ちょっと整理しておきたいのですが…

- 生物情報工学（バイオインフォマティクス）ってなに？

分子生物学研究の結果、大量のDNA配列データが蓄積されてきた。

Gene A: ATGAAGTTTAGACCGATCAGTACT….
Gene B: ATGCAGTACGAAGTACGATAGACAAGT…

新奇遺伝子が見つかった。さて、これは既知のものと同じ機能か否か？

Novel Gene: ATGCAGTACTAAGTTTAGACCGAT….

さらに、ゲノムプロジェクトの進展で大量のDNA配列データが手に入った。
さて、配列が分かってもどこが遺伝子か分からない…。

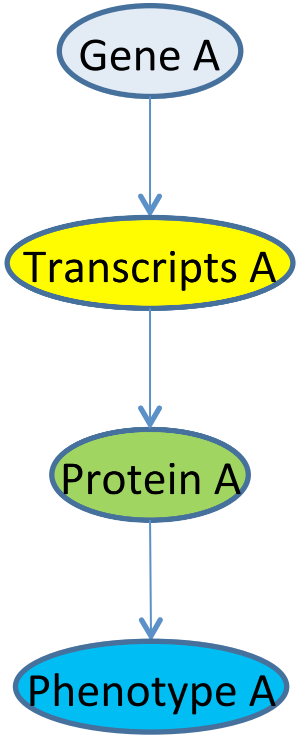
じゃあ、過去の知見をもとに遺伝子領域を予測しよう！
BLAST、ORF finder、Softberry/FGENESH

DNAシーケンサーの発達により、ゲノム配列情報がさらに充実。
ゲノムを種間比較して、進化学的な研究をしよう⇒比較ゲノミクス

ちょっと整理しておきたいのですが…

- 生物情報工学（バイオインフォマティクス）ってなに？

古典的な分子生物学



Gene A

Transcripts A

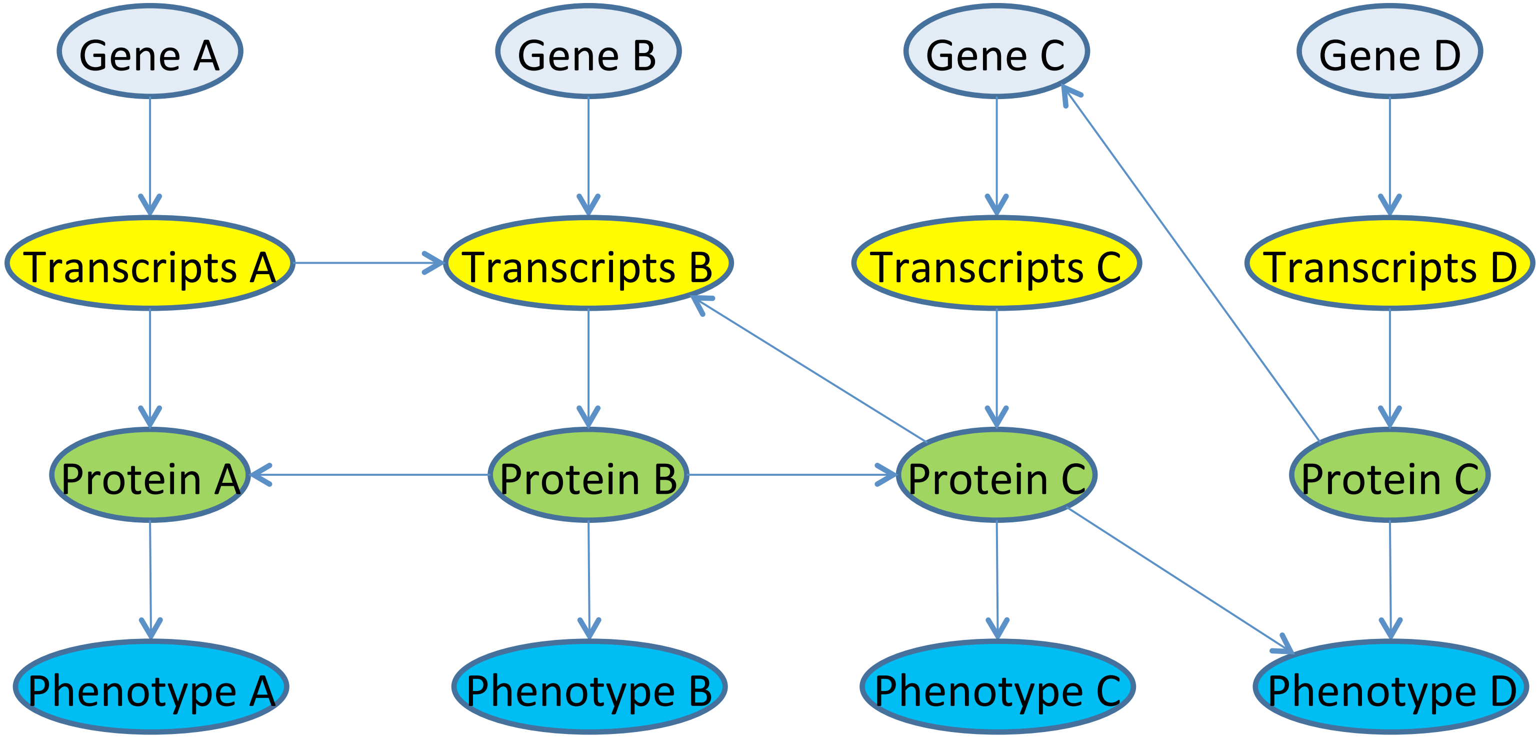
Protein A

Phenotype A

ちょっと整理しておきたいのですが…

- 生物情報工学（バイオインフォマティクス）ってなに？

分子生物学の発展

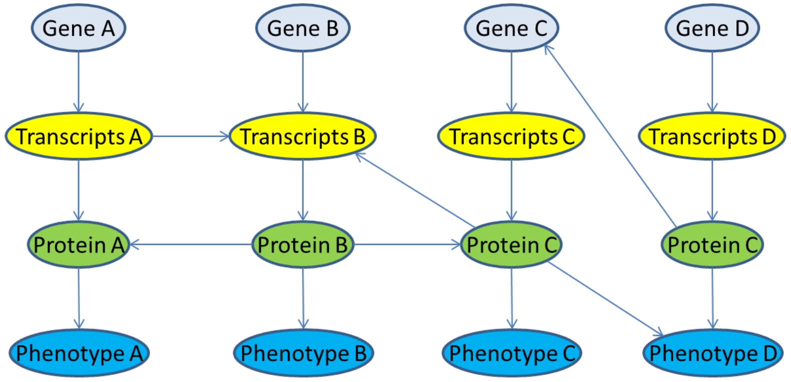

Gene A
Gene B
Gene C
Gene D
Transcripts A
Transcripts B
Transcripts C
Transcripts D
Protein A
Protein B
Protein C
Protein C
Phenotype A
Phenotype B
Phenotype C
Phenotype D

ゲノム、転写産物、たんぱく質、表現型の各階層内・階層間での複雑な相互作用

一つ一つの要素だけに注目していても、生命現象の本質的な理解には至らない？
木を見て森を見ず？

ちょっと整理しておきたいのですが…

➢ 生物情報工学（バイオインフォマティクス）ってなに？


Gene A
Gene B
Gene C
Gene D
Transcripts A
Transcripts B
Transcripts C
Transcripts D
Protein A
Protein B
Protein C
Protein C
Phenotype A
Phenotype B
Phenotype C
Phenotype D

分子生物学の発展

ゲノム、転写産物、たんぱく質、表現型の各階層内・階層間での複雑な相互作用

複雑な相互作用ネットワークから成る生命システムを分解せず複雑なネットワークのまま理解する。

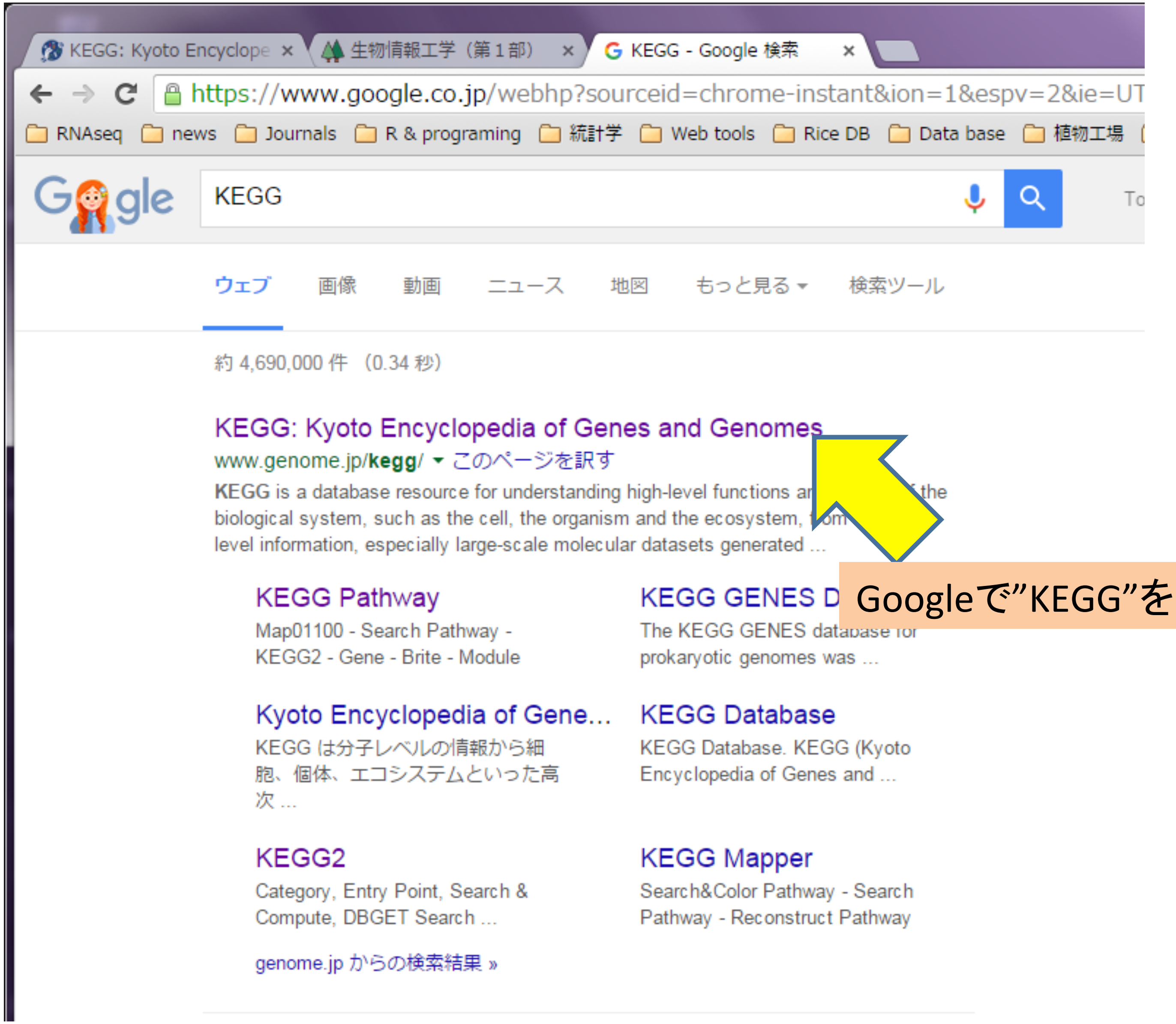
オミクス(Omics)

- Genomics （ゲノム）
- Transcriptomics （転写産物）
- Proteomics （タンパク質）
- Metabolomics （代謝産物）
- Glycomics （糖鎖付加）
- Epigenomics （ゲノム修飾）
- Phenomics （表現型）

データを数理モデルやネットワークモデルに落とし込んで、生命システムを理解したい。

⇒ システムバイオロジー

システムバイオロジーの申し子「KEGG」


KEGG: Kyoto Encyclope
生物情報工学（第１部）
KEGG - Google 検索
https://www.google.co.jp/webhp?sourceid=chrome-instant&ion=1&espv=2&ie=UT
RNAseq
news
Journals
R & programing
統計学
Web tools
Rice DB
Data base
植物工場
KEGG
ウェブ
画像
動画
ニュース
地図
もっと見る
検索ツール

約 4,690,000 件 （0.34 秒）

KEGG: Kyoto Encyclopedia of Genes and Genomes
www.genome.jp/**kegg**/ ▾ このページを訳す
KEGG is a database resource for understanding high-level functions ar the biological system, such as the cell, the organism and the ecosystem, om level information, especially large-scale molecular datasets generated ...

KEGG Pathway
Map01100 - Search Pathway - KEGG2 - Gene - Brite - Module

KEGG GENES D
The KEGG GENES database for prokaryotic genomes was ...

Kyoto Encyclopedia of Gene...
KEGG は分子レベルの情報から細胞、個体、エコシステムといった高次 ...

KEGG Database
KEGG Database. KEGG (Kyoto Encyclopedia of Genes and ...

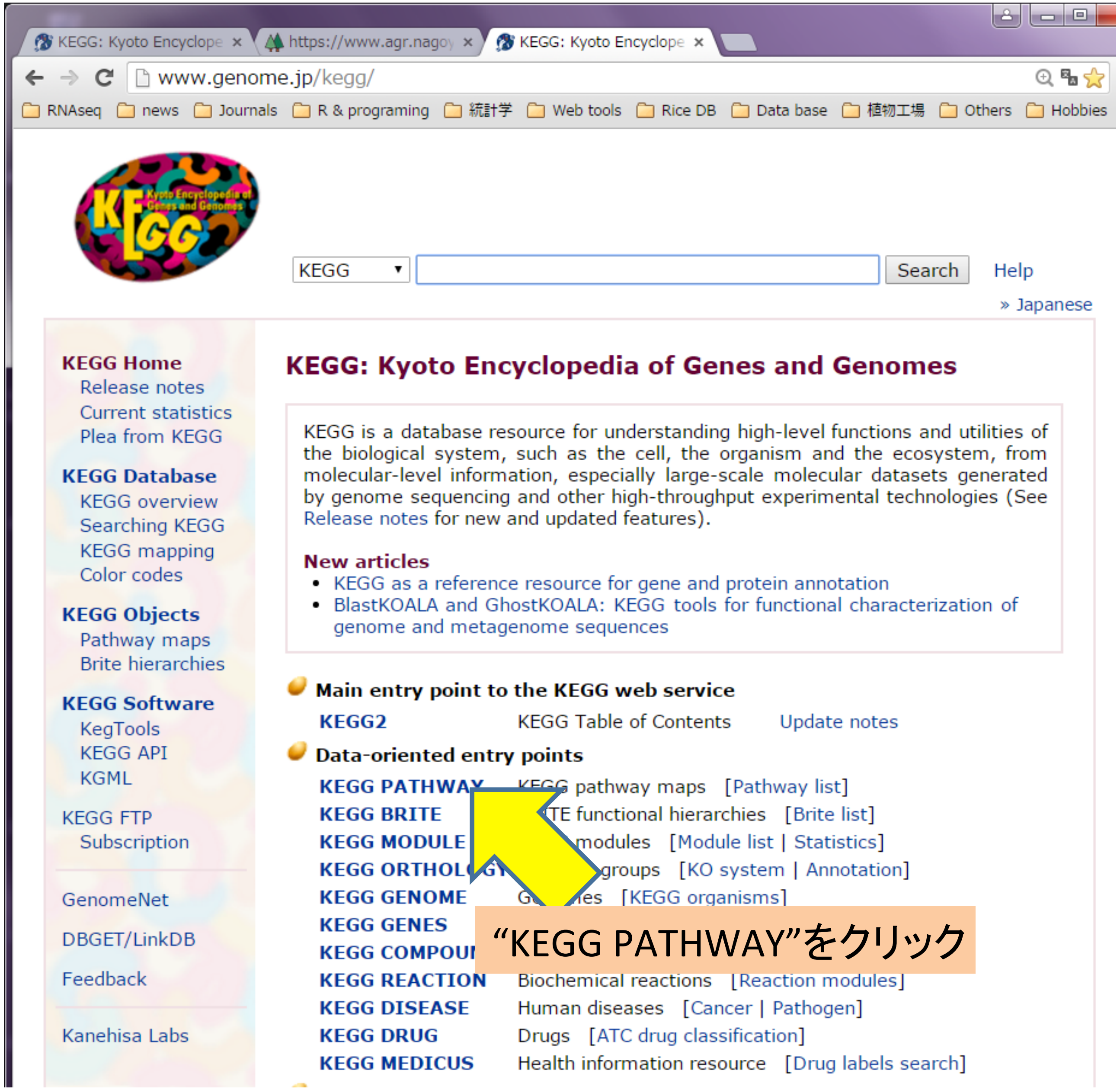
KEGG2
Category, Entry Point, Search & Compute, DBGET Search ...

KEGG Mapper
Search&Color Pathway - Search Pathway - Reconstruct Pathway

genome.jp からの検索結果 »

Googleで”KEGG”を検索

システムバイオロジーの申し子「KEGG」


KEGG: Kyoto Encyclope
https://www.agr.nagoy
KEGG: Kyoto Encyclope
www.genome.jp/kegg/
RNAseq
news
Journals
R & programing
統計学
Web tools
Rice DB
Data base
植物工場
Others
Hobbies
KEGG Kyoto Encyclopedia of Genes and Genomes
KEGG
Search
Help
» Japanese
KEGG Home
Release notes
Current statistics
Plea from KEGG
KEGG Database
KEGG overview
Searching KEGG
KEGG mapping
Color codes
KEGG Objects
Pathway maps
Brite hierarchies
KEGG Software
KegTools
KEGG API
KGML
KEGG FTP
Subscription
GenomeNet
DBGET/LinkDB
Feedback
Kanehisa Labs

KEGG: Kyoto Encyclopedia of Genes and Genomes

KEGG is a database resource for understanding high-level functions and utilities of the biological system, such as the cell, the organism and the ecosystem, from molecular-level information, especially large-scale molecular datasets generated by genome sequencing and other high-throughput experimental technologies (See Release notes for new and updated features).

New articles

- KEGG as a reference resource for gene and protein annotation
- BlastKOALA and GhostKOALA: KEGG tools for functional characterization of genome and metagenome sequences

Main entry point to the KEGG web service

KEGG2	KEGG Table of Contents	Update notes

Data-oriented entry points

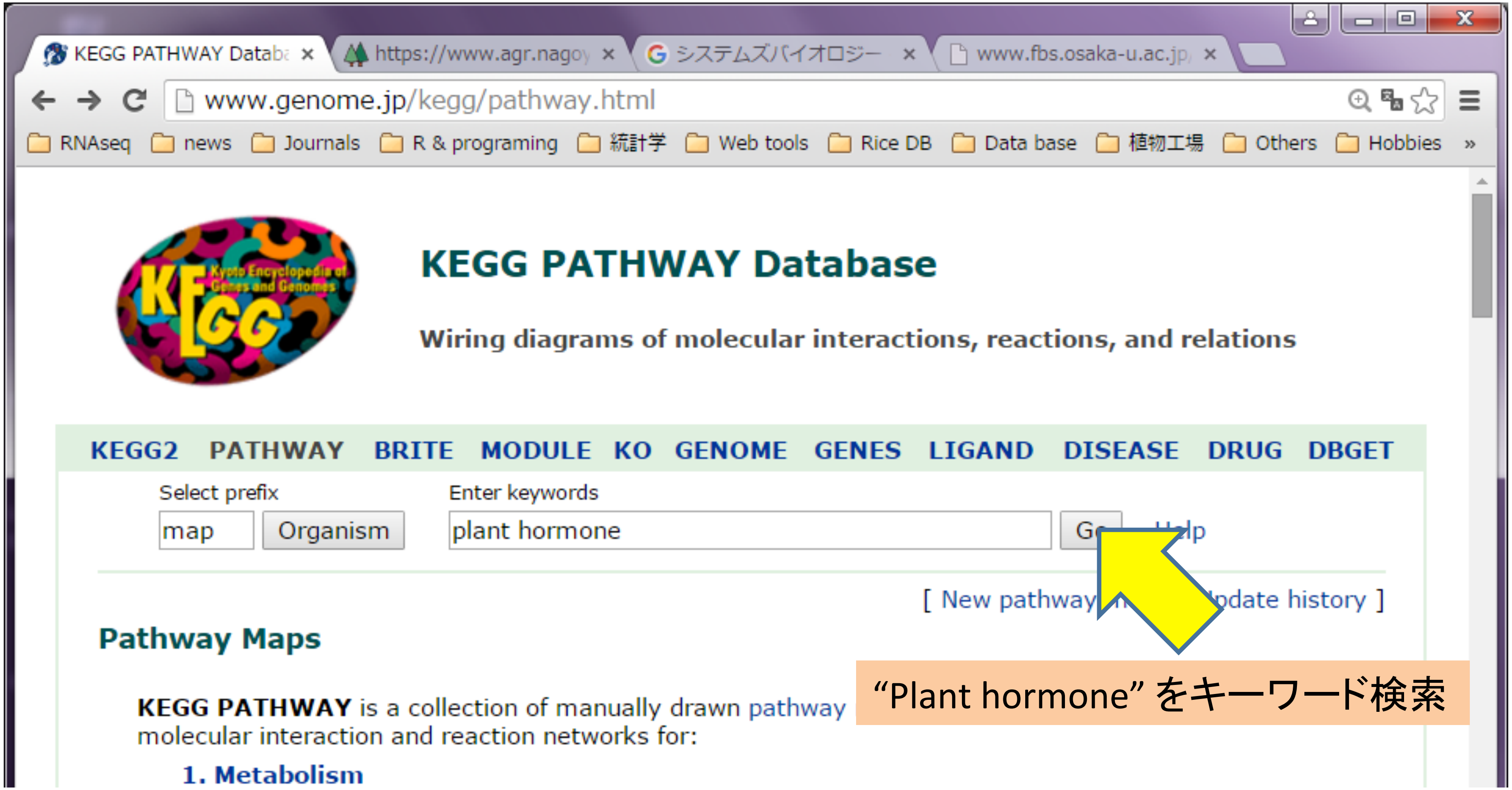
KEGG PATHWAY	KEGG pathway maps [Pathway list]
KEGG BRITE	TE functional hierarchies [Brite list]
KEGG MODULE	modules [Module list | Statistics]
KEGG ORTHOLOGY	groups [KO system | Annotation]
KEGG GENOME	G es [KEGG organisms]
KEGG GENES	
KEGG COMPOU	
KEGG REACTION	Biochemical reactions [Reaction modules]
KEGG DISEASE	Human diseases [Cancer | Pathogen]
KEGG DRUG	Drugs [ATC drug classification]
KEGG MEDICUS	Health information resource [Drug labels search]

“KEGG PATHWAY”をクリック

KEGG

京都大学バイオインフォマティクスセンターが管理しているバイオインフォマティクス研究用データベース。
システムバイオジー的なコンセプトを基にしており、遺伝子間、分子間の相互作用ネットワークに関する情報をデータベース化してある。

KEGGのコアデータベースKEGG PATHWAY



KEGG PATHWAY Datab
https://www.agr.nagoy
システムズバイオロジー
www.fbs.osaka-u.ac.jp
www.genome.jp/kegg/pathway.html
RNAseq
news
Journals
R & programing
統計学
Web tools
Rice DB
Data base
植物工場
Others
Hobbies
Kyoto Encyclopedia of Genes and Genomes
KEGG
KEGG2
PATHWAY
BRITE
MODULE
KO
GENOME
GENES
LIGAND
DISEASE
DRUG
DBGET
Organism
Go
Help
[New pathway
pdate history]

