生物情報工学 *BioInformatics*

５　ゲノムデータベース

ゲノムデータベースを見てみる

GenomeNet

KEGG KEGG2 PATHWAY BRITE MEDICUS DBGET

[English | Japanese]

Search 統合データベース for Go Clear

ゲノムネット
- ゲノムネットとは
- お知らせ
- 謝辞

統合データベース
- 統合DBの概要
- DBGETの概要
- リリース情報

医薬品データベース

KEGG

varDB

研究支援データベース

計算ツール
- その他のツール

FTP

フィードバック

ゲノムネットデータベースリソース

ゲノムネット統合データベース
- DBGET search
- LinkDB search

KEGG MEDICUS: 疾患・医薬品統合リソース
- 医薬品検索 / 疾患検索 / お薬手帳

KEGG: 生命システム情報統合データベース
- KEGG2 - 目次のページ
- KEGG PATHWAY - システム情報: パスウェイ
- KEGG BRITE - システム情報: オントロジー
- KEGG Organisms - 生物種ごとの入口
- KEGG GENES - ゲノム情報
- KEGG LIGAND - ケミカル情報

Reaction Ontology: 反応パターンと分類

varDB: 抗原変異データベース

研究支援データベース
- CYORF - シアノバクテリア
- BSORF - 枯草菌
- EXPRESSION - 遺伝子発現プロフィール

ゲノムネット計算ツール

配列解析

KEGG パスウェイ一覧
BRITE 機能階層 (日本語) 一覧
KEGG 生物種一覧
- メタゲノム
- ドラフトゲノム

データベース間のリンク

http://www.genome.jp/ja/ ゲノムネットにつなぐ。

KEGG GENOME Databaseへアクセスする

KEGG: Kyoto Encyclopedia of Genes and Genomes

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生命システムレベルの機能や有用性を理解するためのリソースです。とくにゲノムをはじめとしたハイスループットデータの生物学的意味解釈に広く利用されています。また KEGG MEDICUS では医薬品添付文書など社会的ニーズの高いデータとの統合も行われています。医薬品相互作用チェックや KEGG お薬手帳をお試しください。

KEGG の主要エントリーポイント

KEGG2	KEGG 全体の目次のページ	Update notes

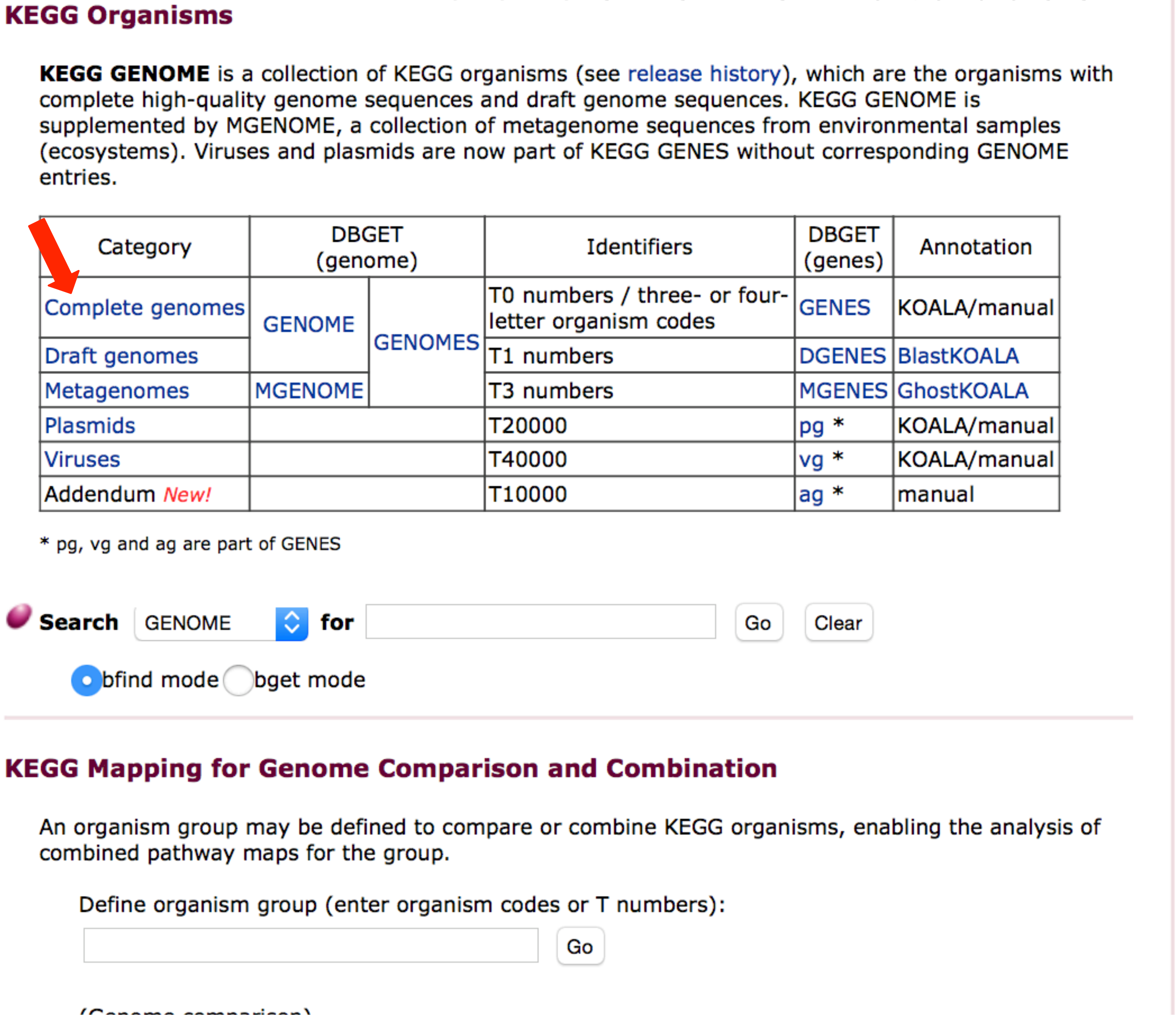
データタイプごとのエントリーポイント

KEGG PATHWAY	パスウェイマップ [パスウェイ一覧]
KEGG BRITE	機能階層・オントロジー (一部日本語) [Brite 一覧]
KEGG MODULE	KEGG モジュール [モジュール一覧]
KEGG DISEASE	病気 (日本語) [がん | 感染症]
KEGG DRUG	医薬品 (日本語) [薬効分類 ATC 分類]
KEGG ORTHOLOGY	オーソログアノテーション
→ **KEGG GENOME**	ゲノム [KEGG 生物種一覧]
KEGG GENES	遺伝子・タンパク質
KEGG LIGAND	化合物・化学反応・糖鎖 [反応モジュール]

一般向けのエントリーポイント

KEGG MEDICUS	ゲノムと疾患・医薬品の統合リソース (日本語) [お薬手帳]

KEGG Genome Database



KEGG Organisms

KEGG GENOME is a collection of KEGG organisms (see release history), which are the organisms with complete high-quality genome sequences and draft genome sequences. KEGG GENOME is supplemented by MGENOME, a collection of metagenome sequences from environmental samples (ecosystems). Viruses and plasmids are now part of KEGG GENES without corresponding GENOME entries.

Category	DBGET (genome)		Identifiers	DBGET (genes)	Annotation
Complete genomes	GENOME	GENOMES	T0 numbers / three- or four-letter organism codes	GENES	KOALA/manual
Draft genomes			T1 numbers	DGENES	BlastKOALA
Metagenomes	MGENOME		T3 numbers	MGENES	GhostKOALA
Plasmids			T20000	pg *	KOALA/manual
Viruses			T40000	vg *	KOALA/manual
Addendum *New!*			T10000	ag *	manual

* pg, vg and ag are part of GENES

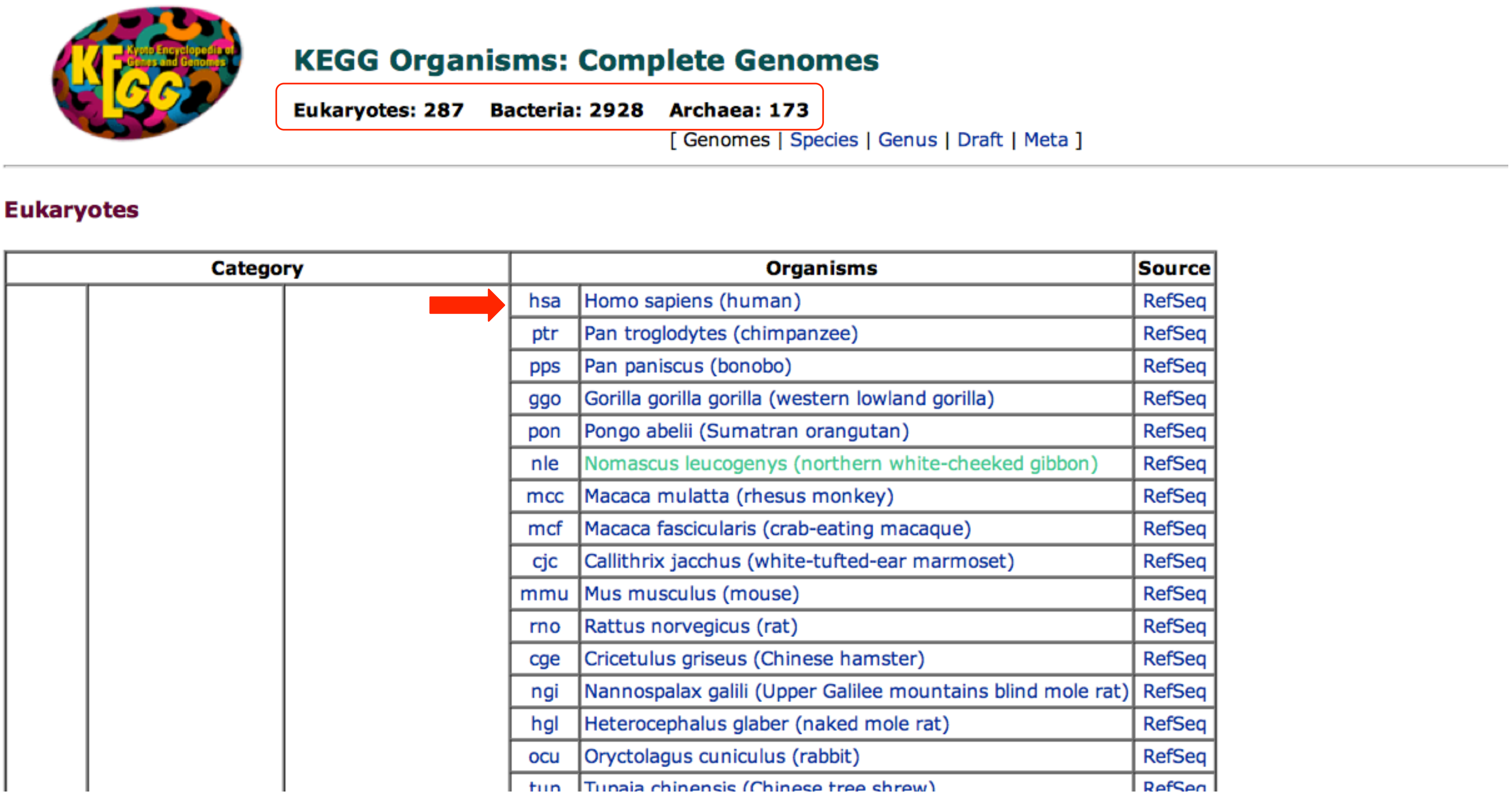
KEGG Mapping for Genome Comparison and Combination

An organism group may be defined to compare or combine KEGG organisms, enabling the analysis of combined pathway maps for the group.

Define organism group (enter organism codes or T numbers):

(Genome comparison)

Complete Genomes in KEGG



KEGG Organisms: Complete Genomes

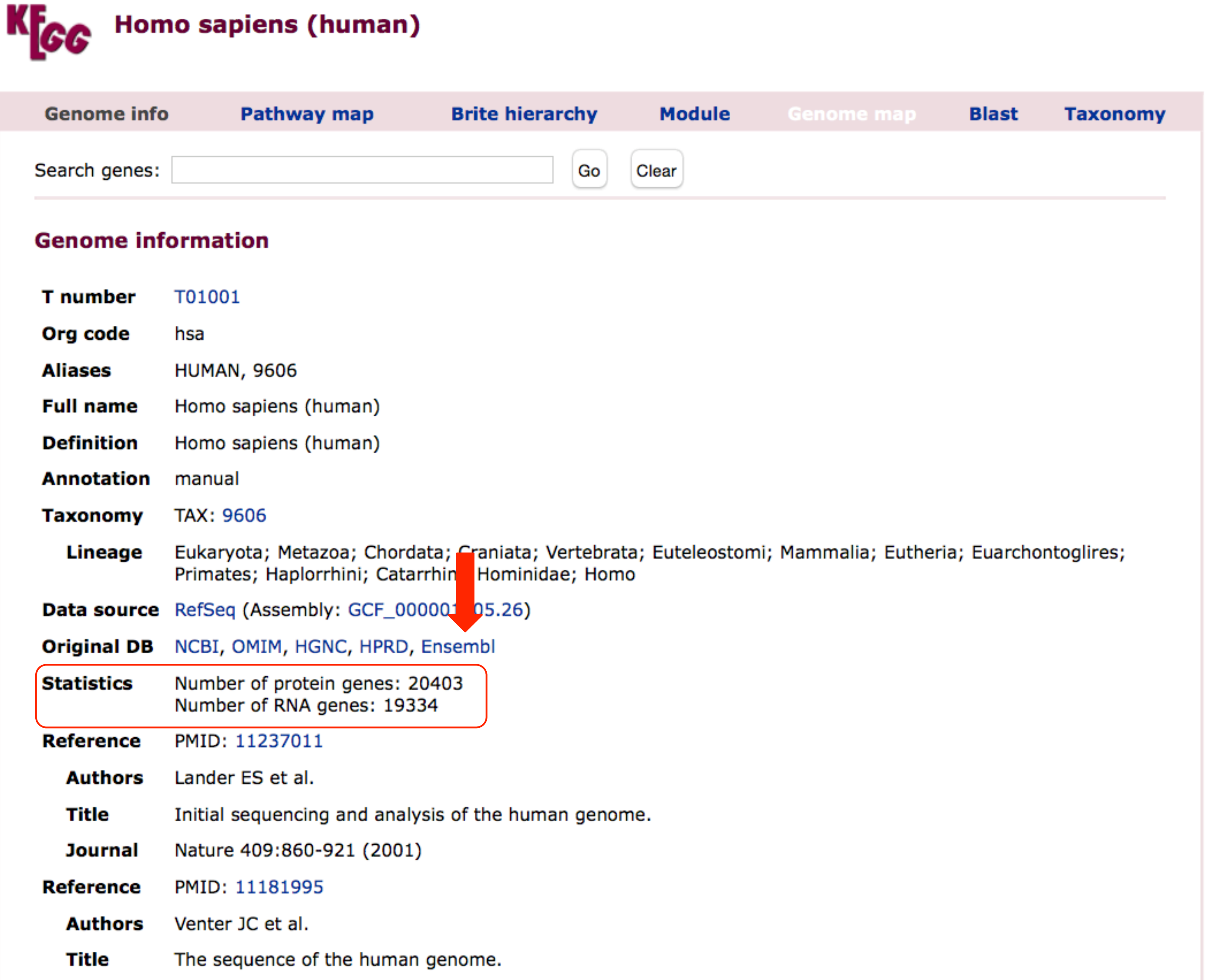
Eukaryotes: 287 **Bacteria: 2928** **Archaea: 173**

[Genomes | Species | Genus | Draft | Meta]

Eukaryotes

Category			Organisms		Source
			hsa	Homo sapiens (human)	RefSeq
			ptr	Pan troglodytes (chimpanzee)	RefSeq
			pps	Pan paniscus (bonobo)	RefSeq
			ggo	Gorilla gorilla gorilla (western lowland gorilla)	RefSeq
			pon	Pongo abelii (Sumatran orangutan)	RefSeq
			nle	Nomascus leucogenys (northern white-cheeked gibbon)	RefSeq
			mcc	Macaca mulatta (rhesus monkey)	RefSeq
			mcf	Macaca fascicularis (crab-eating macaque)	RefSeq
			cjc	Callithrix jacchus (white-tufted-ear marmoset)	RefSeq
			mmu	Mus musculus (mouse)	RefSeq
			rno	Rattus norvegicus (rat)	RefSeq
			cge	Cricetulus griseus (Chinese hamster)	RefSeq
			ngi	Nannospalax galili (Upper Galilee mountains blind mole rat)	RefSeq
			hgl	Heterocephalus glaber (naked mole rat)	RefSeq
			ocu	Oryctolagus cuniculus (rabbit)	RefSeq
			tun	Tupaia chinensis (Chinese tree shrew)	RefSeq

Homo sapiens genome dataに関する情報

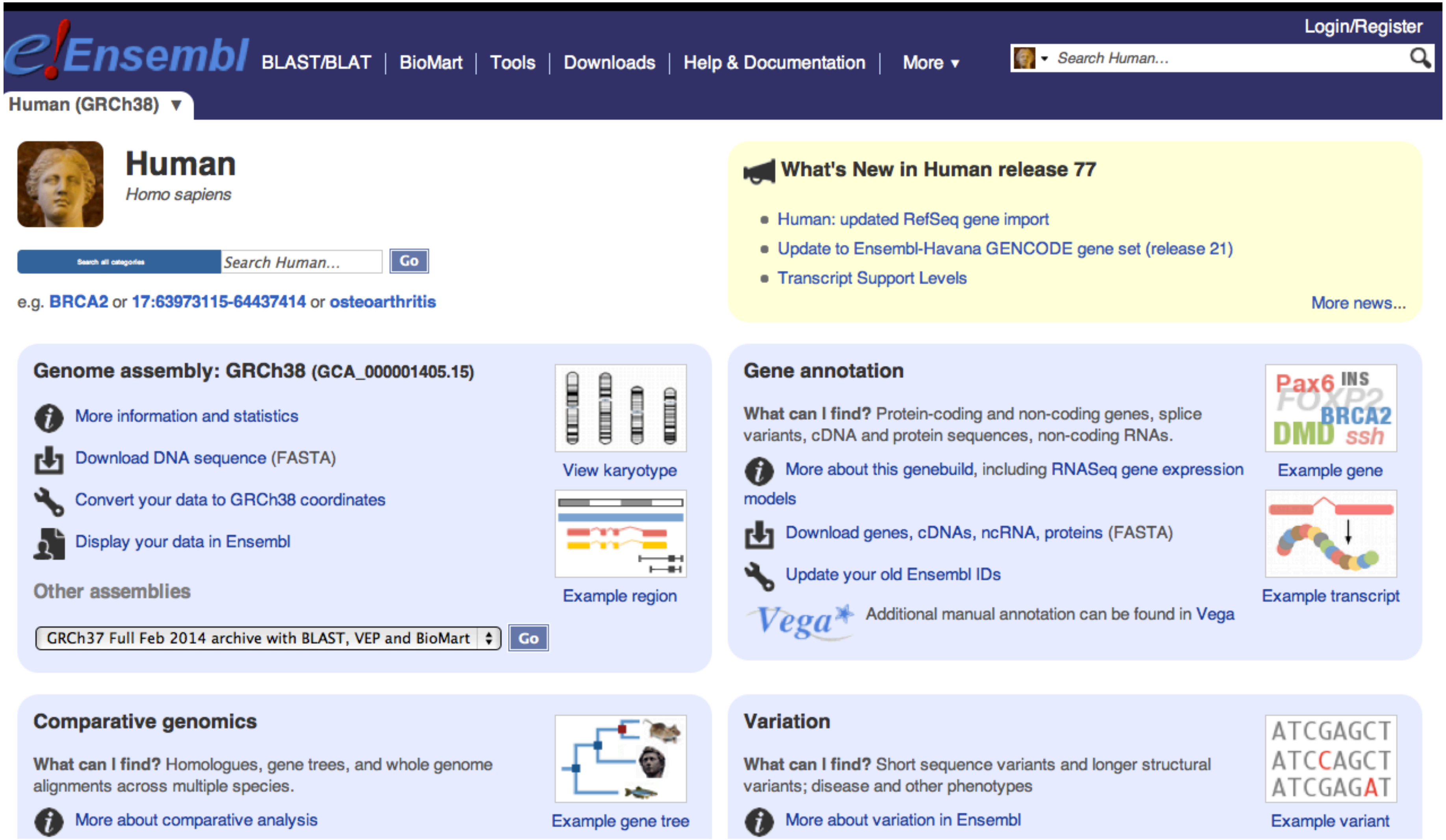


Homo sapiens (human)

Genome information

T number	T01001
Org code	hsa
Aliases	HUMAN, 9606
Full name	Homo sapiens (human)
Definition	Homo sapiens (human)
Annotation	manual
Taxonomy	TAX: 9606
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini; Catarrhin Hominidae; Homo
Data source	RefSeq (Assembly: GCF_000001 05.26)
Original DB	NCBI, OMIM, HGNC, HPRD, Ensembl
Statistics	Number of protein genes: 20403 Number of RNA genes: 19334
Reference	PMID: 11237011
Authors	Lander ES et al.
Title	Initial sequencing and analysis of the human genome.
Journal	Nature 409:860-921 (2001)
Reference	PMID: 11181995
Authors	Venter JC et al.
Title	The sequence of the human genome.

Ensembl Human



Human

Homo sapiens

e.g. **BRCA2** or **17:63973115-64437414** or **osteoarthritis**

What's New in Human release 77

- Human: updated RefSeq gene import
- Update to Ensembl-Havana GENCODE gene set (release 21)
- Transcript Support Levels

More news...

Genome assembly: GRCh38 (GCA_000001405.15)

More information and statistics

Download DNA sequence (FASTA)

Convert your data to GRCh38 coordinates

Display your data in Ensembl

View karyotype

Example region

Other assemblies

GRCh37 Full Feb 2014 archive with BLAST, VEP and BioMart

Gene annotation

What can I find? Protein-coding and non-coding genes, splice variants, cDNA and protein sequences, non-coding RNAs.

More about this genebuild, including RNASeq gene expression models

Download genes, cDNAs, ncRNA, proteins (FASTA)

Update your old Ensembl IDs

Additional manual annotation can be found in Vega

Example gene

Example transcript

Comparative genomics

What can I find? Homologues, gene trees, and whole genome alignments across multiple species.

More about comparative analysis

Example gene tree

Variation

What can I find? Short sequence variants and longer structural variants; disease and other phenotypes

