

Wheat3BMine

a data warehouse dedicated to wheat 3B chromosome data









T. Letellier¹, L. Couderc¹, F. Choulet², M. Spannagl³, C. Pommier¹, J. Ll. Gelpi⁴, P. Kersey⁵,

H. Quesneville¹, D. Steinbach¹ & M. Alaux¹

thomas.letellier@versailles.inra.fr

- ¹ INRA, UR1164 URGI, route de Saint-Cyr, RD 10, 78026 Versailles, France
- ² INRA GDEC, 5 chemin de Beaulieu, Clermont-Ferrand, 63039, France
- ³ MIPS/IBIS, Helmholtz Zentrum München, 85764 Neuhererg, Germany
- ⁴ BSC-INB, University of Barcelona, Spain
- ⁵ EBI, Wellcome Trust Genome Campus, Hinxton, Cambdrige CB10 1SD, UK



Integration and analysis of complex biological data is a key challenge of modern bioinformatics. For this purpose, we developed Wheat3BMine at URGI, (INRA research unit in genomics and bioinformatics dedicated to plants and crop parasites) in the frame of the transPLANT and 3BSEQ projects.

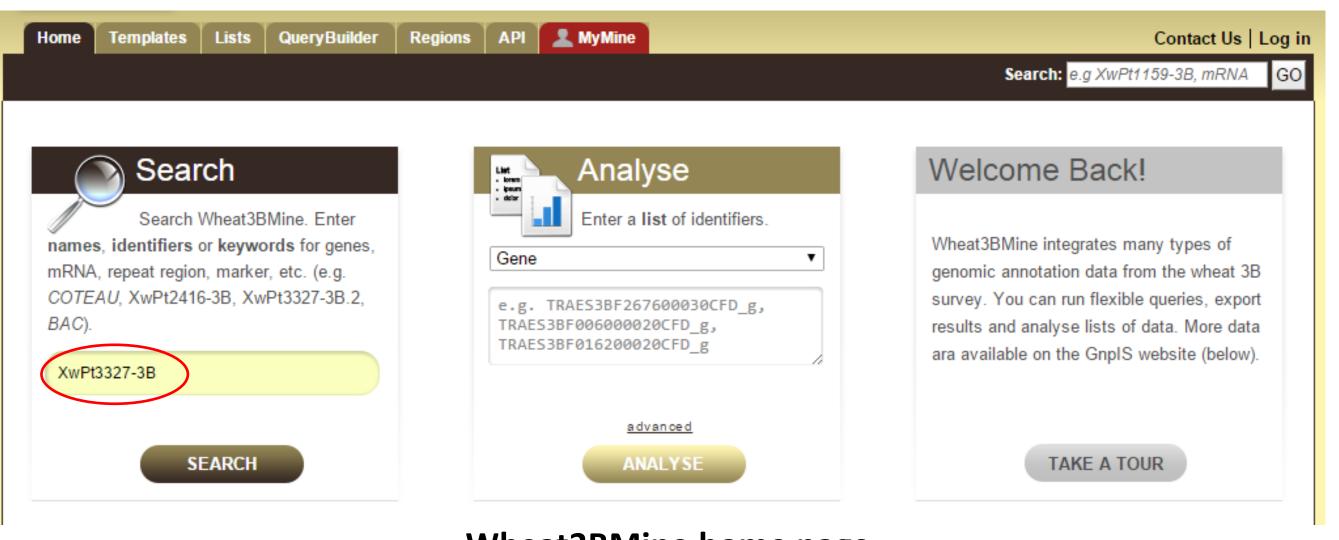
Wheat3BMine is a data warehouse dedicated to the Wheat 3B chromosome:

http://urgi.versailles.inra.fr/Wheat3BMine/

It is developed using InterMine technology, providing a fast, flexible and user friendly access to integrated data by multiple ways: a browser, a query builder, a region search tool and so on. Moreover data can be filtered and exported in many formats (GFF3, BED or XML for example).

Wheat3BMine users can make lists of their favorite features and save their own queries, an online documentation and pre-computed queries help them to extract relevant information. Our data warehouse contains heterogeneous data and is gene-centered. Wheat3BMine provides access to genomic annotation data (genes, mRNA, polypeptides), polymorphisms data (markers, transposable elements), genetic mapping data (QTL, metaQTL) or phenotyping data (accessions, evaluation data). In fact our typical gene card centralizes relevant information like function, ontologies or features which overlap this gene.

