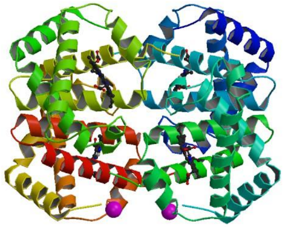
名古屋大学　農学部

生物情報工学II

11月29日

生物情報工学（Bioinfomatics）ってなに？

＞生物が持っている物質（DNA、タンパク質、その他代謝産物など）の情報を分析する学問分野。



あるタンパク質Aがあります。

アミノ酸配列
コードする遺伝子のDNA配列
生体内でのタンパク質の量
コードする遺伝子の転写産物の量

＞情報をもとにその物質の機能や構造を推定。

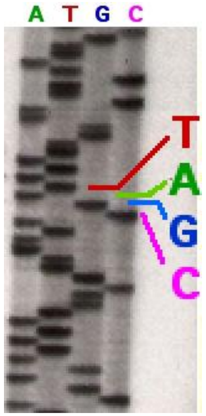
＞ただし、解析には様々な物質に関する情報の蓄積が必要。

Bioinfomaticsの台頭 - DNA配列解析の場合 -

ABI社DNA analyzerで、配列取得に10年、データ解析に３年の歳月と3000億円の費用をかけて解析。 ⇨ Illumina社HiseqXで、5名分のゲノム情報を10日70万円で解析完了。

https://jp.illumina.com/content/dam/illumina-marketing/apac/japan/documents/pdf/primer_illumina_sequencing_introduction-j.pdf

1990年-2003年 ヒトゲノム計画



https://upload.wikimedia.org/wikipedia/commons/c/cb/Sequencing.jpg

1977年 Dideoxy法(サンガー法)

https://upload.wikimedia.org/wikipedia/commons/thumb/7/78/370A_automated_DNA_sequencer.jpg/738px-370A_automated_DNA_sequencer.jpg

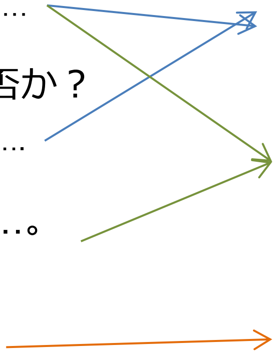
1987年 ABI社370
DNA sequencer発売

http://www.biochemsoctrans.org/content/ppbiost/43/1/1/F4.medium.gif

2006年 Solexa社(現Illumina社)
Genome Analyzer発売

http://www.biotechniques.com/multimedia/archive/00190/2013-04-03-read-len_190429a.png

2011年 Pacific bioscience社
Pacbio RS発売



分子生物学研究の結果、DNA配列情報とその機能情報が蓄積

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….

ゲノムプロジェクトのDNA配列情報、どこが遺伝子か分からない….。

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。

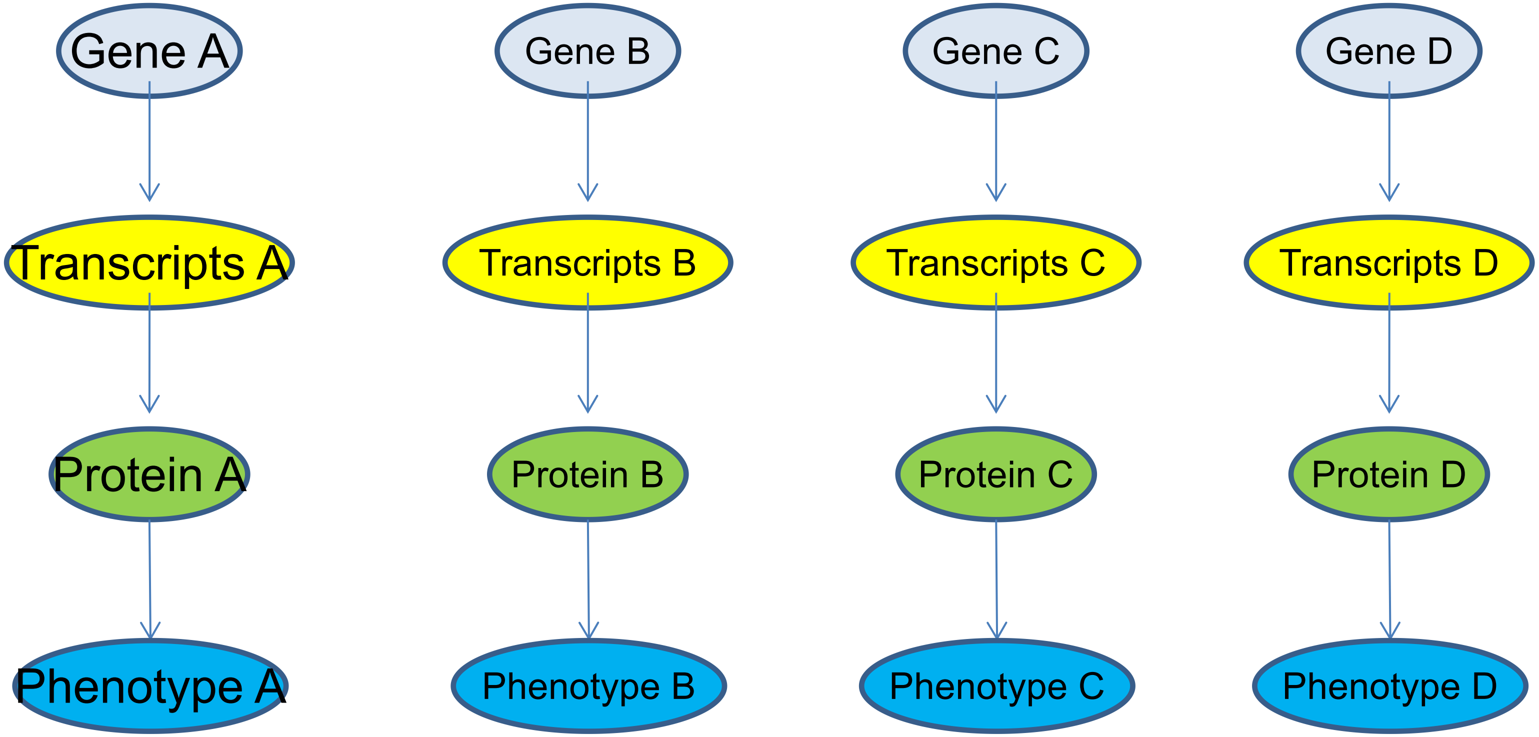
Sequence alignment

BLAST
ORF finder
Softberry/FGENESH

種間比較などによる
比較ゲノミクス

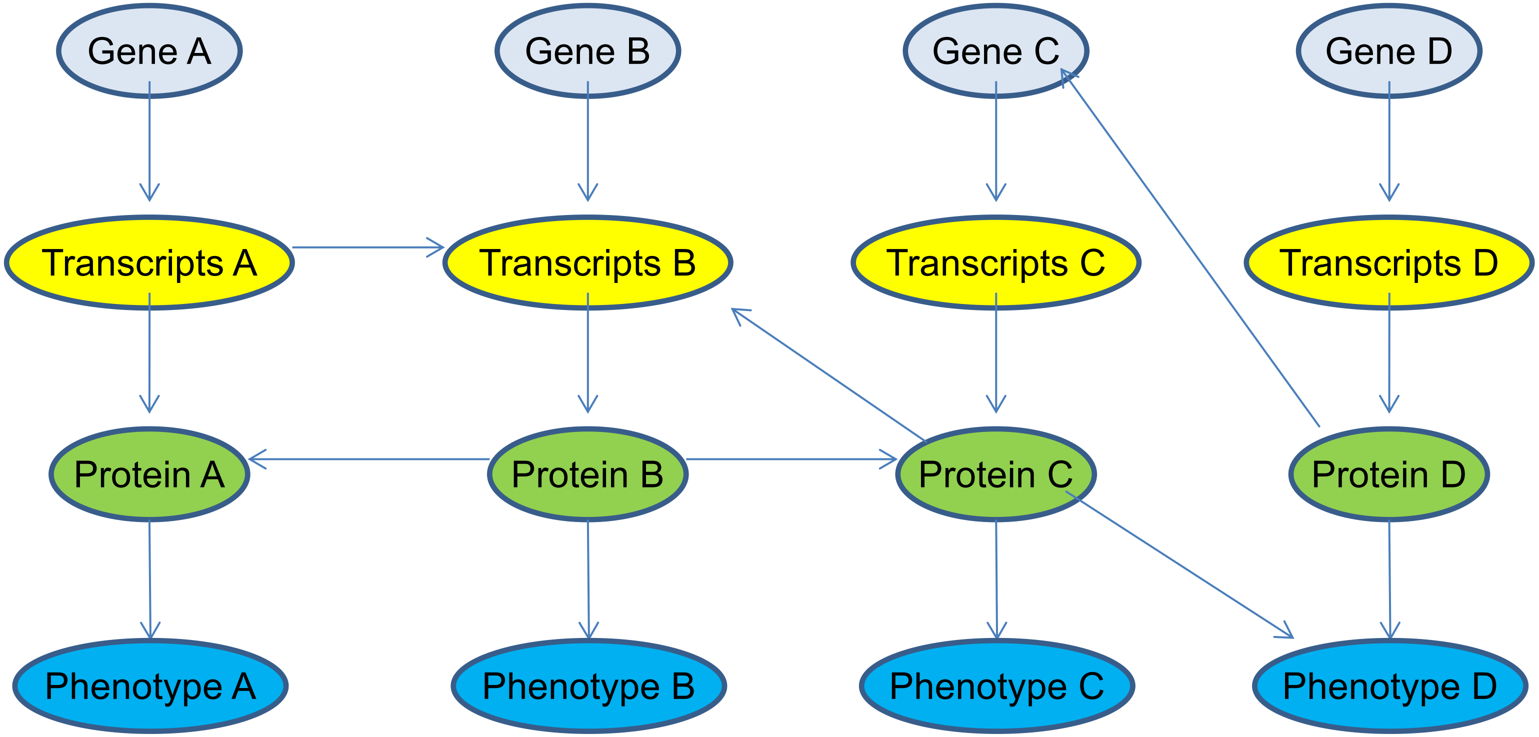
Bioinfomaticsの必要性と分子生物学的アプローチの発展

古典的な分子生物学



Bioinfomaticsの必要性と分子生物学的アプローチの発展

現在の分子生物学

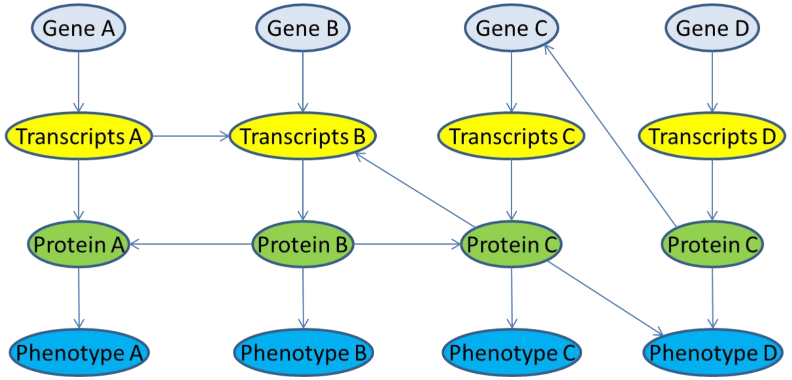


ゲノム、転写産物、たんぱく質、表現型の各階層内・階層間での複雑な相互作用

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？

Bioinfomaticsの必要性と分子生物学的アプローチの発展

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

各階層におけるデータを収集

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）

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として理解する。

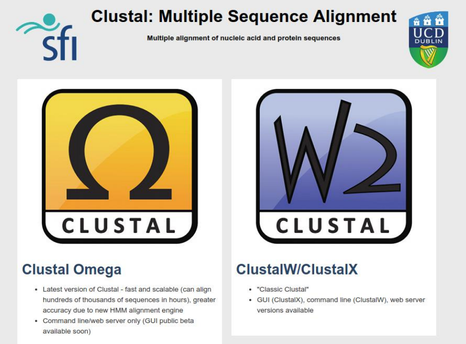
システムバイオロジー

オミクスデータをもとに、統計学やグラフ理論を駆使して、それぞれの要素の間にある相互関係を解き明かし、ネットワーク動態で生命現象を説明する。

けど、今のところ生命システムが複雑すぎて無理ゲー。

ひたすらオミクスで情報を蓄積させている。

Bioinfomaticsの必要性と分子生物学的アプローチの発展


Clustal: Multiple Sequence Alignment

Multiple alignment of nucleic acid and protein sequences

Clustal Omega

- Latest version of Clustal - fast and scalable (can align hundreds of thousands of sequences in hours), greater accuracy due to new HMM alignment engine
- Command line/web server only (GUI public beta available soon)

ClustalW/ClustalX

- "Classic Clustal"
- GUI (ClustalX), command line (ClustalW), web server versions available

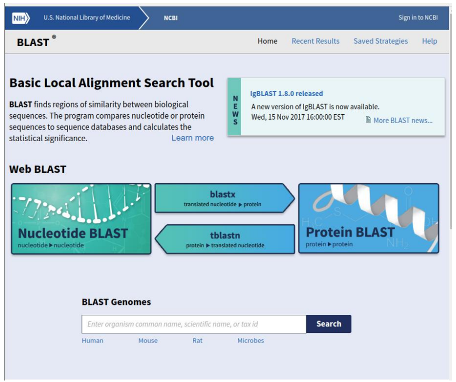
http://www.clustal.org/

単純な配列情報における相同性解析

＊2つの配列の相同性とか

より複雑な配列情報における相同性解析

＊多数の配列や長い配列における相同性



Basic Local Alignment Search Tool

BLAST finds regions of similarity between biological sequences. The program compares nucleotide or protein sequences to sequence databases and calculates the statistical significance. Learn more

NEWS

IgBLAST 1.8.0 released

A new version of IgBLAST is now available.

Wed, 15 Nov 2017 16:00:00 EST

More BLAST news...

Web BLAST

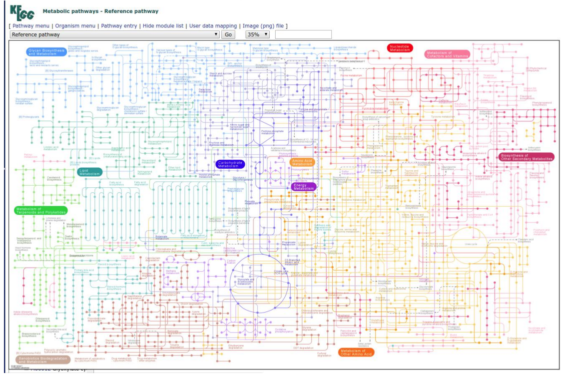
BLAST Genomes

https://blast.ncbi.nlm.nih.gov/Blast.cgi

分子生物学・オミクスとの融合

シーケンサーの発展に伴う
利用できるゲノム情報の増加

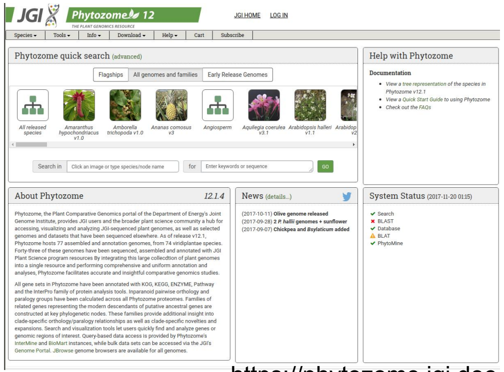
システムバイオロジー



http://www.genome.jp/kegg/kegg2.html

KEGG

比較ゲノミクス



Phytozome quick search (advanced)

Help with Phytozome

Documentation

- View a tree representation of the species in Phytozome v12.1
- View a Quick Start Guide to using Phytozome
- Check out the FAQs

About Phytozome 12.1.4

Phytozome, the Plant Comparative Genomics portal of the Department of Energy's Joint Genome Institute, provides JGI users and the broader plant science community a hub for accessing, visualizing and analyzing JGI-sequenced plant genomes, as well as selected genomes and datasets that have been sequenced elsewhere. As of release v12.1, Phytozome hosts 77 assembled and annotation genomes, from 74 viridiplantae species. Forty-three of these genomes have been sequenced, assembled and annotated with JGI Plant Science program resources By integrating this large collecdtion of plant genomes into a single resource and performing comprehensive and uniform annotation and analyses, Phytozome facilitates accurate and insightful comparative genomics studies.

All gene sets in Phytozome have been annotated with KOG, KEGG, ENZYME, Pathway and the InterPro family of protein analysis tools. Inparanoid pairwise orthology and paralogy groups have been calculated across all Phytozome proteomes. Families of related genes representing the modern descendants of putative ancestral genes are constructed at key phylogenetic nodes. These families provide additional insight into clade-specific orthology/paralogy relationships as well as clade-specific novelties and expansions. Search and visualization tools let users quickly find and analyze genes or genomic regions of interest. Query-based data access is provided by Phytozome's InterMine and BioMart instances, while bulk data sets can be accessed via the JGI's Genome Portal. JBrowse genome browsers are available for all genomes.

News (details...)

(2017-10-11) **Olive genome released**
(2017-09-28) **2 *P. hallii* genomes + sunflower**
(2017-09-07) **Chickpea and *Bsylaticum* added**

System Status (2017-11-20 01:15)

- ✓ Search
- ✗ BLAST
- ✓ Database
- ⚠ BLAT
- ✓ PhytoMine

https://phytozome.jgi.doe.gov/pz/portal.html#

Phytozome

システムバイオロジーの申し子 「KEGG」

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 dat
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 ...

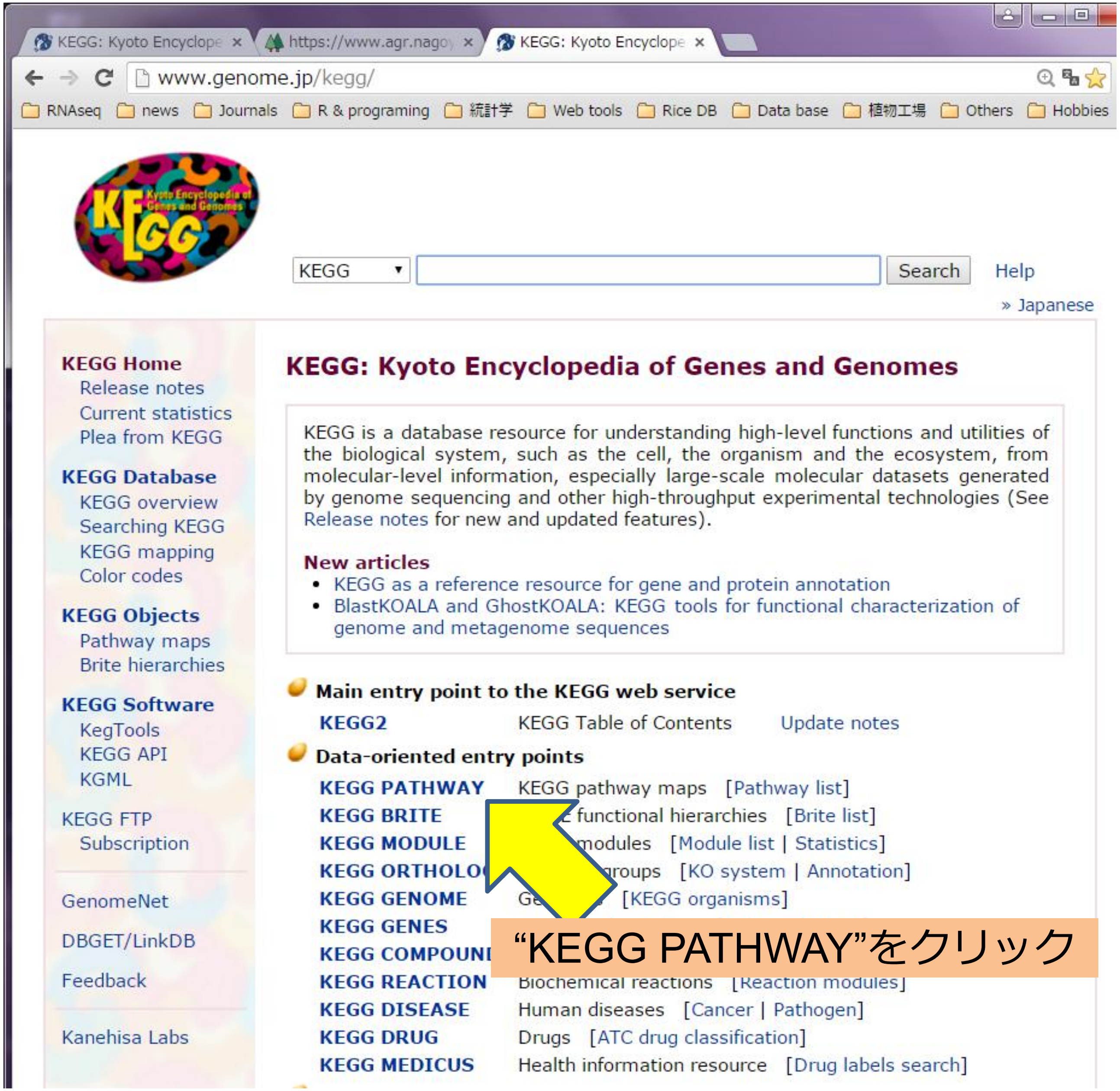
KEGG2
Category, Entry Point, Search & Compute, DBGET Search ...

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 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

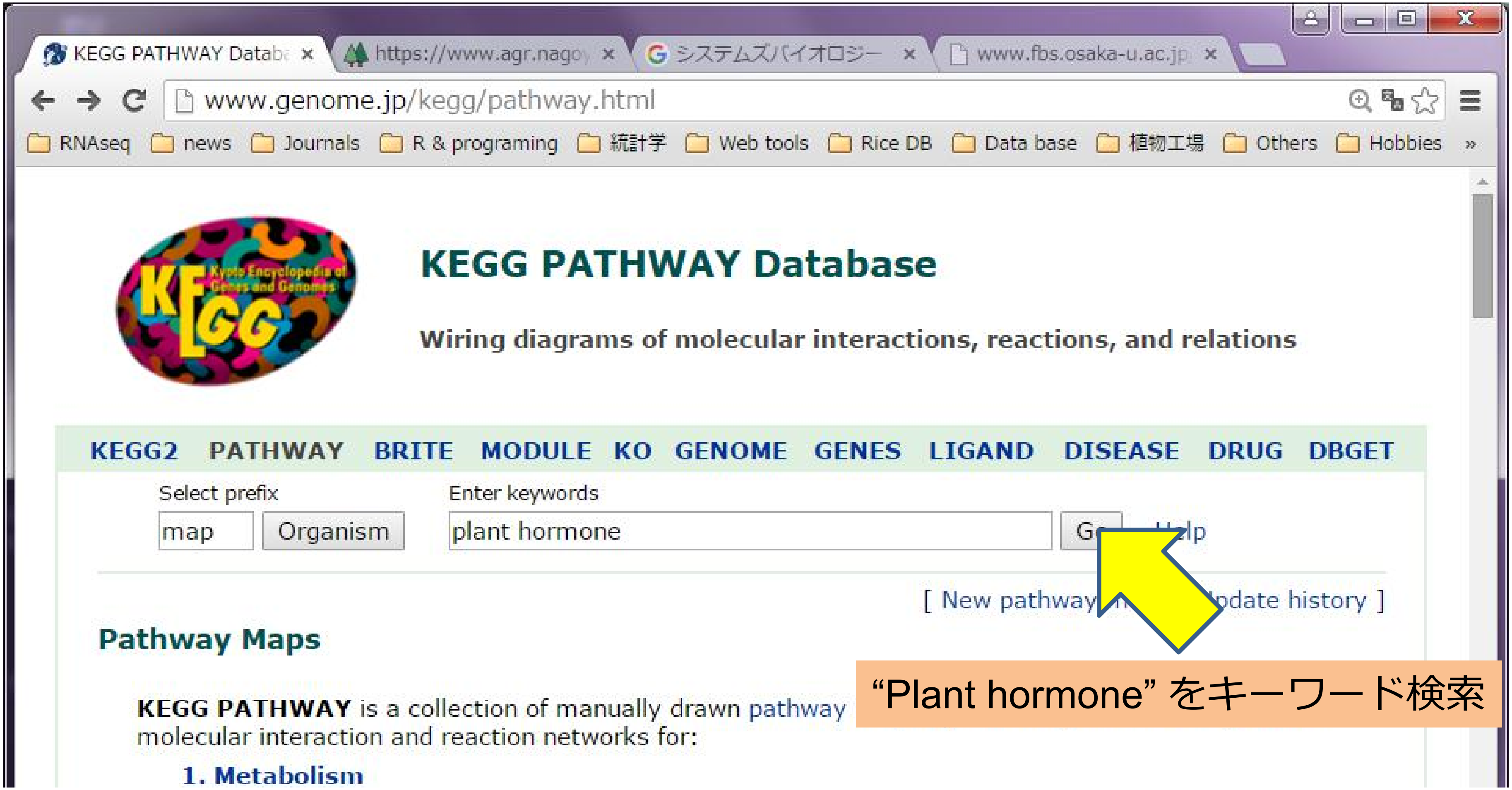
KEGG PATHWAY	KEGG pathway maps [Pathway list]
KEGG BRITE	functional hierarchies [Brite list]
KEGG MODULE	modules [Module list | Statistics]
KEGG ORTHOLO	roups [KO system | Annotation]
KEGG GENOME	Ge [KEGG organisms]
KEGG GENES	
KEGG COMPOUNI	
KEGG REACTION	Biochemical reactions [Reaction modules]
KEGG 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 Database

Wiring diagrams of molecular interactions, reactions, and relations

Select prefix: map

Enter keywords: plant hormone

[New pathway maps | Update history]

