KusakiDB Tools: Search System

Hayai_annotation_v2.0 | KusakiDB_v1.0 | kusakiDB/kusakiDBv1_tutorial

Not Secure | pgdbjsnp.kazusa.or.jp/app/kusakidb

KusakiDB v1.0

A novel approach for assessing existence and completeness of orthogroups in plant species

Search KusakiDB | OG Assessment | OG Management | OG Management User Data | Help

Search proteins within species or family level

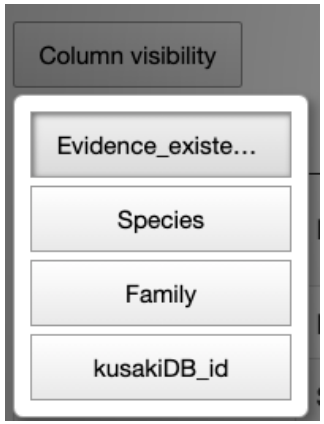
Select Taxon Level: Species or Family

Select Species or Family

Taxon Level: Species

Taxon Name: Zea mays

Filter your results



Column visibility

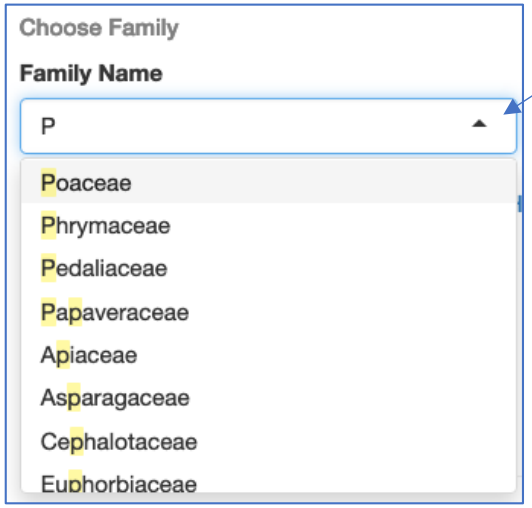
Search:

OrthoDB_Group	OrthoDB_Protein_Name	Accession	Accession_Protein_Name	Evidence_existence
201674at33090	RNA-binding domain, S1	P46618	Translation initiation factor IF-1, chloroplastic	Yes
80872at33090	EGF-like calcium-binding, conserved site	A0A0A7ENQ5	Wall-associated kinase	Yes
70014at33090	SecY/SEC61-alpha family	B8A1R6	SecY protein transport family protein	Yes
187354at33090	Ubiquitin-conjugating enzyme E2	A0A3L6DUL2	Ubiquitin-conjugating enzyme E2 36	Yes
184484at33090	Ubiquitin-conjugating enzyme E2	A0A3L6FR20	Ubiquitin-conjugating enzyme E2 2	Yes
218158at33090	Sm-like protein LSM2	A0A3L6F5V8	Sm-like protein LSM2	Yes
155756at33090	Small GTPase	B4FE06	Uncharacterized Protein	Yes
234012at33090	RNA polymerase archaeal subunit P/eukaryotic subunit RPABC4	A0A3L6E0I6	DNA-directed RNA polymerases II, IV and V subunit 12	Yes
209311at33090	Histone H2A	A0A3L6ET91	Histone H2A	Yes
157046at33090	DNA recombination and repair protein Rad51-like, C-terminal	B4FMC1	Meiotic recombination protein DMC1	Yes

Results of KusakiDB data

KusakiDB Tools: OG Assessment

Select a Family from KusakiDB



Results of KusakiDB data

Hayai_annotation_v2.0 | KusakiDB_v1.0 | kusakiDB/kusakiDBv1_tutorial

Not Secure | pgdbjsnp.kazusa.or.jp/app/kusakidb

KusakiDB v1.0

A novel approach for assessing existence and completeness of orthogroups in plant species

