

The background features a dark blue gradient with faint, light blue circular diagrams and a scale. The scale is a large arc on the left side, with numerical markings from 150 to 260 in increments of 10. Several circular diagrams are scattered across the background, some with arrows indicating a clockwise direction. The overall aesthetic is technical and scientific.

GENOMOK ÉS GENOMBÖNGÉSZŐK

MAKAI SZABOLCS, PHD

PLANTS.ENSEMBL.ORG

The background is a gradient of dark blue to purple, filled with a field of small, light-colored stars. Several faint, white circular patterns are overlaid on the background. One large pattern in the top right corner features concentric circles and a scale from 0 to 210 degrees. Other smaller patterns are scattered in the top left, bottom left, and bottom right.

ENSEMBLE GENOMES

- 1999: Start of Ensembl project (Human Genome)
- 2001: First release of data and web interface
- 2002: Mouse, mosquito, fugu, zebrafish and rat added
- ...
- 2009: First release of Ensembl Genomes
- ...
- 2012: Ensembl (v69): 71 genomes
- 2012: Ensembl Genomes (v16): 359 genomes

Search: for

 e.g. [Carboxy*](#) or [chx28](#)

All genomes

- [View full list of all Ensembl Plants species](#)
- [Edit your favourites](#)

Favourite genomes



Arabidopsis thaliana

TAIR10



Oryza sativa Japonica Group

IRGSP-1.0



Triticum aestivum

IWGSC



Hordeum vulgare

IBSC_v2



Zea mays

B73_RefGen_v4



Physcomitrella patens

Phypa_V3

New wheat assembly

This release of Ensembl Plants hosts the [latest wheat assembly](#) from the IWGSC (RefSeq v1.0). Current data includes:

- The IWGSC RefSeq v1.1 gene annotation.
- Alignment of 98,270 high confidence genes from the TGACv1 annotation.
- The Axiom 820K SNP Array from CerealsDB.
- EMS-induced mutations from sequenced TILLING populations (Kronos and Cadensa).
- Assembly to assembly mapping and gene ID mapping to the previous TGAC v1 assembly and annotation.
- Whole genome alignments to rice, brachypodium and barley.
- The TGACv1 assembly will still be available via the [Ensembl Plants archive site](#).

Polyploid View Enabled

Polyploid view for [wheat](#) has been enabled, allowing users to view alignments between the three wheat components [simultaneously](#).

Funding

Ensembl Plants datasets are constructed in a direct collaboration with the [Gramene](#) resource, funded by the United States [National Science Foundation award #1127112](#). Read [more about our collaboration with Gramene](#).



The development of resources for wheat is funded by the BBSRC-funded [Designing Future Wheat ISP](#).



ADAT TÍPUSOK

- Genomic sequence
- Gene / transcript / protein models
- External references
- Mapped sequences
 - cDNAs, proteins, repeats, markers, probes, etc.
- Variation data:
 - sequence variants
 - structural variants

 **Triticum aestivum** (IWGSC) ▾

Search

e.g. [TraesCS3D02G273600](#) or [3D:2585940-2634711](#) or [Carboxy*](#)


For information about the assembly and annotation please view the [IWGSC announcement](#).
 The previous wheat assembly ([TGACv1](#)) and every other plant from release 31 is available in the new [Ensembl Plants archive](#) site.

About *Triticum aestivum*





Triticum aestivum (bread wheat) is a major global cereal grain essential to human nutrition. Wheat was one of the first cereals to be domesticated, originating in the [fertile crescent](#) around 7000 years ago. Bread wheat is hexaploid, with a genome size estimated at ~17 Gbp, composed of three closely-related and independently maintained genomes that are the result of a series of naturally occurring hybridization events. The ancestral progenitor genomes are considered to be [Triticum urartu](#) (the A-genome donor) and an unknown grass thought to be related to *Aegilops speltoides* (the B-genome donor). This first hybridization event produced tetraploid emmer wheat (AABB, *T. dicoccoides*) which hybridized again with [Aegilops tauschii](#) (the D-genome donor) to produce modern bread wheat.

Taxonomy ID [4565](#)

Data source [International Wheat Genome Sequencing Consortium](#)

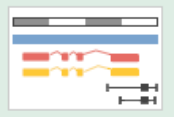
 [More information and statistics](#)

Genome assembly: [IWGSC](#)

-  [More information and statistics](#)
-  [Download DNA sequence \(FASTA\)](#)
-  [Convert your data to IWGSC coordinates](#)
-  [Display your data in Ensembl Plants](#)






[View karyotype](#)



[Example region](#)

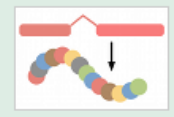
Gene annotation

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

-  [More about this genebuild](#)
-  [Download genes, cDNAs, ncRNA, proteins - FASTA - GFF3](#)
-  [Update your old Ensembl IDs](#)



[Example gene](#)



[Example transcript](#)

Comparative genomics

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




-  [More about comparative analyses](#)
-  [Phylogenetic overview of gene families](#)
-  [Download alignments \(EMF\)](#)
-  [Genomic alignments \[5\] \[Show»\]](#)

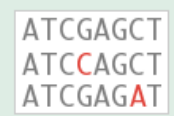


[Example gene tree](#)


Variation

What can I find? Short sequence variants.