KEGG PATHWAY Database

Wiring diagrams of molecular interactions, reactions, and relations

Select prefix: map

Enter keywords: plant hormone

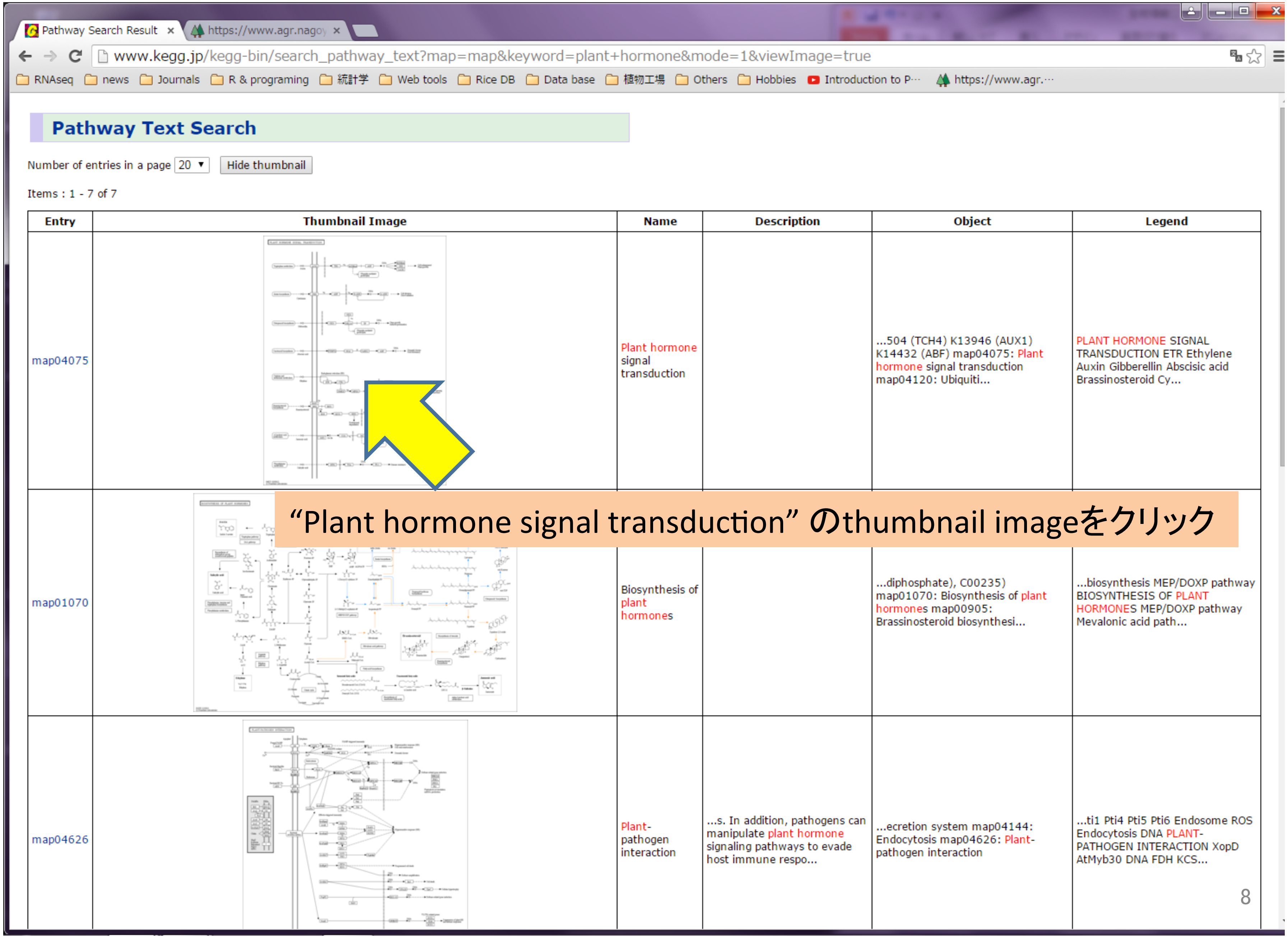
Pathway Maps

KEGG PATHWAY is a collection of manually drawn pathway
molecular interaction and reaction networks for:

1. Metabolism

“Plant hormone” をキーワード検索

KEGGで植物ホルモンシグナル伝達系を俯瞰する


Pathway Search Result
https://www.agr.nagoy
www.kegg.jp/kegg-bin/search_pathway_text?map=map&keyword=plant+hormone&mode=1&viewImage=true
RNAseq
news
Journals
R & programing
統計学
Web tools
Rice DB
Data base
植物工場
Others
Hobbies
Introduction to P···
https://www.agr.···

Pathway Text Search

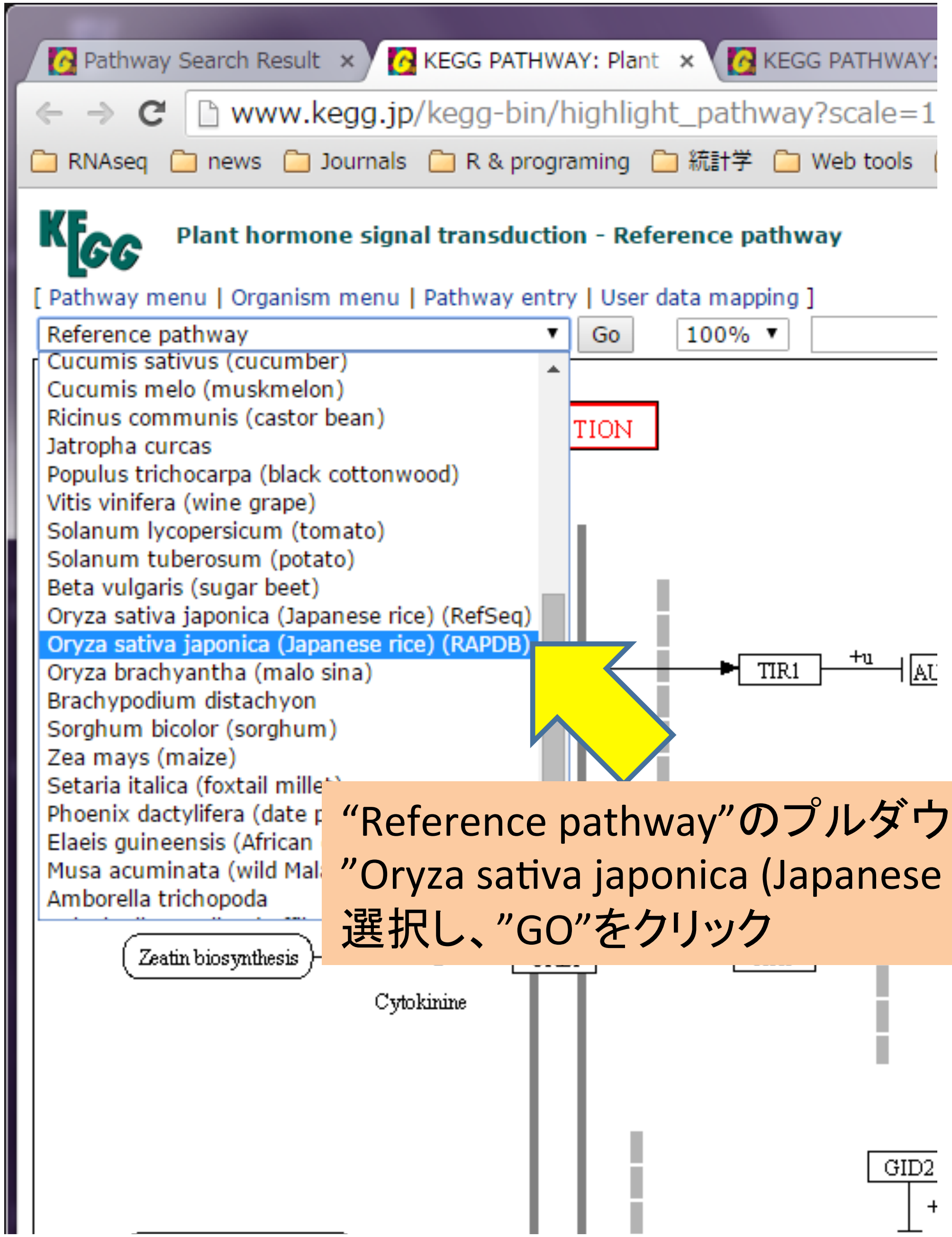
Number of entries in a page 20 ▾ Hide thumbnail

Items : 1 - 7 of 7

Entry	Thumbnail Image	Name	Description	Object	Legend
map04075		Plant hormone signal transduction		...504 (TCH4) K13946 (AUX1) K14432 (ABF) map04075: Plant hormone signal transduction map04120: Ubiquiti...	PLANT HORMONE SIGNAL TRANSDUCTION ETR Ethylene Auxin Gibberellin Abscisic acid Brassinosteroid Cy...
map01070		Biosynthesis of plant hormones		...diphosphate), C00235) map01070: Biosynthesis of plant hormones map00905: Brassinosteroid biosynthesi...	...biosynthesis MEP/DOXP pathway BIOSYNTHESIS OF PLANT HORMONES MEP/DOXP pathway Mevalonic acid path...
map04626		Plant-pathogen interaction	...s. In addition, pathogens can manipulate plant hormone signaling pathways to evade host immune respo...	...ecretion system map04144: Endocytosis map04626: Plant-pathogen interaction	...ti1 Pti4 Pti5 Pti6 Endosome ROS Endocytosis DNA PLANT-PATHOGEN INTERACTION XopD AtMyb30 DNA FDH KCS...

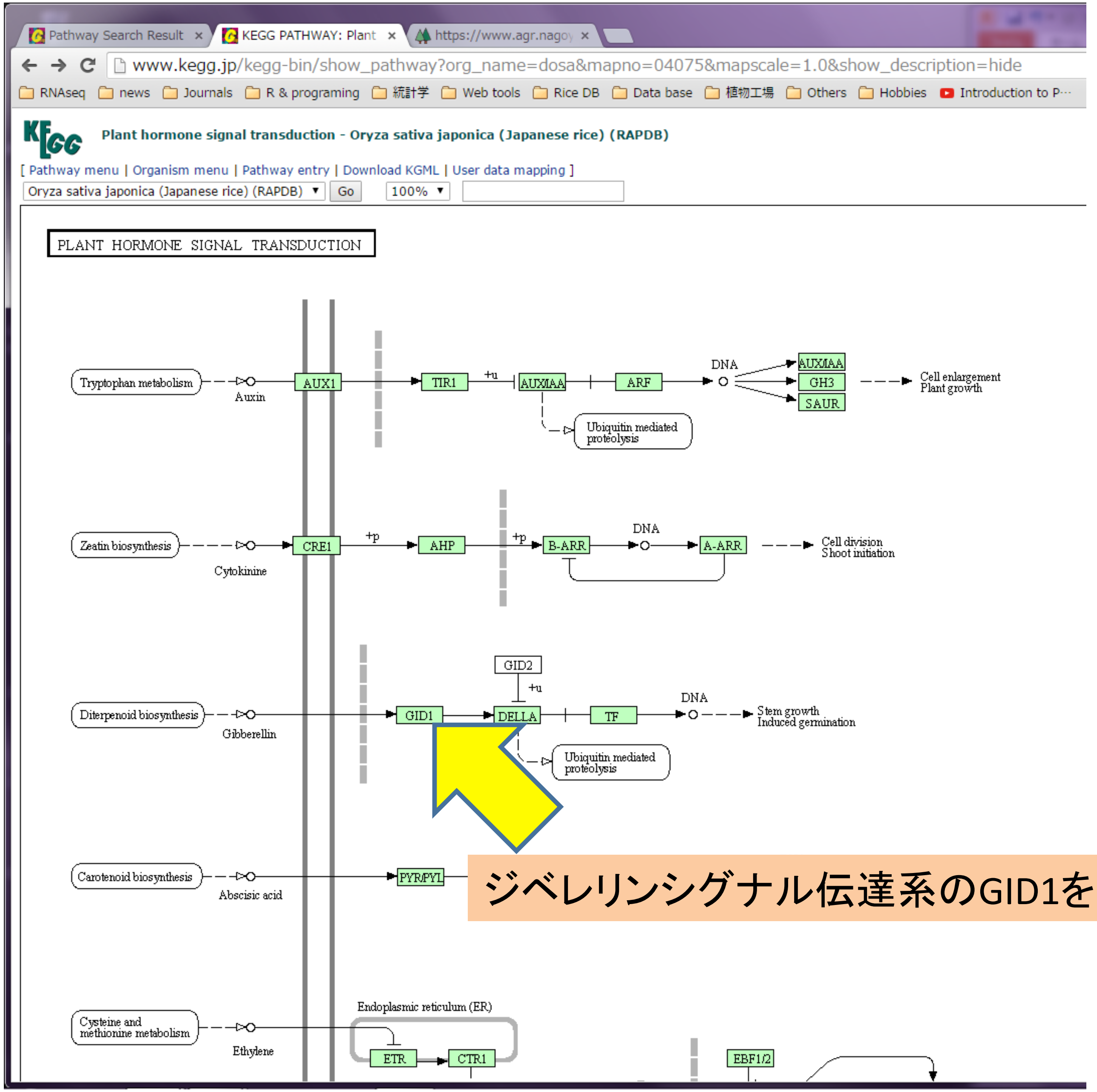
“Plant hormone signal transduction” のthumbnail imageをクリック

イネにおける植物ホルモンシグナル伝達系遺伝子


Pathway Search Result
KEGG PATHWAY: Plant
KEGG PATHWAY:
www.kegg.jp/kegg-bin/highlight_pathway?scale=1
RNAseq
news
Journals
R & programing
統計学
Web tools
KEGG
Plant hormone signal transduction - Reference pathway
[Pathway menu | Organism menu | Pathway entry | User data mapping]
Reference pathway
Go
100%
Cucumis sativus (cucumber)
Cucumis melo (muskmelon)
Ricinus communis (castor bean)
Jatropha curcas
Populus trichocarpa (black cottonwood)
Vitis vinifera (wine grape)
Solanum lycopersicum (tomato)
Solanum tuberosum (potato)
Beta vulgaris (sugar beet)
Oryza sativa japonica (Japanese rice) (RefSeq)
Oryza sativa japonica (Japanese rice) (RAPDB)
Oryza brachyantha (malo sina)
Brachypodium distachyon
Sorghum bicolor (sorghum)
Zea mays (maize)
Setaria italica (foxtail millet)
Phoenix dactylifera (date p
Elaeis guineensis (African
Musa acuminata (wild Mal
Amborella trichopoda
TION
TIR1
+u
AU
Zeatin biosynthesis
Cytokinine
GID2
+

“Reference pathway”のプルダウンメニューから ”Oryza sativa japonica (Japanese rice)(RAPDB)”を選択し、”GO”をクリック

イネのジベレリン受容体



Pathway Search Result ×　KEGG PATHWAY: Plant ×　https://www.agr.nagoy ×

www.kegg.jp/kegg-bin/show_pathway?org_name=dosa&mapno=04075&mapscale=1.0&show_description=hide

RNAseq　news　Journals　R & programing　統計学　Web tools　Rice DB　Data base　植物工場　Others　Hobbies　Introduction to P···

Plant hormone signal transduction - Oryza sativa japonica (Japanese rice) (RAPDB)

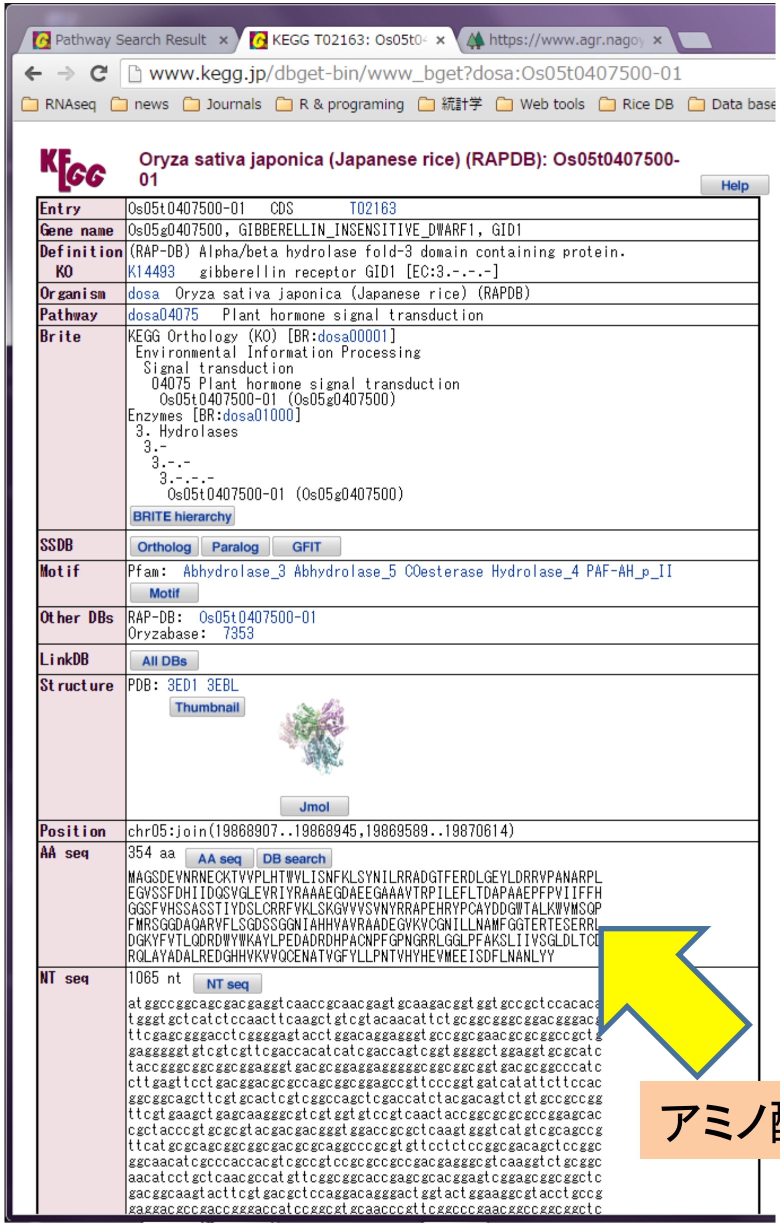
[Pathway menu | Organism menu | Pathway entry | Download KGML | User data mapping]

Oryza sativa japonica (Japanese rice) (RAPDB) ▼　Go　100% ▼

KEGG
PLANT HORMONE SIGNAL TRANSDUCTION
Tryptophan metabolism
Auxin
AUX1
TIR1
+u
AUX/IAA
ARF
DNA
AUX/IAA
GH3
SAUR
Cell enlargement
Plant growth
Ubiquitin mediated proteolysis
Zeatin biosynthesis
Cytokinine
CRE1
+p
AHP
+p
B-ARR
DNA
A-ARR
Cell division
Shoot initiation
GID2
+u
Diterpenoid biosynthesis
Gibberellin
GID1
DELLA
TF
DNA
Stem growth
Induced germination
Ubiquitin mediated proteolysis
Carotenoid biosynthesis
Abscisic acid
PYR/PYL
Endoplasmic reticulum (ER)
Cysteine and methionine metabolism
Ethylene
ETR
CTR1
EBF1/2

ジベレリンシグナル伝達系のGID1をクリック

ジベレリン受容体配列を用いてモチーフサーチ

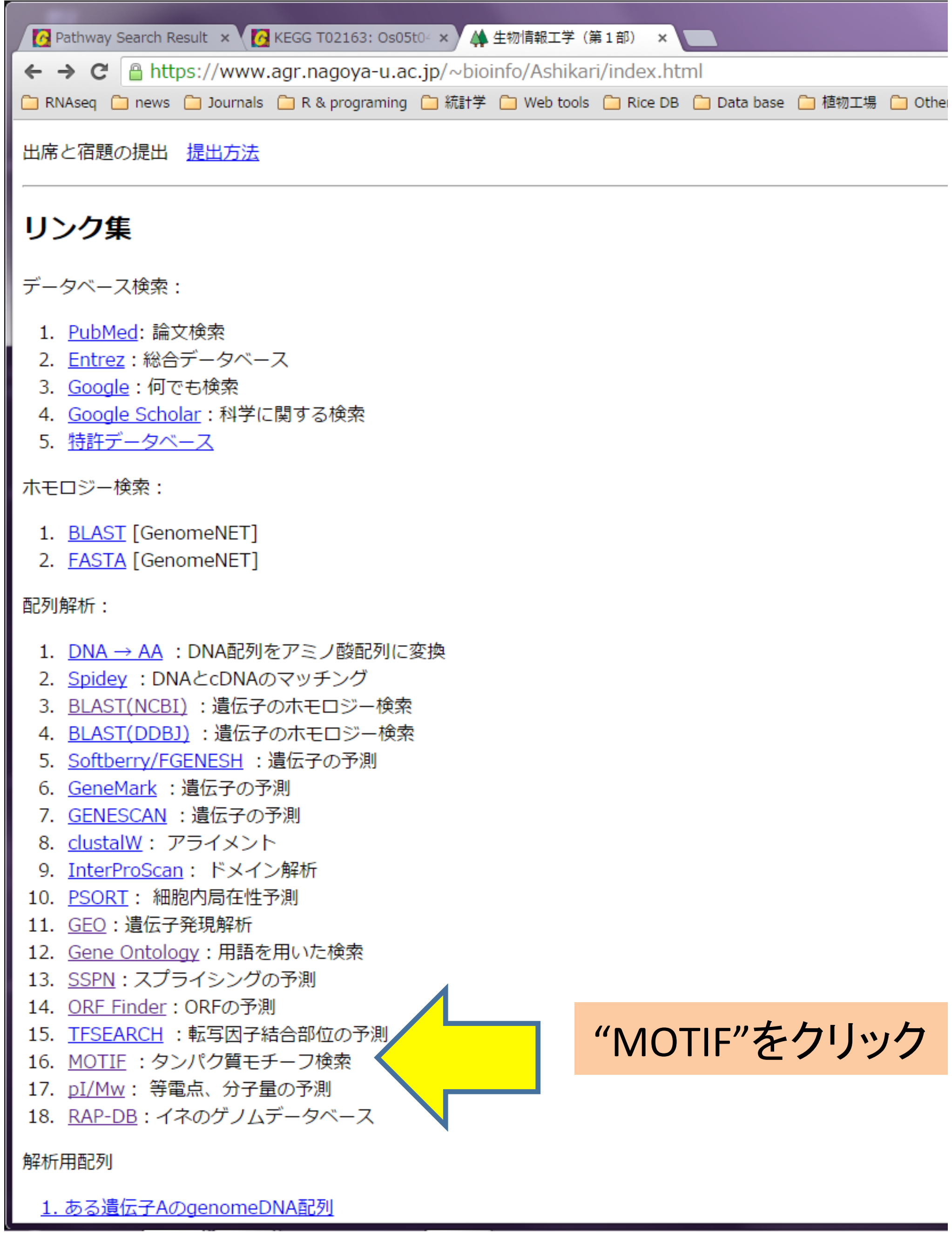

Pathway Search Result
KEGG T02163: Os05t0
https://www.agr.nagoy
www.kegg.jp/dbget-bin/www_bget?dosa:Os05t0407500-01
RNAseq
news
Journals
R & programing
統計学
Web tools
Rice DB
Data base
Help
BRITE hierarchy
Ortholog
Paralog
GFIT
Motif
All DBs
Thumbnail
Jmol
AA seq
DB search
NT seq

Oryza sativa japonica (Japanese rice) (RAPDB): Os05t0407500-01

Entry	Os05t0407500-01 CDS T02163
Gene name	Os05g0407500, GIBBERELLIN_INSENSITIVE_DWARF1, GID1
Definition	(RAP-DB) Alpha/beta hydrolase fold-3 domain containing protein.
KO	K14493 gibberellin receptor GID1 [EC:3.-.-.-]
Organism	dosa Oryza sativa japonica (Japanese rice) (RAPDB)
Pathway	dosa04075 Plant hormone signal transduction
Brite	KEGG Orthology (KO) [BR:dosa00001] Environmental Information Processing Signal transduction 04075 Plant hormone signal transduction Os05t0407500-01 (Os05g0407500) Enzymes [BR:dosa01000] 3. Hydrolases 3.- 3.-.- 3.-.-.- Os05t0407500-01 (Os05g0407500)
SSDB	
Motif	Pfam: Abhydrolase_3 Abhydrolase_5 COesterase Hydrolase_4 PAF-AH_p_II
Other DBs	RAP-DB: Os05t0407500-01 Oryzabase: 7353
LinkDB	
Structure	PDB: 3ED1 3EBL
Position	chr05:join(19868907..19868945,19869589..19870614)
AA seq	354 aa MAGSDEVNRNECKTVVPLHTWVLISNFKLSYNILRRADGTFERDLGEYLDRRVPANARPL EGVSSFDHIIDQSVGLEVRIYRAAAEGDAEEGAAAVTRPILEFLTDAPAAEPFPVIIFFH GGSFVHSSASSTIYDSLCRRFVKLSKGVVVSVNYRRAPEHRYPCAYDDGWTALKWVMSQP FMRSGGDAQARVFLSGDSSGGNIAHHVAVRAADEGVKVCGNILLNAMFGGTERTESERRL DGKYFVTLQDRDWYWKAYLPEDADRDHPACNPFGPNGRRLGGLPFAKSLIIVSGLDLTCD RQLAYADALREDGHHVKVVQCENATVGFYLLPNTVHYHEVMEEISDFLNANLYY
NT seq	1065 nt atggccggcagcgacgaggtcaaccgcaacgagtgcaagacggtggtgccgctccacaca tgggtgctcatctccaacttcaagctgtcgtacaacattctgcggcgggcggacgggacg ttcgagcgggacctcggggagtacctggacaggagggtgccggcgaacgcgcggccgctg gagggggtgtcgtcgttcgaccacatcatcgaccagtcggtggggctggaggtgcgcatc taccgggcggcggcggagggtgacgcggaggagggggcggcggcggtgacgcggcccatc cttgagttcctgacggacgcgccagcggcggagccgttcccggtgatcatattcttccac ggcggcagcttcgtgcactcgtcggccagctcgaccatctacgacagtctgtgccgccgg ttcgtgaagctgagcaagggcgtcgtggtgtccgtcaactaccggcgcgcgccggagcac cgctacccgtgcgcgtacgacgacgggtggaccgcgctcaagtgggtcatgtcgcagccg ttcatgcgcagcggcggcgacgcgcaggcccgcgtgttcctctccggcgacagctccggc ggcaacatcgcccaccacgtcgccgtccgcgccgccgacgagggcgtcaaggtctgcggc aacatcctgctcaacgccatgttcggcggcaccgagcgcacggagtcggagcggcggctc gacggcaagtacttcgtgacgctccaggacagggactggtactggaaggcgtacctgccg gaggacgccgaccgggaccatccggcgtgcaacccgttcggcccgaacggccggcggctc