1. Search for a gene or a marker in the quick search



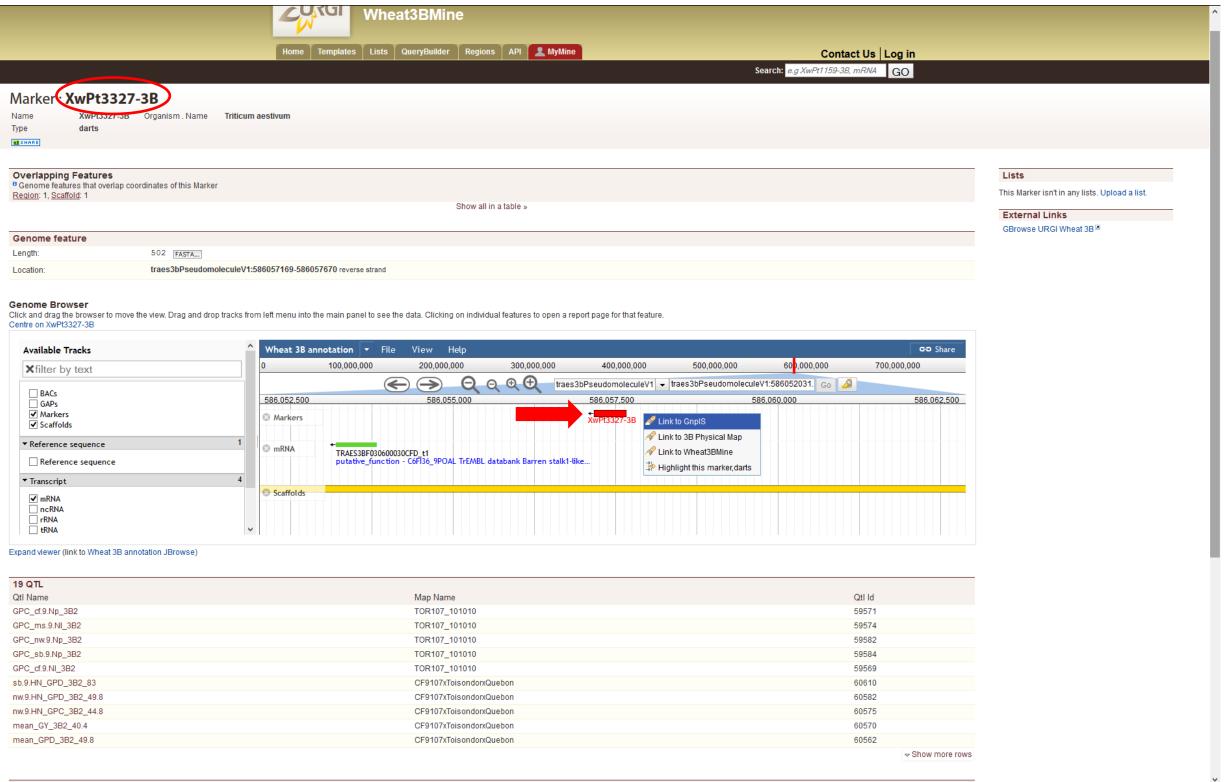
Wheat3BMine home page



Marker: WPT3327

Triticum aestivun

All species



Wheat3BMine marker card

Landmark or Region traes3bPseudomoleculeV1:294,989 Search Download Decorated FASTA File ▼ | Configure... | Go | Examples: traes3bPseudomoleculeV1:9.577.253..9.587.252. Data Source Scroll/Zoom: Show 100 kbp ▼ → Flip Wheat annotation viewer: 3B 295038909 .. 295039410 Positions Length Overview traes3bPseudomoleculeV1 Reference Zoom to this feature Detailed Report Link to Marker card in GnpIS Link to Wheat3BMine Link to 3B Physical Map _____ _____ ★ ■ 🖾 🖾 🗷 🛏 🛍 CDS TRAES3BF030500010CFD_ta ★ ■ X M Z H M Pseudomolecul

