

Resource Summary Report

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Saskatoon Arabidopsis T-DNA mutant population SK Collection

RRID:SCR_004939

Type: Tool

Proper Citation

Saskatoon Arabidopsis T-DNA mutant population SK Collection (RRID:SCR_004939)

Resource Information

URL: <http://aaafc-aac.usask.ca/fst/>

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Description: Population of almost 50,000 activation tagged Arabidopsis thaliana lines that have been archived as individual lines to the T3 generation. The population is an excellent tool for both reverse and forward genetic screens and has been used successfully to identify a number of novel mutants. Flanking sequence tags (FST) have been generated and mapped for 15,507 lines to enable further application of the population, while providing a clear distribution of T-DNA insertions across the genome. The population is being screened for a number of biochemical and developmental phenotypes. The population provides an additional tool for plant researcher's to assist with determining gene function for the many as yet uncharacterized genes annotated within the Arabidopsis genome sequence. The presence of enhancer elements on the inserted T-DNA element (pSKI015) allows both knock-out and dominant activation phenotypes to be identified for traits of interest.

Abbreviations: SK-FST

Synonyms: SK population

Resource Type: biomaterial supply resource, material resource

Defining Citation: [PMID:19646253](#), [PMID:19347643](#)

Keywords: arabidopsis thaliana, genetics, mutant, biochemical, developmental, phenotype, gene function, flanking sequence tag, trait, t-dna

Funding: AAFC Canadian Crop Genomics Initiative ;
NSERC

Availability: Free, Public

Resource Name: Saskatoon Arabidopsis T-DNA mutant population SK Collection

Resource ID: SCR_004939

Alternate IDs: nlx_91019

Record Creation Time: 20220129T080227+0000

Record Last Update: 20260919T195750+0000

Ratings and Alerts

No rating or validation information has been found for Saskatoon Arabidopsis T-DNA mutant population SK Collection.

No alerts have been found for Saskatoon Arabidopsis T-DNA mutant population SK Collection.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 4 mentions in open access literature.

Listed below are recent publications. The full list is available at [nidm-terms](#) .

Luo Q, et al. (2022) Structural insights into molecular mechanism for N6-adenosine methylation by MT-A70 family methyltransferase METTL4. Nature communications, 13(1), 5636.

Bu Z, et al. (2014) Regulation of arabidopsis flowering by the histone mark readers MRG1/2 via interaction with CONSTANS to modulate FT expression. PLoS genetics, 10(9), e1004617.

Bolle C, et al. (2011) Perspectives on Systematic Analyses of Gene Function in Arabidopsis thaliana: New Tools, Topics and Trends. Current genomics, 12(1), 1.

Robinson SJ, et al. (2009) An archived activation tagged population of Arabidopsis thaliana to facilitate forward genetics approaches. BMC plant biology, 9, 101.