

## Access Free Identification Of Triticum Aestivum L Triticum Spelta L

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### **Identification Of Triticum Aestivum L**

Identification of the TaBTF3 gene in wheat (*Triticum aestivum* L.) and the effect of its silencing on wheat chloroplast, mitochondria and mesophyll cell development. The full-length cDNA (882bp) and DNA (1742bp) sequences encoding a basic transcription factor 3, designated as TaBTF3, were first isolated from common wheat (*Triticum aestivum* L.).

### **Identification of the TaBTF3 gene in wheat (Triticum ...**

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The generic name Triticum derives from the Latin for threshing or bruising, and the specific epithet aestivum is from the Latin for summer. Triticum aestivum is a cultigen (a plant that has been altered by humans through a process of selective breeding) and as such is only known in cultivation.

### **Triticum aestivum L. | Plants of the World Online | Kew ...**

Triticum aestivum subsp. aestivum - MHNT Common wheat (Triticum aestivum), also known as bread wheat, is a cultivated wheat species. About 95% of wheat produced worldwide is common wheat; it is the most widely grown of all crops and the cereal with the highest monetary yield.

### **Common wheat - Wikipedia**

Triticum aestivum. common wheat. This plant can be weedy or invasive according to the authoritative sources noted below. This plant may be known by one or more common names in different

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places, and some are listed above. Click on an acronym to view each weed list, or click here for a composite list of Weeds of the U.S. SWSS.

### **Plants Profile for Triticum aestivum (common wheat)**

Identification of Circular RNAs and Their Targets in Leaves of Triticum aestivum L. under Dehydration Stress Introduction. Wheat ( Triticum aestivum) is the most widely grown and important food staple grain. During the life span... Materials and Methods. Seeds of wheat cultivars ( Triticum aestivum ...

### **Frontiers | Identification of Circular RNAs and Their ...**

Identification of candidate genes, regions and markers for pre-harvest sprouting resistance in wheat (Triticum aestivum L.) Adrian L Cabral , Mark C Jordan , Curt A McCartney , Frank M You , D Gavin Humphreys , Ron MacLachlan , and Curtis J Pozniak

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## **Identification of candidate genes, regions and markers for ...**

Common wheat (*Triticum aestivum*) is one of the most important crop species and together with maize and rice provides > 60% of the calories and proteins for humans. Comprehensive identification of miRNAs in the common bread wheat is therefore of great importance.

## **Identification and characterization of a subset of ...**

International Wheat Genome Sequencing Consortium (IWGSC) (<http://www.wheatgenome.org/>) has published survey sequence assemblies of the 21 individual chromosomes of Chinese Spring (*Triticum aestivum* L.). Firstly, the SSR markers were developed by using the survey sequence assembly of chromosome 5DL.

## **Identification and characterization of a high kernel ...**

Identification and Validation of Markers Linked to

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Broad-Spectrum Stem Rust Resistance Gene Sr2 in Wheat  
(Triticum aestivum L.)

## **Identification and Validation of Markers Linked to Broad**

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Despite several studies on WRKYs in wheat (Triticum aestivum L.), functional annotation information about wheat WRKYs is limited. Results Here, 171 TaWRKY TFs were identified from the whole wheat genome and compared with proteins from 19 other species representing nine major plant lineages.

## **Genome-wide analysis of WRKY transcription factors in ...**

Computational identification of microRNAs and their targets in wheat (Triticum aestivum L.) YouSheng Han 1, FuLei Luan 1, HongLiang Zhu 1, Yi Shao 1, ... Zhang B H, Pan X P, Wang Q L, et al. Identification and characterization of new plant microRNAs using EST analysis. Cell Res, 2005, 15: 336-360,

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10.1038/sj.cr.7290302, 15916721.

## **Computational identification of microRNAs and their ...**

Identification of wheat (*Triticum aestivum* L.) genotypes for food safety on two different cadmium contaminated soils Article in Environmental Science and Pollution Research 27 (1-2) · December 2019...

## **Identification of wheat (*Triticum aestivum* L.) genotypes ...**

Identification and validation of QTL for spike fertile floret and fruiting efficiencies in hexaploid wheat (*Triticum aestivum* L.) ... Miralles DJ, González FG (2017) Fruiting efficiency in wheat (*Triticum aestivum* L): trait response to different growing conditions and its relation to spike dry weight at anthesis and grain weight at harvest ...

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## **Identification and validation of QTL for spike fertile ...**

Identification of candidate genes, regions and markers for pre-harvest sprouting resistance in wheat (*Triticum aestivum* L.)

Adrian L Cabral 1 , 3 Mark C Jordan 1

## **Identification of candidate genes, regions and markers for ...**

Genome-wide identification and analysis of the MADS-box gene family in bread wheat (*Triticum aestivum* L.) The MADS-box genes encode transcription factors with key roles in plant growth and development.

## **Genome-wide identification and analysis of the MADS-box**

...

Identification of genes involved in male sterility in wheat (*Triticum aestivum* L.) which could be used in a genic hybrid breeding system Matthew J. Milner. The John Bingham



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Laboratory, NIAB, Cambridge, UK. Search for more papers by this author. Melanie Craze.

## **Identification of genes involved in male sterility in ...**

Identification and validation of stable quantitative trait loci for grain filling rate in common wheat (*Triticum aestivum* L.) Article in Theoretical and Applied Genetics 133(11) · May 2020 with ...

## **Identification and validation of stable quantitative trait**

...

However, with respect to the larger families of CBLs and CIPKs, few CBL-CIPK complexes have been functionally characterized, especially in bread wheat (*Triticum aestivum* L.), which is one of the most important food crops. Bread wheat has an allohexaploid genome with a size of approximately 17 GB, making it one of the largest and most complex ...

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## **Identification and comprehensive analyses of the CBL and**

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Research article; Open Access; Published: 14 September 2020  
Genome-wide identification and expression analysis of the  
calmodulin-binding transcription activator (CAMTA) gene family  
in wheat (*Triticum aestivum* L.) Fan Yang 1 na1,

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