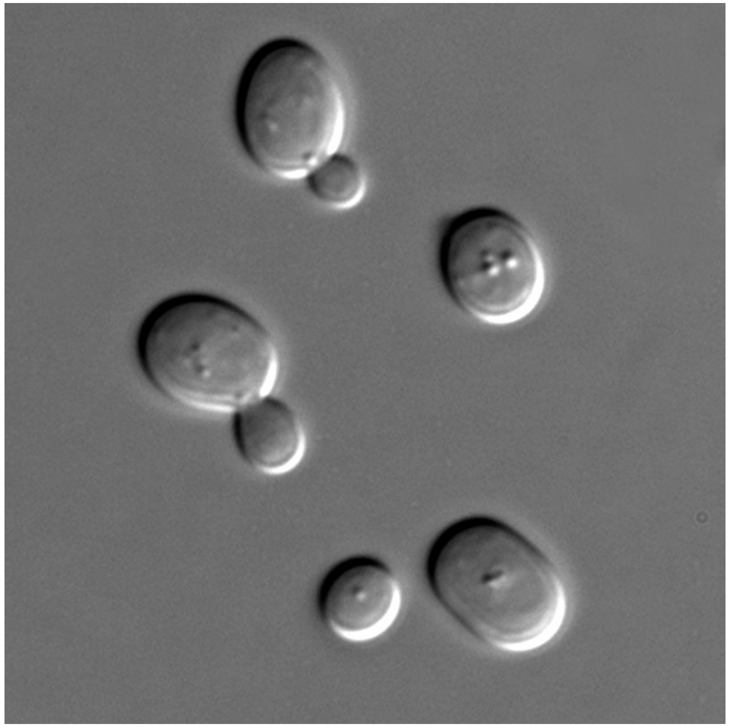
More about variation in Ensembl

Example variant

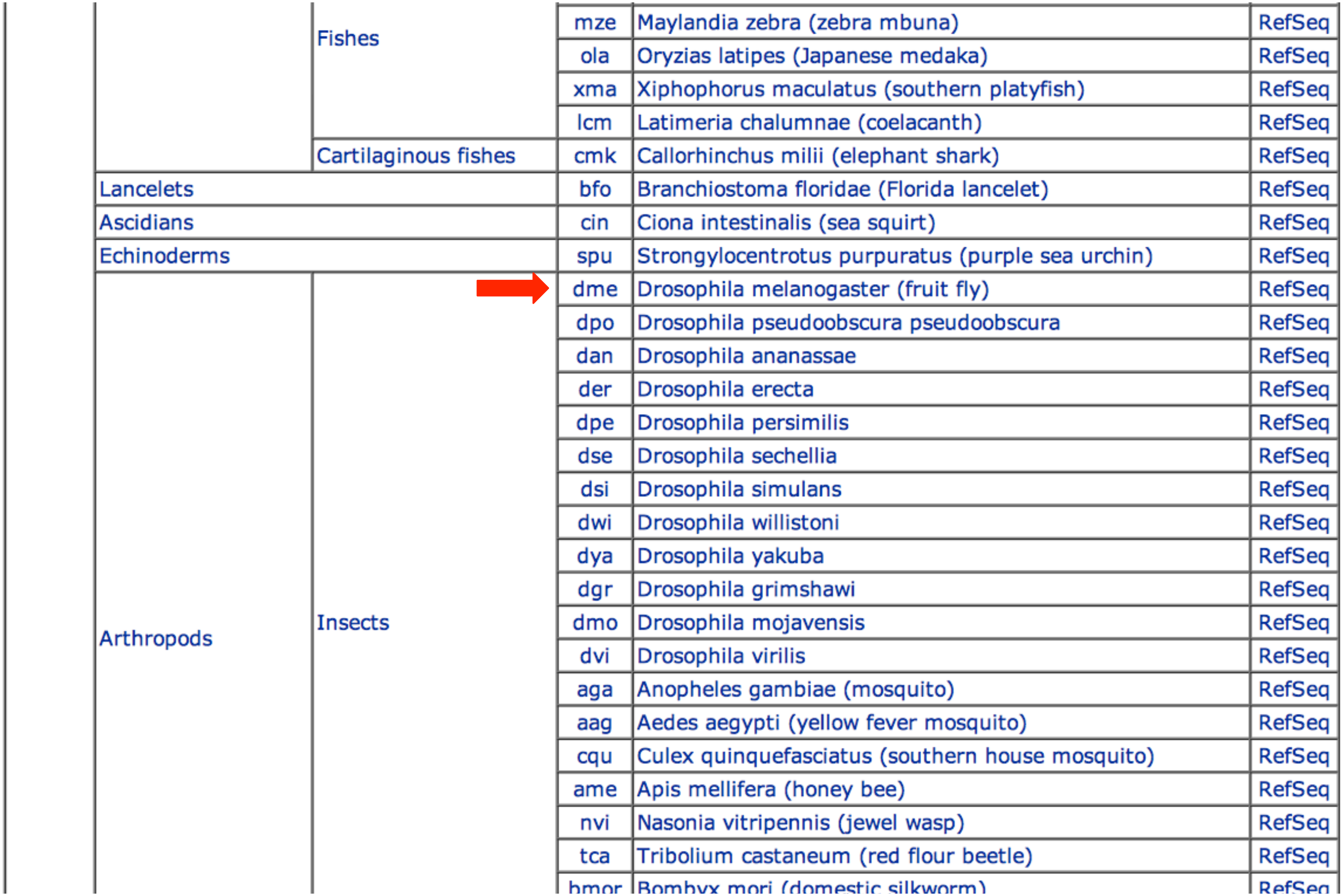
出芽酵母のゲノムについて見てみよう

学名：*Saccharomyces cerevisiae*

細胞周期研究のなどのモデル生物

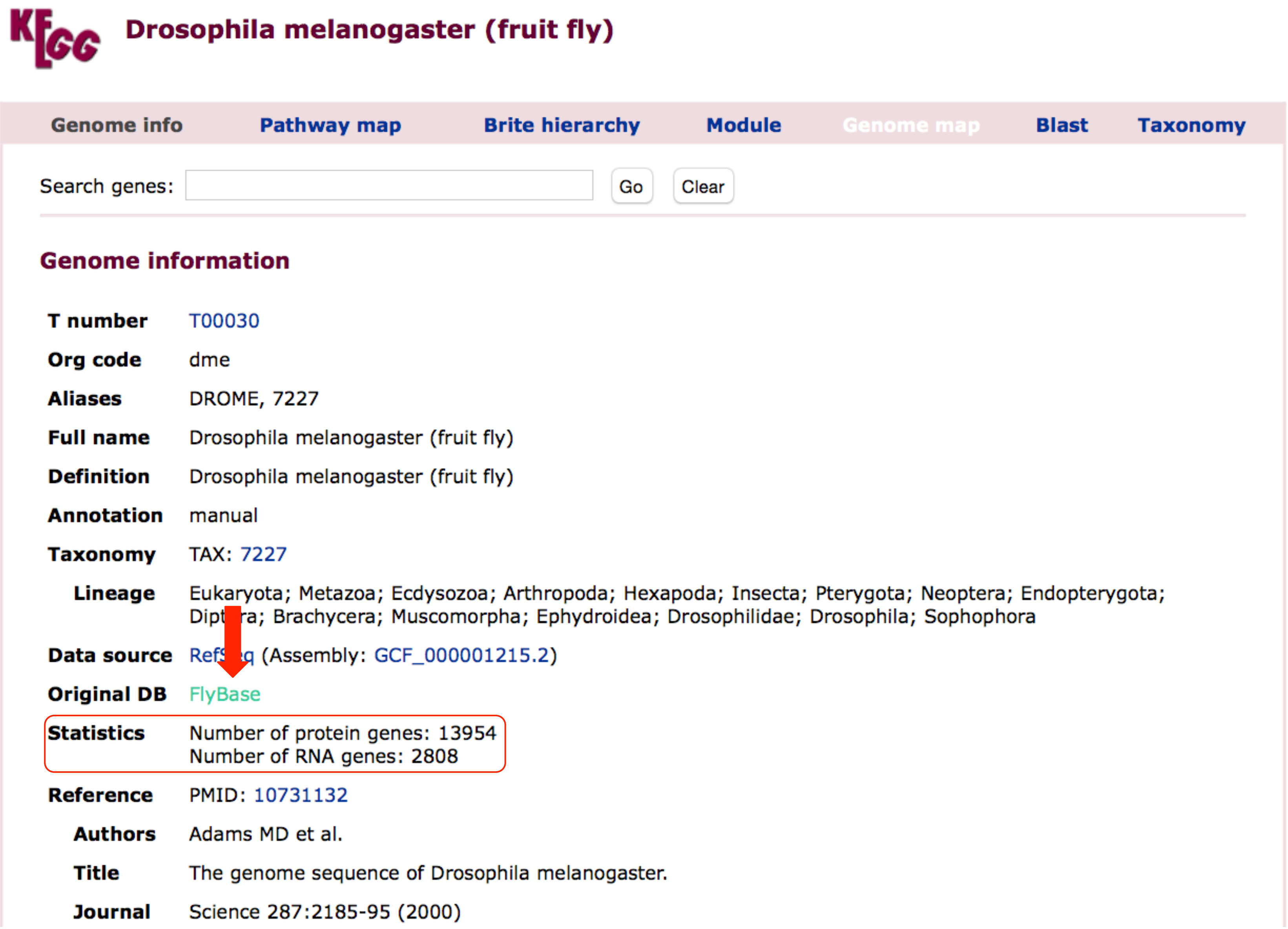


モデル生物　ショウジョウバエ（*Drosophila melanogaster*）について見てみる



		Fishes	mze	Maylandia zebra (zebra mbuna)	RefSeq
			ola	Oryzias latipes (Japanese medaka)	RefSeq
			xma	Xiphophorus maculatus (southern platyfish)	RefSeq
			lcm	Latimeria chalumnae (coelacanth)	RefSeq
		Cartilaginous fishes	cmk	Callorhinchus milii (elephant shark)	RefSeq
	Lancelets		bfo	Branchiostoma floridae (Florida lancelet)	RefSeq
	Ascidians		cin	Ciona intestinalis (sea squirt)	RefSeq
	Echinoderms		spu	Strongylocentrotus purpuratus (purple sea urchin)	RefSeq
	Arthropods	Insects	dme	Drosophila melanogaster (fruit fly)	RefSeq
			dpo	Drosophila pseudoobscura pseudoobscura	RefSeq
			dan	Drosophila ananassae	RefSeq
			der	Drosophila erecta	RefSeq
			dpe	Drosophila persimilis	RefSeq
			dse	Drosophila sechellia	RefSeq
			dsi	Drosophila simulans	RefSeq
			dwi	Drosophila willistoni	RefSeq
			dya	Drosophila yakuba	RefSeq
			dgr	Drosophila grimshawi	RefSeq
			dmo	Drosophila mojavensis	RefSeq
			dvi	Drosophila virilis	RefSeq
			aga	Anopheles gambiae (mosquito)	RefSeq
			aag	Aedes aegypti (yellow fever mosquito)	RefSeq
			cqu	Culex quinquefasciatus (southern house mosquito)	RefSeq
			ame	Apis mellifera (honey bee)	RefSeq
			nvi	Nasonia vitripennis (jewel wasp)	RefSeq
			tca	Tribolium castaneum (red flour beetle)	RefSeq
			bmor	Bombyx mori (domestic silkworm)	RefSeq

ショウジョウバエ ゲノムに関する情報

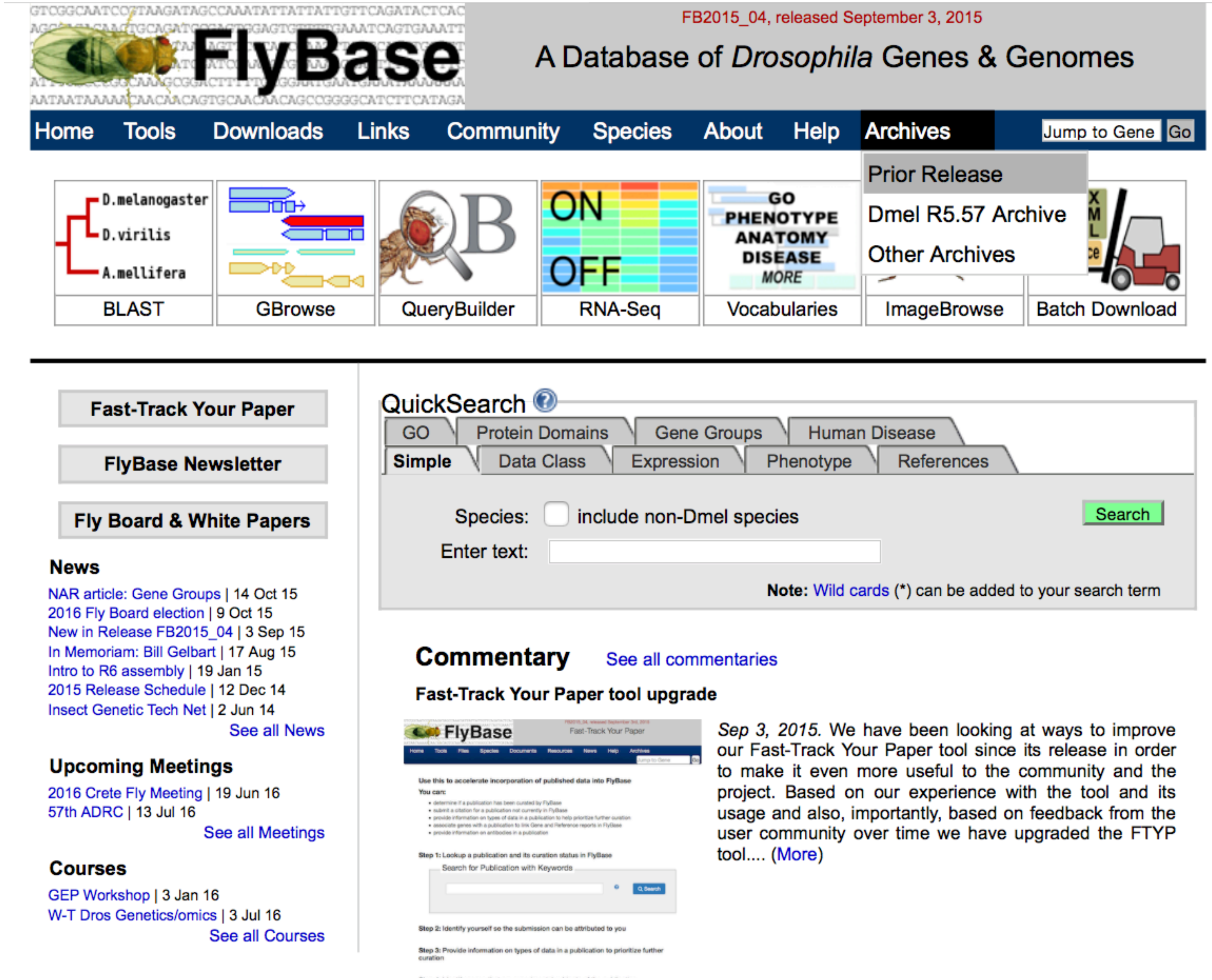


Drosophila melanogaster (fruit fly)

Genome information

T number	T00030
Org code	dme
Aliases	DROME, 7227
Full name	Drosophila melanogaster (fruit fly)
Definition	Drosophila melanogaster (fruit fly)
Annotation	manual
Taxonomy	TAX: 7227
Lineage	Eukaryota; Metazoa; Ecdysozoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila; Sophophora
Data source	RefSeq (Assembly: GCF_000001215.2)
Original DB	FlyBase
Statistics	Number of protein genes: 13954 Number of RNA genes: 2808
Reference	PMID: 10731132
Authors	Adams MD et al.
Title	The genome sequence of Drosophila melanogaster.
Journal	Science 287:2185-95 (2000)

FlyBase: ショウジョウバエのゲノムデータベース



FB2015_04, released September 3, 2015

A Database of *Drosophila* Genes & Genomes

News

NAR article: Gene Groups | 14 Oct 15
2016 Fly Board election | 9 Oct 15
New in Release FB2015_04 | 3 Sep 15
In Memoriam: Bill Gelbart | 17 Aug 15
Intro to R6 assembly | 19 Jan 15
2015 Release Schedule | 12 Dec 14
Insect Genetic Tech Net | 2 Jun 14
See all News

Upcoming Meetings

2016 Crete Fly Meeting | 19 Jun 16
57th ADRC | 13 Jul 16
See all Meetings

Courses

GEP Workshop | 3 Jan 16
W-T Dros Genetics/omics | 3 Jul 16
See all Courses

Species: ☐ include non-Dmel species

Enter text:

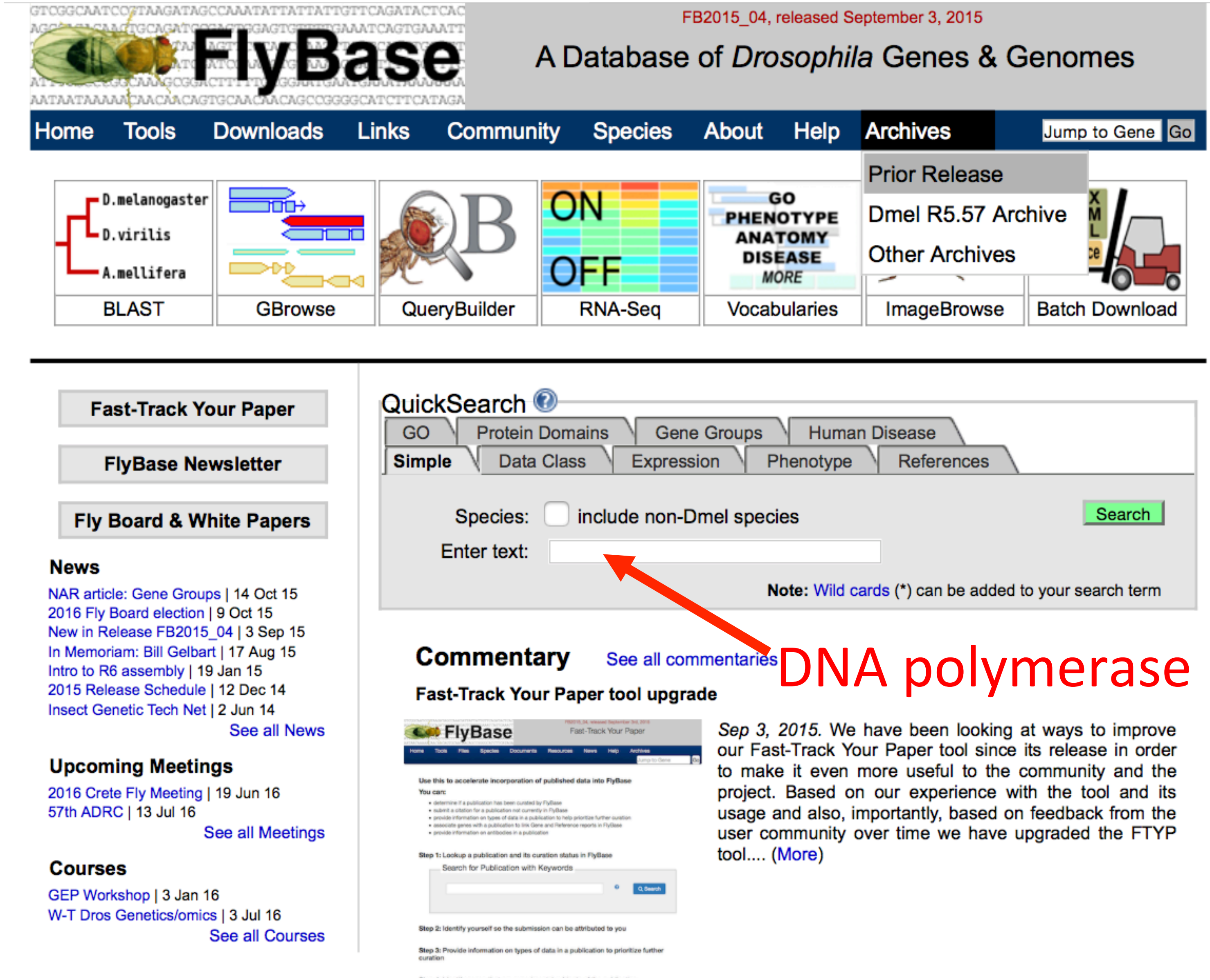
Note: Wild cards (*) can be added to your search term

Commentary See all commentaries

Fast-Track Your Paper tool upgrade

Sep 3, 2015. We have been looking at ways to improve our Fast-Track Your Paper tool since its release in order to make it even more useful to the community and the project. Based on our experience with the tool and its usage and also, importantly, based on feedback from the user community over time we have upgraded the FTYP tool.... (More)

検索ボックスにサーチワードを入れてみる



FB2015_04, released September 3, 2015

A Database of *Drosophila* Genes & Genomes

Species: ☐ include non-Dmel species

Enter text:

Note: Wild cards (*) can be added to your search term

DNA polymerase

News

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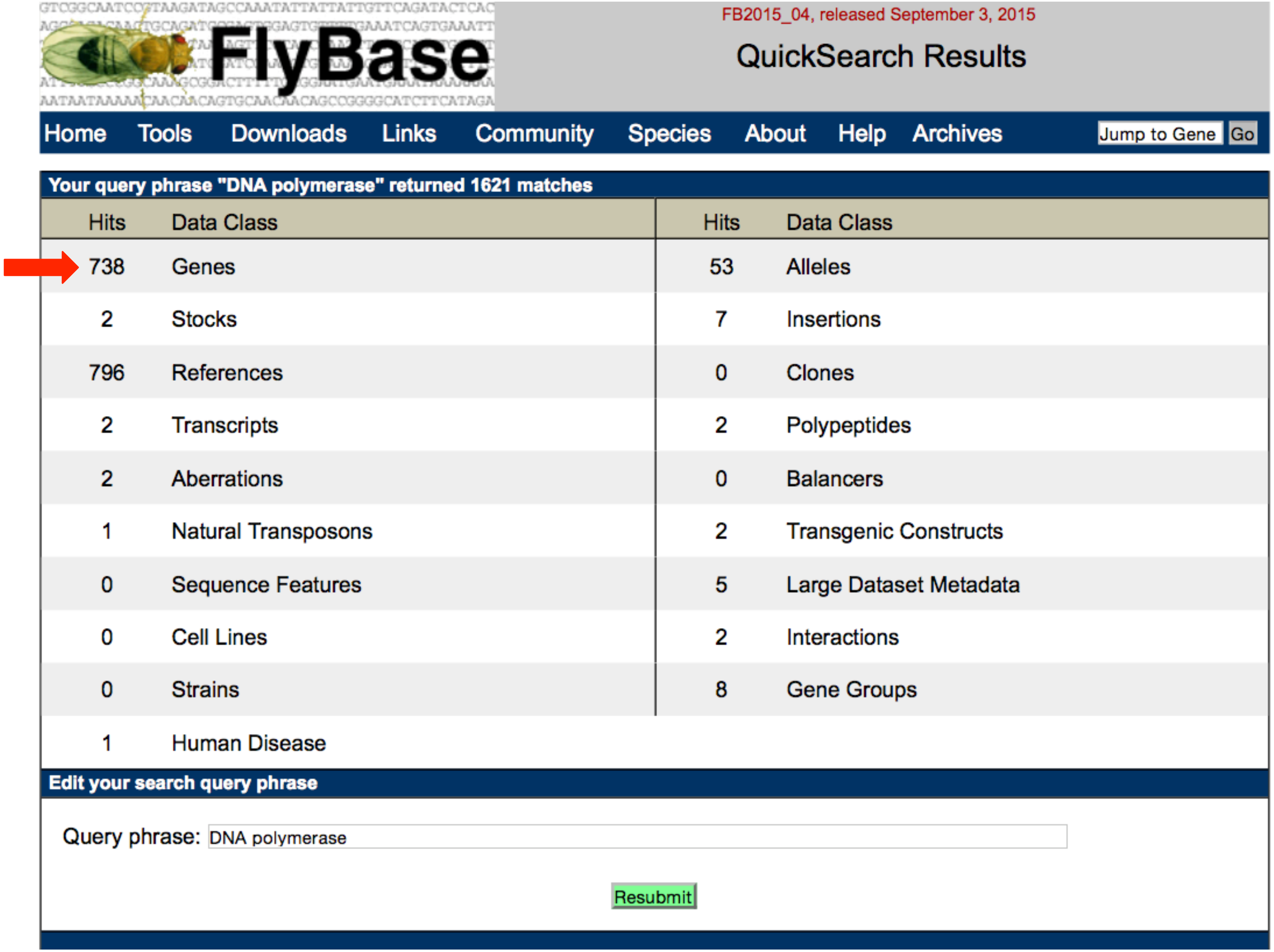
各項目のヒットした件数が標示される



QuickSearch Results

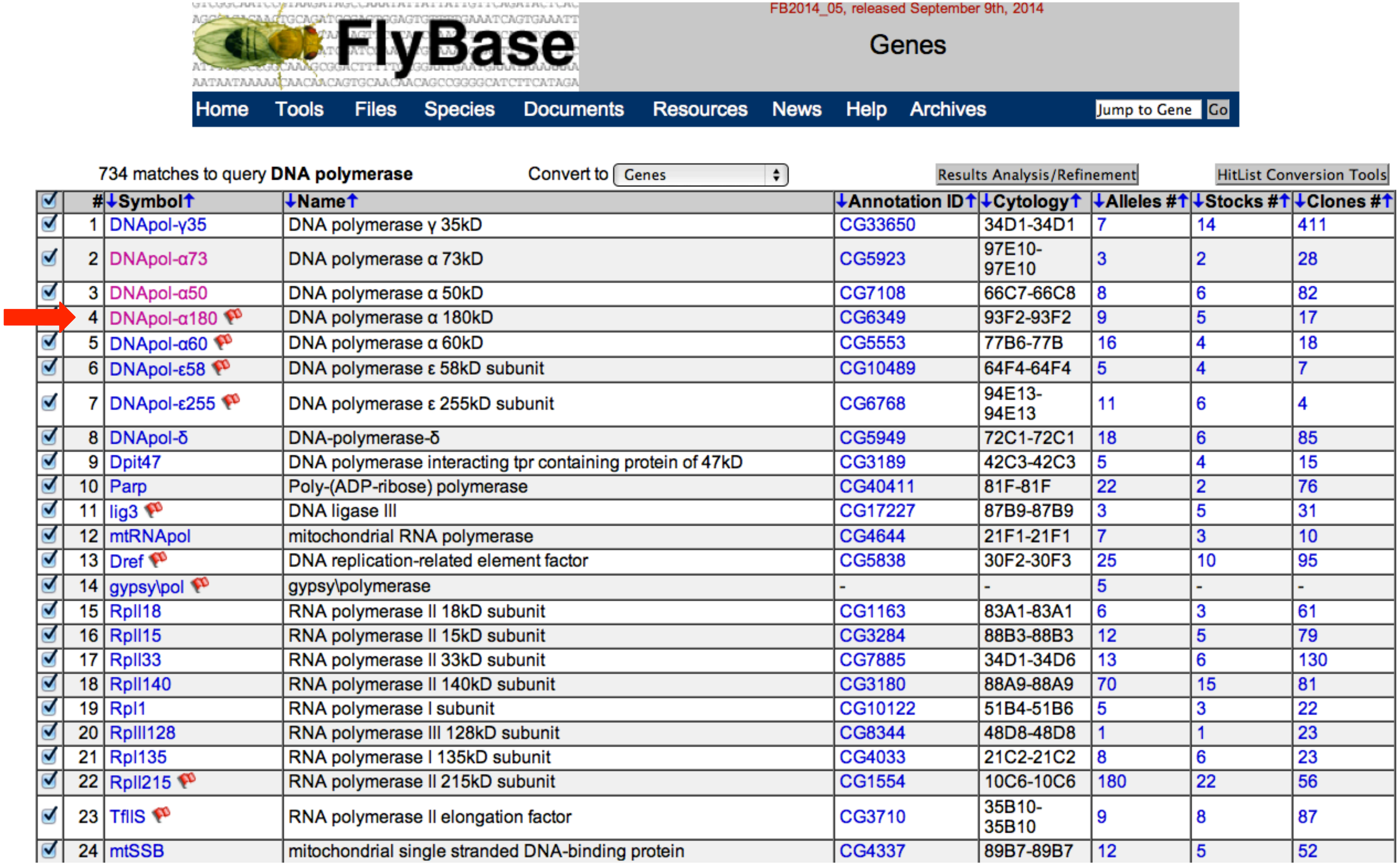
Your query phrase "DNA polymerase" returned 1621 matches

Hits	Data Class	Hits	Data Class
738	Genes	53	Alleles
2	Stocks	7	Insertions
796	References	0	Clones
2	Transcripts	2	Polypeptides
2	Aberrations	0	Balancers
1	Natural Transposons	2	Transgenic Constructs
0	Sequence Features	5	Large Dataset Metadata
0	Cell Lines	2	Interactions
0	Strains	8	Gene Groups
1	Human Disease		

