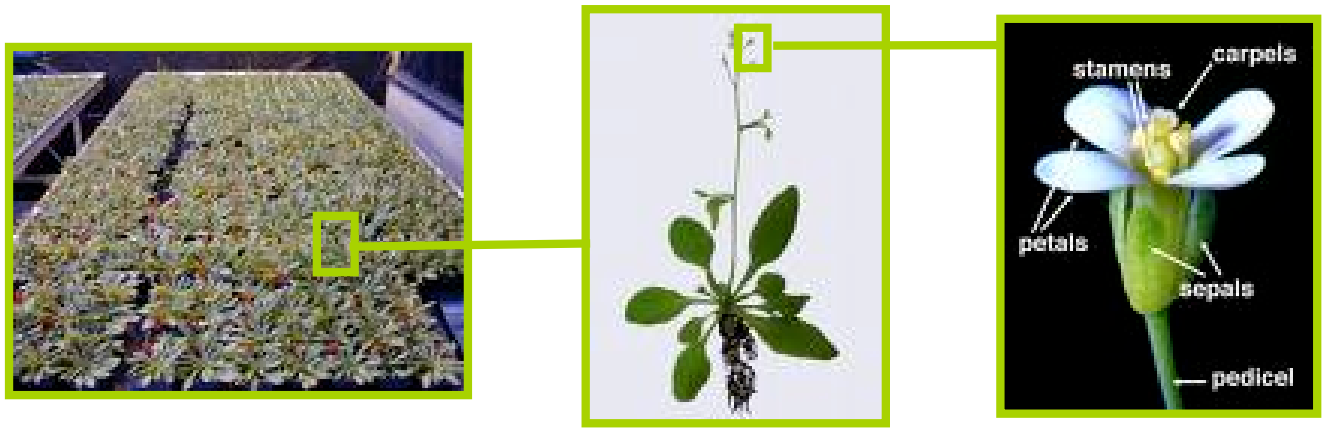
TAIR User Interface

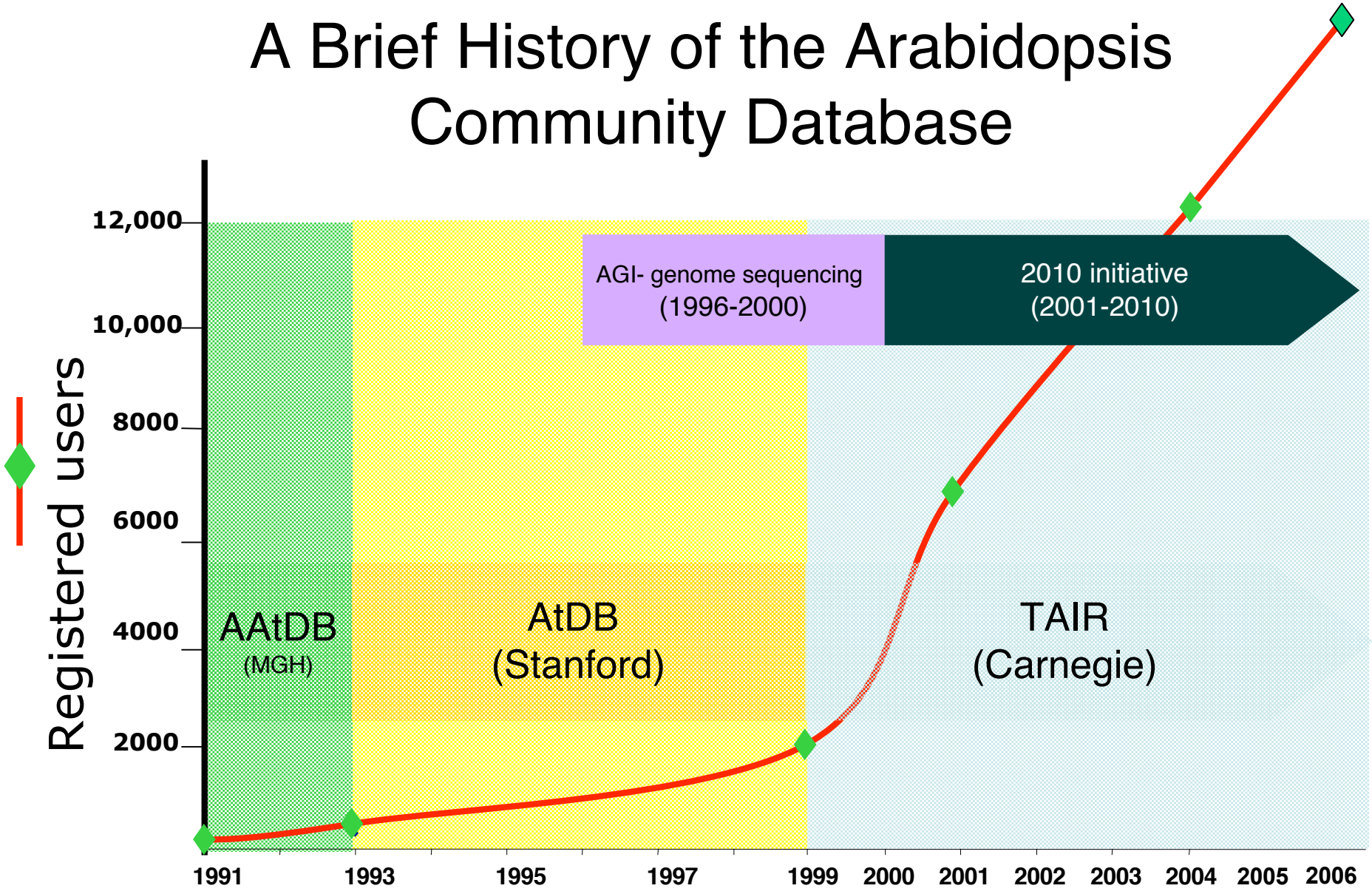
MOD User Interface Caucus

Talk outline

- TAIR intro
  - The Arabidopsis Information Resource
- 2 lessons learned
- Measuring usability
- TAIR interface examples



A Brief History of the Arabidopsis Community Database



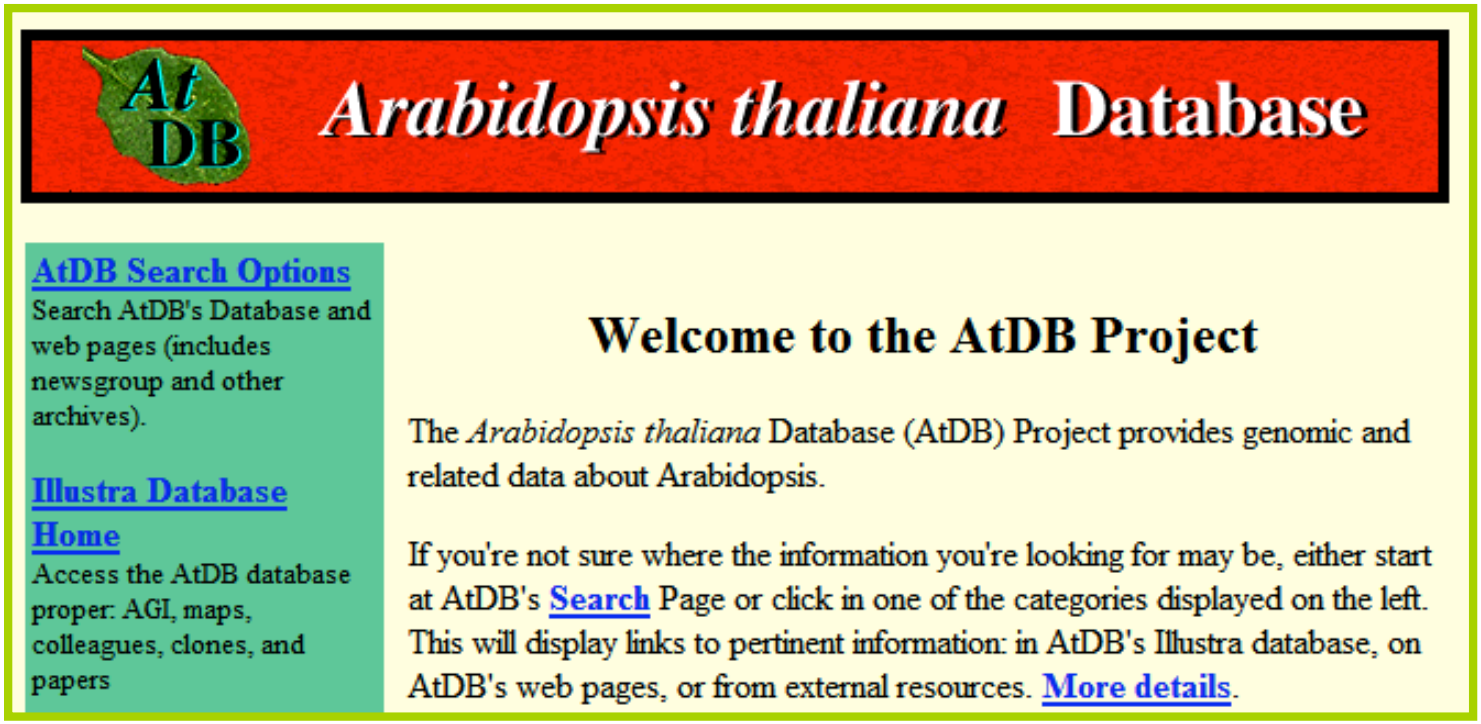
As of Aug 28 2006, 15,627 registered users.

Two lessons learned

- When designing a web interface:
  - How to use it must be obvious
  - It must function as expected

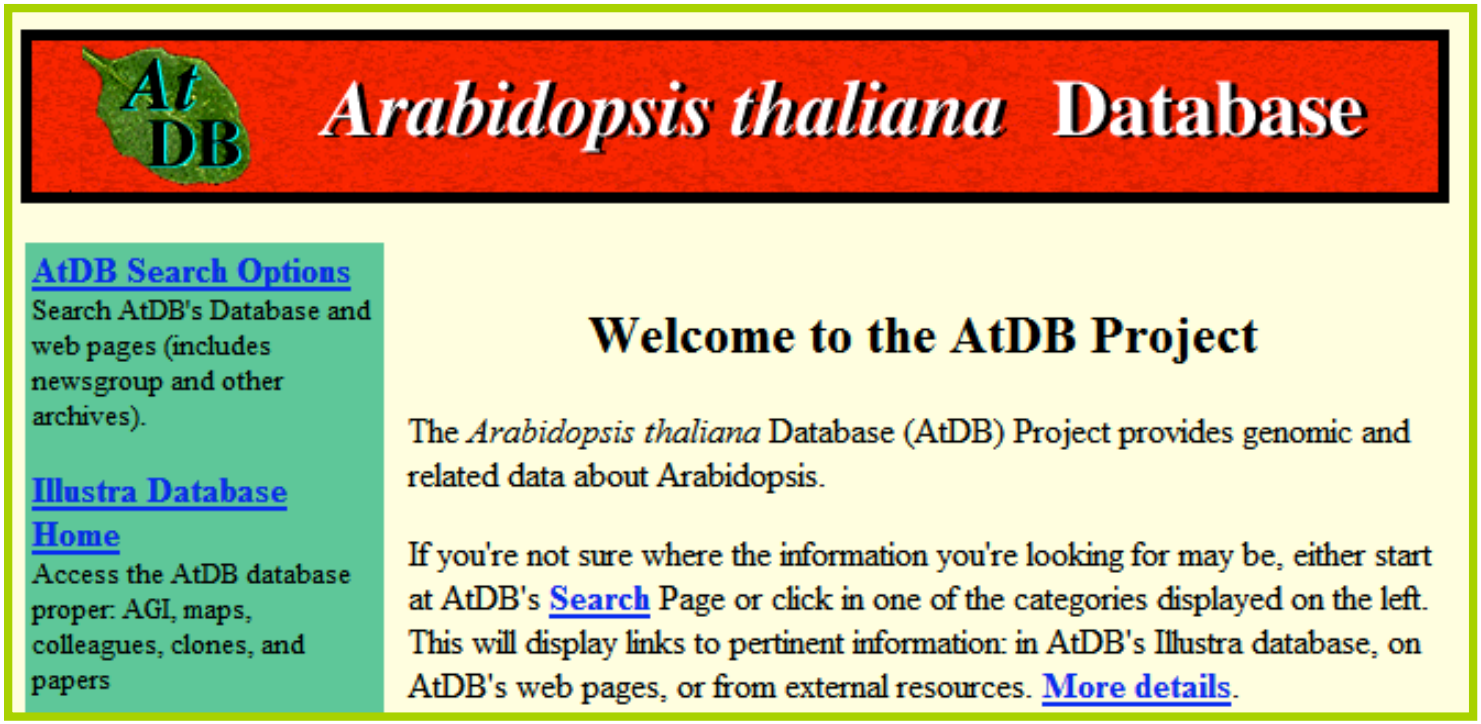
Obviousness

- 1999 AtDB search



Obviousness

- 1999 AtDB search
  - No box to enter a search term



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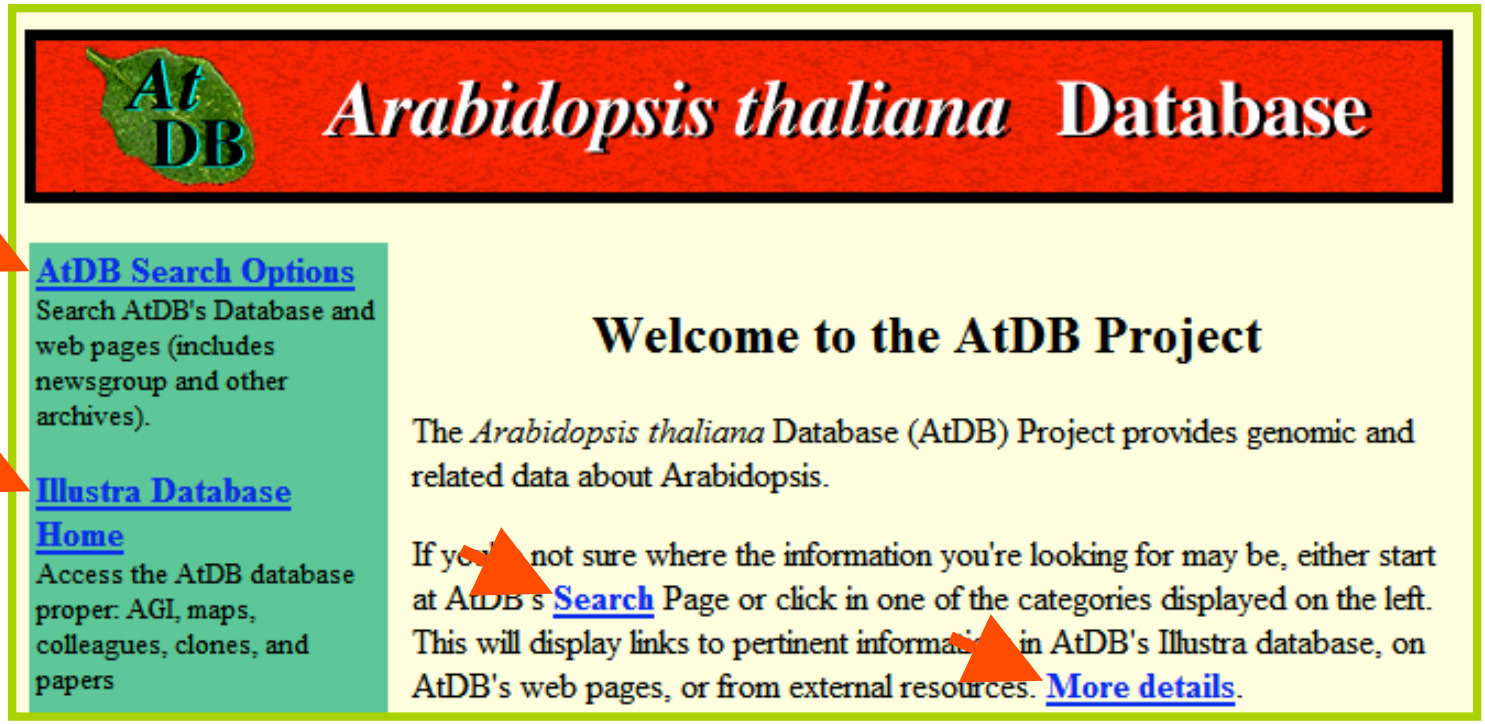

