

Resource Summary Report

Generated by [NIF](#) on Aug 28, 2026

Bahler Laboratory: Genome Regulation

RRID:SCR_008422

Type: Tool

Proper Citation

Bahler Laboratory: Genome Regulation (RRID:SCR_008422)

Resource Information

URL: http://www.sanger.ac.uk/PostGenomics/S_pombe/

Proper Citation: Bahler Laboratory: Genome Regulation (RRID:SCR_008422)

Description: The laboratory studies global gene expression programs in fission yeast (*S. pombe*). They apply a wide range of integrated approaches to analyse regulatory networks during cell proliferation, differentiation and quiescence including genetic and environmental perturbations. They are also interested in genetic diversity, genome evolution, and the complex interactions between genotypes, phenotypes, and the environment. The relative simplicity of the yeast cell promises a deeply satisfying, systems-level understanding of its inner workings within our life time Sponsors: This research is mainly funded by Cancer Research UK and the EC FP7 PhenOxiGEN project. Keywords: Gene, Expression, *S.pombe*, Yeast, Cell, Proliferation, Differentiation, Environmental, Genetic, Diversity, Genome, Evolution, Genotype, Phenotype, Environment,

Abbreviations: BahlerLab

Synonyms: The Bahler Laboratory: Genome Regulation

Resource Type: data or information resource, laboratory portal, organization portal, portal

Resource Name: Bahler Laboratory: Genome Regulation

Resource ID: SCR_008422

Alternate IDs: nif-0000-30160

Record Creation Time: 20220129T080247+0000

Record Last Update: 20260821T193840+0000

Ratings and Alerts

No rating or validation information has been found for Bahler Laboratory: Genome Regulation.

No alerts have been found for Bahler Laboratory: Genome Regulation.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 9 mentions in open access literature.

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

Tange Y, et al. (2012) The CCR4-NOT complex is implicated in the viability of aneuploid yeasts. PLoS genetics, 8(6), e1002776.

Skjølberg HC, et al. (2009) Global transcriptional response after exposure of fission yeast cells to ultraviolet light. BMC cell biology, 10, 87.

Anders A, et al. (2008) Improved tools for efficient mapping of fission yeast genes: identification of microtubule nucleation modifier mod22-1 as an allele of chromatin-remodelling factor gene swr1. Yeast (Chichester, England), 25(12), 913.

Lackner DH, et al. (2007) A network of multiple regulatory layers shapes gene expression in fission yeast. Molecular cell, 26(1), 145.

Mata J, et al. (2007) Transcriptional regulatory network for sexual differentiation in fission yeast. Genome biology, 8(10), R217.

Rustici G, et al. (2007) Global transcriptional responses of fission and budding yeast to changes in copper and iron levels: a comparative study. Genome biology, 8(5), R73.

Chikashige Y, et al. (2006) Meiotic proteins bqt1 and bqt2 tether telomeres to form the bouquet arrangement of chromosomes. Cell, 125(1), 59.

Hermand D, et al. (2006) F-box proteins: more than baits for the SCF? Cell division, 1, 30.

Rodríguez-Gabriel MA, et al. (2003) RNA-binding protein Csx1 mediates global control of gene expression in response to oxidative stress. The EMBO journal, 22(23), 6256.