Edit your search query phrase

Query phrase: DNA polymerase

関連性の高いものから標示される



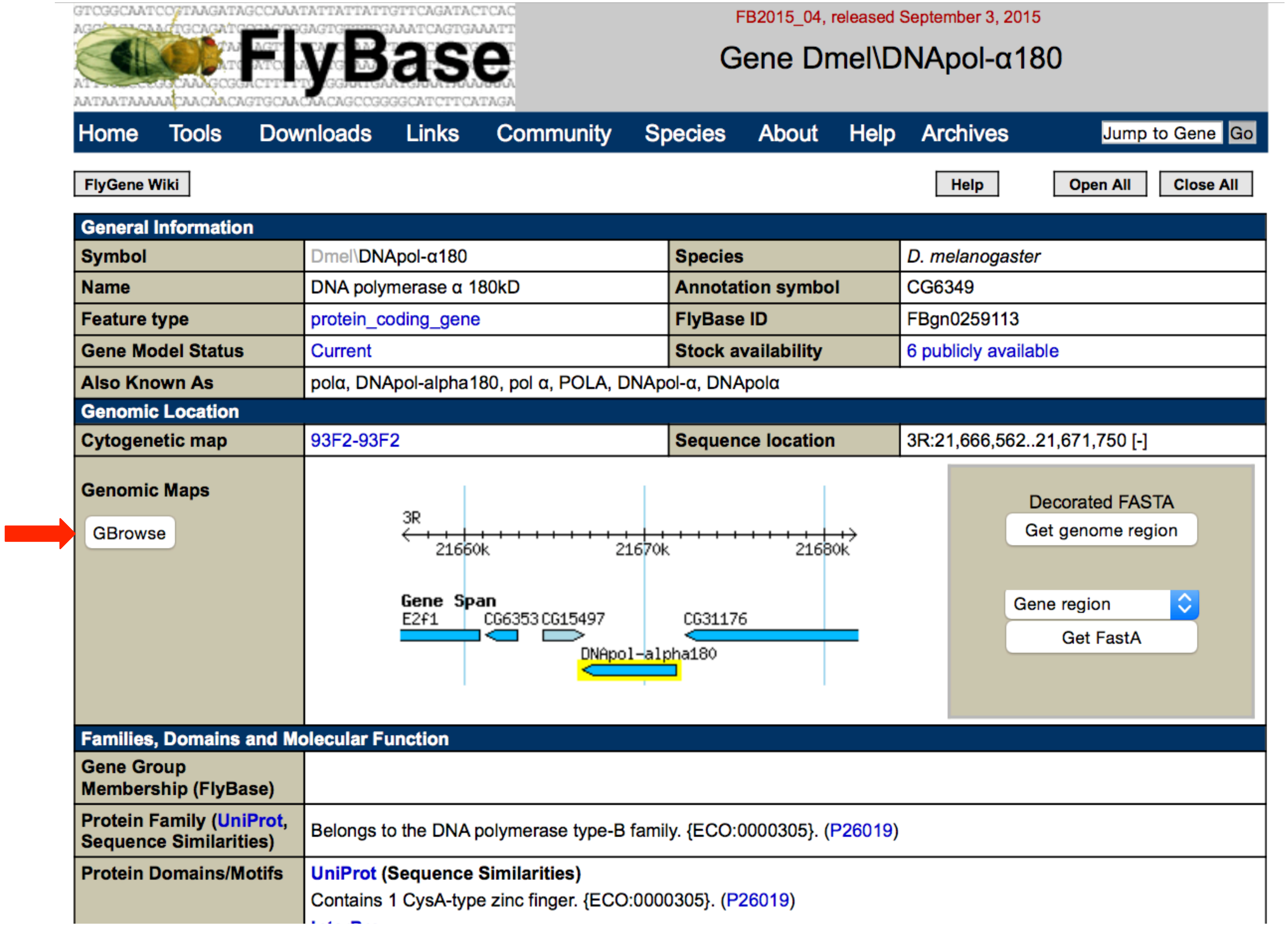
FB2014_05, released September 9th, 2014

Genes

734 matches to query **DNA polymerase**   Convert to Genes

☑	#	↓Symbol↑	↓Name↑	↓Annotation ID↑	↓Cytology↑	↓Alleles #↑	↓Stocks #↑	↓Clones #↑
☑	1	DNApol-γ35	DNA polymerase γ 35kD	CG33650	34D1-34D1	7	14	411
☑	2	DNApol-α73	DNA polymerase α 73kD	CG5923	97E10-97E10	3	2	28
☑	3	DNApol-α50	DNA polymerase α 50kD	CG7108	66C7-66C8	8	6	82
☑	4	DNApol-α180	DNA polymerase α 180kD	CG6349	93F2-93F2	9	5	17
☑	5	DNApol-α60	DNA polymerase α 60kD	CG5553	77B6-77B	16	4	18
☑	6	DNApol-ε58	DNA polymerase ε 58kD subunit	CG10489	64F4-64F4	5	4	7
☑	7	DNApol-ε255	DNA polymerase ε 255kD subunit	CG6768	94E13-94E13	11	6	4
☑	8	DNApol-δ	DNA-polymerase-δ	CG5949	72C1-72C1	18	6	85
☑	9	Dpit47	DNA polymerase interacting tpr containing protein of 47kD	CG3189	42C3-42C3	5	4	15
☑	10	Parp	Poly-(ADP-ribose) polymerase	CG40411	81F-81F	22	2	76
☑	11	lig3	DNA ligase III	CG17227	87B9-87B9	3	5	31
☑	12	mtRNApol	mitochondrial RNA polymerase	CG4644	21F1-21F1	7	3	10
☑	13	Dref	DNA replication-related element factor	CG5838	30F2-30F3	25	10	95
☑	14	gypsy\pol	gypsy\polymerase	-	-	5	-	-
☑	15	RpII18	RNA polymerase II 18kD subunit	CG1163	83A1-83A1	6	3	61
☑	16	RpII15	RNA polymerase II 15kD subunit	CG3284	88B3-88B3	12	5	79
☑	17	RpII33	RNA polymerase II 33kD subunit	CG7885	34D1-34D6	13	6	130
☑	18	RpII140	RNA polymerase II 140kD subunit	CG3180	88A9-88A9	70	15	81
☑	19	RpI1	RNA polymerase I subunit	CG10122	51B4-51B6	5	3	22
☑	20	RpIII128	RNA polymerase III 128kD subunit	CG8344	48D8-48D8	1	1	23
☑	21	RpI135	RNA polymerase I 135kD subunit	CG4033	21C2-21C2	8	6	23
☑	22	RpII215	RNA polymerase II 215kD subunit	CG1554	10C6-10C6	180	22	56
☑	23	TfIIS	RNA polymerase II elongation factor	CG3710	35B10-35B10	9	8	87
☑	24	mtSSB	mitochondrial single stranded DNA-binding protein	CG4337	89B7-89B7	12	5	52

DNAポリメラーゼα 180kDサブユニットの情報



FB2015_04, released September 3, 2015

Gene Dmel\DNApol-α180

General Information

Symbol	Dmel\DNApol-α180	**Species**	*D. melanogaster*
Name	DNA polymerase α 180kD	**Annotation symbol**	CG6349
Feature type	protein_coding_gene	**FlyBase ID**	FBgn0259113
Gene Model Status	Current	**Stock availability**	6 publicly available
Also Known As	polα, DNApol-alpha180, pol α, POLA, DNApol-α, DNApolα		

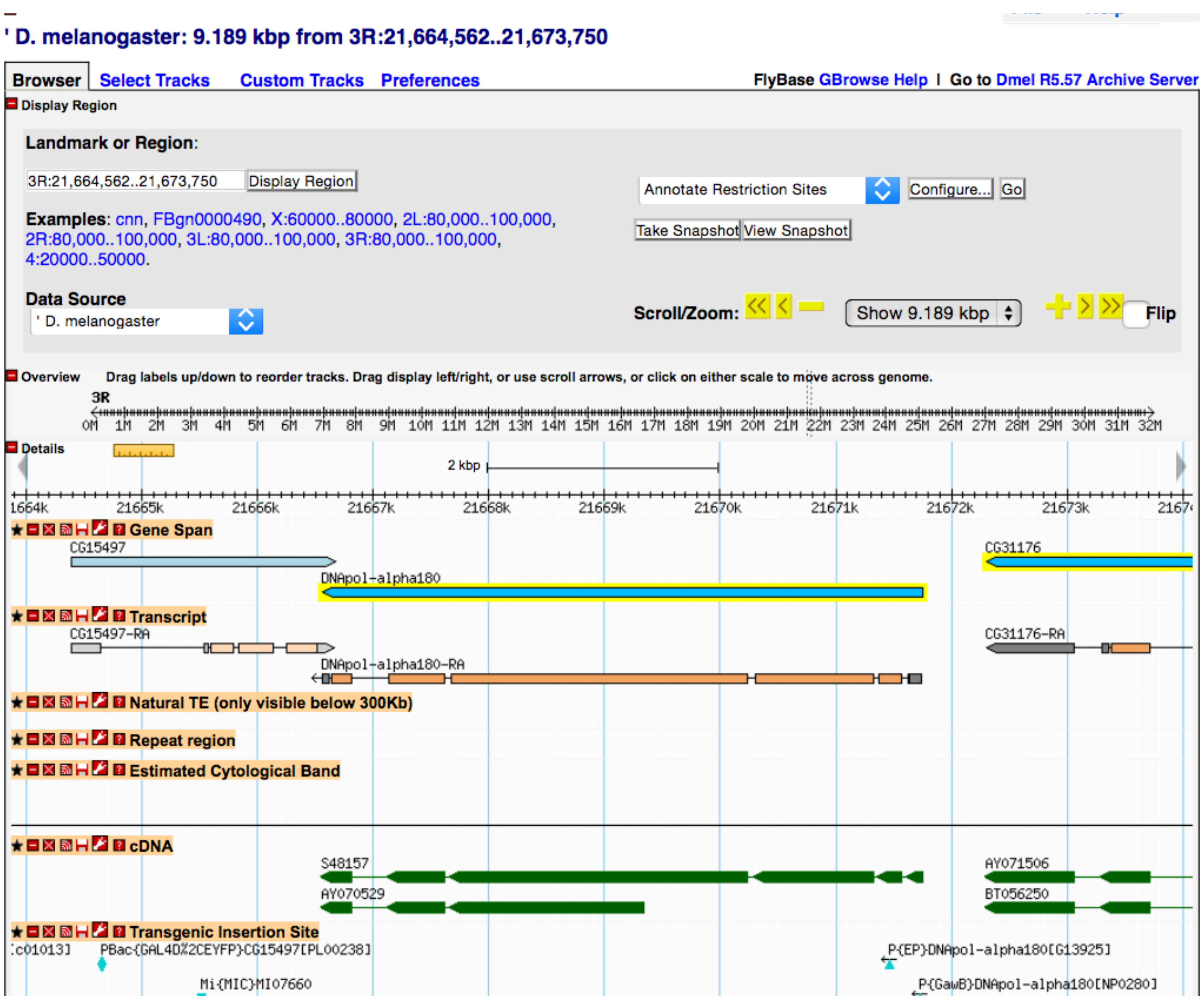
Genomic Location

Cytogenetic map	93F2-93F2	**Sequence location**	3R:21,666,562..21,671,750 [-]
Genomic Maps			

Families, Domains and Molecular Function

Gene Group Membership (FlyBase)	
Protein Family (UniProt, Sequence Similarities)	Belongs to the DNA polymerase type-B family. {ECO:0000305}. (P26019)
Protein Domains/Motifs	**UniProt (Sequence Similarities)** Contains 1 CysA-type zinc finger. {ECO:0000305}. (P26019)

DNAポリメラーゼα 180kD遺伝子のゲノム領域の様子



D. melanogaster: 9.189 kbp from 3R:21,664,562..21,673,750

Landmark or Region: 3R:21,664,562..21,673,750

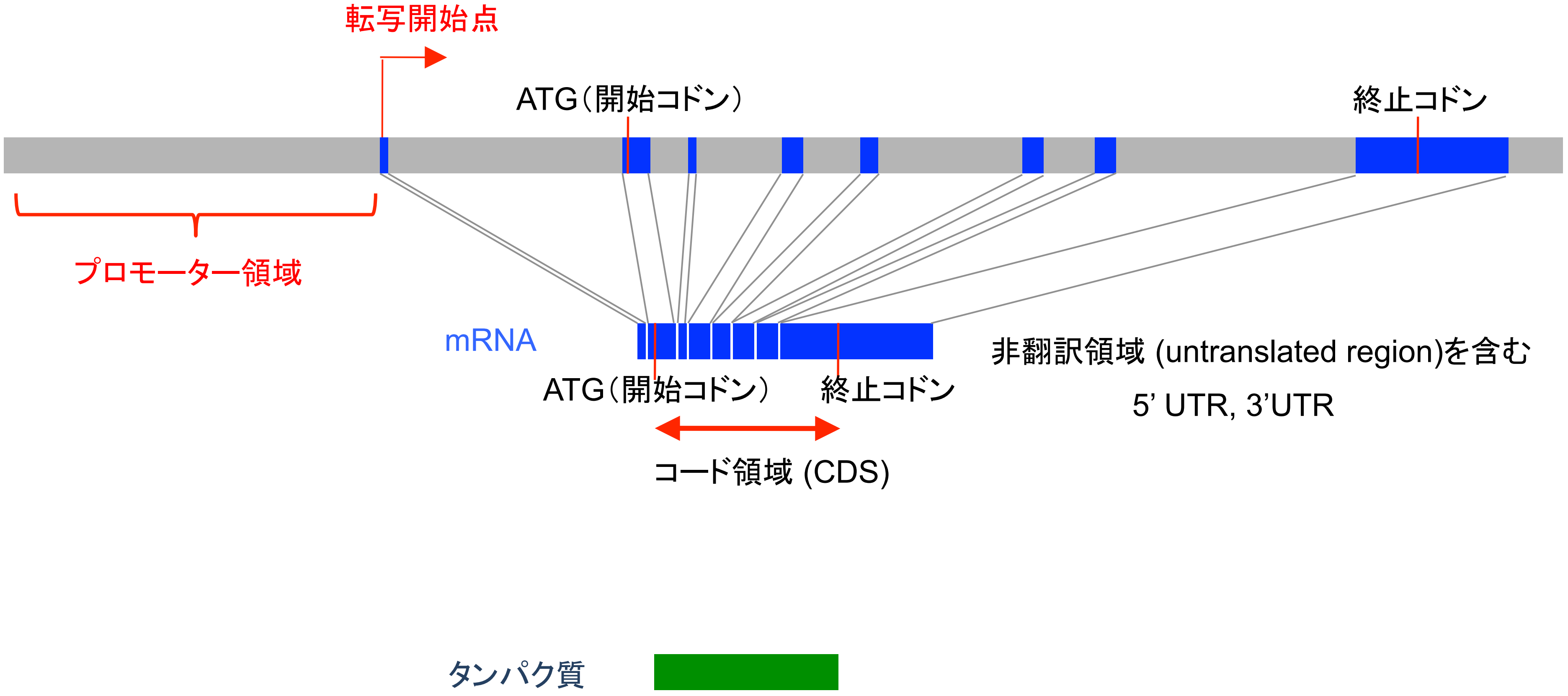
Examples: cnn, FBgn0000490, X:60000..80000, 2L:80,000..100,000, 2R:80,000..100,000, 3L:80,000..100,000, 3R:80,000..100,000, 4:20000..50000.

Data Source: D. melanogaster

Drag labels up/down to reorder tracks. Drag display left/right, or use scroll arrows, or click on either scale to move across genome.

遺伝子の構造

転写を制御するプロモーター領域



転写開始点

ATG（開始コドン）

終止コドン

プロモーター領域

mRNA

ATG（開始コドン）　終止コドン

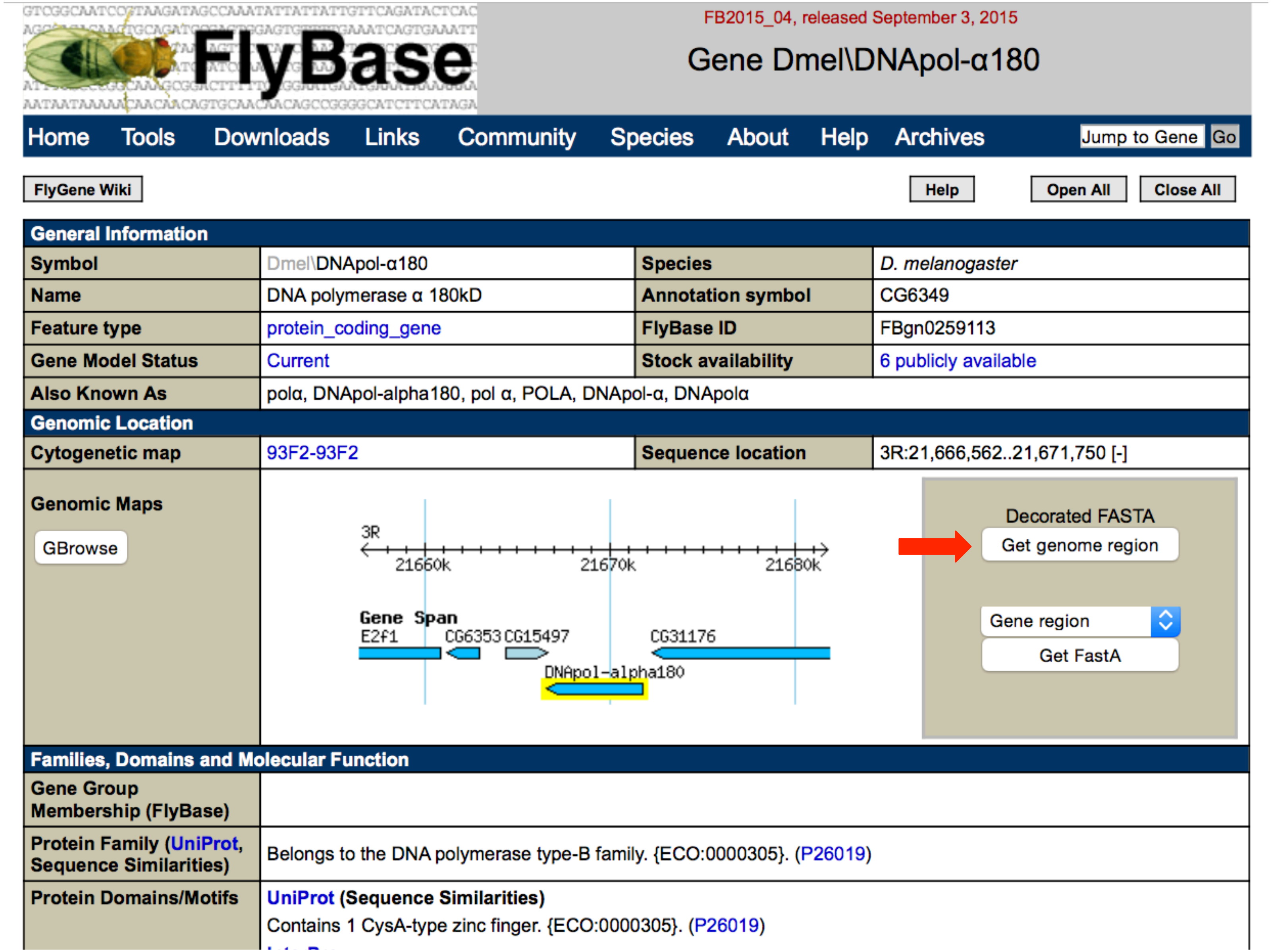
非翻訳領域 (untranslated region)を含む

5’ UTR, 3’UTR

コード領域 (CDS)

タンパク質

DNAポリメラーゼα 180kDの配列情報を見る（1）



FB2015_04, released September 3, 2015

Gene Dmel\DNApol-α180

General Information

Symbol	Dmel\DNApol-α180	**Species**	*D. melanogaster*
Name	DNA polymerase α 180kD	**Annotation symbol**	CG6349
Feature type	protein_coding_gene	**FlyBase ID**	FBgn0259113
Gene Model Status	Current	**Stock availability**	6 publicly available
Also Known As	polα, DNApol-alpha180, pol α, POLA, DNApol-α, DNApolα		

Genomic Location

Cytogenetic map	93F2-93F2	**Sequence location**	3R:21,666,562..21,671,750 [-]

Genomic Maps

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Gene Group Membership (FlyBase)	
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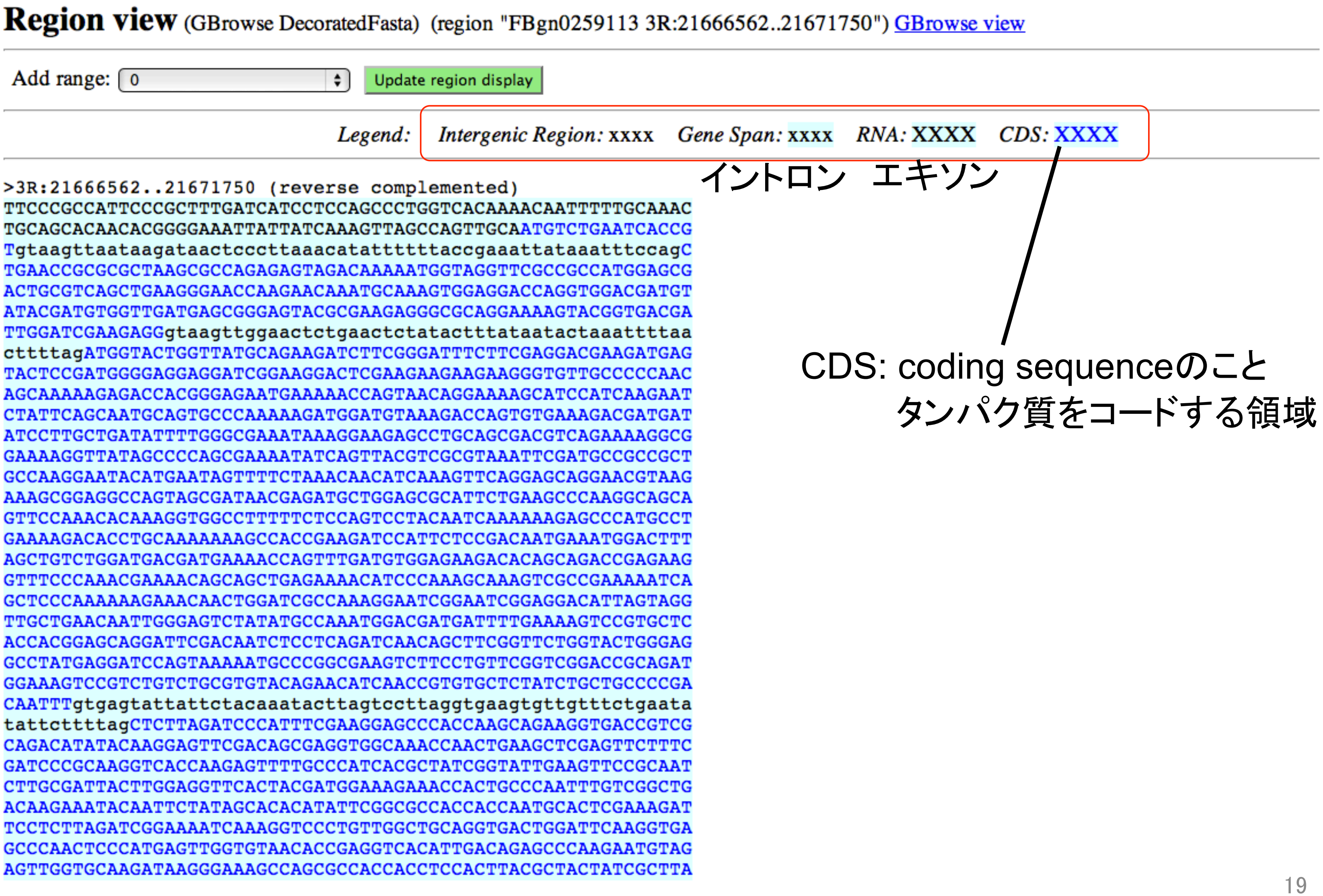
Protein Domains/Motifs	**UniProt (Sequence Similarities)** Contains 1 CysA-type zinc finger. {ECO:0000305}. (P26019)

DNAポリメラーゼα 180kDサブユニットの配列情報



Region view (GBrowse DecoratedFasta) (region "FBgn0259113 3R:21666562..21671750") GBrowse view

