Resource Summary Report

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Stem Cell Discovery Engine

RRID:SCR_004453
Type: Tool

Proper Citation

Stem Cell Discovery Engine (RRID:SCR_004453)

Resource Information

URL: http://discovery.hsci.harvard.edu/

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Description: An online database of curated cancer stem cell (CSC) experiments coupled to the Galaxy analytical framework. Driven by a need to improve our understanding of molecular processes that are common and unique across cancer stem cells (CSCs), the SCDE allows users to consistently describe, share and compare CSC data at the gene and pathway level. The initial focus has been on carefully curating tissue and cancer stem cell-related experiments from blood, intestine and brain to create a high quality resource containing 53 public studies and 1098 assays. The experimental information is captured and stored in the multi-omics Investigation/Study/Assay (ISA-Tab) format and can be queried in the data repository. A linked Galaxy framework provides a comprehensive, flexible environment populated with novel tools for gene list comparisons against molecular signatures in GeneSigDB and MSigDB, curated experiments in the SCDE and pathways in WikiPathways. Investigation/Study/Assay (ISA) infrastructure is the first general-purpose format and freely available desktop software suite targeted to experimentalists, curators and developers and that: * assists in the reporting and local management of experimental metadata (i.e. sample characteristics, technology and measurement types, sample-to-data relationships) from studies employing one or a combination of technologies; * empowers users to uptake community-defined minimum information checklists and ontologies, where required; * formats studies for submission to a growing number of international public repositories endorsing the tools, currently ENA (genomics), PRIDE (proteomics) and ArrayExpress (transcriptomics). Galaxy allows you to do analyses you cannot do anywhere else without the need to install or download anything. You can analyze multiple alignments, compare genomic annotations, profile metagenomic samples and much much more. Best of all, Galaxy""s history system provides a complete analyses record that can be shared. Every history is an analysis workflow, which can be used to reproduce the entire experiment. The code for this Galaxy instance is available for download from BitBucket.

Abbreviations: SCDE

Synonyms: Harvard Stem Cell Discovery Engine, SCDE - Stem Cell Discovery Engine

Resource Type: source code, service resource, production service resource, database, analysis service resource, data or information resource, software resource, storage service resource, data repository

Defining Citation: PMID:22121217

Keywords: stem cell, analysis, cancer stem cell, galaxy, gene, pathway, molecular signature, tissue, bio.tools, FASEB list

Related Condition: Cancer

Funding: NCI 1RC2CA148222-01

Availability: Free, The community can contribute to this resource

Resource Name: Stem Cell Discovery Engine

Resource ID: SCR_004453

Alternate IDs: biotools:scde_discovery, nlx_44656

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

Record Creation Time: 20220129T080224+0000

Record Last Update: 20250517T055640+0000

Ratings and Alerts

No rating or validation information has been found for Stem Cell Discovery Engine.

No alerts have been found for Stem Cell Discovery Engine.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 57 mentions in open access literature.

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

Xue J, et al. (2024) Comparative study on differential expression analysis methods for single-cell RNA sequencing data with small biological replicates: Based on single-cell transcriptional data of PBMCs from COVID-19 severe patients. PloS one, 19(3), e0299358.

Bose A, et al. (2024) Increased heterogeneity in expression of genes associated with cancer progression and drug resistance. Translational oncology, 41, 101879.

Reuter C, et al. (2023) Vector-borne Trypanosoma brucei parasites develop in artificial human skin and persist as skin tissue forms. Nature communications, 14(1), 7660.

Reinhardt J, et al. (2022) Distinguishing activated T regulatory cell and T conventional cells by single-cell technologies. Immunology, 166(1), 121.

Huang S, et al. (2021) Lymph nodes are innervated by a unique population of sensory neurons with immunomodulatory potential. Cell, 184(2), 441.

Chen J, et al. (2021) DeepDRIM: a deep neural network to reconstruct cell-type-specific gene regulatory network using single-cell RNA-seq data. Briefings in bioinformatics, 22(6).

Taftaf R, et al. (2021) ICAM1 initiates CTC cluster formation and trans-endothelial migration

in lung metastasis of breast cancer. Nature communications, 12(1), 4867.

Hagey DW, et al. (2020) CYCLIN-B1/2 and -D1 act in opposition to coordinate cortical progenitor self-renewal and lineage commitment. Nature communications, 11(1), 2898.

Vargo AHS, et al. (2020) A rank-based marker selection method for high throughput scRNA-seq data. BMC bioinformatics, 21(1), 477.

Nelson L, et al. (2020) A living biobank of ovarian cancer ex vivo models reveals profound mitotic heterogeneity. Nature communications, 11(1), 822.

Simon LM, et al. (2020) DrivAER: Identification of driving transcriptional programs in single-cell RNA sequencing data. GigaScience, 9(12).

Ramirez AK, et al. (2020) Single-cell transcriptional networks in differentiating preadipocytes suggest drivers associated with tissue heterogeneity. Nature communications, 11(1), 2117.

Ziegler CGK, et al. (2020) SARS-CoV-2 Receptor ACE2 Is an Interferon-Stimulated Gene in Human Airway Epithelial Cells and Is Detected in Specific Cell Subsets across Tissues. Cell, 181(5), 1016.

Mizrak D, et al. (2020) Single-Cell Profiling and SCOPE-Seq Reveal Lineage Dynamics of Adult Ventricular-Subventricular Zone Neurogenesis and NOTUM as a Key Regulator. Cell reports, 31(12), 107805.

Finkelstein J, et al. (2020) Informatics Approaches for Harmonized Intelligent Integration of Stem Cell Research. Stem cells and cloning : advances and applications, 13, 1.

Plemel JR, et al. (2020) Microglia response following acute demyelination is heterogeneous and limits infiltrating macrophage dispersion. Science advances, 6(3), eaay6324.

Mu T, et al. (2020) Embryonic liver developmental trajectory revealed by single-cell RNA sequencing in the Foxa2eGFP mouse. Communications biology, 3(1), 642.

Neri T, et al. (2019) Human pre-valvular endocardial cells derived from pluripotent stem cells recapitulate cardiac pathophysiological valvulogenesis. Nature communications, 10(1), 1929.

Pang L, et al. (2019) Discovering Rare Genes Contributing to Cancer Stemness and Invasive Potential by GBM Single-Cell Transcriptional Analysis. Cancers, 11(12).

Fuchs YF, et al. (2019) Gene Expression-Based Identification of Antigen-Responsive CD8+ T Cells on a Single-Cell Level. Frontiers in immunology, 10, 2568.