-  [More about variation in Triticum aestivum](#)
-  [More about variation in Ensembl Plants](#)
-  [Download all variants - GVF - VCF - VEP](#)



[Example variant](#)

[Variant Effect Predictor](#) 

Genome

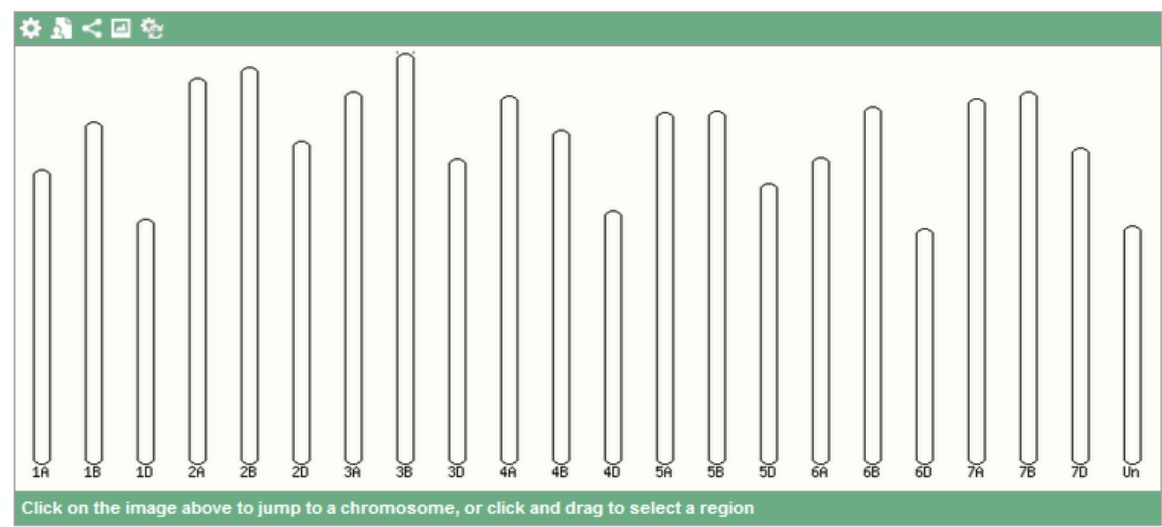
- Location-based displays
- Whole genome
 - Chromosome summary
 - Region overview
 - Region in detail
 - Comparative Genomics
 - Synteny
 - Alignments (image)
 - Alignments (text)
 - Region Comparison
 - Polyploid view
 - Genetic Variation
 - Variant table
 - Resequencing
 - Strain table
 - Linkage Data
 - Markers

- Configure this page
- Custom tracks
- Export data
- Share this page
- Bookmark this page

[Ensembl Plants is produced in collaboration with Gramene](#)

Whole genome ?

+ Add features



Summary

Assembly	IWGSC, INSDC Assembly GCA_900519105.1 , Jul 2018
Database version	94.4
Base Pairs	14,547,261,565
Golden Path Length	14,547,261,565
Genebuild by	IWGSC
Genebuild method	Imported from IWGSC
Data source	International Wheat Genome Sequencing Consortium

Gene counts

Coding genes	107,891
Non coding genes	12,853
Small non coding genes	12,491
Long non coding genes	362
Gene transcripts	146,597

Other

Short Variants	14,142,687
----------------	------------

Triticum aestivum (IWGSC)

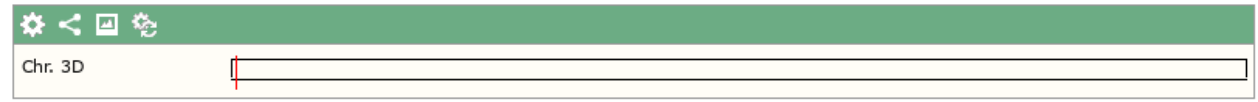
Location: 3D:2,585,940-2,634,711

- Location-based displays
 - Whole genome
 - Chromosome summary
 - Region overview
 - Region in detail**
- Comparative Genomics
 - Synteny
 - Alignments (image)
 - Alignments (text)
 - Region Comparison
 - Polyploid view
- Genetic Variation
 - Variant table
 - Resequencing
 - Linkage Data
- Markers

