

Resource Summary Report

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EUROpean Saccharomyces Cerevisiae ARchive for Functional Analysis

RRID:SCR_003093

Type: Tool

Proper Citation

EUROpean Saccharomyces Cerevisiae ARchive for Functional Analysis
(RRID:SCR_003093)

Resource Information

URL: <http://www.euroscarf.de/index.php?name=News>

Proper Citation: EUROpean Saccharomyces Cerevisiae ARchive for Functional Analysis
(RRID:SCR_003093)

Description: Archive of yeast strains and plasmids that were generated during various yeast functional analysis projects.

Abbreviations: EUROSCARF

Resource Type: biomaterial supply resource, material resource, organism supplier

Keywords: plasmid, strain, wild type, deletion, tap fusion, degron, orf, functional analysis, yeast

Funding: BMBF ;
European UnionROFAN I and II ;
European yeast industrial platform ;
federal state of Hessen

Availability: Free, Freely available

Resource Name: EUROpean Saccharomyces Cerevisiae ARchive for Functional Analysis

Resource ID: SCR_003093

Alternate IDs: nif-0000-30504

Old URLs: <http://www.uni-frankfurt.de/fb15/mikro/EUROSCARF/indexhtml>

Record Creation Time: 20220129T080217+0000

Ratings and Alerts

No rating or validation information has been found for EUROpean Saccharomyces Cerevisiae ARchive for Functional Analysis.

No alerts have been found for EUROpean Saccharomyces Cerevisiae ARchive for Functional Analysis.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 43 mentions in open access literature.

Listed below are recent publications. The full list is available at [kravitz2](#) .

Cao L, et al. (2025) Molecular characterization of Tetragonia tetragonoides (Pall.) Aquaporin (AQP) members and their roles in the response to combined high salinity-alkalinity-drought and heat stress. BMC plant biology, 25(1), 1488.

Huang Z, et al. (2024) Genome-Wide Identification and Expression Analyses of the Thaumatin-Like Protein Gene Family in Tetragonia tetragonoides (Pall.) Kuntze Reveal Their Functions in Abiotic Stress Responses. Plants (Basel, Switzerland), 13(17).

Liu H, et al. (2023) Identification of the Absciscic Acid-, Stress-, and Ripening-Induced (ASR) Family Involved in the Adaptation of Tetragonia tetragonoides (Pall.) Kuntze to Saline-Alkaline and Drought Habitats. International journal of molecular sciences, 24(21).

Barton RE, et al. (2022) Eco1-dependent cohesin acetylation anchors chromatin loops and cohesion to define functional meiotic chromosome domains. eLife, 11.

Mao P, et al. (2022) Genome-Wide Identification and Functional Characterization of the Chloride Channel TaCLC Gene Family in Wheat (Triticum aestivum L.). Frontiers in genetics, 13, 846795.

Lin R, et al. (2021) Genome-wide identification and expression analysis of aquaporin family in Canavalia rosea and their roles in the adaptation to saline-alkaline soils and drought stress. BMC plant biology, 21(1), 333.

Zheng J, et al. (2021) Ectopic Expression of CrPIP2;3, a Plasma Membrane Intrinsic Protein Gene from the Halophyte Canavalia rosea, Enhances Drought and Salt-Alkali Stress Tolerance in Arabidopsis. International journal of molecular sciences, 22(2).

Zoni V, et al. (2021) Pre-existing bilayer stresses modulate triglyceride accumulation in the ER versus lipid droplets. eLife, 10.

Go?ci?ska K, et al. (2020) Eukaryotic Elongation Factor 3 Protects *Saccharomyces cerevisiae* Yeast from Oxidative Stress. *Genes*, 11(12).

Maitra N, et al. (2020) Translational control of one-carbon metabolism underpins ribosomal protein phenotypes in cell division and longevity. *eLife*, 9.

Blank HM, et al. (2020) Abundances of transcripts, proteins, and metabolites in the cell cycle of budding yeast reveal coordinate control of lipid metabolism. *Molecular biology of the cell*, 31(10), 1069.

Gao Y, et al. (2020) Genome-Wide Identification of Metal Tolerance Protein Genes in *Populus trichocarpa* and Their Roles in Response to Various Heavy Metal Stresses. *International journal of molecular sciences*, 21(5).

Schäfer IB, et al. (2019) Molecular Basis for poly(A) RNP Architecture and Recognition by the Pan2-Pan3 Deadenylase. *Cell*, 177(6), 1619.

Zhang M, et al. (2018) Functional Identification of Salt-Stress-Related Genes Using the FOX Hunting System from *Ipomoea pes-caprae*. *International journal of molecular sciences*, 19(11).

Powles J, et al. (2018) Alternative splice variants of rhomboid proteins: Comparative analysis of database entries for select model organisms and validation of functional potential. *F1000Research*, 7, 139.

Howe FS, et al. (2017) CRISPRi is not strand-specific at all loci and redefines the transcriptional landscape. *eLife*, 6.

Zhang M, et al. (2017) Identification of a rice metal tolerance protein OsMTP11 as a manganese transporter. *PloS one*, 12(4), e0174987.

Krietenstein N, et al. (2016) Genomic Nucleosome Organization Reconstituted with Pure Proteins. *Cell*, 167(3), 709.

Ouyang LL, et al. (2016) Site-Directed Mutagenesis from Arg195 to His of a Microalgal Putatively Chloroplastidial Glycerol-3-Phosphate Acyltransferase Causes an Increase in Phospholipid Levels in Yeast. *Frontiers in plant science*, 7, 286.

Pais P, et al. (2016) Membrane Proteomics Analysis of the *Candida glabrata* Response to 5-Flucytosine: Unveiling the Role and Regulation of the Drug Efflux Transporters CgFlr1 and CgFlr2. *Frontiers in microbiology*, 7, 2045.