Resource Summary Report

Generated by NIF on Apr 27, 2025

TRIPLES- a database of TRansposon-Insertion Phenotypes Localization and Expression in Saccharomyces

RRID:SCR_005714
Type: Tool

Proper Citation

TRIPLES- a database of TRansposon-Insertion Phenotypes Localization and Expression in Saccharomyces (RRID:SCR_005714)

Resource Information

URL: http://ygac.med.yale.edu

Proper Citation: TRIPLES- a database of TRansposon-Insertion Phenotypes Localization and Expression in Saccharomyces (RRID:SCR_005714)

Description: THIS RESOURCE IS NO LONGER IN SERVICE, documented on July 15, 2013. TRIPLES provides full public access to the data and reagents generated from ongoing functional analysis of the yeast genome. Using a novel transposon-tagging approach, we have analyzed disruption phenotypes, gene expression, and protein localization on a genome-wide scale in Saccharomyces. The data generated from this study may be accessed through our database, TRIPLES ; additionally, all reagents generated in this study are freely available from on-line order forms (linked to TRIPLES as well). multipurpose, mini-transposon, mutant alleles, phenotypes, protein localization, gene expression, Saccharomyces cerevisiae, Web-accessible database, transposon-mutagenized yeast strains, downloaded, tab-delimited, text file, protein localization data, fluorescent micrographs, staining patterns, indirect immunofluorescence analysis of indicated epitope-tagged proteins, subcellular localization of the yeast proteome, visual library, Nucleic Acid Sequence Data Library (GenBank), clone report, graphic map, transposon insertions (represented as flags)

Synonyms: TRIPLES

Resource Type: data or information resource, database

Keywords: fluorescent micrographs, fungus genome, gene expression, genome, clone report, downloaded, genomics, graphic map, indirect immunofluorescence analysis of indicated epitope-tagged proteins, microarray data, mini-transposon, multipurpose, mutant alleles, nucleic acid sequence data library (genbank), phenotypes, protein localization, protein localization data, saccharomyces cerevisiae, staining patterns, subcellular localization of the yeast proteome, tab-delimited, text file, transposon insertions (represented as flags), transposon-mutagenized yeast strains, visual library, web-accessible database, yeast

Funding:

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: TRIPLES- a database of TRansposon-Insertion Phenotypes Localization and Expression in Saccharomyces

Resource ID: SCR_005714

Alternate IDs: nif-0000-03589

Record Creation Time: 20220129T080232+0000

Record Last Update: 20250426T055808+0000

Ratings and Alerts

No rating or validation information has been found for TRIPLES- a database of TRansposon-Insertion Phenotypes Localization and Expression in Saccharomyces.

No alerts have been found for TRIPLES- a database of TRansposon-Insertion Phenotypes Localization and Expression in Saccharomyces.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 3 mentions in open access literature.

Listed below are recent publications. The full list is available at NIF.

Furukawa K, et al. (2011) Efficient construction of homozygous diploid strains identifies genes required for the hyper-filamentous phenotype in Saccharomyces cerevisiae. PloS one, 6(10), e26584.

Marques AC, et al. (2008) Functional diversification of duplicate genes through subcellular adaptation of encoded proteins. Genome biology, 9(3), R54.

Scherens B, et al. (2004) The uses of genome-wide yeast mutant collections. Genome biology, 5(7), 229.