アミノ酸配列をコピー

ジベレリン受容体配列を用いてモチーフサーチ


Pathway Search Result
KEGG T02163: Os05t0
生物情報工学（第１部）
https://www.agr.nagoya-u.ac.jp/~bioinfo/Ashikari/index.html
RNAseq
news
Journals
R & programing
統計学
Web tools
Rice DB
Data base
植物工場
Othe

出席と宿題の提出　提出方法

リンク集

データベース検索：

1. PubMed: 論文検索
2. Entrez：総合データベース
3. Google：何でも検索
4. Google Scholar：科学に関する検索
5. 特許データベース

ホモロジー検索：

1. BLAST [GenomeNET]
2. FASTA [GenomeNET]

配列解析：

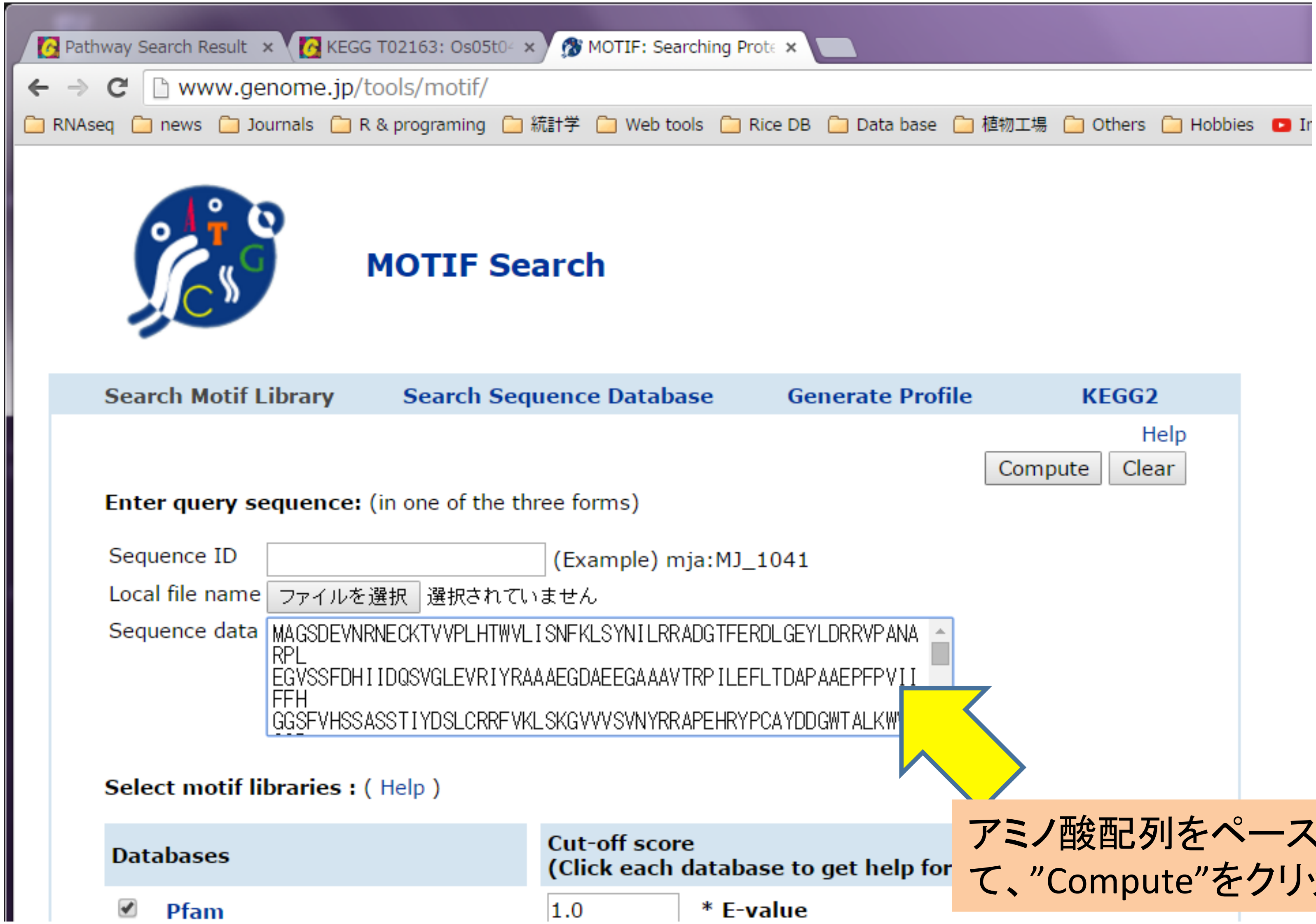
1. DNA → AA ：DNA配列をアミノ酸配列に変換
2. Spidey ：DNAとcDNAのマッチング
3. BLAST(NCBI) ：遺伝子のホモロジー検索
4. BLAST(DDBJ) ：遺伝子のホモロジー検索
5. Softberry/FGENESH ：遺伝子の予測
6. GeneMark ：遺伝子の予測
7. GENESCAN ：遺伝子の予測
8. clustalW： アライメント
9. InterProScan： ドメイン解析
10. PSORT： 細胞内局在性予測
11. GEO：遺伝子発現解析
12. Gene Ontology：用語を用いた検索
13. SSPN：スプライシングの予測
14. ORF Finder：ORFの予測
15. TFSEARCH ：転写因子結合部位の予測
16. MOTIF ：タンパク質モチーフ検索
17. pI/Mw： 等電点、分子量の予測
18. RAP-DB：イネのゲノムデータベース

解析用配列

1. ある遺伝子AのgenomeDNA配列

“MOTIF”をクリック

ジベレリン受容体配列を用いてモチーフサーチ


Pathway Search Result
KEGG T02163: Os05t0-
MOTIF: Searching Prote
www.genome.jp/tools/motif/
RNAseq
news
Journals
R & programing
統計学
Web tools
Rice DB
Data base
植物工場
Others
Hobbies
MOTIF Search
Search Motif Library
Search Sequence Database
Generate Profile
KEGG2
Help
Compute
Clear

Enter query sequence: (in one of the three forms)

Sequence ID (Example) mja:MJ_1041

Local file name ファイルを選択 選択されていません

Sequence data

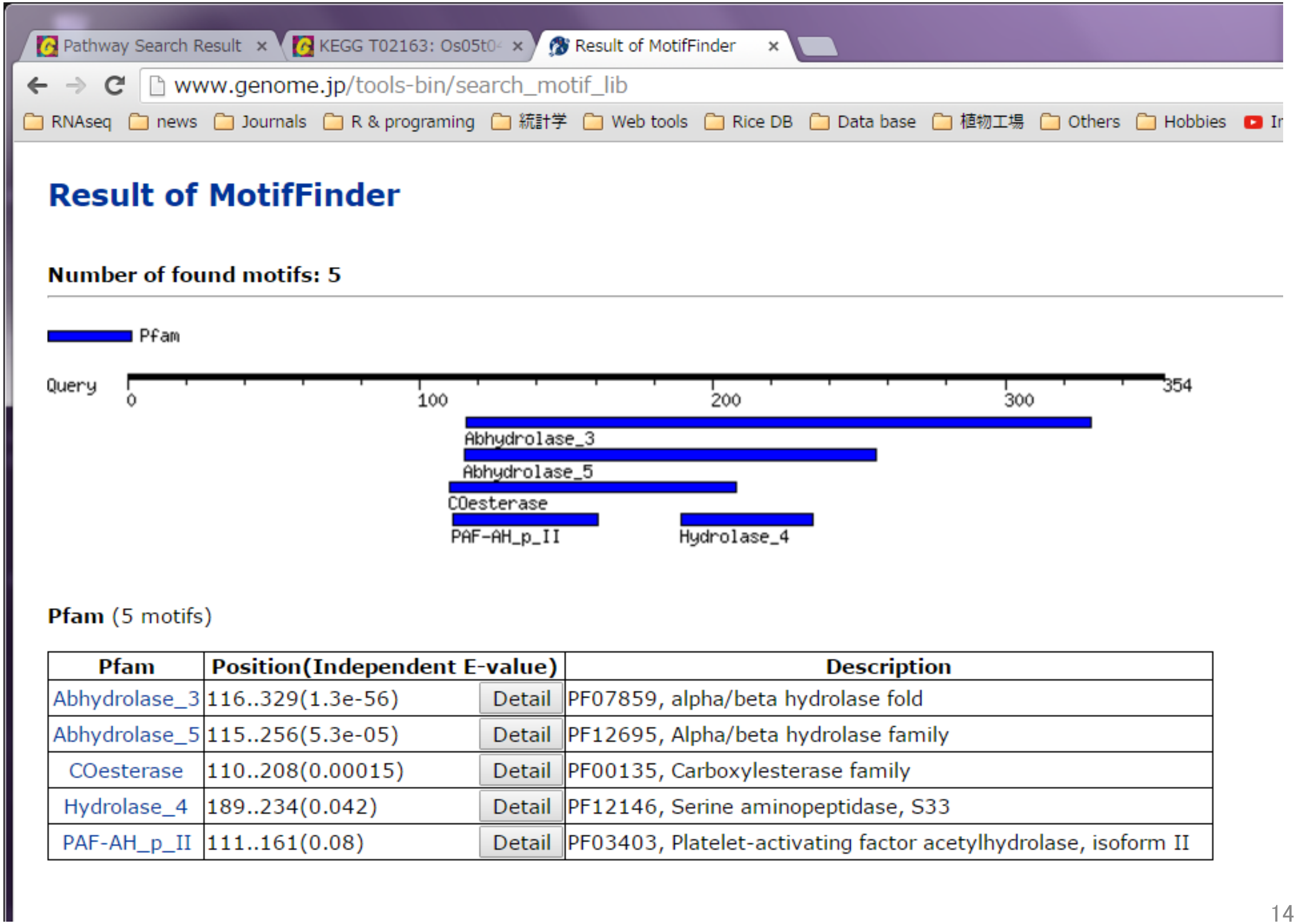
```
MAGSDEVNRNECKTVVPLHTWVLISNFKLSYNILRRADGTFERDLGEYLDRRVPANA
RPL
EGVSSFDHIIDQSVGLEVRIYRAAAEGDAEEGAAAVTRPILEFLTDAPAAEPFPVII
FFH
GGSFVHSSASSTIYDSLCRRFVKLSKGVVVSVNYRRAPEHRYPCAYDDGWTALKW
```

Select motif libraries : (Help)

Databases	**Cut-off score (Click each database to get help for**
☑ **Pfam**	1.0 *** E-value**

アミノ酸配列をペーストして、”Compute”をクリック

ジベレリン受容体配列を用いてモチーフサーチ


Pathway Search Result
KEGG T02163: Os05t0
Result of MotifFinder
www.genome.jp/tools-bin/search_motif_lib
RNAseq
news
Journals
R & programing
統計学
Web tools
Rice DB
Data base
植物工場
Others
Hobbies
Ir
Pfam
Query
0
100
200
300
354
Abhydrolase_3
Abhydrolase_5
COesterase
PAF-AH_p_II
Hydrolase_4

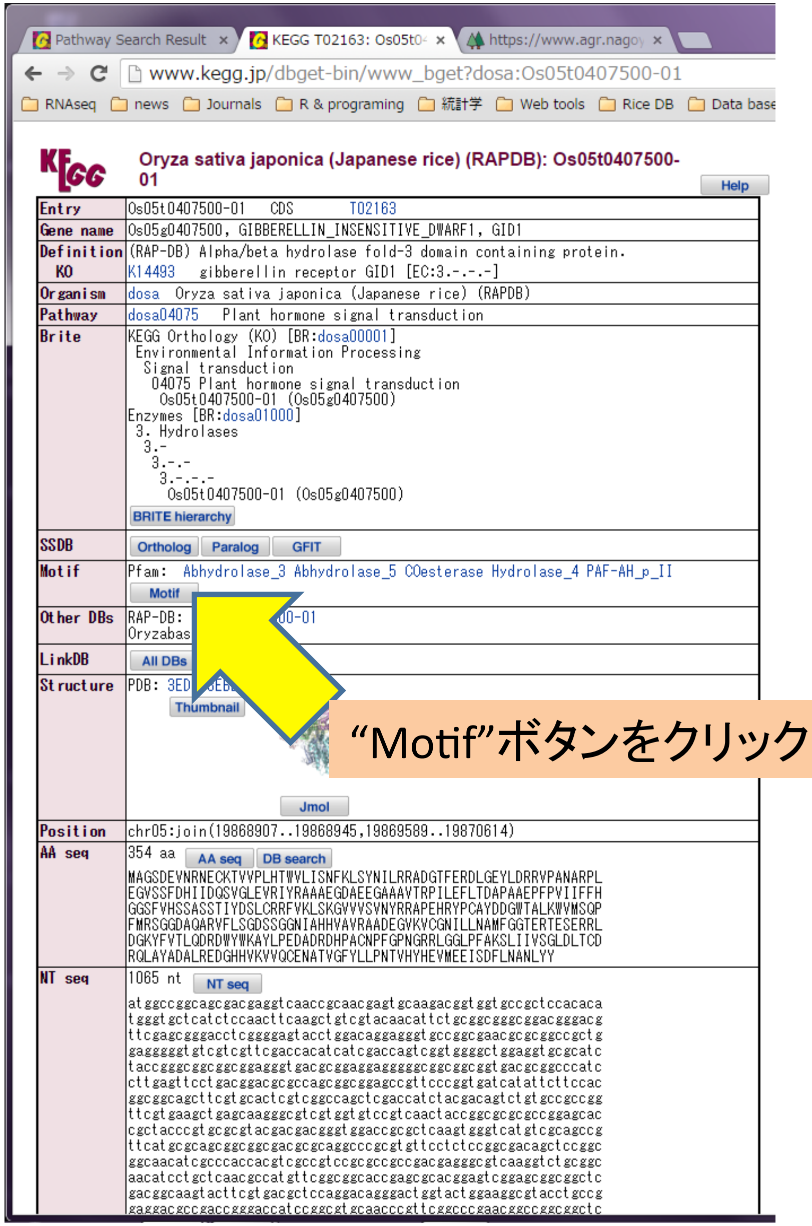
Result of MotifFinder

Number of found motifs: 5

Pfam (5 motifs)

Pfam	Position(Independent E-value)	Description
Abhydrolase_3	116..329(1.3e-56) Detail	PF07859, alpha/beta hydrolase fold
Abhydrolase_5	115..256(5.3e-05) Detail	PF12695, Alpha/beta hydrolase family
COesterase	110..208(0.00015) Detail	PF00135, Carboxylesterase family
Hydrolase_4	189..234(0.042) Detail	PF12146, Serine aminopeptidase, S33
PAF-AH_p_II	111..161(0.08) Detail	PF03403, Platelet-activating factor acetylhydrolase, isoform II

KEGG からモチーフサーチ結果への直接リンク


Pathway Search Result
KEGG T02163: Os05t0
https://www.agr.nagoy
www.kegg.jp/dbget-bin/www_bget?dosa:Os05t0407500-01
RNAseq
news
Journals
R & programing
統計学
Web tools
Rice DB
Data base
Help
BRITE hierarchy
Ortholog
Paralog
GFIT
Motif
All DBs
Thumbnail
Jmol
AA seq
DB search
NT seq

Oryza sativa japonica (Japanese rice) (RAPDB): Os05t0407500-01

Entry	Os05t0407500-01 CDS T02163
Gene name	Os05g0407500, GIBBERELLIN_INSENSITIVE_DWARF1, GID1
Definition	(RAP-DB) Alpha/beta hydrolase fold-3 domain containing protein.
KO	K14493 gibberellin receptor GID1 [EC:3.-.-.-]
Organism	dosa Oryza sativa japonica (Japanese rice) (RAPDB)
Pathway	dosa04075 Plant hormone signal transduction

Brite

```
KEGG Orthology (KO) [BR:dosa00001]
 Environmental Information Processing
  Signal transduction
   04075 Plant hormone signal transduction
    Os05t0407500-01 (Os05g0407500)
Enzymes [BR:dosa01000]
 3. Hydrolases
  3.-
   3.-.-
    3.-.-.-
     Os05t0407500-01 (Os05g0407500)
```

SSDB	
Motif	Pfam: Abhydrolase_3 Abhydrolase_5 COesterase Hydrolase_4 PAF-AH_p_II
Other DBs	RAP-DB: 00-01 Oryzabas
LinkDB	
Structure	PDB: 3ED 3EB
Position	chr05:join(19868907..19868945,19869589..19870614)

AA seq

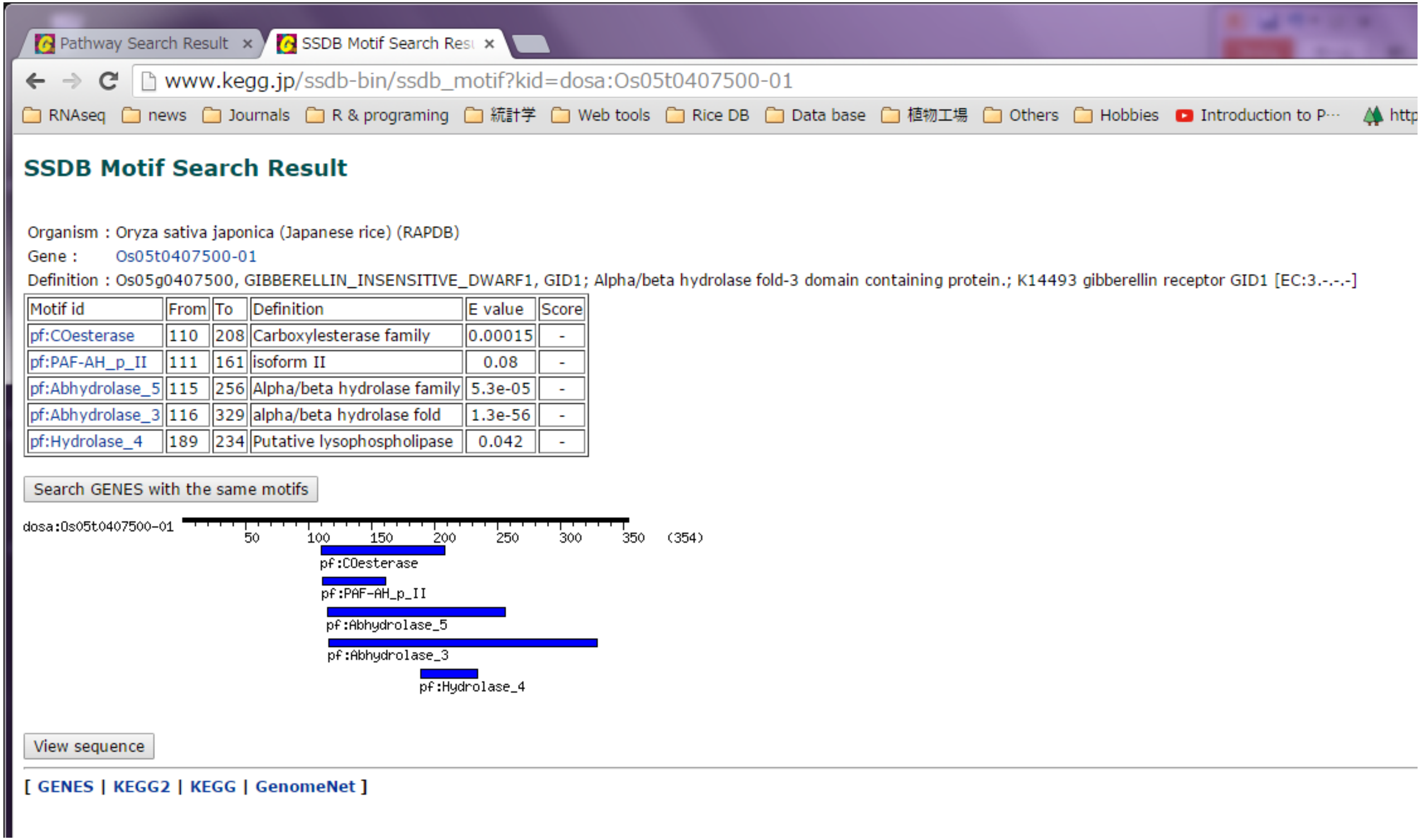
```
354 aa
MAGSDEVNRNECKTVVPLHTWVLISNFKLSYNILRRADGTFERDLGEYLDRRVPANARPL
EGVSSFDHIIDQSVGLEVRIYRAAAEGDAEEGAAAVTRPILEFLTDAPAAEPFPVIIFFH
GGSFVHSSASSTIYDSLCRRFVKLSKGVVVSVNYRRAPEHRYPCAYDDGWTALKWVMSQP
FMRSGGDAQARVFLSGDSSGGNIAHHVAVRAADEGVKVCGNILLNAMFGGTERTESERRL
DGKYFVTLQDRDWYWKAYLPEDADRDHPACNPFGPNGRRLGGLPFAKSLIIVSGLDLTCD
RQLAYADALREDGHHVKVVQCENATVGFYLLPNTVHYHEVMEEISDFLNANLYY
```

NT seq

```
1065 nt
atggccggcagcgacgaggtcaaccgcaacgagtgcaagacggtggtgccgctccacaca
tgggtgctcatctccaacttcaagctgtcgtacaacattctgcggcgggcggacgggacg
ttcgagcgggacctcggggagtacctggacaggagggtgccggcgaacgcgcggccgctg
gaggggggtgtcgtcgttcgaccacatcatcgaccagtcggtggggctggaggtgcgcatc
taccgggcggcggcggagggtgacgcggaggagggggcggcggcggtgacgcggcccatc
cttgagttcctgacggacgcgccagcggcggagccgttcccggtgatcatattcttccac
ggcggcagcttcgtgcactcgtcggccagctcgaccatctacgacagtctgtgccgccgg
ttcgtgaagctgagcaagggcgtcgtggtgtccgtcaactaccggcgcgcgccggagcac
cgctacccgtgcgcgtacgacgacgggtggaccgcgctcaagtgggtcatgtcgcagccg
ttcatgcgcagcggcggcgacgcgcaggcccgcgtgttcctctccggcgacagctccggc
ggcaacatcgcccaccacgtcgccgtccgcgccgccgacgagggcgtcaaggtctgcggc
aacatcctgctcaacgccatgttcggcggcaccgagcgcacggagtcggagcggcggctc
gacggcaagtacttcgtgacgctccaggacagggactggtactggaaggcgtacctgccg
gaggacgccgaccgggaccatccggcgtgcaacccgttcggcccgaacggccggcggctc
```

“Motif”ボタンをクリック

KEGG からモチーフサーチ結果への直接リンク


Pathway Search Result
SSDB Motif Search Resu
www.kegg.jp/ssdb-bin/ssdb_motif?kid=dosa:Os05t0407500-01
RNAseq
news
Journals
R & programing
統計学
Web tools
Rice DB
Data base
植物工場
Others
Hobbies
Introduction to P…
http

SSDB Motif Search Result

Organism : Oryza sativa japonica (Japanese rice) (RAPDB)
Gene : Os05t0407500-01
Definition : Os05g0407500, GIBBERELLIN_INSENSITIVE_DWARF1, GID1; Alpha/beta hydrolase fold-3 domain containing protein.; K14493 gibberellin receptor GID1 [EC:3.-.-.-]

Motif id	From	To	Definition	E value	Score
pf:COesterase	110	208	Carboxylesterase family	0.00015	-
pf:PAF-AH_p_II	111	161	isoform II	0.08	-
pf:Abhydrolase_5	115	256	Alpha/beta hydrolase family	5.3e-05	-
pf:Abhydrolase_3	116	329	alpha/beta hydrolase fold	1.3e-56	-
pf:Hydrolase_4	189	234	Putative lysophospholipase	0.042	-