URGI Wheat 3B Annotation GBrowse

FEATURE TYPE

Repeat Region •

Repeat Region 6

Assembly Gap B

Region B

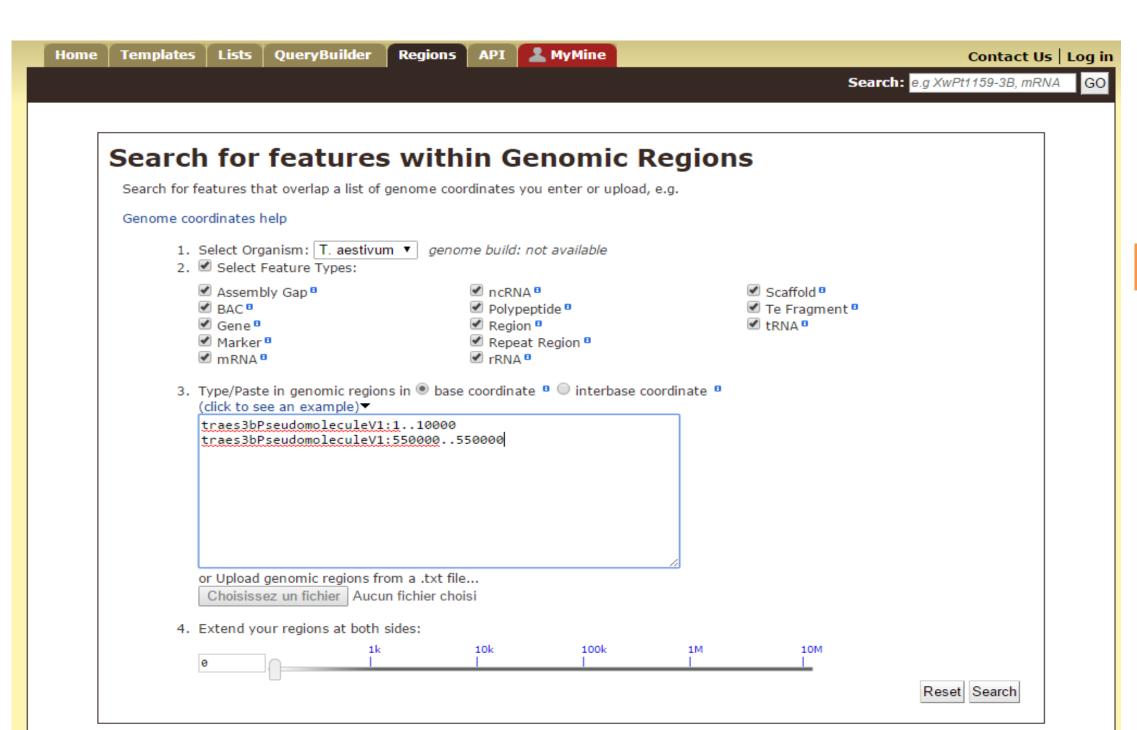
BAC B

Region •

Scaffold B

Wheat3BMine provides a strong interoperability with GnpIS, URGI JBrowse and GBrowse

2. Search for features with genomic ranges



GFF3, BED, FASTA, TAB and CSV exports are available

v443_1685 v443_1685

TaaCsp3BFhA 0218J19

1_v443_1685 1_v443_1685

4_v443_1685 4_v443_1685

5_v443_1685 5_v443_1685

v443_1715 v443_1715

TaaCsp3BFhA_0045H14

TaaCsp3BFhA_0322K03

traes3bPseudomoleculeV1 traes3bPseudomoleculeV1

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Region search results

Create and store lists of your favourite features

Selected feature types: Assembly Gap, ncRNA, Scaffold, BAC, Polypeptide, Te Fragment, Gene, Region, tRNA, Marker, Repeat Region, mRNA, rRNA

Export for all regions: TAB CSV GFF3 FASTA BED FASTA.... or Create List by feature type: Assembly Gap ▼ Go

traes3bPseudomoleculeV1:1..10000 FASTA.

traes3bPseudomoleculeV1:550000..550000 FASTA...

TAB CSV GFFB FASTA BED GALAXY

TAB CSV GFF3 FASTA BED GALAXY

Create List by BAC ▼ Go

Create List by Assembly Gap ▼ Go



Region search form





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traes3bPseudomoleculeV1:1..243120

traes3bPseudomoleculeV1:1097..4232

traes3bPseudomoleculeV1:4233..4491

traes3bPseudomoleculeV1:4499..11095

traes3bPseudomoleculeV1:6954..10959

traes3bPseudomoleculeV1:1..774434471

traes3bPseudomoleculeV1:243221..607166

traes3bPseudomoleculeV1:387299..556101

traes3bPseudomoleculeV1:486988..606495