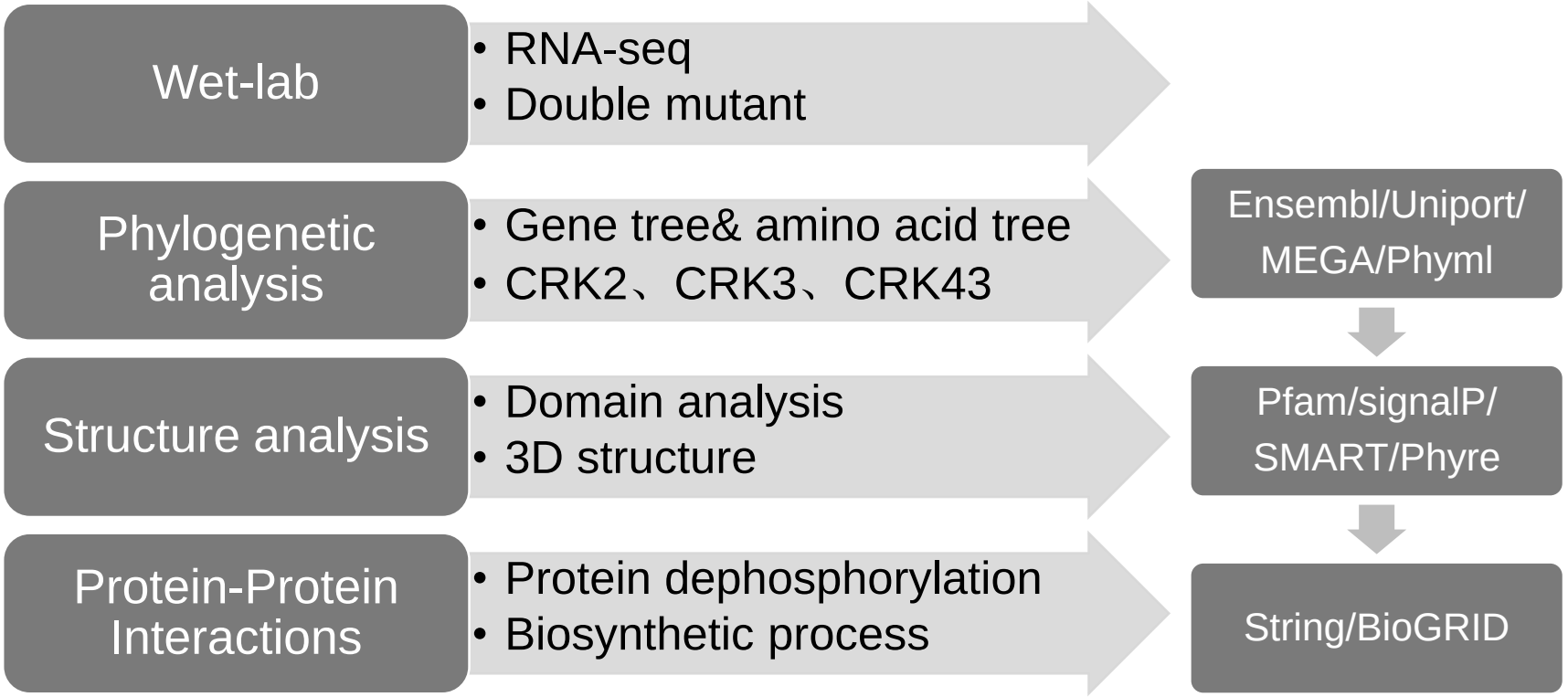
CRK2&42 蛋白互作网络分析



BioGRID

Summary


Wet-lab
• RNA-seq
• Double mutant
Phylogenetic analysis
• Gene tree& amino acid tree
• CRK2、CRK3、CRK43
Structure analysis
• Domain analysis
• 3D structure
Protein-Protein Interactions
• Protein dephosphorylation
• Biosynthetic process
Ensembl/Uniport/ MEGA/Phyml
Pfam/signalP/ SMART/Phyre
String/BioGRID

Acknowledgement

G01	G02	G03
• 吉雅晴 • 仇心钰 • 王龙腾 • 吴鑫凯	• 范昱 • 张延松 • 邹恭鲁 • 项薇	• 马文平 • 杨旖旎 • 庄元

感谢罗老师的指导和助教的帮助~

Thank you!