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IWGSC sequence repository: how to facilitate pseudomolecule assembly?

Michael M. Alaux, Frédéric Choulet, Loïc Couderc, Françoise F. Alfama-Depauw, Véronique Jamilloux, Thomas Letellier, Raphaël-Gauthier R.-G. Flores, Claire Guerche, Mikaël Loaec, Etienne Paux, et al.

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IWGSC Sequence Repository: How to facilitate pseudomolecule assembly ?

Michael Alaux



Wheat@URGI website



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Wheat@URGI



<http://wheat-urgi.versailles.inra.fr>



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Sequence Repository

Create an account

- Home
- Access Status
- FAQ
- BLAST
- Accessories
- Reference sequences
- Genes & annotations
- Physical maps
- Transcriptions
- IRV-Seq
- Publication
- Support to assembly and data submissions

BLAST

- ➔ [FASTA BLAST](#)
- ➔ [BLAST 2](#) in the [genbank](#) database for wheat and other related species genomes
- ➔ [FASTA BLAST](#) in the [genbank](#) database for wheat and other related species genomes
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<http://wheat-urgi.versailles.inra.fr/Seq-Repository> Michael Alaux

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<http://wheat-urgi.versailles.inra.fr/Seq-Repository> Michael Alaux

Sequence Repository

The screenshot shows the 'Sequence Repository' website. On the left is a vertical navigation menu with items: 'Create an account', 'Home', 'Access Status', 'FAQ', 'BLAST', 'Accessories', 'Reference sequences', 'Genes & annotations', 'Physical maps', 'Transcriptome', 'BIM-Seq', 'Publication', and 'Support to assembly and data submission'. The main content area includes sections for 'New sequences', 'Publications', 'Reference sequences', and 'BIM-Seq'.



<http://wheat-urgi.versailles.inra.fr/Seq-Repository>

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Sequence Repository: 3B example

This collage shows several screenshots from the Sequence Repository website. Red arrows highlight various features: a search bar, a list of sequences, a detailed view of a sequence with its annotations, and a visualization of sequence data. The screenshots demonstrate the user interface for exploring genomic data.



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BLAST

BLAST



- **Public BLAST**
<https://urgi.versailles.inra.fr/blast/>
- More than 250 000 BLAST searches the past 2 years !



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<https://urgi.versailles.inra.fr/blast/>

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BLAST

This screenshot shows the BLAST search interface. The 'Database' dropdown menu is open, showing a list of databases. The 'wheat-urgi' database is highlighted with a red circle, indicating it is the selected database for the search.



<https://urgi.versailles.inra.fr/blast/>

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BLAST

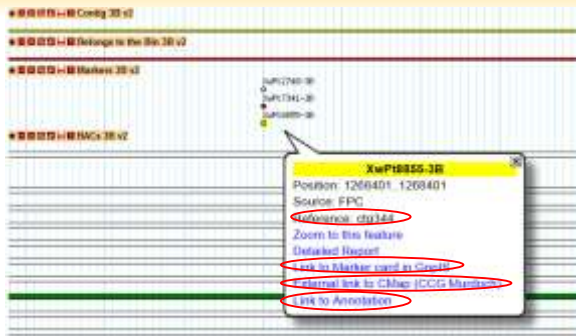
This screenshot shows the 'Advanced search' options in the BLAST interface. It includes settings for 'Expect threshold', 'Word size', 'Matrix/Scoring scheme', 'Gap costs', 'Filter', 'Mask', 'Alignment', and 'Output format'. The 'Mask' option is checked, and the 'Output format' is set to 'table'.