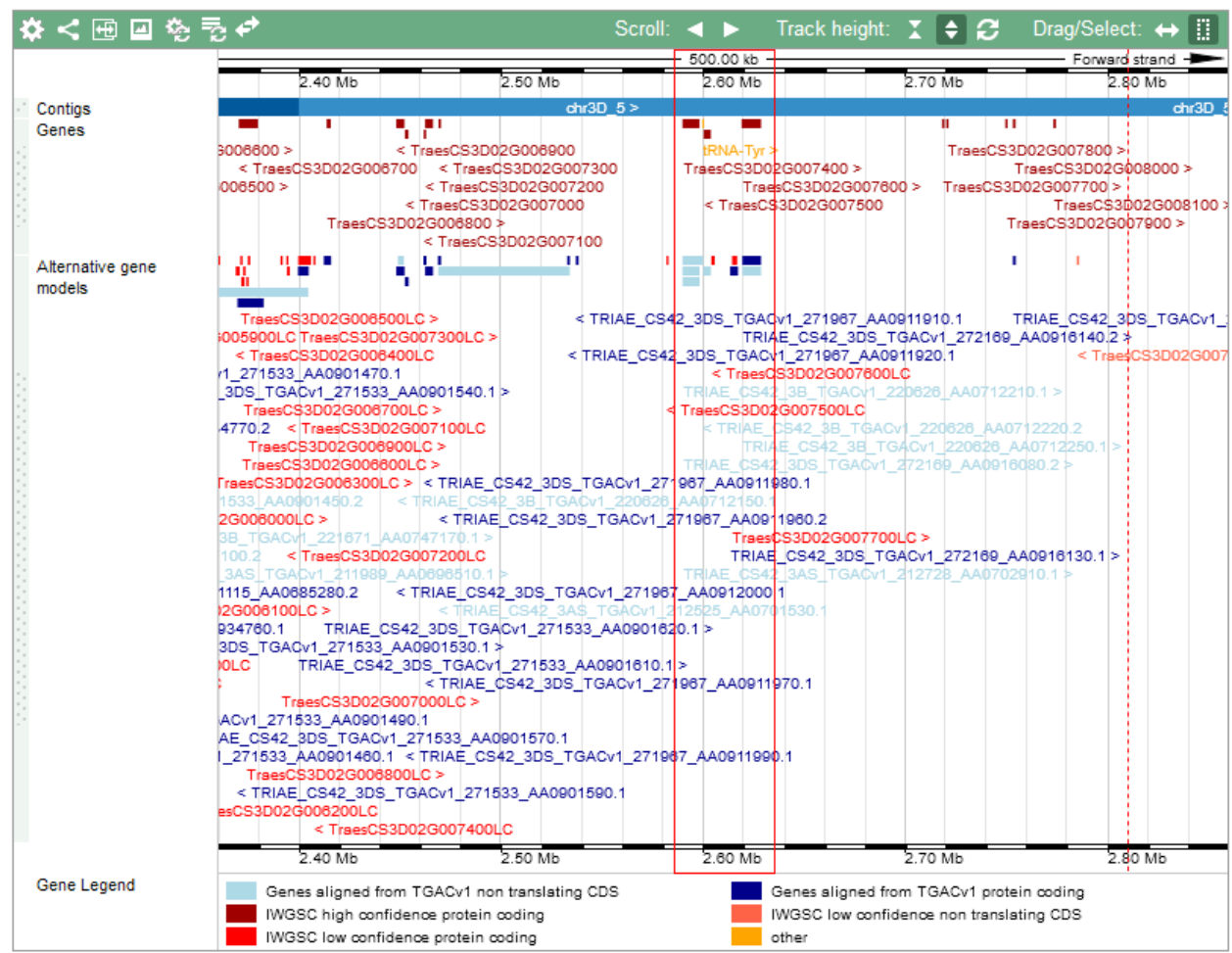
- Configure this page
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Ensembl Plants is produced in collaboration with Gramene

Chromosome 3D: 2,585,940-2,634,711



Region in detail



Location: 3D:2585940-2634711

Go

Gene:

Go



Drag/Select:

Alternative gene models.....

Genes.....

Contigs.....

Genes.....

Alternative gene models.....

Variant - All sources.....

%GC.....