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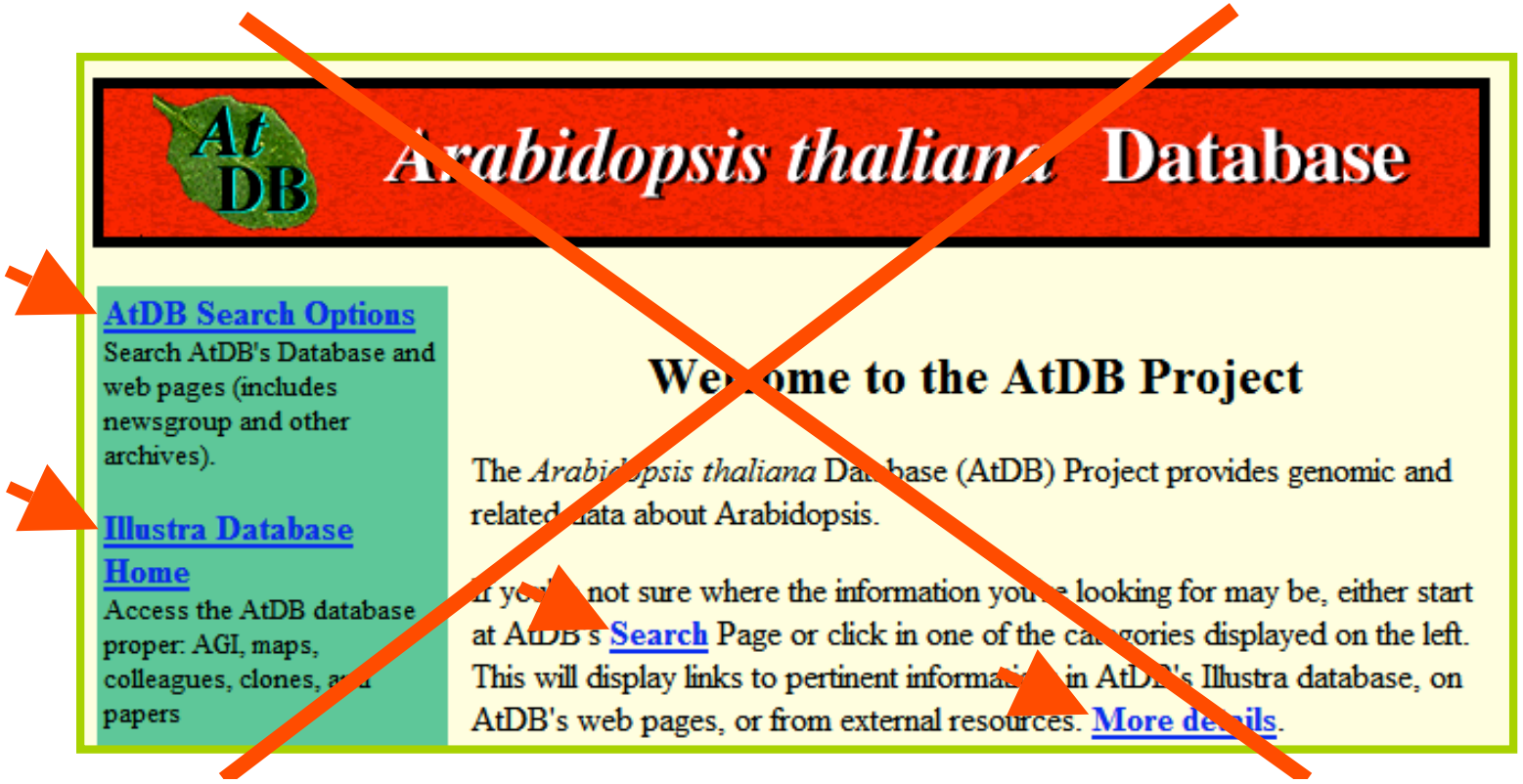
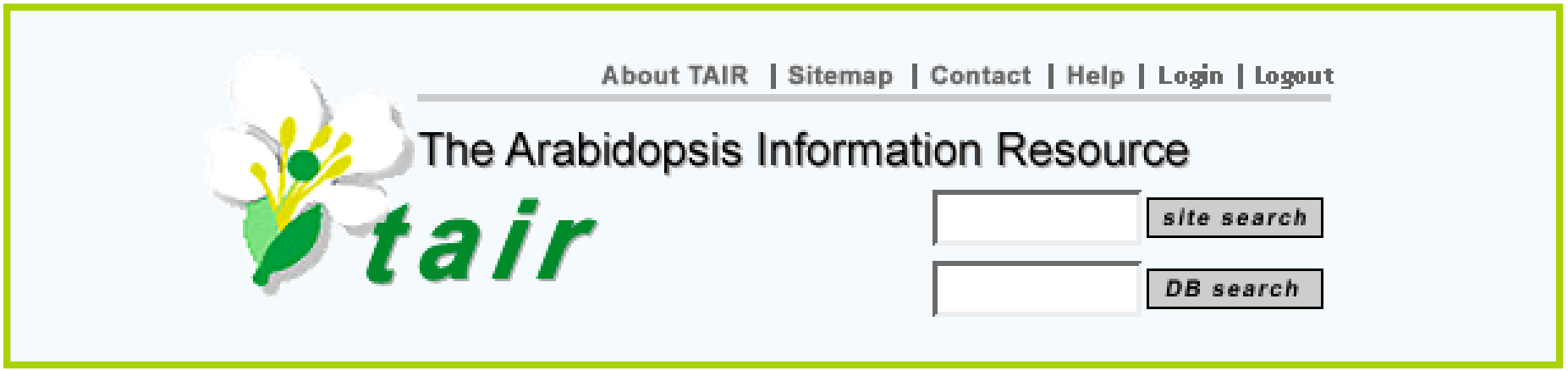


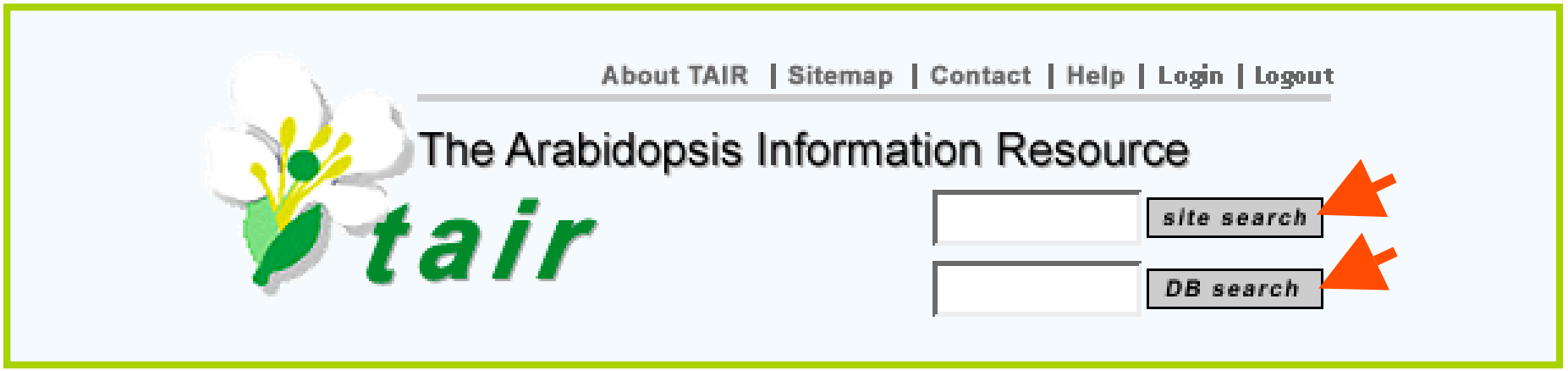
Expectations vs. results

- 2001 TAIR search



Expectations vs. results

- 2001 TAIR search
  - Why are there two search boxes?



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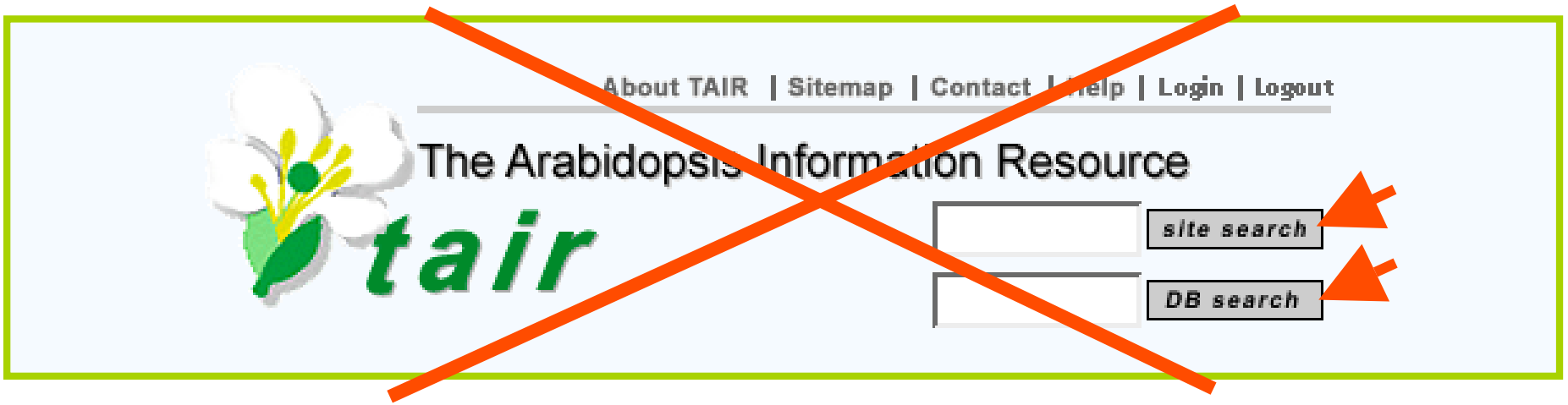

Expectations vs. results

- 2003 TAIR search

Expectations vs. results

- 2003 TAIR search
  - Function is unclear
    - What objects can I search for?
    - “Exact” or “contains” searching?
    - Just names, or also descriptions?

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Will this search for any object in the database containing “kinase”? **No.**

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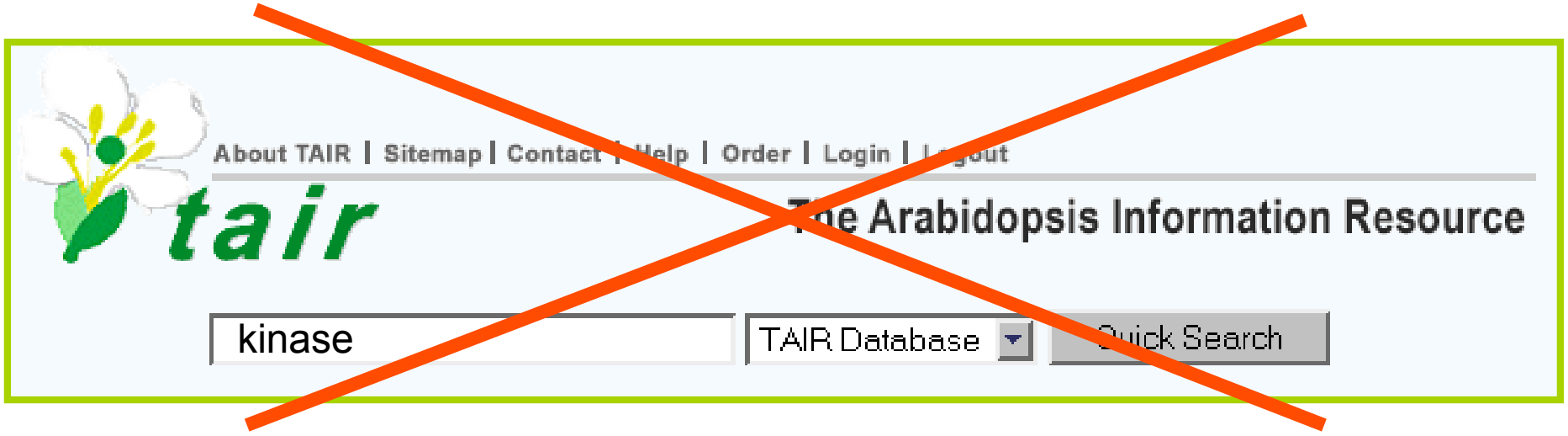

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Expectations vs. results

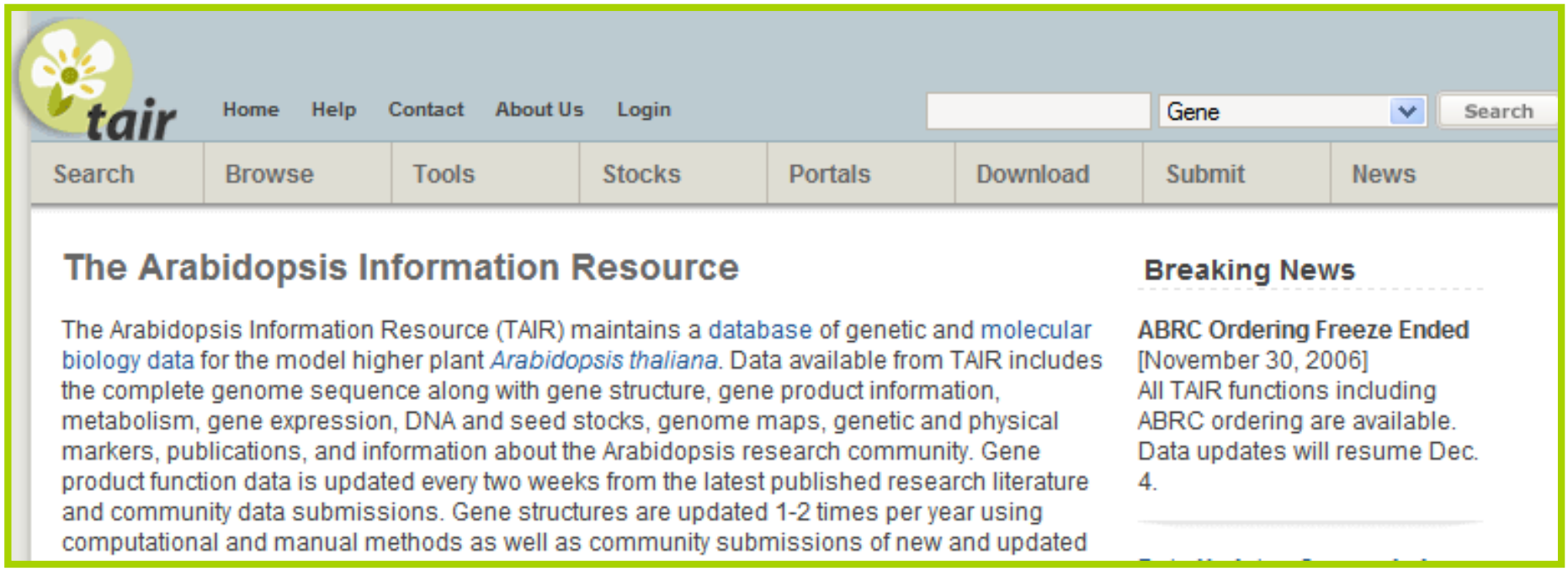
- How can we match expectations to results?
  - Alter results to fix expectations?
  - Alter expectations to fit results?

Expectations vs. results

- How can we match expectations to results?
  - Alter results to fix expectations?
  - Alter expectations to fit results?
  - A bit of both?

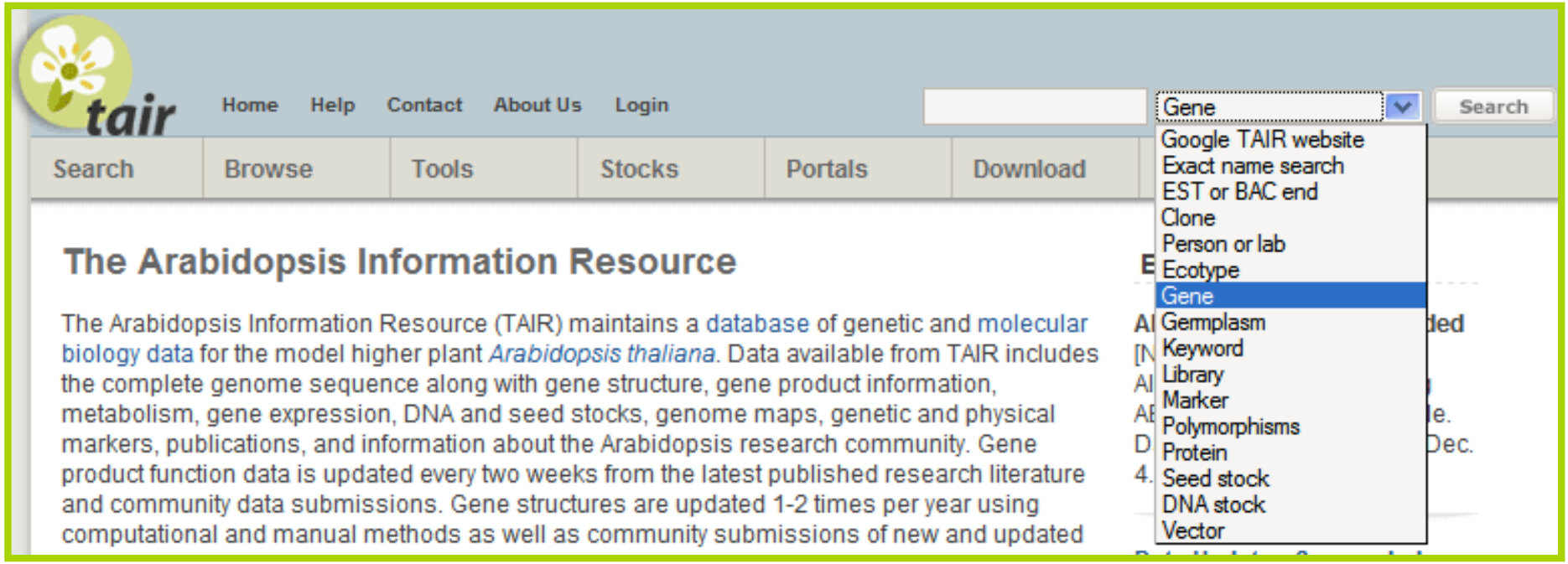
Expectations vs. results

- 2006 TAIR search
  - Use is obvious
  - Expectations are clearer
  - Functions as expected by most users



Expectations vs. results

- 2006 TAIR search
  - Searches Gene by default
  - BUT other searches are still accessible