<https://urgi.versailles.inra.fr/blast/>

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Physical maps



https://urgi.versailles.inra.fr/gb2/gbrowse/wheat_phys_pub/

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3B reference sequence annotation



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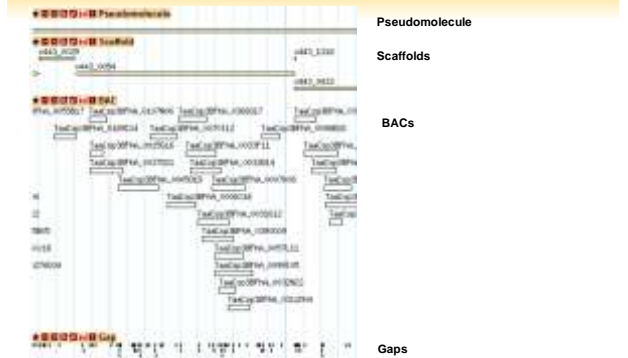
3B annotation



https://urgi.versailles.inra.fr/gb2/gbrowse/wheat_annot_3B

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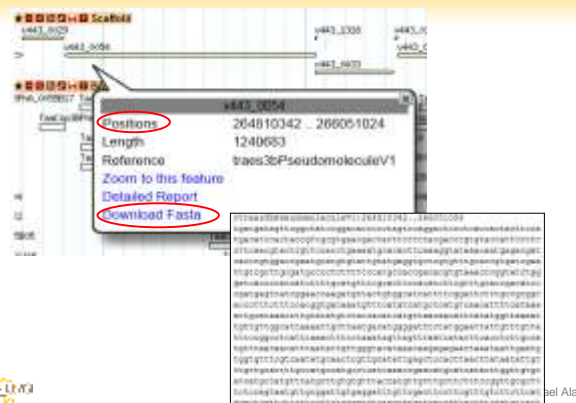
3B annotation



https://urgi.versailles.inra.fr/gb2/gbrowse/wheat_annot_3B

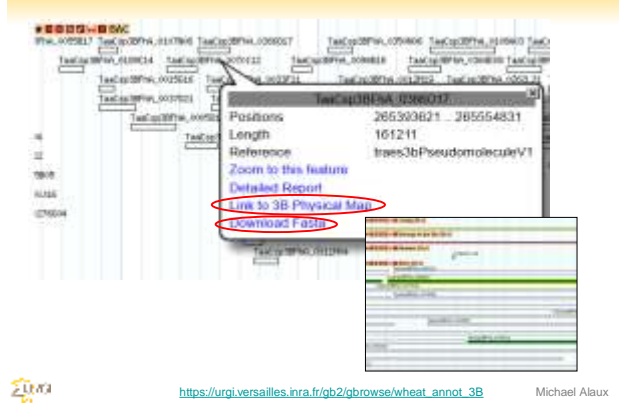
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3B annotation: Scaffold



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3B annotation: BAC



https://urgi.versailles.inra.fr/gb2/gbrowse/wheat_annot_3B

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3B annotation



https://urgi.versailles.inra.fr/gb2/gbrowse/wheat_annot_3B

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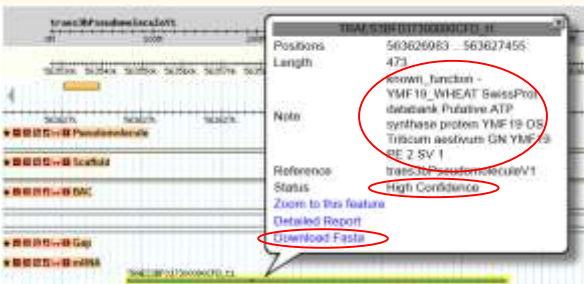
3B annotation: Marker



https://urgi.versailles.inra.fr/gb2/gbrowse/wheat_annot_3B

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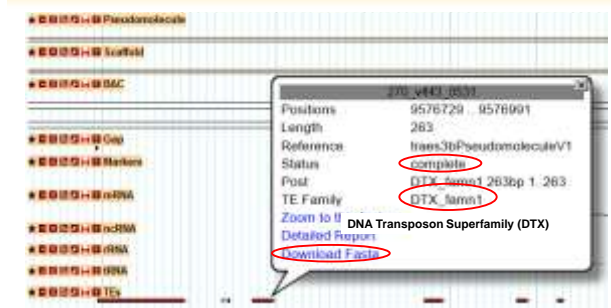
3B annotation: Gene



