

Resource Summary Report

Generated by [NIF](#) on Oct 20, 2026

SwissRegulon

RRID:SCR_005333

Type: Tool

Proper Citation

SwissRegulon (RRID:SCR_005333)

Resource Information

URL: <http://swissregulon.unibas.ch/cgi/sr/swissregulon>

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Description: A database of genome-wide annotations of regulatory sites. The predictions are based on Bayesian probabilistic analysis of a combination of input information including: * Experimentally determined binding sites reported in the literature. * Known sequence-specificities of transcription factors. * ChIP-chip and ChIP-seq data. * Alignments of orthologous non-coding regions. Predictions were made using the PhyloGibbs, MotEvo, IRUS and ISMARA algorithms developed in their group, depending on the data available for each organism. Annotations can be viewed in a Gbrowse genome browser and can also be downloaded in flat file format.

Abbreviations: SwissRegulon

Synonyms: SwissRegulon Database

Resource Type: data or information resource, database

Defining Citation: [PMID:23180783](#), [PMID:17130146](#)

Keywords: genome, binding site, transcription factor, genome-wide annotation, annotation, chip-chip, chip-seq, non-coding region, promoter, motif, transcript, regulatory motif, genome browser, FASEB list

Availability: Acknowledgement requested

Resource Name: SwissRegulon

Resource ID: SCR_005333

Alternate IDs: nif-0000-03524, OMICS_00543

Record Creation Time: 20220129T080229+0000

Record Last Update: 20261017T203324+0000

Ratings and Alerts

No rating or validation information has been found for SwissRegulon.

No alerts have been found for SwissRegulon.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We have not found any literature mentions for this resource.