Gene Legend

Protein Coding

- protein coding
- IWGSC low confidence protein coding
- Genes aligned from TGACv1 protein coding

Non-Protein Coding

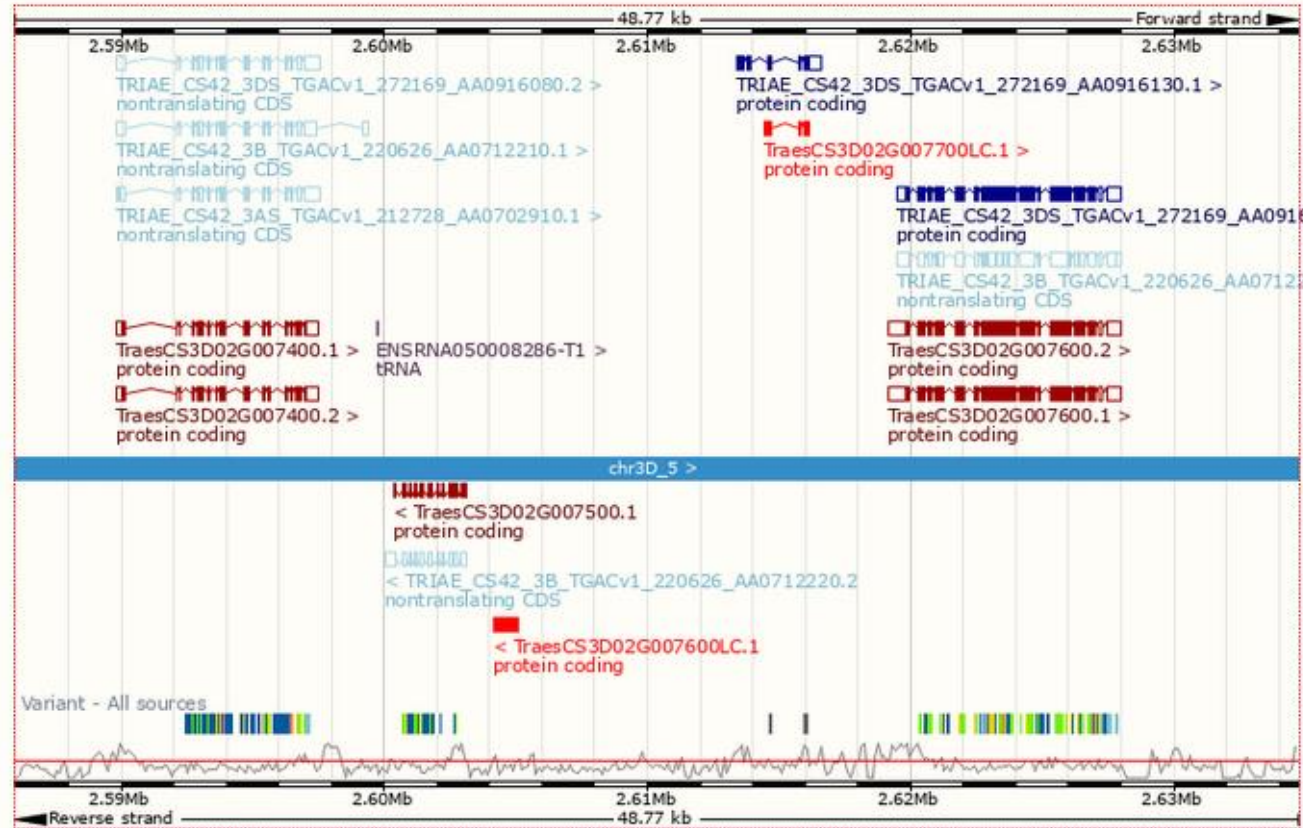
- RNA gene
- Genes aligned from TGACv1 non translating CDS

Variant Legend

- splice donor variant
- missense variant
- synonymous variant
- intron variant
- splice acceptor variant
- splice region variant
- 3 prime UTR variant
- intergenic variant

There are currently 42 tracks turned off.

Ensembl Plants Triticum aestivum version 94.4 (IWGSC) Chromosome 3D: 2,585,940 - 2,634,711