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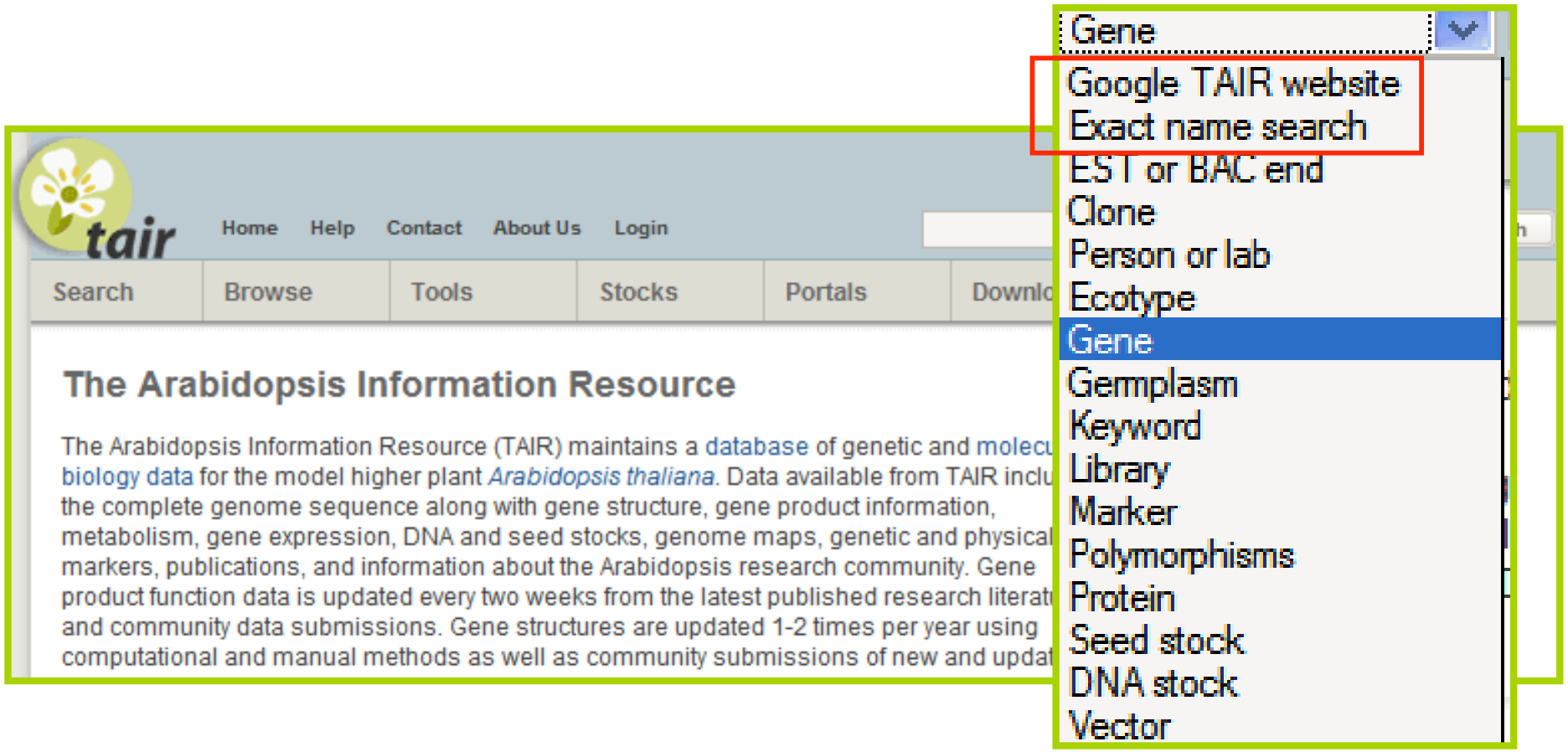
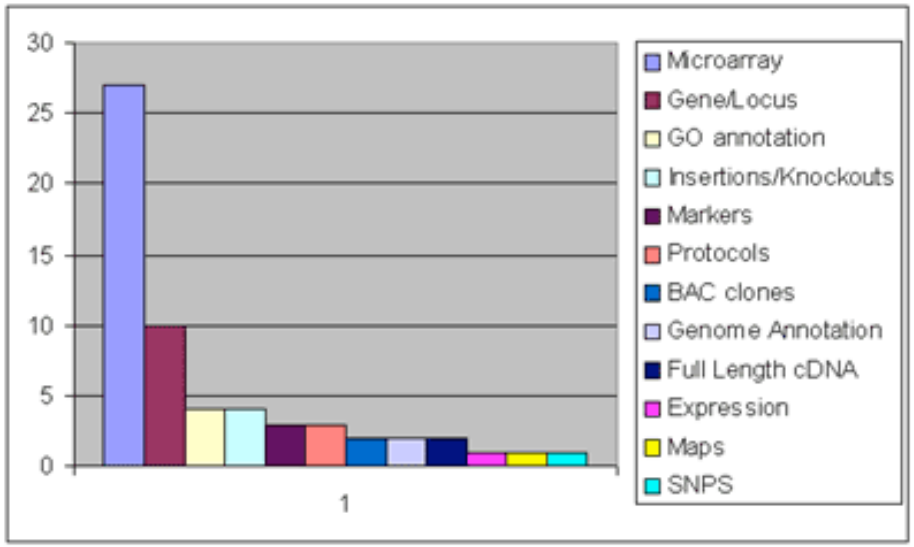


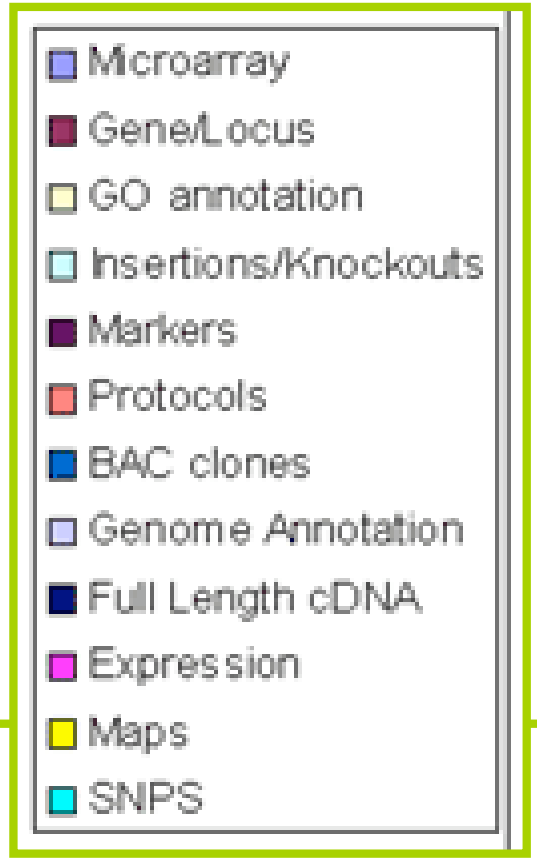
Measuring usability

- Community feedback
  - Email questions
  - Workshops
  - Surveys
- Site logging
- Live usability tests

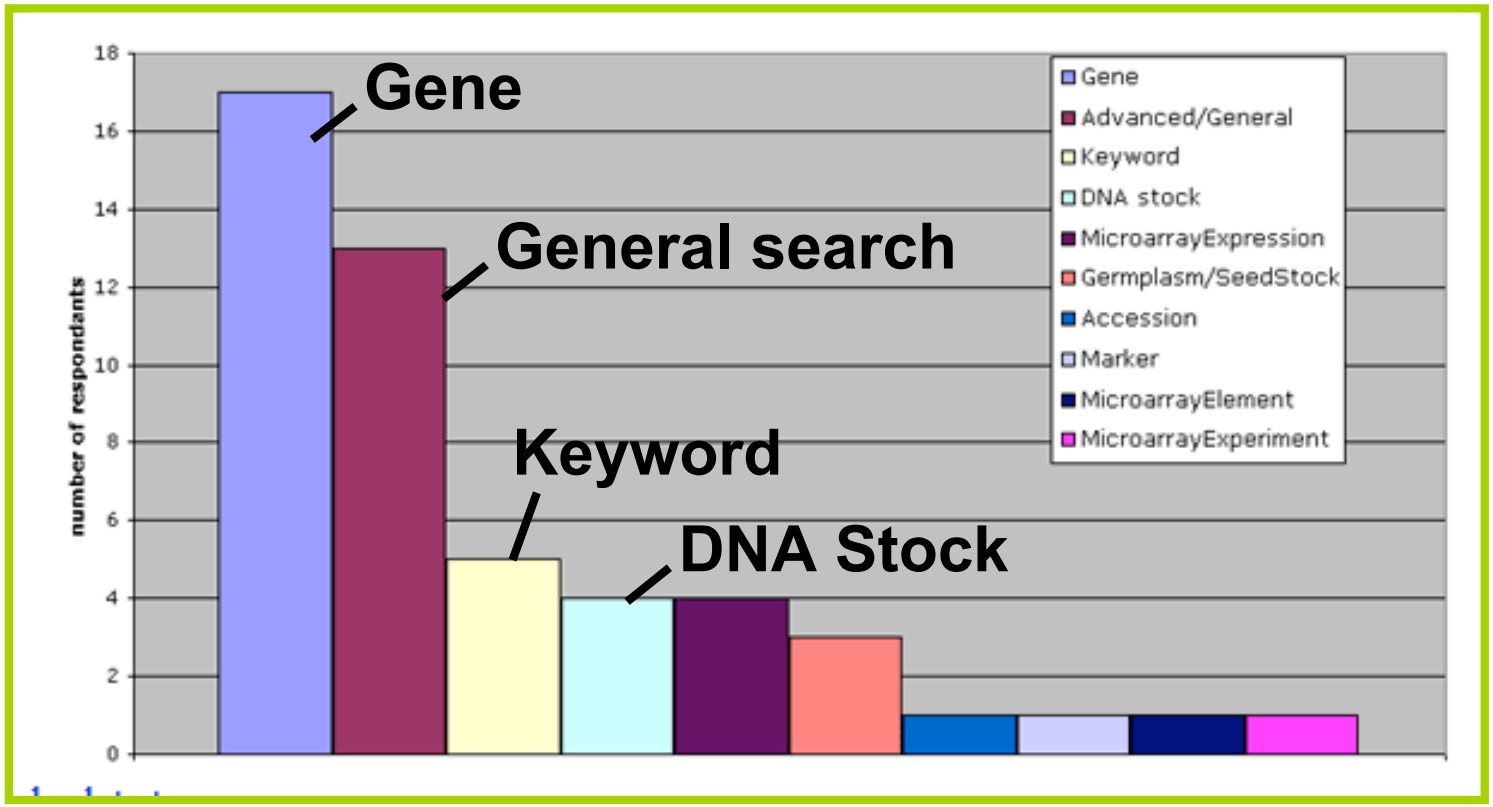
Surveys

Question 3 Results (What tools/searches/information do you find most difficult to use at TAIR and why?)





Surveys



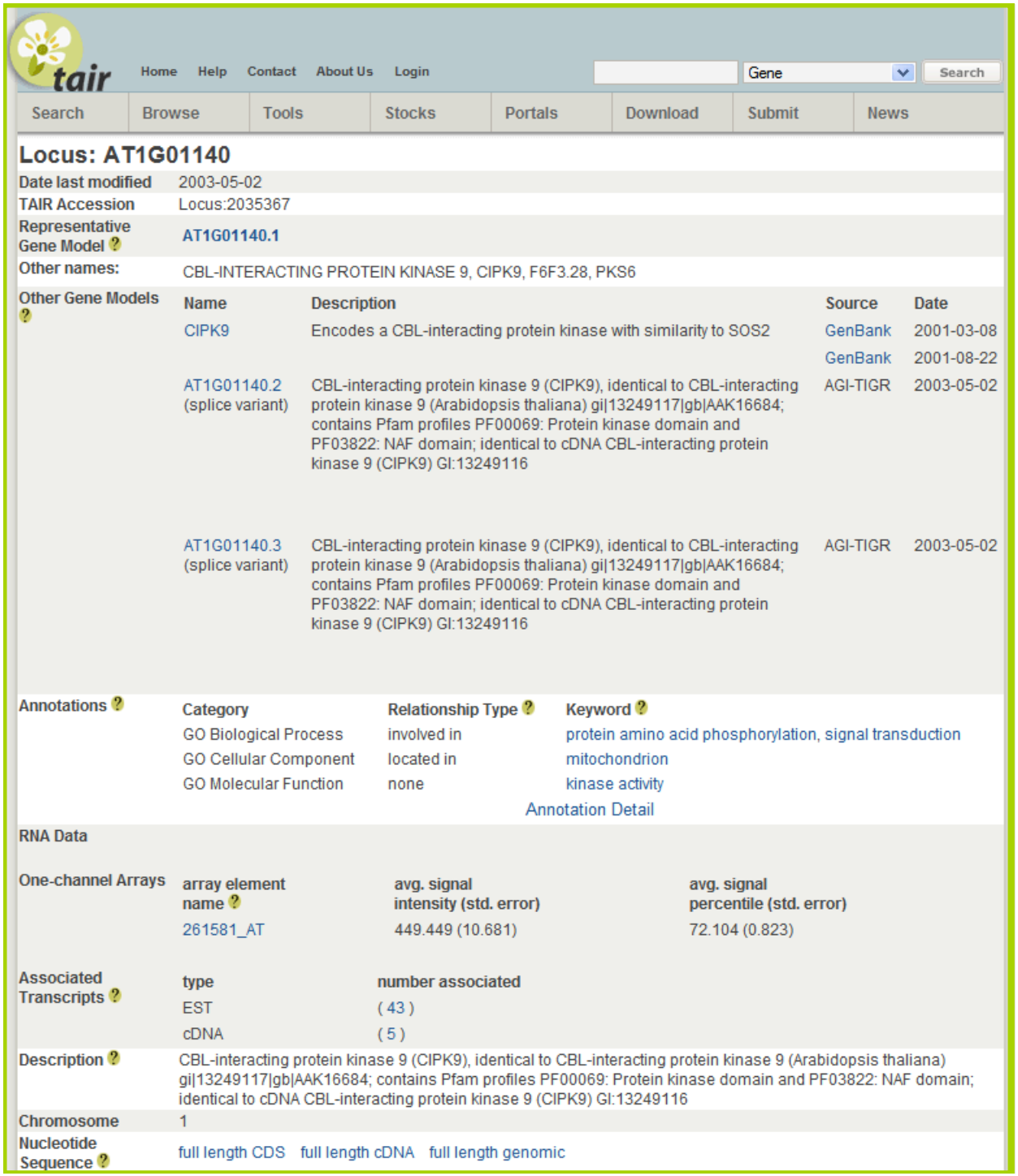
Which searches give the most trouble?

Site Logging

- Log query strings with 0 results
- Eliminate misspellings, objects not stored
- Why did remainder fail?
  - Requires ‘contained in’ search
  - Requires separate matching of each word
  - General concept not associated to object

GMOD interface topics

- Gene search
- Locus/gene page
- Search for gene by phenotype or GO annotation
- Custom report on some aspect of gene
- Bulk output based on a query
- Combine results with info from other data sources



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Locus: AT1G01140

Date last modified	2003-05-02
TAIR Accession	Locus:2035367
Representative Gene Model	AT1G01140.1
Other names:	CBL-INTERACTING PROTEIN KINASE 9, CIPK9, F6F3.28, PKS6

Other Gene Models

Name	Description	Source	Date
CIPK9	Encodes a CBL-interacting protein kinase with similarity to SOS2	GenBank	2001-03-08
		GenBank	2001-08-22
AT1G01140.2 (splice variant)	CBL-interacting protein kinase 9 (CIPK9), identical to CBL-interacting protein kinase 9 (Arabidopsis thaliana) gi|13249117|gb|AAK16684; contains Pfam profiles PF00069: Protein kinase domain and PF03822: NAF domain; identical to cDNA CBL-interacting protein kinase 9 (CIPK9) GI:13249116	AGI-TIGR	2003-05-02
AT1G01140.3 (splice variant)	CBL-interacting protein kinase 9 (CIPK9), identical to CBL-interacting protein kinase 9 (Arabidopsis thaliana) gi|13249117|gb|AAK16684; contains Pfam profiles PF00069: Protein kinase domain and PF03822: NAF domain; identical to cDNA CBL-interacting protein kinase 9 (CIPK9) GI:13249116	AGI-TIGR	2003-05-02

Annotations

Category	Relationship Type	Keyword
GO Biological Process	involved in	protein amino acid phosphorylation, signal transduction
GO Cellular Component	located in	mitochondrion
GO Molecular Function	none	kinase activity

Annotation Detail

RNA Data

One-channel Arrays

array element name	avg. signal intensity (std. error)	avg. signal percentile (std. error)
261581_AT	449.449 (10.681)	72.104 (0.823)