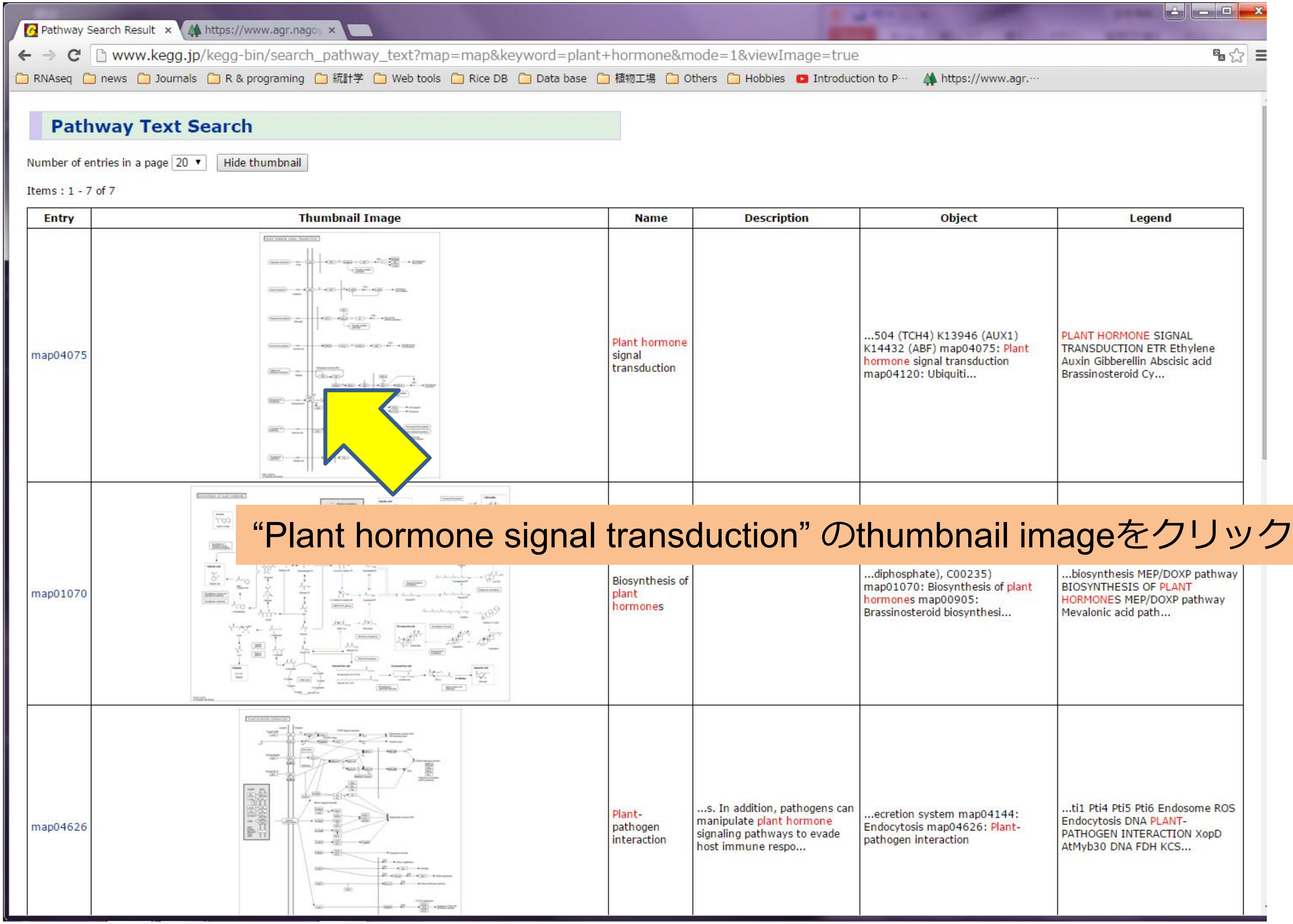
Pathway Maps

KEGG PATHWAY is a collection of manually drawn pathway maps representing our knowledge on the 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



www.kegg.jp/kegg-bin/search_pathway_text?map=map&keyword=plant+hormone&mode=1&viewImage=true

Pathway Text Search

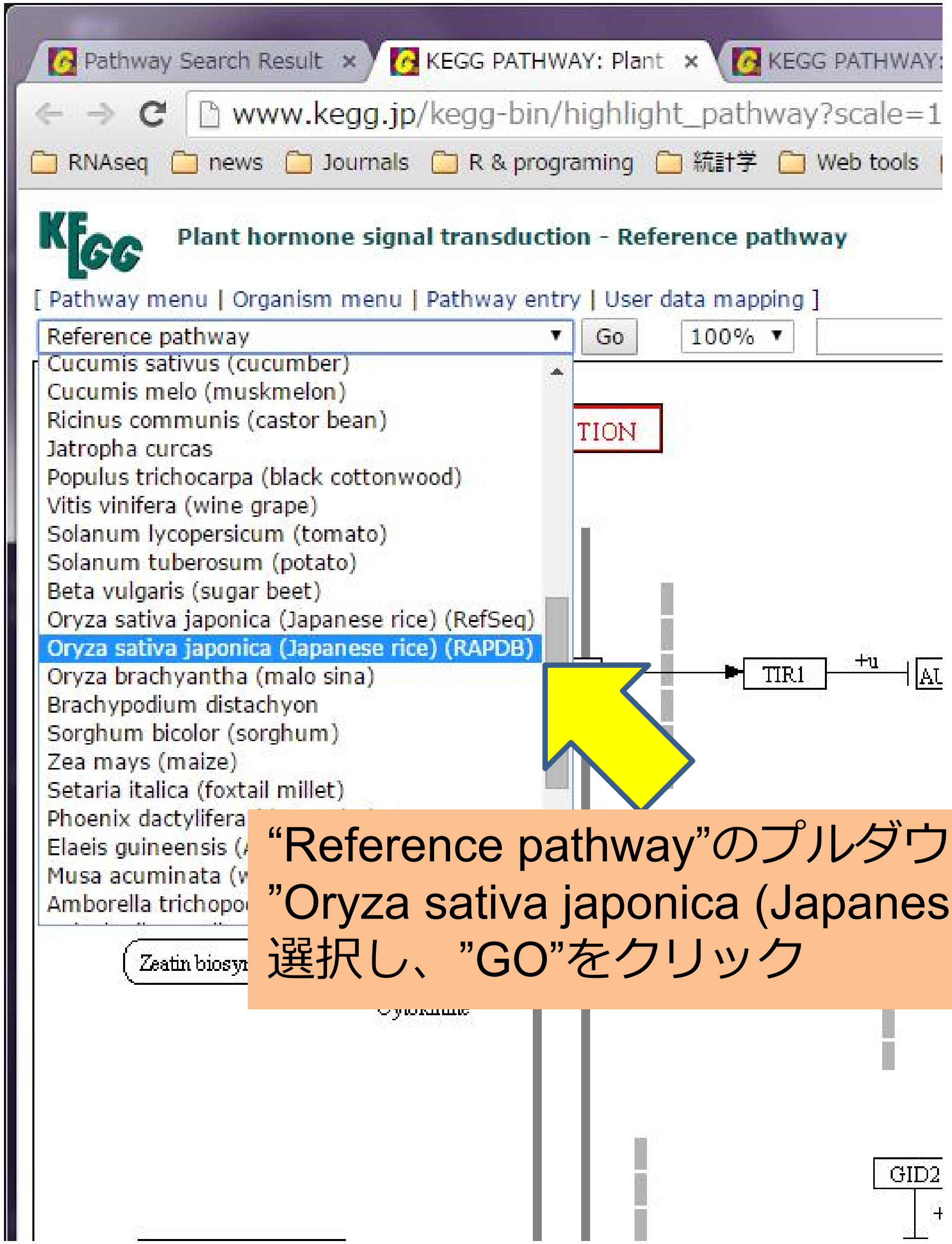
Number of entries in a page: 20 ▾ [Hide thumbnail]

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...

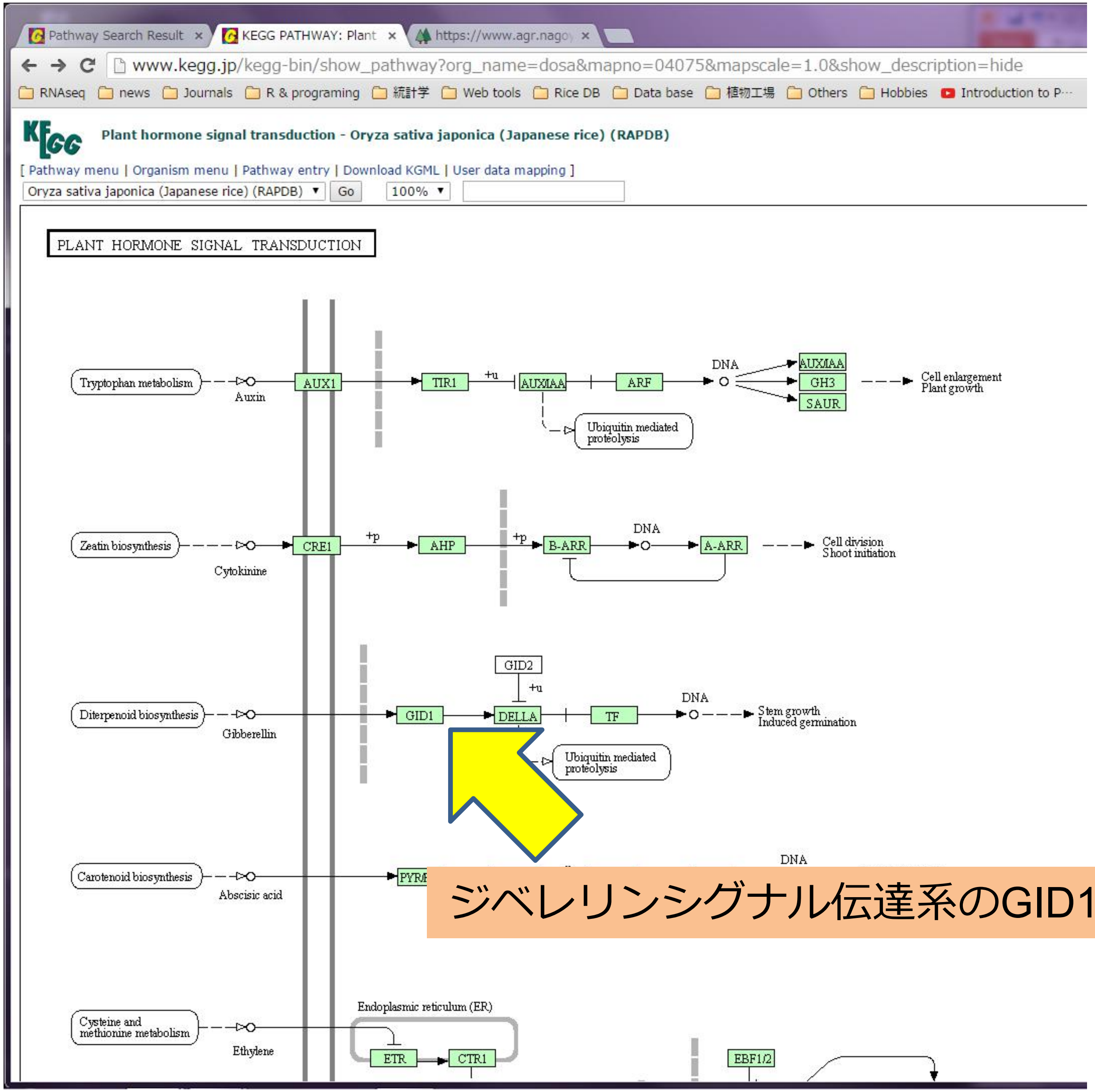
“Plant hormone signal transduction” のthumbnail imageをクリック

イネにおける植物ホルモンシグナル伝達系遺伝子



“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.nago ×

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

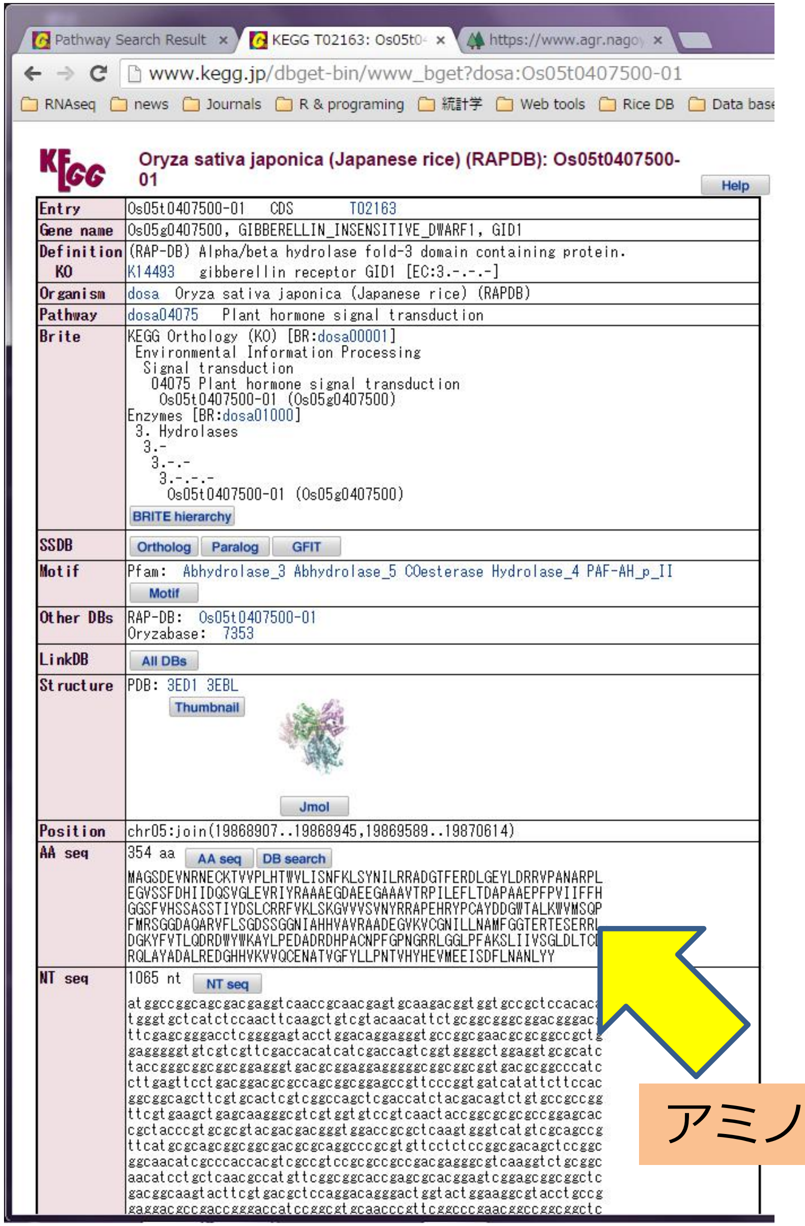
Plant hormone signal transduction - Oryza sativa japonica (Japanese rice) (RAPDB)

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

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

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



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) BRITE hierarchy
SSDB	Ortholog Paralog GFIT
Motif	Pfam: Abhydrolase_3 Abhydrolase_5 COesterase Hydrolase_4 PAF-AH_p_II Motif
Other DBs	RAP-DB: Os05t0407500-01 Oryzabase: 7353
LinkDB	All DBs
Structure	PDB: 3ED1 3EBL Thumbnail Jmol
Position	chr05:join(19868907..19868945,19869589..19870614)
AA seq	354 aa AA seq DB search MAGSDEVNRNECKTVVPLHTWVLISNFKLSYNILRRADGTFERDLGEYLDRRVPANARPL EGVSSFDHIIDQSVGLEVRIYRAAAEGDAEEGAAAVTRPILEFLTDAPAAEPFPVIIFFH GGSFVHSSASSTIYDSLCRRFVKLSKGVVVSVNYRRAPEHRYPCAYDDGWTALKWVMSQP FMRSGGDAQARVFLSGDSSGGNIAHHVAVRAADEGVKVCGNILLNAMFGGTERTESERRL DGKYFVTLQDRDWYWKAYLPEDADRDHPACNPFGPNGRRLGGLPFAKSLIIVSGLDLTC RQLAYADALREDGHHVKVVQCENATVGFYLLPNTVHYHEVMEEISDFLNANLYY
NT seq	1065 nt NT seq atggccggcagcgacgaggtcaaccgcaacgagtgcaagacggtggtgccgctccacac tgggtgctcatctccaacttcaagctgtcgtacaacattctgcggcgggcggacgggac ttcgagcgggacctcggggagtacctggacaggagggtgccggcgaacgcgcggccgct 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

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

MOTIF Search

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

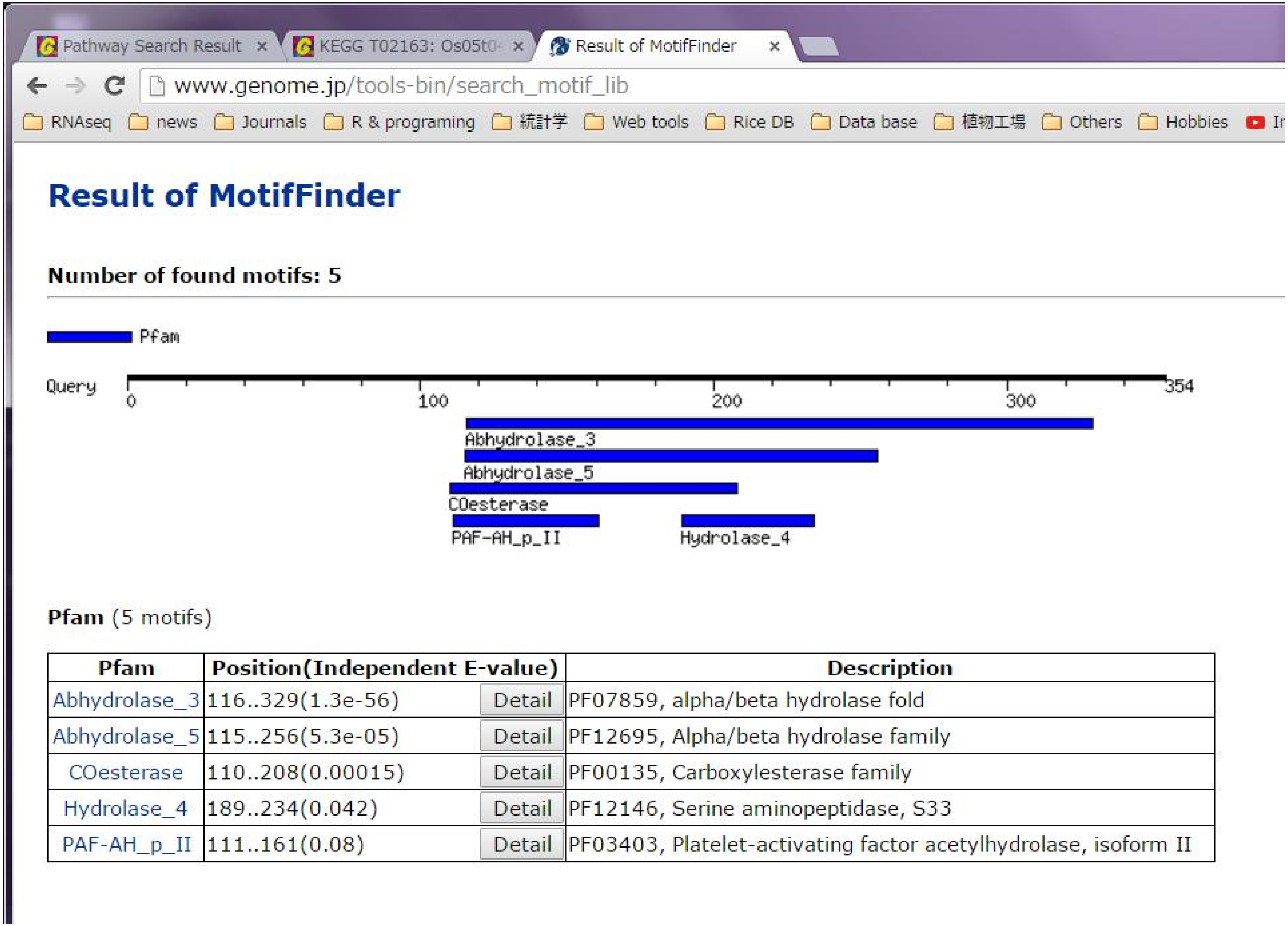
```
MAGSDEVNRNECKTVVPLHTWVLISNFKLSYNILRRADGTFERDLGEYLDRRVPANA
RPL
EGVSSFDHIIDQSVGLEVRIYRAAAEGDAEEGAAAVTRPILEFLTDAPAAEPFPVII
FFH
GGSFVHSSASSTIYDSLCRRFVKLSKGVVVSVNYRRAPEHRYPCAYDDGWTALKW
```

Select motif libraries : (Help)

Databases	Cut-off score (Click each database to g
☑ 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



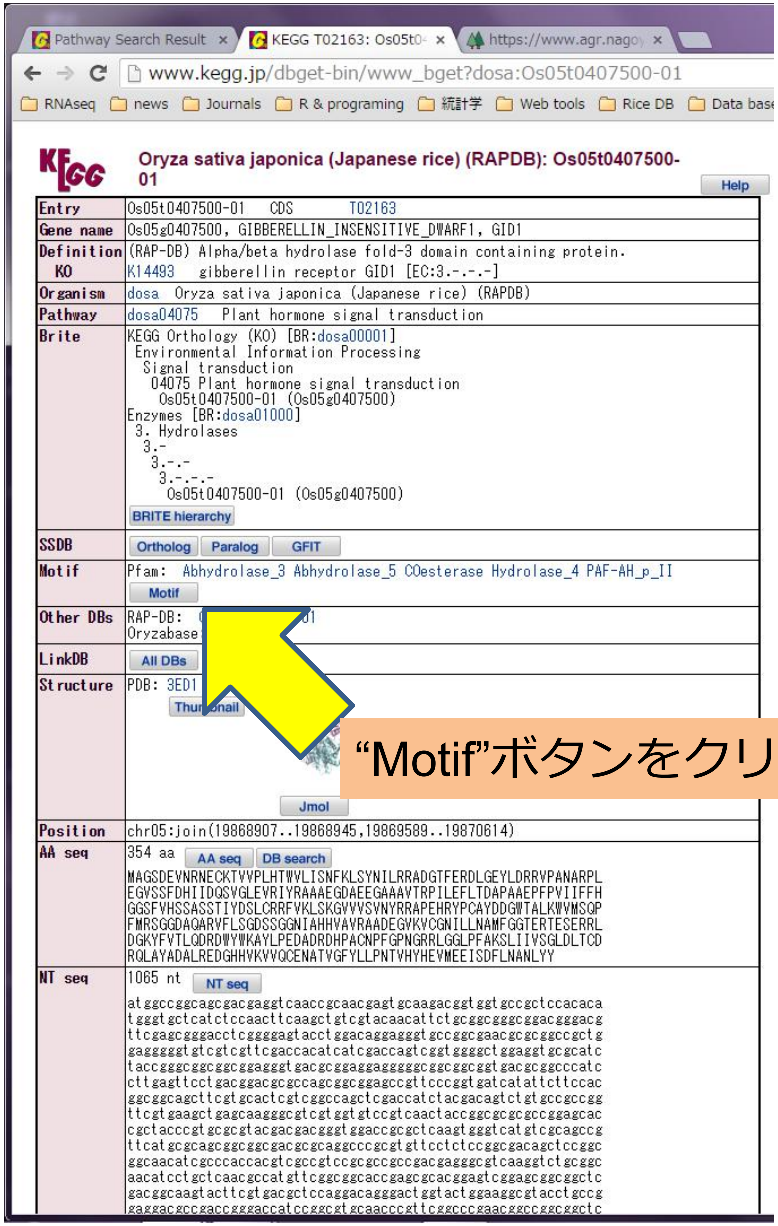
Result of MotifFinder

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



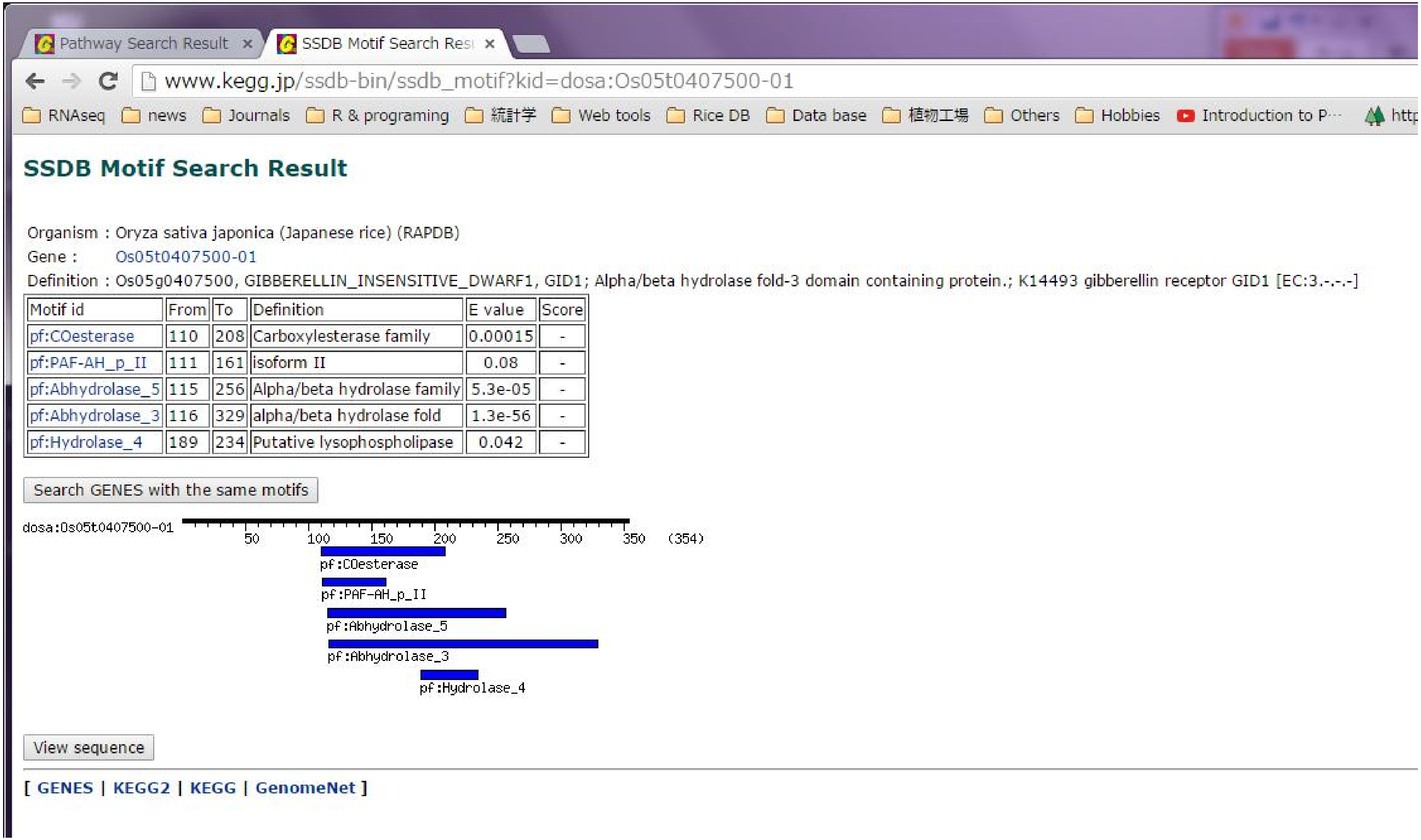
www.kegg.jp/dbget-bin/www_bget?dosa:Os05t0407500-01

