Resource Summary Report

Generated by NIF on May 25, 2025

FastQ Screen

RRID:SCR_000141
Type: Tool

Proper Citation

FastQ Screen (RRID:SCR_000141)

Resource Information

URL: http://www.bioinformatics.babraham.ac.uk/projects/fastq_screen/

Proper Citation: FastQ Screen (RRID:SCR_000141)

Description: Software that allows you to screen a library of sequences in FastQ format against a set of sequence databases so you can see if the composition of the library matches with what you expect.

Abbreviations: FastQ Screen

Resource Type: software resource

Defining Citation: PMID:30254741

Keywords: perl, FASEB list

Funding:

Availability: Free, Freely available

Resource Name: FastQ Screen

Resource ID: SCR_000141

Alternate IDs: OMICS_01042

License: GNU General Public License, v3 or later

Record Creation Time: 20220129T080159+0000

Record Last Update: 20250525T030524+0000

Ratings and Alerts

No rating or validation information has been found for FastQ Screen.

No alerts have been found for FastQ Screen.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 41 mentions in open access literature.

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

Rachubinski AL, et al. (2024) JAK inhibition decreases the autoimmune burden in Down syndrome. eLife, 13.

Wong CH, et al. (2024) Genome-scale requirements for dynein-based transport revealed by a high-content arrayed CRISPR screen. The Journal of cell biology, 223(5).

Tapia Contreras C, et al. (2024) KRASG 12C-inhibitor-based combination therapies for pancreatic cancer: insights from drug screening. Molecular oncology.

Gargiulo E, et al. (2023) Extracellular Vesicle Secretion by Leukemia Cells In Vivo Promotes CLL Progression by Hampering Antitumor T-cell Responses. Blood cancer discovery, 4(1), 54.

Ludwig MP, et al. (2023) Proteasome Inhibition Sensitizes Liposarcoma to MDM2 Inhibition with Nutlin-3 by Activating the ATF4/CHOP Stress Response Pathway. Cancer research, 83(15), 2543.

Qi W, et al. (2022) The haplotype-resolved chromosome pairs of a heterozygous diploid African cassava cultivar reveal novel pan-genome and allele-specific transcriptome features. GigaScience, 11.

Hunter AL, et al. (2022) HNF4A modulates glucocorticoid action in the liver. Cell reports, 39(3), 110697.

Cheng N, et al. (2022) STAG2 promotes the myelination transcriptional program in oligodendrocytes. eLife, 11.

Sullivan KD, et al. (2021) The COVIDome Explorer researcher portal. Cell reports, 36(7), 109527.

Galbraith MD, et al. (2021) Seroconversion stages COVID19 into distinct pathophysiological

states. eLife, 10.

Mordaunt CE, et al. (2020) Cord blood DNA methylome in newborns later diagnosed with autism spectrum disorder reflects early dysregulation of neurodevelopmental and X-linked genes. Genome medicine, 12(1), 88.

Stanney W, et al. (2020) Combinatorial action of NF-Y and TALE at embryonic enhancers defines distinct gene expression programs during zygotic genome activation in zebrafish. Developmental biology, 459(2), 161.

Domenger C, et al. (2018) RNA-Seq Analysis of an Antisense Sequence Optimized for Exon Skipping in Duchenne Patients Reveals No Off-Target Effect. Molecular therapy. Nucleic acids, 10, 277.

Masson F, et al. (2018) In Vitro Culture of the Insect Endosymbiont Spiroplasma poulsonii Highlights Bacterial Genes Involved in Host-Symbiont Interaction. mBio, 9(2).

Simões-Sousa S, et al. (2018) The p38? Stress Kinase Suppresses Aneuploidy Tolerance by Inhibiting Hif-1?. Cell reports, 25(3), 749.

Maddaloni G, et al. (2018) Serotonin depletion causes valproate-responsive manic-like condition and increased hippocampal neuroplasticity that are reversed by stress. Scientific reports, 8(1), 11847.

Cazet AS, et al. (2018) Targeting stromal remodeling and cancer stem cell plasticity overcomes chemoresistance in triple negative breast cancer. Nature communications, 9(1), 2897.

Grand Moursel L, et al. (2018) Brain Transcriptomic Analysis of Hereditary Cerebral Hemorrhage With Amyloidosis-Dutch Type. Frontiers in aging neuroscience, 10, 102.

Lasecka-Dykes L, et al. (2018) Full Genome Sequencing Reveals New Southern African Territories Genotypes Bringing Us Closer to Understanding True Variability of Foot-and-Mouth Disease Virus in Africa. Viruses, 10(4).

Maixner F, et al. (2018) The Iceman's Last Meal Consisted of Fat, Wild Meat, and Cereals. Current biology : CB, 28(14), 2348.