Resource Summary Report

Generated by dkNET on May 19, 2025

Regulatory Sequence Analysis Tools

RRID:SCR_008560
Type: Tool

Proper Citation

Regulatory Sequence Analysis Tools (RRID:SCR_008560)

Resource Information

URL: http://rsat.ulb.ac.be/rsat/

Proper Citation: Regulatory Sequence Analysis Tools (RRID:SCR_008560)

Description: THIS RESOURCE IS NO LONGER IN SERVICE. Documented on February 28,2023. Retrieve-ensembl-seq is included in the software suite regulatory sequence analysis tools (RSAT), allowing instant submission of retrieved sequences to further analysis tools. AVAILABILITY: retrieve-ensembl-seq is integrated in the RSAT suite: http://rsat.ulb.ac.be/rsat. Web site: http://rsat.ulb.ac.be/rsat/retrieve-ensembl-seq_form.cgi. Web services: http://rsat.ulb.ac.be/rsat/web_services/RSATWS.wsdl. Stand-alone distribution: freely available under an academic licence to download from the RSAT web site. The complete manual, a convenient tutorial and demos are available from the RSAT website. Additional help can be found on the RSAT public forum.

Synonyms: RSAT

Resource Type: database, data or information resource

Defining Citation: DOI:10.1093/nar/gkv362

Keywords: bio.tools, FASEB list

Funding:

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: Regulatory Sequence Analysis Tools

Resource ID: SCR_008560

Alternate IDs: biotools:rsat, nif-0000-31437, OMICS_08097

Alternate URLs: https://bio.tools/rsat

Old URLs: https://sources.debian.org/src/rsat/

Record Creation Time: 20220129T080248+0000

Record Last Update: 20250517T055902+0000

Ratings and Alerts

No rating or validation information has been found for Regulatory Sequence Analysis Tools.

No alerts have been found for Regulatory Sequence Analysis Tools.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 106 mentions in open access literature.

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

Guo A, et al. (2025) The miR3367-lncRNA67-GhCYP724B module regulates male sterility by modulating brassinosteroid biosynthesis and interacting with Aorf27 in Gossypium hirsutum. Journal of integrative plant biology, 67(1), 169.

Chen L, et al. (2022) The Essential Role of OmpR in Acidithiobacillus caldus Adapting to the High Osmolarity and Its Regulation on the Tetrathionate-Metabolic Pathway. Microorganisms, 11(1).

Yoshua SB, et al. (2021) Integration host factor bends and bridges DNA in a multiplicity of binding modes with varying specificity. Nucleic acids research, 49(15), 8684.

Sánchez-Sánchez AV, et al. (2021) The Embryonic Key Pluripotent Factor NANOG Mediates Glioblastoma Cell Migration via the SDF1/CXCR4 Pathway. International journal of molecular sciences, 22(19).

Keffeler EC, et al. (2021) Influence of the Alternative Sigma Factor RpoN on Global Gene Expression and Carbon Catabolism in Enterococcus faecalis V583. mBio, 12(3).

Demircio?lu D, et al. (2019) A Pan-cancer Transcriptome Analysis Reveals Pervasive Regulation through Alternative Promoters. Cell, 178(6), 1465.

Kumar P, et al. (2018) Pivotal role of bZIPs in amylose biosynthesis by genome survey and transcriptome analysis in wheat (Triticum aestivum L.) mutants. Scientific reports, 8(1), 17240.

Sardina JL, et al. (2018) Transcription Factors Drive Tet2-Mediated Enhancer Demethylation to Reprogram Cell Fate. Cell stem cell, 23(5), 727.

Znaidi S, et al. (2018) Systematic gene overexpression in Candida albicans identifies a regulator of early adaptation to the mammalian gut. Cellular microbiology, 20(11), e12890.

He BZ, et al. (2017) Evolution of reduced co-activator dependence led to target expansion of a starvation response pathway. eLife, 6.

Karijolich J, et al. (2017) Genome-wide mapping of infection-induced SINE RNAs reveals a role in selective mRNA export. Nucleic acids research, 45(10), 6194.

Reimegård J, et al. (2017) Genome-wide identification of physically clustered genes suggests chromatin-level co-regulation in male reproductive development in Arabidopsis thaliana. Nucleic acids research, 45(6), 3253.

Lin C, et al. (2017) YAP is essential for mechanical force production and epithelial cell proliferation during lung branching morphogenesis. eLife, 6.

Tardu M, et al. (2017) MerR and ChrR mediate blue light induced photo-oxidative stress response at the transcriptional level in Vibrio cholerae. Scientific reports, 7, 40817.

Chattopadhyay I, et al. (2017) Src promotes castration-recurrent prostate cancer through androgen receptor-dependent canonical and non-canonical transcriptional signatures. Oncotarget, 8(6), 10324.

Navarro-Tapia E, et al. (2016) Ethanol Cellular Defense Induce Unfolded Protein Response in Yeast. Frontiers in microbiology, 7, 189.

Anderson BR, et al. (2016) Identification of consensus binding sites clarifies FMRP binding determinants. Nucleic acids research, 44(14), 6649.

Conteduca G, et al. (2016) AIRE polymorphism, melanoma antigen-specific T cell immunity, and susceptibility to melanoma. Oncotarget, 7(38), 60872.

Salazar-Henao JE, et al. (2016) Discriminative gene co-expression network analysis uncovers novel modules involved in the formation of phosphate deficiency-induced root hairs in Arabidopsis. Scientific reports, 6, 26820.

Marbach-Bar N, et al. (2016) DTIE, a novel core promoter element that directs start site selection in TATA-less genes. Nucleic acids research, 44(3), 1080.