Resource Summary Report

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ROSE

RRID:SCR_017390
Type: Tool

Proper Citation

ROSE (RRID:SCR_017390)

Resource Information

URL: http://younglab.wi.mit.edu/super_enhancer_code.html

Proper Citation: ROSE (RRID:SCR_017390)

Description: To create stitched enhancers, and to separate super enhancers from typical enhancers using sequencing data given file of previously identified constituent enhancers .

Abbreviations: ROSE

Synonyms: Rank Ordering of Super Enhancers, RANK ORDERING OF SUPER-ENHANCERS

Resource Type: software resource, software application, data processing software

Keywords: Stitched, enhancer, separate, super, sequencing, data, file, identified, previously, constituent

Funding:

Availability: Free, Freely available

Resource Name: ROSE

Resource ID: SCR_017390

License: MIT X11 License

Record Creation Time: 20220129T080335+0000

Record Last Update: 20250411T055941+0000

Ratings and Alerts

No rating or validation information has been found for ROSE.

No alerts have been found for ROSE.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 52 mentions in open access literature.

Listed below are recent publications. The full list is available at FDI Lab - SciCrunch.org.

Cigrang M, et al. (2025) Pan-inhibition of super-enhancer-driven oncogenic transcription by next-generation synthetic ecteinascidins yields potent anti-cancer activity. Nature communications, 16(1), 512.

Kaufman ME, et al. (2024) Characterizing Relationships between T-cell Inflammation and Outcomes in Patients with High-Risk Neuroblastoma According to Mesenchymal and Adrenergic Signatures. Cancer research communications, 4(8), 2255.

Prutsch N, et al. (2024) STAT3 couples activated tyrosine kinase signaling to the oncogenic core transcriptional regulatory circuitry of anaplastic large cell lymphoma. Cell reports. Medicine, 5(3), 101472.

Abeywardana T, et al. (2024) Regulation of Enhancers by SUMOylation Through TFAP2C Binding and Recruitment of HDAC Complex to the Chromatin. Research square.

Shan L, et al. (2024) SP1 undergoes phase separation and activates RGS20 expression through super-enhancers to promote lung adenocarcinoma progression. Proceedings of the National Academy of Sciences of the United States of America, 121(29), e2401834121.

Wei X, et al. (2024) Super-enhancer-driven ZFP36L1 promotes PD-L1 expression in infiltrative gastric cancer. eLife, 13.

Obinata D, et al. (2024) Patient-derived castration-resistant prostate cancer model revealed CTBP2 upregulation mediated by OCT1 and androgen receptor. BMC cancer, 24(1), 554.

Weng Y, et al. (2024) Zfp260 choreographs the early stage osteo-lineage commitment of skeletal stem cells. Nature communications, 15(1), 10186.

Likasitwatanakul P, et al. (2024) Chemical perturbations impacting histone acetylation govern colorectal cancer differentiation. bioRxiv : the preprint server for biology.

Hamamoto R, et al. (2023) Analysis of super-enhancer using machine learning and its application to medical biology. Briefings in bioinformatics, 24(3).

Kim M, et al. (2023) Super-enhancer-associated transcription factors collaboratively regulate trophoblast-active gene expression programs in human trophoblast stem cells. Nucleic acids research, 51(8), 3806.

Tanaka M, et al. (2023) HEY1-NCOA2 expression modulates chondrogenic differentiation and induces mesenchymal chondrosarcoma in mice. JCI insight, 8(10).

Youngblood MW, et al. (2023) Super-enhancer hijacking drives ectopic expression of hedgehog pathway ligands in meningiomas. Nature communications, 14(1), 6279.

Tanaka M, et al. (2023) ASPSCR1::TFE3 orchestrates the angiogenic program of alveolar soft part sarcoma. Nature communications, 14(1), 1957.

Mohan DR, et al. (2023) ?-Catenin-Driven Differentiation Is a Tissue-Specific Epigenetic Vulnerability in Adrenal Cancer. Cancer research, 83(13), 2123.

Singh DK, et al. (2023) 5-Azacytidine- and retinoic-acid-induced reprogramming of DCCs into dormancy suppresses metastasis via restored TGF-?-SMAD4 signaling. Cell reports, 42(6), 112560.

Durbin AD, et al. (2022) EP300 Selectively Controls the Enhancer Landscape of MYCN-Amplified Neuroblastoma. Cancer discovery, 12(3), 730.

Hsu JY, et al. (2022) SIX1 reprograms myogenic transcription factors to maintain the rhabdomyosarcoma undifferentiated state. Cell reports, 38(5), 110323.

Panditharatna E, et al. (2022) BAF Complex Maintains Glioma Stem Cells in Pediatric H3K27M Glioma. Cancer discovery, 12(12), 2880.

Tang S, et al. (2022) A genome-scale CRISPR screen reveals PRMT1 as a critical regulator of androgen receptor signaling in prostate cancer. Cell reports, 38(8), 110417.