Legend: *Intergenic Region:* xxxx *Gene Span:* xxxx *RNA:* XXXX *CDS:* XXXX

```
>3R:21666562..21671750 (reverse complemented)
TTCCCGCCATTCCCGCTTTGATCATCCTCCAGCCCTGGTCACAAAACAATTTTTGCAAAC
TGCAGCACAACACGGGGAAATTATTATCAAAGTTAGCCAGTTGCAATGTCTGAATCACCG
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TACTCCGATGGGGAGGAGGATCGGAAGGACTCGAAGAAGAAGAAGGGTGTTGCCCCCAAC
AGCAAAAAGAGACCACGGGAGAATGAAAAACCAGTAACAGGAAAAGCATCCATCAAGAAT
CTATTCAGCAATGCAGTGCCCAAAAAGATGGATGTAAAGACCAGTGTGAAAGACGATGAT
ATCCTTGCTGATATTTTGGGCGAAATAAAGGAAGAGCCTGCAGCGACGTCAGAAAAGGCG
GAAAAGGTTATAGCCCCAGCGAAAATATCAGTTACGTCGCGTAAATTCGATGCCGCCGCT
GCCAAGGAATACATGAATAGTTTTCTAAACAACATCAAAGTTCAGGAGCAGGAACGTAAG
AAAGCGGAGGCCAGTAGCGATAACGAGATGCTGGAGCGCATTCTGAAGCCCAAGGCAGCA
GTTCCAAACACAAAGGTGGCCTTTTTCTCCAGTCCTACAATCAAAAAAGAGCCCATGCCT
GAAAAGACACCTGCAAAAAAAGCCACCGAAGATCCATTCTCCGACAATGAAATGGACTTT
AGCTGTCTGGATGACGATGAAAACCAGTTTGATGTGGAGAAGACACAGCAGACCGAGAAG
GTTTCCCAAACGAAAACAGCAGCTGAGAAAACATCCCAAAGCAAAGTCGCCGAAAAATCA
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GGAAAGTCCGTCTGTCTGCGTGTACAGAACATCAACCGTGTGCTCTATCTGCTGCCCCGA
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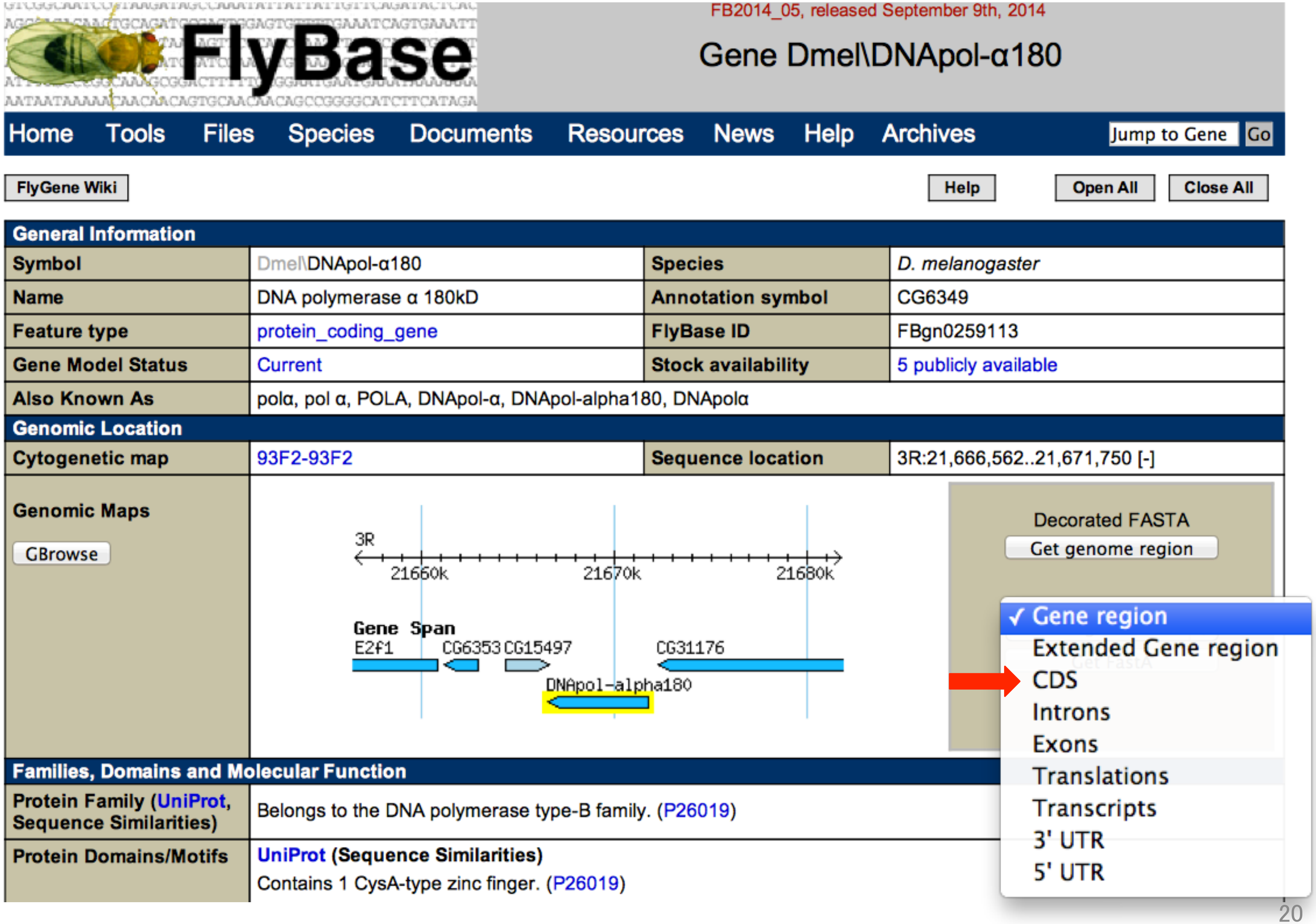
CAGACATATACAAGGAGTTCGACAGCGAGGTGGCAAACCAACTGAAGCTCGAGTTCTTTC
GATCCCGCAAGGTCACCAAGAGTTTTGCCCATCACGCTATCGGTATTGAAGTTCCGCAAT
CTTGCGATTACTTGGAGGTTCACTACGATGGAAAGAAACCACTGCCCAATTTGTCGGCTG
ACAAGAAATACAATTCTATAGCACACATATTCGGCGCCACCACCAATGCACTCGAAAGAT
TCCTCTTAGATCGGAAAATCAAAGGTCCCTGTTGGCTGCAGGTGACTGGATTCAAGGTGA
GCCCAACTCCCATGAGTTGGTGTAACACCGAGGTCACATTGACAGAGCCCAAGAATGTAG
AGTTGGTGCAAGATAAGGGAAAGCCAGCGCCACCACCTCCACTTACGCTACTATCGCTTA
```

イントロン　エキソン

CDS: coding sequenceのこと
タンパク質をコードする領域

演習：いろいろな配列情報を見てみよう



FB2014_05, released September 9th, 2014

Gene Dmel\DNApol-α180

General Information			
Symbol	Dmel\DNApol-α180	**Species**	*D. melanogaster*
Name	DNA polymerase α 180kD	**Annotation symbol**	CG6349
Feature type	protein_coding_gene	**FlyBase ID**	FBgn0259113
Gene Model Status	Current	**Stock availability**	5 publicly available
Also Known As	polα, pol α, POLA, DNApol-α, DNApol-alpha180, DNApolα		
Genomic Location			
Cytogenetic map	93F2-93F2	**Sequence location**	3R:21,666,562..21,671,750 [-]
Genomic Maps			
Families, Domains and Molecular Function			
Protein Family (UniProt, Sequence Similarities)	Belongs to the DNA polymerase type-B family. (P26019)		
Protein Domains/Motifs	**UniProt (Sequence Similarities)** Contains 1 CysA-type zinc finger. (P26019)		

課題

ショウジョウバエのRNA polymerase I 135kD subunitについて以下のことを調べて、テキストファイルに整理する。

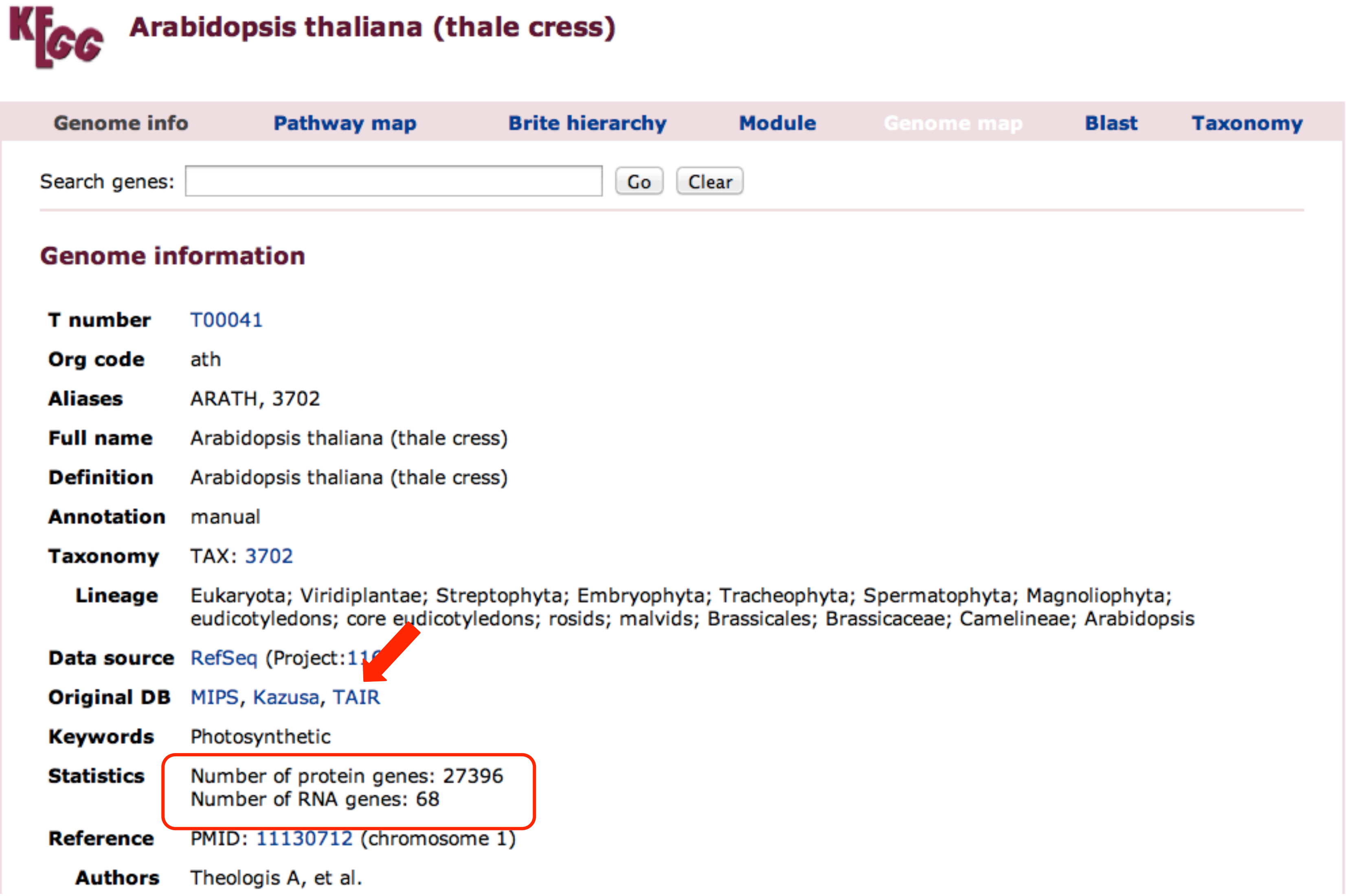
1. この遺伝子が存在する染色体の番号、またこの染色体上での位置（塩基の番号）
2. エキソンの数
3. コードするタンパク質のアミノ酸配列
4. この遺伝子の隣（上流側および下流側）に位置する遺伝子の名称（記号でよい）

- テキストファイルをメールに添付して提出
- 講義５課題１

シロイヌナズナのデータベース

	Placozoans		tad	Trichoplax adhaerens	RefSeq
	Poriferans		aqu	Amphimedon queenslandica (sponge)	RefSeq
Plants	Eudicots	Mustard family	ath	Arabidopsis thaliana (thale cress)	RefSeq
			aly	Arabidopsis lyrata (lyrate rockcress)	RefSeq
		Pea family	gmx	Glycine max (soybean)	RefSeq
			mtr	Medicago truncatula (barrel medic)	RefSeq
			cam	Cicer arietinum (chickpea)	RefSeq
		Rose family	fve	Fragaria vesca (woodland strawberry)	RefSeq
		Cucumber family	csv	Cucumis sativus (cucumber)	RefSeq
		Spurge family	rcu	Ricinus communis (castor bean)	RefSeq
		Willow family	pop	Populus trichocarpa (black cottonwood)	RefSeq
		Grape family	vvi	Vitis vinifera (wine grape)	RefSeq
		Nightshade family	sly	Solanum lycopersicum (tomato)	RefSeq
	Monocots	Grass family	osa	Oryza sativa japonica (Japanese rice) (RefSeq)	RefSeq
			dosa	Oryza sativa japonica (Japanese rice) (RAPDB)	RAP-DB
			bdi	Brachypodium distachyon	RefSeq
			sbi	Sorghum bicolor (sorghum)	RefSeq
			zma	Zea mays (maize)	RefSeq
			sita	Setaria italica (foxtail millet)	RefSeq
	Ferns		smo	Selaginella moellendorffii	RefSeq
	Mosses		ppp	Physcomitrella patens subsp. patens	RefSeq
	Green algae		cre	Chlamydomonas reinhardtii	RefSeq
			vcn	Volvox carteri f. nagariensis	RefSeq
			olu	Ostreococcus lucimarinus	RefSeq
			ota	Ostreococcus tauri	RefSeq
			mis	Micromonas sp. RCC299	RefSeq
			mpp	Micromonas pusilla	RefSeq
	Red algae		cme	Cyanidioschyzon merolae	U Tokyo
			sce	Saccharomyces cerevisiae (budding yeast)	RefSeq

TAIRにアクセスする

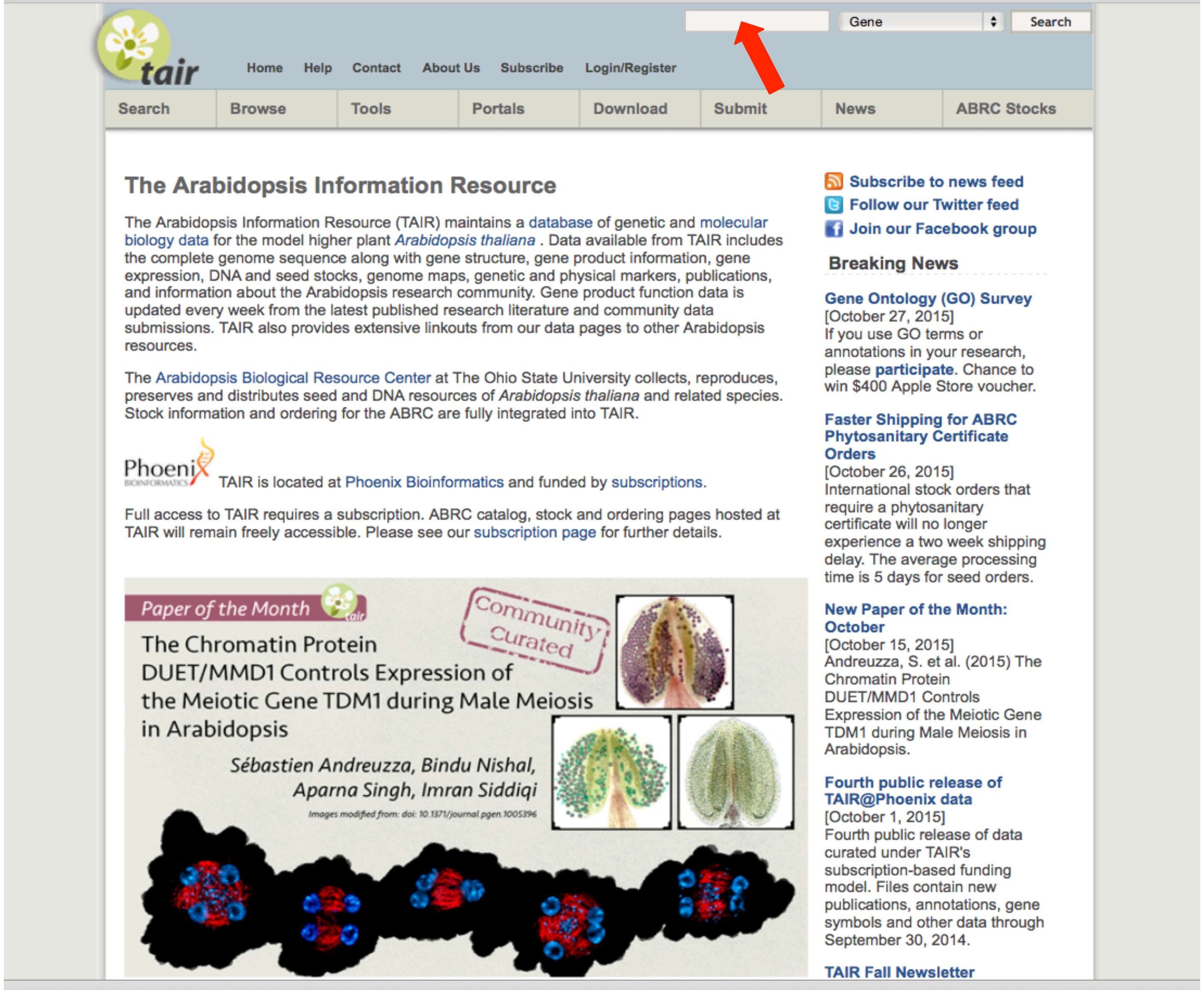


Arabidopsis thaliana (thale cress)

Genome information

T number	T00041
Org code	ath
Aliases	ARATH, 3702
Full name	Arabidopsis thaliana (thale cress)
Definition	Arabidopsis thaliana (thale cress)
Annotation	manual
Taxonomy	TAX: 3702
Lineage	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; malvids; Brassicales; Brassicaceae; Camelineae; Arabidopsis
Data source	RefSeq (Project:11
Original DB	MIPS, Kazusa, TAIR
Keywords	Photosynthetic
Statistics	Number of protein genes: 27396 Number of RNA genes: 68
Reference	PMID: 11130712 (chromosome 1)
Authors	Theologis A, et al.

演習（検索ボックスに「GL2」と入力）



The Arabidopsis Information Resource

The Arabidopsis Information Resource (TAIR) maintains a database of genetic and molecular biology data for the model higher plant *Arabidopsis thaliana* . Data available from TAIR includes the complete genome sequence along with gene structure, gene product information, gene expression, DNA and seed stocks, genome maps, genetic and physical markers, publications, and information about the Arabidopsis research community. Gene product function data is updated every week from the latest published research literature and community data submissions. TAIR also provides extensive linkouts from our data pages to other Arabidopsis resources.

The Arabidopsis Biological Resource Center at The Ohio State University collects, reproduces, preserves and distributes seed and DNA resources of *Arabidopsis thaliana* and related species. Stock information and ordering for the ABRC are fully integrated into TAIR.

Phoenix BIOINFORMATICS TAIR is located at Phoenix Bioinformatics and funded by subscriptions.

Full access to TAIR requires a subscription. ABRC catalog, stock and ordering pages hosted at TAIR will remain freely accessible. Please see our subscription page for further details.

Paper of the Month

The Chromatin Protein DUET/MMD1 Controls Expression of the Meiotic Gene TDM1 during Male Meiosis in Arabidopsis

Sébastien Andreuzza, Bindu Nishal, Aparna Singh, Imran Siddiqi

Images modified from: doi: 10.1371/journal.pgen.1005396

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Breaking News

Gene Ontology (GO) Survey
[October 27, 2015]
If you use GO terms or annotations in your research, please **participate**. Chance to win $400 Apple Store voucher.

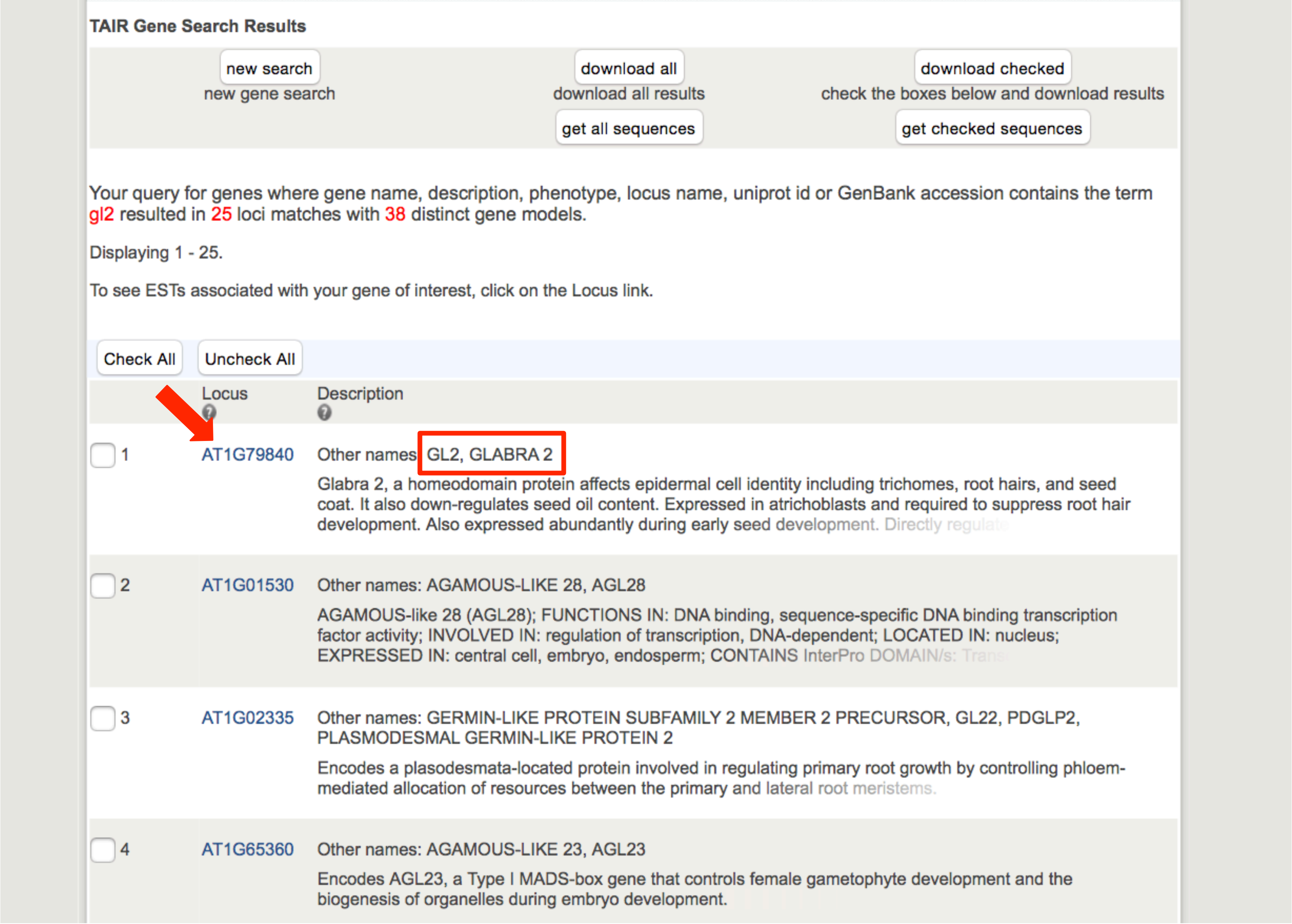
Faster Shipping for ABRC Phytosanitary Certificate Orders
[October 26, 2015]
International stock orders that require a phytosanitary certificate will no longer experience a two week shipping delay. The average processing time is 5 days for seed orders.

New Paper of the Month: October
[October 15, 2015]
Andreuzza, S. et al. (2015) The Chromatin Protein DUET/MMD1 Controls Expression of the Meiotic Gene TDM1 during Male Meiosis in Arabidopsis.

Fourth public release of TAIR@Phoenix data
[October 1, 2015]
Fourth public release of data curated under TAIR's subscription-based funding model. Files contain new publications, annotations, gene symbols and other data through September 30, 2014.

TAIR Fall Newsletter

結果1



TAIR Gene Search Results

new gene search

download all results

check the boxes below and download results

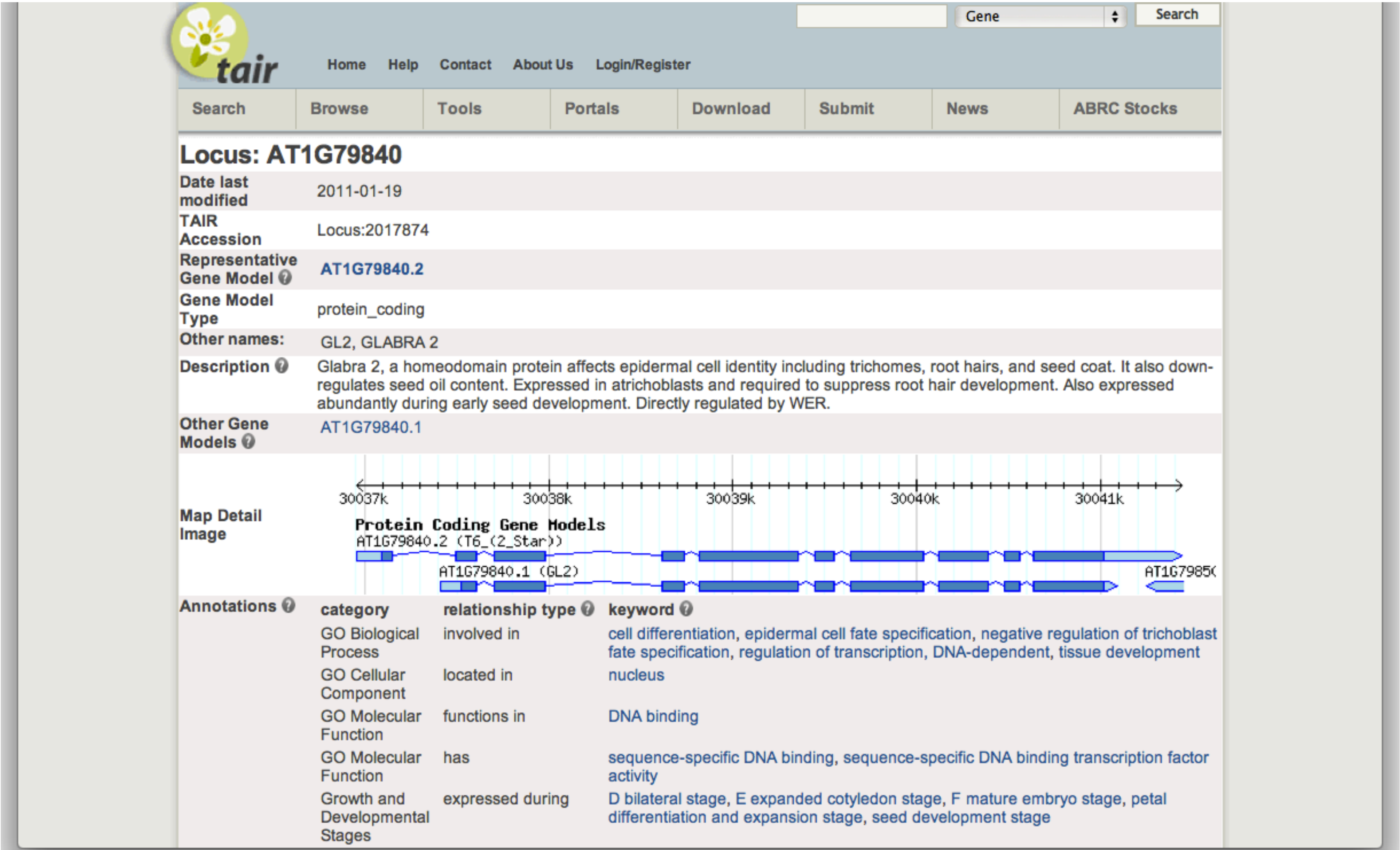
Your query for genes where gene name, description, phenotype, locus name, uniprot id or GenBank accession contains the term gl2 resulted in 25 loci matches with 38 distinct gene models.

Displaying 1 - 25.

To see ESTs associated with your gene of interest, click on the Locus link.

	Locus	Description
☐ 1	AT1G79840	Other names: GL2, GLABRA 2 Glabra 2, a homeodomain protein affects epidermal cell identity including trichomes, root hairs, and seed coat. It also down-regulates seed oil content. Expressed in atrichoblasts and required to suppress root hair development. Also expressed abundantly during early seed development. Directly regulate
☐ 2	AT1G01530	Other names: AGAMOUS-LIKE 28, AGL28 AGAMOUS-like 28 (AGL28); FUNCTIONS IN: DNA binding, sequence-specific DNA binding transcription factor activity; INVOLVED IN: regulation of transcription, DNA-dependent; LOCATED IN: nucleus; EXPRESSED IN: central cell, embryo, endosperm; CONTAINS InterPro DOMAIN/s: Trans
☐ 3	AT1G02335	Other names: GERMIN-LIKE PROTEIN SUBFAMILY 2 MEMBER 2 PRECURSOR, GL22, PDGLP2, PLASMODESMAL GERMIN-LIKE PROTEIN 2 Encodes a plasodesmata-located protein involved in regulating primary root growth by controlling phloem-mediated allocation of resources between the primary and lateral root meristems.
☐ 4	AT1G65360	Other names: AGAMOUS-LIKE 23, AGL23 Encodes AGL23, a Type I MADS-box gene that controls female gametophyte development and the biogenesis of organelles during embryo development.