Search GENES with the same motifs
dosa:Os05t0407500-01
50
100
150
200
250
300
350
(354)
pf:COesterase
pf:PAF-AH_p_II
pf:Abhydrolase_5
pf:Abhydrolase_3
pf:Hydrolase_4
View sequence

[GENES | KEGG2 | KEGG | GenomeNet]

ジベレリン受容体GID1は、加水分解酵素！？

ジベレリン受容体GID1は、加水分解酵素！？

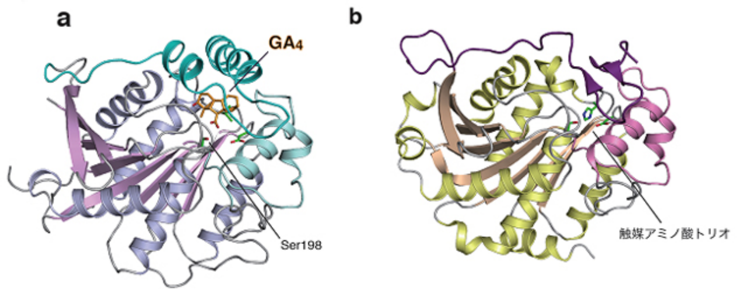

a
b
GA4
Ser198
触媒アミノ酸トリオ

図１　リボンモデルで表示したジベレリン受容体とリパーゼの立体構造の比較
a ジベレリン受容体、b リパーゼ。両者の基本構造は非常によく似ている。a、bにおいてそれぞれ薄紫色、金色で示したのがα/β水解酵素型構造。a、bにおいてそれぞれ濃緑色、濃紫色で示したのがN末端のリッド（ふた）。

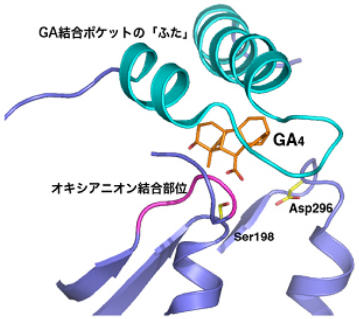
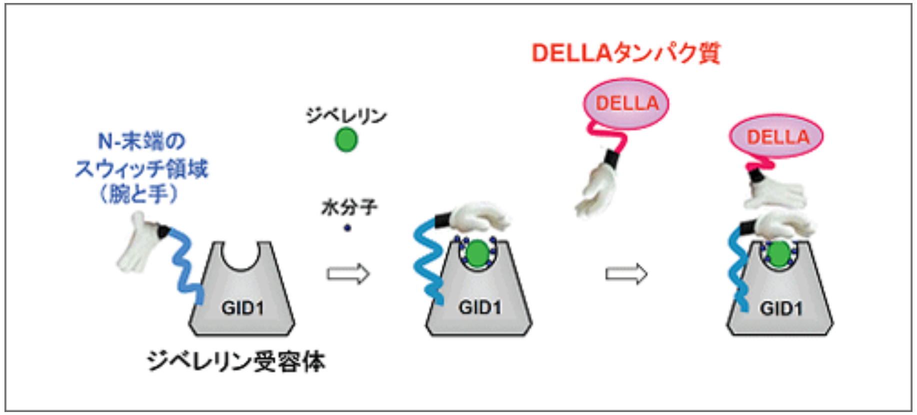

GA結合ポケットの「ふた」
GA4
オキシアニオン結合部位
Asp296
Ser198

図２　ジベレリン受容体のジベレリン（GA）結合ポケットの拡大図
活性型ジベレリン(GA4)は炭素原子をオレンジ、酸素原子を赤で表示した。リパーゼ触媒アミノ酸トリオに相当するSer198とAsp296は、炭素原子を黄色、酸素原子を赤で表示した。オキシアニオン結合部位は紫色、ジベレリン結合ポケットの「ふた」は水色で表示した。

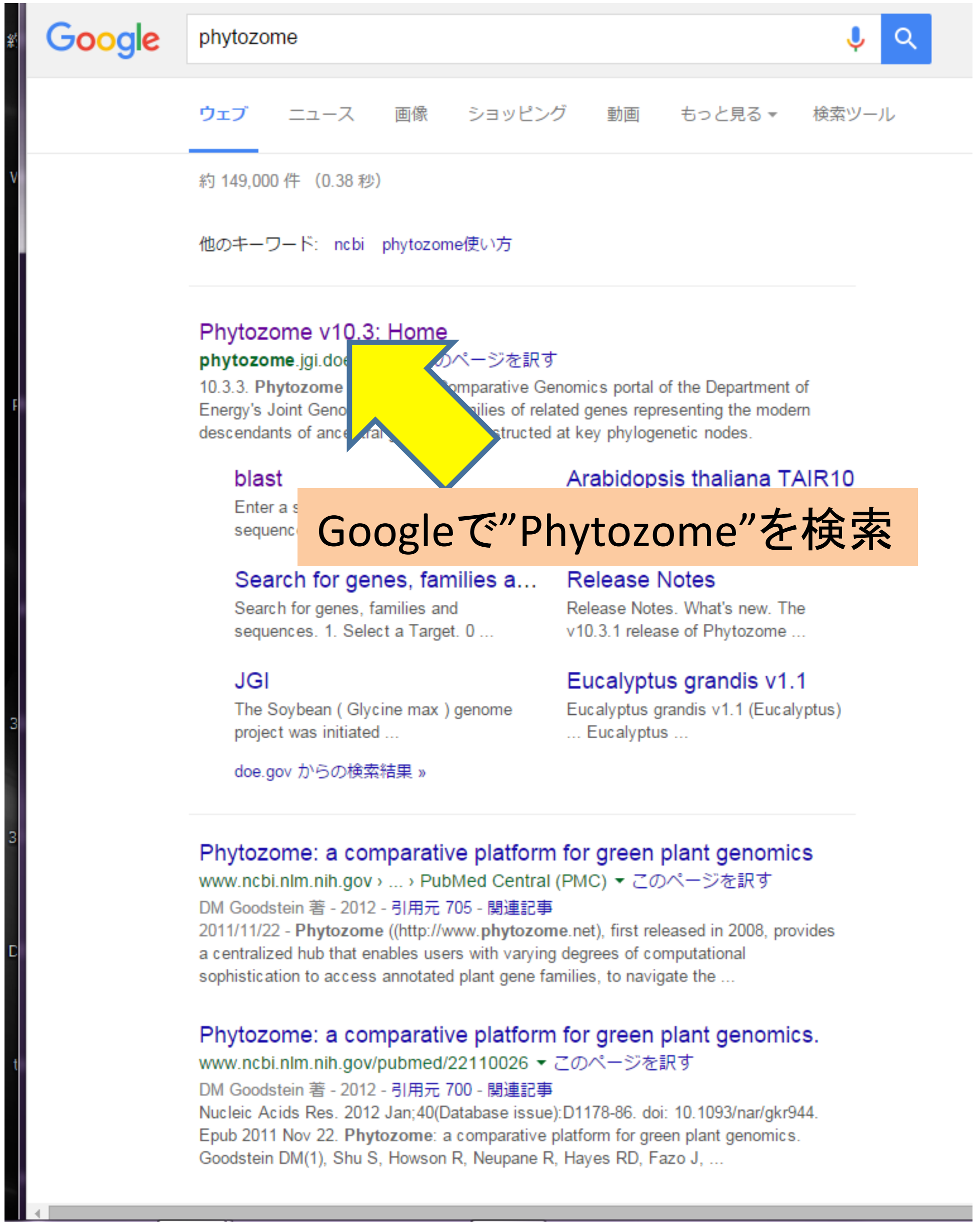
http://www.kyoto-u.ac.jp/static/ja/news_data/h/h1/news6/2008/081127_1.htm


DELLAタンパク質
DELLA
DELLA
ジベレリン
N-末端の
スウィッチ領域
（腕と手）
水分子
GID1
GID1
GID1
ジベレリン受容体

ジベレリンを分解することなく、結合による構造変化でシグナルを伝達。

脂質加水分解酵素リパーゼの基質結合部位に変異が起こり、ジベレリンと結合できるようになった。

バイオインフォマティクスの真骨頂：比較ゲノミクス



phytozome

約 149,000 件 （0.38 秒）

他のキーワード: ncbi phytozome使い方

Phytozome v10.3: Home
phytozome.jgi.doe のページを訳す
10.3.3. Phytozome omparative Genomics portal of the Department of Energy's Joint Geno ilies of related genes representing the modern descendants of ance tral structed at key phylogenetic nodes.

blast
Enter a s
sequenc

Arabidopsis thaliana TAIR10

Search for genes, families a...
Search for genes, families and sequences. 1. Select a Target. 0 ...

Release Notes
Release Notes. What's new. The v10.3.1 release of Phytozome ...

JGI
The Soybean (Glycine max) genome project was initiated ...

Eucalyptus grandis v1.1
Eucalyptus grandis v1.1 (Eucalyptus) ... Eucalyptus ...

doe.gov からの検索結果 »

Phytozome: a comparative platform for green plant genomics
www.ncbi.nlm.nih.gov › ... › PubMed Central (PMC) ▾ このページを訳す
DM Goodstein 著 - 2012 - 引用元 705 - 関連記事
2011/11/22 - **Phytozome** ((http://www.**phytozome**.net), first released in 2008, provides a centralized hub that enables users with varying degrees of computational sophistication to access annotated plant gene families, to navigate the ...

Phytozome: a comparative platform for green plant genomics.
www.ncbi.nlm.nih.gov/pubmed/22110026 ▾ このページを訳す
DM Goodstein 著 - 2012 - 引用元 700 - 関連記事
Nucleic Acids Res. 2012 Jan;40(Database issue):D1178-86. doi: 10.1093/nar/gkr944. Epub 2011 Nov 22. **Phytozome**: a comparative platform for green plant genomics. Goodstein DM(1), Shu S, Howson R, Neupane R, Hayes RD, Fazo J, ...

Googleで”Phytozome”を検索

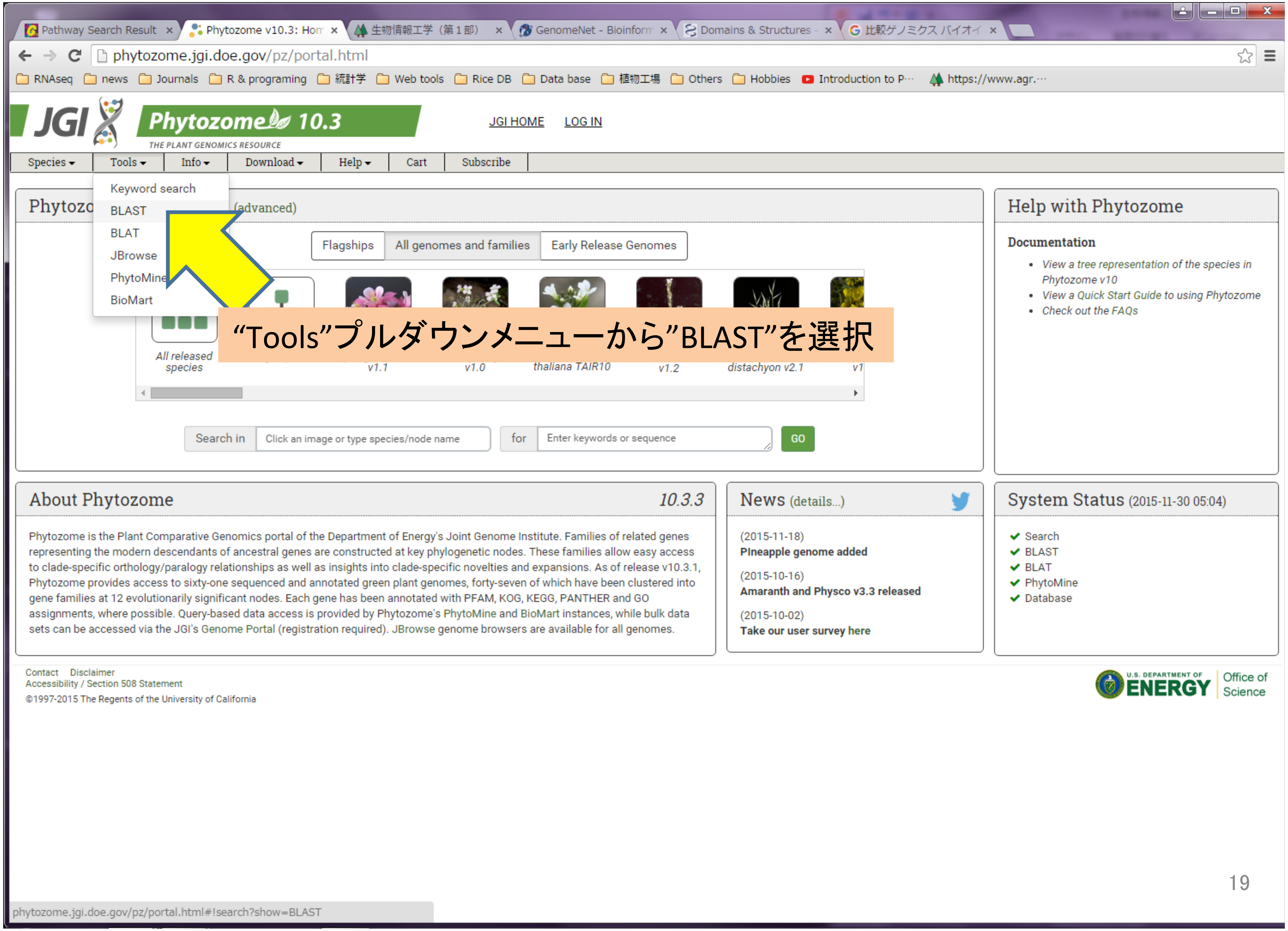
Phytozome

数十の植物種のゲノム情報を統合し、そのゲノム情報を比較する目的に特化したデータベース。

植物種間横断的にBLAST解析を行ったり、とある遺伝子のホモログやパラログを容易に検索できる。

通常のNCBIのBLASTなどに比べて、検索される情報が整理されているので扱いが容易。

Phytozomeでお手軽比較ゲノミクス的解析



“Tools”プルダウンメニューから”BLAST”を選択

Pathway Search Result
Phytozome v10.3: Hom
生物情報工学（第１部）
GenomeNet - Bioinform
Domains & Structures -
比較ゲノミクス バイオイ
phytozome.jgi.doe.gov/pz/portal.html
RNAseq
news
Journals
R & programing
統計学
Web tools
Rice DB
Data base
植物工場
Others
Hobbies
Introduction to P…
https://www.agr.…
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THE PLANT GENOMICS RESOURCE
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Download
Help
Cart
Subscribe
Keyword search
BLAST
BLAT
JBrowse
PhytoMine
BioMart
Phytozo
(advanced)
Flagships
All genomes and families
Early Release Genomes
All released species
v1.1
v1.0
thaliana TAIR10
v1.2
distachyon v2.1
v1
Search in
Click an image or type species/node name
for
Enter keywords or sequence
GO
phytozome.jgi.doe.gov/pz/portal.html#!search?show=BLAST

Help with Phytozome

Documentation

- *View a tree representation of the species in Phytozome v10*
- *View a Quick Start Guide to using Phytozome*
- *Check out the FAQs*

About Phytozome *10.3.3*

Phytozome is the Plant Comparative Genomics portal of the Department of Energy's Joint Genome Institute. Families of related genes representing the modern descendants of ancestral genes are constructed at key phylogenetic nodes. These families allow easy access to clade-specific orthology/paralogy relationships as well as insights into clade-specific novelties and expansions. As of release v10.3.1, Phytozome provides access to sixty-one sequenced and annotated green plant genomes, forty-seven of which have been clustered into gene families at 12 evolutionarily significant nodes. Each gene has been annotated with PFAM, KOG, KEGG, PANTHER and GO assignments, where possible. Query-based data access is provided by Phytozome's PhytoMine and BioMart instances, while bulk data sets can be accessed via the JGI's Genome Portal (registration required). JBrowse genome browsers are available for all genomes.

News (details...)

(2015-11-18)
Pineapple genome added

(2015-10-16)
Amaranth and Physco v3.3 released

(2015-10-02)
Take our user survey here

System Status (2015-11-30 05:04)

- ✓ Search
- ✓ BLAST
- ✓ BLAT
- ✓ PhytoMine
- ✓ Database

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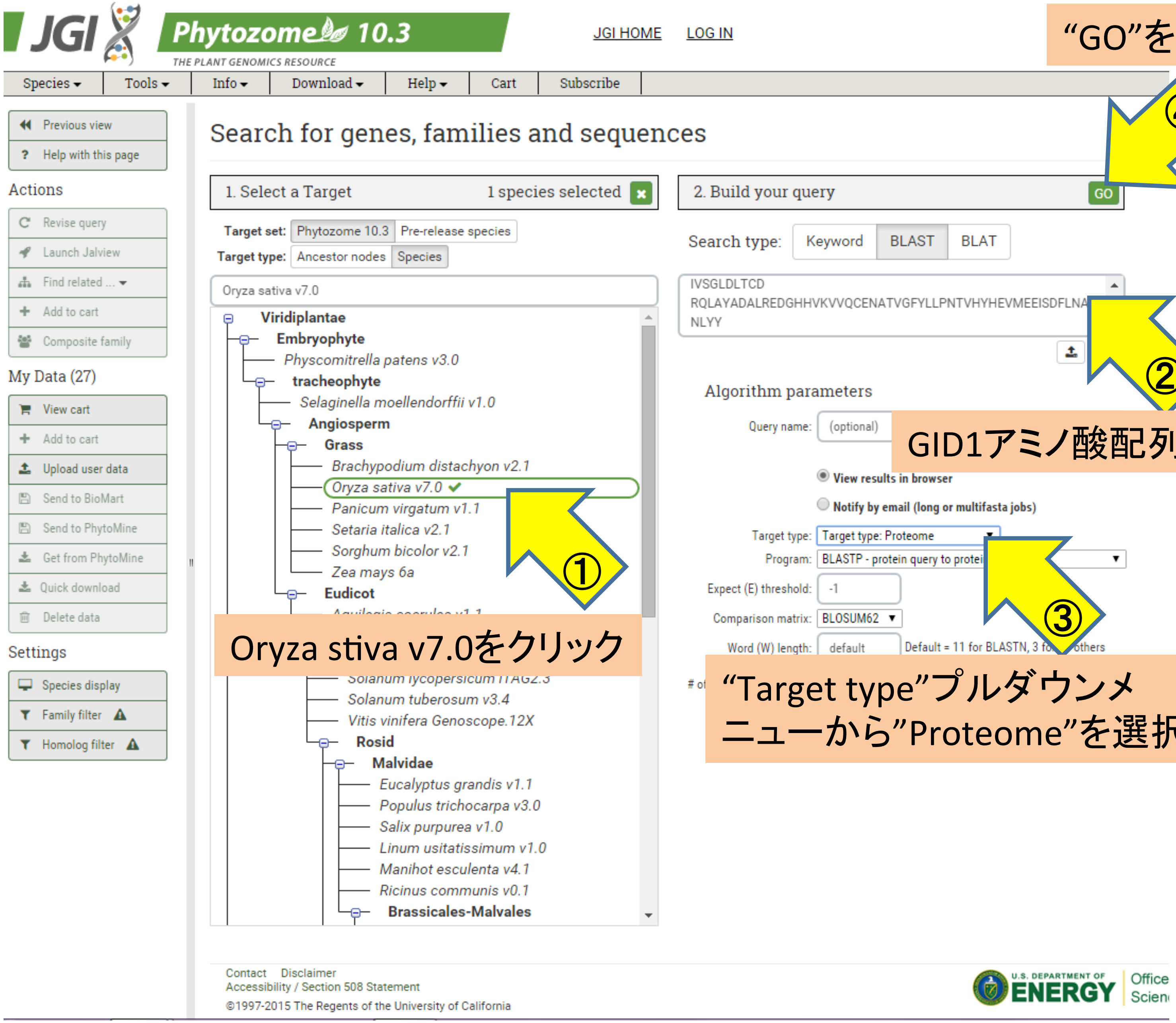
Phytozomeでお手軽比較ゲノミクス的解析


JGI
Phytozome 10.3
THE PLANT GENOMICS RESOURCE
JGI HOME
LOG IN
Species
Tools
Info
Download
Help
Cart
Subscribe
Previous view
Help with this page
Actions
Revise query
Launch Jalview
Find related ...
Add to cart
Composite family
My Data (27)
View cart
Add to cart
Upload user data
Send to BioMart
Send to PhytoMine
Get from PhytoMine
Quick download
Delete data
Settings
Species display
Family filter
Homolog filter
Search for genes, families and sequences
1. Select a Target
1 species selected
2. Build your query
GO
Keyword
BLAST
BLAT
Algorithm parameters
Viridiplantae
Embryophyte
Physcomitrella patens v3.0
tracheophyte
Selaginella moellendorffii v1.0
Angiosperm
Grass
Brachypodium distachyon v2.1
Oryza sativa v7.0 ✓
Panicum virgatum v1.1
Setaria italica v2.1
Sorghum bicolor v2.1
Zea mays 6a
Eudicot
Solanum lycopersicum iTAG2.3
Solanum tuberosum v3.4
Vitis vinifera Genoscope.12X
Rosid
Malvidae
Eucalyptus grandis v1.1
Populus trichocarpa v3.0
Salix purpurea v1.0
Linum usitatissimum v1.0
Manihot esculenta v4.1
Ricinus communis v0.1
Brassicales-Malvales
① ② ③ ④
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Target set: Phytozome 10.3 | Pre-release species

Target type: Ancestor nodes | Species

Oryza sativa v7.0

Search type: BLAST

IVSGLDLTCD
RQLAYADALREDGHHVKVVQCENATVGFYLLPNTVHYHEVMEEISDFLNA
NLYY

Query name: (optional)

● View results in browser

○ Notify by email (long or multifasta jobs)

Target type: Target type: Proteome

Program: BLASTP - protein query to protei

Expect (E) threshold: -1

Comparison matrix: BLOSUM62

Word (W) length: default Default = 11 for BLASTN, 3 fo others

“GO”をクリック

④

GID1アミノ酸配列をペースト

②

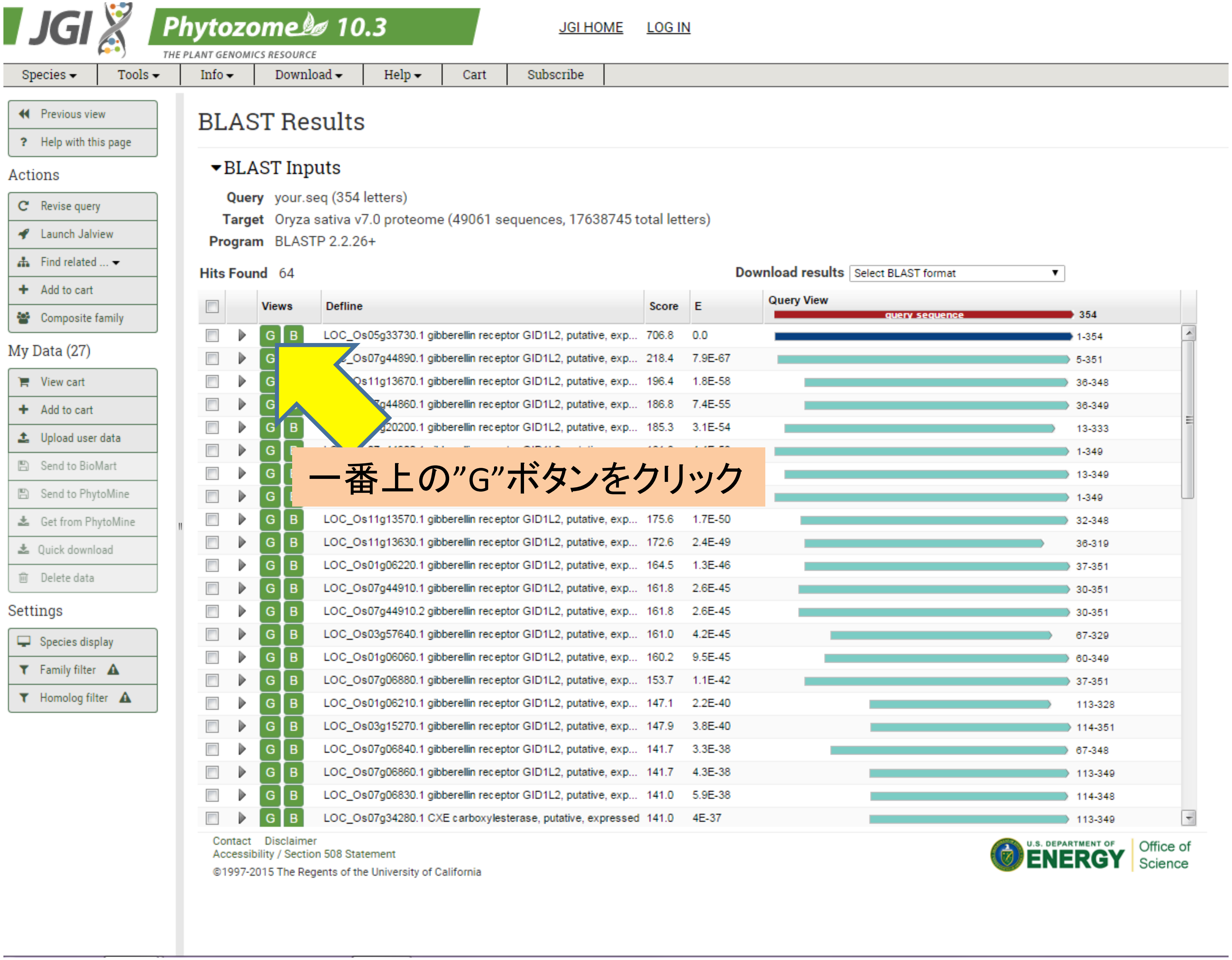
Oryza stiva v7.0をクリック

①

“Target type”プルダウンメニューから”Proteome”を選択

③

Phytozomeでお手軽比較ゲノミクス的解析


JGI
Phytozome 10.3
THE PLANT GENOMICS RESOURCE
JGI HOME
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Species ▾
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Revise query
Launch Jalview
Find related ... ▾
Add to cart
Composite family
My Data (27)
View cart
Add to cart
Upload user data
Send to BioMart
Send to PhytoMine
Get from PhytoMine
Quick download
Delete data
Settings
Species display
Family filter
Homolog filter