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: Oryzabase
LinkDB	
Structure	PDB: 3ED1
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 taccgggcggcggcggagggtgacgcggaggaggggcggcggcggtgacgcggcccatc 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



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	-

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！？

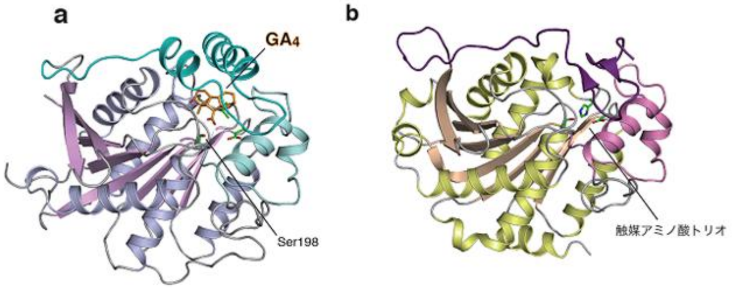


図１　リボンモデルで表示したジベレリン受容体とリパーゼの立体構造の比較
a ジベレリン受容体、b リパーゼ。両者の基本構造は非常によく似ている。a、bにおいてそれぞれ薄紫色、金色で示したのがα/β水解酵素型構造。a、bにおいてそれぞれ濃緑色、濃紫色で示したのがN末端のリッド（ふた）。

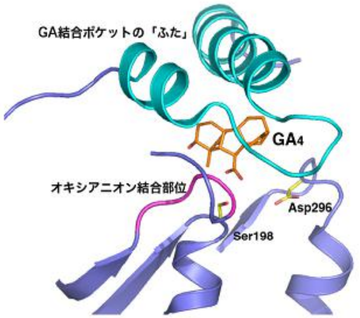
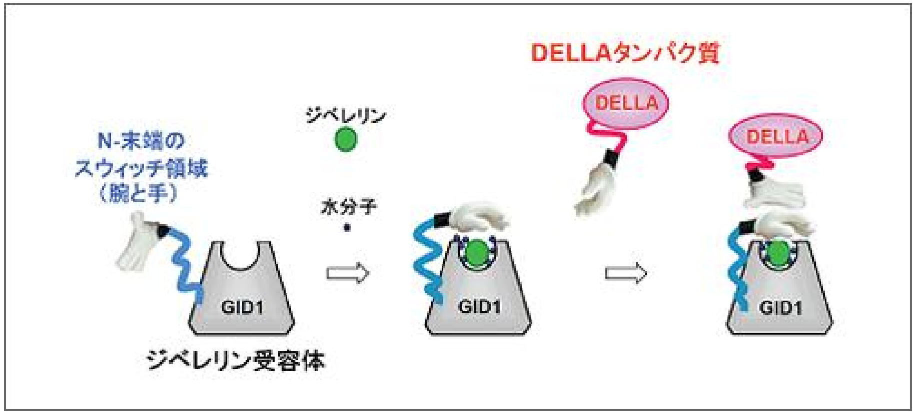


図２　ジベレリン受容体のジベレリン（GA）結合ポケットの拡大図
活性型ジベレリン(GA4)は炭素原子をオレンジ、酸素原子を赤で表示した。リパーゼ触媒アミノ酸トリオに相当するSer198とAsp296は、炭素原子を黄色、酸素原子を赤で表示した。オキシアニオン結合部位は紫色、ジベレリン結合ポケットの「ふた」は水色で表示した。

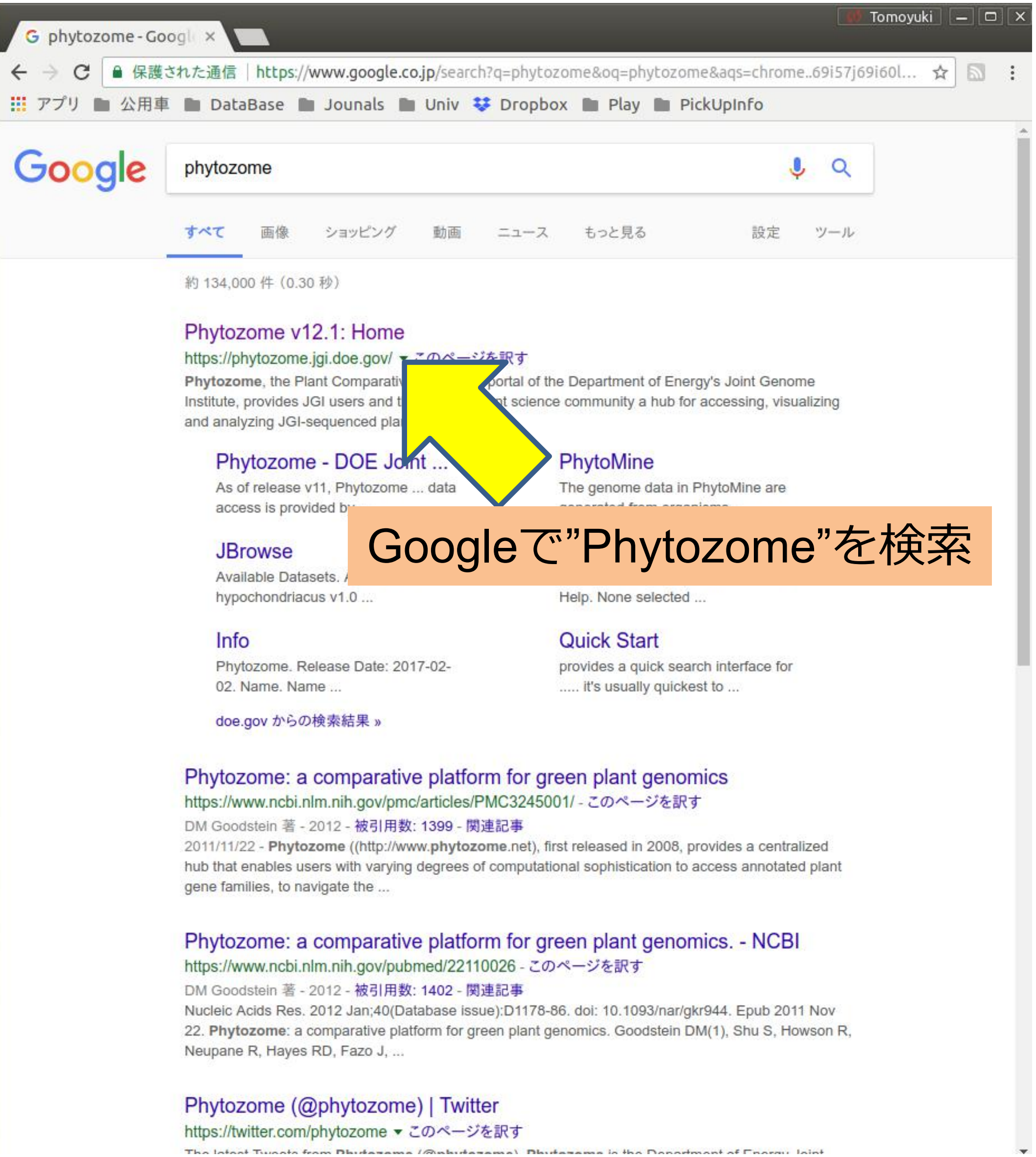
http://www.kyoto-u.ac.jp/static/ja/news_data/h/h1/news6/2008/081127_1.htm



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



約 134,000 件（0.30 秒）

Phytozome v12.1: Home
https://phytozome.jgi.doe.gov/
Phytozome, the Plant Comparativ … portal of the Department of Energy's Joint Genome Institute, provides JGI users and t … t science community a hub for accessing, visualizing and analyzing JGI-sequenced pla

Phytozome - DOE Jo nt ...
As of release v11, Phytozome ... data access is provided b

PhytoMine
The genome data in PhytoMine are

JBrowse
Available Datasets.
hypochondriacus v1.0 ...

Help. None selected ...

Info
Phytozome. Release Date: 2017-02-02. Name. Name ...

Quick Start
provides a quick search interface for ..... it's usually quickest to ...

doe.gov からの検索結果 »

Phytozome: a comparative platform for green plant genomics
https://www.ncbi.nlm.nih.gov/pmc/articles/PMC3245001/ - このページを訳す
DM Goodstein 著 - 2012 - 被引用数: 1399 - 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. - NCBI
https://www.ncbi.nlm.nih.gov/pubmed/22110026 - このページを訳す
DM Goodstein 著 - 2012 - 被引用数: 1402 - 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, ...

Phytozome (@phytozome) | Twitter
https://twitter.com/phytozome ▾ このページを訳す

Googleで”Phytozome”を検索

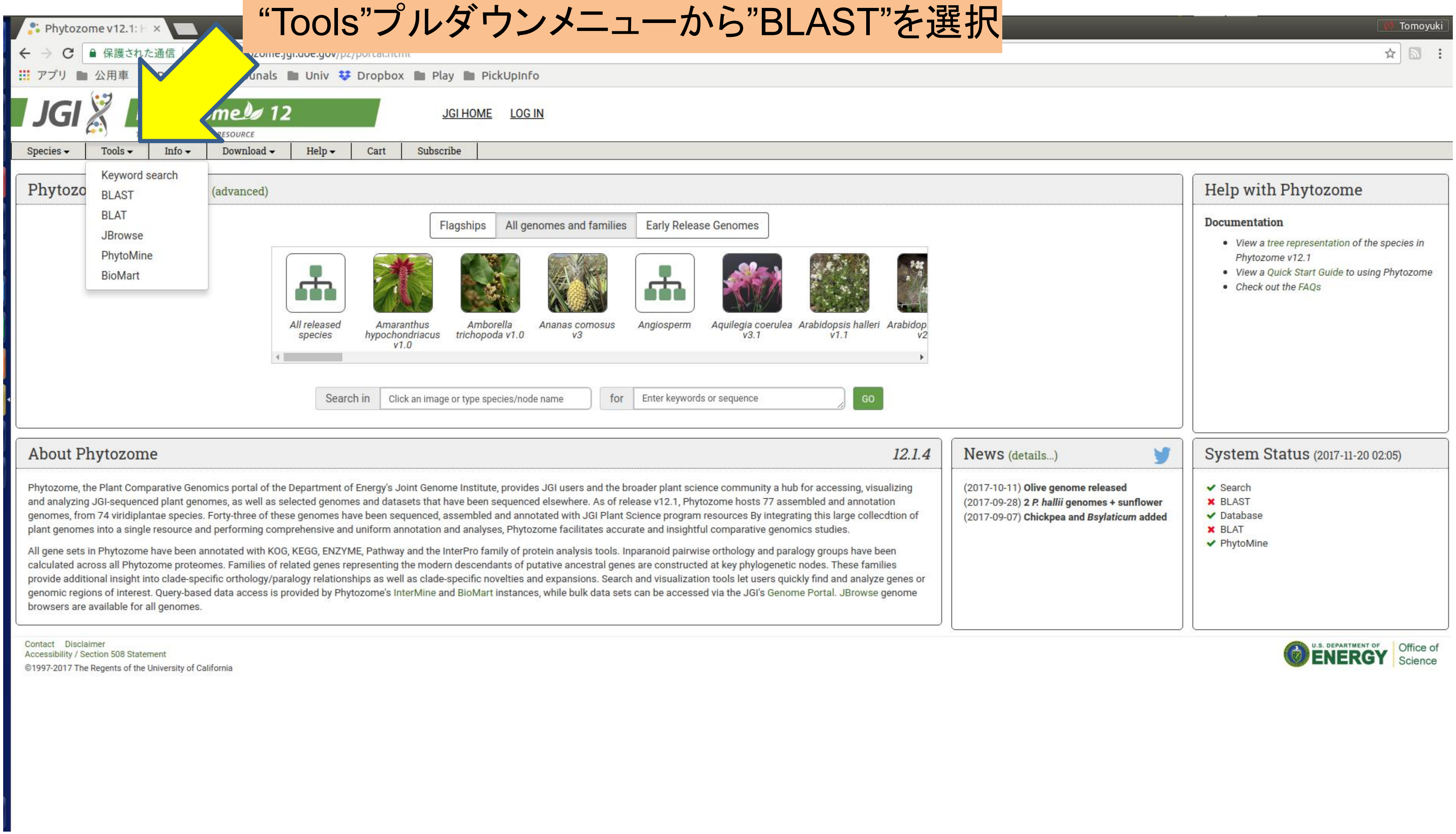
Phytozome
数十の植物種のゲノム情報を統合し、そのゲノム情報を比較する目的に特化したデータベース。

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



Help with Phytozome

Documentation

- View a tree representation of the species in Phytozome v12.1
- View a Quick Start Guide to using Phytozome
- Check out the FAQs

About Phytozome

12.1.4

Phytozome, the Plant Comparative Genomics portal of the Department of Energy's Joint Genome Institute, provides JGI users and the broader plant science community a hub for accessing, visualizing and analyzing JGI-sequenced plant genomes, as well as selected genomes and datasets that have been sequenced elsewhere. As of release v12.1, Phytozome hosts 77 assembled and annotation genomes, from 74 viridiplantae species. Forty-three of these genomes have been sequenced, assembled and annotated with JGI Plant Science program resources By integrating this large collecdtion of plant genomes into a single resource and performing comprehensive and uniform annotation and analyses, Phytozome facilitates accurate and insightful comparative genomics studies.

All gene sets in Phytozome have been annotated with KOG, KEGG, ENZYME, Pathway and the InterPro family of protein analysis tools. Inparanoid pairwise orthology and paralogy groups have been calculated across all Phytozome proteomes. Families of related genes representing the modern descendants of putative ancestral genes are constructed at key phylogenetic nodes. These families provide additional insight into clade-specific orthology/paralogy relationships as well as clade-specific novelties and expansions. Search and visualization tools let users quickly find and analyze genes or genomic regions of interest. Query-based data access is provided by Phytozome's InterMine and BioMart instances, while bulk data sets can be accessed via the JGI's Genome Portal. JBrowse genome browsers are available for all genomes.

News (details...)

(2017-10-11) **Olive genome released**
(2017-09-28) **2 *P. hallii* genomes + sunflower**
(2017-09-07) **Chickpea and *Bsylaticum* added**

System Status (2017-11-20 02:05)

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

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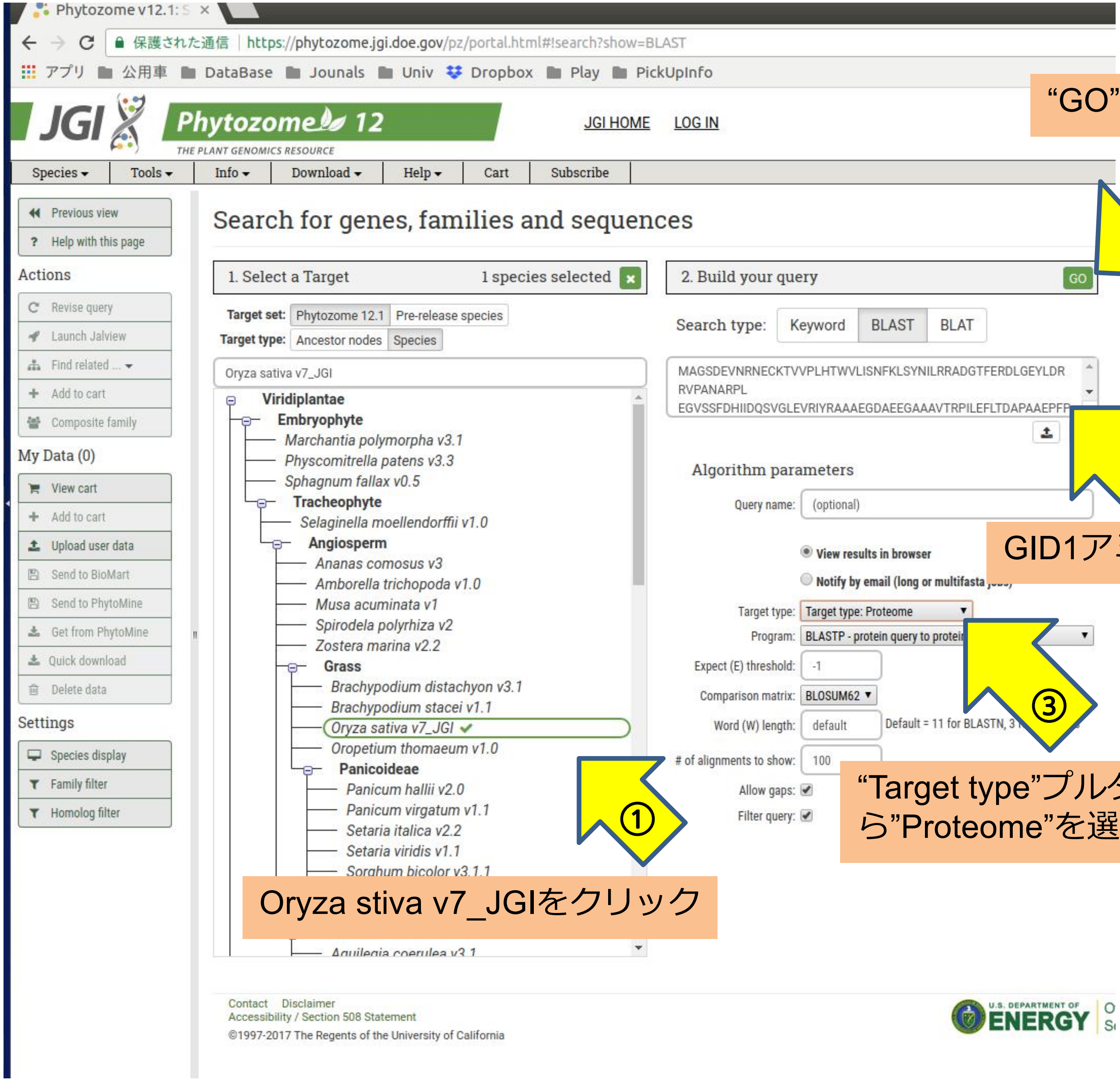
U.S. DEPARTMENT OF ENERGY Office of Science

Phytozomeでお手軽比較ゲノミクス的解析



Search for genes, families and sequences

1. Select a Target 1 species selected

Target set: Phytozome 12.1 | Pre-release species

Target type: Ancestor nodes | Species

Oryza sativa v7_JGI

- Viridiplantae
  - Embryophyte
    - *Marchantia polymorpha v3.1*
    - *Physcomitrella patens v3.3*
    - *Sphagnum fallax v0.5*
    - Tracheophyte
      - *Selaginella moellendorffii v1.0*
      - Angiosperm
        - *Ananas comosus v3*
        - *Amborella trichopoda v1.0*
        - *Musa acuminata v1*
        - *Spirodela polyrhiza v2*
        - *Zostera marina v2.2*
        - Grass
          - *Brachypodium distachyon v3.1*
          - *Brachypodium stacei v1.1*
          - *Oryza sativa v7_JGI* ✓
          - *Oropetium thomaeum v1.0*
          - Panicoideae
            - *Panicum hallii v2.0*
            - *Panicum virgatum v1.1*
            - *Setaria italica v2.2*
            - *Setaria viridis v1.1*
            - *Sorghum bicolor v3.1.1*
        - *Aquilegia coerulea v3.1*

2. Build your query

Search type: BLAST

MAGSDEVNRNECKTVVPLHTWVLISNFKLSYNILRRADGTFERDLGEYLDR
RVPANARPL
EGVSSFDHIIDQSVGLEVRIYRAAAEGDAEEGAAAVTRPILEFLTDAPAAEPFP

Algorithm parameters

Query name: (optional)

● View results in browser

○ Notify by email (long or multifasta jobs)

Target type: Target type: Proteome

Program: BLASTP - protein query to protein

Expect (E) threshold: -1

Comparison matrix: BLOSUM62

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

# of alignments to show: 100

Allow gaps: ☑

Filter query: ☑

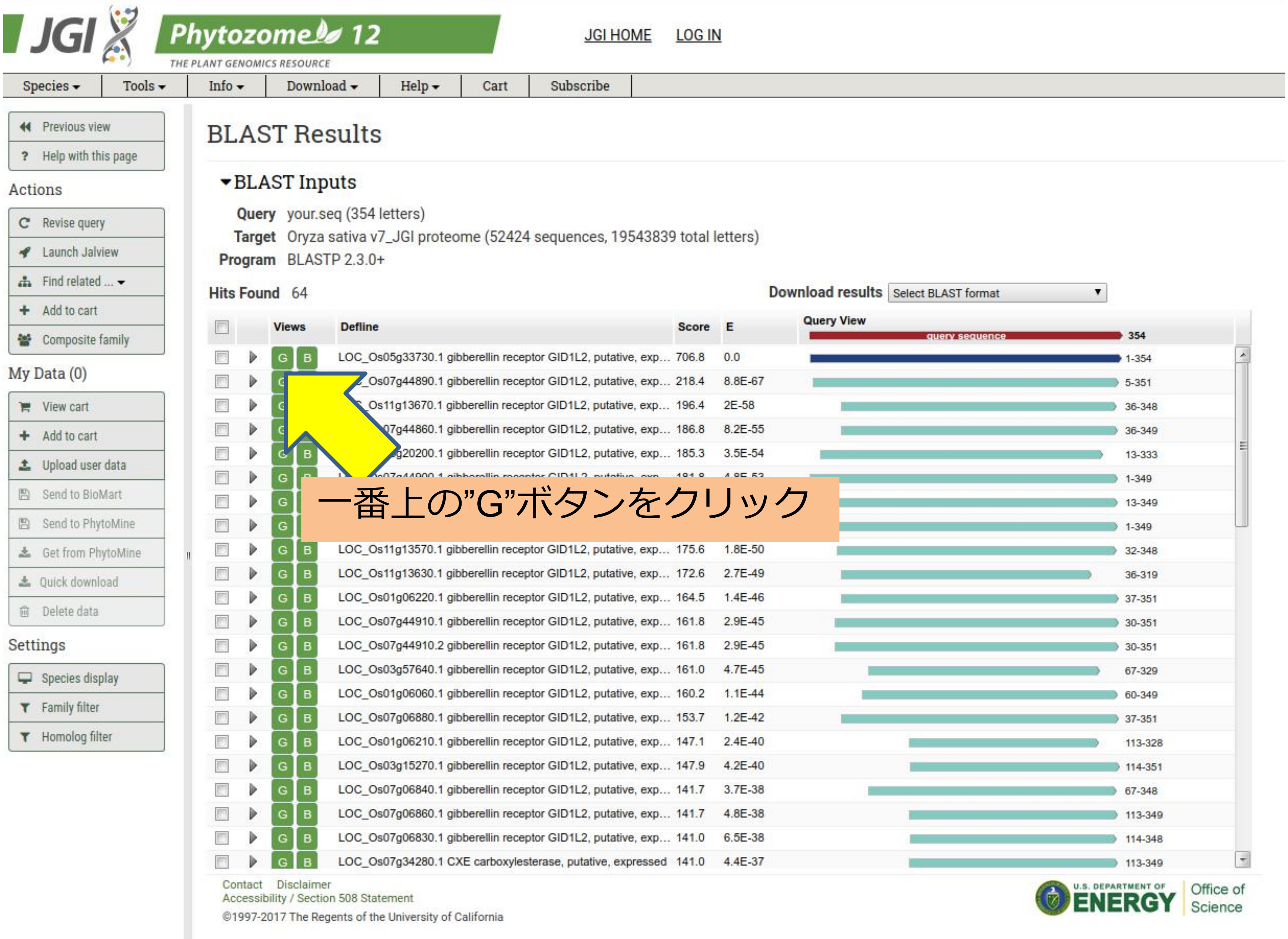
① Oryza stiva v7_JGIをクリック

② GID1アミノ酸配列をペースト

③ “Target type”プルダウンメニューから”Proteome”を選択

④ “GO”をクリック

Phytozomeでお手軽比較ゲノミクス的解析



BLAST Results

▾BLAST Inputs

Query your.seq (354 letters)
Target Oryza sativa v7_JGI proteome (52424 sequences, 19543839 total letters)
Program BLASTP 2.3.0+