結果2



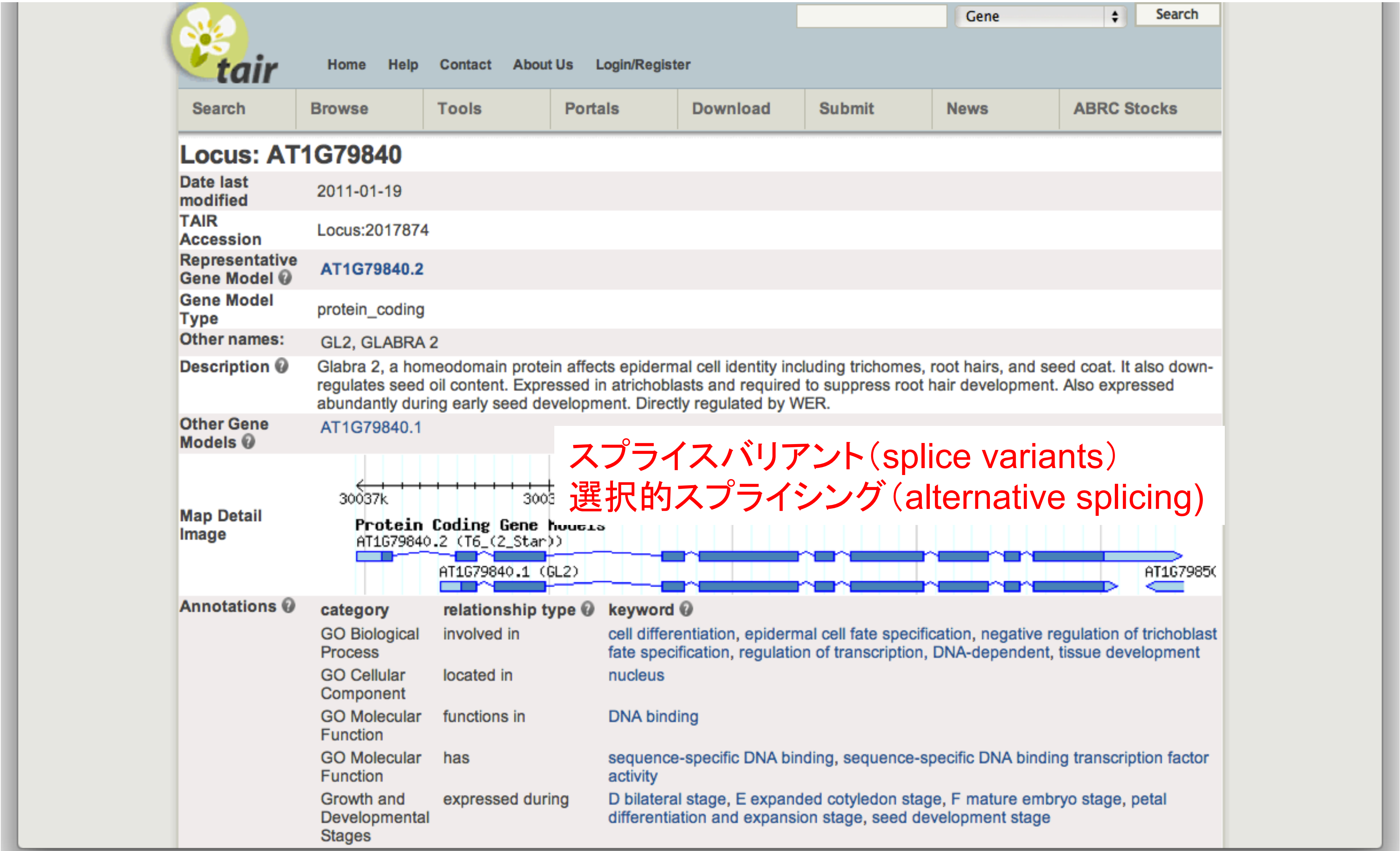
Locus: AT1G79840

Date last modified	2011-01-19
TAIR Accession	Locus:2017874
Representative Gene Model	AT1G79840.2
Gene Model Type	protein_coding
Other names:	GL2, GLABRA 2
Description	Glabra 2, a homeodomain protein affects epidermal cell identity including trichomes, root hairs, and seed coat. It also down-regulates seed oil content. Expressed in atrichoblasts and required to suppress root hair development. Also expressed abundantly during early seed development. Directly regulated by WER.
Other Gene Models	AT1G79840.1
Map Detail Image	

Annotations

category	relationship type	keyword
GO Biological Process	involved in	cell differentiation, epidermal cell fate specification, negative regulation of trichoblast fate specification, regulation of transcription, DNA-dependent, tissue development
GO Cellular Component	located in	nucleus
GO Molecular Function	functions in	DNA binding
GO Molecular Function	has	sequence-specific DNA binding, sequence-specific DNA binding transcription factor activity
Growth and Developmental Stages	expressed during	D bilateral stage, E expanded cotyledon stage, F mature embryo stage, petal differentiation and expansion stage, seed development stage

結果2



Locus: AT1G79840

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Map Detail Image	

Annotations

category	relationship type	keyword
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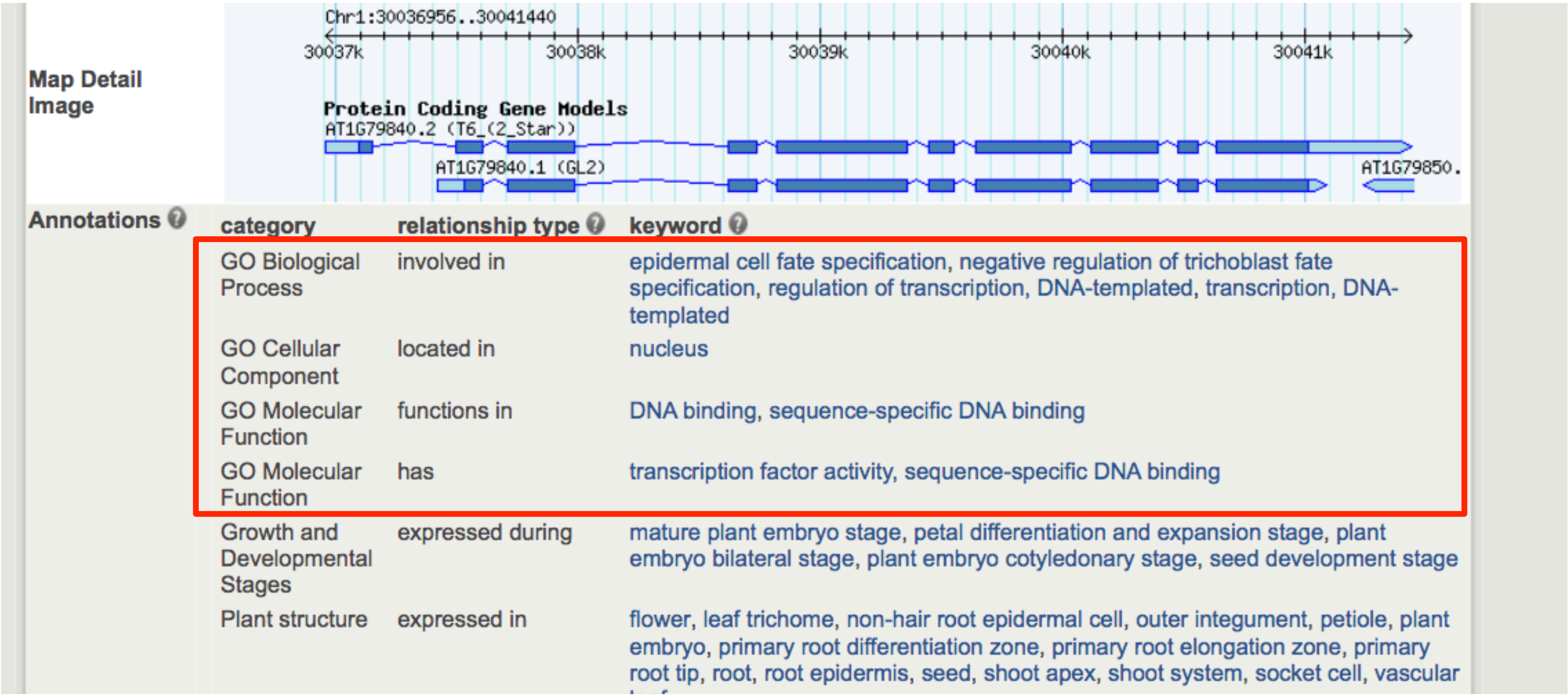
GO Cellular Component	located in	nucleus
GO Molecular Function	functions in	DNA binding
GO Molecular Function	has	sequence-specific DNA binding, sequence-specific DNA binding transcription factor activity
Growth and Developmental Stages	expressed during	D bilateral stage, E expanded cotyledon stage, F mature embryo stage, petal differentiation and expansion stage, seed development stage

スプライスバリアント（splice variants）
選択的スプライシング（alternative splicing)

結果3

GO (Gene Ontology) について



Annotations

category	relationship type	keyword
GO Biological Process	involved in	epidermal cell fate specification, negative regulation of trichoblast fate specification, regulation of transcription, DNA-templated, transcription, DNA-templated
GO Cellular Component	located in	nucleus
GO Molecular Function	functions in	DNA binding, sequence-specific DNA binding
GO Molecular Function	has	transcription factor activity, sequence-specific DNA binding
Growth and Developmental Stages	expressed during	mature plant embryo stage, petal differentiation and expansion stage, plant embryo bilateral stage, plant embryo cotyledonary stage, seed development stage
Plant structure	expressed in	flower, leaf trichome, non-hair root epidermal cell, outer integument, petiole, plant embryo, primary root differentiation zone, primary root elongation zone, primary root tip, root, root epidermis, seed, shoot apex, shoot system, socket cell, vascular

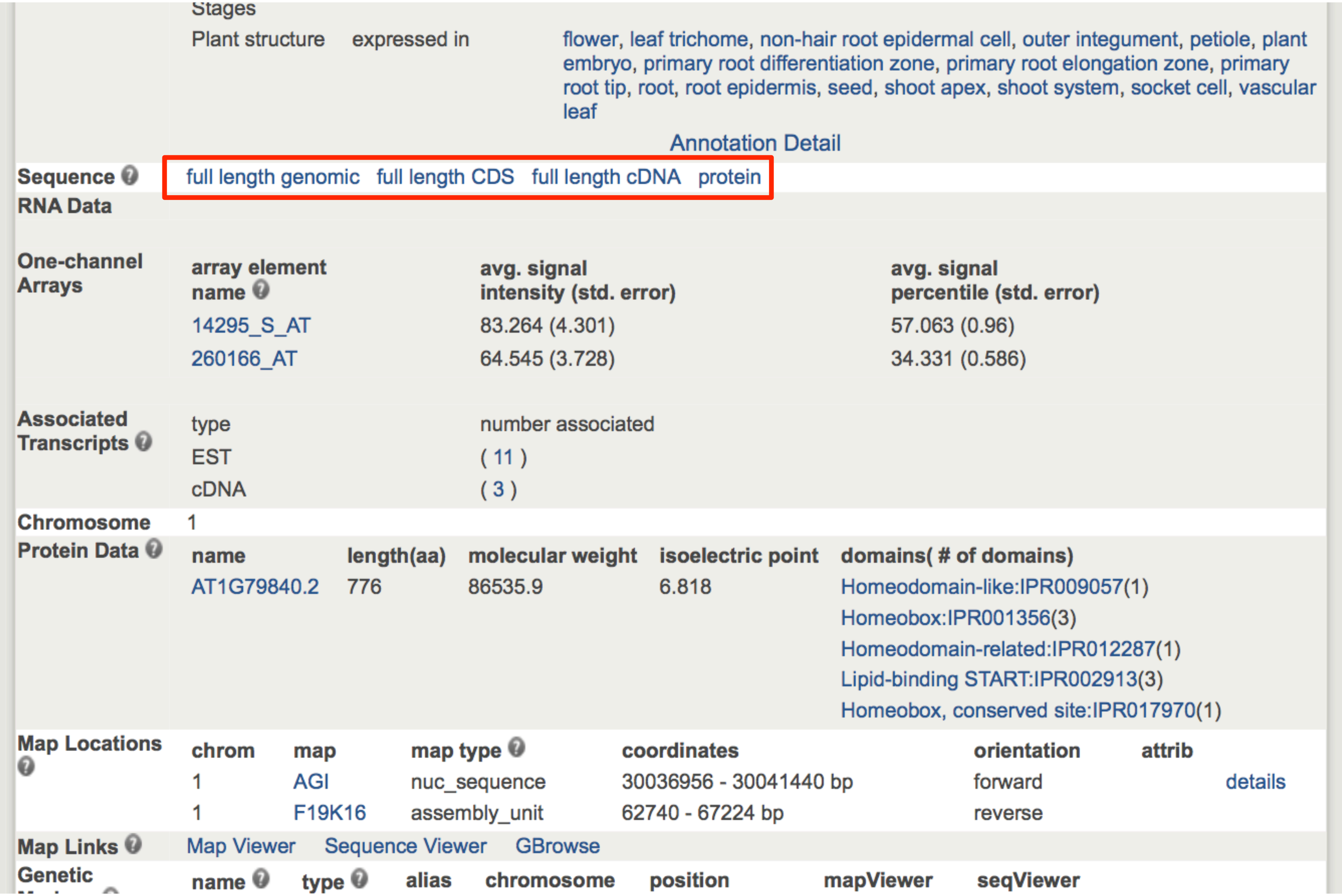
GO (Gene Ontology) :

遺伝子に関する情報を共通のワードを用いて表現し、データベース化することにより、系統的に整理するプロジェクト。遺伝子間、生物間の横断的な比較が可能になる。

Biological Process, Molecular Function, Cellular component

結果4

塩基配列をみる



Stages

Plant structure expressed in flower, leaf trichome, non-hair root epidermal cell, outer integument, petiole, plant embryo, primary root differentiation zone, primary root elongation zone, primary root tip, root, root epidermis, seed, shoot apex, shoot system, socket cell, vascular leaf

Annotation Detail

Sequence full length genomic full length CDS full length cDNA protein

RNA Data

One-channel Arrays

array element name	avg. signal intensity (std. error)	avg. signal percentile (std. error)
14295_S_AT	83.264 (4.301)	57.063 (0.96)
260166_AT	64.545 (3.728)	34.331 (0.586)

Associated Transcripts

type	number associated
EST	(11)
cDNA	(3)

Chromosome 1

Protein Data

name	length(aa)	molecular weight	isoelectric point	domains(# of domains)
AT1G79840.2	776	86535.9	6.818	Homeodomain-like:IPR009057(1) Homeobox:IPR001356(3) Homeodomain-related:IPR012287(1) Lipid-binding START:IPR002913(3) Homeobox, conserved site:IPR017970(1)

Map Locations

chrom	map	map type	coordinates	orientation	attrib
1	AGI	nuc_sequence	30036956 - 30041440 bp	forward	details
1	F19K16	assembly_unit	62740 - 67224 bp	reverse	

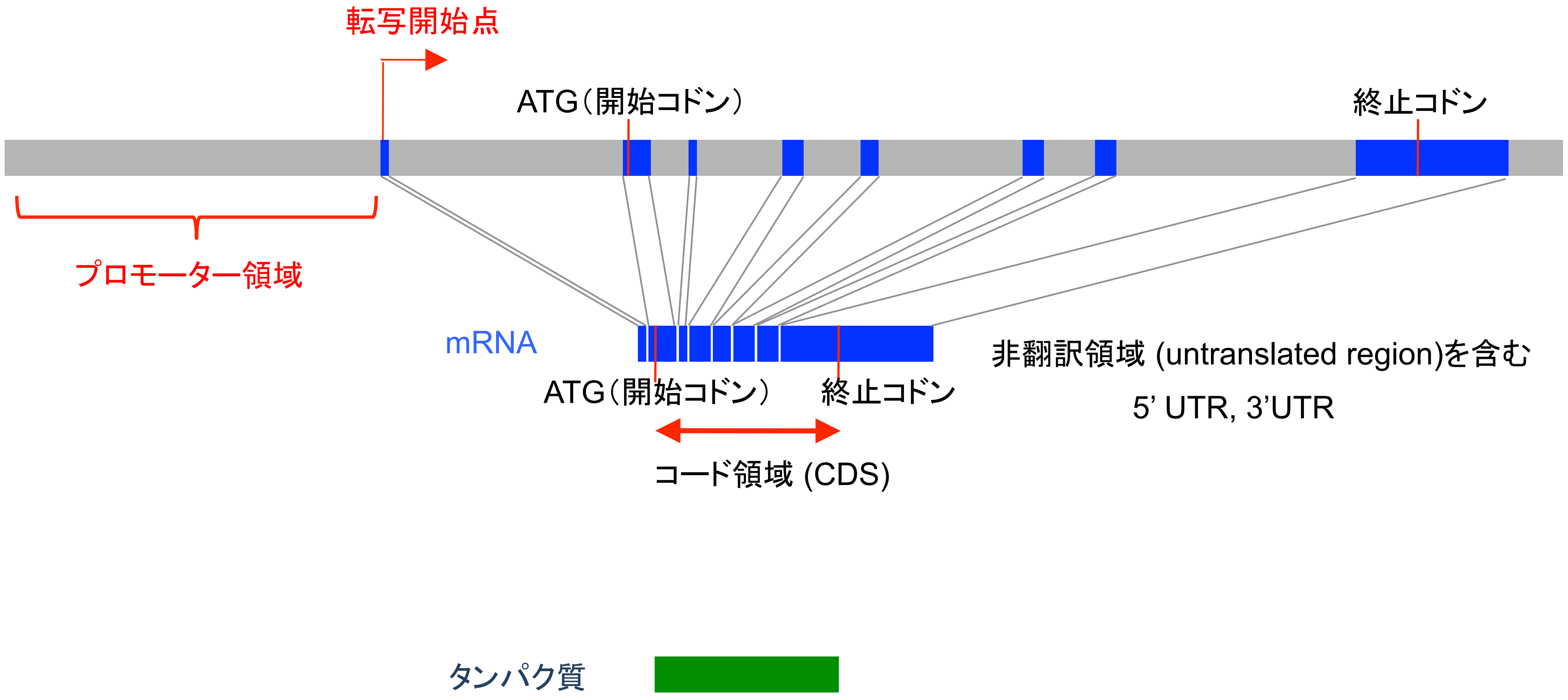
Map Links Map Viewer Sequence Viewer GBrowse

Genetic

name	type	alias	chromosome	position	mapViewer	seqViewer

遺伝子の構造

転写を制御するプロモーター領域



転写開始点

ATG（開始コドン）

終止コドン

プロモーター領域

mRNA

ATG（開始コドン）

終止コドン

非翻訳領域 (untranslated region)を含む

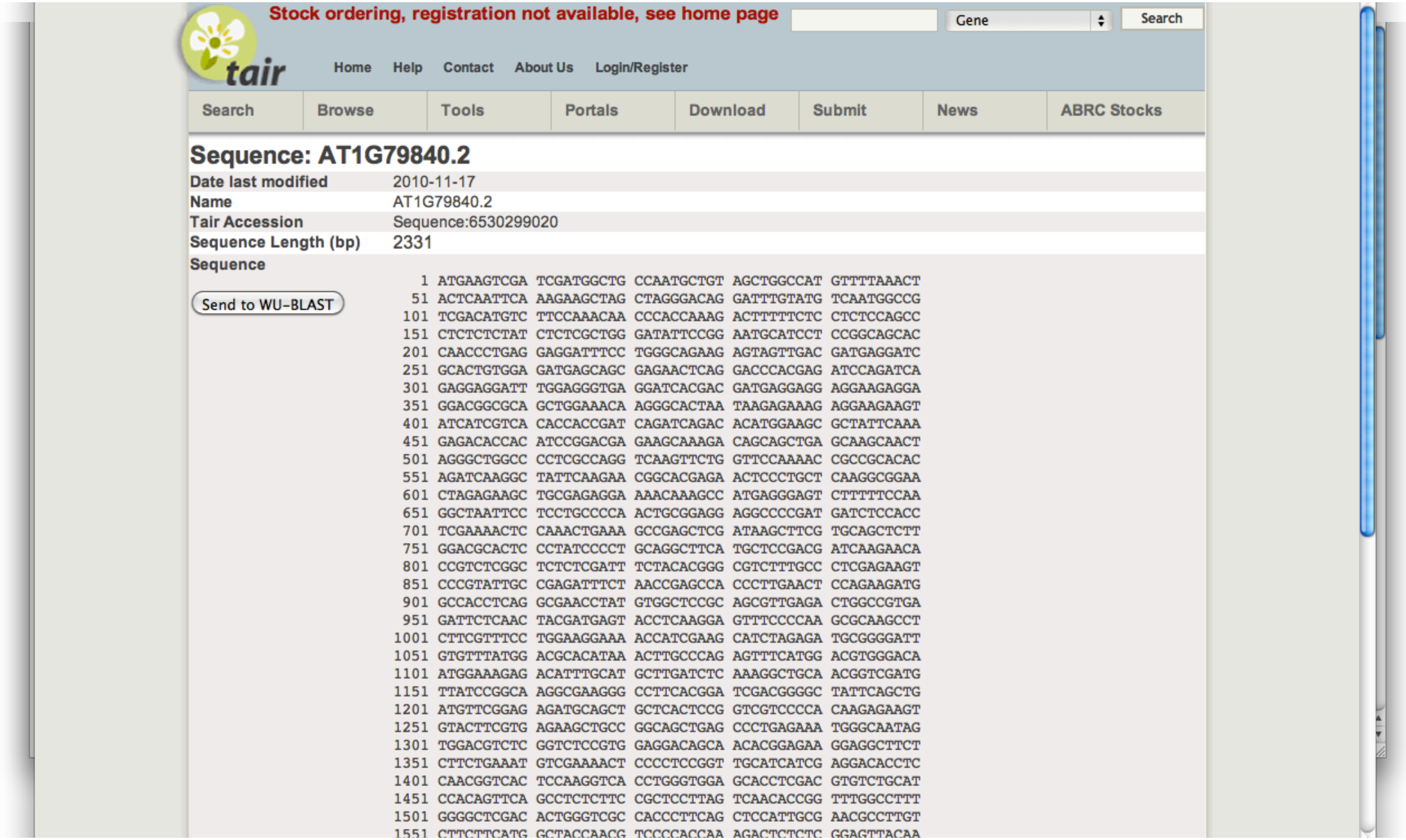
5’ UTR, 3’UTR

コード領域 (CDS)

タンパク質

結果5

塩基配列をみる



Sequence: AT1G79840.2

Date last modified	2010-11-17
Name	AT1G79840.2
Tair Accession	Sequence:6530299020
Sequence Length (bp)	2331
Sequence	

