Resource Summary Report

Generated by Kravitz on Sep 10, 2026

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

Availability: Free, Available for download, 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: 20260905T132414+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 50 mentions in open access literature.

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

Thege FI, et al. (2026) An autochthonous CRISPR activation screening platform for characterizing tissue-specific oncogene selection. Cell reports. Medicine, 7(5), 102759.

Dunn LN, et al. (2026) Altered hepatic metabolism in Down syndrome. Cell reports, 45(1), 116835.

Mariancini A, et al. (2026) IL1R2 Deficiency Unleashes Neutrophil-Mediated Antitumor Potential in Sarcoma. Cancer immunology research, 14(5), 751.

Miller CN, et al. (2025) A single-nuclei transcriptome census of the Arabidopsis maturing root identifies that MYB67 controls phellem cell maturation. Developmental cell, 60(9), 1377.

Tighe A, et al. (2025) Screening a living biobank identifies cabazitaxel as a strategy to combat acquired taxol resistance in high-grade serous ovarian cancer. Cell reports. Medicine, 6(6), 102160.

Littler S, et al. (2025) Targeting SUMOylation in ovarian cancer: Sensitivity, resistance, and the role of MYC. iScience, 28(6), 112555.

Stupichev D, et al. (2025) AI-driven multimodal algorithm predicts immunotherapy and targeted therapy outcomes in clear cell renal cell carcinoma. Cell reports. Medicine, 6(8), 102299.

Araya P, et al. (2025) Interferon signaling modulates Down syndrome-associated Alzheimer's disease pathology in a mouse model. iScience, 28(8), 113130.

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

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).

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

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.

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.

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.

Petrillo M, et al. (2022) Evidence of SARS-CoV-2 bacteriophage potential in human gut microbiota. F1000Research, 11, 292.

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.

Galbraith MD, et al. (2021) Seroconversion stages COVID19 into distinct pathophysiological states. eLife, 10.

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

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.