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
☐	▶		_Os07g44890.1 gibberellin receptor GID1L2, putative, exp...	218.4	8.8E-67	5-351
☐	▶		_Os11g13670.1 gibberellin receptor GID1L2, putative, exp...	196.4	2E-58	36-348
☐	▶		07g44860.1 gibberellin receptor GID1L2, putative, exp...	186.8	8.2E-55	36-349
☐	▶	B	g20200.1 gibberellin receptor GID1L2, putative, exp...	185.3	3.5E-54	13-333
☐	▶	G				1-349
☐	▶	G				13-349
☐	▶	G				1-349
☐	▶	G B	LOC_Os11g13570.1 gibberellin receptor GID1L2, putative, exp...	175.6	1.8E-50	32-348
☐	▶	G B	LOC_Os11g13630.1 gibberellin receptor GID1L2, putative, exp...	172.6	2.7E-49	36-319
☐	▶	G B	LOC_Os01g06220.1 gibberellin receptor GID1L2, putative, exp...	164.5	1.4E-46	37-351
☐	▶	G B	LOC_Os07g44910.1 gibberellin receptor GID1L2, putative, exp...	161.8	2.9E-45	30-351
☐	▶	G B	LOC_Os07g44910.2 gibberellin receptor GID1L2, putative, exp...	161.8	2.9E-45	30-351
☐	▶	G B	LOC_Os03g57640.1 gibberellin receptor GID1L2, putative, exp...	161.0	4.7E-45	67-329
☐	▶	G B	LOC_Os01g06060.1 gibberellin receptor GID1L2, putative, exp...	160.2	1.1E-44	60-349
☐	▶	G B	LOC_Os07g06880.1 gibberellin receptor GID1L2, putative, exp...	153.7	1.2E-42	37-351
☐	▶	G B	LOC_Os01g06210.1 gibberellin receptor GID1L2, putative, exp...	147.1	2.4E-40	113-328
☐	▶	G B	LOC_Os03g15270.1 gibberellin receptor GID1L2, putative, exp...	147.9	4.2E-40	114-351
☐	▶	G B	LOC_Os07g06840.1 gibberellin receptor GID1L2, putative, exp...	141.7	3.7E-38	67-348
☐	▶	G B	LOC_Os07g06860.1 gibberellin receptor GID1L2, putative, exp...	141.7	4.8E-38	113-349
☐	▶	G B	LOC_Os07g06830.1 gibberellin receptor GID1L2, putative, exp...	141.0	6.5E-38	114-348
☐	▶	G B	LOC_Os07g34280.1 CXE carboxylesterase, putative, expressed	141.0	4.4E-37	113-349

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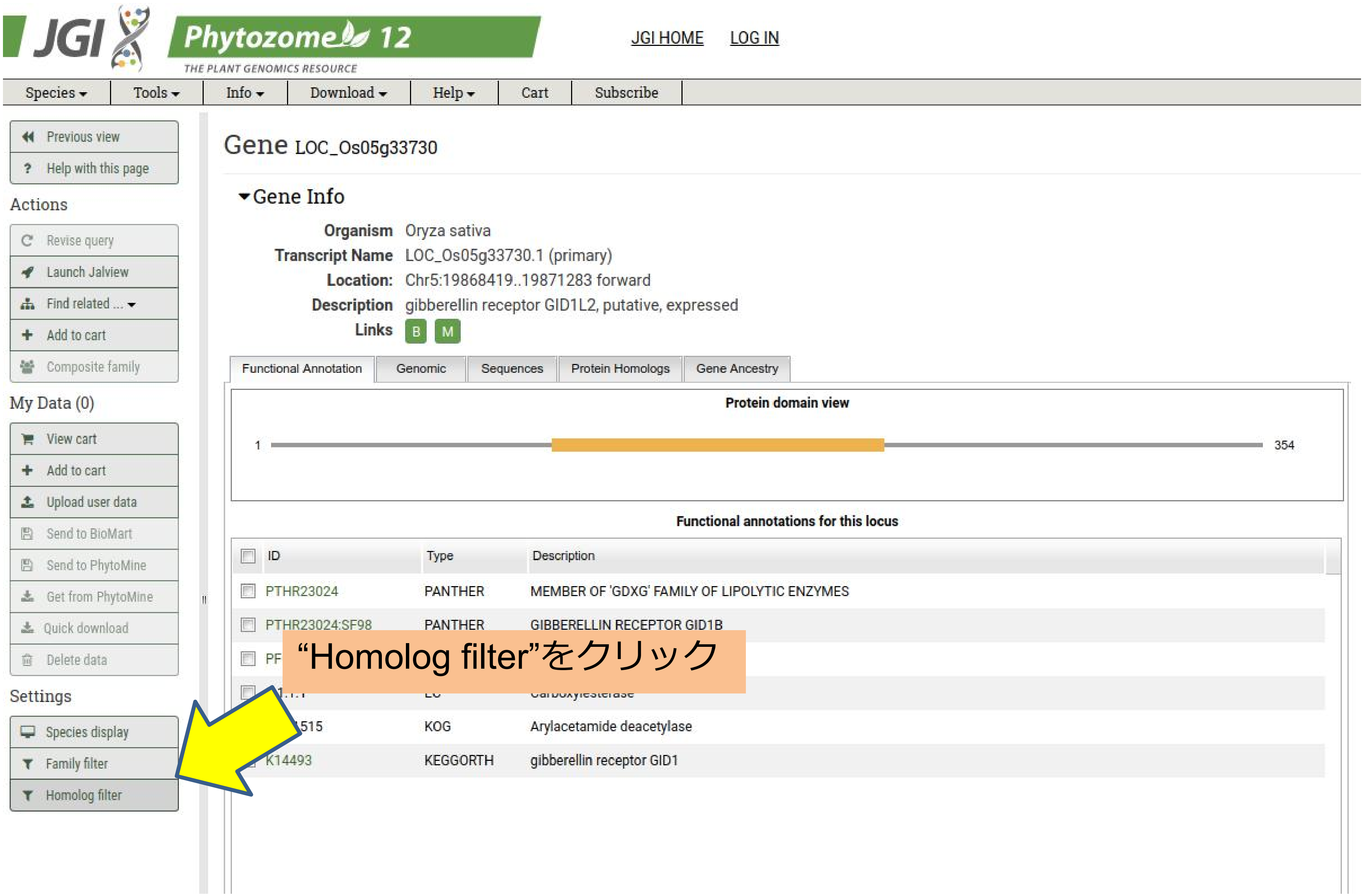
一番上の”G”ボタンをクリック

Phytozomeでお手軽比較ゲノミクス的解析



Gene LOC_Os05g33730

Gene Info

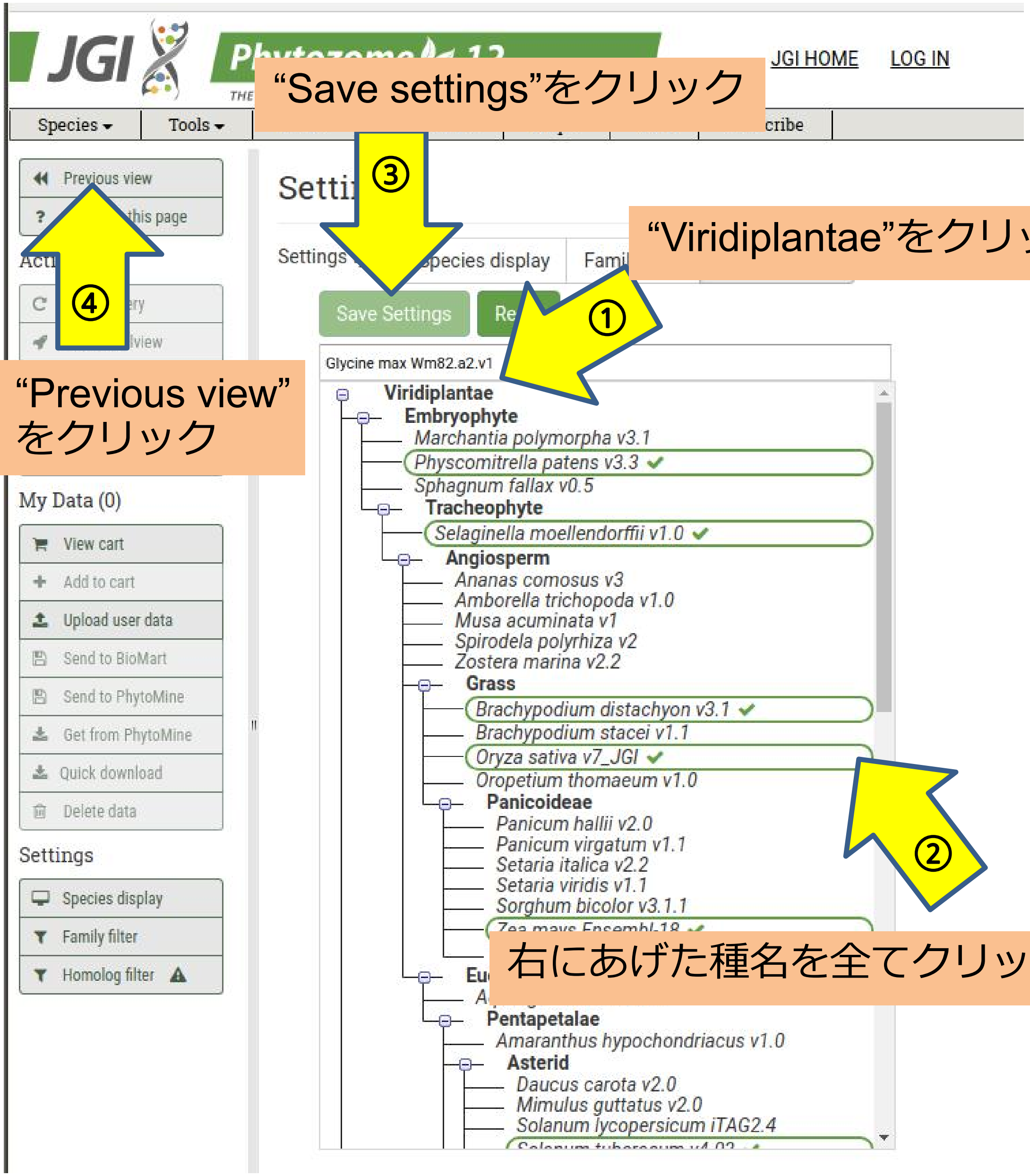
Organism Oryza sativa
Transcript Name LOC_Os05g33730.1 (primary)
Location: Chr5:19868419..19871283 forward
Description gibberellin receptor GID1L2, putative, expressed
Links B M

Functional annotations for this locus

☐	ID	Type	Description
☐	PTHR23024	PANTHER	MEMBER OF 'GDXG' FAMILY OF LIPOLYTIC ENZYMES
☐	PTHR23024:SF98	PANTHER	GIBBERELLIN RECEPTOR GID1B
☐	PF		
☐	.1.1.1	EC	Carboxylesterase
	515	KOG	Arylacetamide deacetylase
	K14493	KEGGORTH	gibberellin receptor GID1

“Homolog filter”をクリック

Phytozomeでお手軽比較ゲノミクス的解析



“Save settings”をクリック

③

“Viridiplantae”をクリック

①

“Previous view”
をクリック

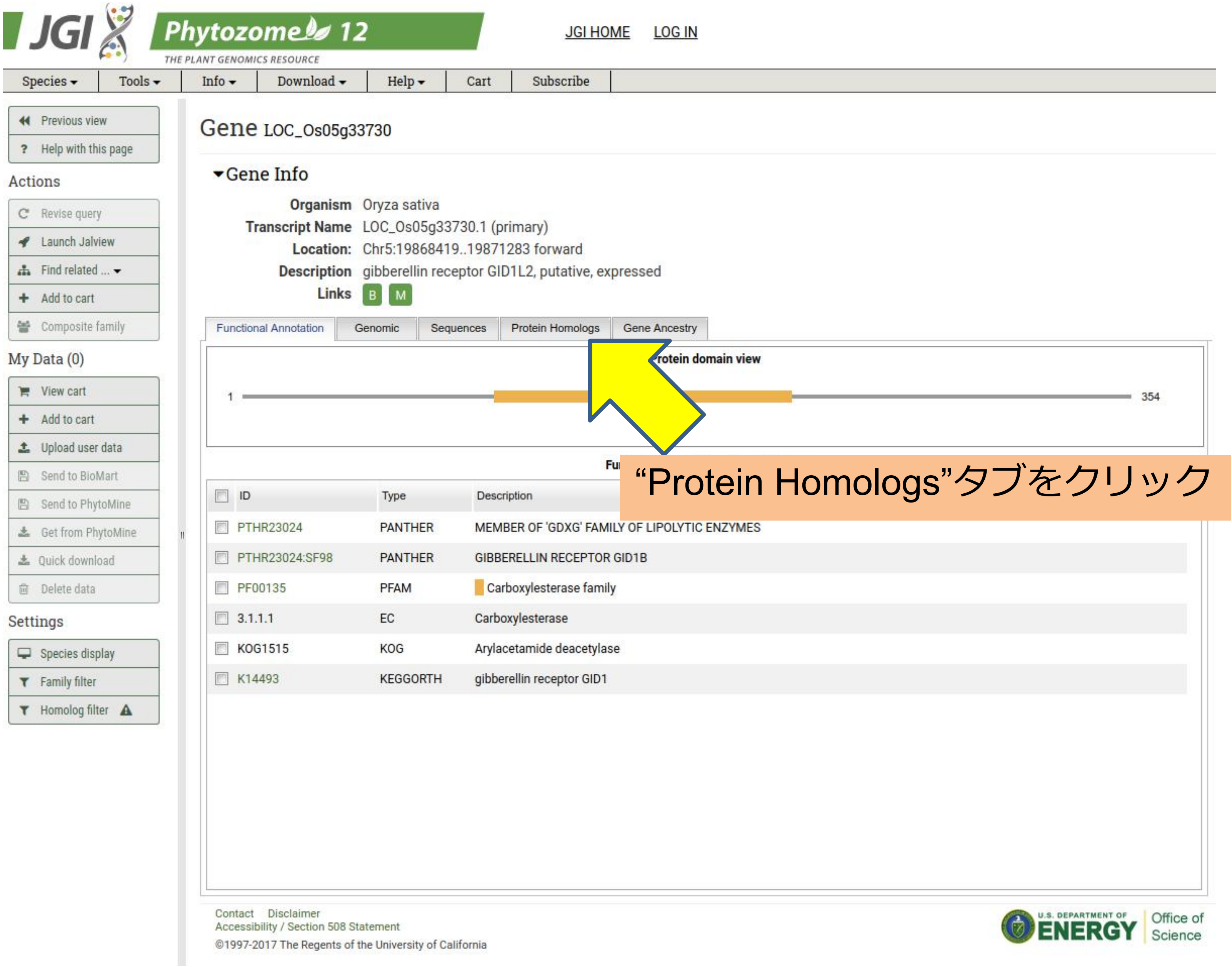
④

②

右にあげた種名を全てクリック

Embryophyte
Physcomitrella patens v3.3
Tracheophyte
Selaginella moellendorffii v1.0
Grass
Brachypodium distachyon v3.1
Oryza sativa v7_JGI
Panicoideae
Zea mays Ensembl-18
Asterid
Solanum tuberosum v4.03
Malpighiales
Populus trichocarpa v3.0
Citrus
Citrus sinensis v1.1
Brassicaceae
Arabidopsis thaliana TAIR10
Fabidae
Glycine max Wm82.a2.v1

Phytozomeでお手軽比較ゲノミクス的解析



Gene LOC_Os05g33730

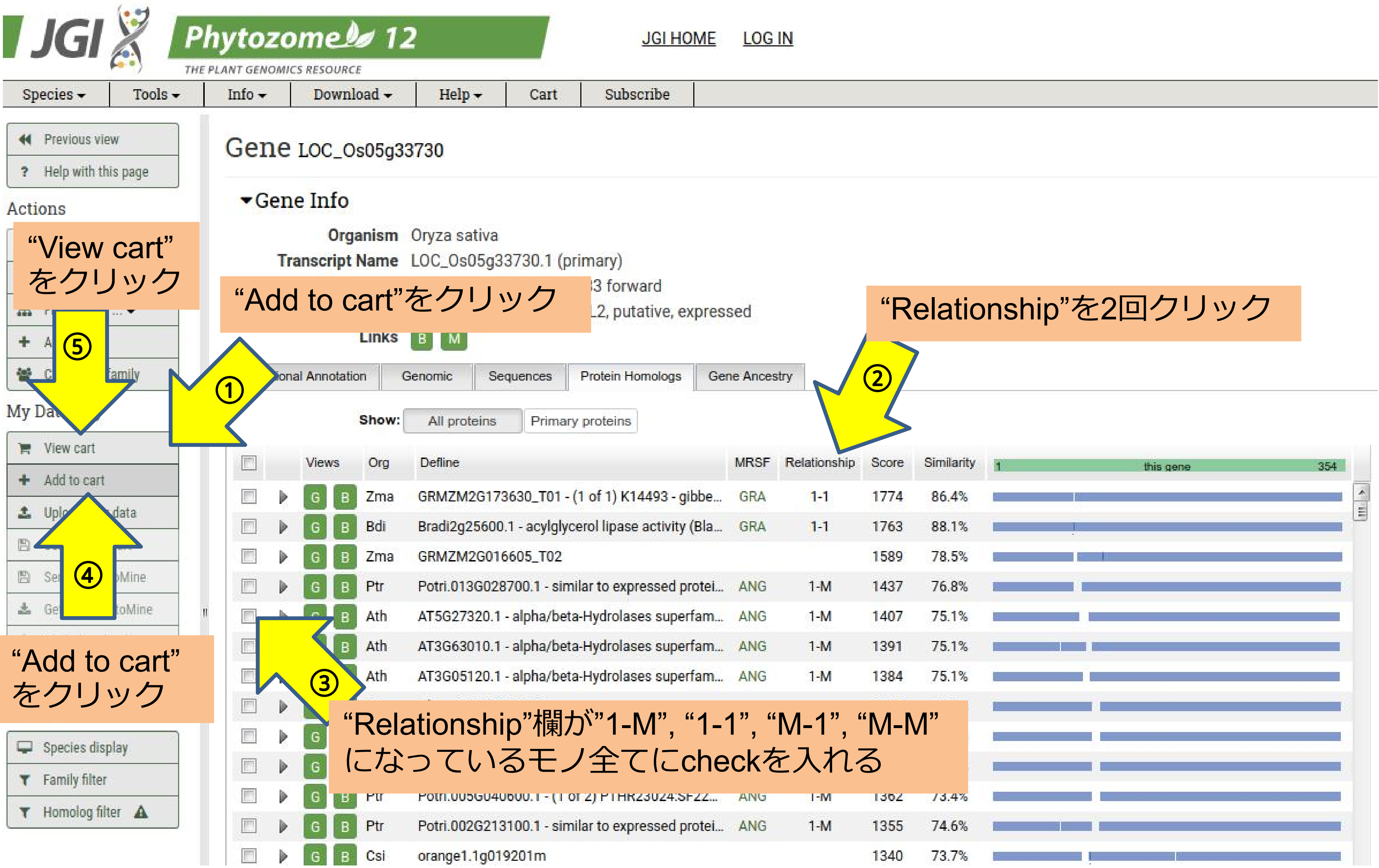
Gene Info

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

☐	ID	Type	Description
☐	PTHR23024	PANTHER	MEMBER OF 'GDXG' FAMILY OF LIPOLYTIC ENZYMES
☐	PTHR23024:SF98	PANTHER	GIBBERELLIN RECEPTOR GID1B
☐	PF00135	PFAM	🟧 Carboxylesterase family
☐	3.1.1.1	EC	Carboxylesterase
☐	KOG1515	KOG	Arylacetamide deacetylase
☐	K14493	KEGGORTH	gibberellin receptor GID1

“Protein Homologs”タブをクリック

Phytozomeでお手軽比較ゲノミクス的解析



Gene LOC_Os05g33730

Organism Oryza sativa
Transcript Name LOC_Os05g33730.1 (primary)

Show: All proteins | Primary proteins

☐	Views	Org	Define	MRSF	Relationship	Score	Similarity
☐	G B	Zma	GRMZM2G173630_T01 - (1 of 1) K14493 - gibbe...	GRA	1-1	1774	86.4%
☐	G B	Bdi	Bradi2g25600.1 - acylglycerol lipase activity (Bla...	GRA	1-1	1763	88.1%
☐	G B	Zma	GRMZM2G016605_T02			1589	78.5%
☐	G B	Ptr	Potri.013G028700.1 - similar to expressed protei...	ANG	1-M	1437	76.8%
☐	B	Ath	AT5G27320.1 - alpha/beta-Hydrolases superfam...	ANG	1-M	1407	75.1%
☐	B	Ath	AT3G63010.1 - alpha/beta-Hydrolases superfam...	ANG	1-M	1391	75.1%
☐		Ath	AT3G05120.1 - alpha/beta-Hydrolases superfam...	ANG	1-M	1384	75.1%
☐	G B	Ptr	Potri.005G040600.1 - (1 of 2) PTHR23024:SF22...	ANG	1-M	1362	73.4%
☐	G B	Ptr	Potri.002G213100.1 - similar to expressed protei...	ANG	1-M	1355	74.6%
☐	G B	Csi	orange1.1g019201m			1340	73.7%

①
“Add to cart”をクリック

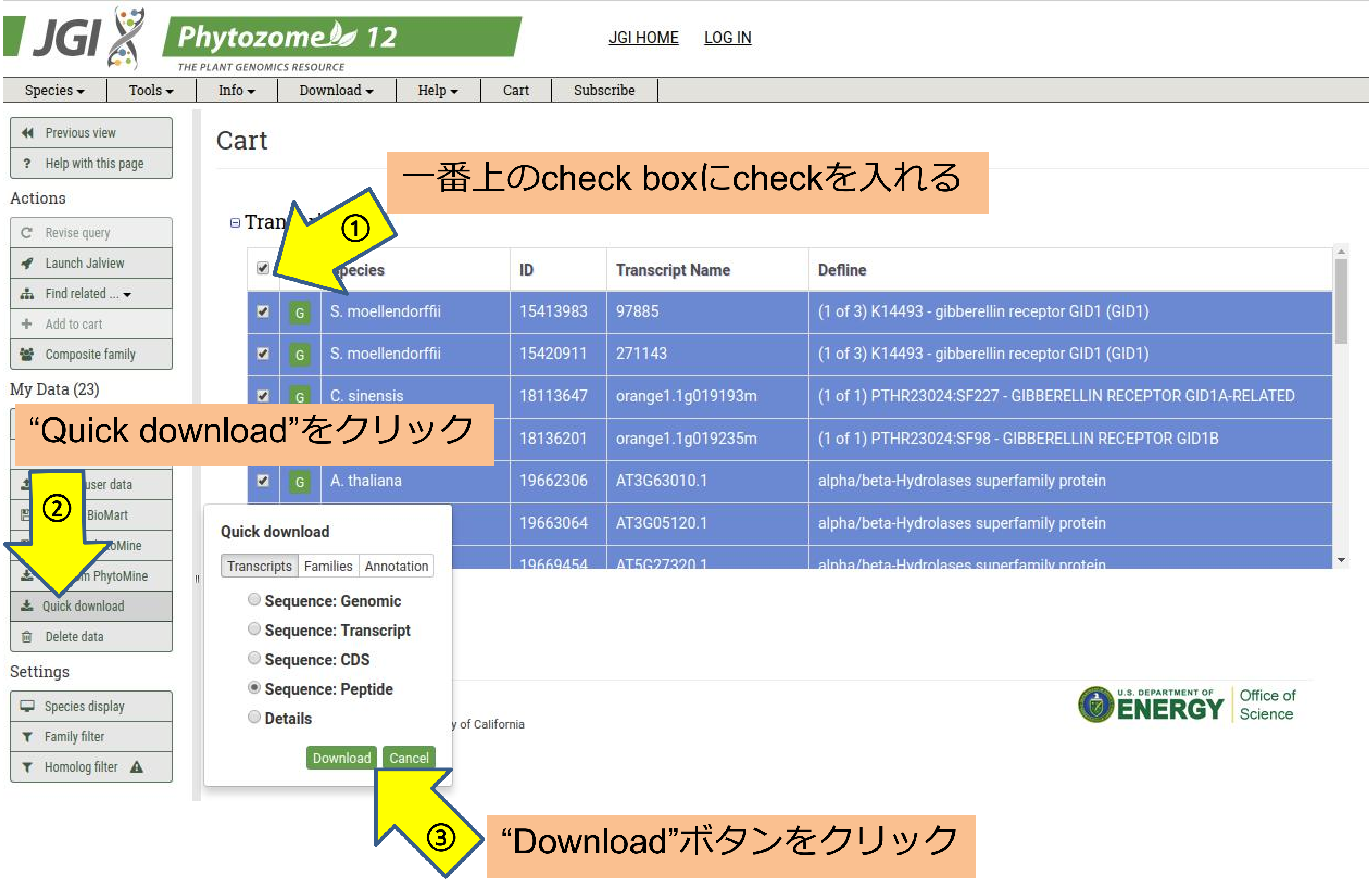
②
“Relationship”を2回クリック

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



Cart

Tran

① 一番上のcheck boxにcheckを入れる

☑		pecies	ID	Transcript Name	Define
☑	G	S. moellendorffii	15413983	97885	(1 of 3) K14493 - gibberellin receptor GID1 (GID1)
☑	G	S. moellendorffii	15420911	271143	(1 of 3) K14493 - gibberellin receptor GID1 (GID1)
☑	G	C. sinensis	18113647	orange1.1g019193m	(1 of 1) PTHR23024:SF227 - GIBBERELLIN RECEPTOR GID1A-RELATED
			18136201	orange1.1g019235m	(1 of 1) PTHR23024:SF98 - GIBBERELLIN RECEPTOR GID1B
☑	G	A. thaliana	19662306	AT3G63010.1	alpha/beta-Hydrolases superfamily protein
			19663064	AT3G05120.1	alpha/beta-Hydrolases superfamily protein
			19669454	AT5G27320.1	alpha/beta-Hydrolases superfamily protein