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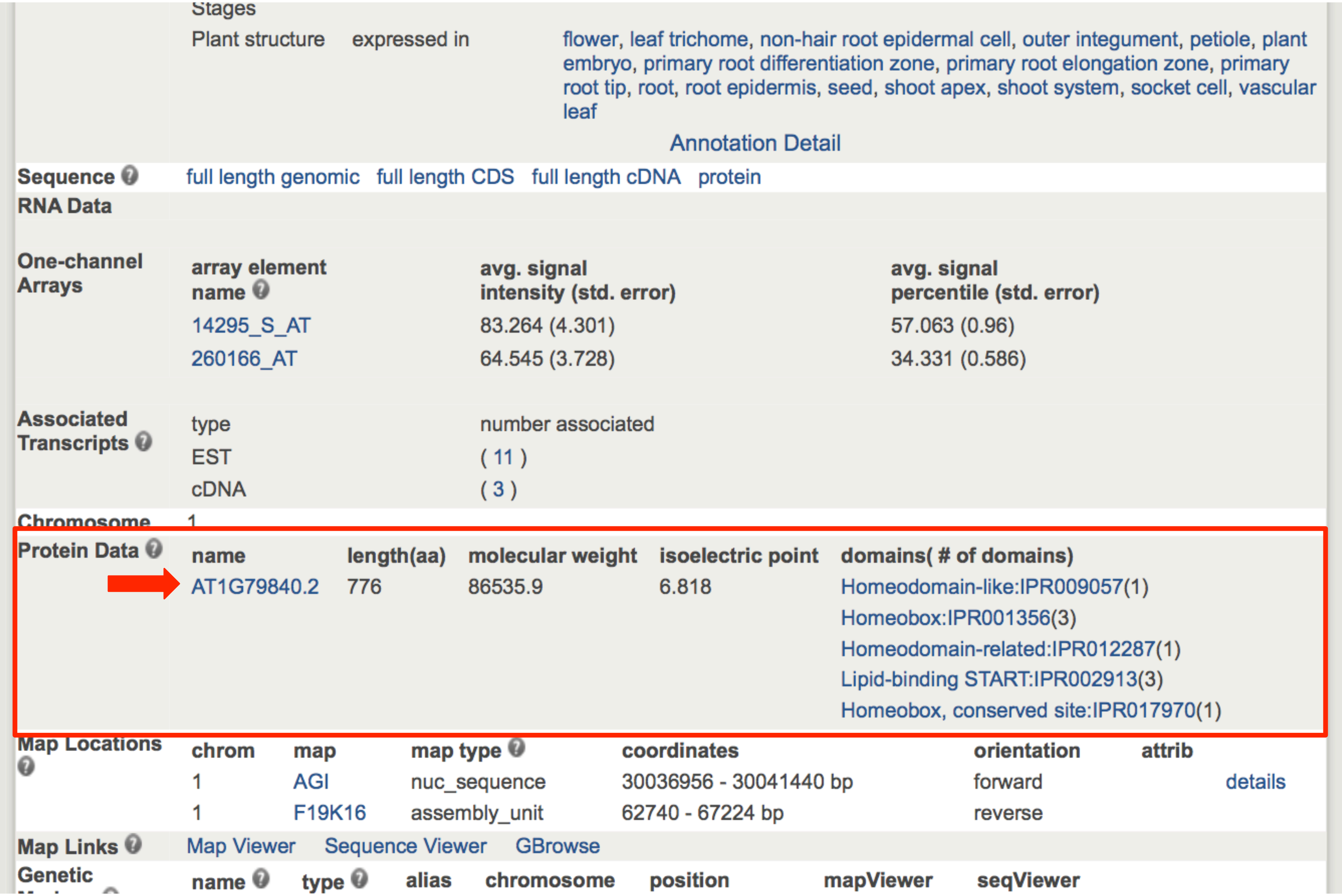
  51 ACTCAATTCA AAGAAGCTAG CTAGGGACAG GATTTGTATG TCAATGGCCG
 101 TCGACATGTC TTCCAAACAA CCCACCAAAG ACTTTTTCTC CTCTCCAGCC
 151 CTCTCTCTAT CTCTCGCTGG GATATTCCGG AATGCATCCT CCGGCAGCAC
 201 CAACCCTGAG GAGGATTTCC TGGGCAGAAG AGTAGTTGAC GATGAGGATC
 251 GCACTGTGGA GATGAGCAGC GAGAACTCAG GACCCACGAG ATCCAGATCA
 301 GAGGAGGATT TGGAGGGTGA GGATCACGAC GATGAGGAGG AGGAAGAGGA
 351 GGACGGCGCA GCTGGAAACA AGGGCACTAA TAAGAGAAAG AGGAAGAAGT
 401 ATCATCGTCA CACCACCGAT CAGATCAGAC ACATGGAAGC GCTATTCAAA
 451 GAGACACCAC ATCCGGACGA GAAGCAAAGA CAGCAGCTGA GCAAGCAACT
 501 AGGGCTGGCC CCTCGCCAGG TCAAGTTCTG GTTCCAAAAC CGCCGCACAC
 551 AGATCAAGGC TATTCAAGAA CGGCACGAGA ACTCCCTGCT CAAGGCGGAA
 601 CTAGAGAAGC TGCGAGAGGA AAACAAAGCC ATGAGGGAGT CTTTTTCCAA
 651 GGCTAATTCC TCCTGCCCCA ACTGCGGAGG AGGCCCCGAT GATCTCCACC
 701 TCGAAAACTC CAAACTGAAA GCCGAGCTCG ATAAGCTTCG TGCAGCTCTT
 751 GGACGCACTC CCTATCCCCT GCAGGCTTCA TGCTCCGACG ATCAAGAACA
 801 CCGTCTCGGC TCTCTCGATT TCTACACGGG CGTCTTTGCC CTCGAGAAGT
 851 CCCGTATTGC CGAGATTTCT AACCGAGCCA CCCTTGAACT CCAGAAGATG
 901 GCCACCTCAG GCGAACCTAT GTGGCTCCGC AGCGTTGAGA CTGGCCGTGA
 951 GATTCTCAAC TACGATGAGT ACCTCAAGGA GTTTCCCCAA GCGCAAGCCT
1001 CTTCGTTTCC TGGAAGGAAA ACCATCGAAG CATCTAGAGA TGCGGGGATT
1051 GTGTTTATGG ACGCACATAA ACTTGCCCAG AGTTTCATGG ACGTGGGACA
1101 ATGGAAAGAG ACATTTGCAT GCTTGATCTC AAAGGCTGCA ACGGTCGATG
1151 TTATCCGGCA AGGCGAAGGG CCTTCACGGA TCGACGGGGC TATTCAGCTG
1201 ATGTTCGGAG AGATGCAGCT GCTCACTCCG GTCGTCCCCA CAAGAGAAGT
1251 GTACTTCGTG AGAAGCTGCC GGCAGCTGAG CCCTGAGAAA TGGGCAATAG
1301 TGGACGTCTC GGTCTCCGTG GAGGACAGCA ACACGGAGAA GGAGGCTTCT
1351 CTTCTGAAAT GTCGAAAACT CCCCTCCGGT TGCATCATCG AGGACACCTC
1401 CAACGGTCAC TCCAAGGTCA CCTGGGTGGA GCACCTCGAC GTGTCTGCAT
1451 CCACAGTTCA GCCTCTCTTC CGCTCCTTAG TCAACACCGG TTTGGCCTTT
1501 GGGGCTCGAC ACTGGGTCGC CACCCTTCAG CTCCATTGCG AACGCCTTGT
1551 CTTCTTCATG GCTACCAACG TCCCCACCAA AGACTCTCTC GGAGTTACAA
```

結果6

アミノ酸配列をみる



Stages

Plant structure expressed in flower, leaf trichome, non-hair root epidermal cell, outer integument, petiole, plant embryo, primary root differentiation zone, primary root elongation zone, primary root tip, root, root epidermis, seed, shoot apex, shoot system, socket cell, vascular leaf

Annotation Detail

Sequence full length genomic full length CDS full length cDNA protein

RNA Data

One-channel Arrays

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260166_AT	64.545 (3.728)	34.331 (0.586)

Associated Transcripts

type	number associated
EST	(11)
cDNA	(3)

Chromosome 1

Protein Data

name	length(aa)	molecular weight	isoelectric point	domains(# of domains)
AT1G79840.2	776	86535.9	6.818	Homeodomain-like:IPR009057(1) Homeobox:IPR001356(3) Homeodomain-related:IPR012287(1) Lipid-binding START:IPR002913(3) Homeobox, conserved site:IPR017970(1)

Map Locations

chrom	map	map type	coordinates	orientation	attrib
1	AGI	nuc_sequence	30036956 - 30041440 bp	forward	details
1	F19K16	assembly_unit	62740 - 67224 bp	reverse	

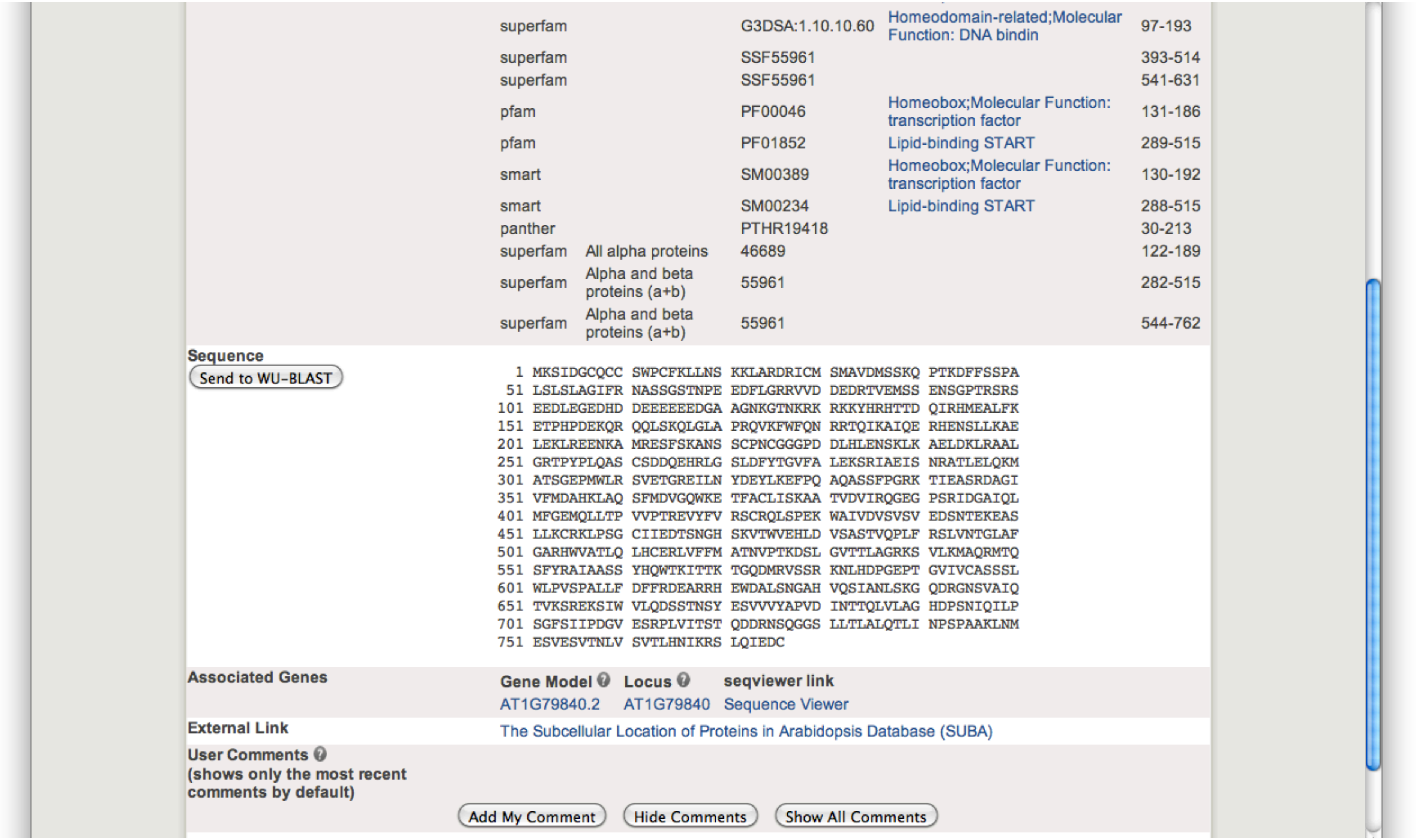
Map Links Map Viewer Sequence Viewer GBrowse

Genetic

name	type	alias	chromosome	position	mapViewer	seqViewer

結果7

アミノ酸配列をみる



superfam		G3DSA:1.10.10.60	Homeodomain-related;Molecular Function: DNA bindin	97-193
superfam		SSF55961		393-514
superfam		SSF55961		541-631
pfam		PF00046	Homeobox;Molecular Function: transcription factor	131-186
pfam		PF01852	Lipid-binding START	289-515
smart		SM00389	Homeobox;Molecular Function: transcription factor	130-192
smart		SM00234	Lipid-binding START	288-515
panther		PTHR19418		30-213
superfam	All alpha proteins	46689		122-189
superfam	Alpha and beta proteins (a+b)	55961		282-515
superfam	Alpha and beta proteins (a+b)	55961		544-762

Sequence