Gene: TraesCS3D02G273600

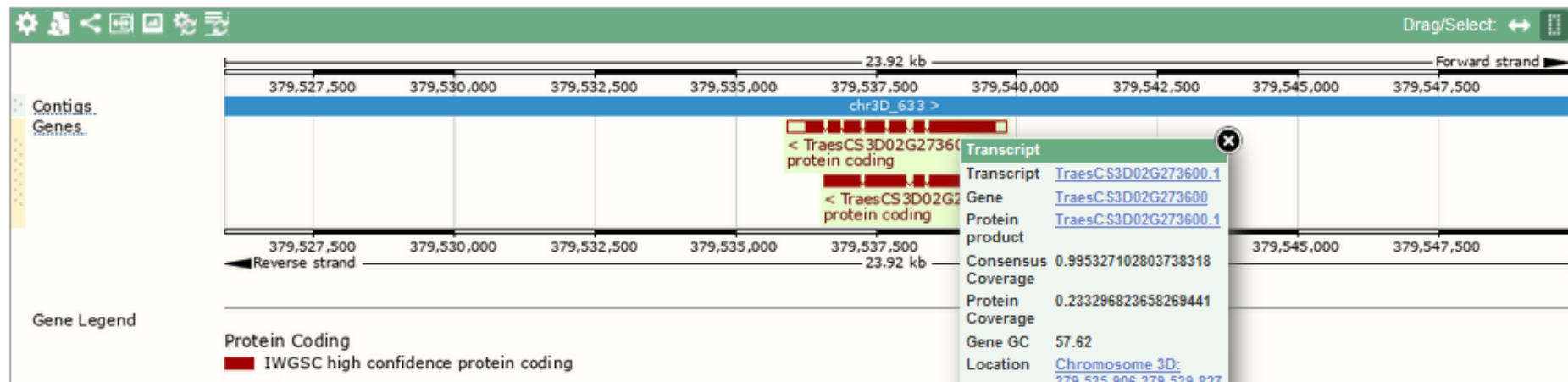
Description Heat shock protein 101 [Source:UniProtKB/TrEMBL;Acc:Q9SPH4 [↗](#)]
Location [Chromosome 3D: 379,535,906-379,539,827](#) reverse strand.
About this gene This gene has 2 transcripts ([splice variants](#)), [80 orthologues](#) and [21 paralogues](#).
Transcripts [Show transcript table](#)

Summary [?](#)

Gene type Protein coding
Annotation method Genes annotated with high confidence by IWGSC



Go to [Region in Detail](#) for more tracks and navigation options (e.g. zooming)



[?](#) Configuring the display

Tip: use the "Configure this page" link on the left to show additional data in this region.

Gene: TraesCS3D02G273600

Description	Heat shock protein 101 [Source:UniProtKB/TrEMBL;Acc:Q9SPH4 ↗]
Location	Chromosome 3D: 379,535,906-379,539,827 reverse strand.
About this gene	This gene has 2 transcripts (splice variants), 80 orthologues and 21 paralogues .
Transcripts	Show transcript table

GO: Molecular function [?](#)

Accession	Term	Evidence	Annotation source	Mapped using	Transcript IDs
GO:0000166 ↗	nucleotide binding	IEA	UniProtKB/TrEMBL:Q9SPH4 ↗		TraesCS3D02G273600.1 <ul style="list-style-type: none">Search BioMartView on karyotype
GO:0005524 ↗	ATP binding	IEA	UniProtKB/TrEMBL:Q9SPH4 ↗ , InterPro:ATPase_AAA_core ↗ , InterPro:ClpA/B_CS1 ↗ , InterPro:ClpA/B ↗		TraesCS3D02G273600.2 TraesCS3D02G273600.1 <ul style="list-style-type: none">Search BioMartView on karyotype

Gene: TraesCS3D02G273600

Description	Heat shock protein 101 [Source:UniProtKB/TrEMBL;Acc:Q9SPH4 ↗]
Location	Chromosome 3D: 379,535,906-379,539,827 reverse strand.
About this gene	This gene has 2 transcripts (splice variants), 80 orthologues and 21 paralogues .
Transcripts	Show transcript table

GO: Biological process [?](#)

Accession	Term	Evidence	Annotation source	Mapped using	Transcript IDs
GO:0019538 ↗	protein metabolic process	IEA	UniProtKB/TrEMBL:Q9SPH4 ↗ , InterPro:Clp_N_dom_sf ↗		TraesCS3D02G273600.1 TraesCS3D02G273600.2 <ul style="list-style-type: none">Search BioMartView on karyotype

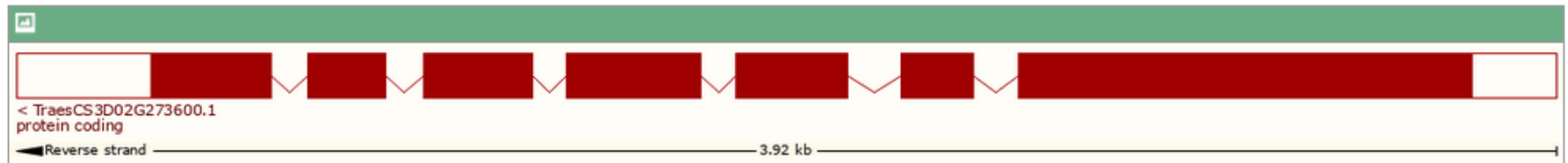
Gene: [TraesCS3D02G273600](#)

Trans: [TraesCS3D02G273600.1](#)

Transcript: [TraesCS3D02G273600.1](#)

Description	Heat shock protein 101 [Source:UniProtKB/TrEMBL;Acc: Q9SPH4]
Location	Chromosome 3D: 379,535,906-379,539,827 reverse strand.
About this transcript	This transcript has 7 exons , is annotated with 32 domains and features and is associated with 130 variations .
Gene	This transcript is a product of gene TraesCS3D02G273600 Show transcript table

Summary



Statistics	Exons: 7, Coding exons: 7, Transcript length: 3,297 bps, Translation length: 913 residues
Version	TraesCS3D02G273600.1.
Type	Protein coding
Annotation Method	Genes annotated with high confidence by IWGSC

Transcript: TraesCS3D02G273600.1

Description Heat shock protein 101 [Source:UniProtKB/TrEMBL;Acc:Q9SPH4]

Location [Chromosome 3D: 379,535,906-379,539,827](#) reverse strand.