Search KusakiDB | OG Assessment | OG Management | OG Management User Data | Help

Assess conservation of orthogroups within complete genomes

Choose Family

Family Name

Poaceae

Or analyse your own data. Click here to create Hayai-annotation file

Upload Hayai_annotation_v2.0.tsv

Browse... No file selected

Submit

Users' Data

KusakiDB Complete Genomes Data

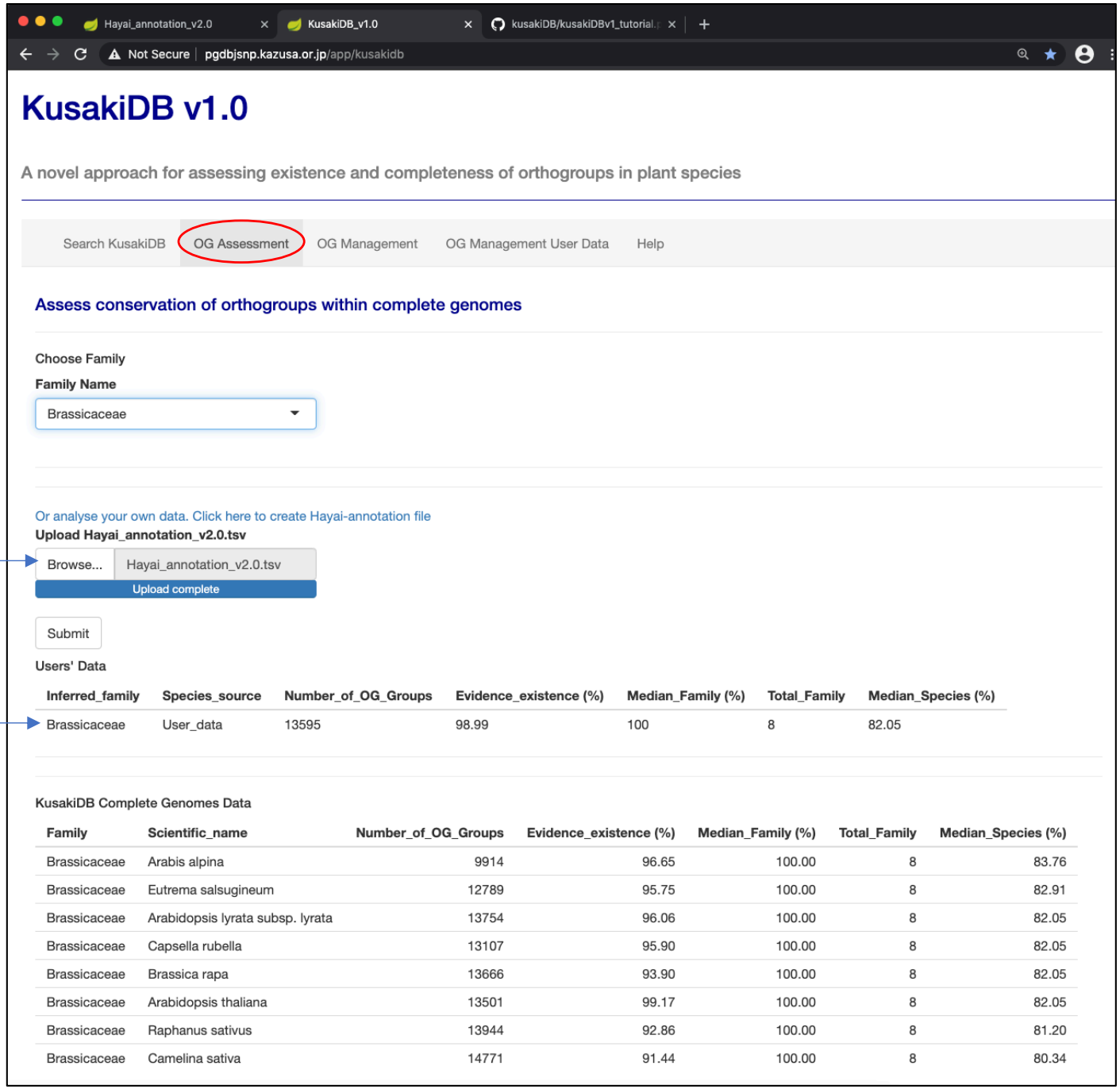
Family	Scientific_name	Number_of_OG_Groups	Evidence_existence (%)	Median_Family (%)	Total_Family	Median_Species (%)
Poaceae	Oryza brachyantha	11801	96.95	90.91	11	83.76
Poaceae	Triticum urartu	10512	91.83	90.91	11	82.91
Poaceae	Brachypodium distachyon	12833	95.11	90.91	11	82.91
Poaceae	Zea mays	13021	96.84	90.91	11	82.05
Poaceae	Oryza sativa Japonica Group	13128	96.95	90.91	11	82.05
Poaceae	Sorghum bicolor	13314	94.88	90.91	11	82.05
Poaceae	Dichanthelium oligosanthes	11988	93.45	90.91	11	82.05
Poaceae	Panicum hallii	13708	92.08	90.91	11	82.05
Poaceae	Setaria italica	13190	93.49	90.91	11	82.05
Poaceae	Aegilops tauschii	15967	80.14	81.82	11	78.63
Poaceae	Triticum aestivum	10932	59.80	45.45	11	9.40

