

Resource Summary Report

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MAGeCK

RRID:SCR_025016

Type: Tool

Proper Citation

MAGeCK (RRID:SCR_025016)

Resource Information

URL: <https://sourceforge.net/p/mageck/wiki/Home/>

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Description: Software tool to identify important genes from genome-scale CRISPR-Cas9 screens. Used for prioritizing single-guide RNAs, genes and pathways in genome-scale CRISPR/Cas9 knockout screens.

Synonyms: Model-based Analysis of Genome-wide CRISPR-Cas9 Knockout

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

Defining Citation: [PMID:25476604](#)

Keywords: identify genes, genome scale CRISPR-Cas9 screens,

Funding: NIGMS R01 GM099409;
Dana-Farber Cancer Institute

Availability: Free, Available for download, Freely available

Resource Name: MAGeCK

Resource ID: SCR_025016

Alternate URLs: <https://github.com/liulab-dfci/MAGeCK>

License: 3-clause Berkeley Software Distribution

Record Creation Time: 20240221T003954+0000

Record Last Update: 20260811T043746+0000

Ratings and Alerts

No rating or validation information has been found for MAGeCK.

No alerts have been found for MAGeCK.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 232 mentions in open access literature.

Listed below are recent publications. The full list is available at [dkNET](#) .

Long X, et al. (2026) Targeting the host factor HGS-viral membrane protein interaction in coronavirus infection. *The Journal of clinical investigation*, 136(5).

Nguyen QV, et al. (2026) Genome-wide CRISPR screens in primary human natural killer cells identify countermeasures against immunosuppressive environment. *Nature communications*, 17(1).

Shokri L, et al. (2026) STAR Protocols question-and-answer series: CRISPR. *STAR protocols*, 7(3), 104600.

de la Rosa C, et al. (2026) In vivo CRISPR screen reveals regulation of macrophage states in neuroinflammation. *Nature neuroscience*, 29(2), 493.

Shi P, et al. (2026) Decoding the MYC locus reveals a druggable ultraconserved RNA element. *bioRxiv : the preprint server for biology*.

Maeda M, et al. (2026) CRISPR screen of human pancreatic cancer xenografts identifies a KLF5 proliferation vulnerability through epigenetic modifiers NCAPD2 and MTHFD1. *Molecular cancer*, 25(1).

Streicher F, et al. (2026) Type I and III interferon responses restrict infection by tick-borne orthoflaviviruses through IFI6. *Journal of virology*, 100(5), e0076025.

Nyberg WA, et al. (2026) In vivo site-specific engineering to reprogram T cells. *Nature*, 652(8110), 712.

Sun D, et al. (2026) In vivo interrogation of transcriptional and epigenetic regulators of lung epithelial regeneration. *bioRxiv : the preprint server for biology*.

Fernandez Garcia M, et al. (2026) Transcriptomic and phenotypic convergence of neurodevelopmental disorder risk genes in vitro and in vivo. *Nature neuroscience*, 29(5), 1079.

Ly D, et al. (2026) Genome-wide screening reveals producer-cell modifications that improve virus-like particle production and delivery potency. *Nature communications*, 17(1).

Xu F, et al. (2026) Convergent targeting of FUNDC1-dependent mitophagy sensitises and overcomes resistance to EGFR inhibition. *Clinical and translational medicine*, 16(5), e70685.

Xu L, et al. (2026) A Bayesian-Based Integrative Bioinformatics Analysis Nominates Oncogenic Drivers in Neuroblastoma. *Clinical and translational science*, 19(6), e70627.

Chen J, et al. (2026) TOPK Inhibition Promotes Anti-Tumor Immunity Via eIF4F Complex Mediated STAT1 Translation in Gastric Cancer. *Advanced science (Weinheim, Baden-Wurttemberg, Germany)*, 13(13), e17380.

Dogan H, et al. (2026) MDC1 counteracts replication fork reversal and mediates chemosensitivity in BRCA1/2-deficient tumors. *Oncogene*, 45(4), 491.

Drepanos LM, et al. (2026) Balancing off-target and on-target considerations for optimized CRISPR-Cas9 knockout library design. *Cell genomics*, 6(5), 101190.

Price JDW, et al. (2026) Epigenetic control of telomeric RNA maintains heterochromatin in telomerase-driven cancers. *Signal transduction and targeted therapy*, 11(1).

Tanka AT, et al. (2026) Integrative CRISPR Screening and RNA Analyses Discover an Essential Role for PUF60 Interactions with 3' Splice Sites in Cancer Progression. *Cancer research*, 86(7), 1586.

Saini A, et al. (2026) Cell type-specific enhancers regulate IL-22 expression in innate and adaptive type 3 lymphoid cells. *Nature communications*, 17(1).

Zhang H, et al. (2026) Development of a split-toxin CRISPR screening platform to systematically identify regulators of human myoblast fusion. *Nature communications*, 17(1), 547.