② “Quick download”をクリック

Quick download

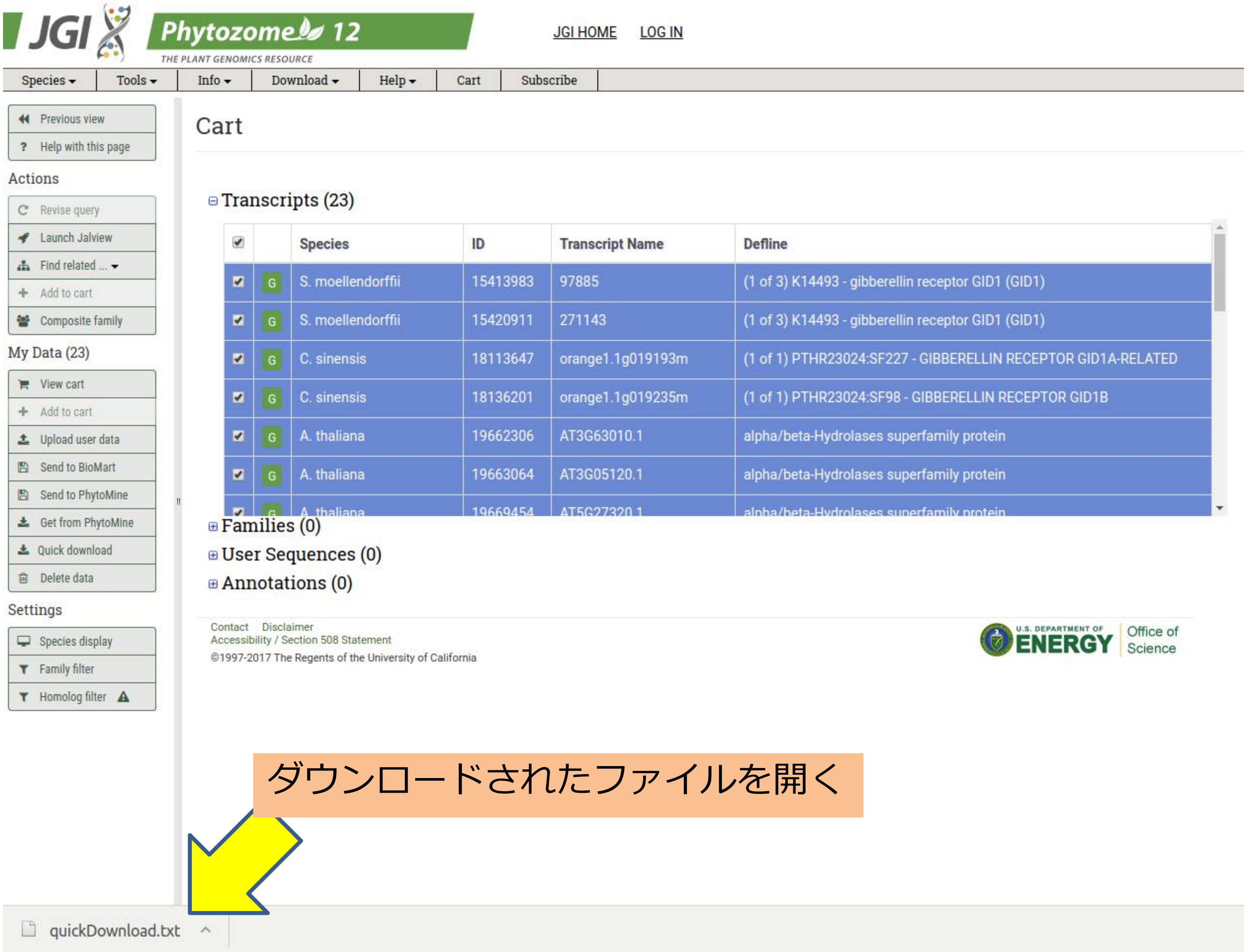
Transcripts | Families | Annotation

- ○ Sequence: Genomic
- ○ Sequence: Transcript
- ○ Sequence: CDS
- ● Sequence: Peptide
- ○ Details

Download　Cancel

③ “Download”ボタンをクリック

Phytozomeでお手軽比較ゲノミクス的解析



Cart

⊟ Transcripts (23)

☑		Species	ID	Transcript Name	Defline
☑	G	S. moellendorffii	15413983	97885	(1 of 3) K14493 - gibberellin receptor GID1 (GID1)
☑	G	S. moellendorffii	15420911	271143	(1 of 3) K14493 - gibberellin receptor GID1 (GID1)
☑	G	C. sinensis	18113647	orange1.1g019193m	(1 of 1) PTHR23024:SF227 - GIBBERELLIN RECEPTOR GID1A-RELATED
☑	G	C. sinensis	18136201	orange1.1g019235m	(1 of 1) PTHR23024:SF98 - GIBBERELLIN RECEPTOR GID1B
☑	G	A. thaliana	19662306	AT3G63010.1	alpha/beta-Hydrolases superfamily protein
☑	G	A. thaliana	19663064	AT3G05120.1	alpha/beta-Hydrolases superfamily protein
☑	G	A. thaliana	19669454	AT5G27320.1	alpha/beta-Hydrolases superfamily protein

⊞ Families (0)

⊞ User Sequences (0)

⊞ Annotations (0)

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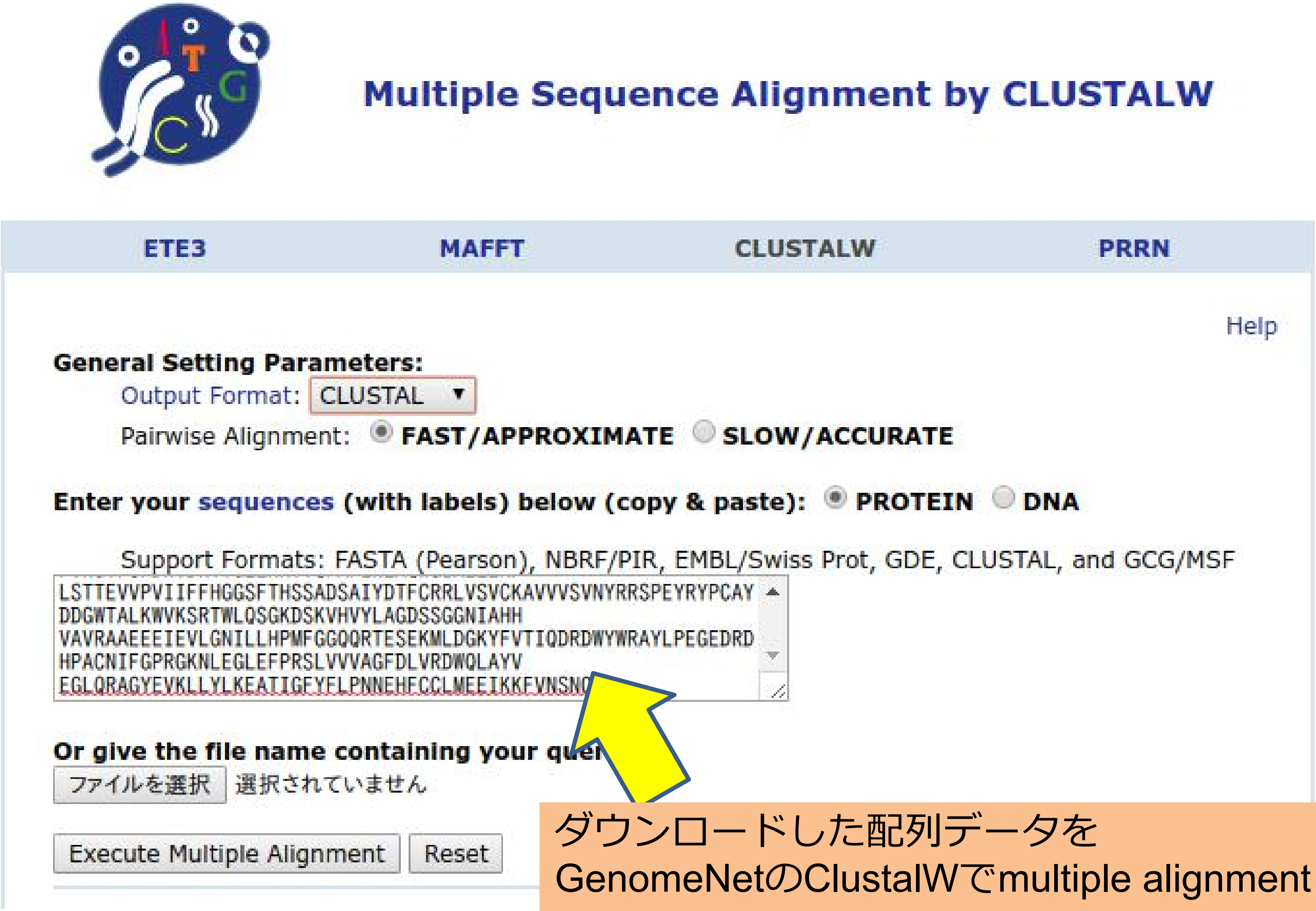
ダウンロードされたファイルを開く

Phytozomeでお手軽比較ゲノミクス的解析



General Setting Parameters:

Output Format: CLUSTAL ▼

Pairwise Alignment: ● FAST/APPROXIMATE ○ SLOW/ACCURATE

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

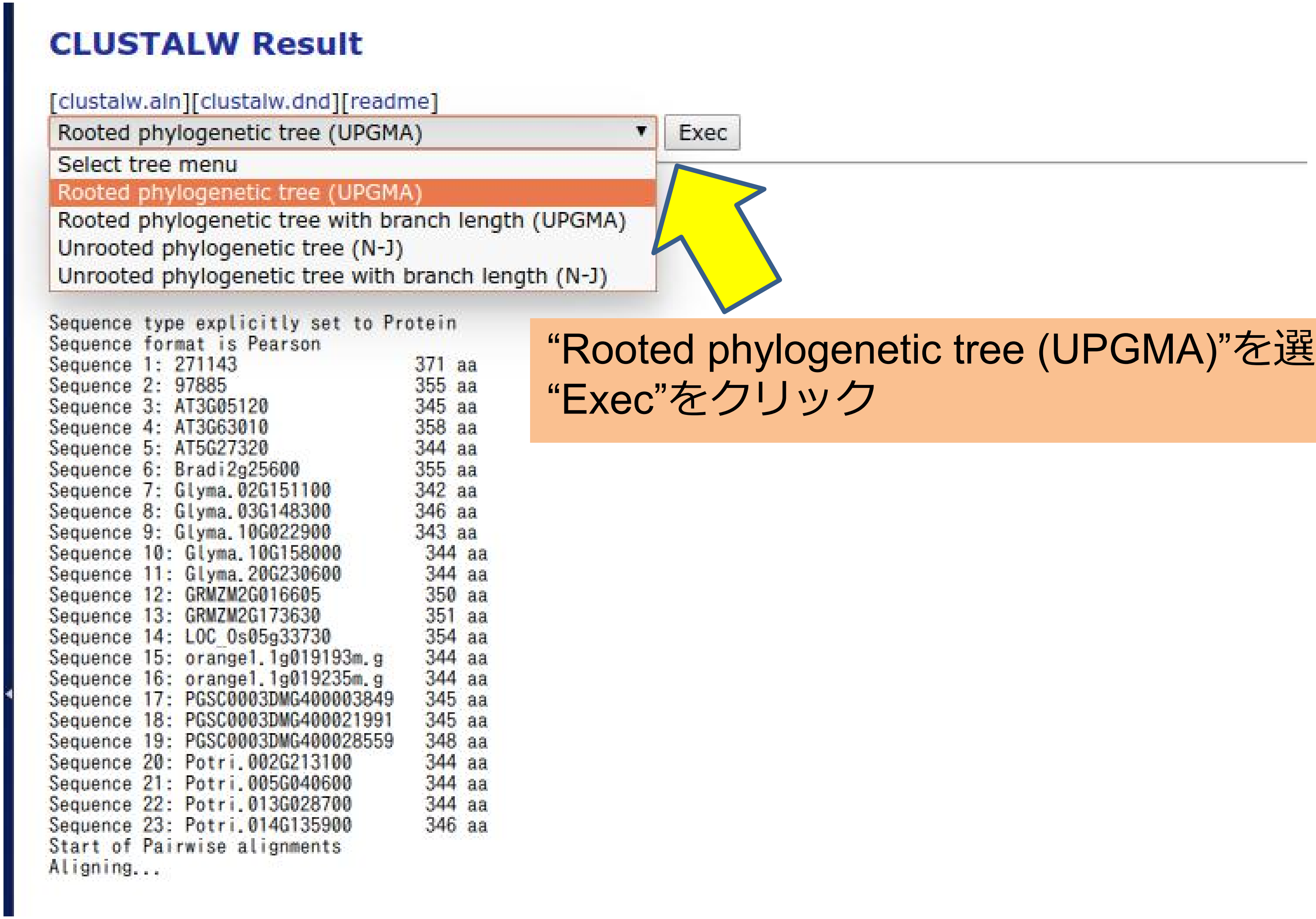
Support Formats: FASTA (Pearson), NBRF/PIR, EMBL/Swiss Prot, GDE, CLUSTAL, and GCG/MSF

```
LSTTEVVPVIIFFHGGSFTHSSADSAIYDTFCRRLVSVCKAVVVSVNYRRSPEYRYPCAY
DDGWTALKWVKSRTWLQSGKDSKVHVYLAGDSSGGNIAHH
VAVRAAEEEIEVLGNILLHPMFGGQQRTESEKMLDGKYFVTIQDRDWYWRAYLPEGEDRD
HPACNIFGPRGKNLEGLEFPRSLVVVAGFDLVRDWQLAYV
EGLQRAGYEVKLLYLKEATIGFYFLPNNEHFCCLMEEIKKFVNSN
```

Or give the file name containing your que

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

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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: GRMZM2G016605          350 aa
Sequence 13: GRMZM2G173630          351 aa
Sequence 14: LOC_Os05g33730         354 aa
Sequence 15: orange1.1g019193m.g    344 aa
Sequence 16: orange1.1g019235m.g    344 aa
Sequence 17: PGSC0003DMG400003849   345 aa
Sequence 18: PGSC0003DMG400021991   345 aa
Sequence 19: PGSC0003DMG400028559   348 aa
Sequence 20: Potri.002G213100       344 aa
Sequence 21: Potri.005G040600       344 aa
Sequence 22: Potri.013G028700       344 aa
Sequence 23: Potri.014G135900       346 aa
Start of Pairwise alignments
Aligning...
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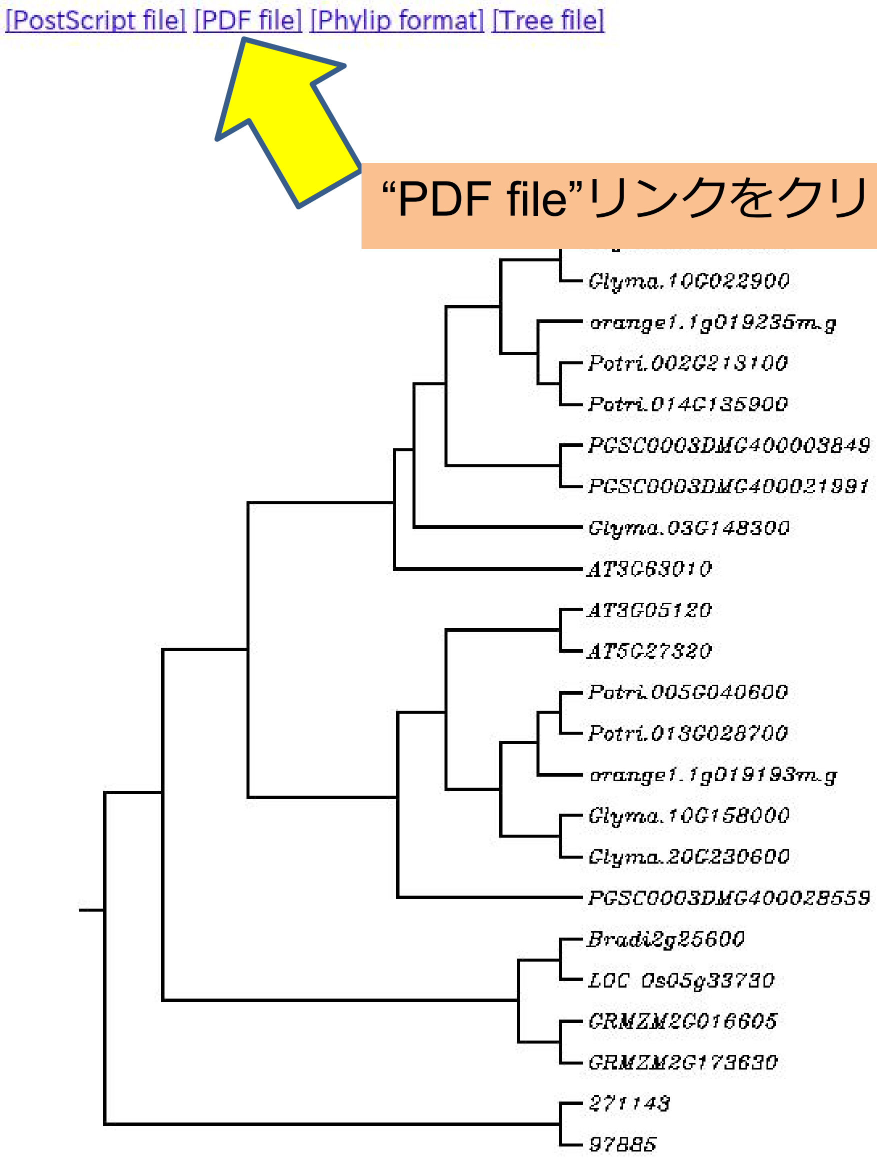
Phytozomeでお手軽比較ゲノミクス的解析



[PostScript file] [PDF file] [Phylip format] [Tree file]

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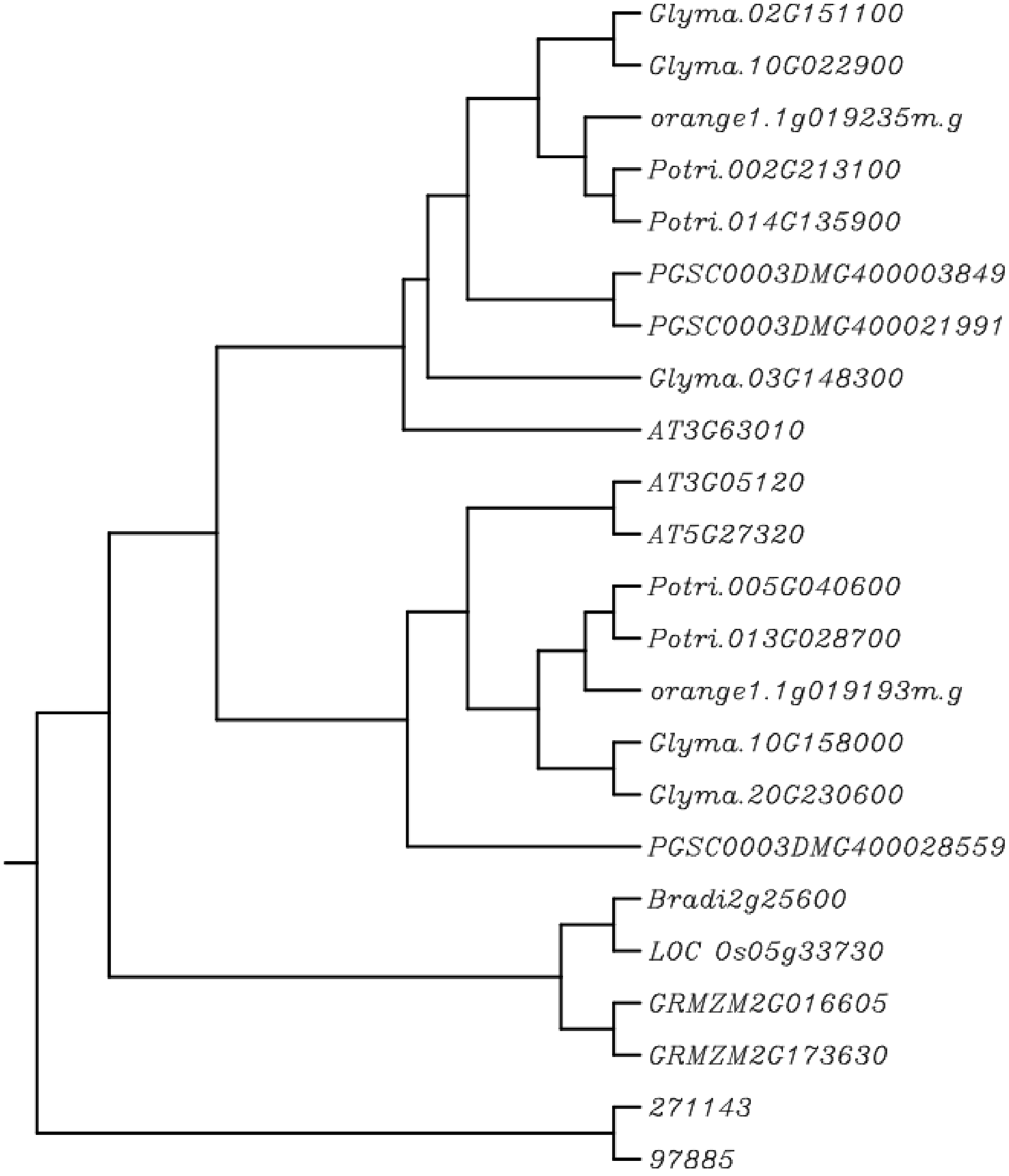
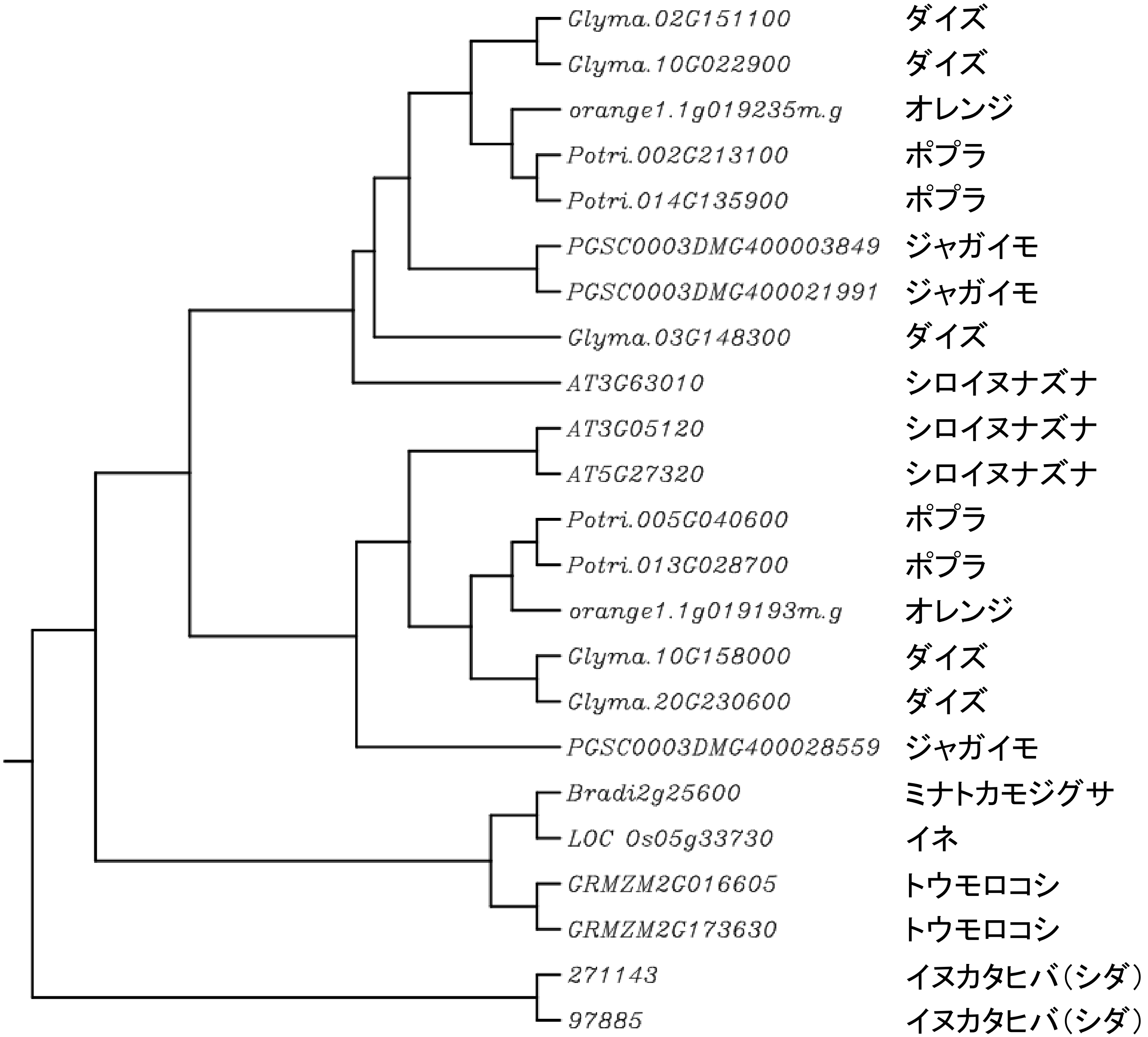
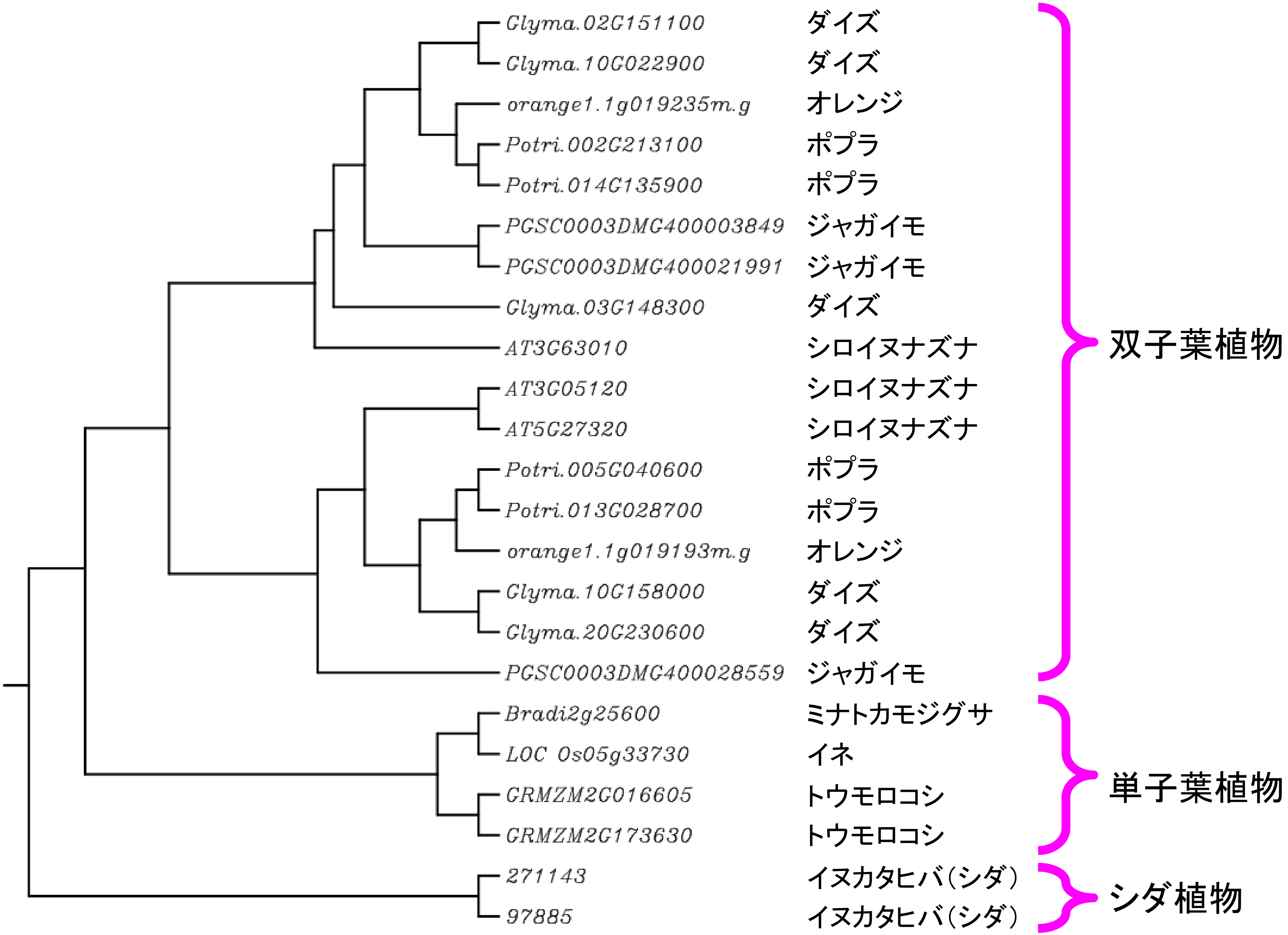
Phytozomeでお手軽比較ゲノミクス的解析