KusakiDB OG Assessment accepts user's data

KusakiDB Tools: OG Assessment

Upload your own data annotated by Hayai-annotation v2.0

User's data result:
KusakiDB predicts family and calculate number of validated OGs, median of OG within same family and median of OG within all species



OG Assessment Equations

Median of OGs within a family (median family):

Median_Family (%) = $median(\frac{rep_{fam}}{Total_{family}} \times 100)$, where:

rep_{fam} is the count of unique sequences in an OG, per species, within a family.
$Total_{family}$ is the total number of species in each family.

Median of OGs within all species (median species):

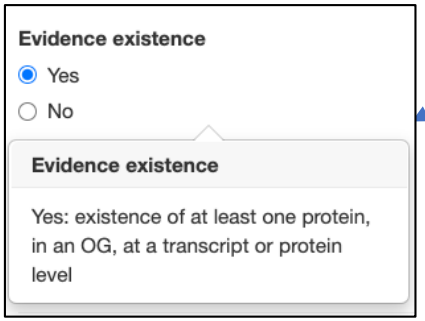
Median_Species (%) = $median(\frac{rep}{Total_{species}} \times 100)$, where:

rep is the count of unique sequences in an OG, per species.
$Total_{species}$ is the total number of species in KusakiDB.

KusakiDB Tools: OG Management

Select the parameters to compare OGs among all species in KusakiDB, such as:

- Evidence existence tag
- Number of species in each family
- Percentage of species in each family
- Percentage within all species (Percentage of Total Species)