Associated Transcripts

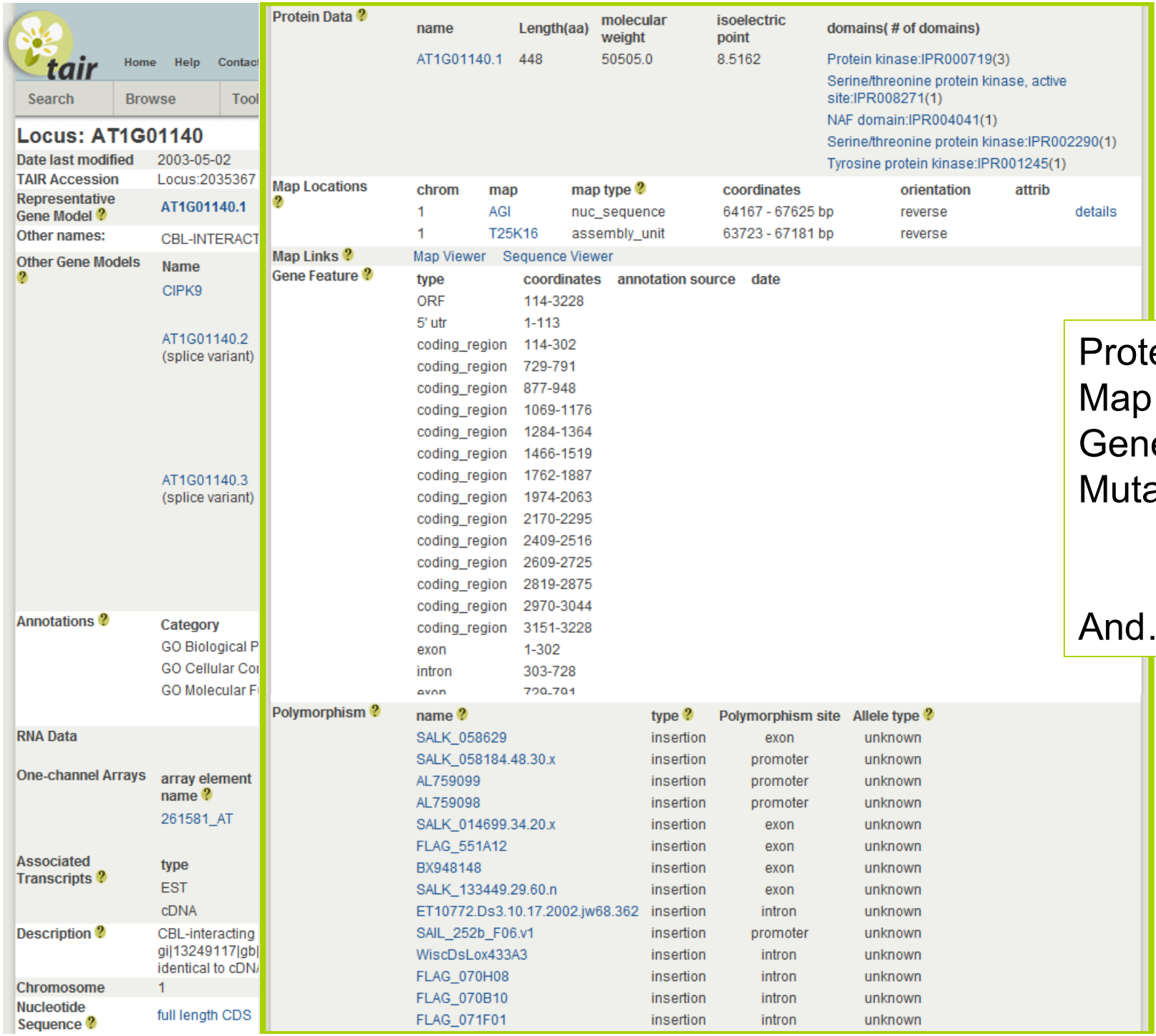
type	number associated
EST	(43)
cDNA	(5)

Description	CBL-interacting protein kinase 9 (CIPK9), identical to CBL-interacting protein kinase 9 (Arabidopsis thaliana) gi|13249117|gb|AAK16684; contains Pfam profiles PF00069: Protein kinase domain and PF03822: NAF domain; identical to cDNA CBL-interacting protein kinase 9 (CIPK9) GI:13249116
Chromosome	1
Nucleotide Sequence	full length CDS full length cDNA full length genomic

Gene Page

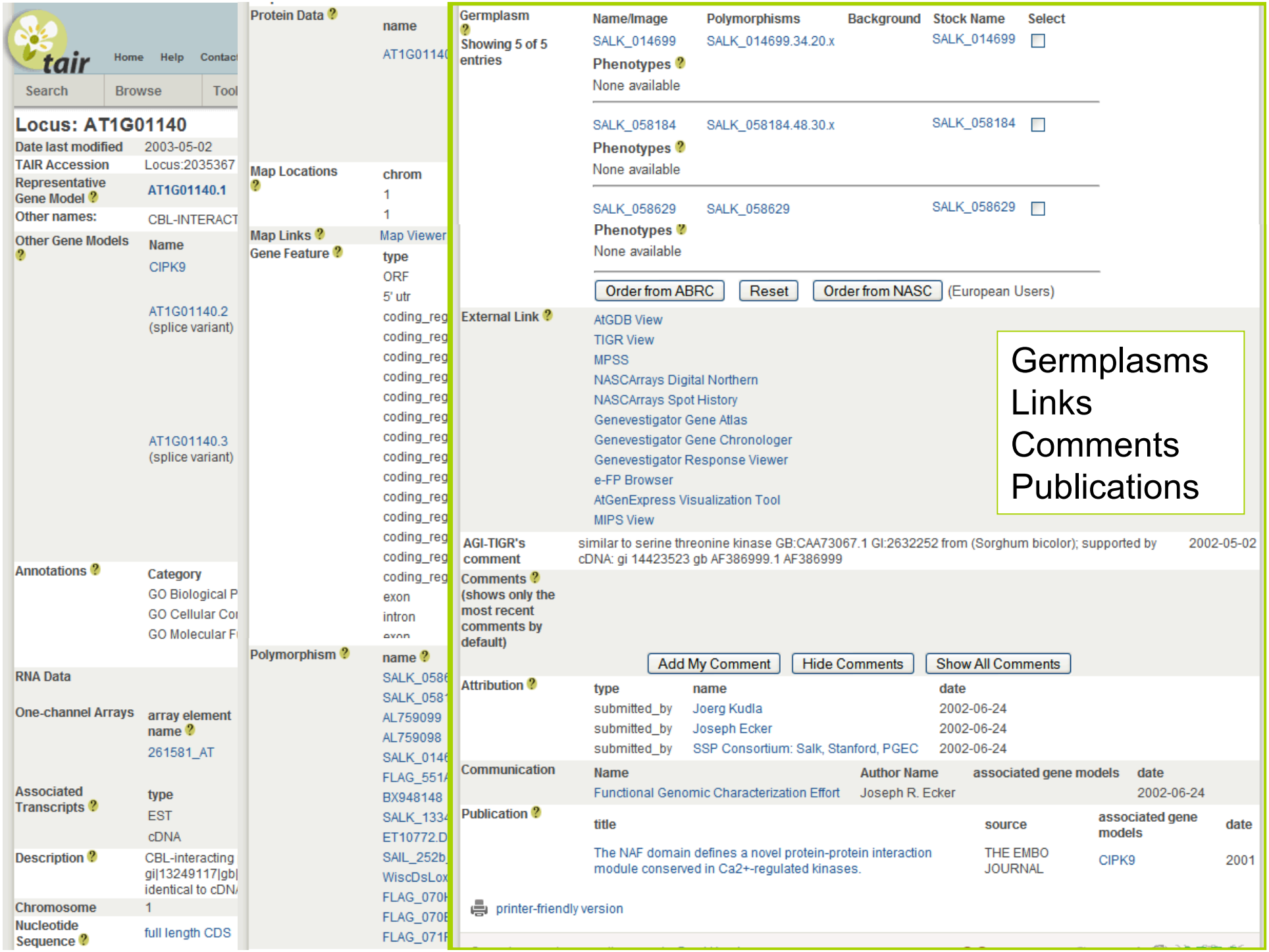
Other names
Splice variants
GO annotations
Expression
Description
Sequences

And…..



Proteins
Map Info
Gene structure
Mutations

And…..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Search
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Tool
Locus: AT1G01140
Date last modified 2003-05-02
TAIR Accession Locus:2035367
Representative Gene Model
AT1G01140.1
Other names: CBL-INTERACT
Other Gene Models
Name
CIPK9
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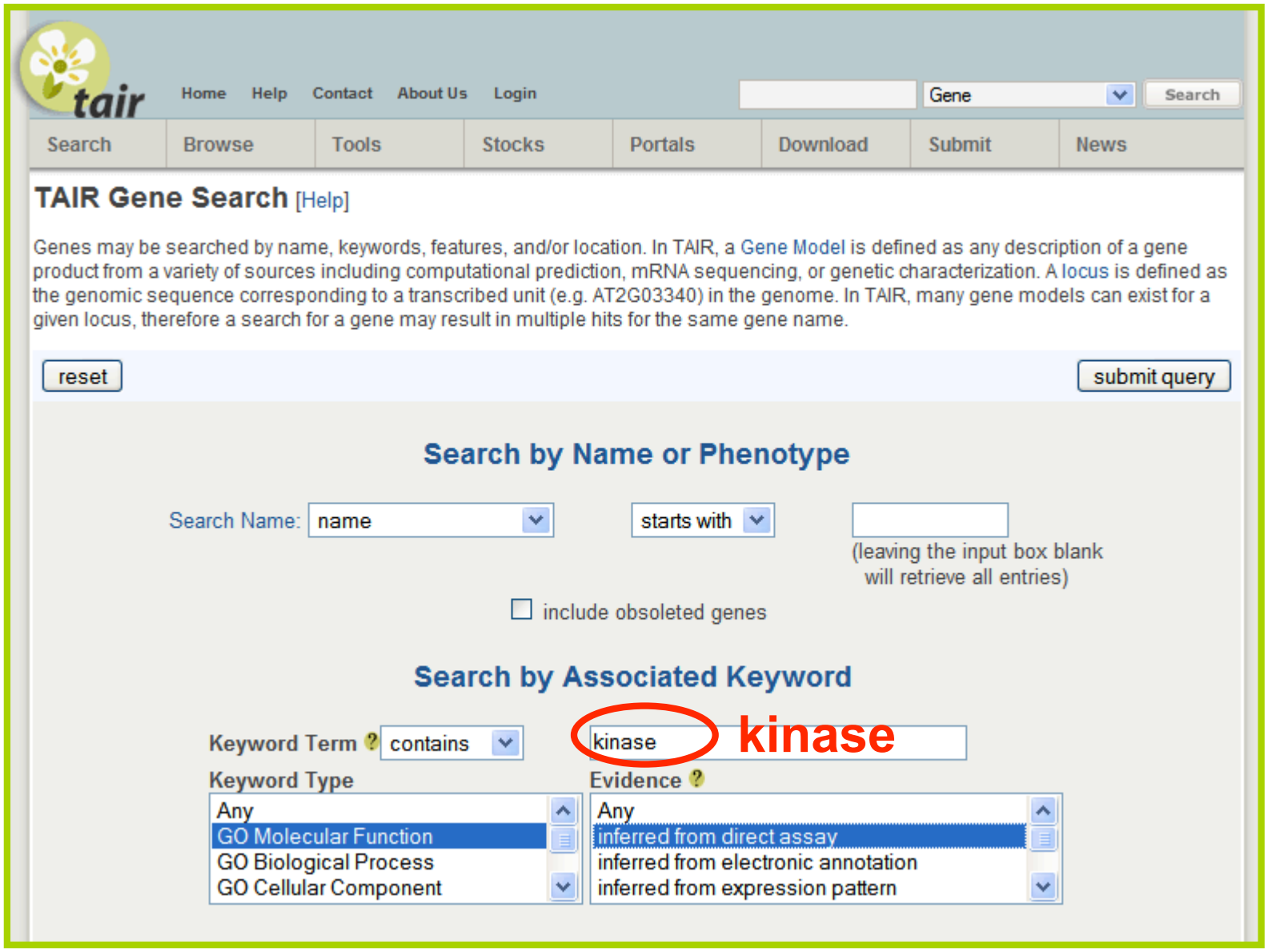
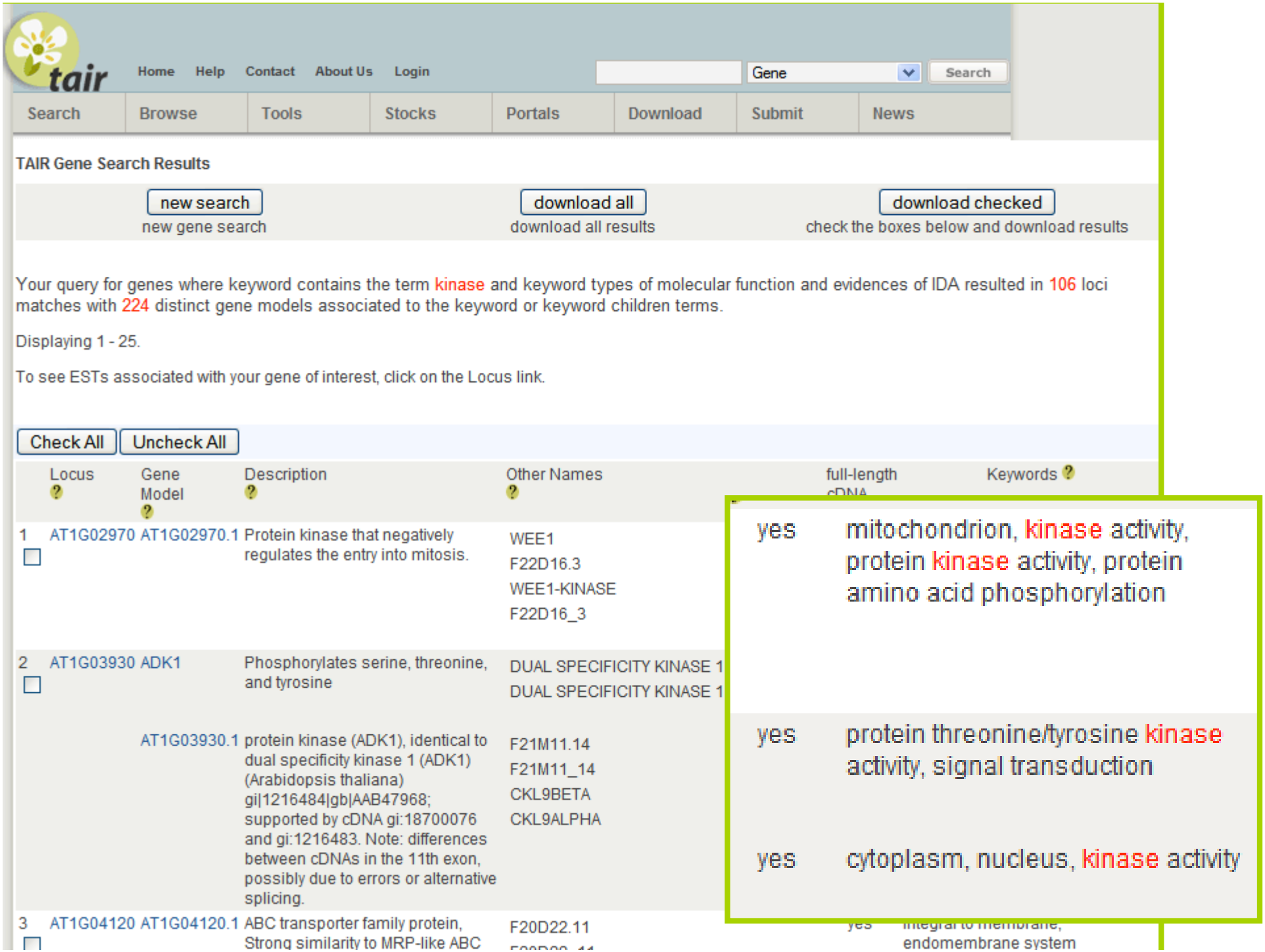
Annotations
Category
GO Biological P
GO Cellular Co
GO Molecular F
RNA Data
One-channel Arrays
array element name
261581_AT
Associated Transcripts
type
EST
cDNA
Description
CBL-interacting
gi|13249117|gb|
identical to cDN
Chromosome 1
Nucleotide Sequence
full length CDS
Protein Data
name
AT1G0114
Map Locations
chrom
1
1
Map Links
Map Viewer
Gene Feature
type
ORF
5' utr
coding_reg
exon
intron
Polymorphism
name
SALK_058
SALK_058
AL759099
AL759098
SALK_014
FLAG_551
BX948148
SALK_133
ET10772.D
SAIL_252b
WiscDsLox
FLAG_070
FLAG_070
FLAG_071
Germplasm
Showing 5 of 5 entries
Name/Image
Polymorphisms
Background
Stock Name
Select
SALK_014699
SALK_014699.34.20.x
SALK_014699
Phenotypes
None available
SALK_058184
SALK_058184.48.30.x
SALK_058184
Phenotypes
None available
SALK_058629
SALK_058629
SALK_058629
Phenotypes
None available
Order from ABRC
Reset
Order from NASC
(European Users)
External Link
AtGDB View
TIGR View
MPSS
NASCArrays Digital Northern
NASCArrays Spot History
Genevestigator Gene Atlas
Genevestigator Gene Chronologer
Genevestigator Response Viewer
e-FP Browser
AtGenExpress Visualization Tool
MIPS View
Germplasms
Links
Comments
Publications
AGI-TIGR's comment
similar to serine threonine kinase GB:CAA73067.1 GI:2632252 from (Sorghum bicolor); supported by cDNA: gi 14423523 gb AF386999.1 AF386999
2002-05-02
Comments (shows only the most recent comments by default)
Add My Comment
Hide Comments
Show All Comments
Attribution
type
name
date
submitted_by
Joerg Kudla
2002-06-24
submitted_by
Joseph Ecker
2002-06-24
submitted_by
SSP Consortium: Salk, Stanford, PGEC
2002-06-24
Communication
Name
Author Name
associated gene models
date
Functional Genomic Characterization Effort
Joseph R. Ecker
2002-06-24
Publication
title
source
associated gene models
date
The NAF domain defines a novel protein-protein interaction module conserved in Ca2+-regulated kinases.
THE EMBO JOURNAL
CIPK9
2001
printer-friendly version