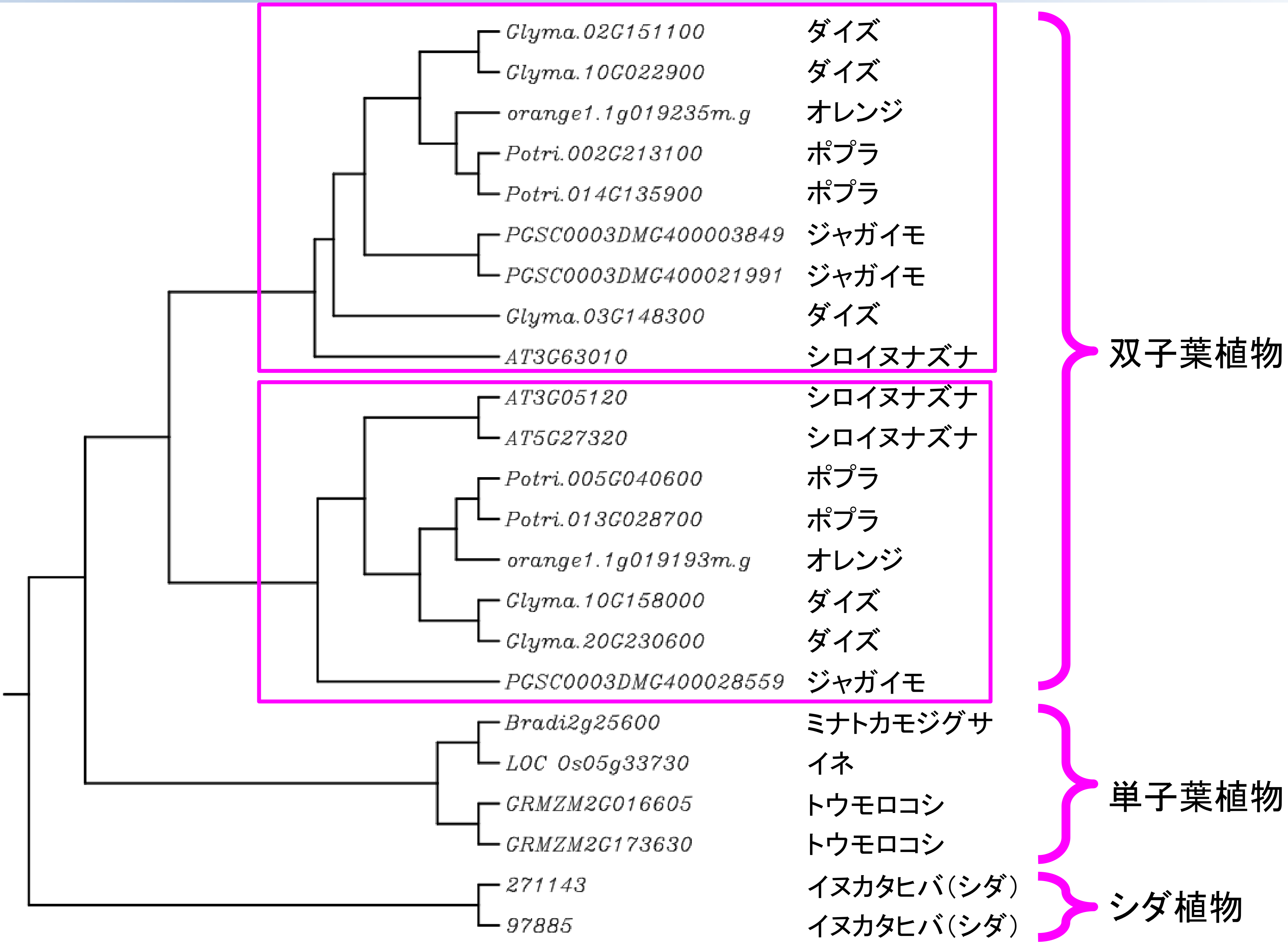
Phytozomeでお手軽比較ゲノミクス的解析



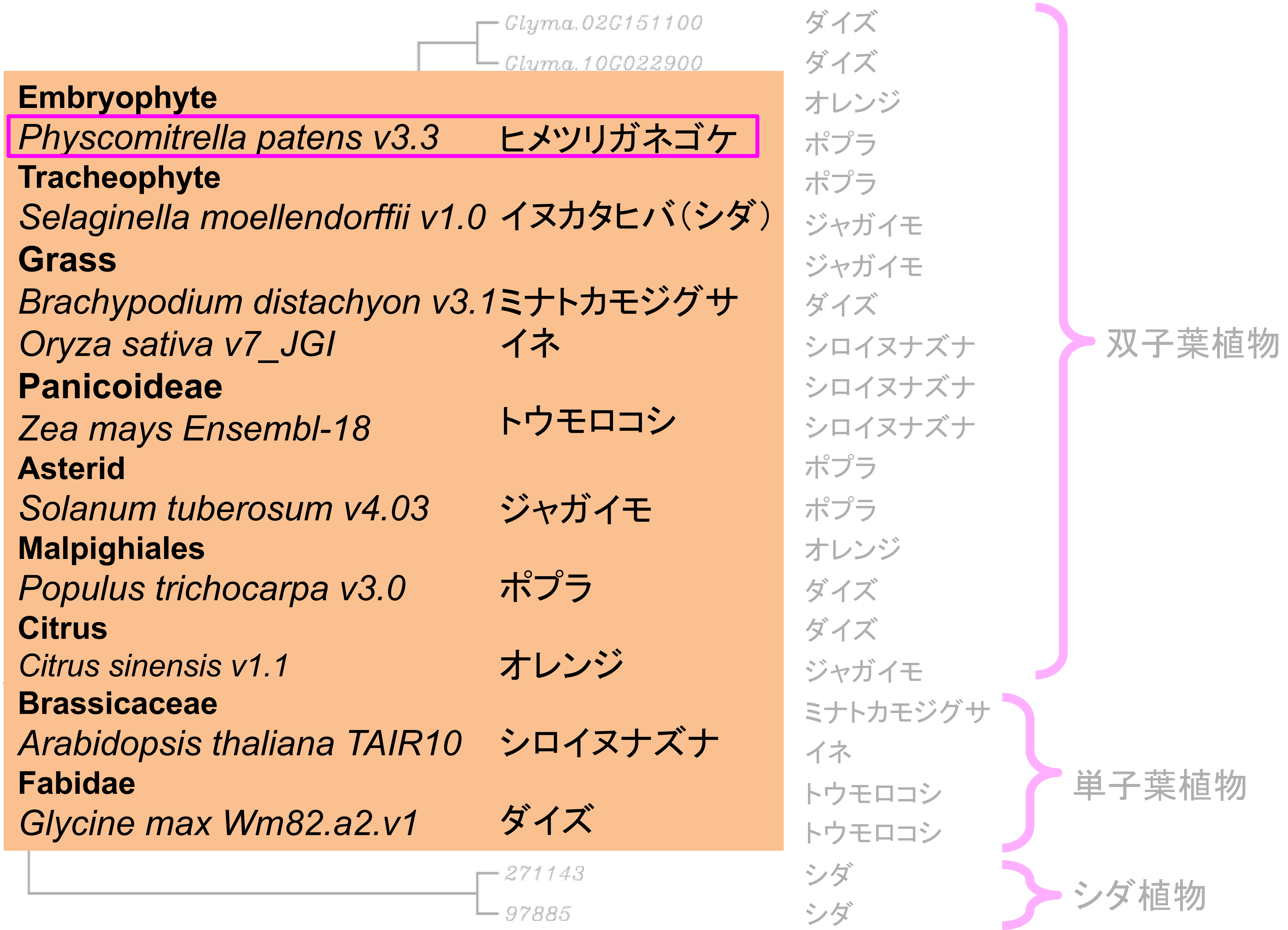
Phytozomeでお手軽比較ゲノミクス的解析



Phytozomeでお手軽比較ゲノミクス的解析

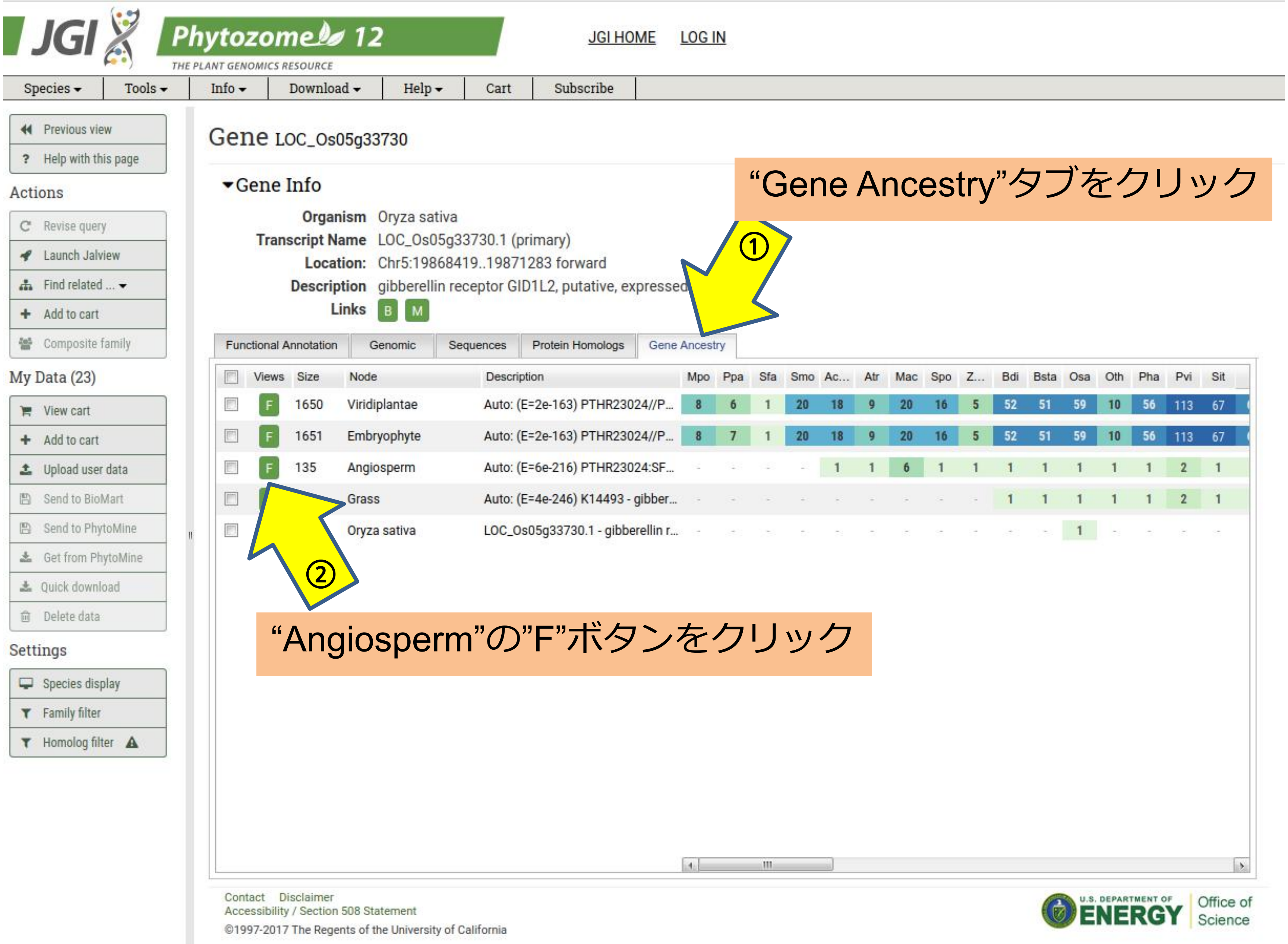


Phytozomeでお手軽比較ゲノミクス的解析



Embryophyte
Physcomitrella patens v3.3 ヒメツリガネゴケ
Tracheophyte
Selaginella moellendorffii v1.0 イヌカタヒバ（シダ）
Grass
Brachypodium distachyon v3.1 ミナトカモジグサ
Oryza sativa v7_JGI イネ
Panicoideae
Zea mays Ensembl-18 トウモロコシ
Asterid
Solanum tuberosum v4.03 ジャガイモ
Malpighiales
Populus trichocarpa v3.0 ポプラ
Citrus
Citrus sinensis v1.1 オレンジ
Brassicaceae
Arabidopsis thaliana TAIR10 シロイヌナズナ
Fabidae
Glycine max Wm82.a2.v1 ダイズ

Phytozomeでお手軽比較ゲノミクス的解析



Gene LOC_Os05g33730

Gene Info

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

☐	Views	Size	Node	Description	Mpo	Ppa	Sfa	Smo	Ac...	Atr	Mac	Spo	Z...	Bdi	Bsta	Osa	Oth	Pha	Pvi	Sit
☐	F	1650	Viridiplantae	Auto: (E=2e-163) PTHR23024//P...	8	6	1	20	18	9	20	16	5	52	51	59	10	56	113	67
☐	F	1651	Embryophyte	Auto: (E=2e-163) PTHR23024//P...	8	7	1	20	18	9	20	16	5	52	51	59	10	56	113	67
☐	F	135	Angiosperm	Auto: (E=6e-216) PTHR23024:SF...	-	-	-	-	1	1	6	1	1	1	1	1	1	1	2	1
☐			Grass	Auto: (E=4e-246) K14493 - gibber...	-	-	-	-	-	-	-	-	-	1	1	1	1	1	2	1
☐			Oryza sativa	LOC_Os05g33730.1 - gibberellin r...	-	-	-	-	-	-	-	-	-	-	-	1	-	-	-	-

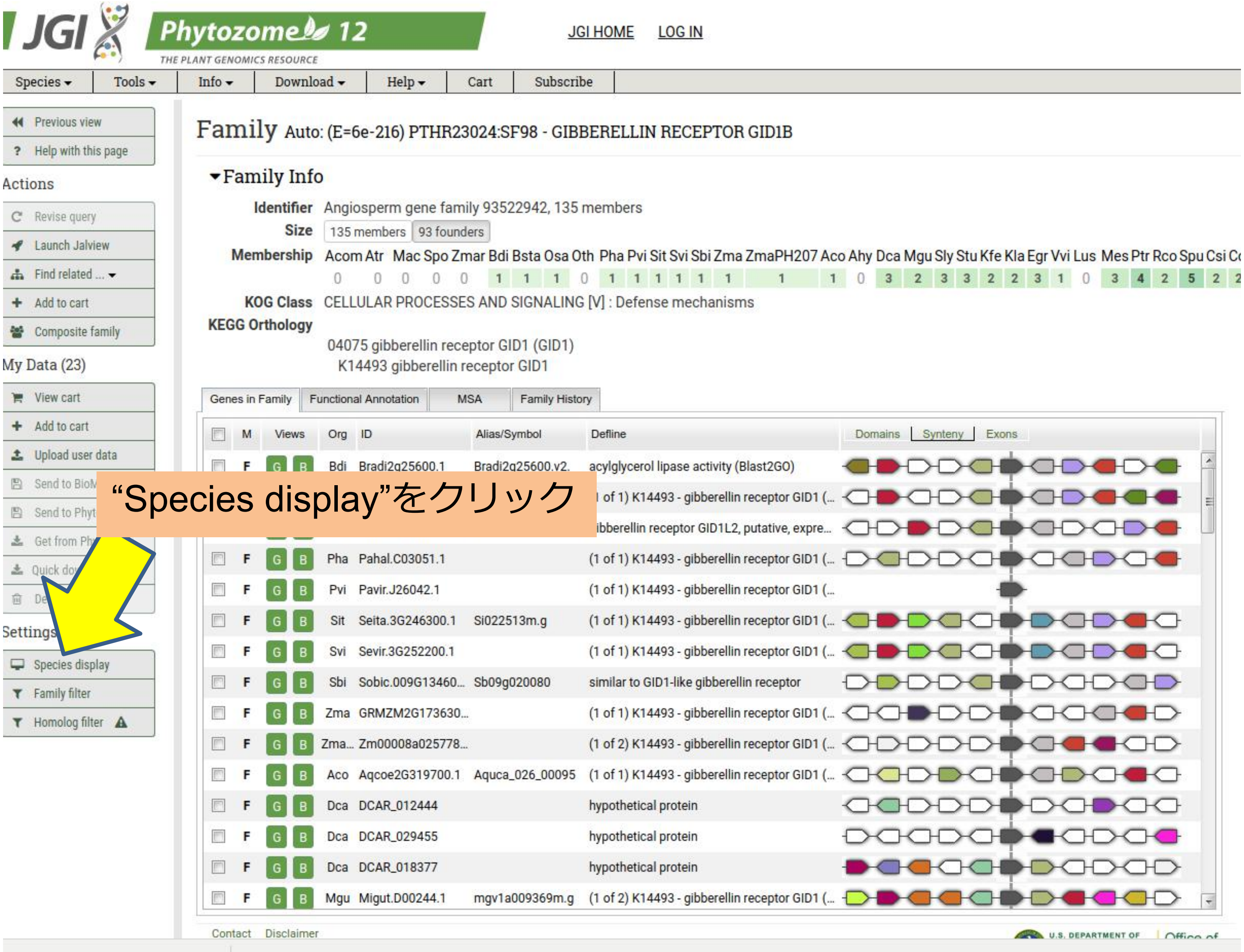
“Gene Ancestry”タブをクリック

①

②

“Angiosperm”の”F”ボタンをクリック

Phytozomeでお手軽比較ゲノミクス的解析



“Species display”をクリック

Family Auto: (E=6e-216) PTHR23024:SF98 - GIBBERELLIN RECEPTOR GID1B

Family Info

Identifier Angiosperm gene family 93522942, 135 members

Size 135 members 93 founders

Membership

Acom	Atr	Mac	Spo	Zmar	Bdi	Bsta	Osa	Oth	Pha	Pvi	Sit	Svi	Sbi	Zma	ZmaPH207	Aco	Ahy	Dca	Mgu	Sly	Stu	Kfe	Kla	Egr	Vvi	Lus	Mes	Ptr	Rco	Spu	Csi
0	0	0	0	0	1	1	1	0	1	1	1	1	1	1	1	1	0	3	2	3	3	2	2	3	1	0	3	4	2	5	2

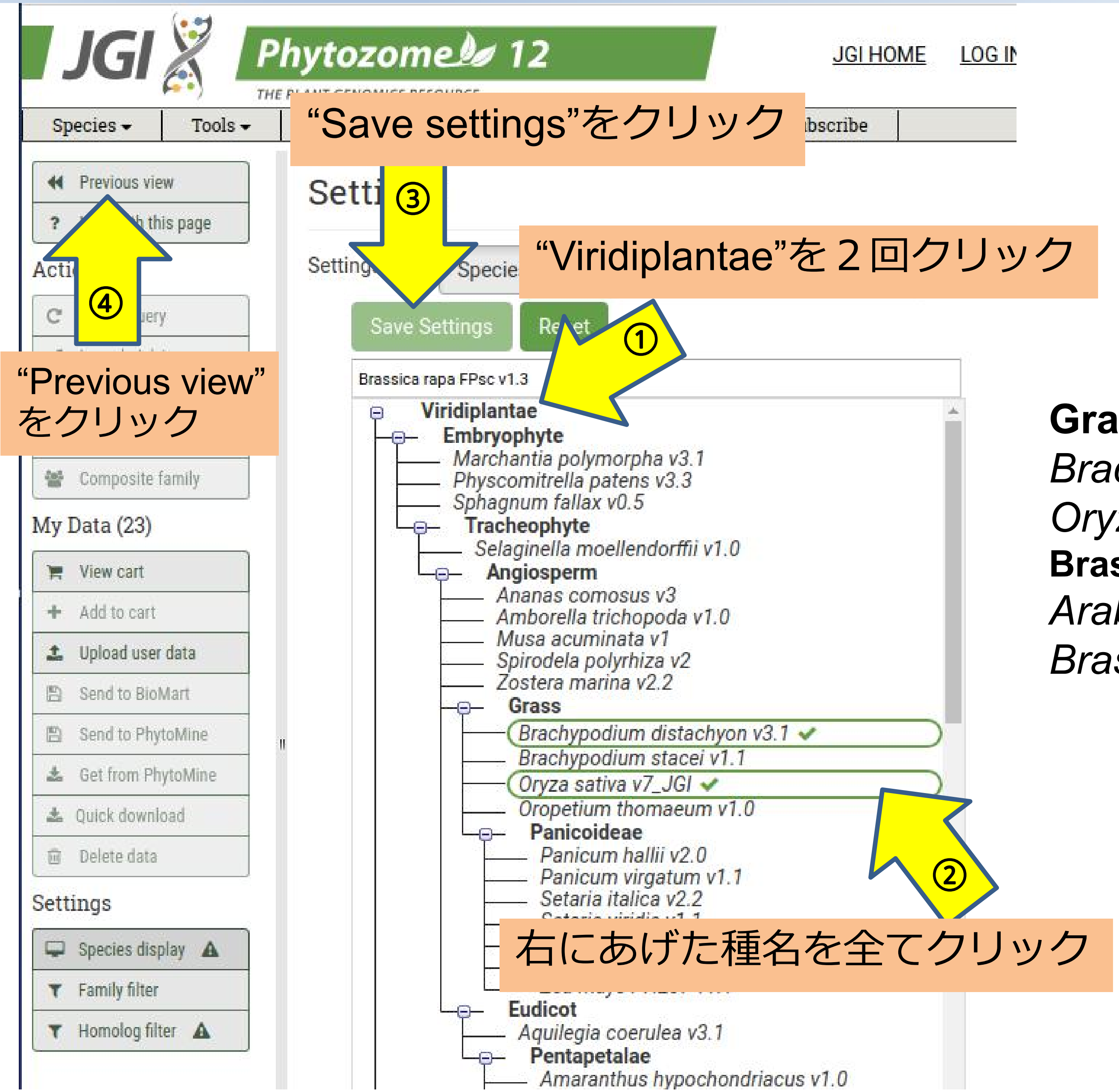
KOG Class CELLULAR PROCESSES AND SIGNALING [V] : Defense mechanisms

KEGG Orthology

04075 gibberellin receptor GID1 (GID1)
K14493 gibberellin receptor GID1

☐	M	Views	Org	ID	Alias/Symbol	Define
☐	F	G B	Bdi	Bradi2g25600.1	Bradi2g25600.v2.	acylglycerol lipase activity (Blast2GO)
						of 1) K14493 - gibberellin receptor GID1 (...
						ibberellin receptor GID1L2, putative, expre...
☐	F	G B	Pha	Pahal.C03051.1		(1 of 1) K14493 - gibberellin receptor GID1 (...
☐	F	G B	Pvi	Pavir.J26042.1		(1 of 1) K14493 - gibberellin receptor GID1 (...
☐	F	G B	Sit	Seita.3G246300.1	Si022513m.g	(1 of 1) K14493 - gibberellin receptor GID1 (...
☐	F	G B	Svi	Sevir.3G252200.1		(1 of 1) K14493 - gibberellin receptor GID1 (...
☐	F	G B	Sbi	Sobic.009G13460...	Sb09g020080	similar to GID1-like gibberellin receptor
☐	F	G B	Zma	GRMZM2G173630...		(1 of 1) K14493 - gibberellin receptor GID1 (...
☐	F	G B	Zma...	Zm00008a025778...		(1 of 2) K14493 - gibberellin receptor GID1 (...
☐	F	G B	Aco	Aqcoe2G319700.1	Aquca_026_00095	(1 of 1) K14493 - gibberellin receptor GID1 (...
☐	F	G B	Dca	DCAR_012444		hypothetical protein
☐	F	G B	Dca	DCAR_029455		hypothetical protein
☐	F	G B	Dca	DCAR_018377		hypothetical protein
☐	F	G B	Mgu	Migut.D00244.1	mgv1a009369m.g	(1 of 2) K14493 - gibberellin receptor GID1 (...