https://urgi.versailles.inra.fr/gb2/gbrowse/wheat_annot_3B

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3B annotation: TE



https://urgi.versailles.inra.fr/gb2/gbrowse/wheat_annot_3B

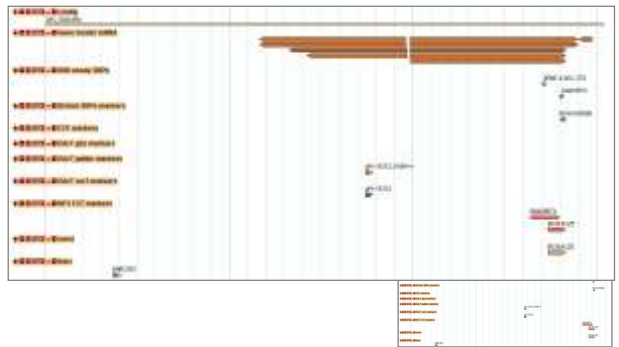
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Survey sequence browser



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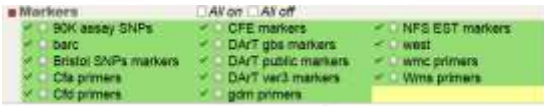
Survey sequence



https://urgi.versailles.inra.fr/gb2/gbrowse/wheat_survey_sequence_annotation

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Survey sequence



Support to assembly and data submission



https://urgi.versailles.inra.fr/gb2/gbrowse/wheat_survey_sequence_annotation

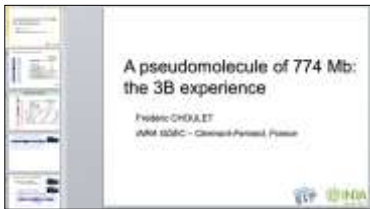
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BAC sequence assembly

4 BAC (sequence assembly)
 Frédéric Choulet, Stéphane Bouchon, Frédéric Choulet, Stéphane Bouchon, Frédéric Choulet, Stéphane Bouchon
<http://urgi.versailles.inra.fr/Seq-Repository>



- 3B MTP BAC sequencing
- 3B physical map
- Assembly and scaffolding
- Ordering scaffolds
- Perform the Annotation
- Bioinformatic tools

BAC sequence assembly

What are the needs?
 i.e. distribute the bioinformatics softwares



<http://wheat-urgi.versailles.inra.fr/Seq-Repository>

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Data submission



Wheat dataflow overview



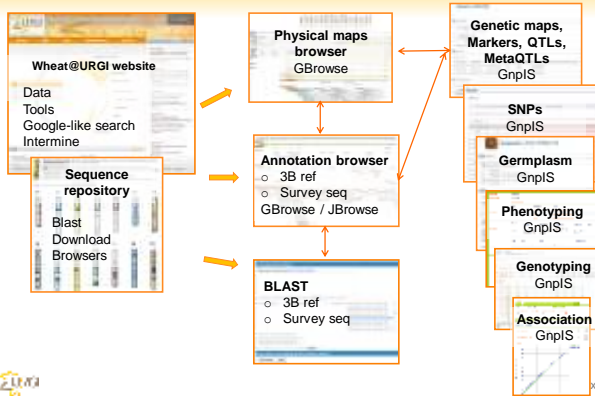
<http://wheat-urgi.versailles.inra.fr/Seq-Repository>

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Wheat dataflow overview



Acknowledgments



Alaux M.
Letellier T.
Couderc L.
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Jamilloux V.
Flores R.
Guerche C.
Loaec M.
Steinbach D.
Quesneville H.



Choulet F.
Paux E.



Rogers J.
Eversole K.

All data providers



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Questions

Sequence Repository

<http://wheat-urgi.versailles.inra.fr/Seq-Repository>

BLAST (public)

<https://urgi.versailles.inra.fr/blast/>

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