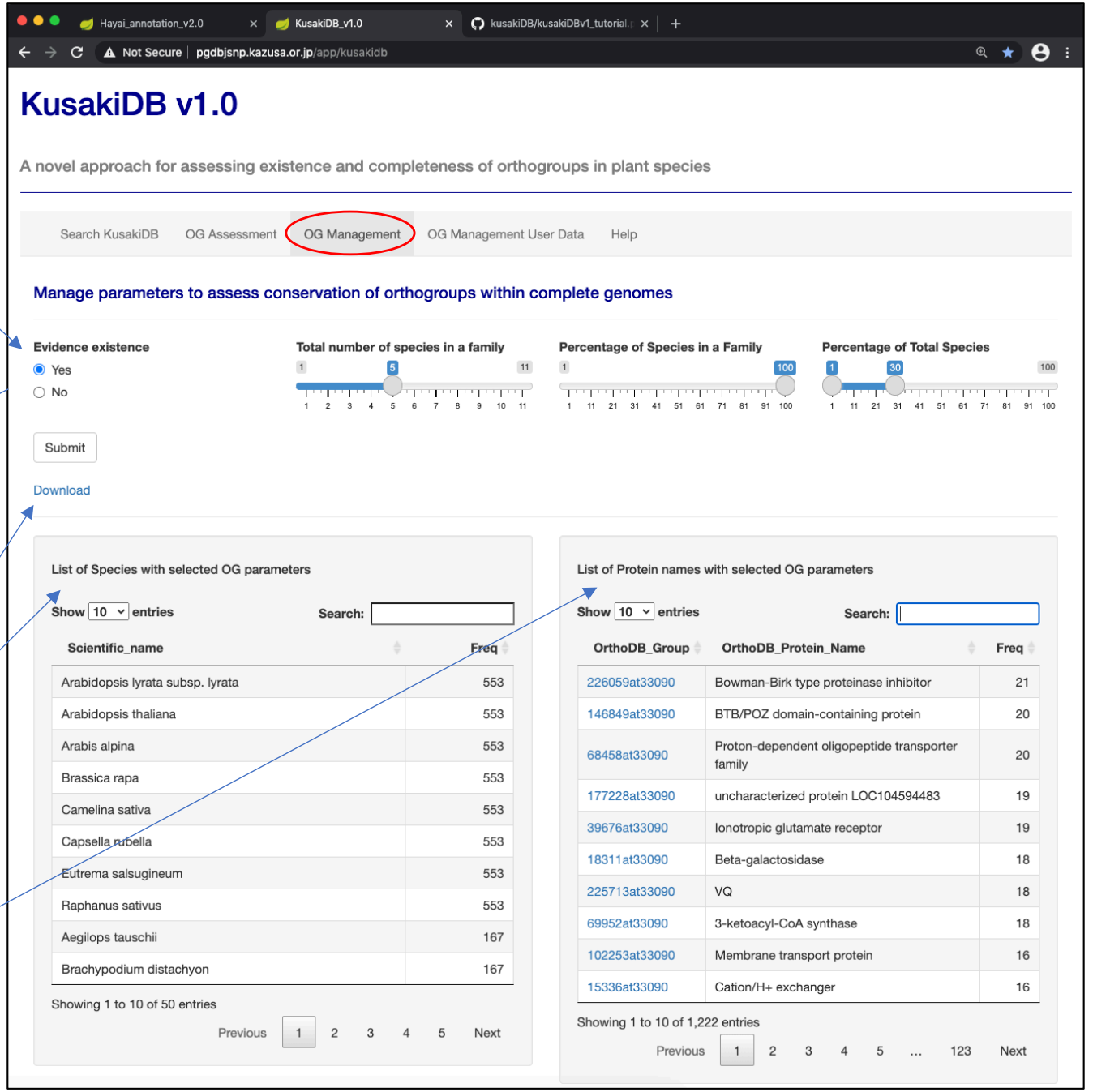


Pop-up

User can download the results

The results with the selected parameters are shown in two table:

- List of species and correspondent number of OGs/species
- List of protein names and correspondent number of species/OrthoDB protein name