About this transcript This transcript has [7 exons](#), is annotated with [32 domains and features](#) and is associated with [130 variations](#).

Gene This transcript is a product of gene [TraesCS3D02G273600](#) [Show transcript table](#)

Domains & features

Domains

Domain source	Start	End	Description	Accession	InterPro
PANTHER	1	859	-	PTHR11638	-
PANTHER	1	859	-	PTHR11638:SF146	-
Gene3D	152	345	-	3.40.50.300	-
CDD	184	344	-	cd00009	-
Gene3D	346	546	-	3.40.50.300	-
Gene3D	552	767	-	3.40.50.300	-
CDD	596	767	-	cd00009	-
Gene3D	768	864	-	1.10.8.60	-
SMART	201	346	AAA+ ATPase domain	SM00382	IPR003593 [Display all genes with this domain]
SMART	599	742	AAA+ ATPase domain	SM00382	IPR003593 [Display all genes with this domain]
Pfam	206	322	ATPase, AAA-type, core	PF00004	IPR003959 [Display all genes with this domain]
Pfam	599	762	ATPase, AAA-type, core	PF07724	IPR003959 [Display all genes with this domain]
Pfam	768	847	Clp ATPase, C-terminal	PF10431	IPR019489 [Display all genes with this domain]
SMART	768	859	Clp ATPase, C-terminal	SM01086	IPR019489 [Display all genes with this domain]
Pfam	17	67	Clp, N-terminal	PF02861	IPR004176 [Display all genes with this domain]
Pfam	98	148	Clp, N-terminal	PF02861	IPR004176 [Display all genes with this domain]
Gene3D	3	151	Clp, N-terminal domain superfamily	1.10.1780.10	IPR036628 [Display all genes with this domain]
Superfamily	4	158	Clp, N-terminal domain superfamily	SSF81923	IPR036628 [Display all genes with this domain]
Prints	603	621	ClpA/B family	PR00300	IPR001270 [Display all genes with this domain]
Prints	648	666	ClpA/B family	PR00300	IPR001270 [Display all genes with this domain]
Prints	677	695	ClpA/B family	PR00300	IPR001270 [Display all genes with this domain]
Prints	710	724	ClpA/B family	PR00300	IPR001270 [Display all genes with this domain]
PROSITE patterns	297	309	ClpA/B, conserved site 1	PS00870	IPR018368 [Display all genes with this domain]
PROSITE patterns	633	651	ClpA/B, conserved site 2	PS00871	IPR028299 [Display all genes with this domain]
Superfamily	164	547	P-loop containing nucleoside triphosphate hydrolase	SSF52540	IPR027417 [Display all genes with this domain]
Superfamily	548	848	P-loop containing nucleoside triphosphate hydrolase	SSF52540	IPR027417 [Display all genes with this domain]

ARRAY EXPRESS

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ArrayExpress – functional genomics data

ArrayExpress Archive of Functional Genomics Data stores data from high-throughput functional genomics experiments, and provides these data for reuse to the research community.



Data Content

Updated today at 03:00

- 71356 experiments
- 2306133 assays
- 46.86 TB of archived data

Latest News

18 May 2018 - **New single-cell submission and metadata guide**

We are happy to announce the newest addition to our help pages: [The single-cell submission guide!](#)

This is a simple step-by-step guide which leads you through submitting single-cell sequencing submissions and lists the minimum required metadata to include. The guide starts by explaining the expected sample attributes dependent on the experiment design to help you correctly annotate your samples. The next section details the technical information that is required for single cell-specific procedures including pre/post analysis quality control or how single cells were generated. The library and sequencing information section helps you to understand the required information for the library construction protocols, how to include barcode information, and spike-in information where applicable. Lastly, how to prepare the raw data files for your submission.

We hope you find this useful to submit single-cell sequencing data!