Phytozomeでお手軽比較ゲノミクス的解析



① “Viridiplantae”を２回クリック

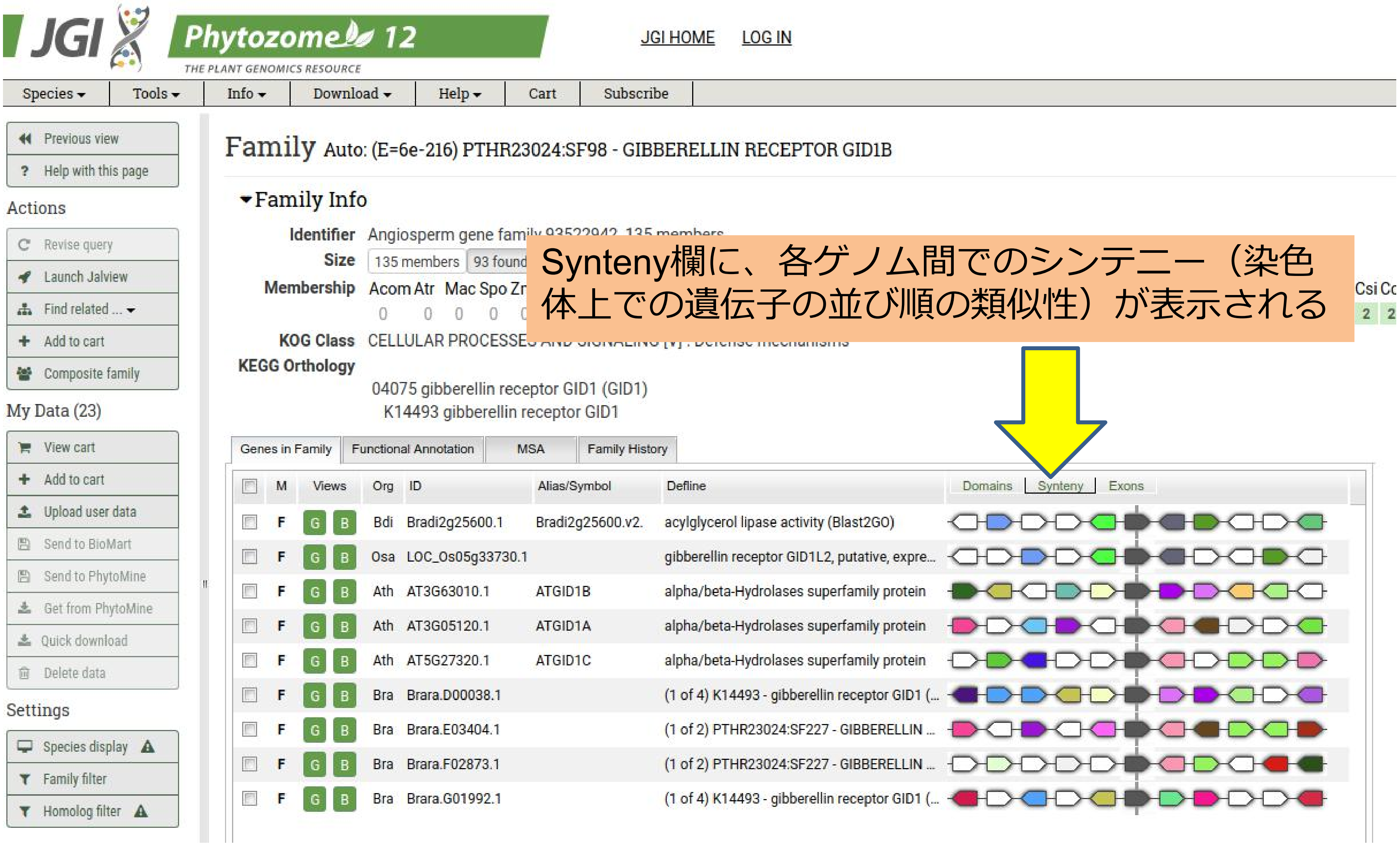
② 右にあげた種名を全てクリック

③ “Save settings”をクリック

④ “Previous view”をクリック

Grass
Brachypodium distachyon v3.1
Oryza sativa v7_JGI
Brassicaceae
Arabidopsis thaliana TAIR10
Brassica rapa FPsc v1.3

Phytozomeでお手軽比較ゲノミクス的解析



Family Auto: (E=6e-216) PTHR23024:SF98 - GIBBERELLIN RECEPTOR GID1B

Family Info

Identifier Angiosperm gene family 93522942, 135 members

Size 135 members 93 found

Membership Acom Atr Mac Spo Zr … Csi Cc
0 0 0 0 0 … 2 2

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

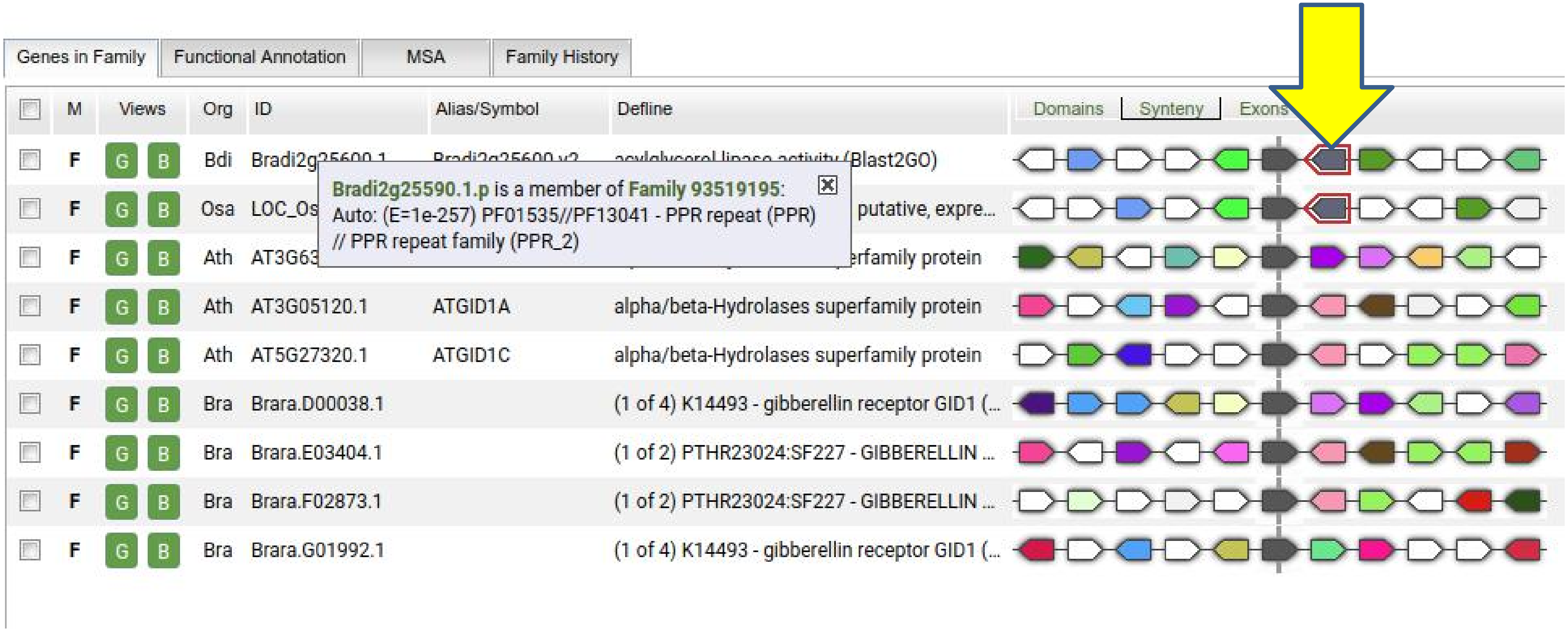
KEGG Orthology
04075 gibberellin receptor GID1 (GID1)
K14493 gibberellin receptor GID1

☐	M	Views	Org	ID	Alias/Symbol	Define	Domains Synteny Exons
☐	F	G B	Bdi	Bradi2g25600.1	Bradi2g25600.v2.	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		(1 of 4) K14493 - gibberellin receptor GID1 (...	
☐	F	G B	Bra	Brara.E03404.1		(1 of 2) PTHR23024:SF227 - GIBBERELLIN ...	
☐	F	G B	Bra	Brara.F02873.1		(1 of 2) PTHR23024:SF227 - GIBBERELLIN ...	
☐	F	G B	Bra	Brara.G01992.1		(1 of 4) K14493 - gibberellin receptor GID1 (...	

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

Phytozomeでお手軽比較ゲノミクス的解析

Osa(イネ)のGID1周辺の遺伝子をクリックするとBdi(ミナトカモジグサ)のGID1周辺遺伝子もハイライトされる。

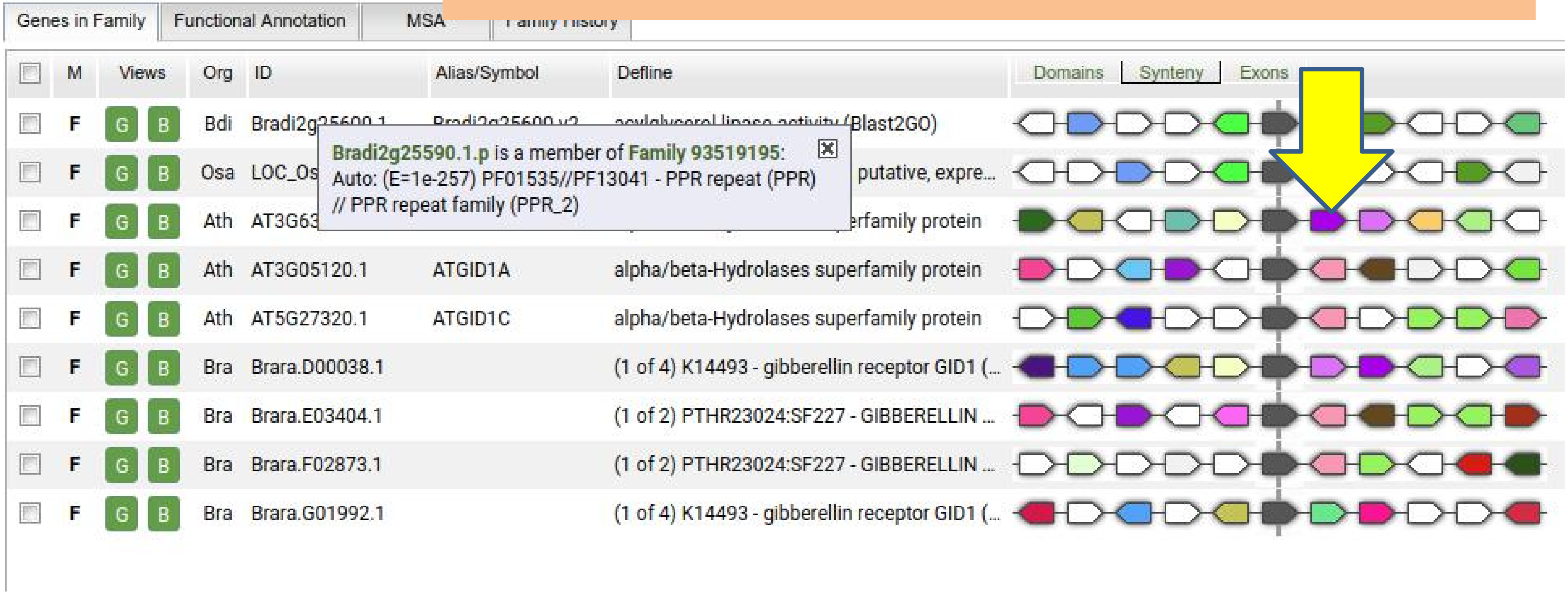


☐	M	Views	Org	ID	Alias/Symbol	Define
☐	F	G B	Bdi	Bradi2g25600.1	Bradi2g25600.v2	acylglycerol lipase activity (Blast2GO)
☐	F	G B	Osa	LOC_Os		putative, expre...
☐	F	G B	Ath	AT3G63		erfamily protein
☐	F	G B	Ath	AT3G05120.1	ATGID1A	alpha/beta-Hydrolases superfamily protein
☐	F	G B	Ath	AT5G27320.1	ATGID1C	alpha/beta-Hydrolases superfamily protein
☐	F	G B	Bra	Brara.D00038.1		(1 of 4) K14493 - gibberellin receptor GID1 (...
☐	F	G B	Bra	Brara.E03404.1		(1 of 2) PTHR23024:SF227 - GIBBERELLIN ...
☐	F	G B	Bra	Brara.F02873.1		(1 of 2) PTHR23024:SF227 - GIBBERELLIN ...
☐	F	G B	Bra	Brara.G01992.1		(1 of 4) K14493 - gibberellin receptor GID1 (...

Bradi2g25590.1.p is a member of **Family 93519195**: ☒
Auto: (E=1e-257) PF01535//PF13041 - PPR repeat (PPR) // PPR repeat family (PPR_2)

Phytozomeでお手軽比較ゲノミクス的解析

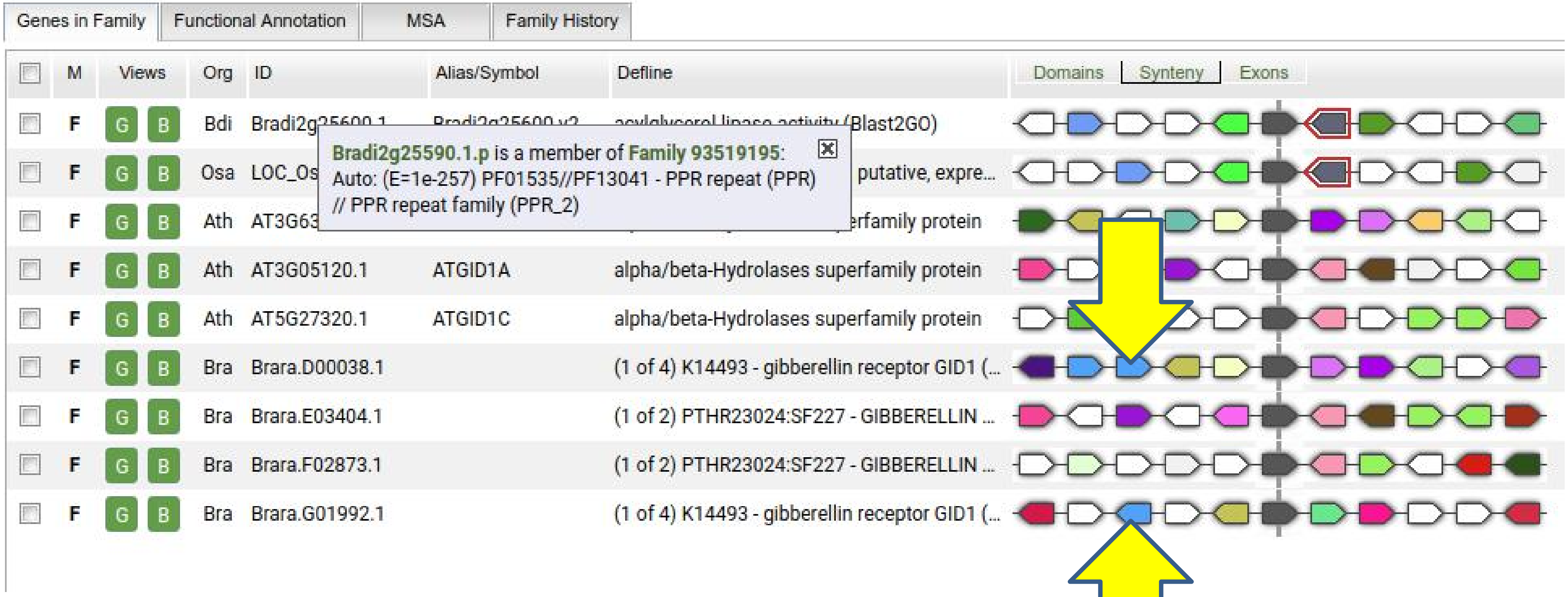
Ath(シロイヌナズナ)のGID1周辺の遺伝子をクリックすると
Bra(ブラシカラパ)のGID1周辺遺伝子もハイライトされる。
ただし、ATGID1BとATGID1AまたはATGID1C周辺では、
ハイライトされる遺伝子が異なる。



☐	M	Views	Org	ID	Alias/Symbol	Define
☐	F	G B	Bdi	Bradi2g25600.1	Bradi2g25600.v2	acylglycerol lipase activity (Blast2GO)
☐	F	G B	Osa	LOC_Os		putative, expre...
☐	F	G B	Ath	AT3G63		erfamily 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		(1 of 4) K14493 - gibberellin receptor GID1 (...
☐	F	G B	Bra	Brara.E03404.1		(1 of 2) PTHR23024:SF227 - GIBBERELLIN ...
☐	F	G B	Bra	Brara.F02873.1		(1 of 2) PTHR23024:SF227 - GIBBERELLIN ...
☐	F	G B	Bra	Brara.G01992.1		(1 of 4) K14493 - gibberellin receptor GID1 (...

Bradi2g25590.1.p is a member of Family 93519195:
Auto: (E=1e-257) PF01535//PF13041 - PPR repeat (PPR)
// PPR repeat family (PPR_2)

Phytozomeでお手軽比較ゲノミクス的解析



☐	M	Views	Org	ID	Alias/Symbol	Define
☐	F	G B	Bdi	Bradi2g25600.1	Bradi2g25600.v2	acylglycerol lipase activity (Blast2GO)
☐	F	G B	Osa	LOC_Os		putative, expre...
☐	F	G B	Ath	AT3G63		erfamily 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		(1 of 4) K14493 - gibberellin receptor GID1 (...
☐	F	G B	Bra	Brara.E03404.1		(1 of 2) PTHR23024:SF227 - GIBBERELLIN ...
☐	F	G B	Bra	Brara.F02873.1		(1 of 2) PTHR23024:SF227 - GIBBERELLIN ...
☐	F	G B	Bra	Brara.G01992.1		(1 of 4) K14493 - gibberellin receptor GID1 (...

Bradi2g25590.1.p is a member of **Family 93519195**:
Auto: (E=1e-257) PF01535//PF13041 - PPR repeat (PPR) // PPR repeat family (PPR_2) ☒

一番下のBra(ブラシカラパ)のGID1周辺遺伝子は、ATGID1B周辺と近いが、どちらかといえばBra(ブラシカラパ)の一番上のエントリーと似ている。

Phytozomeでお手軽比較ゲノミクス的解析

Family Auto: (E=6e-216) PTHR23024:SF98 - GIBBERELLIN RECEPTOR GID1B

Family Info

Identifier Angiosperm gene family 93522942, 135 members

Size 135 members | 93 founders

Membership

Acom	Atr	Mac	Spo	Zmar	Bdi	Bsta	Osa	Oth	Pha	Pvi	Sit	Svi	Sbi	Zma	ZmaPH207	Aco	Ahy	Dca	Mgu	Sly	Stu	Kfe	Kla	Egr	Vvi	Lus	Mes	Ptr	Rco	Spu
0	0	0	0	0	1	1	1	0	1	1	1	1	1	1	1	1	0	3	2	3	3	2	2	3	1	0	3	4	2	5

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

KEGG Orthology

04075 gibberellin receptor GID1 (GID1)

K14493 gibberellin receptor GID1

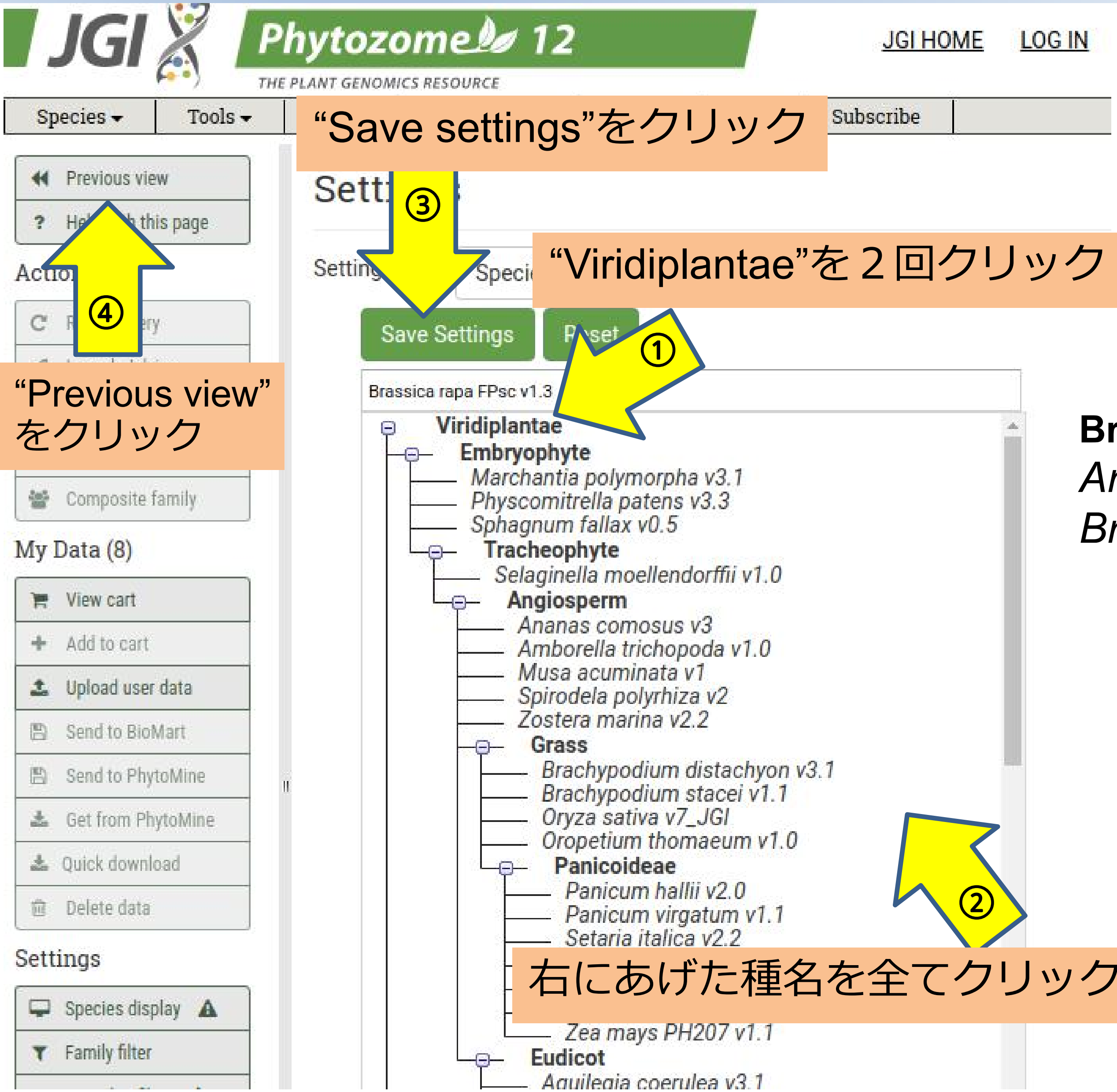
☐	M	Views	Org	ID	Alias/Symbol	Define
☐	F	G B	Bdi	Bradi2g25600.1	Bradi2g25600.v2.	acylglycerol lipase activity (Blast2GO)
☐	F	G B	Osa	LOC_Os05g33730.1		gibberellin receptor GID1L2, putative, expre...
☐	F			AT3G63010.1	ATGID1B	alpha/beta-Hydrolases superfamily protein
☐	F			AT3G05120.1	ATGID1A	alpha/beta-Hydrolases superfamily protein
☐	F	G		AT5G27320.1	ATGID1C	alpha/beta-Hydrolases superfamily protein
☐	F					
☐	F					
☐	F	G B	Bra	Brara.F02873.1		(1 of 2) PTHR23024:SF227 - GIBBERELLIN ...
☐	F	G B	Bra	Brara.G		receptor GID1 (...

