Resource Summary Report

Generated by dkNET on May 18, 2025

GeneProf

RRID:SCR_012927
Type: Tool

Proper Citation

GeneProf (RRID:SCR_012927)

Resource Information

URL: http://www.geneprof.org/GeneProf/

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Description: A database of curated, integrated and reusable high-throughput genomics experiments and a web-based, graphical software suite that allows users to analyse data produced using high-throughput sequencing platforms (RNA-seq and ChIP-seq; Next-Generation Sequencing or NGS). Algorithm developers and computer programmers can develop their own modules and extend the functionality of GeneProf. Existing software can be easily wrapped and integrated in the GeneProf framework and data from GeneProf may be used externally.

Abbreviations: GeneProf

Resource Type: data access protocol, service resource, production service resource, data analysis service, database, analysis service resource, data or information resource, web service, software resource

Defining Citation: PMID:22205509, PMID:24174536

Keywords: next-generation sequencing, bio.tools

Funding: MRC ;
European Union Framework 7 Project EuroSyStem

Availability: Acknowledgement requested

Resource Name: GeneProf

Resource ID: SCR_012927

Alternate IDs: biotools:geneprof, OMICS_00442

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

Record Creation Time: 20220129T080313+0000

Record Last Update: 20250517T060053+0000

Ratings and Alerts

No rating or validation information has been found for GeneProf.

No alerts have been found for GeneProf.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 15 mentions in open access literature.

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

Bruedigam C, et al. (2023) Gene Expression Analyses in Models of Rosiglitazone-Induced Physiological and Pathological Mineralization Identify Novel Targets to Improve Bone and Vascular Health. Cells, 12(20).

Festuccia N, et al. (2018) Esrrb extinction triggers dismantling of naïve pluripotency and marks commitment to differentiation. The EMBO journal, 37(21).

Ansen-Wilson LJ, et al. (2018) Common basis for orofacial clefting and cortical interneuronopathy. Translational psychiatry, 8(1), 8.

Qu J, et al. (2018) Mutant p63 Affects Epidermal Cell Identity through Rewiring the Enhancer Landscape. Cell reports, 25(12), 3490.

Buckle A, et al. (2018) Functional characteristics of novel pancreatic Pax6 regulatory elements. Human molecular genetics, 27(19), 3434.

McGarvey AC, et al. (2017) A molecular roadmap of the AGM region reveals BMPER as a novel regulator of HSC maturation. The Journal of experimental medicine, 214(12), 3731.

Corsinotti A, et al. (2017) Distinct SoxB1 networks are required for naïve and primed

pluripotency. eLife, 6.

Leach DA, et al. (2017) Cell-lineage specificity and role of AP-1 in the prostate fibroblast androgen receptor cistrome. Molecular and cellular endocrinology, 439, 261.

Mazzara PG, et al. (2017) Two factor-based reprogramming of rodent and human fibroblasts into Schwann cells. Nature communications, 8, 14088.

Hildebrand EM, et al. (2016) Regulation of Budding Yeast CENP-A levels Prevents Misincorporation at Promoter Nucleosomes and Transcriptional Defects. PLoS genetics, 12(3), e1005930.

Nazarieh M, et al. (2016) Identification of key player genes in gene regulatory networks. BMC systems biology, 10(1), 88.

Yuan D, et al. (2015) Enrichment Analysis Identifies Functional MicroRNA-Disease Associations in Humans. PloS one, 10(8), e0136285.

Kumar N, et al. (2015) Genome-wide endogenous DAF-16/FOXO recruitment dynamics during lowered insulin signalling in C. elegans. Oncotarget, 6(39), 41418.

Morrison VL, et al. (2014) Loss of beta2-integrin-mediated cytoskeletal linkage reprogrammes dendritic cells to a mature migratory phenotype. Nature communications, 5, 5359.

Boria I, et al. (2013) NGS-Trex: Next Generation Sequencing Transcriptome profile explorer. BMC bioinformatics, 14 Suppl 7(Suppl 7), S10.