Search for gene by GO annotation

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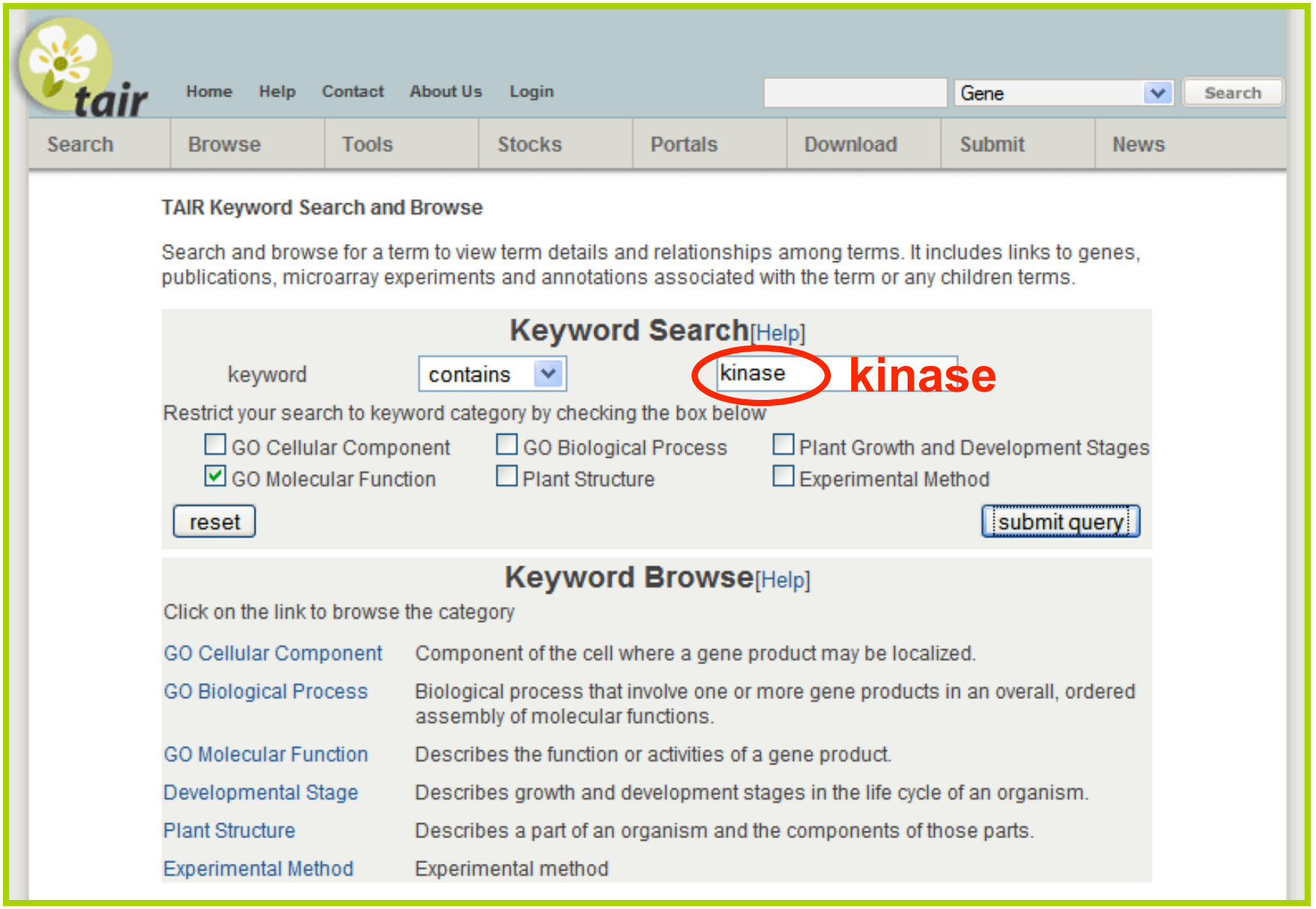
Gene
Search
Search Browse Tools Stocks Portals Download Submit News
TAIR Gene Search Results
new search
new gene search
download all
download all results
download checked
check the boxes below and download results
Your query for genes where keyword contains the term kinase and keyword types of molecular function and evidences of IDA resulted in 106 loci matches with 224 distinct gene models associated to the keyword or keyword children terms.
Displaying 1 - 25.
To see ESTs associated with your gene of interest, click on the Locus link.
Check All
Uncheck All
Locus
Gene Model
Description
Other Names
full-length cDNA
Keywords
1 AT1G02970 AT1G02970.1 Protein kinase that negatively regulates the entry into mitosis.
WEE1
F22D16.3
WEE1-KINASE
F22D16_3
yes
mitochondrion, kinase activity, protein kinase activity, protein amino acid phosphorylation
2 AT1G03930 ADK1 Phosphorylates serine, threonine, and tyrosine
DUAL SPECIFICITY KINASE 1
DUAL SPECIFICITY KINASE 1
AT1G03930.1 protein kinase (ADK1), identical to dual specificity kinase 1 (ADK1) (Arabidopsis thaliana) gi|1216484|gb|AAB47968; supported by cDNA gi:18700076 and gi:1216483. Note: differences between cDNAs in the 11th exon, possibly due to errors or alternative splicing.
F21M11.14
F21M11_14
CKL9BETA
CKL9ALPHA
yes
protein threonine/tyrosine kinase activity, signal transduction
yes
cytoplasm, nucleus, kinase activity
3 AT1G04120 AT1G04120.1 ABC transporter family protein, Strong similarity to MRP-like ABC
F20D22.11
yes
integral to membrane, endomembrane system

Search or browse keywords/GO terms



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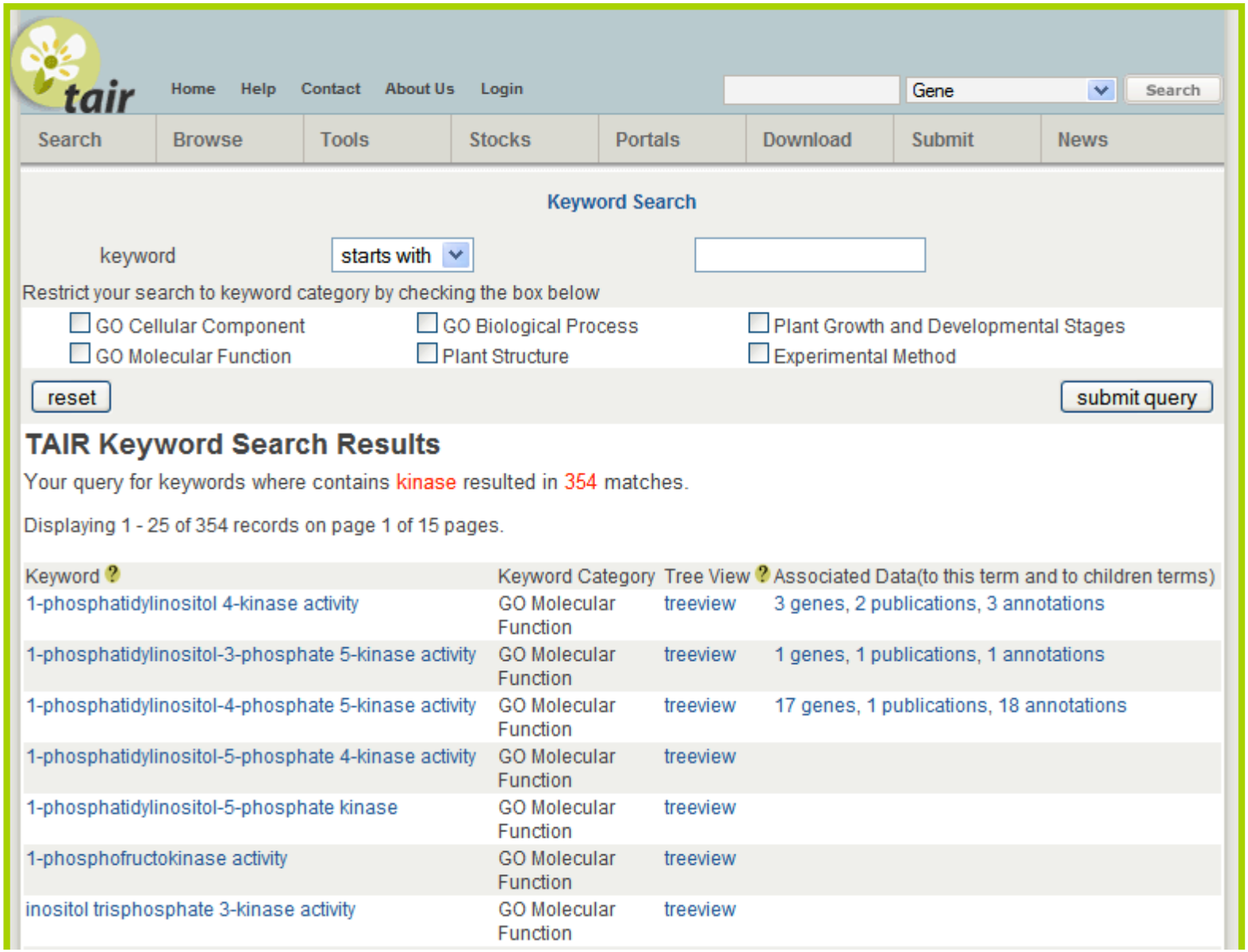
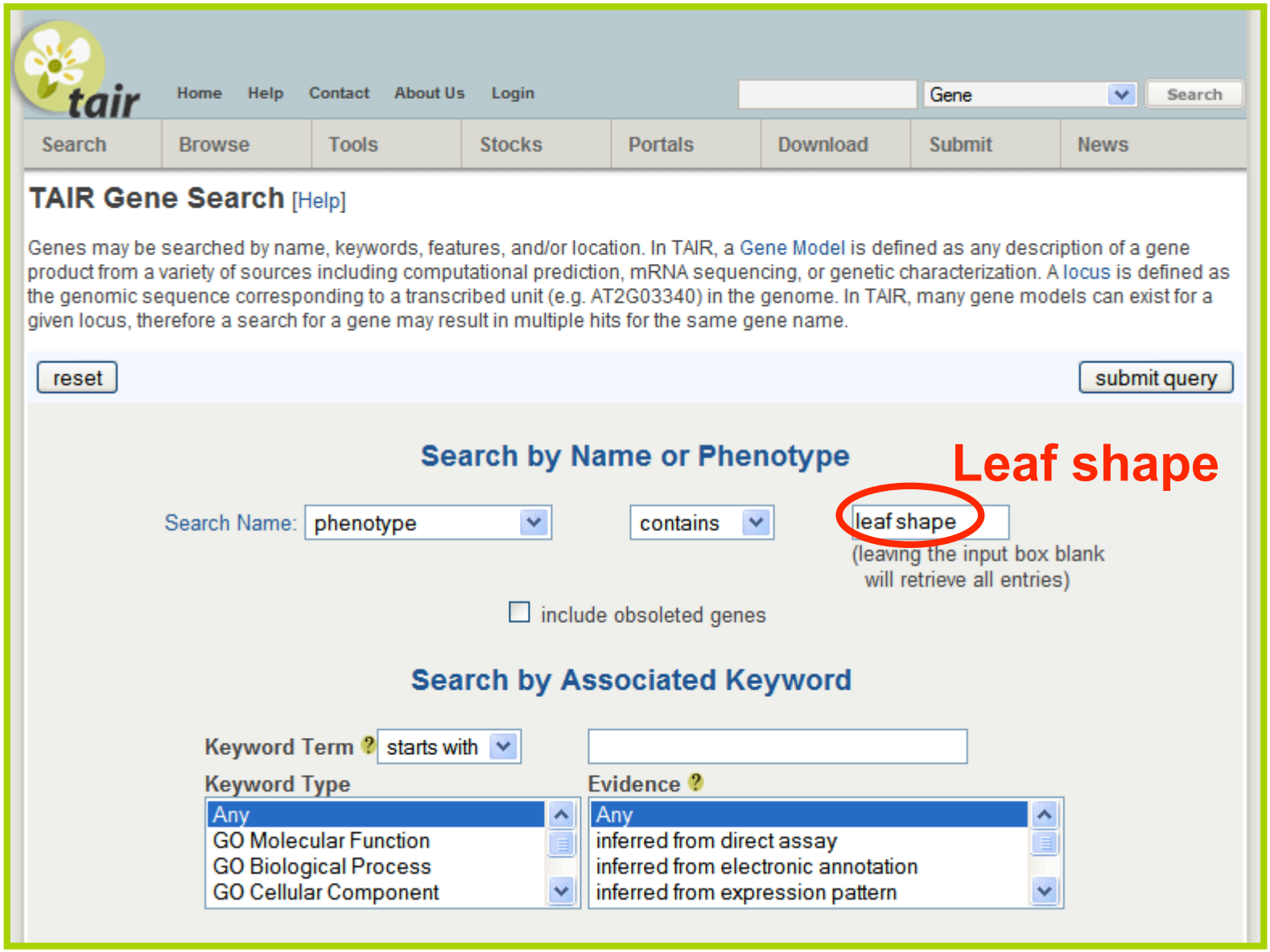
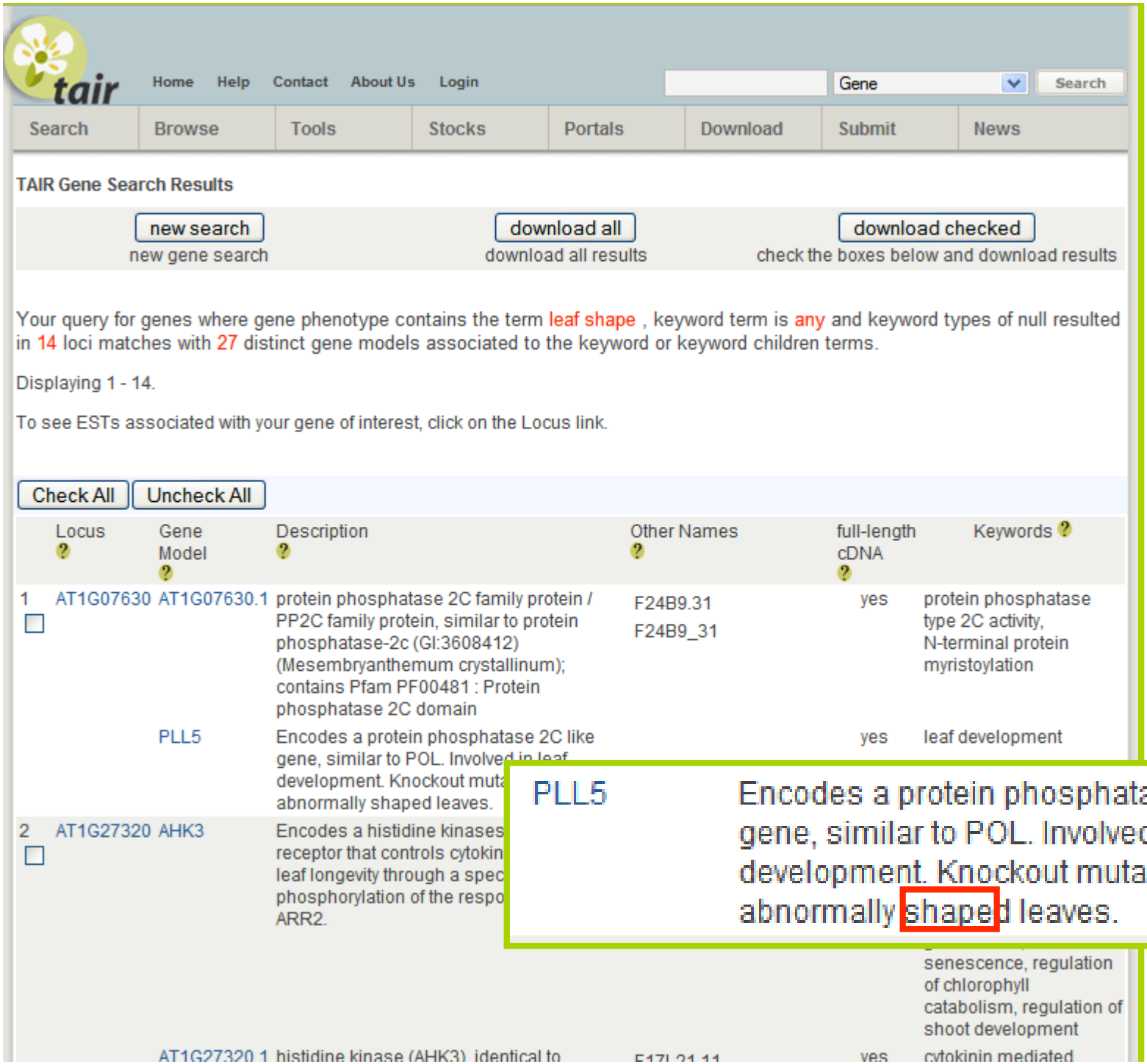