Filter search results

Filtered by organism **Triticum aestivum**, experiment type **"rna assay"**, experiment type **"sequencing assay"**

Page **1** [2](#)

Showing **1 - 25** of **46** experiments

Page size **25** [50](#) [100](#) [250](#) [500](#)

Accession	Title	Type	Organism	Assays	Released	Processed	Raw	Views	Atlas
E-MTAB-5898	RNAseq of roots and leaves of tender wheat (<i>Triticum aestivum</i> cv chinese Spring) during interactions with mycorrhizal fungi (<i>Funneliformis mossae</i>) with and without a pathogen attack by <i>Xanthomonas translucens</i>	RNA-seq of coding RNA	Triticum aestivum	12	01/06/2018	-		52	Atlas
E-MTAB-6398	RNA-seq of pericarp of purple-grain wheat Luozhen No.1 of 20 days (D20) shading treatment after pollination, against 20 DAP untreated controls	RNA-seq of coding RNA	Triticum aestivum	2	30/03/2018	Link		82	-
E-MTAB-5975	RNA-seq of pericarp of <i>Triticum aestivum</i> Luozhen No.1, field study in Tai'an (China) at 15 and 20 days post pollination in response to shading treatment after pollination compared to untreated controls	RNA-seq of coding RNA	Triticum aestivum	8	26/03/2018	Download		86	-
E-MTAB-6383	Transcriptomic analysis of <i>F. graminearum</i> disease response in near-isogenic resistant and susceptible hexaploid wheat lines	RNA-seq of coding RNA	Triticum aestivum	22	28/02/2018	-		101	-
E-MTAB-5891	RNA-seq of wheat leaves and roots in response to <i>Xanthomonas translucens</i> infection	RNA-seq of coding RNA	Triticum aestivum	12	01/09/2017	-		146	Atlas
E-MTAB-4222	RNA-seq of coding RNA of wheat heads from 3, 6, 12, 24, 36, and 48 hours after inoculation of fungal pathogen <i>Fusarium graminearum</i> or mock	RNA-seq of coding RNA	Triticum aestivum	72	31/08/2016	-		619	Atlas

EXPRESSION ATLAS

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Expression Atlas

Gene expression across
species and biological
conditions

Query single cell expression

[To Single Cell Expression Atlas](#)

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Exploring gene expression results across species under different biological conditions

Expression Atlas is an open science resource that gives users a powerful way to find information about gene and protein expression across species and biological conditions such as different tissues, cell types, developmental stages and diseases among others. Expression Atlas aims to help answering questions such as 'where is a certain gene expressed?' or 'how does its expression change in a disease?'.


[Read more about Expression Atlas](#)

Search

Gene set enrichment

Gene / Gene properties

Examples: [REG1B](#), [zinc finger](#), [O14777 \(UniProt\)](#), [GO:0010468 \(regulation of gene expression\)](#)

Organism

Any

Biological conditions

Examples: [lung](#), [leaf](#), [valproic acid](#), [cancer](#)

Search

Clear

Results for leaf OR seed AND Triticum aestivum

Baseline expression | Differential expression

Show anatomograms

Filter your results

Triticum aestivum

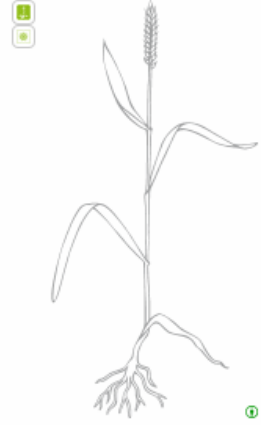
Organism part

Developmental stage

Sampling time point

Organism part

Showing 4 experiments:



By experiment type | Filters | Download

- Cell Types - Pfeifer - 20 days post anthesis
- Cell Types - Pfeifer - 30 days post anthesis
- Cell Types - Pfeifer - 10 days post anthesis
- 3 Tissues - Phillips et al



High Medium Low Below cutoff No data available

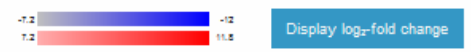
Did you find these results useful?



Results for leaf OR seed AND Triticum aestivum

Baseline expression Differential expression

Filter your results



Download results

- Kingdom**
- Plants
- Species**
- Triticum aestivum
- Experiment type**
- RNA-seq mRNA differential
- Experimental variables**
- Infect
 - Time
 - Organism part
 - Age
 - Environmental stress
- Regulation**
- Down
 - Up