```
  1 MKSIDGCQCC SWPCFKLLNS KKLARDRICM SMAVDMSSKQ PTKDFFSSPA
 51 LSLSLAGIFR NASSGSTNPE EDFLGRRVVD DEDRTVEMSS ENSGPTRSRS
101 EEDLEGEDHD DEEEEEEDGA AGNKGTNKRK RKKYHRHTTD QIRHMEALFK
151 ETPHPDEKQR QQLSKQLGLA PRQVKFWFQN RRTQIKAIQE RHENSLLKAE
201 LEKLREENKA MRESFSKANS SCPNCGGGPD DLHLENSKLK AELDKLRAAL
251 GRTPYPLQAS CSDDQEHRLG SLDFYTGVFA LEKSRIAEIS NRATLELQKM
301 ATSGEPMWLR SVETGREILN YDEYLKEFPQ AQASSFPGRK TIEASRDAGI
351 VFMDAHKLAQ SFMDVGQWKE TFACLISKAA TVDVIRQGEG PSRIDGAIQL
401 MFGEMQLLTP VVPTREVYFV RSCRQLSPEK WAIVDVSVSV EDSNTEKEAS
451 LLKCRKLPSG CIIEDTSNGH SKVTWVEHLD VSASTVQPLF RSLVNTGLAF
501 GARHWVATLQ LHCERLVFFM ATNVPTKDSL GVTTLAGRKS VLKMAQRMTQ
551 SFYRAIAASS YHQWTKITTK TGQDMRVSSR KNLHDPGEPT GVIVCASSSL
601 WLPVSPALLF DFFRDEARRH EWDALSNGAH VQSIANLSKG QDRGNSVAIQ
651 TVKSREKSIW VLQDSSTNSY ESVVVYAPVD INTTQLVLAG HDPSNIQILP
701 SGFSIIPDGV ESRPLVITST QDDRNSQGGS LLTLALQTLI NPSPAAKLNM
751 ESVESVTNLV SVTLHNIKRS LQIEDC
```

Associated Genes

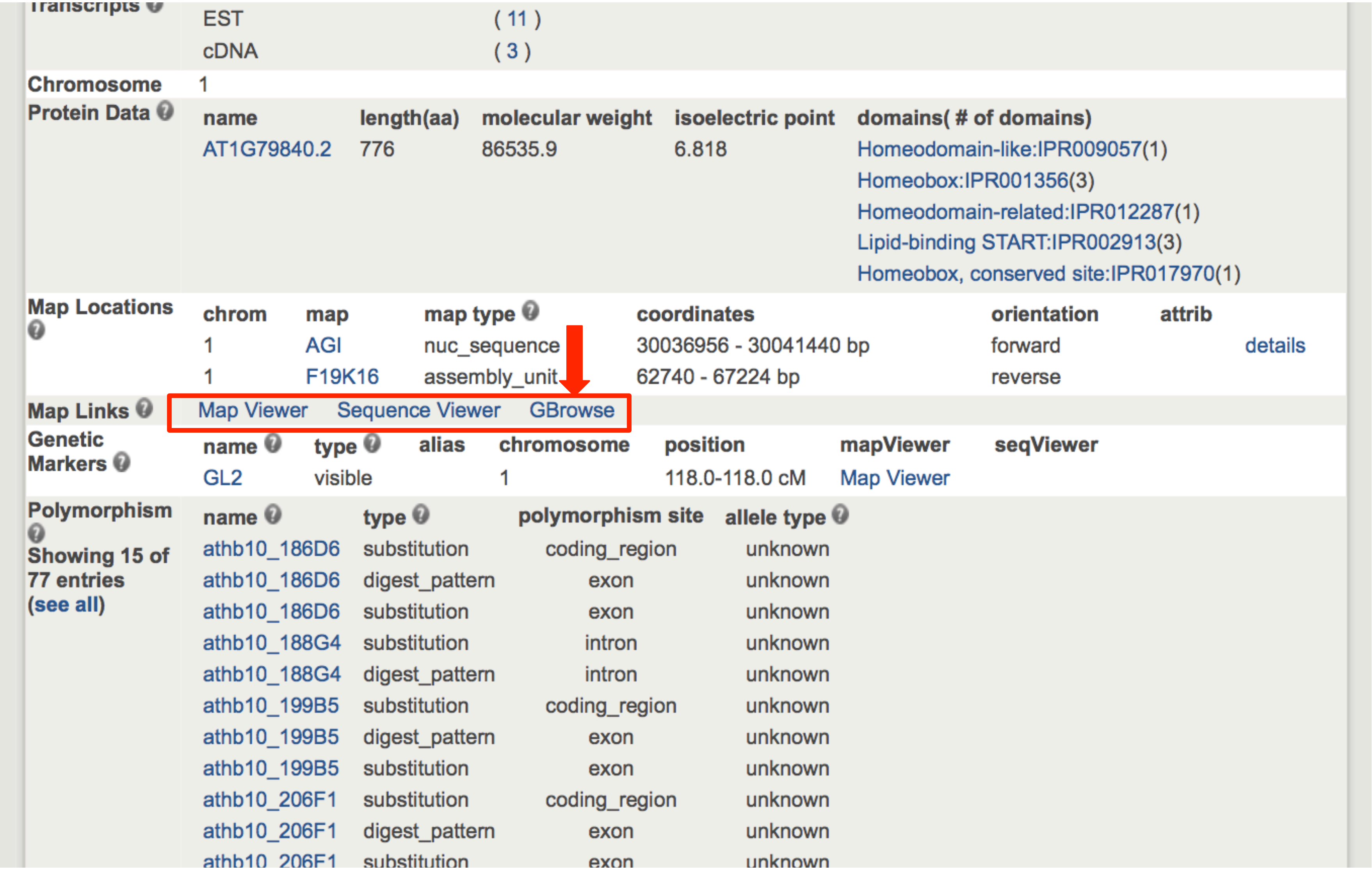
Gene Model	Locus	seqviewer link
AT1G79840.2	AT1G79840	Sequence Viewer

External Link The Subcellular Location of Proteins in Arabidopsis Database (SUBA)

User Comments
(shows only the most recent comments by default)

結果8

ゲノムをみる



Transcripts

EST	(11)
cDNA	(3)

Chromosome 1

Protein Data

name	length(aa)	molecular weight	isoelectric point	domains(# of domains)
AT1G79840.2	776	86535.9	6.818	Homeodomain-like:IPR009057(1) Homeobox:IPR001356(3) Homeodomain-related:IPR012287(1) Lipid-binding START:IPR002913(3) Homeobox, conserved site:IPR017970(1)

Map Locations

chrom	map	map type	coordinates	orientation	attrib
1	AGI	nuc_sequence	30036956 - 30041440 bp	forward	details
1	F19K16	assembly_unit	62740 - 67224 bp	reverse	

Map Links Map Viewer Sequence Viewer GBrowse

Genetic Markers

name	type	alias	chromosome	position	mapViewer	seqViewer
GL2	visible		1	118.0-118.0 cM	Map Viewer	

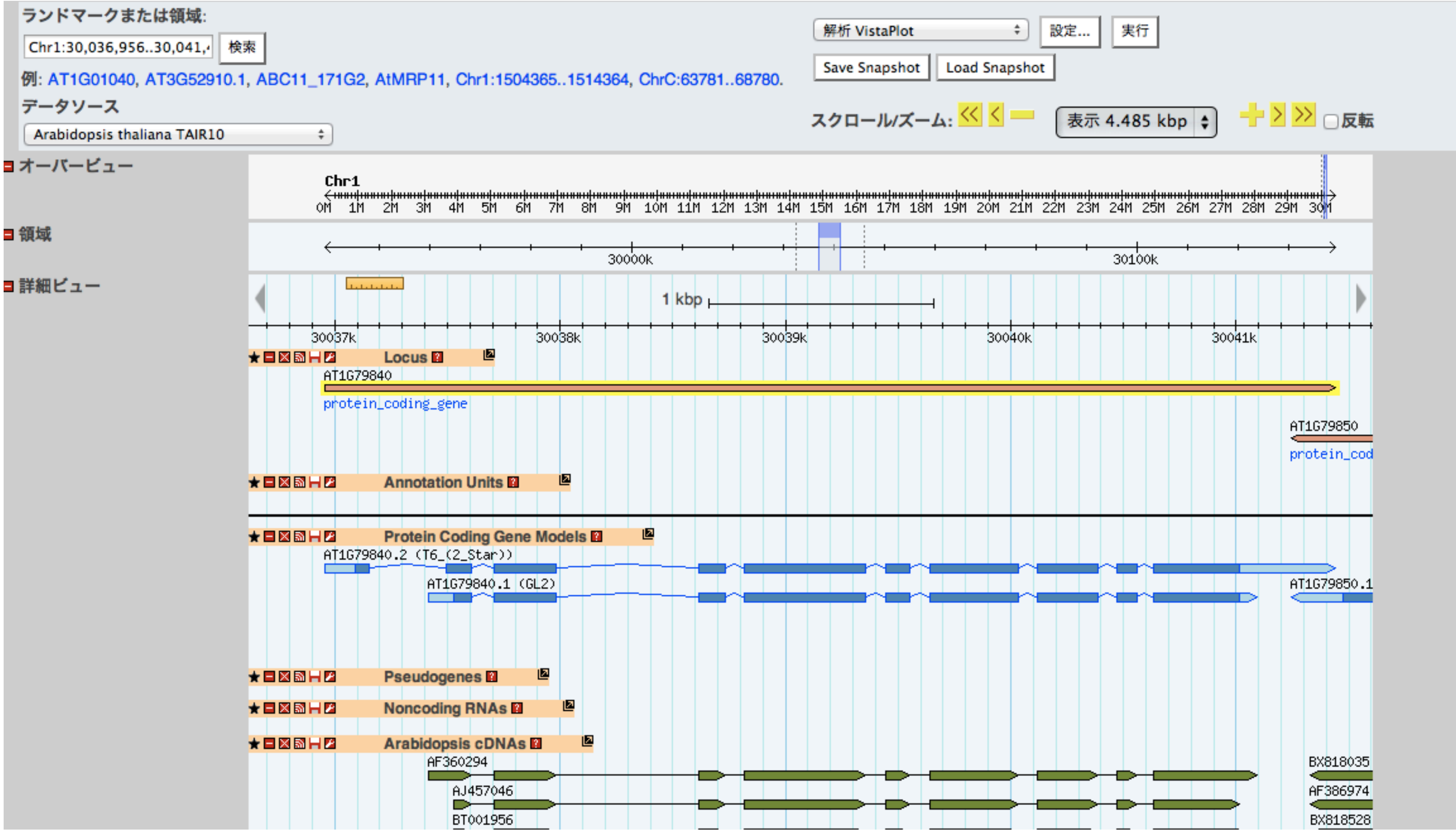
Polymorphism

Showing 15 of 77 entries (see all)

name	type	polymorphism site	allele type
athb10_186D6	substitution	coding_region	unknown
athb10_186D6	digest_pattern	exon	unknown
athb10_186D6	substitution	exon	unknown
athb10_188G4	substitution	intron	unknown
athb10_188G4	digest_pattern	intron	unknown
athb10_199B5	substitution	coding_region	unknown
athb10_199B5	digest_pattern	exon	unknown
athb10_199B5	substitution	exon	unknown
athb10_206F1	substitution	coding_region	unknown
athb10_206F1	digest_pattern	exon	unknown
athb10_206F1	substitution	exon	unknown

結果9

Gbrowseでゲノムをみる



ランドマークまたは領域: Chr1:30,036,956..30,041,

例: AT1G01040, AT3G52910.1, ABC11_171G2, AtMRP11, Chr1:1504365..1514364, ChrC:63781..68780.

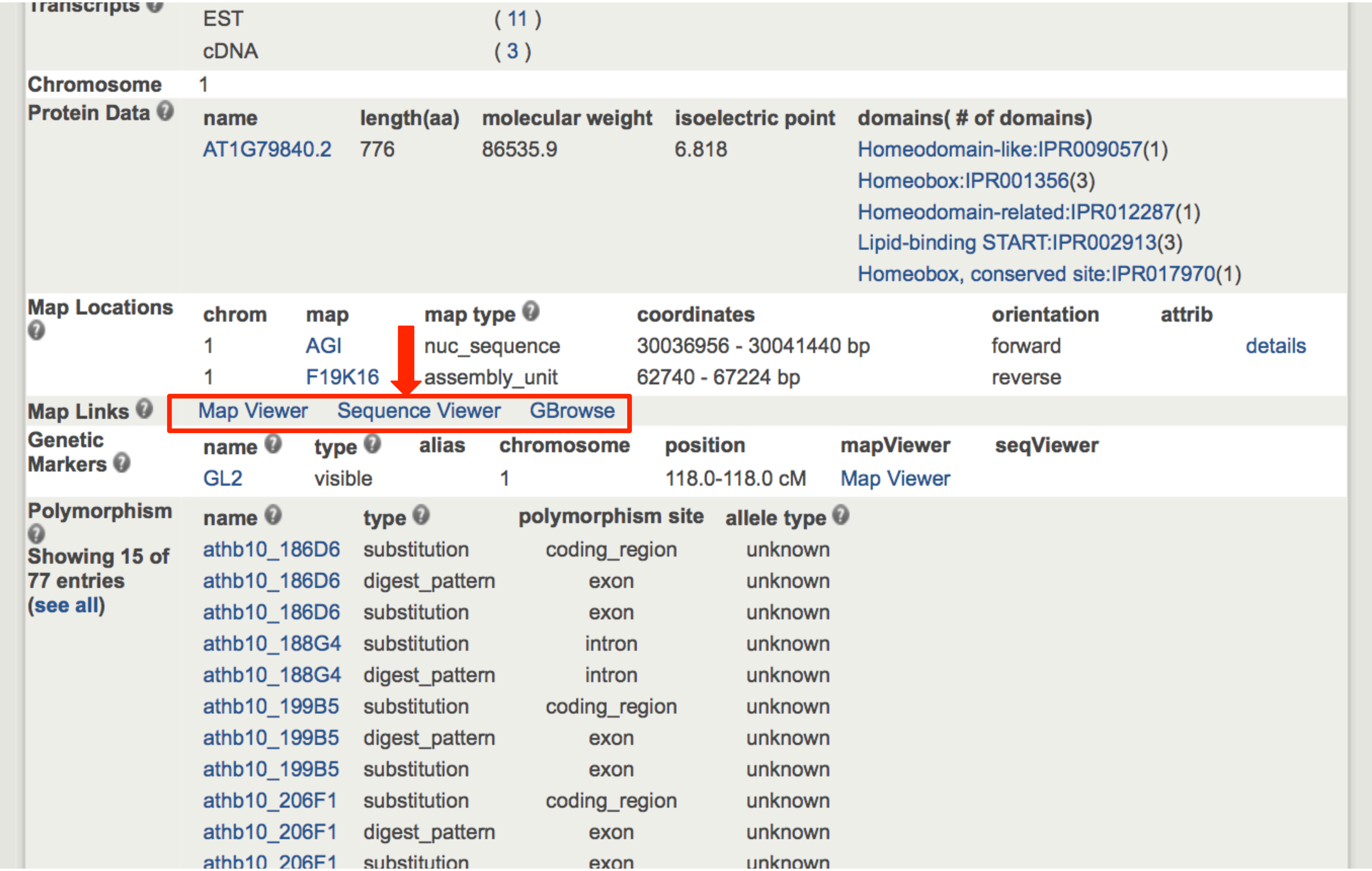
データソース: Arabidopsis thaliana TAIR10

解析 VistaPlot

スクロール/ズーム: 表示 4.485 kbp ☐反転

結果10

ゲノムをみる



Transcripts

EST	(11)
cDNA	(3)

Chromosome 1

Protein Data

name	length(aa)	molecular weight	isoelectric point	domains(# of domains)
AT1G79840.2	776	86535.9	6.818	Homeodomain-like:IPR009057(1) Homeobox:IPR001356(3) Homeodomain-related:IPR012287(1) Lipid-binding START:IPR002913(3) Homeobox, conserved site:IPR017970(1)

Map Locations

chrom	map	map type	coordinates	orientation	attrib
1	AGI	nuc_sequence	30036956 - 30041440 bp	forward	details
1	F19K16	assembly_unit	62740 - 67224 bp	reverse	

Map Links Map Viewer Sequence Viewer GBrowse

Genetic Markers

name	type	alias	chromosome	position	mapViewer	seqViewer
GL2	visible		1	118.0-118.0 cM	Map Viewer	

Polymorphism
Showing 15 of 77 entries
(see all)

name	type	polymorphism site	allele type
athb10_186D6	substitution	coding_region	unknown
athb10_186D6	digest_pattern	exon	unknown
athb10_186D6	substitution	exon	unknown
athb10_188G4	substitution	intron	unknown
athb10_188G4	digest_pattern	intron	unknown
athb10_199B5	substitution	coding_region	unknown
athb10_199B5	digest_pattern	exon	unknown
athb10_199B5	substitution	exon	unknown
athb10_206F1	substitution	coding_region	unknown
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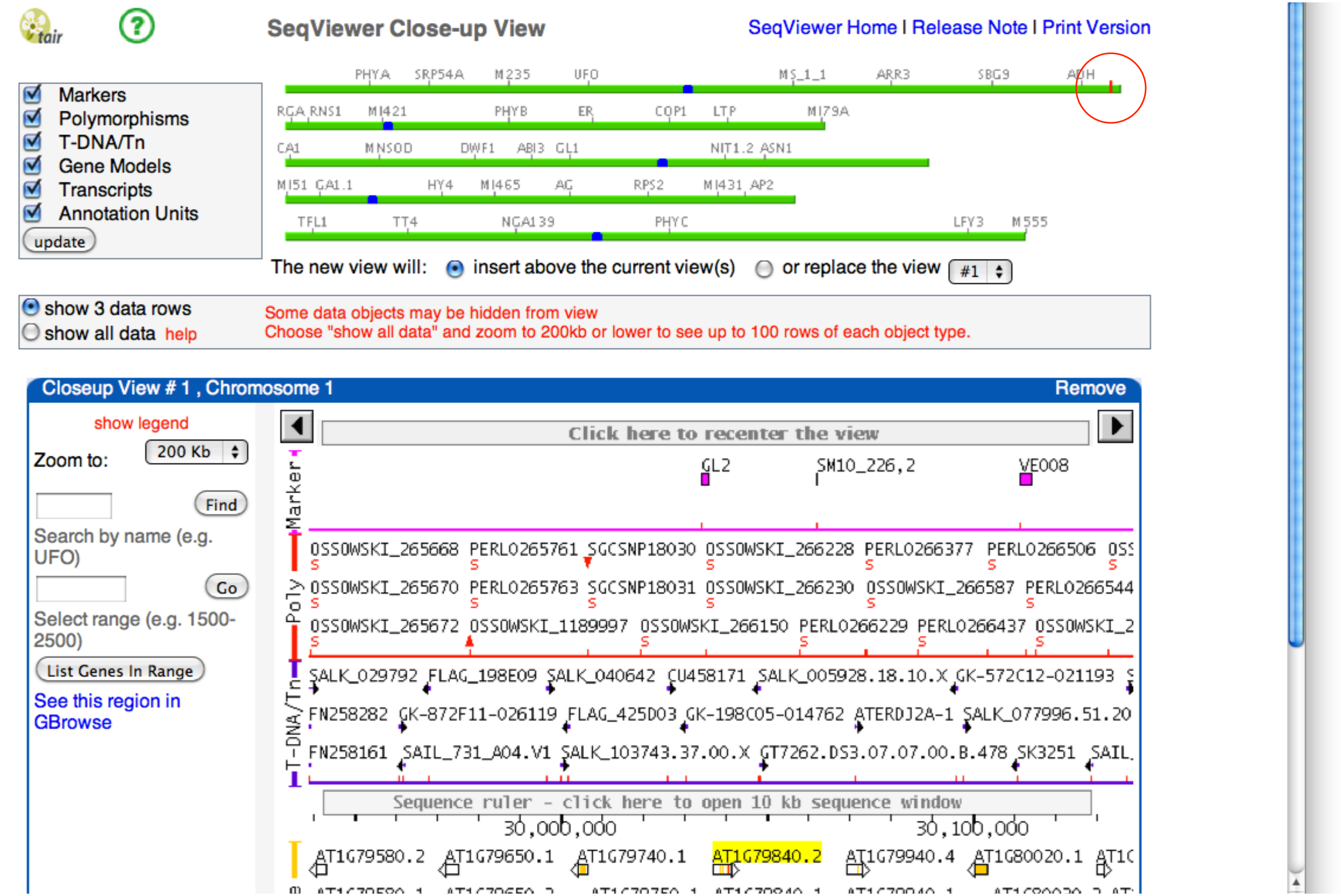
結果11

Sequence Viewerでゲノムをみる



SeqViewer Close-up View

SeqViewer Home | Release Note | Print Version

☑ Markers
☑ Polymorphisms
☑ T-DNA/Tn
☑ Gene Models
☑ Transcripts
☑ Annotation Units

The new view will: ● insert above the current view(s) ○ or replace the view #1

● show 3 data rows
○ show all data help

Some data objects may be hidden from view
Choose "show all data" and zoom to 200kb or lower to see up to 100 rows of each object type.

Closeup View # 1 , Chromosome 1

Zoom to: 200 Kb

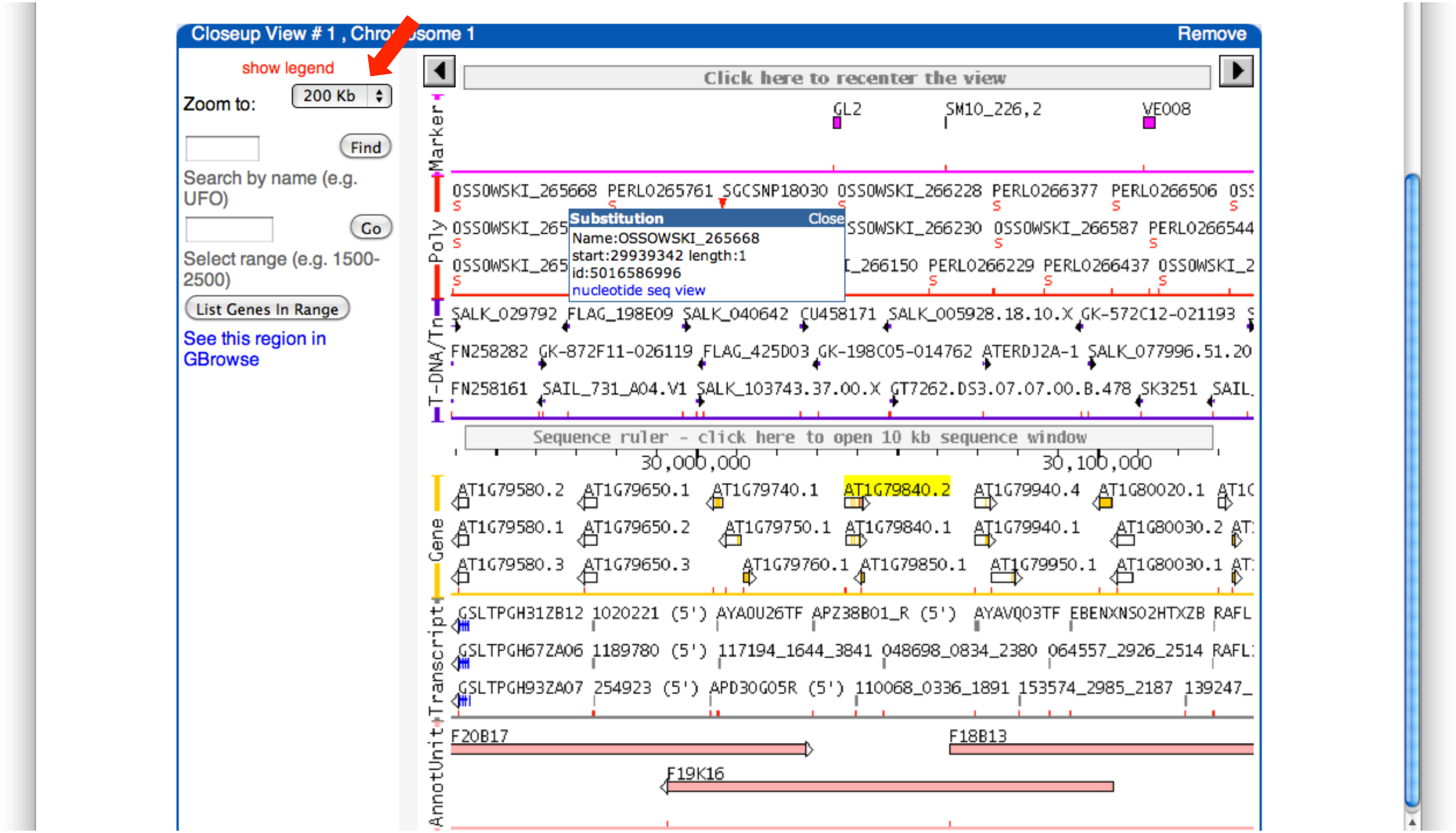
Search by name (e.g. UFO)

Select range (e.g. 1500-2500)

See this region in GBrowse

結果12

Sequence Viewerでゲノムをみる

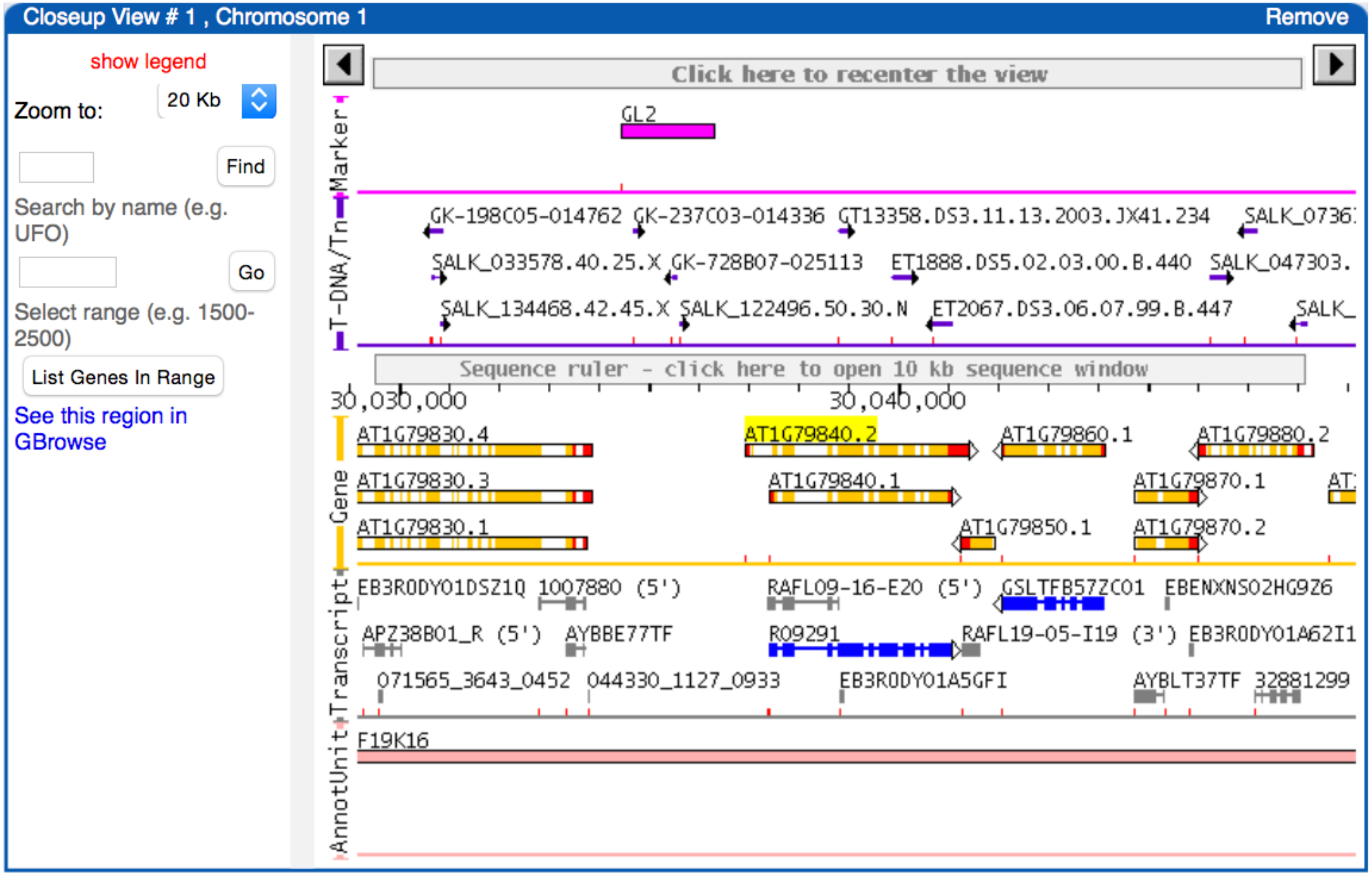


Zoom to: 200 Kb

Substitution Close
Name:OSSOWSKI_265668
start:29939342 length:1
id:5016586996
nucleotide seq view

結果13

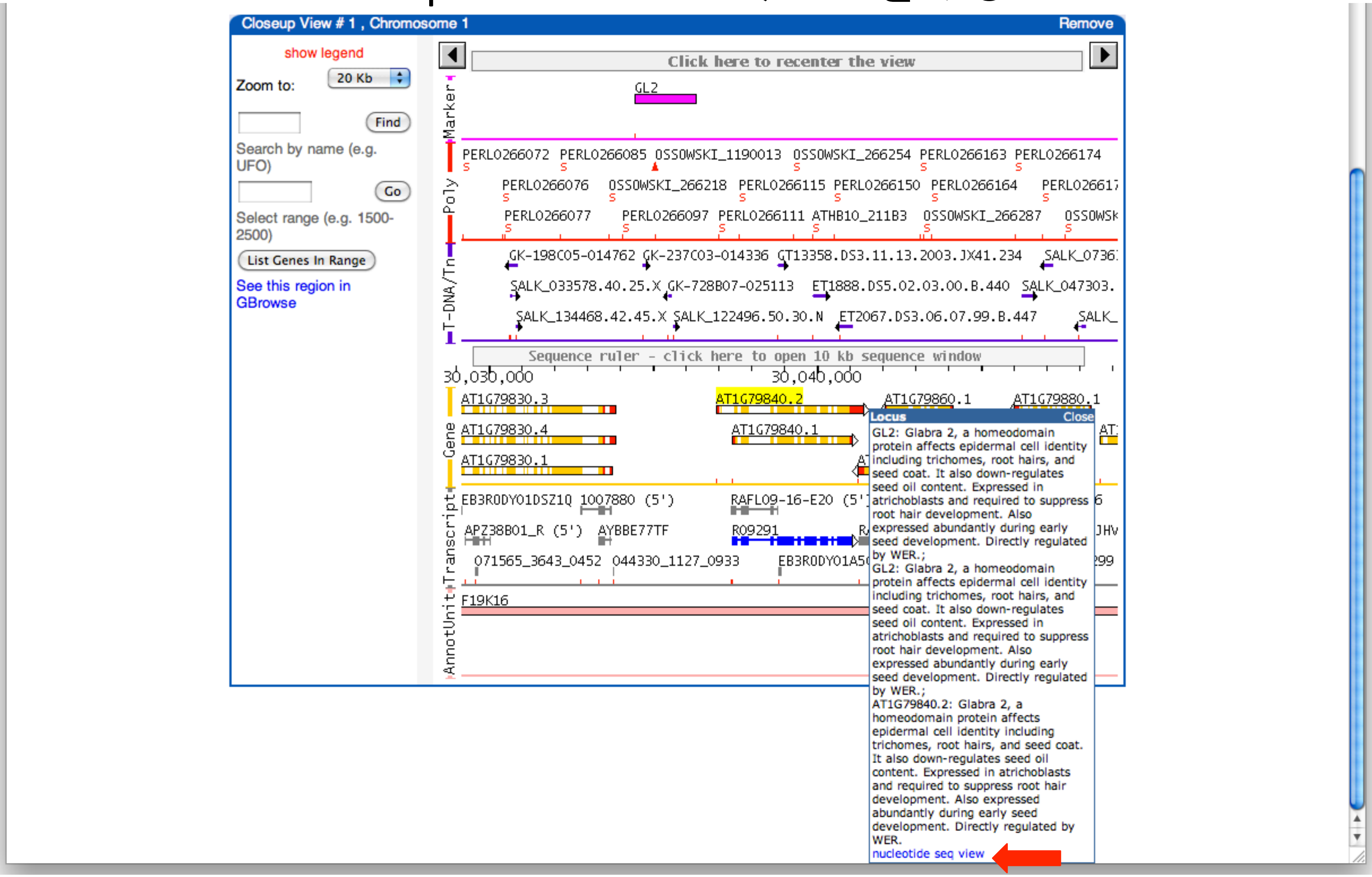
Sequence Viewerでゲノムをみる



Zoom to: 20 Kb

結果14

Sequence Viewerでゲノムをみる



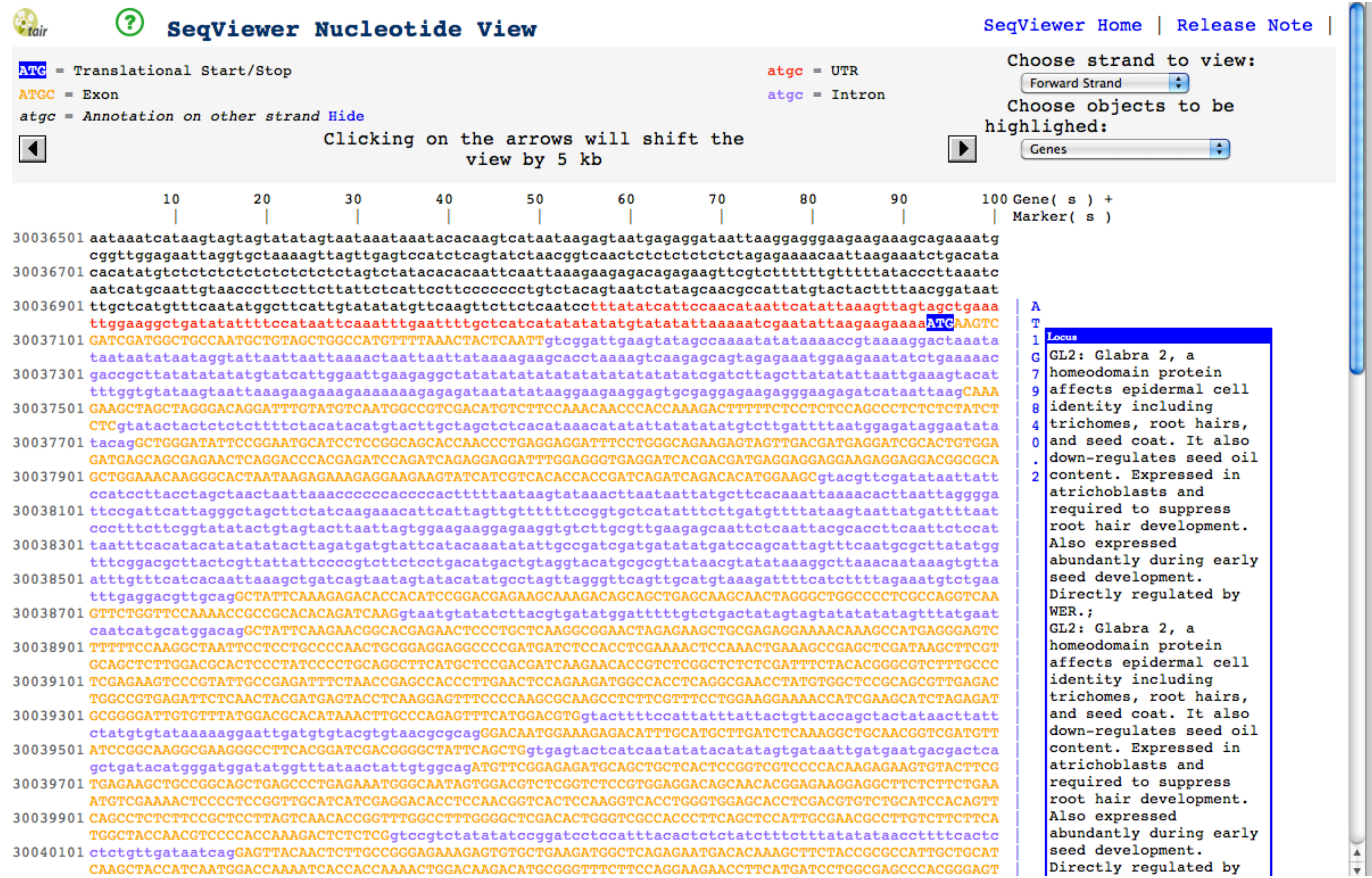
GL2: Glabra 2, a homeodomain protein affects epidermal cell identity including trichomes, root hairs, and seed coat. It also down-regulates seed oil content. Expressed in atrichoblasts and required to suppress root hair development. Also expressed abundantly during early seed development. Directly regulated by WER.;

GL2: Glabra 2, a homeodomain protein affects epidermal cell identity including trichomes, root hairs, and seed coat. It also down-regulates seed oil content. Expressed in atrichoblasts and required to suppress root hair development. Also expressed abundantly during early seed development. Directly regulated by WER.;

AT1G79840.2: Glabra 2, a homeodomain protein affects epidermal cell identity including trichomes, root hairs, and seed coat. It also down-regulates seed oil content. Expressed in atrichoblasts and required to suppress root hair development. Also expressed abundantly during early seed development. Directly regulated by WER.

結果15

配列情報をみる



ATG = Translational Start/Stop
ATGC = Exon
atgc = *Annotation on other strand* Hide
atgc = UTR
atgc = Intron

Clicking on the arrows will shift the view by 5 kb