Brara.F02875.1.p is a member of **Family 93516874**: Auto: (E=0) PF01535//PF13041 - PPR repeat (PPR) // PPR repeat family (PPR_2)

②

Osaのエントリーの”G”ボタンをクリック

Phytozomeでお手軽比較ゲノミクス的解析



Brassica rapa FPsc v1.3

- Viridiplantae
  - Embryophyte
    - *Marchantia polymorpha v3.1*
    - *Physcomitrella patens v3.3*
    - *Sphagnum fallax v0.5*
    - Tracheophyte
      - *Selaginella moellendorffii v1.0*
      - Angiosperm
        - *Ananas comosus v3*
        - *Amborella trichopoda v1.0*
        - *Musa acuminata v1*
        - *Spirodela polyrhiza v2*
        - *Zostera marina v2.2*
        - Grass
          - *Brachypodium distachyon v3.1*
          - *Brachypodium stacei v1.1*
          - *Oryza sativa v7_JGI*
          - *Oropetium thomaeum v1.0*
          - Panicoideae
            - *Panicum hallii v2.0*
            - *Panicum virgatum v1.1*
            - *Setaria italica v2.2*
            - *Zea mays PH207 v1.1*
        - Eudicot
          - *Aquilegia coerulea v3.1*

“Save settings”をクリック

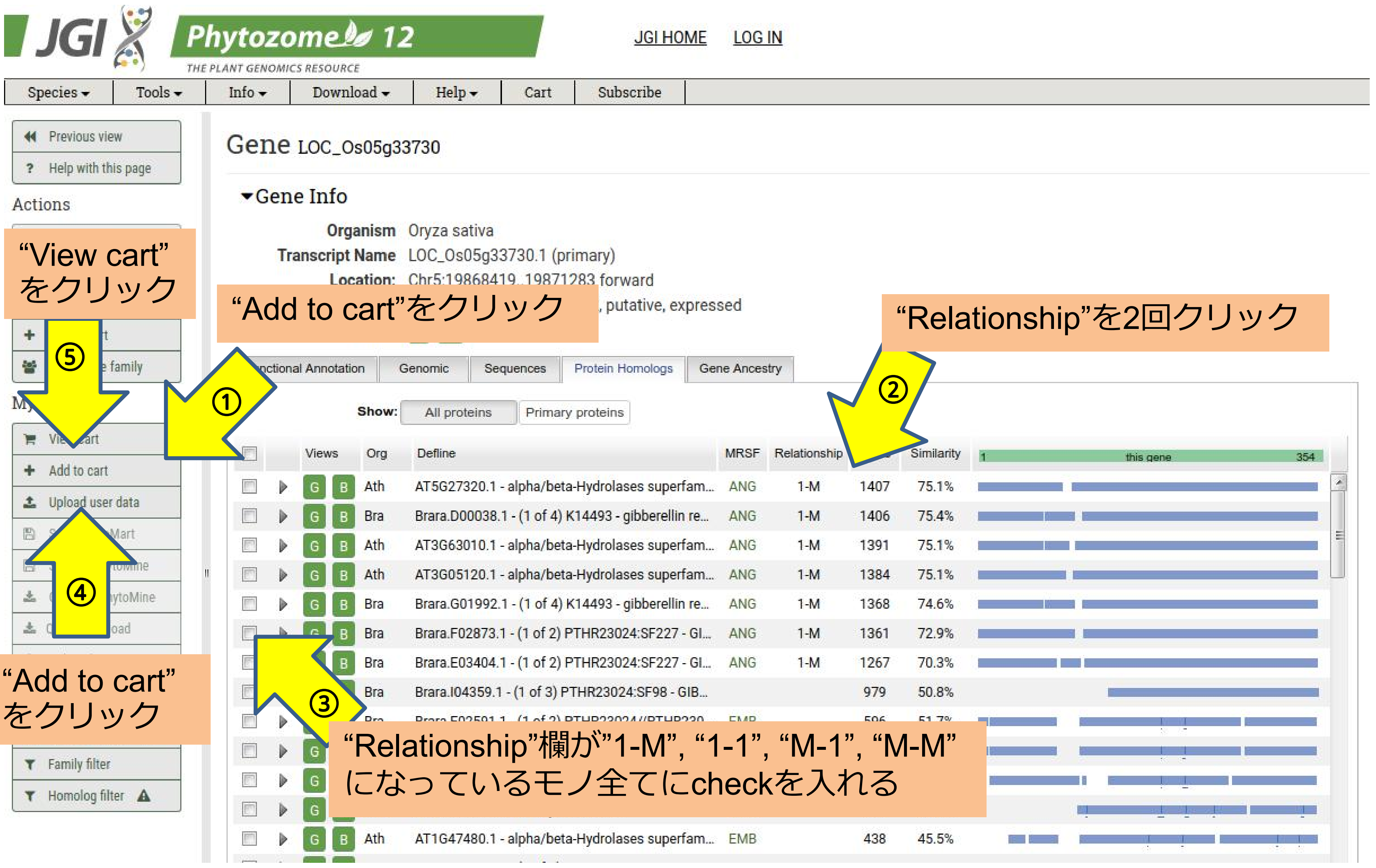
“Viridiplantae”を２回クリック

“Previous view”
をクリック

右にあげた種名を全てクリック

Brassicaceae
Arabidopsis thaliana TAIR10
Brassica rapa FPsc v1.3

Phytozomeでお手軽比較ゲノミクス的解析



“View cart”をクリック

“Add to cart”をクリック

“Relationship”を2回クリック

“Add to cart”をクリック

“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

Gene LOC_Os05g33730

▾Gene Info

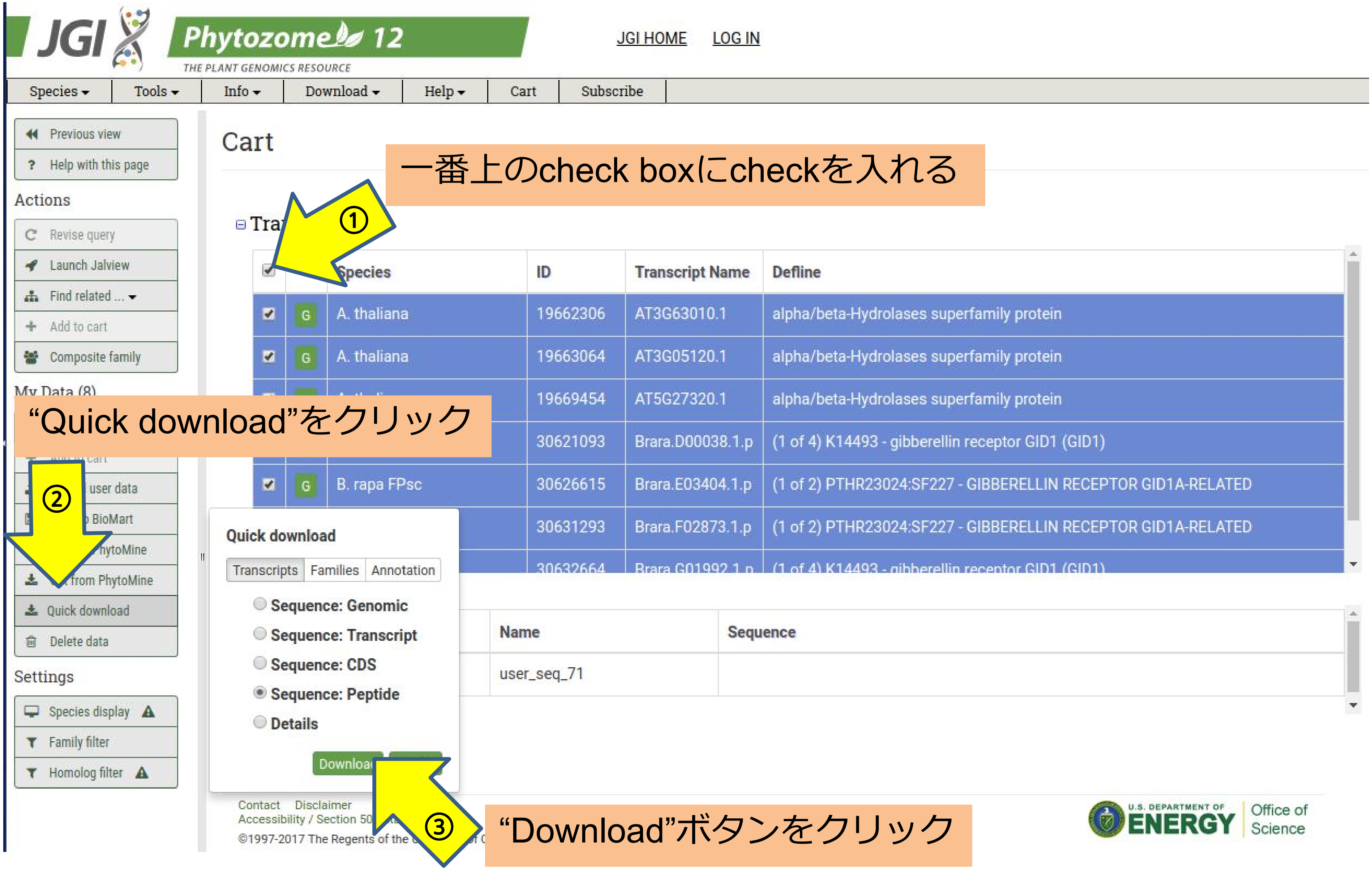
Organism Oryza sativa
Transcript Name LOC_Os05g33730.1 (primary)
Location: Chr5:19868419..19871283 forward
, putative, expressed

nctional Annotation | Genomic | Sequences | Protein Homologs | Gene Ancestry

Show: All proteins | Primary proteins

☐		Views	Org	Defline	MRSF	Relationship		Similarity	1 this gene 354
☐	▶	G B	Ath	AT5G27320.1 - alpha/beta-Hydrolases superfam...	ANG	1-M	1407	75.1%	
☐	▶	G B	Bra	Brara.D00038.1 - (1 of 4) K14493 - gibberellin re...	ANG	1-M	1406	75.4%	
☐	▶	G B	Ath	AT3G63010.1 - alpha/beta-Hydrolases superfam...	ANG	1-M	1391	75.1%	
☐	▶	G B	Ath	AT3G05120.1 - alpha/beta-Hydrolases superfam...	ANG	1-M	1384	75.1%	
☐	▶	G B	Bra	Brara.G01992.1 - (1 of 4) K14493 - gibberellin re...	ANG	1-M	1368	74.6%	
☐	▶	G B	Bra	Brara.F02873.1 - (1 of 2) PTHR23024:SF227 - GI...	ANG	1-M	1361	72.9%	
☐		B	Bra	Brara.E03404.1 - (1 of 2) PTHR23024:SF227 - GI...	ANG	1-M	1267	70.3%	
☐			Bra	Brara.I04359.1 - (1 of 3) PTHR23024:SF98 - GIB...			979	50.8%	
☐	▶		Bra	Brara.F02591.1 - (1 of 2) PTHR23024//PTHR230...	EMB		596	51.7%	
☐	▶	G							
☐	▶	G							
☐	▶	G							
☐	▶	G B	Ath	AT1G47480.1 - alpha/beta-Hydrolases superfam...	EMB		438	45.5%	

Phytozomeでお手軽比較ゲノミクス的解析



☑		Species	ID	Transcript Name	Define
☑	G	A. thaliana	19662306	AT3G63010.1	alpha/beta-Hydrolases superfamily protein
☑	G	A. thaliana	19663064	AT3G05120.1	alpha/beta-Hydrolases superfamily protein
			19669454	AT5G27320.1	alpha/beta-Hydrolases superfamily protein
			30621093	Brara.D00038.1.p	(1 of 4) K14493 - gibberellin receptor GID1 (GID1)
☑	G	B. rapa FPsc	30626615	Brara.E03404.1.p	(1 of 2) PTHR23024:SF227 - GIBBERELLIN RECEPTOR GID1A-RELATED
			30631293	Brara.F02873.1.p	(1 of 2) PTHR23024:SF227 - GIBBERELLIN RECEPTOR GID1A-RELATED
			30632664	Brara.G01992.1.p	(1 of 4) K14493 - gibberellin receptor GID1 (GID1)

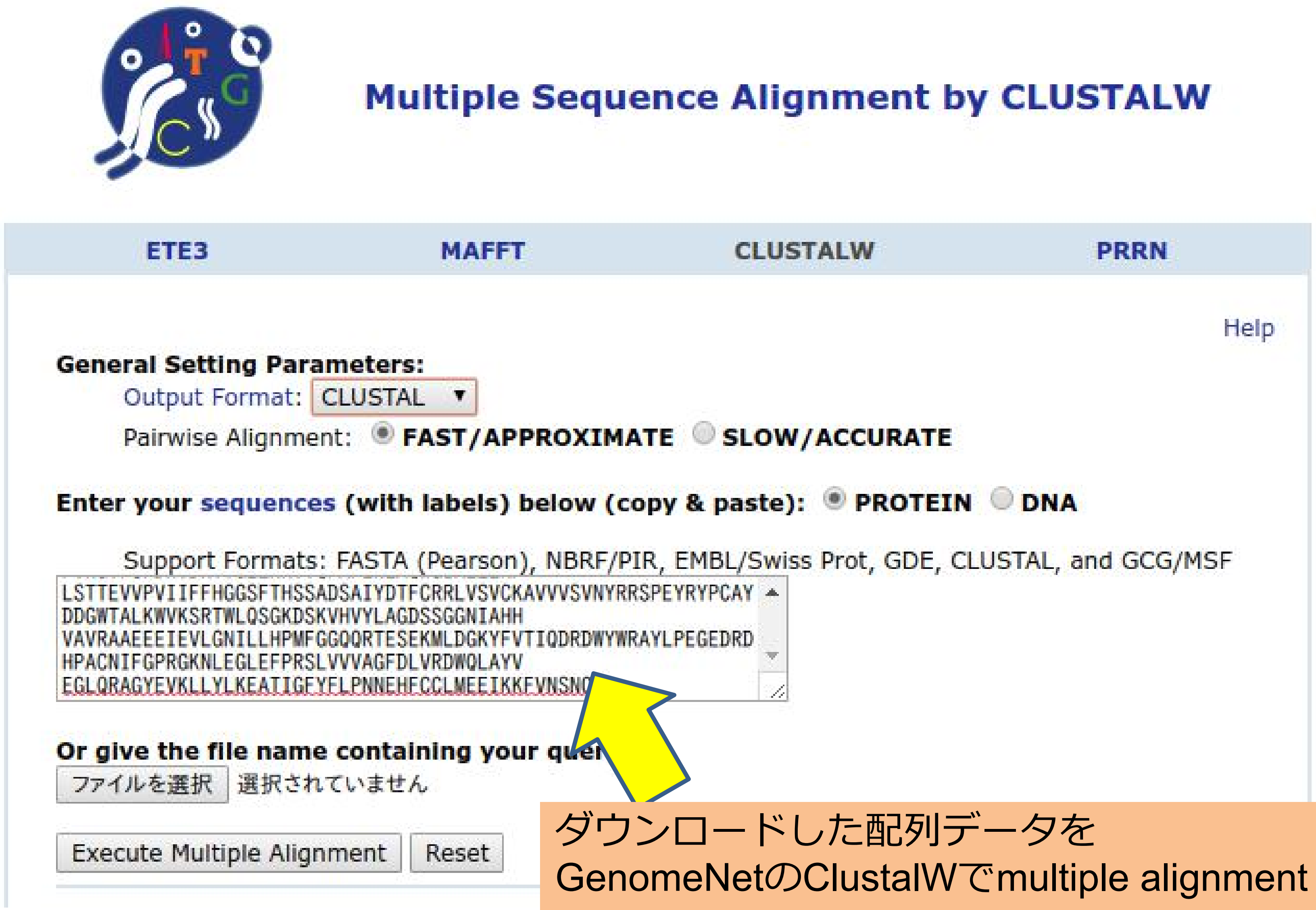
Name	Sequence
user_seq_71	

① 一番上のcheck boxにcheckを入れる

② “Quick download”をクリック

③ “Download”ボタンをクリック

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**

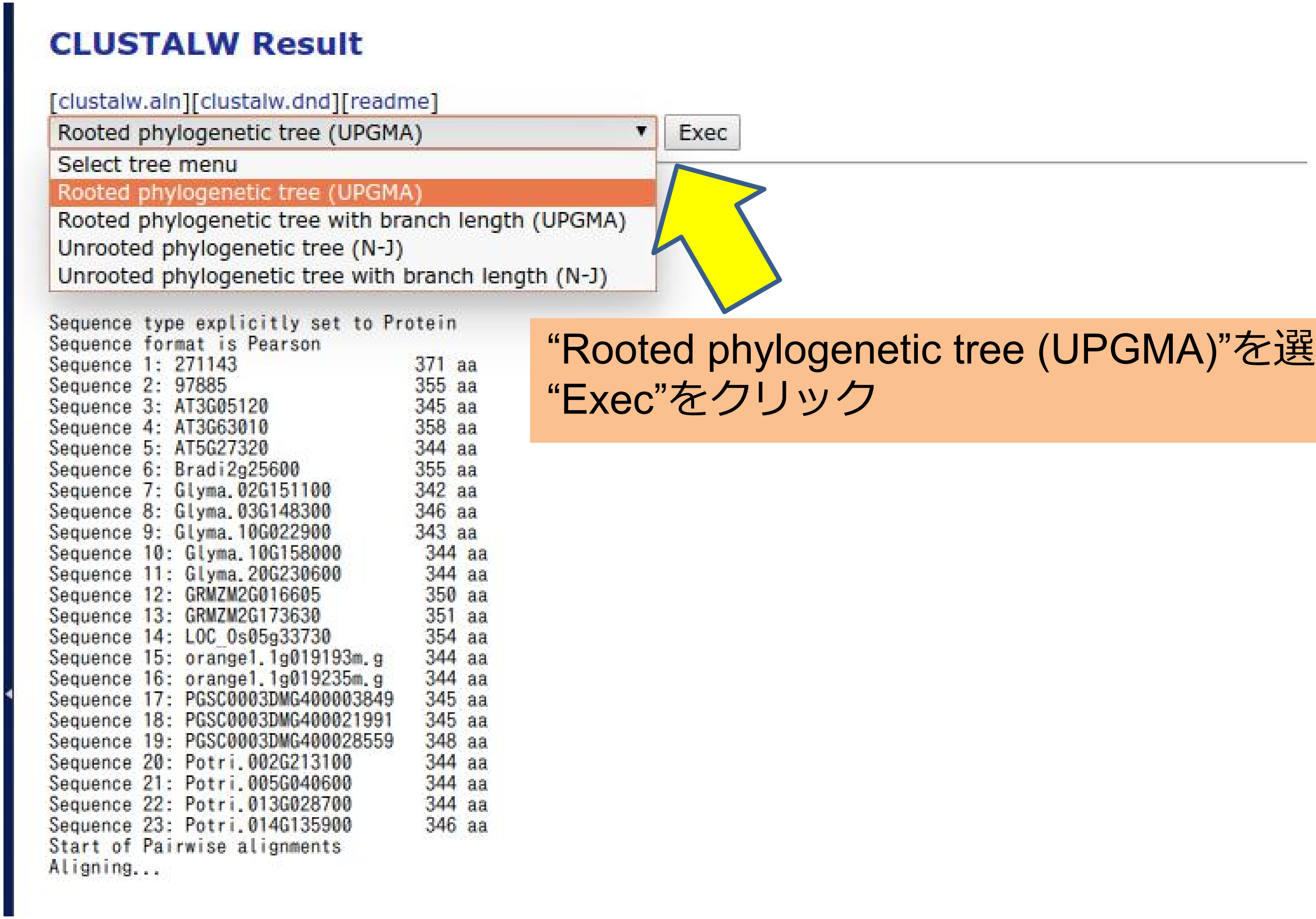
Support Formats: FASTA (Pearson), NBRF/PIR, EMBL/Swiss Prot, GDE, CLUSTAL, and GCG/MSF

```
LSTTEVVPVIIFFHGGSFTHSSADSAIYDTFCRRLVSVCKAVVVSVNYRRSPEYRYPCAY
DDGWTALKWVKSRTWLQSGKDSKVHVYLAGDSSGGNIAHH
VAVRAAEEEIEVLGNILLHPMFGGQQRTESEKMLDGKYFVTIQDRDWYWRAYLPEGEDRD
HPACNIFGPRGKNLEGLEFPRSLVVVAGFDLVRDWQLAYV
EGLQRAGYEVKLLYLKEATIGFYFLPNNEHFCCLMEEIKKFVNSN
```

Or give the file name containing your que

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



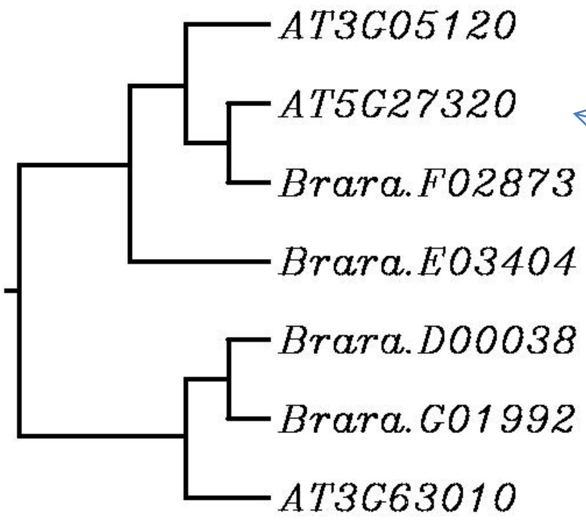
CLUSTALW Result

[clustalw.aln][clustalw.dnd][readme]

```
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: GRMZM2G016605          350 aa
Sequence 13: GRMZM2G173630          351 aa
Sequence 14: LOC_Os05g33730         354 aa
Sequence 15: orange1.1g019193m.g    344 aa
Sequence 16: orange1.1g019235m.g    344 aa
Sequence 17: PGSC0003DMG400003849   345 aa
Sequence 18: PGSC0003DMG400021991   345 aa
Sequence 19: PGSC0003DMG400028559   348 aa
Sequence 20: Potri.002G213100       344 aa
Sequence 21: Potri.005G040600       344 aa
Sequence 22: Potri.013G028700       344 aa
Sequence 23: Potri.014G135900       346 aa
Start of Pairwise alignments
Aligning...
```

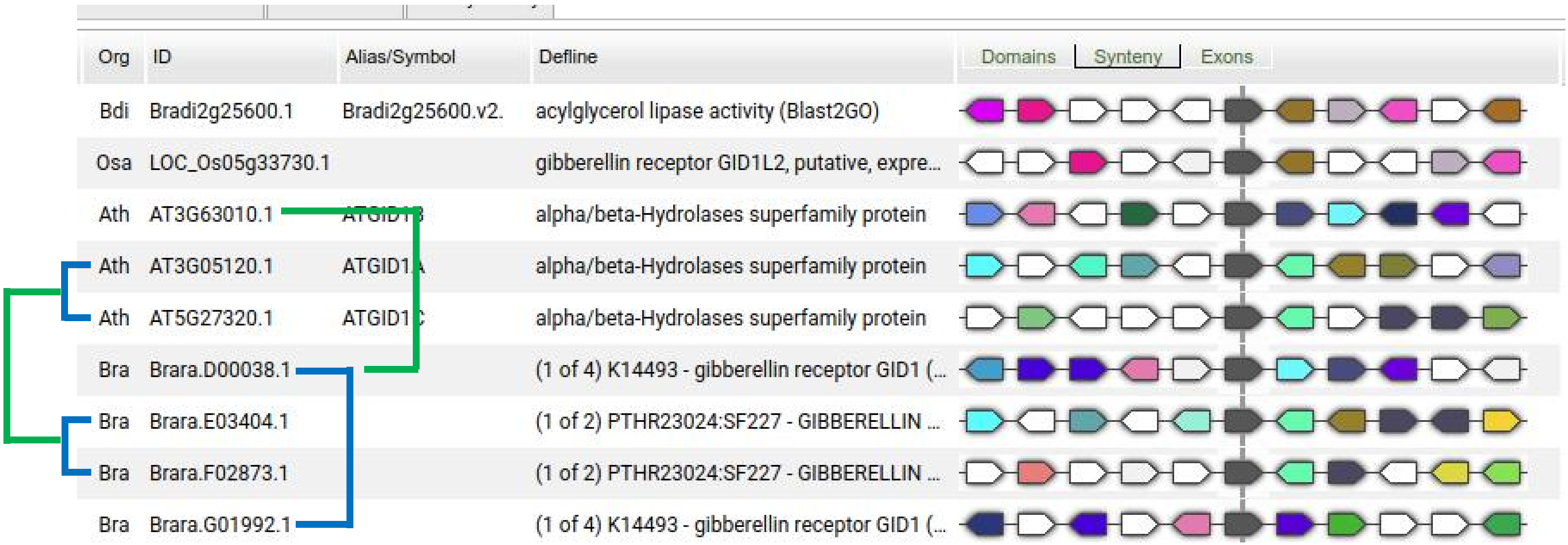
“Rooted phylogenetic tree (UPGMA)”を選択し、
“Exec”をクリック

Phytozomeでお手軽比較ゲノミクス的解析



シロイヌナズナの遺伝子よりブラシカラパの遺伝子と似ており、種分化の前に重複が起きた可能性。

ATGID1Bとの共通祖先遺伝子を持ち、種分化が起きた後に重複が起きた可能性。



Org	ID	Alias/Symbol	Define
Bdi	Bradi2g25600.1	Bradi2g25600.v2.	acylglycerol lipase activity (Blast2GO)
Osa	LOC_Os05g33730.1		gibberellin receptor GID1L2, putative, expre...
Ath	AT3G63010.1	ATGID1B	alpha/beta-Hydrolases superfamily protein
Ath	AT3G05120.1	ATGID1A	alpha/beta-Hydrolases superfamily protein
Ath	AT5G27320.1	ATGID1C	alpha/beta-Hydrolases superfamily protein
Bra	Brara.D00038.1		(1 of 4) K14493 - gibberellin receptor GID1 (...
Bra	Brara.E03404.1		(1 of 2) PTHR23024:SF227 - GIBBERELLIN ...
Bra	Brara.F02873.1		(1 of 2) PTHR23024:SF227 - GIBBERELLIN ...
Bra	Brara.G01992.1		(1 of 4) K14493 - gibberellin receptor GID1 (...