BLAST Results

BLAST Inputs

Query your.seq (354 letters)
Target Oryza sativa v7.0 proteome (49061 sequences, 17638745 total letters)
Program BLASTP 2.2.26+

Hits Found 64

Download results Select BLAST format ▾

☐		Views	Define	Score	E	Query View query sequence 354
☐	▶	G B	LOC_Os05g33730.1 gibberellin receptor GID1L2, putative, exp...	706.8	0.0	1-354
☐	▶	G	_Os07g44890.1 gibberellin receptor GID1L2, putative, exp...	218.4	7.9E-67	5-351
☐	▶	G	Os11g13670.1 gibberellin receptor GID1L2, putative, exp...	196.4	1.8E-58	36-348
☐	▶	G	g44860.1 gibberellin receptor GID1L2, putative, exp...	186.8	7.4E-55	36-349
☐	▶	G B	g20200.1 gibberellin receptor GID1L2, putative, exp...	185.3	3.1E-54	13-333
☐	▶	G				1-349
☐	▶	G				13-349
☐	▶	G				1-349
☐	▶	G B	LOC_Os11g13570.1 gibberellin receptor GID1L2, putative, exp...	175.6	1.7E-50	32-348
☐	▶	G B	LOC_Os11g13630.1 gibberellin receptor GID1L2, putative, exp...	172.6	2.4E-49	36-319
☐	▶	G B	LOC_Os01g06220.1 gibberellin receptor GID1L2, putative, exp...	164.5	1.3E-46	37-351
☐	▶	G B	LOC_Os07g44910.1 gibberellin receptor GID1L2, putative, exp...	161.8	2.6E-45	30-351
☐	▶	G B	LOC_Os07g44910.2 gibberellin receptor GID1L2, putative, exp...	161.8	2.6E-45	30-351
☐	▶	G B	LOC_Os03g57640.1 gibberellin receptor GID1L2, putative, exp...	161.0	4.2E-45	67-329
☐	▶	G B	LOC_Os01g06060.1 gibberellin receptor GID1L2, putative, exp...	160.2	9.5E-45	60-349
☐	▶	G B	LOC_Os07g06880.1 gibberellin receptor GID1L2, putative, exp...	153.7	1.1E-42	37-351
☐	▶	G B	LOC_Os01g06210.1 gibberellin receptor GID1L2, putative, exp...	147.1	2.2E-40	113-328
☐	▶	G B	LOC_Os03g15270.1 gibberellin receptor GID1L2, putative, exp...	147.9	3.8E-40	114-351
☐	▶	G B	LOC_Os07g06840.1 gibberellin receptor GID1L2, putative, exp...	141.7	3.3E-38	67-348
☐	▶	G B	LOC_Os07g06860.1 gibberellin receptor GID1L2, putative, exp...	141.7	4.3E-38	113-349
☐	▶	G B	LOC_Os07g06830.1 gibberellin receptor GID1L2, putative, exp...	141.0	5.9E-38	114-348
☐	▶	G B	LOC_Os07g34280.1 CXE carboxylesterase, putative, expressed	141.0	4E-37	113-349

一番上の”G”ボタンをクリック

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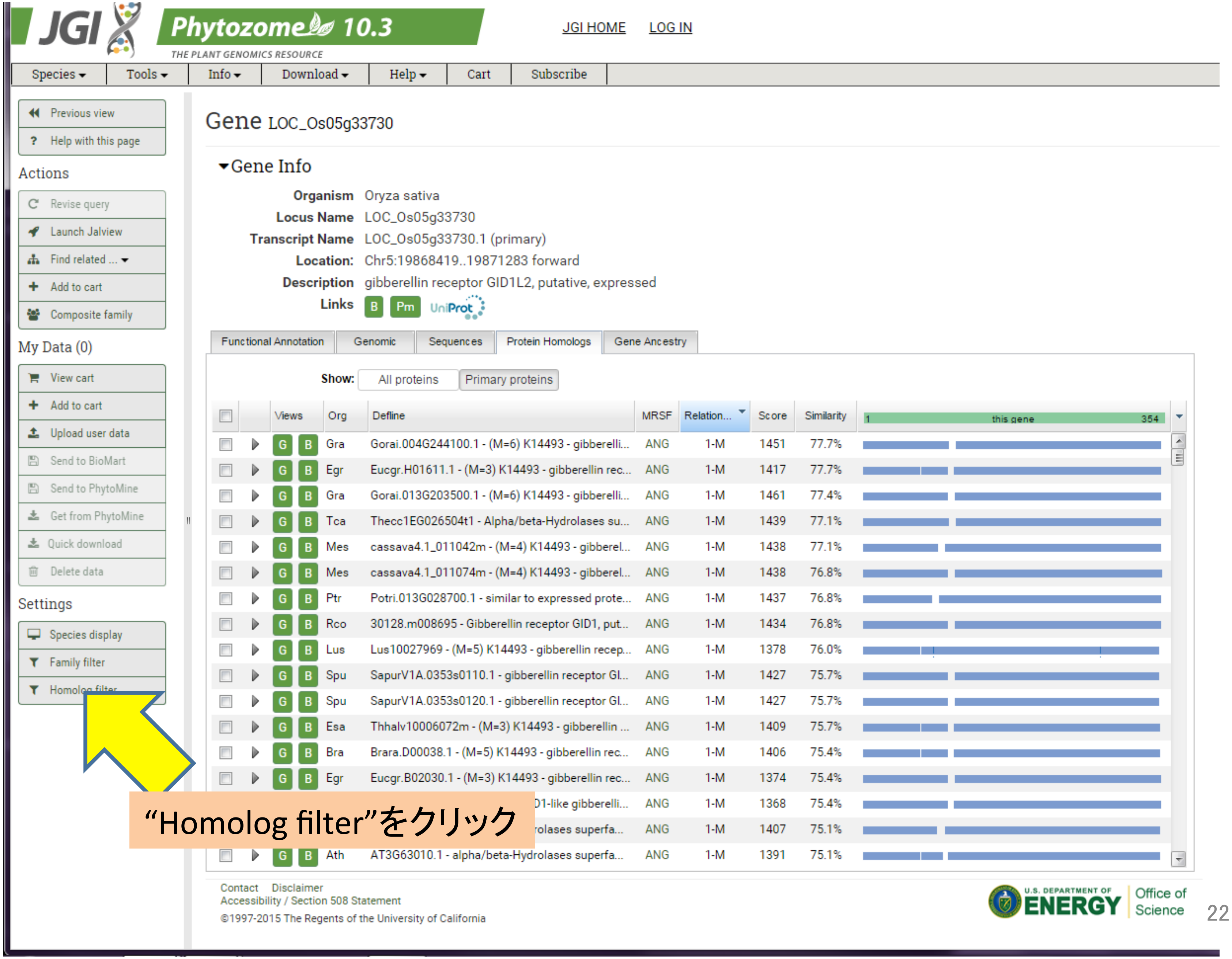
Phytozomeでお手軽比較ゲノミクス的解析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Actions
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Launch Jalview
Find related ...
Add to cart
Composite family
My Data (0)
View cart
Add to cart
Upload user data
Send to BioMart
Send to PhytoMine
Get from PhytoMine
Quick download
Delete data
Settings
Species display
Family filter
Homolog filter
Functional Annotation
Genomic
Sequences
Protein Homologs
Gene Ancestry
Show:
All proteins
Primary proteins
1
this gene
354
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Gene LOC_Os05g33730

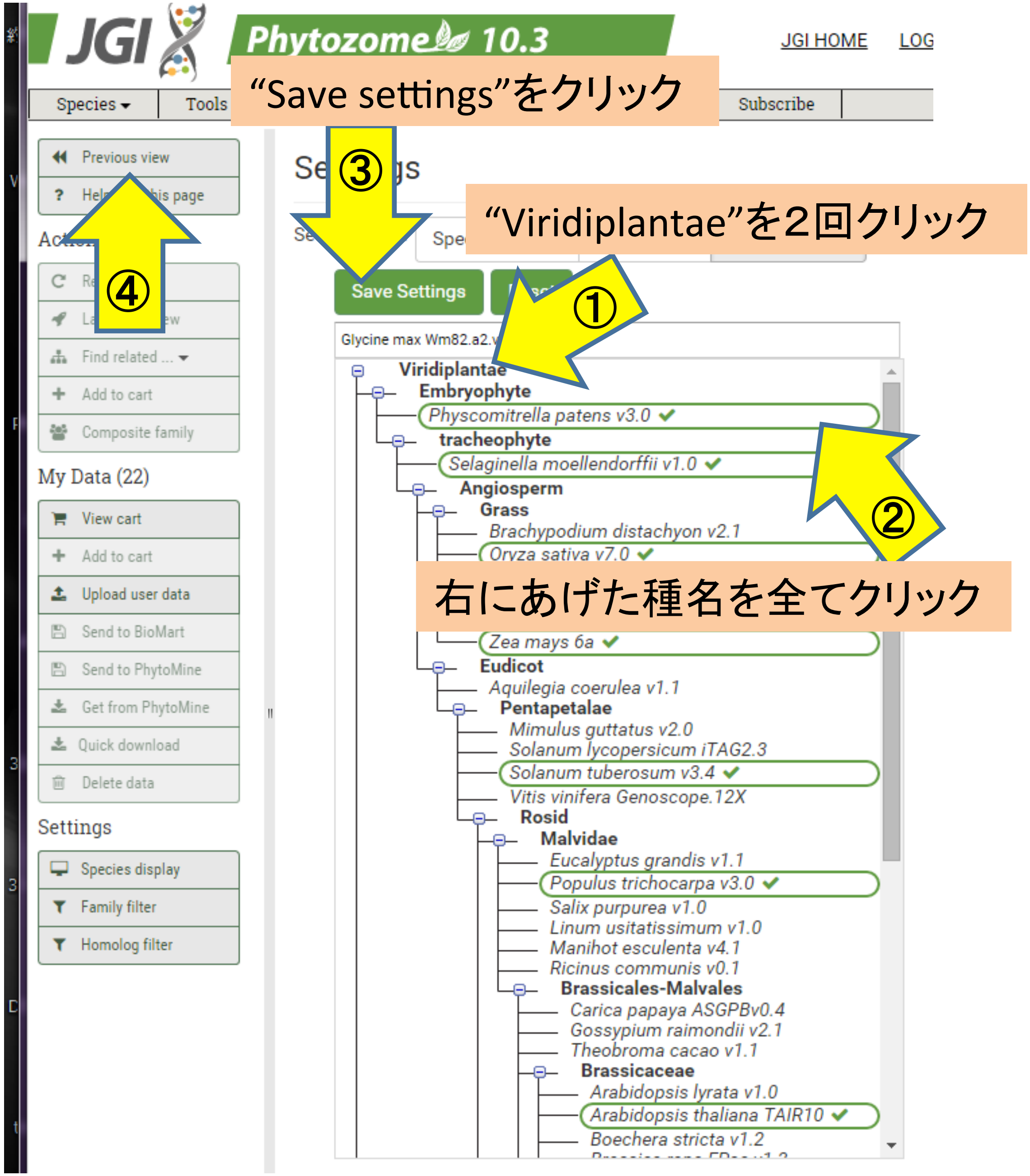
Gene Info

Organism Oryza sativa
Locus Name LOC_Os05g33730
Transcript Name LOC_Os05g33730.1 (primary)
Location: Chr5:19868419..19871283 forward
Description gibberellin receptor GID1L2, putative, expressed
Links B Pm UniProt

☐	Views	Org	Define	MRSF	Relation...	Score	Similarity
☐	G B	Gra	Gorai.004G244100.1 - (M=6) K14493 - gibberelli...	ANG	1-M	1451	77.7%
☐	G B	Egr	Eucgr.H01611.1 - (M=3) K14493 - gibberellin rec...	ANG	1-M	1417	77.7%
☐	G B	Gra	Gorai.013G203500.1 - (M=6) K14493 - gibberelli...	ANG	1-M	1461	77.4%
☐	G B	Tca	Thecc1EG026504t1 - Alpha/beta-Hydrolases su...	ANG	1-M	1439	77.1%
☐	G B	Mes	cassava4.1_011042m - (M=4) K14493 - gibberel...	ANG	1-M	1438	77.1%
☐	G B	Mes	cassava4.1_011074m - (M=4) K14493 - gibberel...	ANG	1-M	1438	76.8%
☐	G B	Ptr	Potri.013G028700.1 - similar to expressed prote...	ANG	1-M	1437	76.8%
☐	G B	Rco	30128.m008695 - Gibberellin receptor GID1, put...	ANG	1-M	1434	76.8%
☐	G B	Lus	Lus10027969 - (M=5) K14493 - gibberellin recep...	ANG	1-M	1378	76.0%
☐	G B	Spu	SapurV1A.0353s0110.1 - gibberellin receptor GI...	ANG	1-M	1427	75.7%
☐	G B	Spu	SapurV1A.0353s0120.1 - gibberellin receptor GI...	ANG	1-M	1427	75.7%
☐	G B	Esa	Thhalv10006072m - (M=3) K14493 - gibberellin ...	ANG	1-M	1409	75.7%
☐	G B	Bra	Brara.D00038.1 - (M=5) K14493 - gibberellin rec...	ANG	1-M	1406	75.4%
☐	G B	Egr	Eucgr.B02030.1 - (M=3) K14493 - gibberellin rec...	ANG	1-M	1374	75.4%
			D1-like gibberelli...	ANG	1-M	1368	75.4%
			rolases superfa...	ANG	1-M	1407	75.1%
☐	G B	Ath	AT3G63010.1 - alpha/beta-Hydrolases superfa...	ANG	1-M	1391	75.1%

“Homolog filter”をクリック

Phytozomeでお手軽比較ゲノミクス的解析


JGI
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Composite family
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Send to BioMart
Send to PhytoMine
Get from PhytoMine
Quick download
Delete data
Settings
Species display
Family filter
Homolog filter
Save Settings
Glycine max Wm82.a2.v
Viridiplantae
Embryophyte
Physcomitrella patens v3.0 ✓
tracheophyte
Selaginella moellendorffii v1.0 ✓
Angiosperm
Grass
Brachypodium distachyon v2.1
Oryza sativa v7.0 ✓
Zea mays 6a ✓
Eudicot
Aquilegia coerulea v1.1
Pentapetalae
Mimulus guttatus v2.0
Solanum lycopersicum iTAG2.3
Solanum tuberosum v3.4 ✓
Vitis vinifera Genoscope.12X
Rosid
Malvidae
Eucalyptus grandis v1.1
Populus trichocarpa v3.0 ✓
Salix purpurea v1.0
Linum usitatissimum v1.0
Manihot esculenta v4.1
Ricinus communis v0.1
Brassicales-Malvales
Carica papaya ASGPBv0.4
Gossypium raimondii v2.1
Theobroma cacao v1.1
Brassicaceae
Arabidopsis lyrata v1.0
Arabidopsis thaliana TAIR10 ✓
Boechera stricta v1.2
①
②
③
④

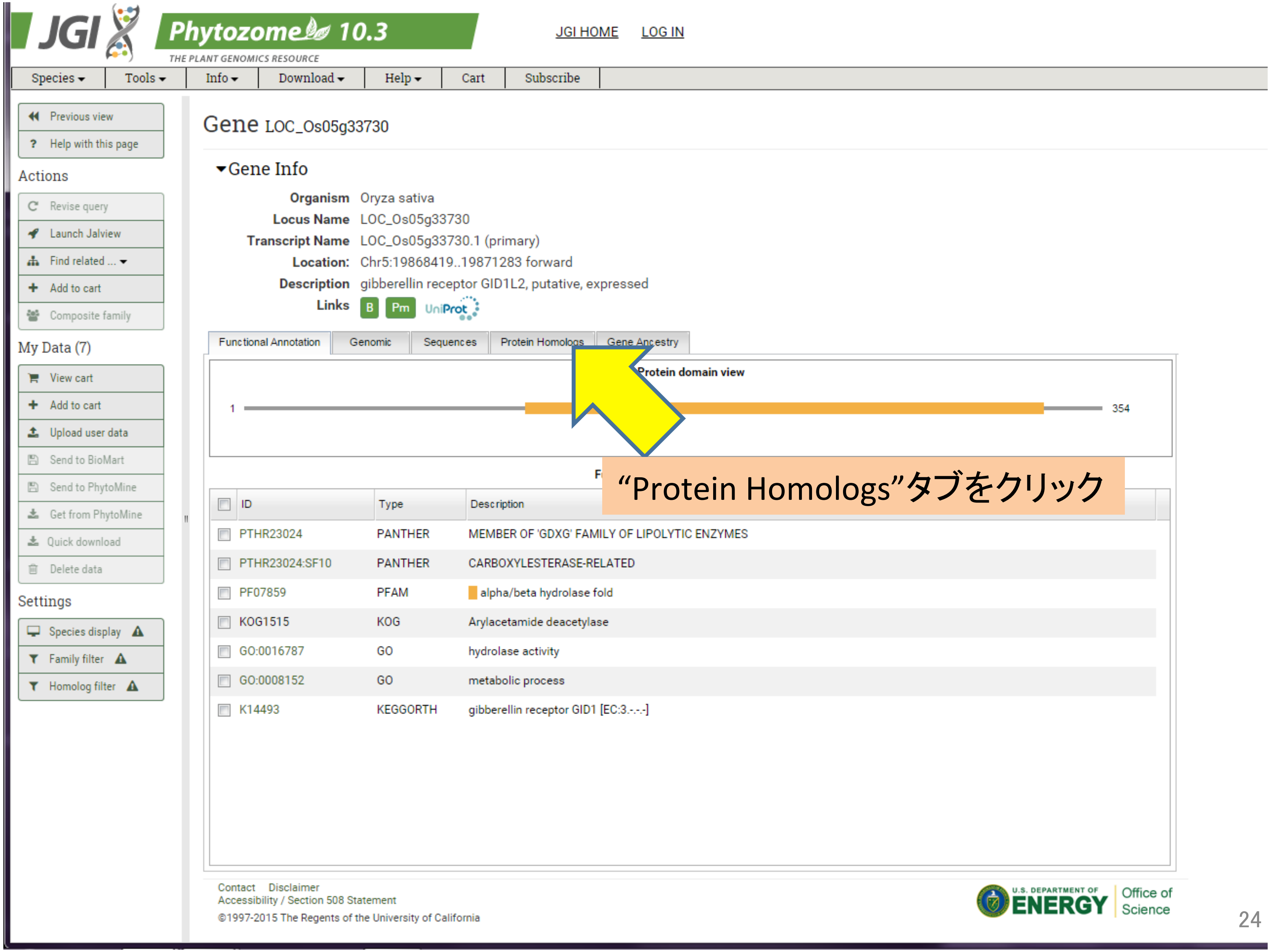
“Save settings”をクリック

“Viridiplantae”を２回クリック

右にあげた種名を全てクリック

Embryophyte
Physcomitrella patens v3.0
Tracheophyte
Selaginella moellendorffii v1.0
Grass
Brachypodium distachyon v2.1
Oryza sativa v7.0
Zea mays 6a
Pentapetalae
Solanum tuberosum v3.4
Malvidae
Populus trichocarpa v3.0
Brassicaceae
Arabidopsis thaliana TAIR10
Citrus
Citrus sinensis v1.1
Fabidae
Glycine max Wm82.a2.v1

Phytozomeでお手軽比較ゲノミクス的解析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UniProt
Functional Annotation
Genomic
Sequences
Protein Homologs
Gene Ancestry
Protein domain view
1
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Gene LOC_Os05g33730

Gene Info

Organism Oryza sativa
Locus Name LOC_Os05g33730
Transcript Name LOC_Os05g33730.1 (primary)
Location: Chr5:19868419..19871283 forward
Description gibberellin receptor GID1L2, putative, expressed
Links

☐	ID	Type	Description
☐	PTHR23024	PANTHER	MEMBER OF 'GDXG' FAMILY OF LIPOLYTIC ENZYMES
☐	PTHR23024:SF10	PANTHER	CARBOXYLESTERASE-RELATED
☐	PF07859	PFAM	🟧 alpha/beta hydrolase fold
☐	KOG1515	KOG	Arylacetamide deacetylase
☐	GO:0016787	GO	hydrolase activity
☐	GO:0008152	GO	metabolic process
☐	K14493	KEGGORTH	gibberellin receptor GID1 [EC:3.-.-.-]

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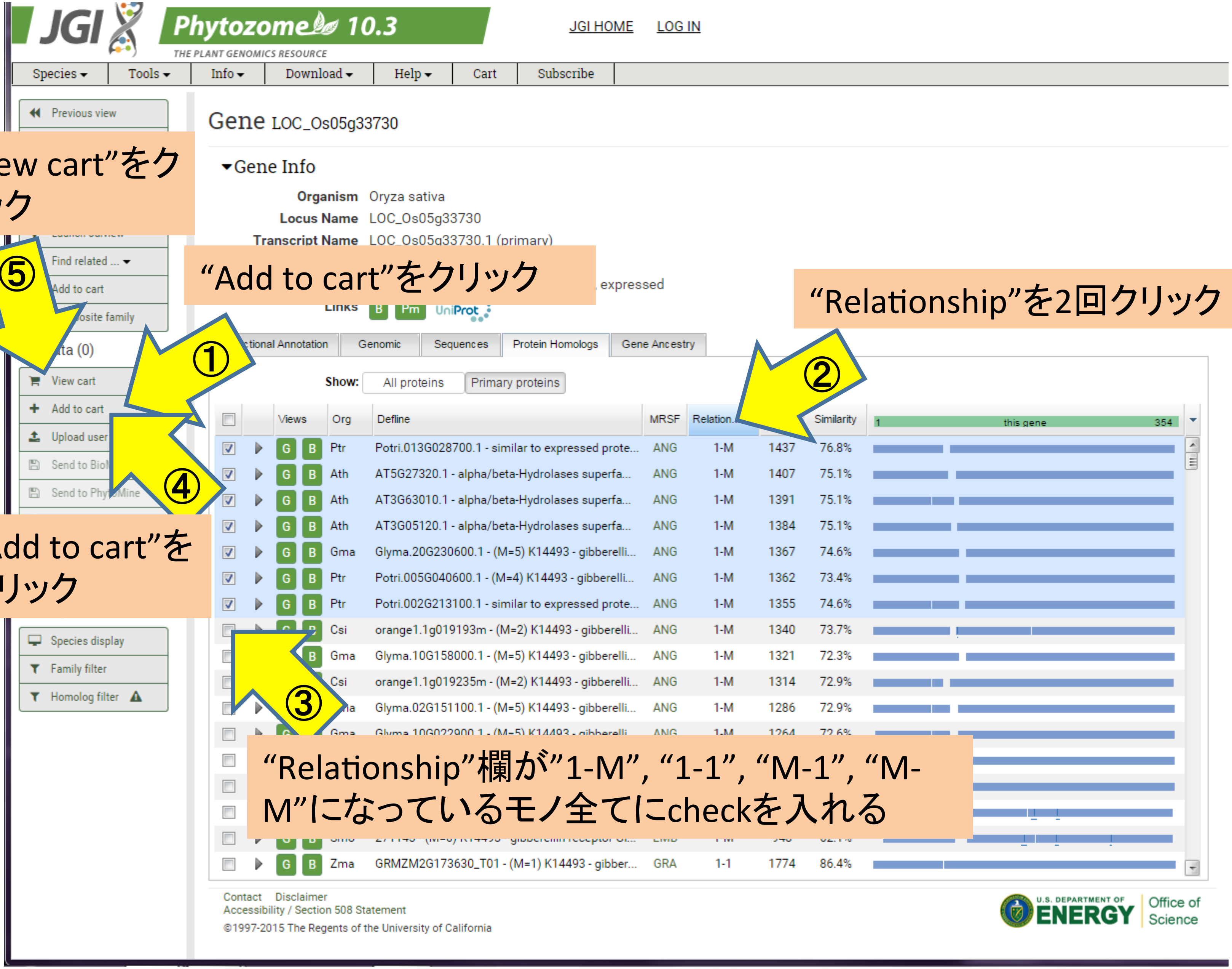
“Protein Homologs”タブをクリック