Search for gene by phenotype

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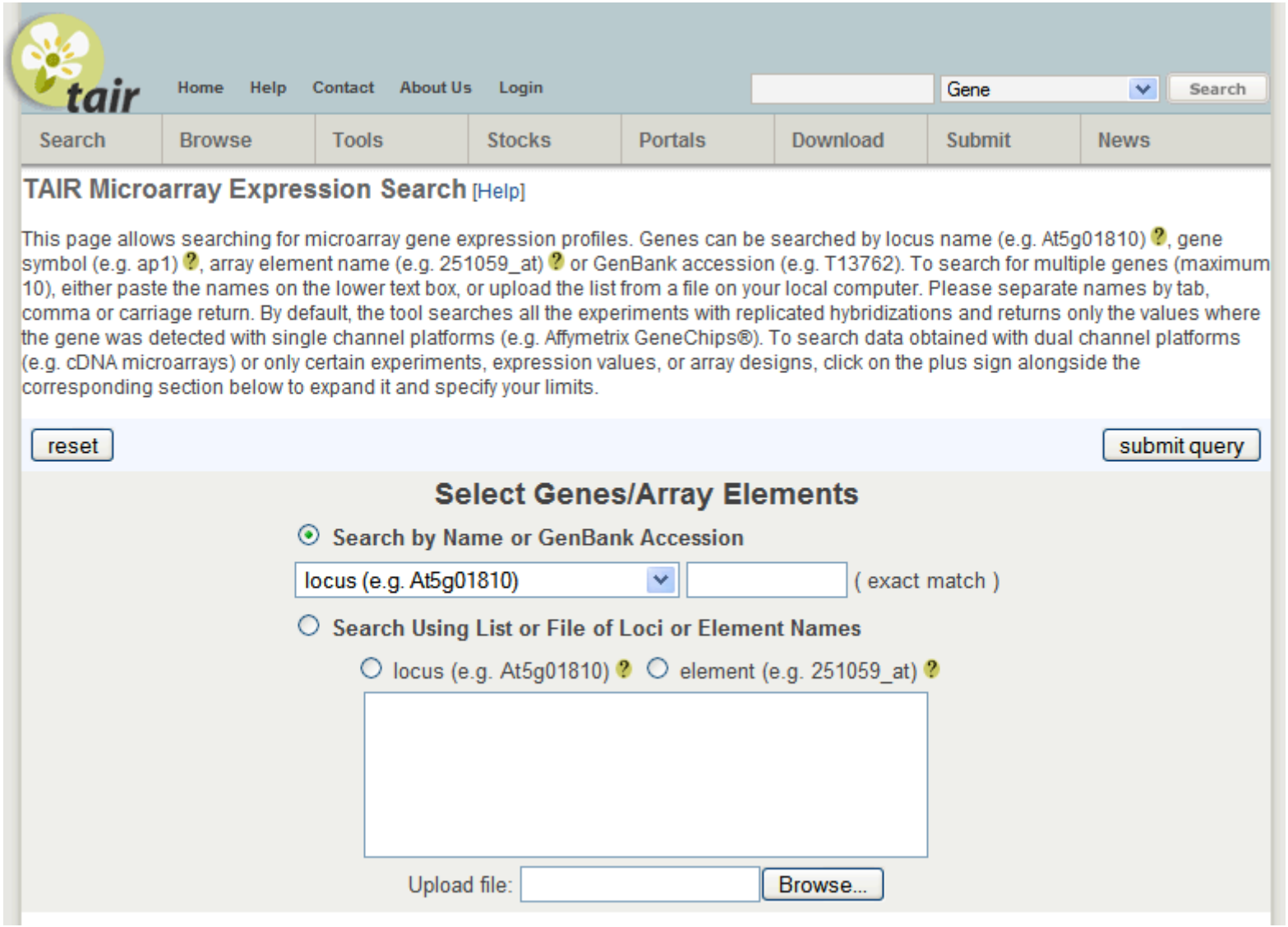
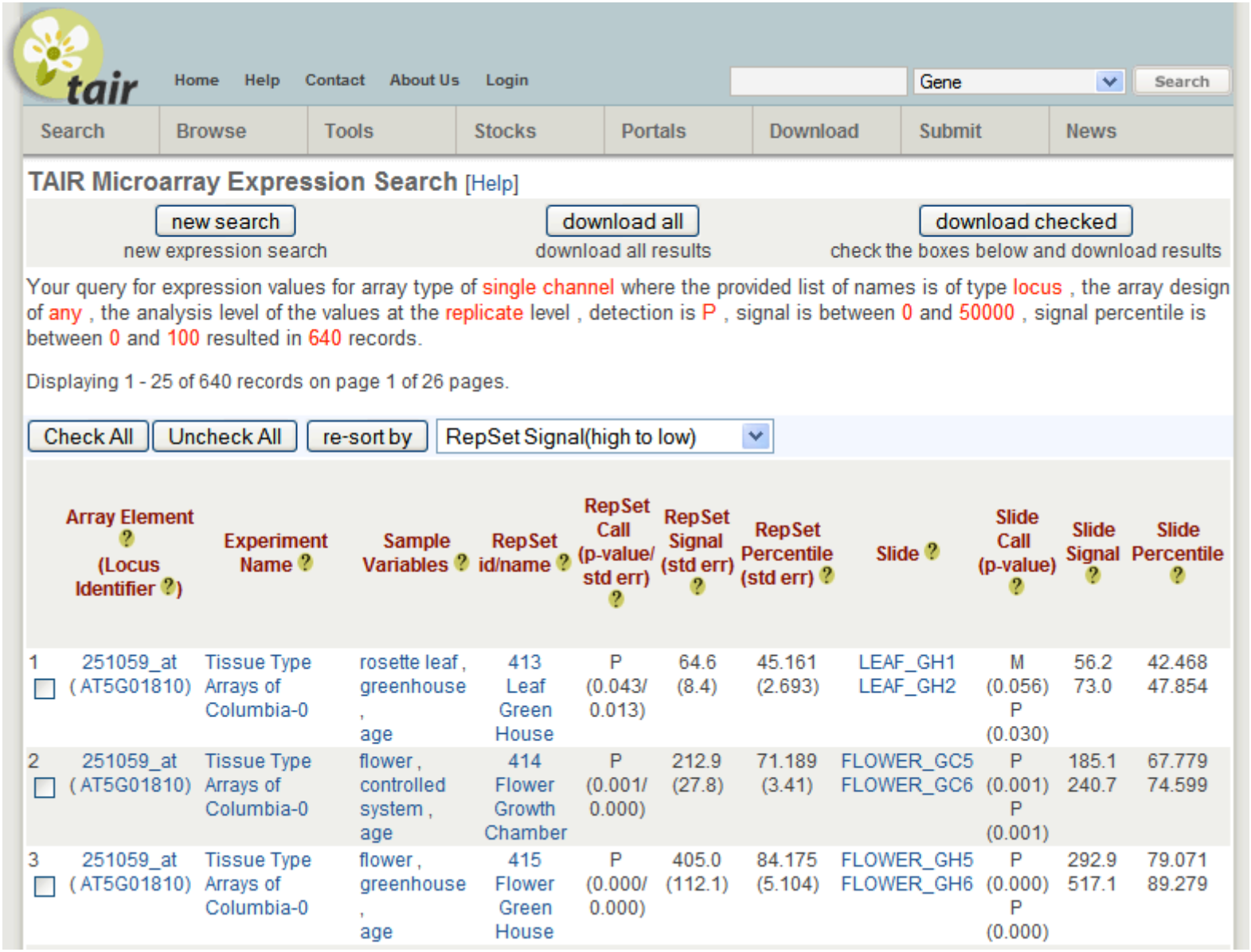
Search Browse Tools Stocks Portals Download Submit News
TAIR Gene Search Results
new search
new gene search
download all
download all results
download checked
check the boxes below and download results
Your query for genes where gene phenotype contains the term leaf shape , keyword term is any and keyword types of null resulted in 14 loci matches with 27 distinct gene models associated to the keyword or keyword children terms.
Displaying 1 - 14.
To see ESTs associated with your gene of interest, click on the Locus link.
Check All
Uncheck All
Locus
Gene Model
Description
Other Names
full-length cDNA
Keywords
1
AT1G07630
AT1G07630.1
protein phosphatase 2C family protein / PP2C family protein, similar to protein phosphatase-2c (GI:3608412) (Mesembryanthemum crystallinum); contains Pfam PF00481 : Protein phosphatase 2C domain
F24B9.31
F24B9_31
yes
protein phosphatase type 2C activity, N-terminal protein myristoylation
PLL5
Encodes a protein phosphatase 2C like gene, similar to POL. Involved in leaf
yes
leaf development
development. Knockout muta
abnormally shaped leaves.
2
AT1G27320
AHK3
Encodes a histidine kinases
receptor that controls cytokin
leaf longevity through a spec
phosphorylation of the respo
ARR2.
senescence, regulation of chlorophyll catabolism, regulation of shoot development
AT1G27320.1
histidine kinase (AHK3), identical to
F17L21.11
yes
cytokinin mediated
PLL5
Encodes a protein phosphatase 2C like gene, similar to POL. Involved in leaf development. Knockout mutants have abnormally shaped leaves.

Custom report on some aspect of gene



Custom report on some aspect of gene



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Gene Search

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TAIR Microarray Expression Search [Help]

new search — new expression search

download all — download all results

download checked — check the boxes below and download results

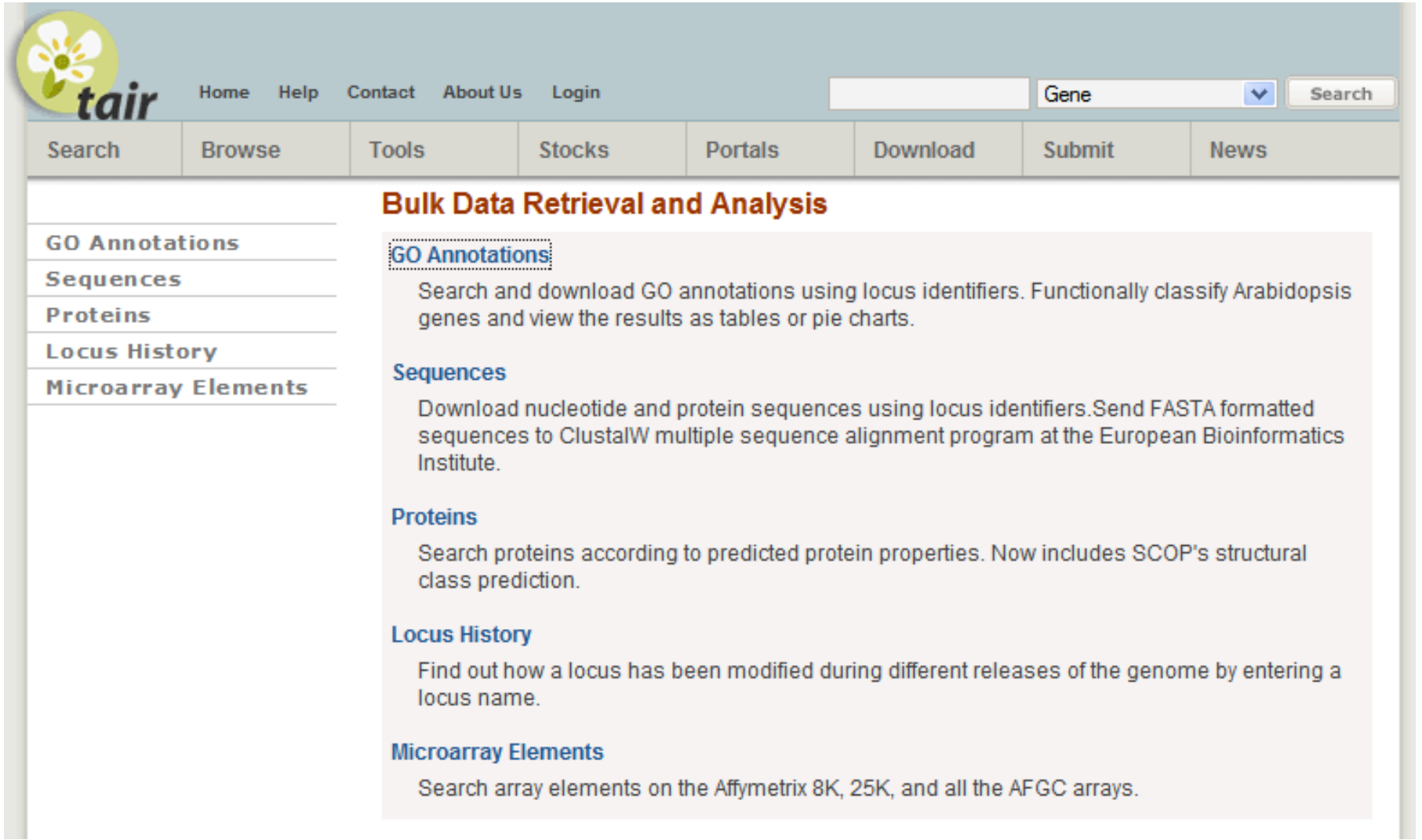
Your query for expression values for array type of single channel where the provided list of names is of type locus , the array design of any , the analysis level of the values at the replicate level , detection is P , signal is between 0 and 50000 , signal percentile is between 0 and 100 resulted in 640 records.

Displaying 1 - 25 of 640 records on page 1 of 26 pages.

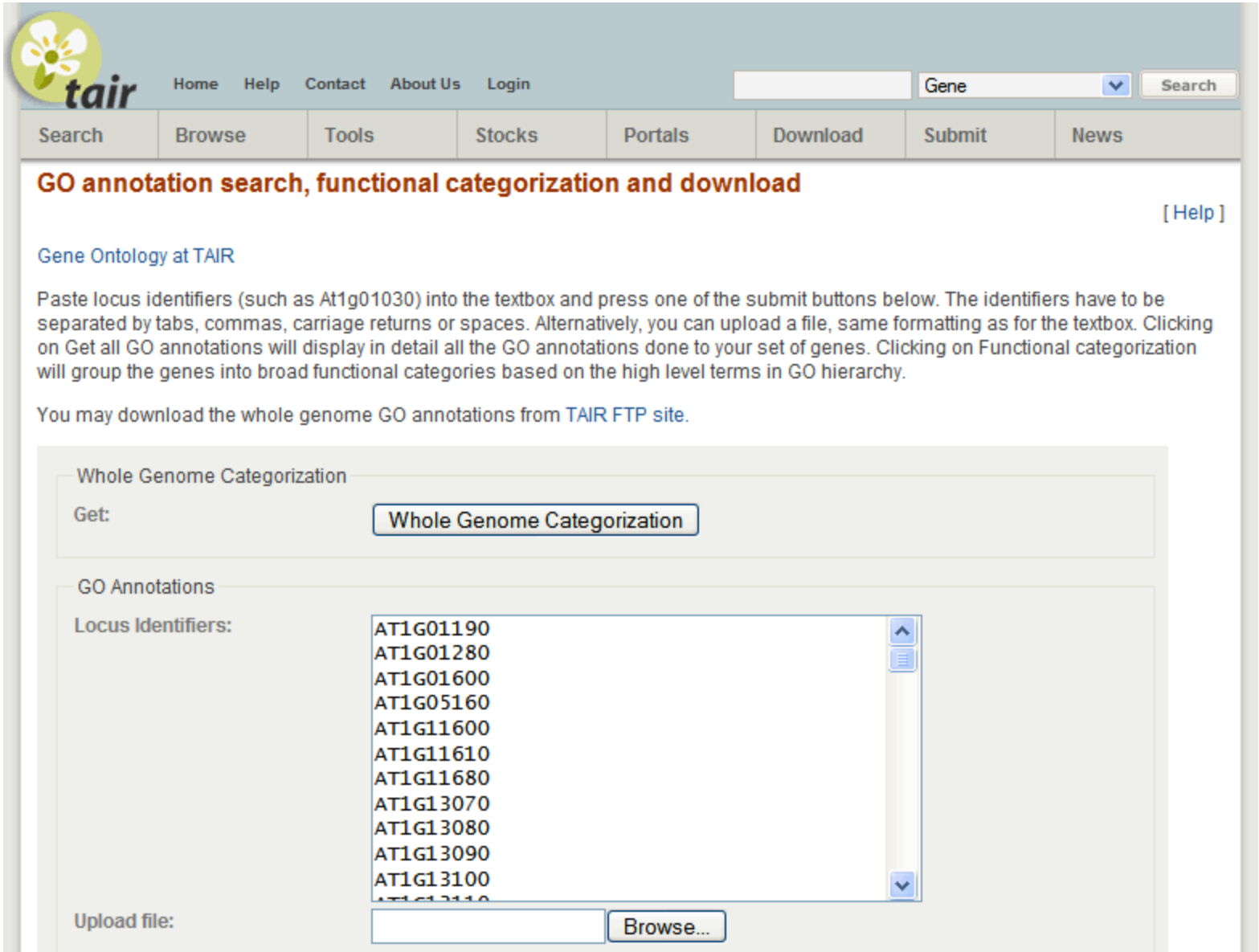
Check All | Uncheck All | re-sort by | RepSet Signal(high to low)

	Array Element (Locus Identifier)	Experiment Name	Sample Variables	RepSet id/name	RepSet Call (p-value/ std err)	RepSet Signal (std err)	RepSet Percentile (std err)	Slide	Slide Call (p-value)	Slide Signal	Slide Percentile
1 ☐	251059_at (AT5G01810)	Tissue Type Arrays of Columbia-0	rosette leaf , greenhouse , age	413 Leaf Green House	P (0.043/ 0.013)	64.6 (8.4)	45.161 (2.693)	LEAF_GH1 LEAF_GH2	M (0.056) P (0.030)	56.2 73.0	42.468 47.854
2 ☐	251059_at (AT5G01810)	Tissue Type Arrays of Columbia-0	flower , controlled system , age	414 Flower Growth Chamber	P (0.001/ 0.000)	212.9 (27.8)	71.189 (3.41)	FLOWER_GC5 FLOWER_GC6	P (0.001) P (0.001)	185.1 240.7	67.779 74.599
3 ☐	251059_at (AT5G01810)	Tissue Type Arrays of Columbia-0	flower , greenhouse , age	415 Flower Green House	P (0.000/ 0.000)	405.0 (112.1)	84.175 (5.104)	FLOWER_GH5 FLOWER_GH6	P (0.000) P (0.000)	292.9 517.1	79.071 89.279

