## **Resource Summary Report**

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# **Systems Transcriptional Activity Reconstruction**

RRID:SCR\_005622 Type: Tool

### **Proper Citation**

Systems Transcriptional Activity Reconstruction (RRID:SCR\_005622)

### **Resource Information**

URL: http://tabit.ucsd.edu/sdec/

Proper Citation: Systems Transcriptional Activity Reconstruction (RRID:SCR\_005622)

**Description:** A next-generation web-based application that aims to provide an integrated solution for both visualization and analysis of deep-sequencing data, along with simple access to public datasets.

Abbreviations: STAR

**Synonyms:** Systems Transcriptional Activity Reconstruction Genome Browser, Systems Transcriptional Activity Reconstruction, STAR Genome Browser

Resource Type: data or information resource, database, service resource

Keywords: genome browser, genome, next generation sequence, visualization, FASEB list

#### Funding:

Availability: Account required, Or Guest login

Resource Name: Systems Transcriptional Activity Reconstruction

Resource ID: SCR\_005622

Alternate IDs: OMICS\_00895

**Record Creation Time:** 20220129T080231+0000

Record Last Update: 20250426T055803+0000

### **Ratings and Alerts**

No rating or validation information has been found for Systems Transcriptional Activity Reconstruction.

No alerts have been found for Systems Transcriptional Activity Reconstruction.

### Data and Source Information

Source: SciCrunch Registry

### **Usage and Citation Metrics**

We found 6465 mentions in open access literature.

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

Dibra D, et al. (2024) Mutant p53 protects triple-negative breast adenocarcinomas from ferroptosis in vivo. Science advances, 10(7), eadk1835.

Jamal T, et al. (2024) Experience-dependent regulation of dopaminergic signaling in the somatosensory cortex. Progress in neurobiology, 239, 102630.

Sun N, et al. (2024) Establishing a 3D culture system for early organogenesis of monkey embryos ex vivo and single-cell transcriptome analysis of cultured embryos. STAR protocols, 5(1), 102835.

Lancaster MS, et al. (2023) Loss of succinyl-CoA synthetase in mouse forebrain results in hypersuccinylation with perturbed neuronal transcription and metabolism. Cell reports, 42(10), 113241.

Podmore L, et al. (2023) Insulin receptor loss impairs mammary tumorigenesis in mice. Cell reports, 42(11), 113251.

Hsieh YP, et al. (2022) Single-Cell RNA Sequencing Analysis for Oncogenic Mechanisms Underlying Oral Squamous Cell Carcinoma Carcinogenesis with Candida albicans Infection. International journal of molecular sciences, 23(9).

Ta AC, et al. (2022) Temporal and spatial transcriptomic dynamics across brain development in Xenopus laevis tadpoles. G3 (Bethesda, Md.), 12(1).

Wesolowski R, et al. (2021) Myeloid transformation by MLL-ENL depends strictly on C/EBP. Life science alliance, 4(1).

Shoguchi E, et al. (2021) A New Dinoflagellate Genome Illuminates a Conserved Gene Cluster Involved in Sunscreen Biosynthesis. Genome biology and evolution, 13(2).

Craig-Schapiro R, et al. (2021) COVID-19 outcomes in patients waitlisted for kidney transplantation and kidney transplant recipients. American journal of transplantation : official journal of the American Society of Transplantation and the American Society of Transplant Surgeons, 21(4), 1576.

Luo X, et al. (2021) RMVar: an updated database of functional variants involved in RNA modifications. Nucleic acids research, 49(D1), D1405.

Worthington M, et al. (2021) A new genome allows the identification of genes associated with natural variation in aluminium tolerance in Brachiaria grasses. Journal of experimental botany, 72(2), 302.

Baschnagel AM, et al. (2021) Development and characterization of patient-derived xenografts from non-small cell lung cancer brain metastases. Scientific reports, 11(1), 2520.

Bruno M, et al. (2021) Comparative host transcriptome in response to pathogenic fungi identifies common and species-specific transcriptional antifungal host response pathways. Computational and structural biotechnology journal, 19, 647.

Himeda CL, et al. (2021) Targeted epigenetic repression by CRISPR/dSaCas9 suppresses pathogenic DUX4-fl expression in FSHD. Molecular therapy. Methods & clinical development, 20, 298.

Fibi-Smetana S, et al. (2021) Research Note: Snapshot of the transcriptome via RNA sequencing in the ileum of broiler chickens fed subtherapeutic concentrations of avilamycin. Poultry science, 100(2), 998.

Monticolo F, et al. (2021) Translation machinery reprogramming in programmed cell death in Saccharomyces cerevisiae. Cell death discovery, 7(1), 17.

Wang W, et al. (2021) Multiregion single-cell sequencing reveals the transcriptional landscape of the immune microenvironment of colorectal cancer. Clinical and translational medicine, 11(1), e253.

Chen LP, et al. (2021) Model-based forecasting for Canadian COVID-19 data. PloS one, 16(1), e0244536.

Klees S, et al. (2021) In Silico Identification of the Complex Interplay between Regulatory SNPs, Transcription Factors, and Their Related Genes in Brassica napus L. Using Multi-Omics Data. International journal of molecular sciences, 22(2).