Phytozomeでお手軽比較ゲノミクス的解析



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Send to PhytoMine
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Family filter
Homolog filter
ctional Annotation
Genomic
Sequences
Protein Homologs
Gene Ancestry
Links
B
Pm
UniProt

Gene LOC_Os05g33730

Gene Info

Organism Oryza sativa
Locus Name LOC_Os05g33730
Transcript Name LOC_Os05g33730.1 (primary)
expressed

Show: All proteins | Primary proteins

☐		Views	Org	Define	MRSF	Relation...		Similarity
☑	▶	G B	Ptr	Potri.013G028700.1 - similar to expressed prote...	ANG	1-M	1437	76.8%
☑	▶	G B	Ath	AT5G27320.1 - alpha/beta-Hydrolases superfa...	ANG	1-M	1407	75.1%
☑	▶	G B	Ath	AT3G63010.1 - alpha/beta-Hydrolases superfa...	ANG	1-M	1391	75.1%
☑	▶	G B	Ath	AT3G05120.1 - alpha/beta-Hydrolases superfa...	ANG	1-M	1384	75.1%
☑	▶	G B	Gma	Glyma.20G230600.1 - (M=5) K14493 - gibberelli...	ANG	1-M	1367	74.6%
☑	▶	G B	Ptr	Potri.005G040600.1 - (M=4) K14493 - gibberelli...	ANG	1-M	1362	73.4%
☑	▶	G B	Ptr	Potri.002G213100.1 - similar to expressed prote...	ANG	1-M	1355	74.6%
☐		B	Csi	orange1.1g019193m - (M=2) K14493 - gibberelli...	ANG	1-M	1340	73.7%
☐		B	Gma	Glyma.10G158000.1 - (M=5) K14493 - gibberelli...	ANG	1-M	1321	72.3%
☐			Csi	orange1.1g019235m - (M=2) K14493 - gibberelli...	ANG	1-M	1314	72.9%
☐	▶		[illegible]	Glyma.02G151100.1 - (M=5) K14493 - gibberelli...	ANG	1-M	1286	72.9%
☐	▶	G	Gma	Glyma.10G022900.1 - (M=5) K14493 - gibberelli...	ANG	1-M	1264	72.6%
☐								
☐								
☐								
☐								
☐	▶	G B	Zma	GRMZM2G173630_T01 - (M=1) K14493 - gibber...	GRA	1-1	1774	86.4%

1
this gene
354

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① “Add to cart”をクリック

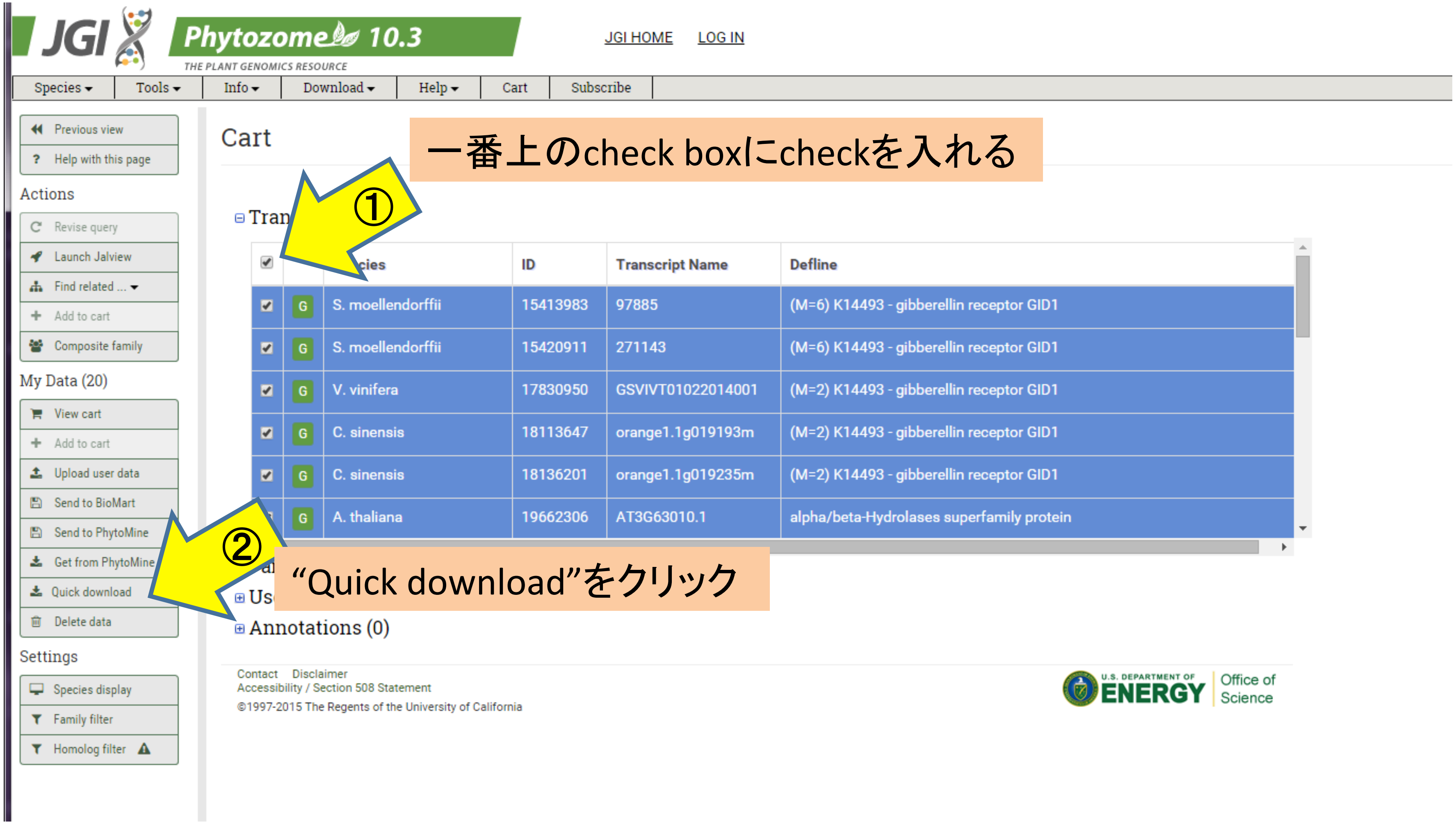
② “Relationship”を2回クリック

③ “Relationship”欄が”1-M”, “1-1”, “M-1”, “M-M”になっているモノ全てにcheckを入れる

④ “Add to cart”をクリック

⑤ “View cart”をクリック

Phytozomeでお手軽比較ゲノミクス的解析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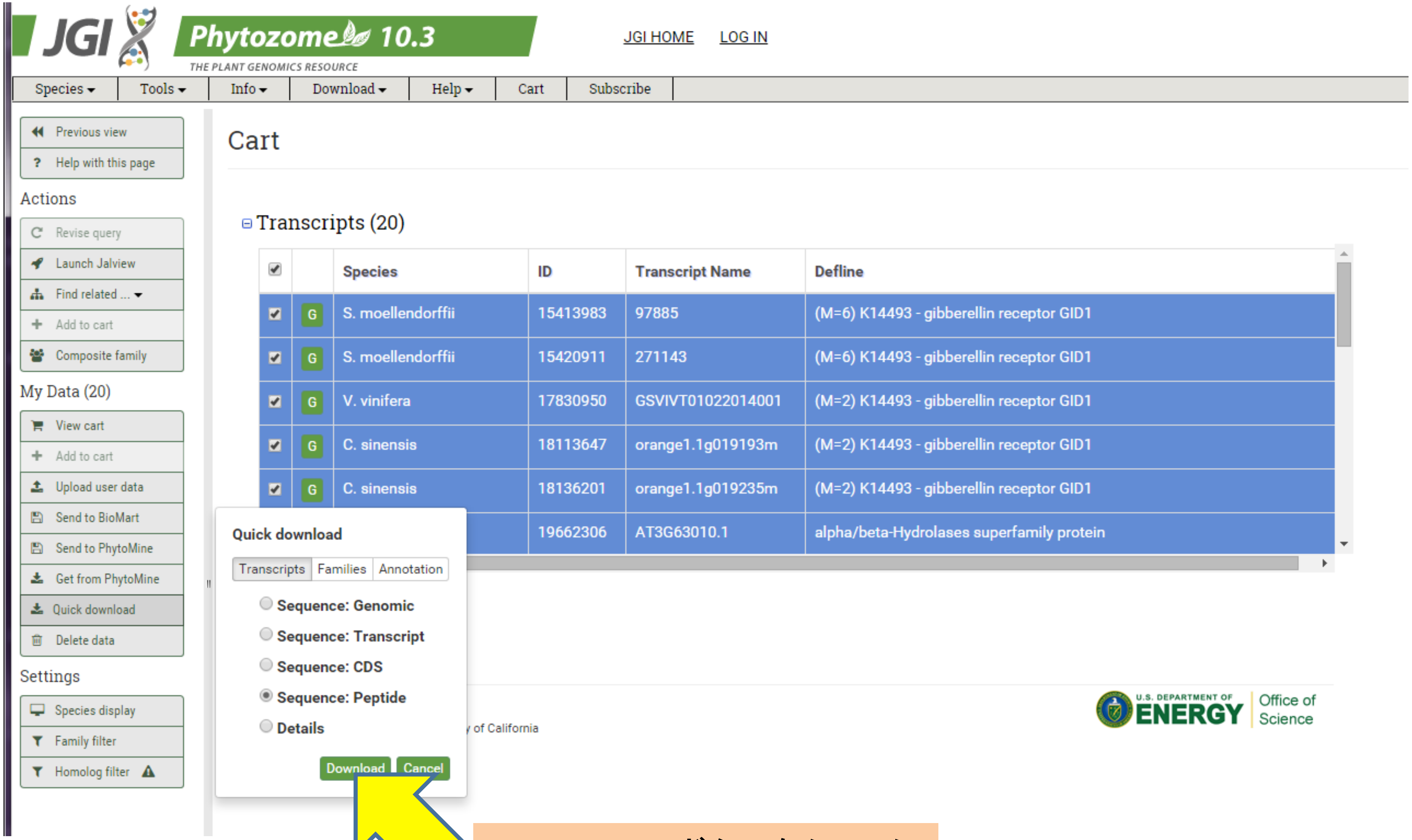
☑		cies	ID	Transcript Name	Defline
☑	G	S. moellendorffii	15413983	97885	(M=6) K14493 - gibberellin receptor GID1
☑	G	S. moellendorffii	15420911	271143	(M=6) K14493 - gibberellin receptor GID1
☑	G	V. vinifera	17830950	GSVIVT01022014001	(M=2) K14493 - gibberellin receptor GID1
☑	G	C. sinensis	18113647	orange1.1g019193m	(M=2) K14493 - gibberellin receptor GID1
☑	G	C. sinensis	18136201	orange1.1g019235m	(M=2) K14493 - gibberellin receptor GID1
	G	A. thaliana	19662306	AT3G63010.1	alpha/beta-Hydrolases superfamily protein

① 一番上のcheck boxにcheckを入れる

② “Quick download”をクリック

Phytozomeでお手軽比較ゲノミクス的解析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Transcripts (20)

☑		Species	ID	Transcript Name	Define
☑	G	S. moellendorffii	15413983	97885	(M=6) K14493 - gibberellin receptor GID1
☑	G	S. moellendorffii	15420911	271143	(M=6) K14493 - gibberellin receptor GID1
☑	G	V. vinifera	17830950	GSVIVT01022014001	(M=2) K14493 - gibberellin receptor GID1
☑	G	C. sinensis	18113647	orange1.1g019193m	(M=2) K14493 - gibberellin receptor GID1
☑	G	C. sinensis	18136201	orange1.1g019235m	(M=2) K14493 - gibberellin receptor GID1
			19662306	AT3G63010.1	alpha/beta-Hydrolases superfamily protein

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Transcripts | Families | Annotation

○ Sequence: Genomic

○ Sequence: Transcript

○ Sequence: CDS

● Sequence: Peptide

○ Details

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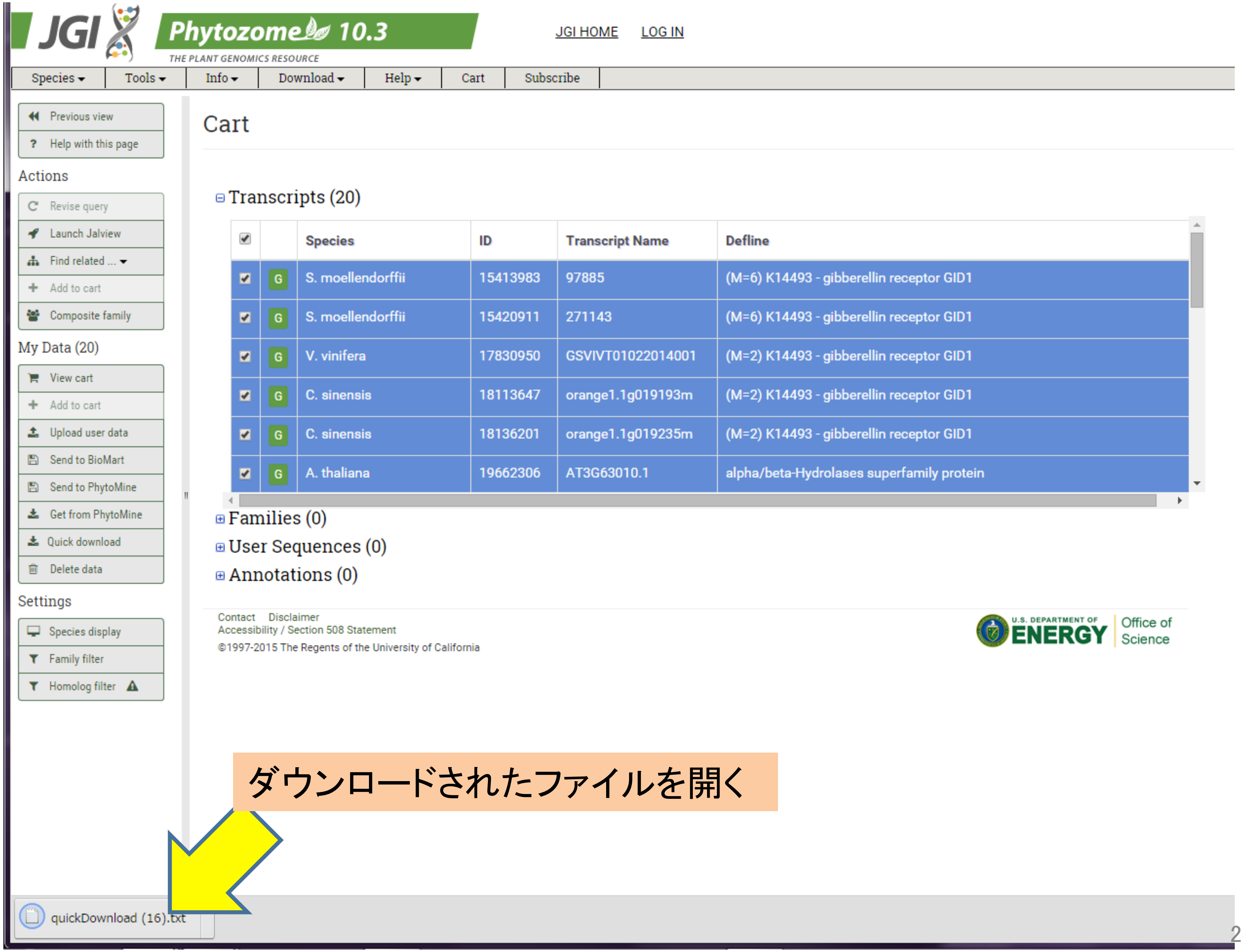
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Families (0)
User Sequences (0)
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☑		Species	ID	Transcript Name	Define
☑	G	S. moellendorffii	15413983	97885	(M=6) K14493 - gibberellin receptor GID1
☑	G	S. moellendorffii	15420911	271143	(M=6) K14493 - gibberellin receptor GID1
☑	G	V. vinifera	17830950	GSVIVT01022014001	(M=2) K14493 - gibberellin receptor GID1
☑	G	C. sinensis	18113647	orange1.1g019193m	(M=2) K14493 - gibberellin receptor GID1
☑	G	C. sinensis	18136201	orange1.1g019235m	(M=2) K14493 - gibberellin receptor GID1
☑	G	A. thaliana	19662306	AT3G63010.1	alpha/beta-Hydrolases superfamily protein

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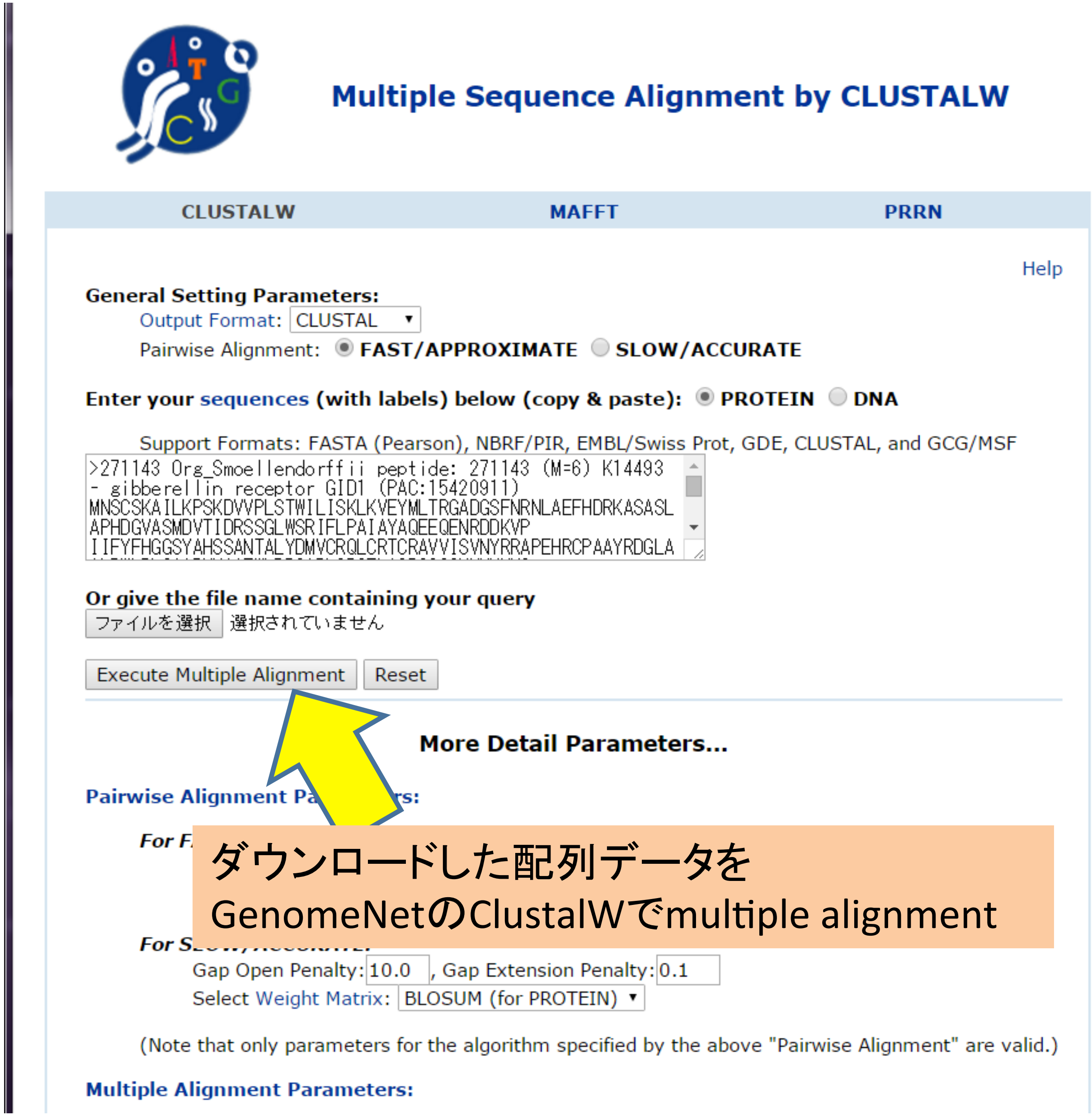
Phytozomeでお手軽比較ゲノミクス的解析



Multiple Sequence Alignment by CLUSTALW

General Setting Parameters:
Output Format: CLUSTAL
Pairwise Alignment: ● FAST/APPROXIMATE ○ SLOW/ACCURATE

Enter your sequences (with labels) below (copy & paste): ● PROTEIN ○ DNA

Support Formats: FASTA (Pearson), NBRF/PIR, EMBL/Swiss Prot, GDE, CLUSTAL, and GCG/MSF

```
>271143 Org_Smoellendorffii peptide: 271143 (M=6) K14493
- gibberellin receptor GID1 (PAC:15420911)
MNSCSKAILKPSKDVVPLSTWILISKLKVEYMLTRGADGSFNRNLAEFHDRKASASL
APHDGVASMDVTIDRSSGLWSRIFLPAIAYAQEEQENRDDKVP
IIFYFHGGSYAHSSANTALYDMVCRQLCRTCRAVVISVNYRRAPEHRCPAAYRDGLA
```

Or give the file name containing your query

More Detail Parameters...

Pairwise Alignment Pa rs:

For F

For S

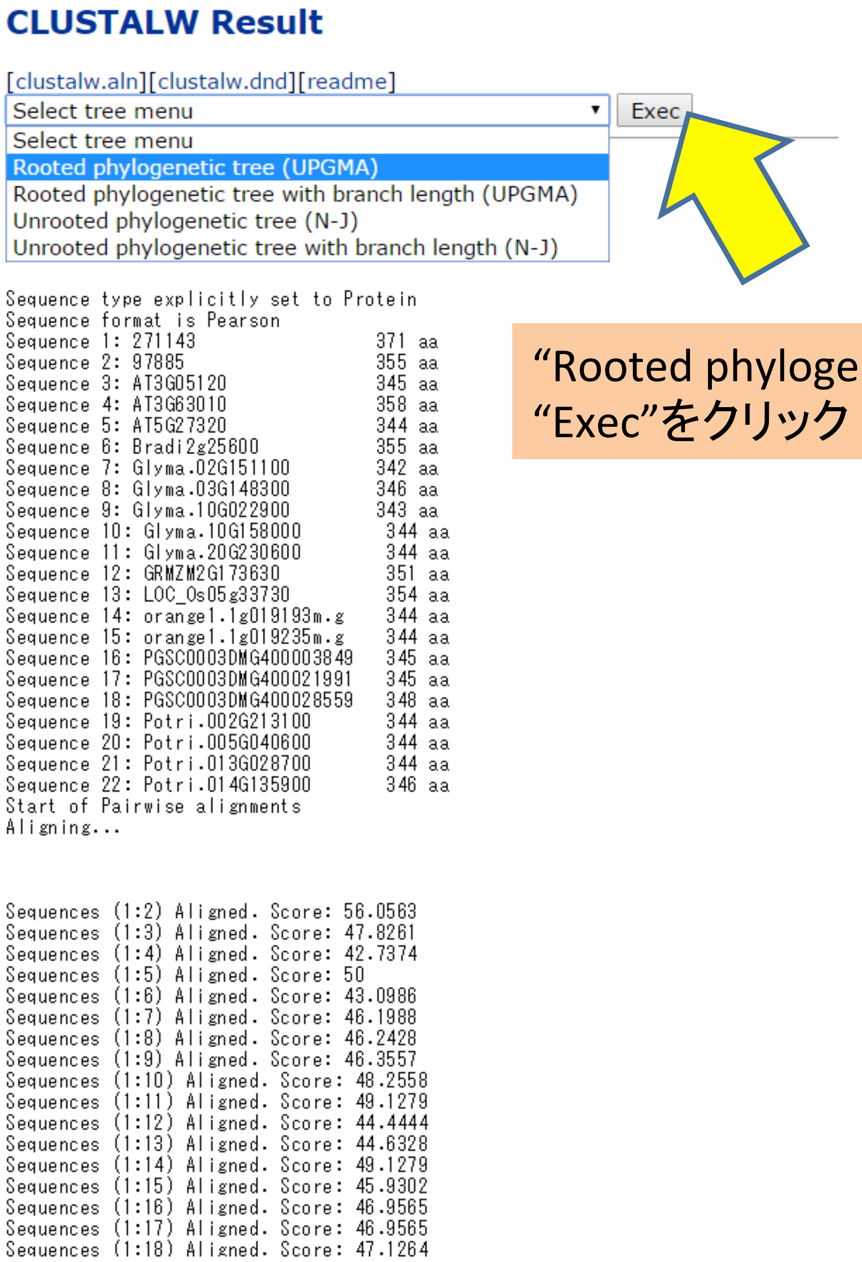
Gap Open Penalty: 10.0 , Gap Extension Penalty: 0.1
Select Weight Matrix: BLOSUM (for PROTEIN)

(Note that only parameters for the algorithm specified by the above "Pairwise Alignment" are valid.)