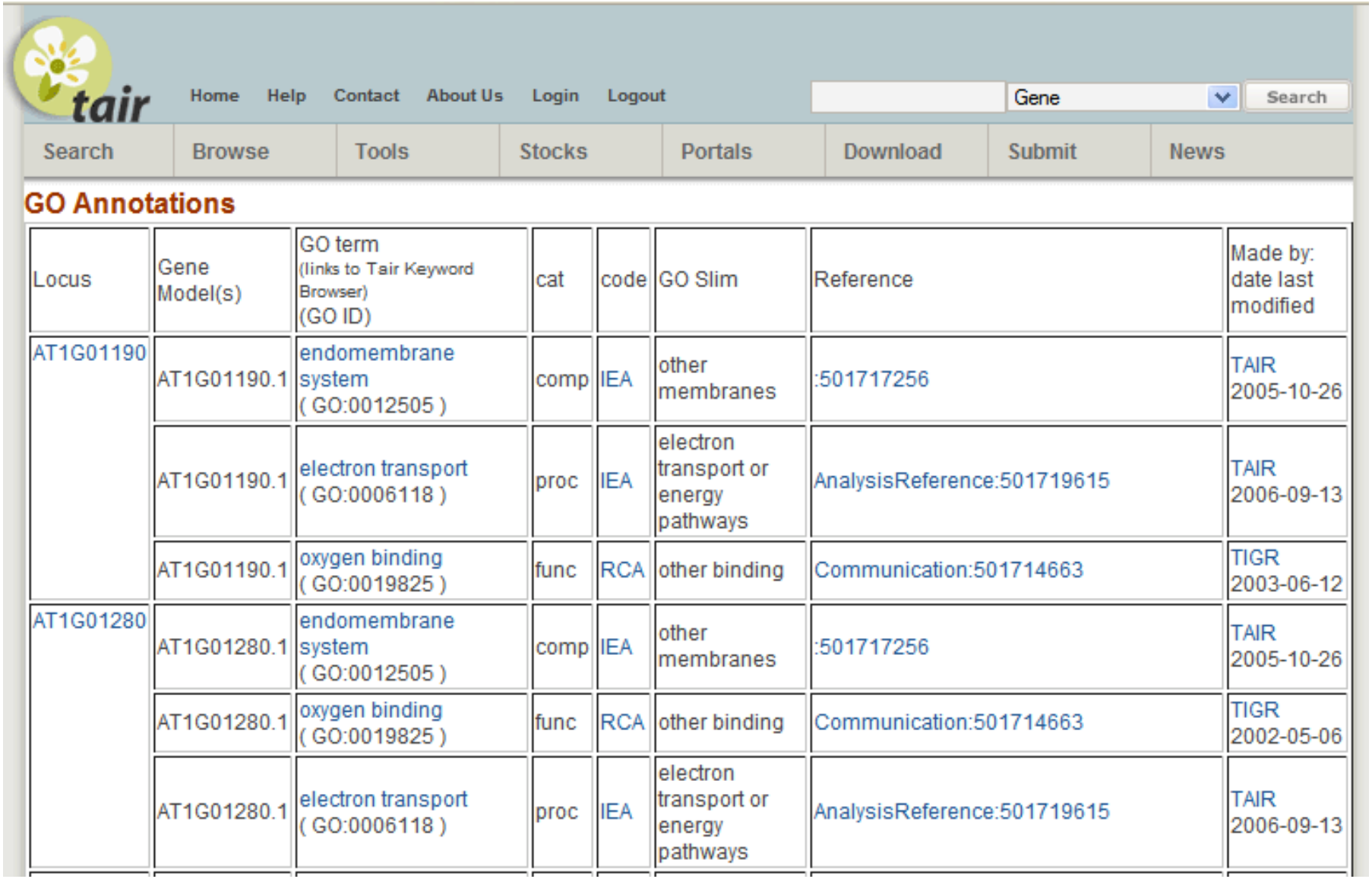
Bulk output based on a query



Bulk query – GO annotations



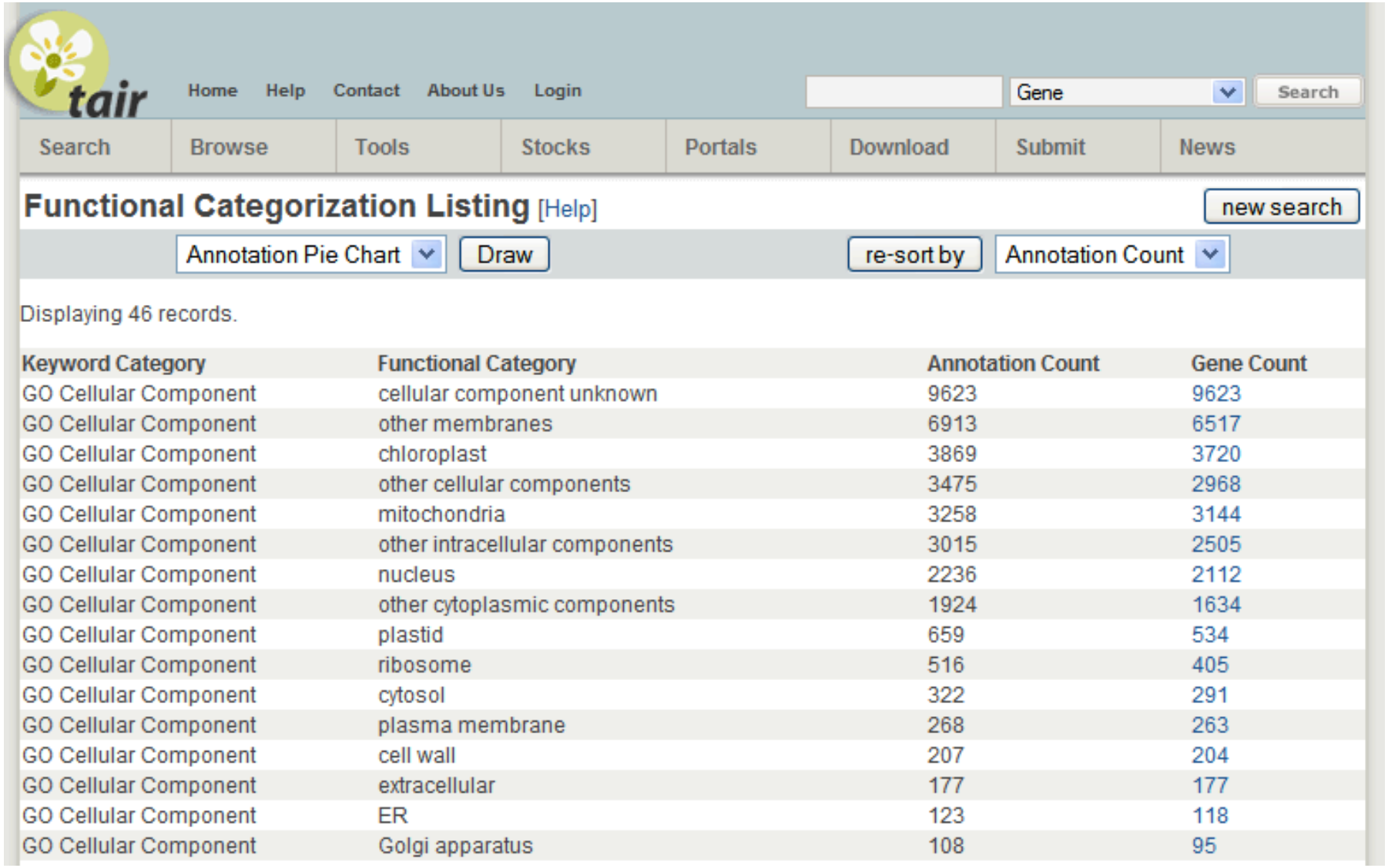
Bulk query – GO annotations



GO Annotations

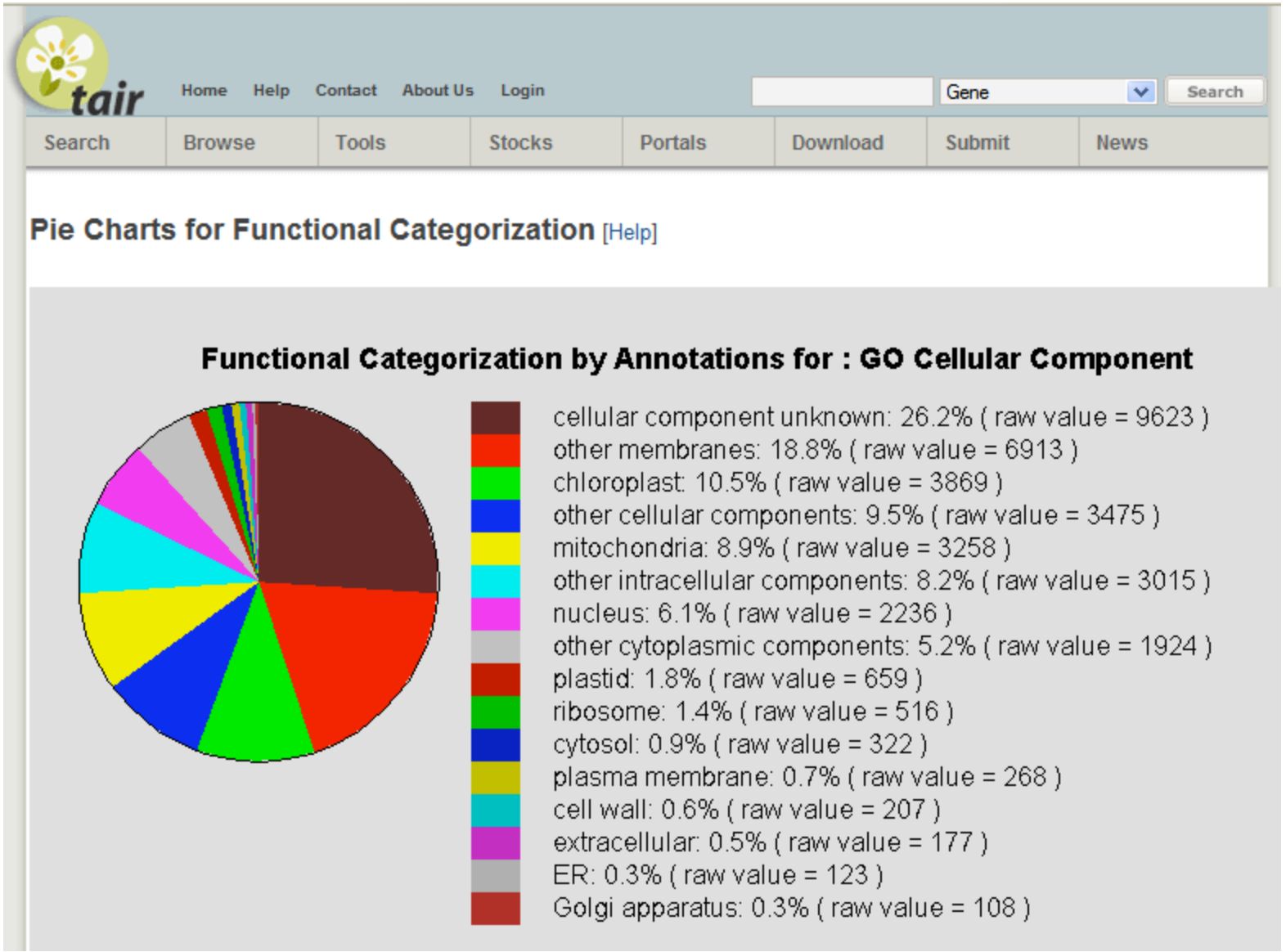
Locus	Gene Model(s)	GO term (links to Tair Keyword Browser) (GO ID)	cat	code	GO Slim	Reference	Made by: date last modified
AT1G01190	AT1G01190.1	endomembrane system (GO:0012505)	comp	IEA	other membranes	:501717256	TAIR 2005-10-26
	AT1G01190.1	electron transport (GO:0006118)	proc	IEA	electron transport or energy pathways	AnalysisReference:501719615	TAIR 2006-09-13
	AT1G01190.1	oxygen binding (GO:0019825)	func	RCA	other binding	Communication:501714663	TIGR 2003-06-12
AT1G01280	AT1G01280.1	endomembrane system (GO:0012505)	comp	IEA	other membranes	:501717256	TAIR 2005-10-26
	AT1G01280.1	oxygen binding (GO:0019825)	func	RCA	other binding	Communication:501714663	TIGR 2002-05-06
	AT1G01280.1	electron transport (GO:0006118)	proc	IEA	electron transport or energy pathways	AnalysisReference:501719615	TAIR 2006-09-13

Bulk query – GO annotations

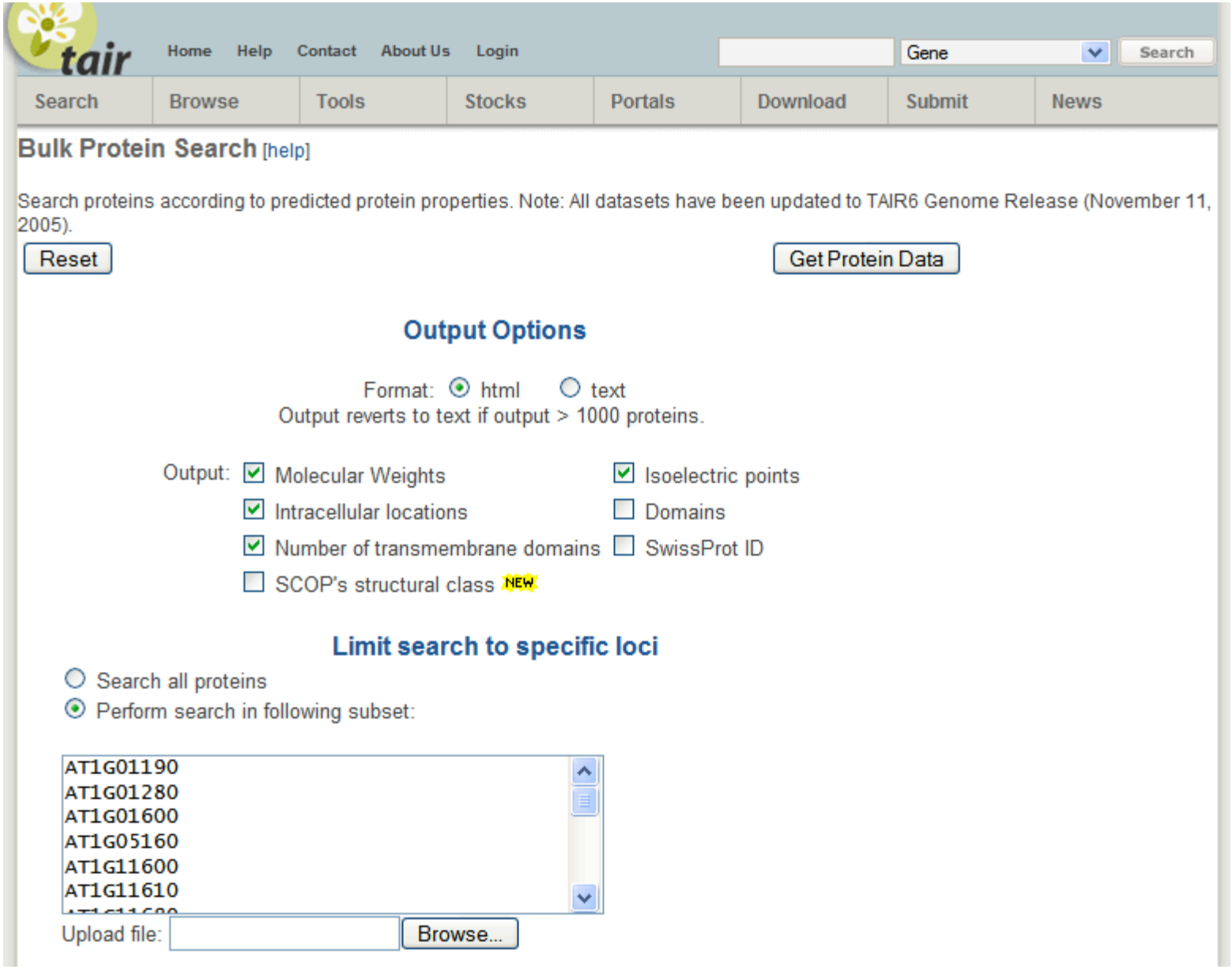


Keyword Category	Functional Category	Annotation Count	Gene Count
GO Cellular Component	cellular component unknown	9623	9623
GO Cellular Component	other membranes	6913	6517
GO Cellular Component	chloroplast	3869	3720
GO Cellular Component	other cellular components	3475	2968
GO Cellular Component	mitochondria	3258	3144
GO Cellular Component	other intracellular components	3015	2505
GO Cellular Component	nucleus	2236	2112
GO Cellular Component	other cytoplasmic components	1924	1634
GO Cellular Component	plastid	659	534
GO Cellular Component	ribosome	516	405
GO Cellular Component	cytosol	322	291
GO Cellular Component	plasma membrane	268	263
GO Cellular Component	cell wall	207	204
GO Cellular Component	extracellular	177	177
GO Cellular Component	ER	123	118
GO Cellular Component	Golgi apparatus	108	95

