

Resource Summary Report

Generated by [NIF](#) on Sep 17, 2026

Liftoff

RRID:SCR_026535

Type: Tool

Proper Citation

Liftoff (RRID:SCR_026535)

Resource Information

URL: <https://github.com/agshumate/Liftoff>

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Description: Software genome annotation lift-over tool capable of mapping genes between two assemblies of the same or closely related species. Aligns genes from reference genome to target genome and finds the mapping that maximizes sequence identity while preserving the structure of each exon, transcript and gene. Used for accurate mapping of gene annotations.

Resource Type: software resource, source code

Defining Citation: [PMID:33320174](#)

Keywords: Aligns genes, reference genome to target genome alignment, mapping of gene annotations, genome annotation lift-over, mapping genes between two assemblies of species, mapping genes, same or closely related species,

Funding: NHGRI R01 HG006677;
NIGMS R35 GM130151

Availability: Free, Available for download, Freely available

Resource Name: Liftoff

Resource ID: SCR_026535

License: GNU GPN v3

Record Creation Time: 20250307T060316+0000

Record Last Update: 20260912T200506+0000

Ratings and Alerts

No rating or validation information has been found for Liftoff.

No alerts have been found for Liftoff.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 10 mentions in open access literature.

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

Corrigan EK, et al. (2025) Conservation and alteration of mammalian striatal interneurons. *Nature*, 647(8088), 187.

Veith AC, et al. (2025) The draft genome of the Wisconsin Miniature SwineTM, a valuable biomedical research tool. *G3 (Bethesda, Md.)*, 15(6).

Irwin D, et al. (2025) The Distribution and Dispersal of Large Haploblocks in a Superspecies. *Molecular ecology*, 34(21), e17731.

Corda L, et al. (2025) Cell line-matched reference enables high-precision functional genomics. *Nature communications*, 16(1), 11194.

Dauban L, et al. (2025) Interactions between the genome and the nuclear lamina are multivalent and cooperative. *Nature structural & molecular biology*, 32(11), 2335.

Parker MT, et al. (2025) Scalable eQTL mapping using single-nucleus RNA-sequencing of recombined gametes from a small number of individuals. *PLoS biology*, 23(4), e3003085.

Movilli A, et al. (2025) Long-read detection of transposable element mobilization in the soma of hypomethylated *Arabidopsis thaliana* individuals. *Genome biology*, 26(1), 231.

Volpe E, et al. (2025) The reference genome of the human diploid cell line RPE-1. *Nature communications*, 16(1), 7751.

Jayakody TB, et al. (2024) Genome-wide evaluation of gene editing outcomes using CRISPR/Cas9 in seed propagated *Camelina sativa* and vegetatively propagated *Solanum tuberosum*. *Frontiers in plant science*, 15, 1496861.

Davenport KM, et al. (2022) An improved ovine reference genome assembly to facilitate in-depth functional annotation of the sheep genome. *GigaScience*, 11.