Multiple Alignment Parameters:

ダウンロードした配列データを
GenomeNetのClustalWでmultiple alignment

Phytozomeでお手軽比較ゲノミクス的解析


CLUSTALW Result
[clustalw.aln][clustalw.dnd][readme]
Select tree menu
Exec
Select tree menu
Rooted phylogenetic tree (UPGMA)
Rooted phylogenetic tree with branch length (UPGMA)
Unrooted phylogenetic tree (N-J)
Unrooted phylogenetic tree with branch length (N-J)

```
Sequence type explicitly set to Protein
Sequence format is Pearson
Sequence 1: 271143                      371 aa
Sequence 2: 97885                       355 aa
Sequence 3: AT3G05120                   345 aa
Sequence 4: AT3G63010                   358 aa
Sequence 5: AT5G27320                   344 aa
Sequence 6: Bradi2g25600                355 aa
Sequence 7: Glyma.02G151100             342 aa
Sequence 8: Glyma.03G148300             346 aa
Sequence 9: Glyma.10G022900             343 aa
Sequence 10: Glyma.10G158000             344 aa
Sequence 11: Glyma.20G230600             344 aa
Sequence 12: GRMZM2G173630               351 aa
Sequence 13: LOC_Os05g33730              354 aa
Sequence 14: orange1.1g019193m.g         344 aa
Sequence 15: orange1.1g019235m.g         344 aa
Sequence 16: PGSC0003DMG400003849        345 aa
Sequence 17: PGSC0003DMG400021991        345 aa
Sequence 18: PGSC0003DMG400028559        348 aa
Sequence 19: Potri.002G213100            344 aa
Sequence 20: Potri.005G040600            344 aa
Sequence 21: Potri.013G028700            344 aa
Sequence 22: Potri.014G135900            346 aa
Start of Pairwise alignments
Aligning...


Sequences (1:2) Aligned. Score: 56.0563
Sequences (1:3) Aligned. Score: 47.8261
Sequences (1:4) Aligned. Score: 42.7374
Sequences (1:5) Aligned. Score: 50
Sequences (1:6) Aligned. Score: 43.0986
Sequences (1:7) Aligned. Score: 46.1988
Sequences (1:8) Aligned. Score: 46.2428
Sequences (1:9) Aligned. Score: 46.3557
Sequences (1:10) Aligned. Score: 48.2558
Sequences (1:11) Aligned. Score: 49.1279
Sequences (1:12) Aligned. Score: 44.4444
Sequences (1:13) Aligned. Score: 44.6328
Sequences (1:14) Aligned. Score: 49.1279
Sequences (1:15) Aligned. Score: 45.9302
Sequences (1:16) Aligned. Score: 46.9565
Sequences (1:17) Aligned. Score: 46.9565
Sequences (1:18) Aligned. Score: 47.1264
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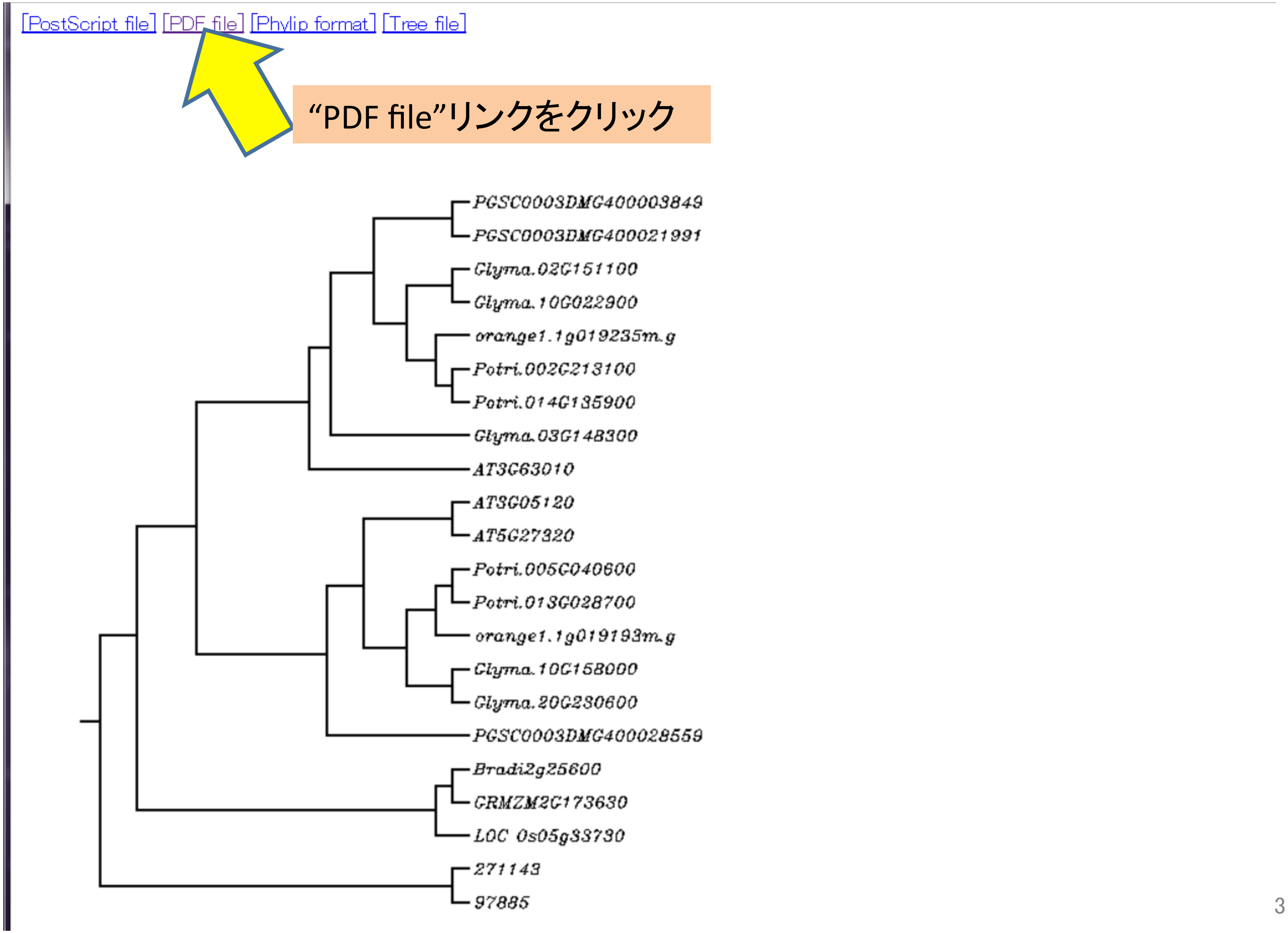
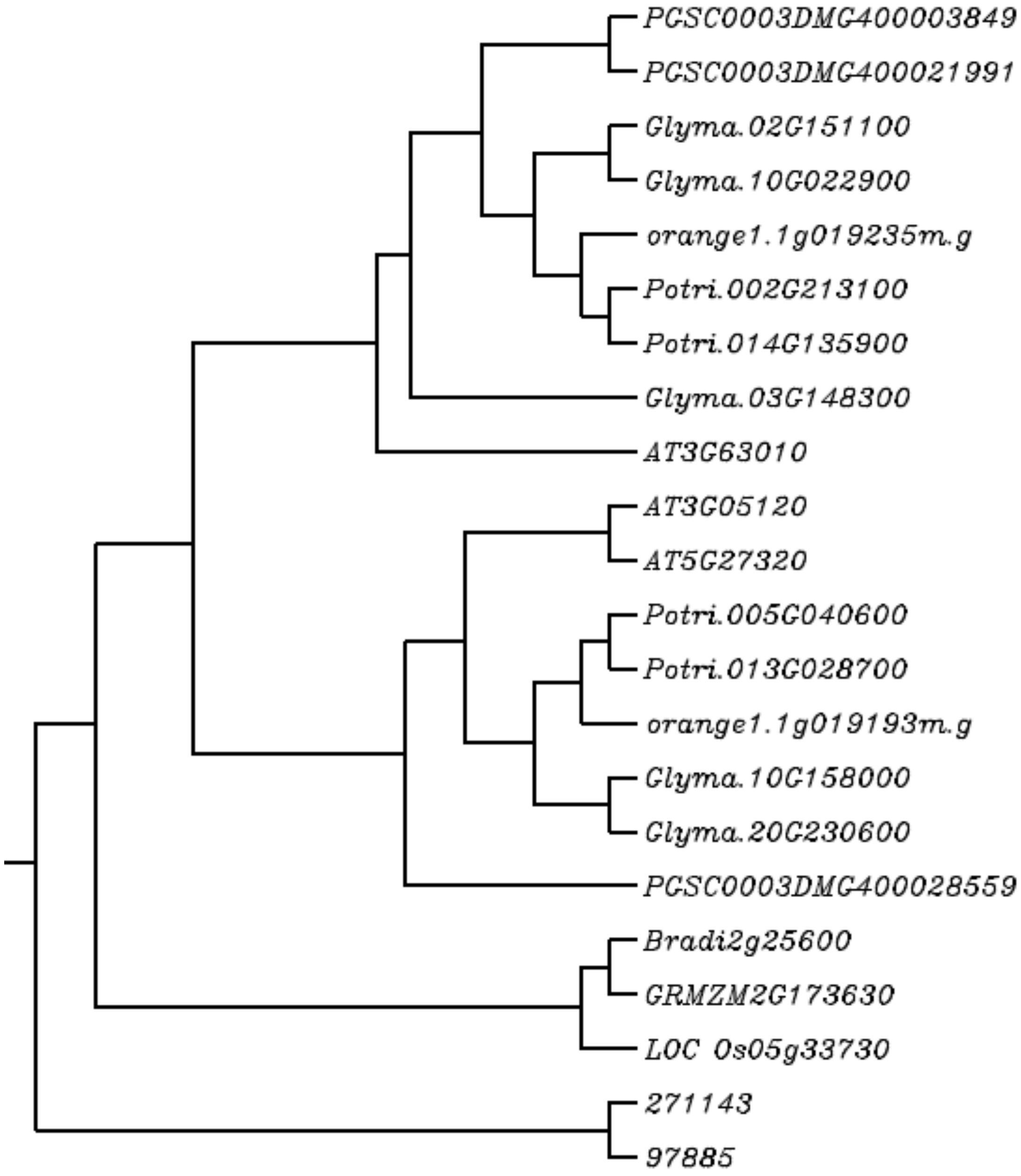
“Rooted phylogenetic tree (UPGMA)”を選択し、
“Exec”をクリック

Phytozomeでお手軽比較ゲノミクス的解析


[PostScript file] [PDF file] [Phylip format] [Tree file]
PGSC0003DMG400003849
PGSC0003DMG400021991
Glyma.02G151100
Glyma.10G022900
orange1.1g019235m.g
Potri.002G213100
Potri.014G135900
Glyma.03G148300
AT3G63010
AT3G05120
AT5G27320
Potri.005G040600
Potri.013G028700
orange1.1g019193m.g
Glyma.10G158000
Glyma.20G230600
PGSC0003DMG400028559
Bradi2g25600
GRMZM2G173630
LOC Os05g33730
271143
97885

“PDF file”リンクをクリック

Phytozomeでお手軽比較ゲノミクス的解析


PCSC0003DMG400003849
PCSC0003DMG400021991
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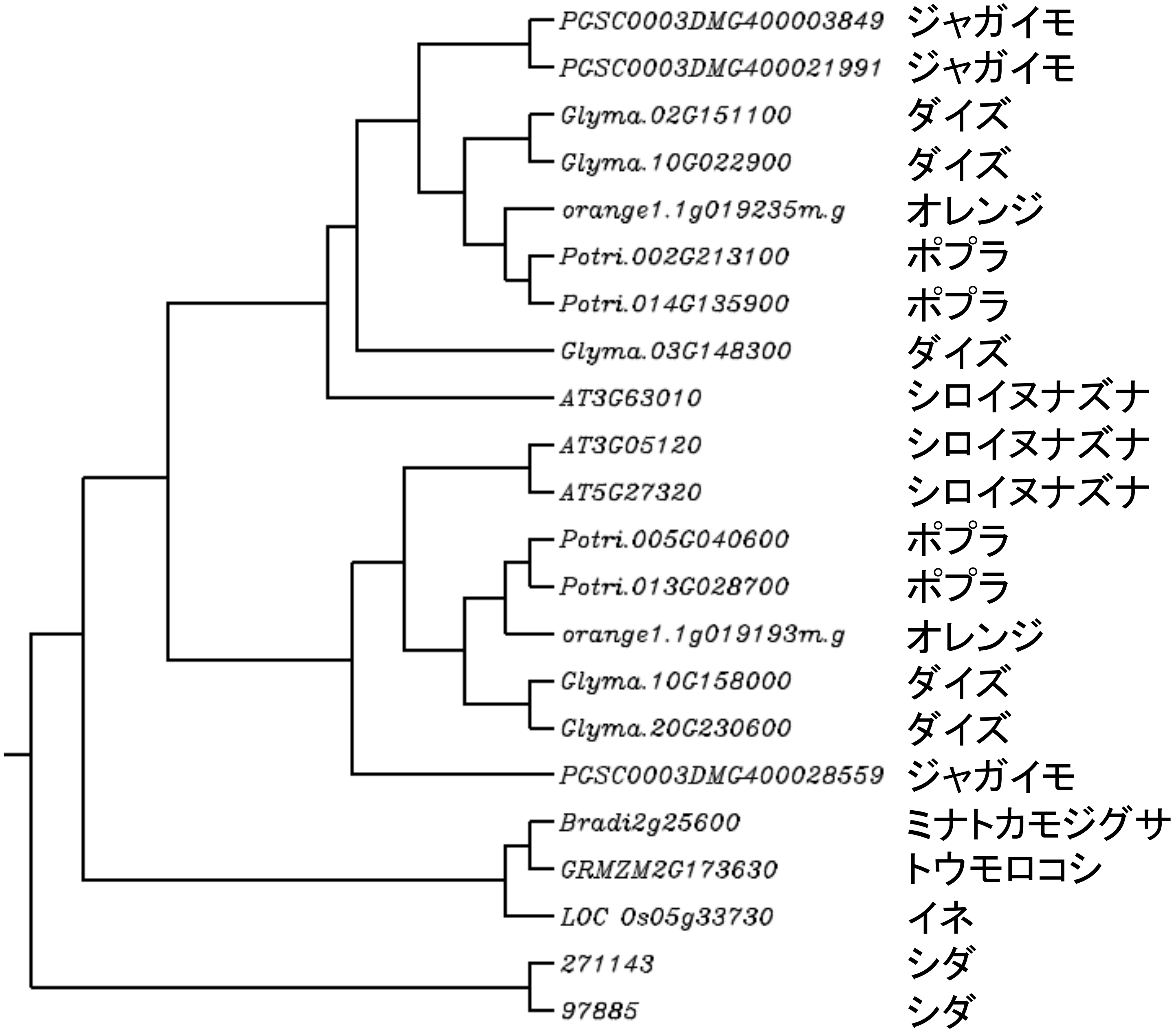
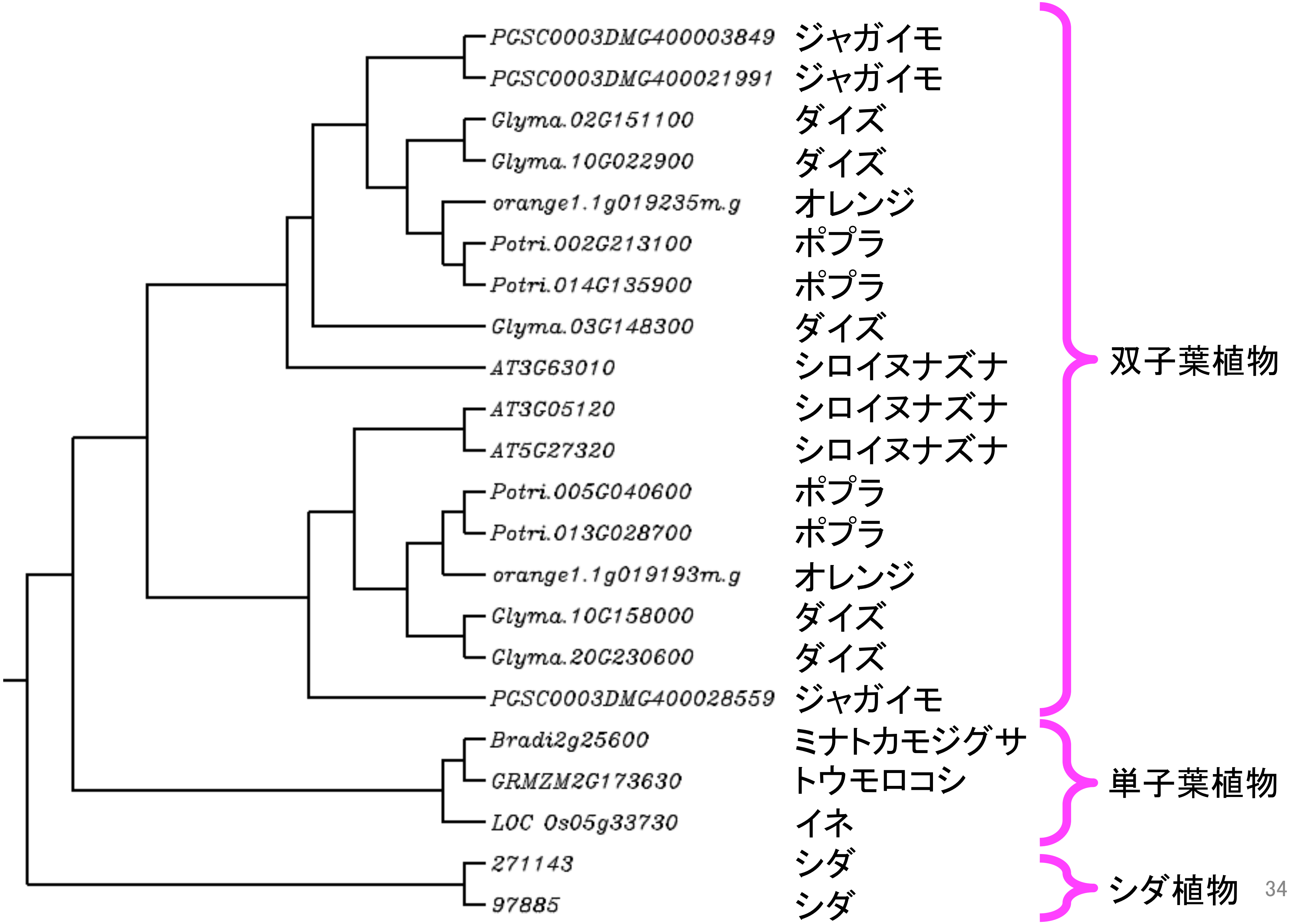
Glyma.10G022900
orange1.1g019235m.g
Potri.002G213100
Potri.014G135900
Glyma.03G148300
AT3G63010
AT3G05120
AT5G27320
Potri.005G040600
Potri.013G028700
orange1.1g019193m.g
Glyma.10G158000
Glyma.20G230600
PCSC0003DMG400028559
Bradi2g25600
GRMZM2G173630
LOC Os05g33730
271143
97885

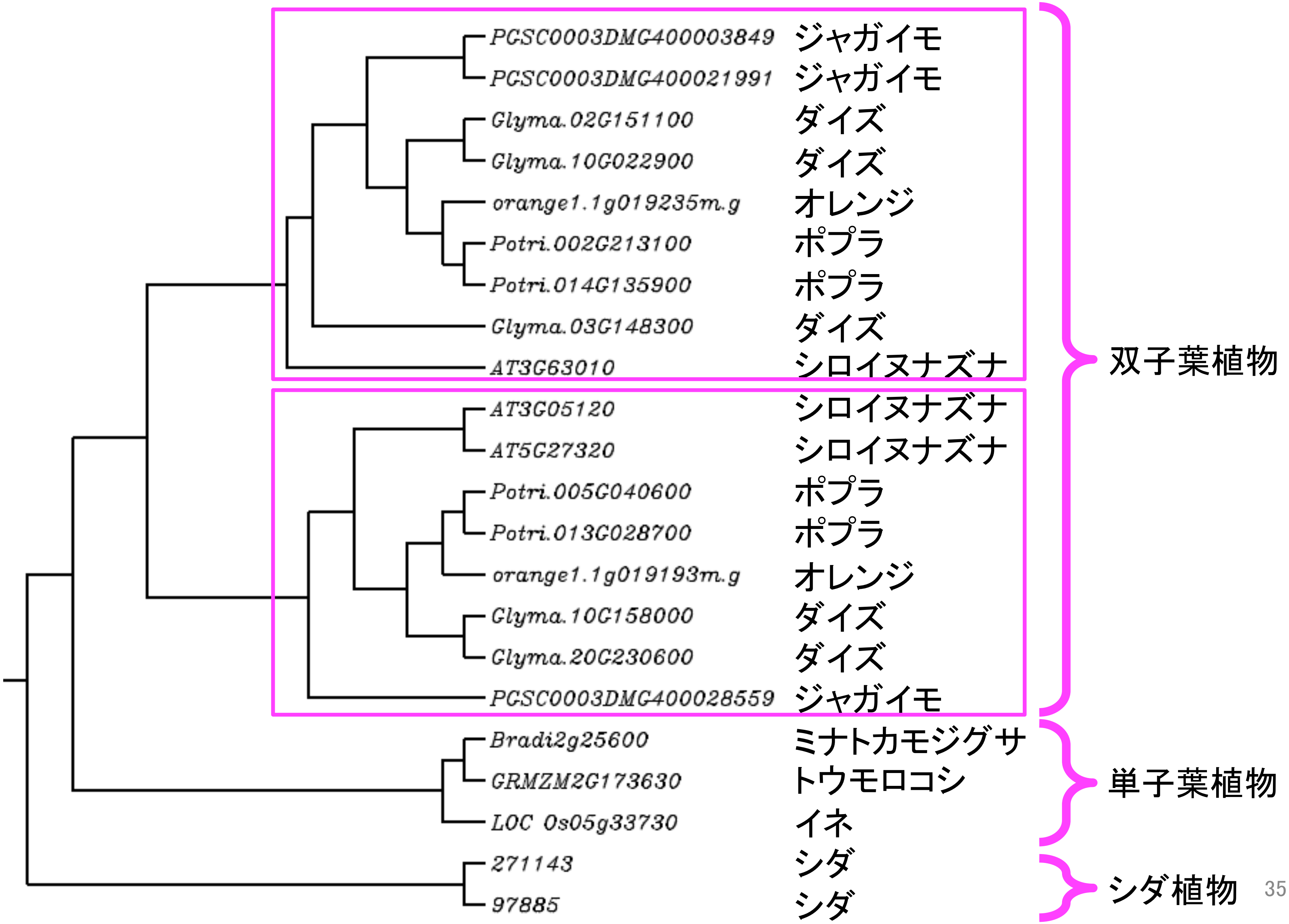
Phytozomeでお手軽比較ゲノミクス的解析


PCSC0003DMG400003849 ジャガイモ
PCSC0003DMG400021991 ジャガイモ
Glyma.02G151100 ダイズ
Glyma.10G022900 ダイズ
orange1.1g019235m.g オレンジ
Potri.002G213100 ポプラ
Potri.014G135900 ポプラ
Glyma.03G148300 ダイズ
AT3G63010 シロイヌナズナ
AT3G05120 シロイヌナズナ
AT5G27320 シロイヌナズナ
Potri.005G040600 ポプラ
Potri.013G028700 ポプラ
orange1.1g019193m.g オレンジ
Glyma.10G158000 ダイズ
Glyma.20G230600 ダイズ
PCSC0003DMG400028559 ジャガイモ
Bradi2g25600 ミナトカモジグサ
GRMZM2G173630 トウモロコシ
LOC Os05g33730 イネ
271143 シダ
97885 シダ

Phytozomeでお手軽比較ゲノミクス的解析

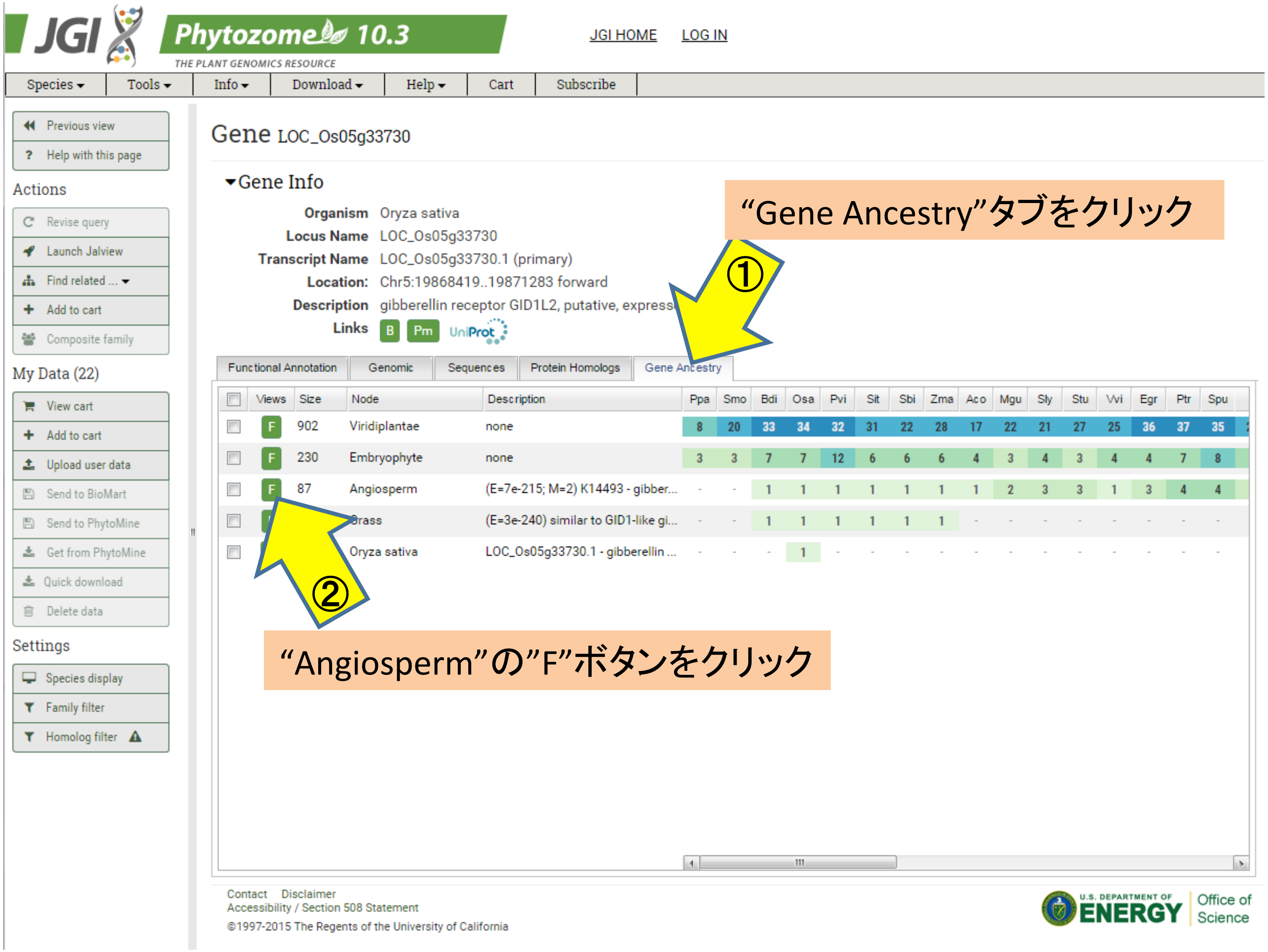

PCSC0003DMG400003849 ジャガイモ
PCSC0003DMG400021991 ジャガイモ
Glyma.02G151100 ダイズ
Glyma.10G022900 ダイズ
orange1.1g019235m.g オレンジ
Potri.002G213100 ポプラ
Potri.014G135900 ポプラ
Glyma.03G148300 ダイズ
AT3G63010 シロイヌナズナ
AT3G05120 シロイヌナズナ
AT5G27320 シロイヌナズナ
Potri.005G040600 ポプラ
Potri.013G028700 ポプラ
orange1.1g019193m.g オレンジ
Glyma.10G158000 ダイズ
Glyma.20G230600 ダイズ
PCSC0003DMG400028559 ジャガイモ
Bradi2g25600 ミナトカモジグサ
GRMZM2G173630 トウモロコシ
LOC Os05g33730 イネ
271143 シダ
97885 シダ
双子葉植物
単子葉植物
シダ植物

Phytozomeでお手軽比較ゲノミクス的解析



PCSC0003DMG400003849 ジャガイモ
PCSC0003DMG400021991 ジャガイモ
Glyma.02G151100 ダイズ
Glyma.10G022900 ダイズ
orange1.1g019235m.g オレンジ
Potri.002G213100 ポプラ
Potri.014G135900 ポプラ
Glyma.03G148300 ダイズ
AT3G63010 シロイヌナズナ
AT3G05120 シロイヌナズナ
AT5G27320 シロイヌナズナ
Potri.005G040600 ポプラ
Potri.013G028700 ポプラ
orange1.1g019193m.g オレンジ
Glyma.10G158000 ダイズ
Glyma.20G230600 ダイズ
PCSC0003DMG400028559 ジャガイモ
Bradi2g25600 ミナトカモジグサ
GRMZM2G173630 トウモロコシ
LOC Os05g33730 イネ
271143 シダ
97885 シダ
双子葉植物
単子葉植物
シダ植物

Phytozomeでお手軽比較ゲノミクス的解析



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Sequences