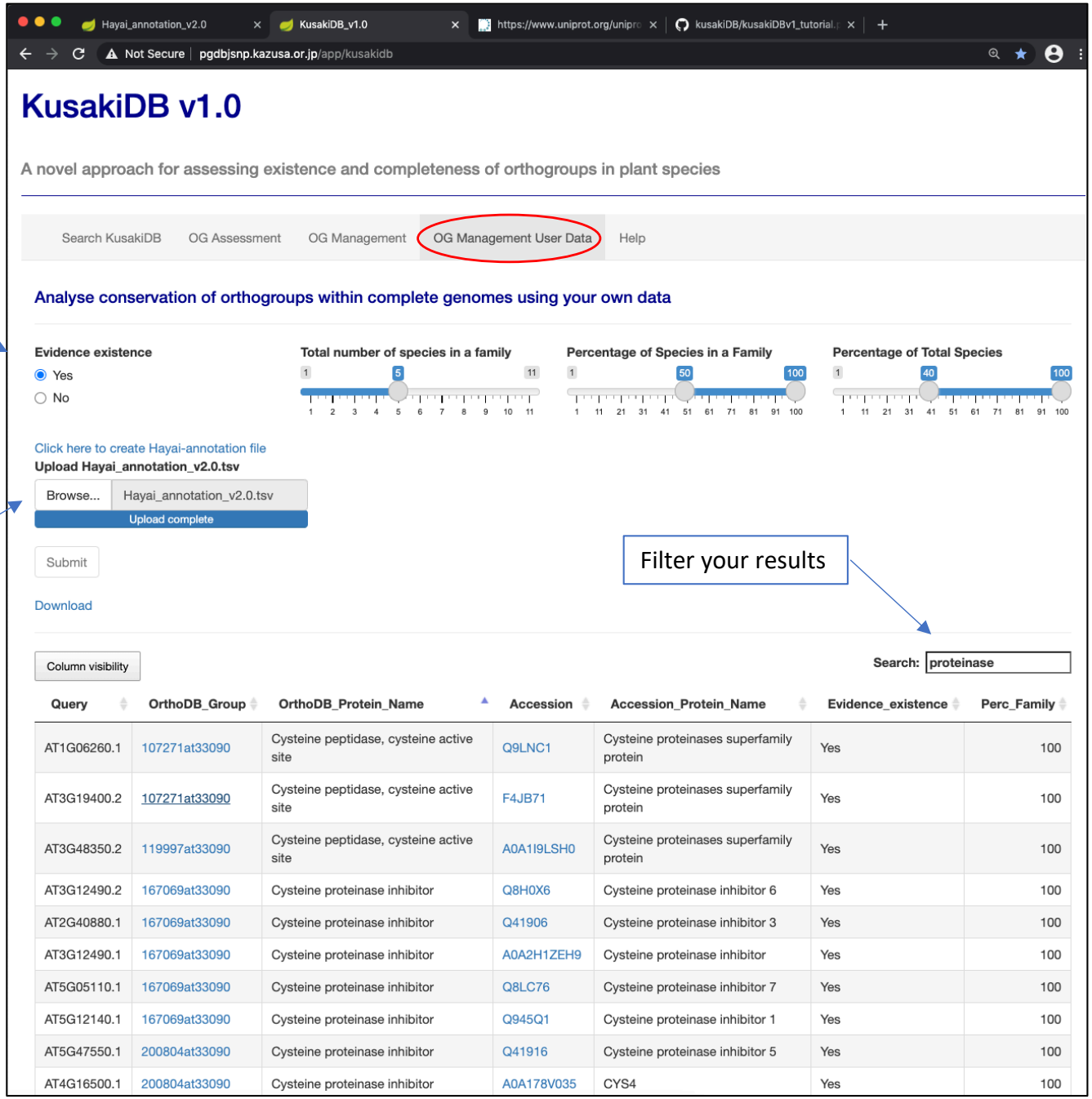
KusakiDB Tools: OG Management User Data

Select the parameters to compare OGs among all species in KusakiDB, such as:

- Evidence existence tag
- Number of species in each family
- Percentage of species in each family
- Percentage within all species (Percentage of Total Species)

Upload the functional annotation performed by Hayai-annotation v2.0

The results show a “filter” of the genes that are selected under the conditions regarding the conservation level for each OG.



Query	OrthoDB_Group	OrthoDB_Protein_Name	Accession	Accession_Protein_Name	Evidence_existence	Perc_Family
AT1G06260.1	107271at33090	Cysteine peptidase, cysteine active site	Q9LNC1	Cysteine proteinases superfamily protein	Yes	100
AT3G19400.2	107271at33090	Cysteine peptidase, cysteine active site	F4JB71	Cysteine proteinases superfamily protein	Yes	100
AT3G48350.2	119997at33090	Cysteine peptidase, cysteine active site	A0A1I9LSH0	Cysteine proteinases superfamily protein	Yes	100
AT3G12490.2	167069at33090	Cysteine proteinase inhibitor	Q8H0X6	Cysteine proteinase inhibitor 6	Yes	100
AT2G40880.1	167069at33090	Cysteine proteinase inhibitor	Q41906	Cysteine proteinase inhibitor 3	Yes	100
AT3G12490.1	167069at33090	Cysteine proteinase inhibitor	A0A2H1ZEH9	Cysteine proteinase inhibitor	Yes	100
AT5G05110.1	167069at33090	Cysteine proteinase inhibitor	Q8LC76	Cysteine proteinase inhibitor 7	Yes	100
AT5G12140.1	167069at33090	Cysteine proteinase inhibitor	Q945Q1	Cysteine proteinase inhibitor 1	Yes	100
AT5G47550.1	200804at33090	Cysteine proteinase inhibitor	Q41916	Cysteine proteinase inhibitor 5	Yes	100
AT4G16500.1	200804at33090	Cysteine proteinase inhibitor	A0A178V035	CYS4	Yes	100