```
         10        20        30        40        50        60        70        80        90       100 Gene( s ) +
          |         |         |         |         |         |         |         |         |         | Marker( s )
30036501 aataaatcataagtagtagtatatagtaataaataaatacacaagtcataataagagtaatgagaggataattaaggagggaagaagaaagcagaaaatg
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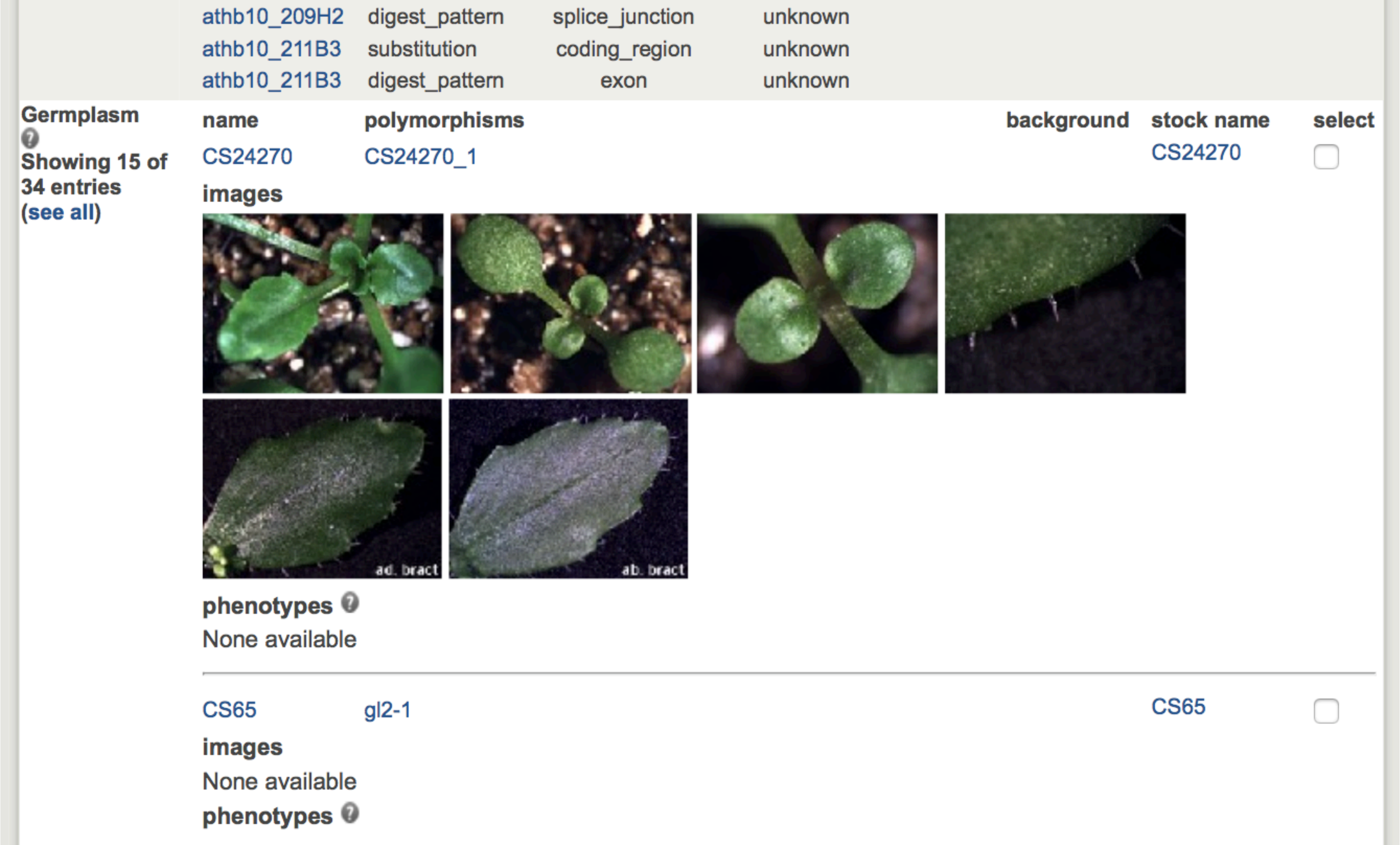
```

GL2: Glabra 2, a homeodomain protein affects epidermal cell identity including trichomes, root hairs, and seed coat. It also down-regulates seed oil content. Expressed in atrichoblasts and required to suppress root hair development. Also expressed abundantly during early seed development. Directly regulated by WER.;

GL2: Glabra 2, a homeodomain protein affects epidermal cell identity including trichomes, root hairs, and seed coat. It also down-regulates seed oil content. Expressed in atrichoblasts and required to suppress root hair development. Also expressed abundantly during early seed development. Directly regulated by

結果16

表現型をみる



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Germplasm

Showing 15 of 34 entries (see all)

name	polymorphisms	background	stock name	select
CS24270	CS24270_1		CS24270	☐

images

phenotypes

None available

name	polymorphisms	background	stock name	select
CS65	gl2-1		CS65	☐

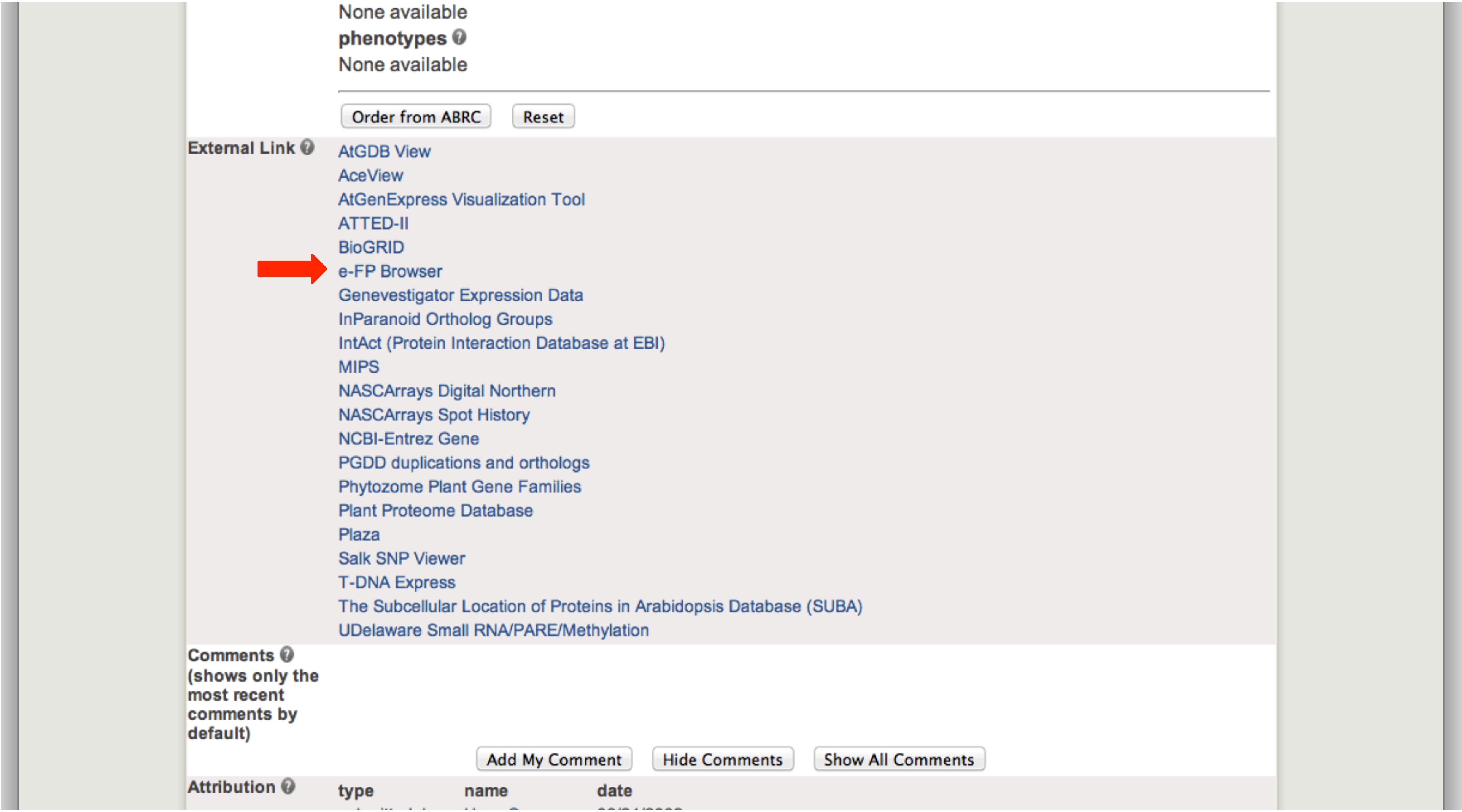
images

None available

phenotypes

結果17

リンクを使って遺伝子発現のパターンをみる



None available

phenotypes

None available

External Link

AtGDB View
AceView
AtGenExpress Visualization Tool
ATTED-II
BioGRID
e-FP Browser
Genevestigator Expression Data
InParanoid Ortholog Groups
IntAct (Protein Interaction Database at EBI)
MIPS
NASCArrays Digital Northern
NASCArrays Spot History
NCBI-Entrez Gene
PGDD duplications and orthologs
Phytozome Plant Gene Families
Plant Proteome Database
Plaza
Salk SNP Viewer
T-DNA Express
The Subcellular Location of Proteins in Arabidopsis Database (SUBA)
UDelaware Small RNA/PARE/Methylation

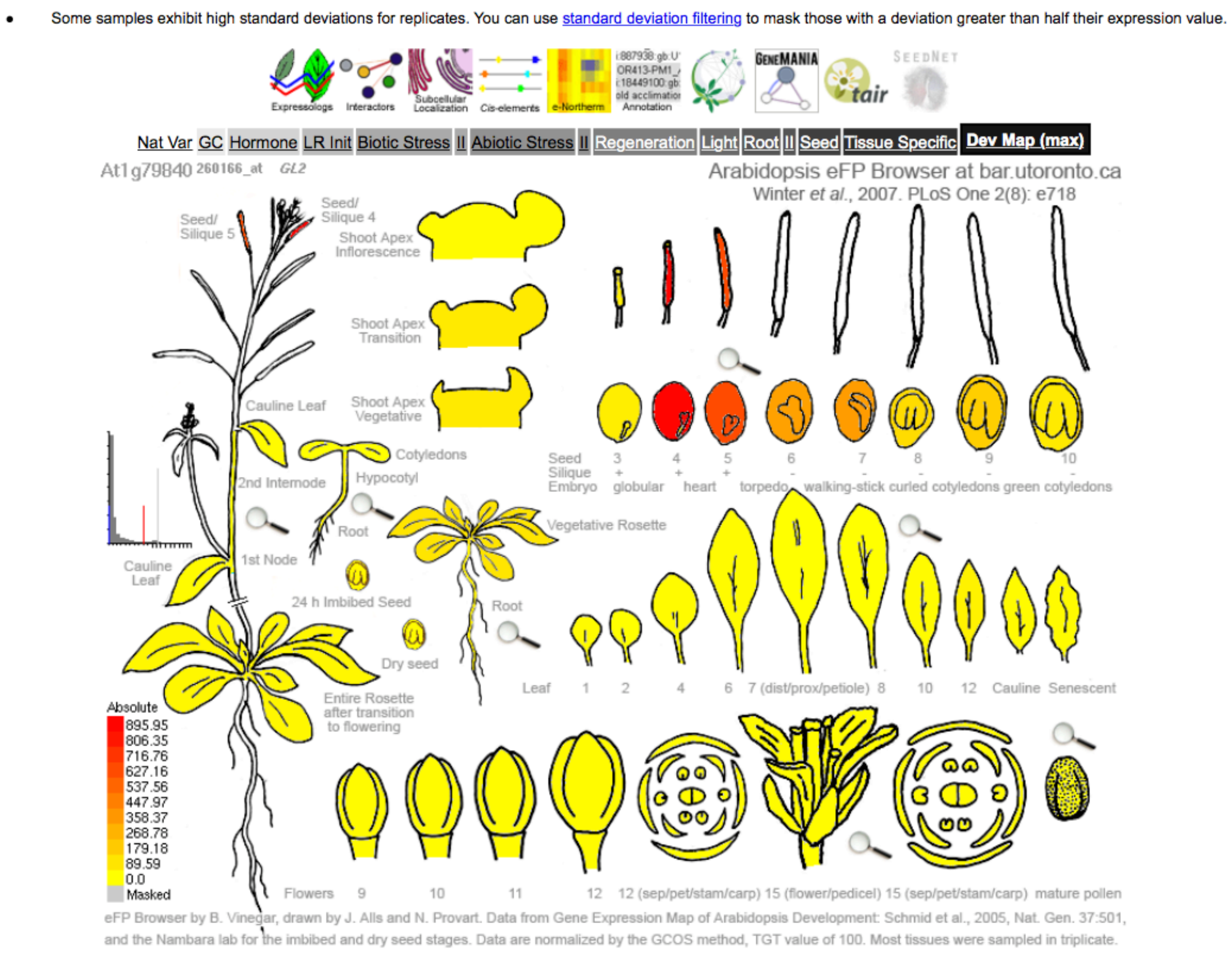
Comments (shows only the most recent comments by default)

Attribution

type	name	date

結果18

リンクを使って遺伝子発現のパターンをみる

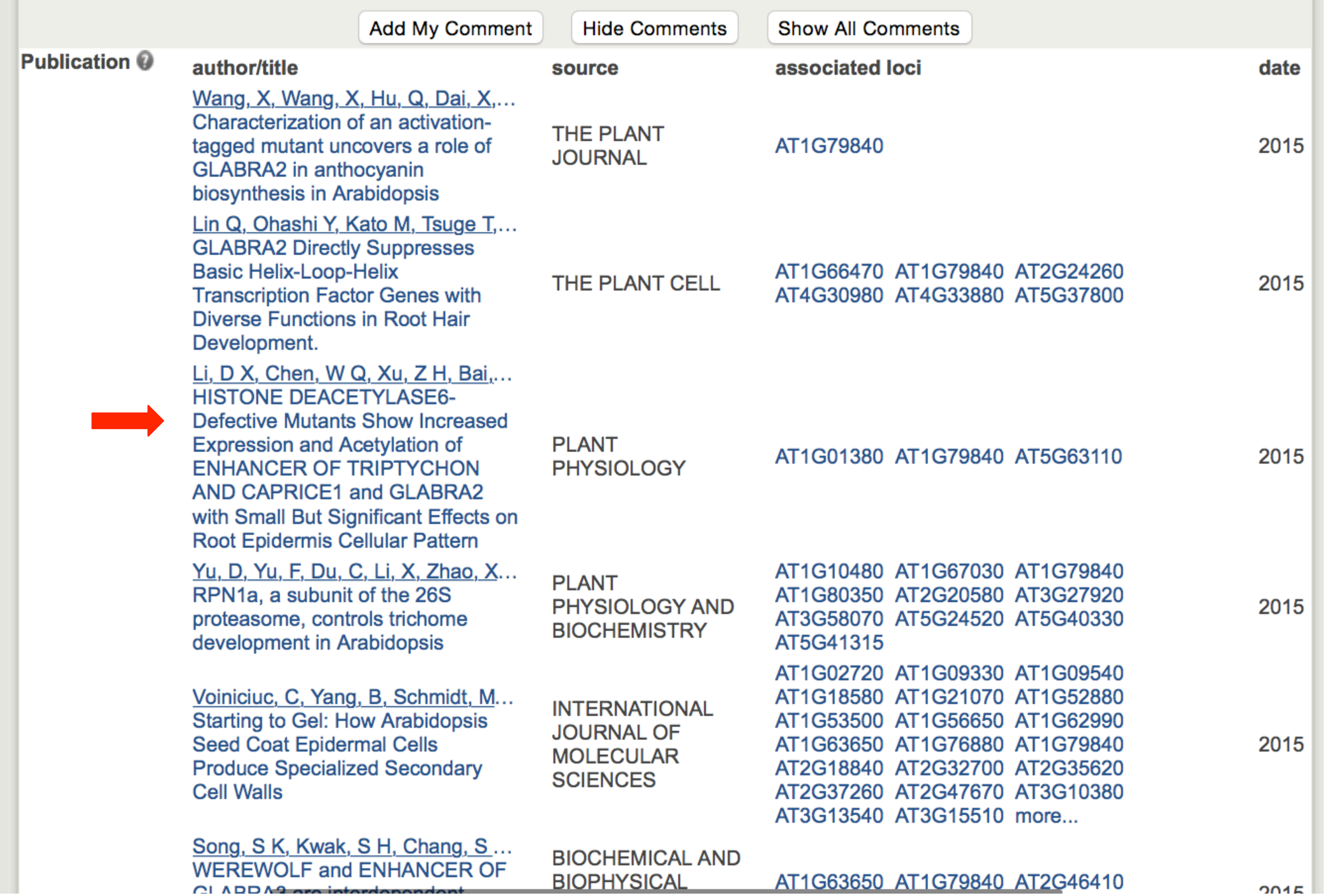


- Some samples exhibit high standard deviations for replicates. You can use standard deviation filtering to mask those with a deviation greater than half their expression value.

eFP Browser by B. Vinegar, drawn by J. Alls and N. Provart. Data from Gene Expression Map of Arabidopsis Development: Schmid et al., 2005, Nat. Gen. 37:501, and the Nambara lab for the imbibed and dry seed stages. Data are normalized by the GCOS method, TGT value of 100. Most tissues were sampled in triplicate.

結果19

文献を調べる



Publication	author/title	source	associated loci	date
	Wang, X, Wang, X, Hu, Q, Dai, X,… Characterization of an activation-tagged mutant uncovers a role of GLABRA2 in anthocyanin biosynthesis in Arabidopsis	THE PLANT JOURNAL	AT1G79840	2015
	Lin Q, Ohashi Y, Kato M, Tsuge T,… GLABRA2 Directly Suppresses Basic Helix-Loop-Helix Transcription Factor Genes with Diverse Functions in Root Hair Development.	THE PLANT CELL	AT1G66470 AT1G79840 AT2G24260 AT4G30980 AT4G33880 AT5G37800	2015
→	Li, D X, Chen, W Q, Xu, Z H, Bai,… HISTONE DEACETYLASE6-Defective Mutants Show Increased Expression and Acetylation of ENHANCER OF TRIPTYCHON AND CAPRICE1 and GLABRA2 with Small But Significant Effects on Root Epidermis Cellular Pattern	PLANT PHYSIOLOGY	AT1G01380 AT1G79840 AT5G63110	2015
	Yu, D, Yu, F, Du, C, Li, X, Zhao, X… RPN1a, a subunit of the 26S proteasome, controls trichome development in Arabidopsis	PLANT PHYSIOLOGY AND BIOCHEMISTRY	AT1G10480 AT1G67030 AT1G79840 AT1G80350 AT2G20580 AT3G27920 AT3G58070 AT5G24520 AT5G40330 AT5G41315	2015
	Voiniciuc, C, Yang, B, Schmidt, M… Starting to Gel: How Arabidopsis Seed Coat Epidermal Cells Produce Specialized Secondary Cell Walls	INTERNATIONAL JOURNAL OF MOLECULAR SCIENCES	AT1G02720 AT1G09330 AT1G09540 AT1G18580 AT1G21070 AT1G52880 AT1G53500 AT1G56650 AT1G62990 AT1G63650 AT1G76880 AT1G79840 AT2G18840 AT2G32700 AT2G35620 AT2G37260 AT2G47670 AT3G10380 AT3G13540 AT3G15510 more...	2015
	Song, S K, Kwak, S H, Chang, S … WEREWOLF and ENHANCER OF	BIOCHEMICAL AND BIOPHYSICAL	AT1G63650 AT1G79840 AT2G46410	

結果20

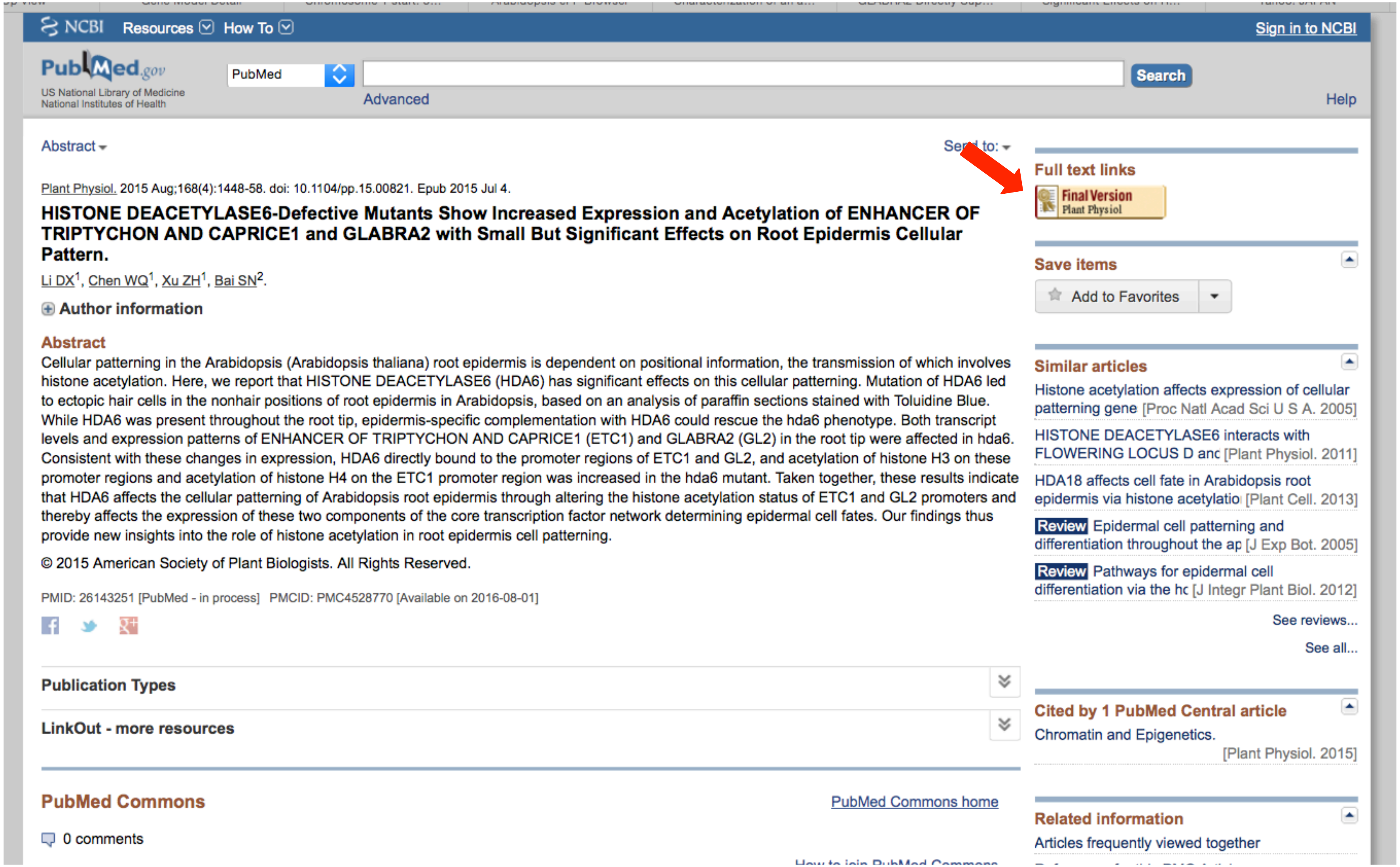
文献を調べる

Title: HISTONE DEACETYLASE6-Defective Mutants Show Increased Expression and Acetylation of ENHANCER OF TRIPTYCHON AND CAPRICE1 and GLABRA2 with Small But Significant Effects on Root Epidermis Cellular Pattern

Authors	Li, D. X., Chen, W. Q., Xu, Z. H., Bai, S. N.
Type	Research_article
Journal	PLANT PHYSIOLOGY
Year	2015
Volume	168
Issue	4
Start Page	1448-58
TAIR accession	Publication:501765610
DOI	10.1104/pp.15.00821
PubMed ID	26143251
Abstract	Cellular patterning in the Arabidopsis (Arabidopsis thaliana) root epidermis is dependent on positional information, the transmission of which involves histone acetylation. Here, we report that HISTONE DEACETYLASE6 (HDA6) has significant effects on this cellular patterning. Mutation of HDA6 led to ectopic hair cells in the nonhair positions of root epidermis in Arabidopsis, based on an analysis of paraffin sections stained with Toluidine Blue. While HDA6 was present throughout the root tip, epidermis-specific complementation with HDA6 could rescue the hda6 phenotype. Both transcript levels and expression patterns of ENHANCER OF TRIPTYCHON AND CAPRICE1 (ETC1) and GLABRA2 (GL2) in the root tip were affected in hda6. Consistent with these changes in expression, HDA6 directly bound to the promoter regions of ETC1 and GL2, and acetylation of histone H3 on these promoter regions and acetylation of histone H4 on the ETC1 promoter region was increased in the hda6 mutant. Taken together, these results indicate that HDA6 affects the cellular patterning of Arabidopsis root epidermis through altering the histone acetylation status of ETC1 and GL2 promoters and thereby affects the expression of these two components of the core transcription factor network determining epidermal cell fates. Our findings thus provide new insights into the role of histone acetylation in root epidermis cell patterning.
	The publisher has kindly granted permission to reproduce this abstract on TAIR.
Associated Keywords	cell; histone acetylation; epidermal cell; root; root epidermis; epidermis; root tip
Associated Loci	AT1G79840 AT1G01380 AT5G63110

結果21

文献を調べる（PubMed)



Plant Physiol. 2015 Aug;168(4):1448-58. doi: 10.1104/pp.15.00821. Epub 2015 Jul 4.

HISTONE DEACETYLASE6-Defective Mutants Show Increased Expression and Acetylation of ENHANCER OF TRIPTYCHON AND CAPRICE1 and GLABRA2 with Small But Significant Effects on Root Epidermis Cellular Pattern.

Li DX[1], Chen WQ[1], Xu ZH[1], Bai SN[2].

Author information

Abstract

Cellular patterning in the Arabidopsis (Arabidopsis thaliana) root epidermis is dependent on positional information, the transmission of which involves histone acetylation. Here, we report that HISTONE DEACETYLASE6 (HDA6) has significant effects on this cellular patterning. Mutation of HDA6 led to ectopic hair cells in the nonhair positions of root epidermis in Arabidopsis, based on an analysis of paraffin sections stained with Toluidine Blue. While HDA6 was present throughout the root tip, epidermis-specific complementation with HDA6 could rescue the hda6 phenotype. Both transcript levels and expression patterns of ENHANCER OF TRIPTYCHON AND CAPRICE1 (ETC1) and GLABRA2 (GL2) in the root tip were affected in hda6. Consistent with these changes in expression, HDA6 directly bound to the promoter regions of ETC1 and GL2, and acetylation of histone H3 on these promoter regions and acetylation of histone H4 on the ETC1 promoter region was increased in the hda6 mutant. Taken together, these results indicate that HDA6 affects the cellular patterning of Arabidopsis root epidermis through altering the histone acetylation status of ETC1 and GL2 promoters and thereby affects the expression of these two components of the core transcription factor network determining epidermal cell fates. Our findings thus provide new insights into the role of histone acetylation in root epidermis cell patterning.

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PMID: 26143251 [PubMed - in process] PMCID: PMC4528770 [Available on 2016-08-01]

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Histone acetylation affects expression of cellular patterning gene [Proc Natl Acad Sci U S A. 2005]

HISTONE DEACETYLASE6 interacts with FLOWERING LOCUS D anc [Plant Physiol. 2011]

HDA18 affects cell fate in Arabidopsis root epidermis via histone acetylatio [Plant Cell. 2013]

Review Epidermal cell patterning and differentiation throughout the ap [J Exp Bot. 2005]

Review Pathways for epidermal cell differentiation via the hc [J Integr Plant Biol. 2012]

See reviews...

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Cited by 1 PubMed Central article

Chromatin and Epigenetics. [Plant Physiol. 2015]

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HISTONE DEACETYLASE6-Defective Mutants Show Increased Expression and Acetylation of ENHANCER OF TRIPTYCHON AND CAPRICE1 and GLABRA2 with Small But Significant Effects on Root Epidermis Cellular Pattern[1]

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Abstract

Cellular patterning in the Arabidopsis (*Arabidopsis thaliana*) root epidermis is dependent on positional information, the transmission of which involves histone acetylation. Here, we report that *HISTONE DEACETYLASE6* (*HDA6*) has significant effects on this cellular patterning. Mutation of *HDA6* led to ectopic hair cells in the nonhair positions of root epidermis in Arabidopsis, based on an analysis of paraffin sections stained with Toluidine Blue. While HDA6 was present throughout the root tip, epidermis-specific complementation with *HDA6* could rescue the *hda6* phenotype. Both transcript levels and expression patterns of *ENHANCER OF TRIPTYCHON AND CAPRICE1* (*ETC1*) and *GLABRA2* (*GL2*) in the root tip were affected in *hda6*. Consistent with these changes in expression, HDA6 directly

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HISTONE DEACETYLASE6-Defective Mutants Show Increased Expression and Acetylation of *ENHANCER OF TRIPTYCHON AND CAPRICE1* and *GLABRA2* with Small But Significant Effects on Root Epidermis Cellular Pattern[1]

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Cellular patterning in the Arabidopsis (*Arabidopsis thaliana*) root epidermis is dependent on positional information, the transmission of which involves histone acetylation. Here, we report that *HISTONE DEACETYLASE6* (*HDA6*) has significant effects on this cellular patterning. Mutation of *HDA6* led to ectopic hair cells in the nonhair positions of root epidermis in Arabidopsis, based on an analysis of paraffin sections stained with Toluidine Blue. While HDA6 was present throughout the root tip, epidermis-specific complementation with *HDA6* could rescue the *hda6* phenotype. Both transcript levels and expression patterns of *ENHANCER OF TRIPTYCHON AND CAPRICE1* (*ETC1*) and *GLABRA2* (*GL2*) in the root tip were affected in *hda6*. Consistent with these changes in expression, HDA6 directly bound to the promoter regions of *ETC1* and *GL2*, and acetylation of histone H3 on these promoter regions and acetylation of histone H4 on the *ETC1* promoter region was increased in the *hda6* mutant. Taken together, these results indicate that HDA6 affects the cellular patterning of Arabidopsis root epidermis through altering the histone acetylation status of *ETC1* and *GL2* promoters and thereby affects the expression of these two components of the core transcription factor network determining epidermal cell fates. Our findings thus provide new insights into the role of histone acetylation in root epidermis cell patterning.

Pattern formation is an important event during the morphogenesis of a multicellular organism. In Arabidopsis (*Arabidopsis thaliana*), root epidermis is a well-established model system for studying pattern formation in plant development (Schiefelbein, 2003; Schiefelbein et al., 2009, 2014; Grebe, 2012). The root epidermis comprises hair cells and nonhair cells. These two types of epidermal cells have different cytoplasmic characteristics, and their fates are determined in a position-dependent manner: epidermal cells overlying two cortical cells (the H position) adopt the hair cell fate, while epidermal

adopt the nonhair cell fate (Dolan et al., 1993; Galway et al., 1994; Berger et al., 1998).

The position-dependent cellular patterning of Arabidopsis root epidermis is regulated mainly by a system consisting of at least three levels. The first level is a GLABRA2 (GL2)-centered transcription factor network including three types of proteins: the Myb domain proteins WEREWOLF (WER), CAPRICE (CPC), TRIPTYCHON (TRY), and ENHANCER OF TRIPTYCHON AND CAPRICE1 (ETC1; Wada et al., 1997; Lee and Schiefelbein, 1999; Schellmann et al., 2002; Kirik et al., 2004); the

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