Protein Homologs
Gene Ancestry
B
Pm
UniProt

Gene LOC_Os05g33730

▾Gene Info

Organism Oryza sativa

Locus Name LOC_Os05g33730

Transcript Name LOC_Os05g33730.1 (primary)

Location: Chr5:19868419..19871283 forward

Description gibberellin receptor GID1L2, putative, express

Links

☐	Views	Size	Node	Description	Ppa	Smo	Bdi	Osa	Pvi	Sit	Sbi	Zma	Aco	Mgu	Sly	Stu	Vvi	Egr	Ptr	Spu
☐	F	902	Viridiplantae	none	8	20	33	34	32	31	22	28	17	22	21	27	25	36	37	35
☐	F	230	Embryophyte	none	3	3	7	7	12	6	6	6	4	3	4	3	4	4	7	8
☐	F	87	Angiosperm	(E=7e-215; M=2) K14493 - gibber...	-	-	1	1	1	1	1	1	1	2	3	3	1	3	4	4
☐			Grass	(E=3e-240) similar to GID1-like gi...	-	-	1	1	1	1	1	1	-	-	-	-	-	-	-	-
☐			Oryza sativa	LOC_Os05g33730.1 - gibberellin ...	-	-	-	1	-	-	-	-	-	-	-	-	-	-	-	-

“Gene Ancestry”タブをクリック

①

②

“Angiosperm”の”F”ボタンをクリック

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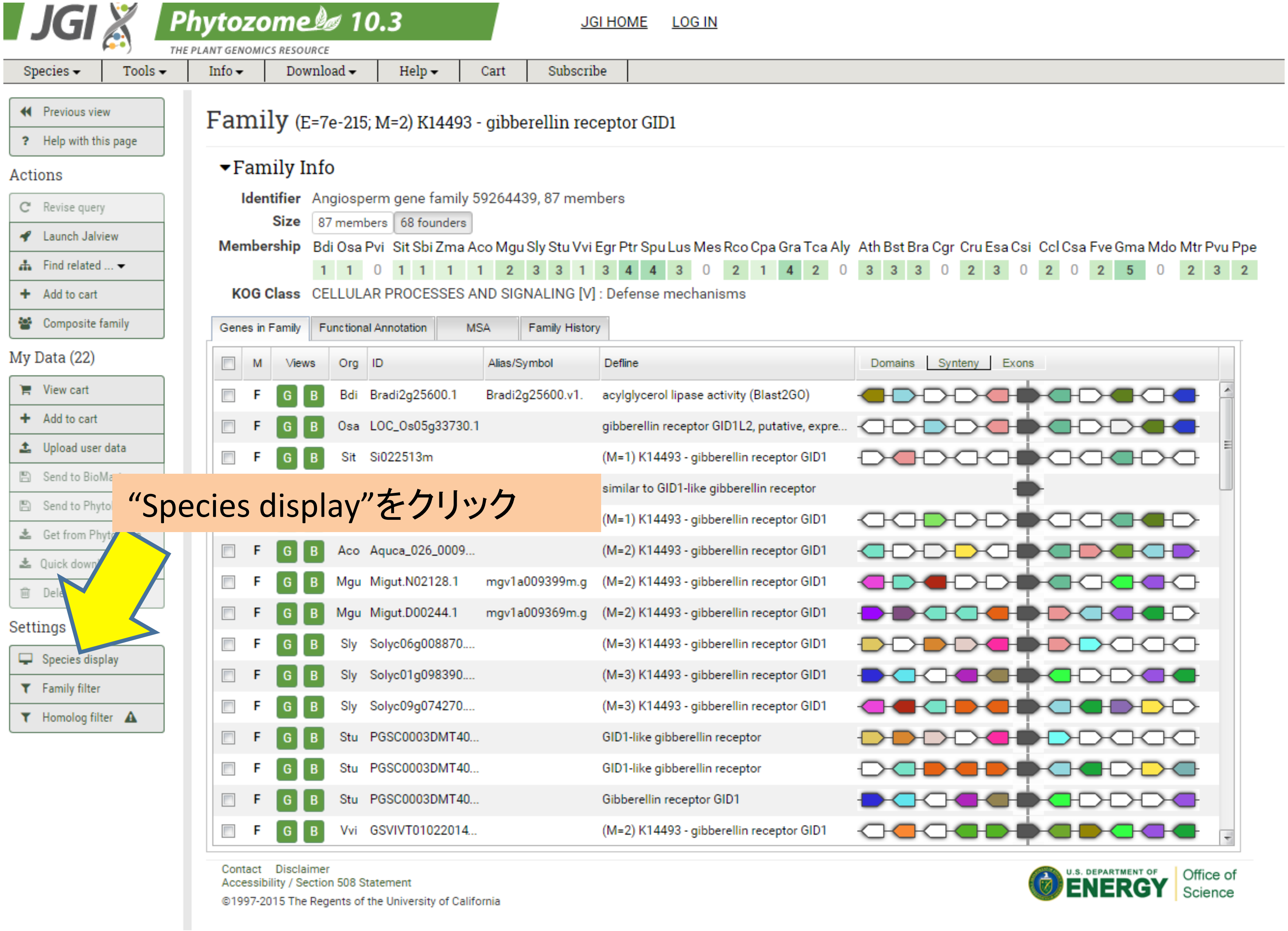
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Species display
Family filter
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Genes in Family
Functional Annotation
MSA
Family History
Domains
Synteny
Exons

Family (E=7e-215; M=2) K14493 - gibberellin receptor GID1

Family Info

Identifier Angiosperm gene family 59264439, 87 members

Size 87 members 68 founders

Membership

Bdi	Osa	Pvi	Sit	Sbi	Zma	Aco	Mgu	Sly	Stu	Vvi	Egr	Ptr	Spu	Lus	Mes	Rco	Cpa	Gra	Tca	Aly	Ath	Bst	Bra	Cgr	Cru	Esa	Csi	Ccl	Csa	Fve	Gma	Mdo	Mtr	Pvu	Ppe
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KOG Class CELLULAR PROCESSES AND SIGNALING [V] : Defense mechanisms

☐	M	Views	Org	ID	Alias/Symbol	Define
☐	F	G B	Bdi	Bradi2g25600.1	Bradi2g25600.v1.	acylglycerol lipase activity (Blast2GO)
☐	F	G B	Osa	LOC_Os05g33730.1		gibberellin receptor GID1L2, putative, expre...
☐	F	G B	Sit	Si022513m		(M=1) K14493 - gibberellin receptor GID1
						similar to GID1-like gibberellin receptor
						(M=1) K14493 - gibberellin receptor GID1
☐	F	G B	Aco	Aquca_026_0009...		(M=2) K14493 - gibberellin receptor GID1
☐	F	G B	Mgu	Migut.N02128.1	mgv1a009399m.g	(M=2) K14493 - gibberellin receptor GID1
☐	F	G B	Mgu	Migut.D00244.1	mgv1a009369m.g	(M=2) K14493 - gibberellin receptor GID1
☐	F	G B	Sly	Solyc06g008870....		(M=3) K14493 - gibberellin receptor GID1
☐	F	G B	Sly	Solyc01g098390....		(M=3) K14493 - gibberellin receptor GID1
☐	F	G B	Sly	Solyc09g074270....		(M=3) K14493 - gibberellin receptor GID1
☐	F	G B	Stu	PGSC0003DMT40...		GID1-like gibberellin receptor
☐	F	G B	Stu	PGSC0003DMT40...		GID1-like gibberellin receptor
☐	F	G B	Stu	PGSC0003DMT40...		Gibberellin receptor GID1
☐	F	G B	Vvi	GSVIVT01022014...		(M=2) K14493 - gibberellin receptor GID1

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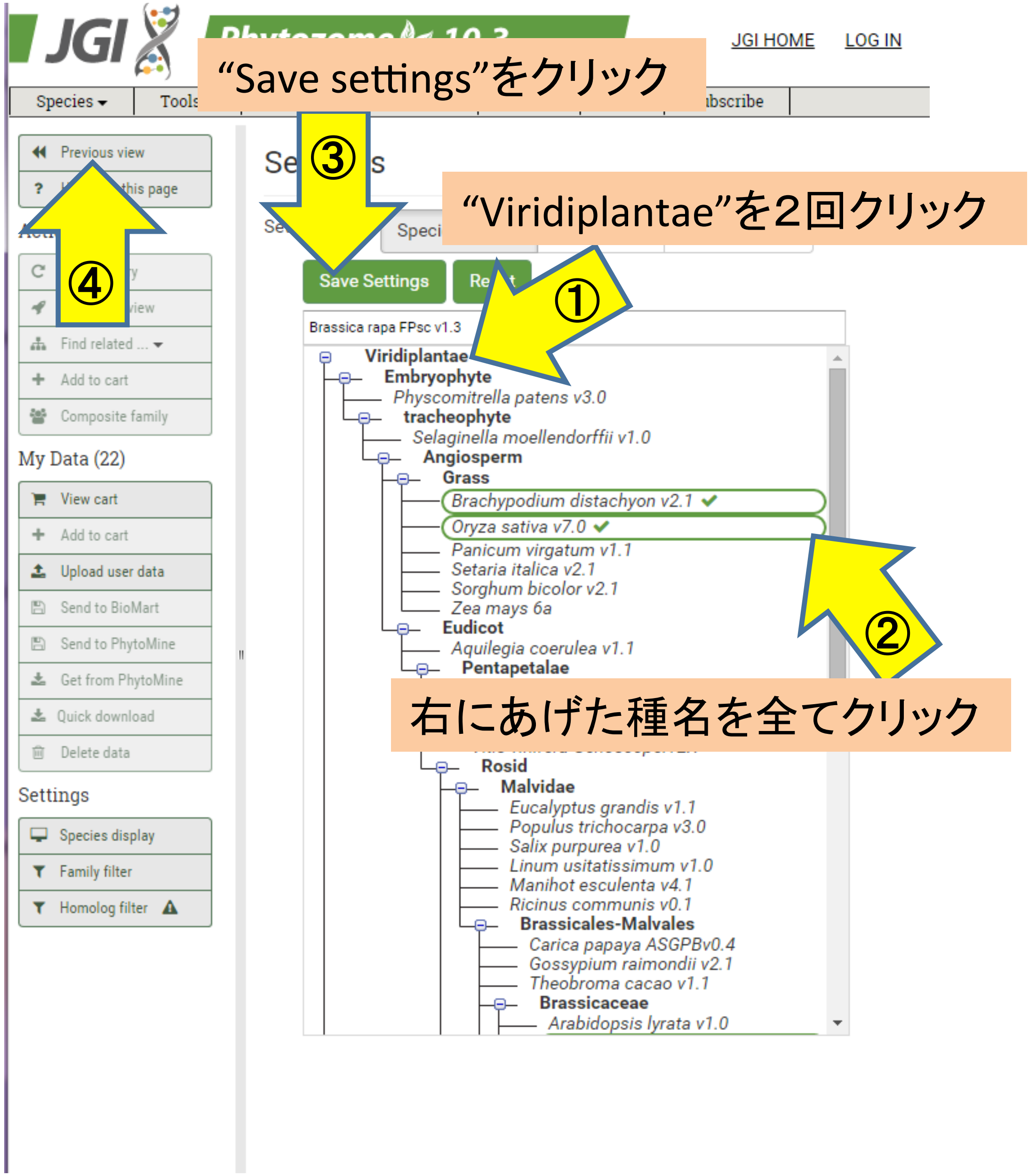
“Species display”をクリック

Phytozomeでお手軽比較ゲノミクス的解析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Viridiplantae
Embryophyte
Physcomitrella patens v3.0
tracheophyte
Selaginella moellendorffii v1.0
Angiosperm
Grass
Brachypodium distachyon v2.1 ✓
Oryza sativa v7.0 ✓
Panicum virgatum v1.1
Setaria italica v2.1
Sorghum bicolor v2.1
Zea mays 6a
Eudicot
Aquilegia coerulea v1.1
Pentapetalae
Rosid
Malvidae
Eucalyptus grandis v1.1
Populus trichocarpa v3.0
Salix purpurea v1.0
Linum usitatissimum v1.0
Manihot esculenta v4.1
Ricinus communis v0.1
Brassicales-Malvales
Carica papaya ASGPBv0.4
Gossypium raimondii v2.1
Theobroma cacao v1.1
Brassicaceae
Arabidopsis lyrata v1.0

③ “Save settings”をクリック

④

① “Viridiplantae”を２回クリック

② 右にあげた種名を全てクリック

Grass

Brachypodium distachyon v2.1

Oryza sativa v7.0

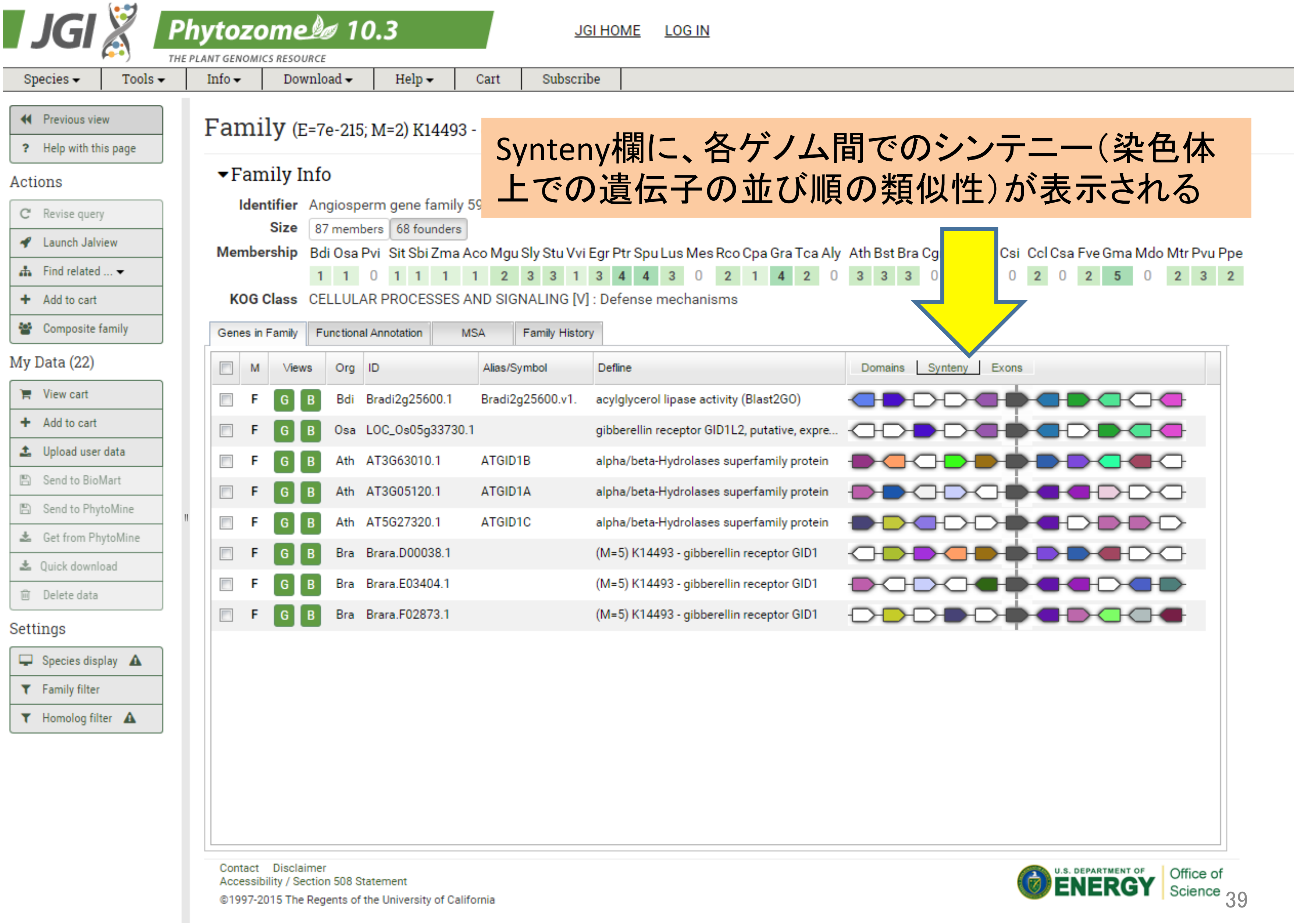
Brassicaceae

Arabidopsis thaliana TAIR10

Brassica rapa FPsc v1.3

Phytozomeでお手軽比較ゲノミクス的解析

Synteny欄に、各ゲノム間でのシンテニー（染色体上での遺伝子の並び順の類似性）が表示される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Genes in Family
Functional Annotation
MSA
Family History
Domains
Synteny
Exons

Family (E=7e-215; M=2) K14493 -

▾Family Info

Identifier Angiosperm gene family 59

Size 87 members 68 founders

Membership

Bdi	Osa	Pvi	Sit	Sbi	Zma	Aco	Mgu	Sly	Stu	Vvi	Egr	Ptr	Spu	Lus	Mes	Rco	Cpa	Gra	Tca	Aly	Ath	Bst	Bra	Cg	Csi	Ccl	Csa	Fve	Gma	Mdo	Mtr	Pvu	Ppe
1	1	0	1	1	1	1	2	3	3	1	3	4	4	3	0	2	1	4	2	0	3	3	3	0	0	2	0	2	5	0	2	3	2

KOG Class CELLULAR PROCESSES AND SIGNALING [V] : Defense mechanisms

☐	M	Views	Org	ID	Alias/Symbol	Defline
☐	F	G B	Bdi	Bradi2g25600.1	Bradi2g25600.v1.	acylglycerol lipase activity (Blast2GO)
☐	F	G B	Osa	LOC_Os05g33730.1		gibberellin receptor GID1L2, putative, expre...
☐	F	G B	Ath	AT3G63010.1	ATGID1B	alpha/beta-Hydrolases superfamily protein
☐	F	G B	Ath	AT3G05120.1	ATGID1A	alpha/beta-Hydrolases superfamily protein
☐	F	G B	Ath	AT5G27320.1	ATGID1C	alpha/beta-Hydrolases superfamily protein
☐	F	G B	Bra	Brara.D00038.1		(M=5) K14493 - gibberellin receptor GID1
☐	F	G B	Bra	Brara.E03404.1		(M=5) K14493 - gibberellin receptor GID1
☐	F	G B	Bra	Brara.F02873.1		(M=5) K14493 - gibberellin receptor GID1

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