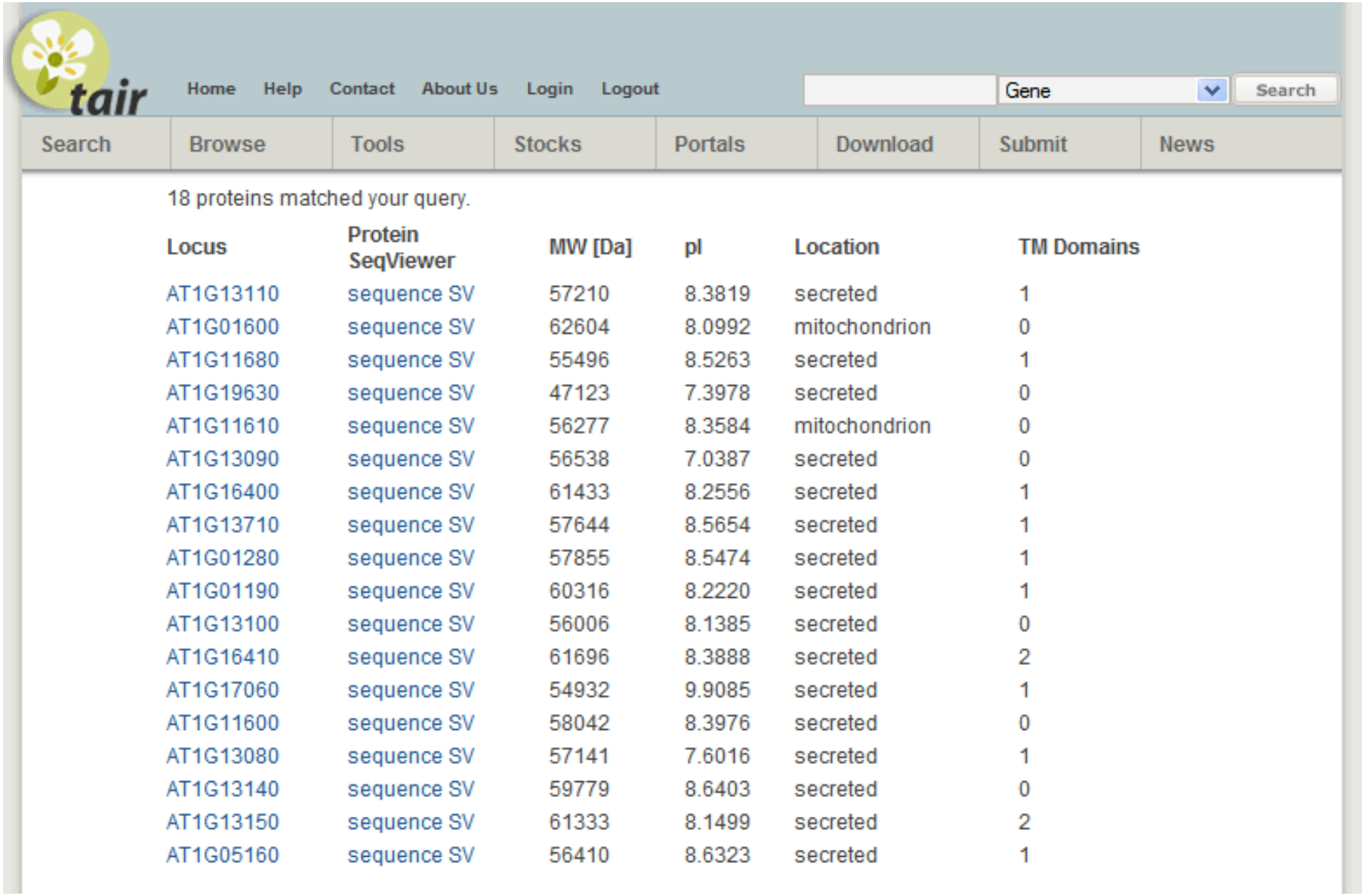
Bulk query – GO annotations



Bulk query - proteins



Bulk query - proteins

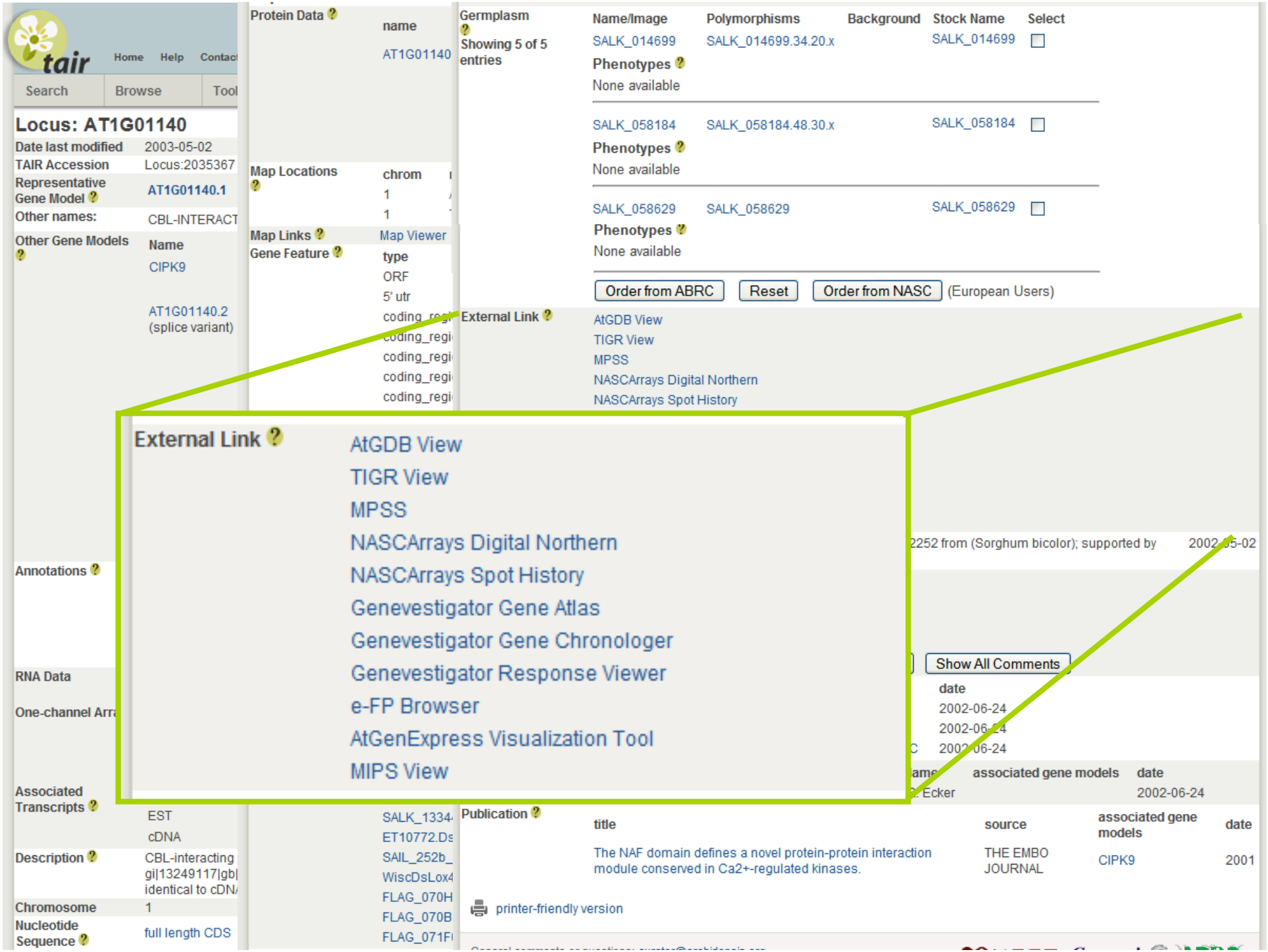


18 proteins matched your query.

Locus	Protein SeqViewer	MW [Da]	pI	Location	TM Domains
AT1G13110	sequence SV	57210	8.3819	secreted	1
AT1G01600	sequence SV	62604	8.0992	mitochondrion	0
AT1G11680	sequence SV	55496	8.5263	secreted	1
AT1G19630	sequence SV	47123	7.3978	secreted	0
AT1G11610	sequence SV	56277	8.3584	mitochondrion	0
AT1G13090	sequence SV	56538	7.0387	secreted	0
AT1G16400	sequence SV	61433	8.2556	secreted	1
AT1G13710	sequence SV	57644	8.5654	secreted	1
AT1G01280	sequence SV	57855	8.5474	secreted	1
AT1G01190	sequence SV	60316	8.2220	secreted	1
AT1G13100	sequence SV	56006	8.1385	secreted	0
AT1G16410	sequence SV	61696	8.3888	secreted	2
AT1G17060	sequence SV	54932	9.9085	secreted	1
AT1G11600	sequence SV	58042	8.3976	secreted	0
AT1G13080	sequence SV	57141	7.6016	secreted	1
AT1G13140	sequence SV	59779	8.6403	secreted	0
AT1G13150	sequence SV	61333	8.1499	secreted	2
AT1G05160	sequence SV	56410	8.6323	secreted	1

Combine results with info from other data sources

- External links on TAIR data pages
  - Links go directly to relevant data in other resource
- Inclusion of IDs from other databases
  - GenBank accession, pubmed ID
- Web services in progress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Contact
Search
Browse
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Locus: AT1G01140
Date last modified 2003-05-02
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Representative Gene Model
AT1G01140.1
Other names: CBL-INTERACT
Other Gene Models
Name
CIPK9
AT1G01140.2 (splice variant)
Protein Data
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AT1G01140
Map Locations
chrom
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Map Links
Map Viewer
Gene Feature
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Background
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Order from ABRC
Reset
Order from NASC
(European Users)
External Link
AtGDB View
TIGR View
MPSS
NASCArrays Digital Northern
NASCArrays Spot History
External Link
AtGDB View
TIGR View
MPSS
NASCArrays Digital Northern
NASCArrays Spot History
Genevestigator Gene Atlas
Genevestigator Gene Chronologer
Genevestigator Response Viewer
e-FP Browser
AtGenExpress Visualization Tool
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EST
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FLAG_070B
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source
associated gene models
date
The NAF domain defines a novel protein-protein interaction module conserved in Ca2+-regulated kinases.
THE EMBO JOURNAL
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2001
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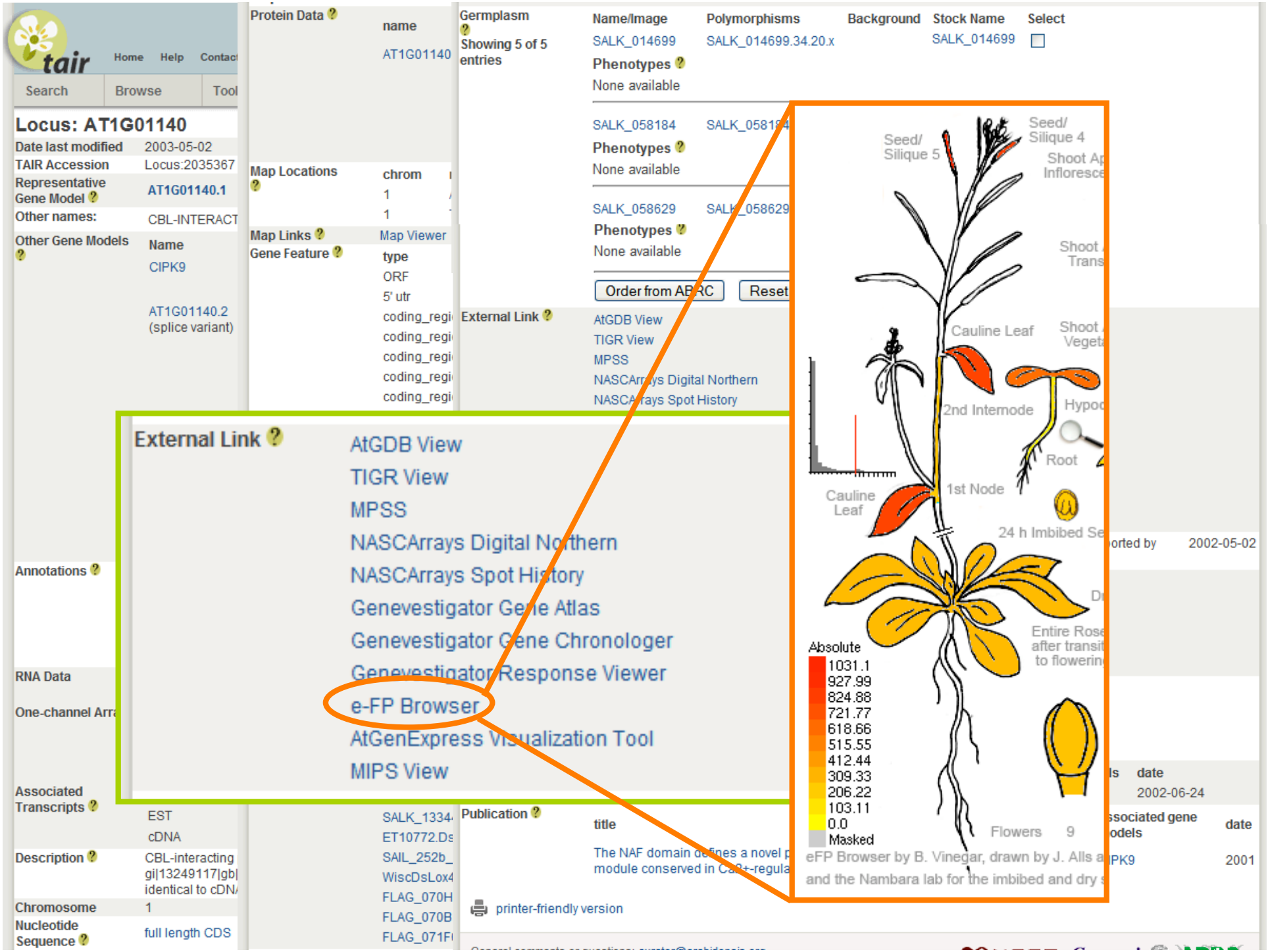
Chromosome 1
Nucleotide Sequence
full length CDS
printer-friendly version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Locus: AT1G01140
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Representative Gene Model
AT1G01140.1
Other names: CBL-INTERACT
Other Gene Models
Name
CIPK9
AT1G01140.2 (splice variant)
Protein Data
name
AT1G01140
Map Locations
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Map Links
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Showing 5 of 5 entries
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Phenotypes
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Reset
External Link
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TIGR View
MPSS
NASCArrays Digital Northern
NASCArrays Spot History
External Link
AtGDB View
TIGR View
MPSS
NASCArrays Digital Northern
NASCArrays Spot History
Genevestigator Gene Atlas
Genevestigator Gene Chronologer
Genevestigator Response Viewer
e-FP Browser
AtGenExpress Visualization Tool
MIPS View
Annotations
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full length CDS
Publication
title
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printer-friendly version
Seed/ Silique 5
Seed/ Silique 4
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Inflorescc
Shoot
Trans
Cauline Leaf
Shoot
Vegeta
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Hypoc
Root
1st Node
Cauline Leaf
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Entire Rose
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to floweri
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721.77
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515.55
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309.33
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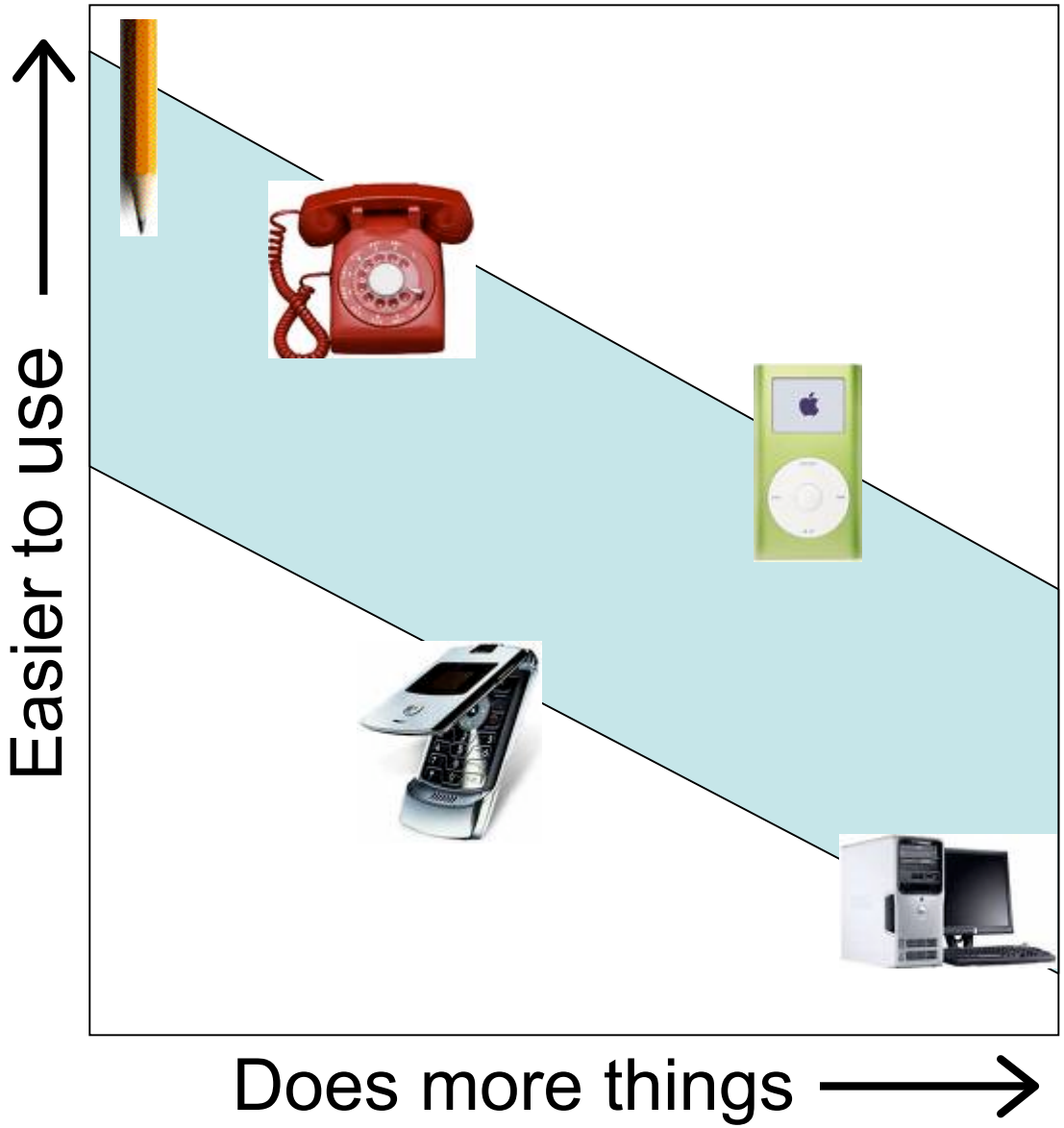
The Tradeoff



A Good Design

- "How to use" is obvious
- Results match expectations