Log ₂ -fold change	Species	Gene name	Comparison	Experimental variables	Experiment name
		TRIAE_CS42_5BL_TGACv1_413043_AA1367940	'4 week; cold temperature regimen' vs '2 week; control'	age, environmental stress	Transcription profiling by high throughput sequencing of wheat in response to low temperature
		TRIAE_CS42_2BL_TGACv1_130091_AA0403600	'4 week; cold temperature regimen' vs '2 week; control'	age, environmental stress	Transcription profiling by high throughput sequencing of wheat in response to low temperature
		TRIAE_CS42_2BL_TGACv1_129997_AA0401280	'4 week; cold temperature regimen' vs '2 week; control'	age, environmental stress	Transcription profiling by high throughput sequencing of wheat in response to low temperature
		TRIAE_CS42_2AL_TGACv1_094560_AA0299650	'4 week; cold temperature regimen' vs '2 week; control'	age, environmental stress	Transcription profiling by high throughput sequencing of wheat in response to low temperature
		TRIAE_CS42_7AS_TGACv1_569613_AA1820410	'4 week; cold temperature regimen' vs '2 week; control'	age, environmental stress	Transcription profiling by high throughput sequencing of wheat in response to low temperature
		TRIAE_CS42_5BL_TGACv1_412328_AA1367790	'4 week; cold temperature regimen' vs '2 week; control'	age, environmental stress	Transcription profiling by high throughput sequencing of wheat in response to low temperature
		TRIAE_CS42_4AL_TGACv1_288169_AA0939290	'4 week; cold temperature regimen' vs '2 week; control'	age, environmental stress	Transcription profiling by high throughput sequencing of wheat in response to low temperature
		TRIAE_CS42_2DL_TGACv1_162669_AA0563320	'4 week; cold temperature regimen' vs '2 week; control'	age, environmental stress	Transcription profiling by high throughput sequencing of wheat in response to low temperature
		TRIAE_CS42_5BL_TGACv1_405520_AA1329310	'4 week; cold temperature regimen' vs '2 week; control'	age, environmental stress	Transcription profiling by high throughput sequencing of wheat in response to low temperature
		TRIAE_CS42_5DL_TGACv1_433492_AA1414670	'4 week; cold temperature regimen' vs '2 week; control'	age, environmental stress	Transcription profiling by high throughput sequencing of wheat in response to low temperature
		TRIAE_CS42_7DS_TGACv1_622753_AA2044770	'4 week; cold temperature regimen' vs '2 week; control'	age, environmental stress	Transcription profiling by high throughput sequencing of wheat in response to low temperature

The background is a dark blue gradient with a field of small white stars. On the right side, there are several technical diagrams: a large circular scale with degree markings from 0 to 210, a smaller circular diagram with arrows, and a dashed circular diagram with an arrow. In the top left and bottom left corners, there are partial circular diagrams with arrows.

RÁADÁS

HA NINCS KÉRDÉS

- [Overview](#)
- [Synonyms](#)
- [Ancestor Chart](#)
- [Child Terms](#)
- [Annotation Guidance](#)
- [GO Discussions](#)
- [Taxon Constraints](#)
- [Blacklist](#)
- [Cross-References](#)
- [Cross-Ontology Relations](#)
- [Protein Complexes](#)
- [Replaces](#)
- [Replaced By](#)
- [Co-occurring Terms](#)
- [GO Slims](#)
- [Change Log](#)

GO:0019538 P 🏠 JSON

protein metabolic process

Biological Process

Definition (GO:0019538 GONUTS page)

The chemical reactions and pathways involving a protein. Includes protein modification.

Secondary IDs

GO:0006411, GO:0044268

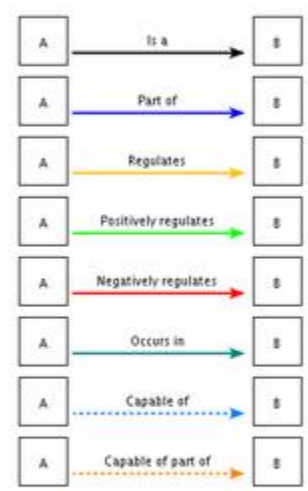
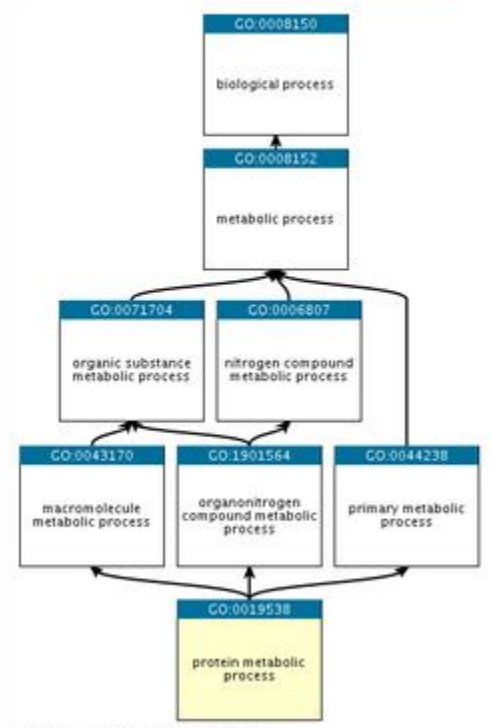
34,157,229 annotations

Synonyms

Ancestor chart

Ancestor chart for GO:0019538

Chart options



Close

