

Resource Summary Report

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CrossMap

RRID:SCR_001173

Type: Tool

Proper Citation

CrossMap (RRID:SCR_001173)

Resource Information

URL: <http://crossmap.sourceforge.net/>

Proper Citation: CrossMap (RRID:SCR_001173)

Description: A software program for convenient conversion of genome coordinates (or annotation files) between different assemblies. It supports most commonly used file formats including SAM/BAM, Wiggle/BigWig, BED, GFF/GTF, VCF. It is designed to lift over genome coordinates between assemblies. It's not a program for aligning sequences to reference genome. CrossMap is not recommend for converting genome coordinates between species.

Abbreviations: CrossMap

Resource Type: software resource

Defining Citation: [PMID:24351709](#)

Keywords: genome, assembly

Availability: GNU General Public License

Resource Name: CrossMap

Resource ID: SCR_001173

Alternate IDs: OMICS_02184

Record Creation Time: 20220129T080206+0000

Record Last Update: 20260912T195520+0000

Ratings and Alerts

No rating or validation information has been found for CrossMap.

No alerts have been found for CrossMap.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 19 mentions in open access literature.

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

Arthur TD, et al. (2025) Multiomic QTL mapping reveals phenotypic complexity of GWAS loci and prioritizes putative causal variants. *Cell genomics*, 5(3), 100775.

Qin N, et al. (2025) Comprehensive Characterization of Somatic Mutation Timing Reveals the Evolutionary Trajectory of Lung Adenocarcinoma in Chinese Patients. *Cancer research*, 85(15), 2905.

Ishikawa R, et al. (2025) Immunohistochemical and molecular evolutionary features of jejunoileal adenocarcinoma unveiled through comparative analysis with colorectal adenocarcinoma. *Neoplasia (New York, N.Y.)*, 66, 101180.

Akopyan M, et al. (2025) Reference genome choice compromises population genetic analyses. *Cell*.

Chang JJ, et al. (2024) Uncovering strain- and age-dependent innate immune responses to SARS-CoV-2 infection in air-liquid-interface cultured nasal epithelia. *iScience*, 27(6), 110009.

Kim JJ, et al. (2024) Multi-ancestry genome-wide association meta-analysis of Parkinson's disease. *Nature genetics*, 56(1), 27.

Golov AK, et al. (2024) A genome-wide nucleosome-resolution map of promoter-centered interactions in human cells corroborates the enhancer-promoter looping model. *eLife*, 12.

Iranzo J, et al. (2023) Protocol for comparing gene-level selection on coding mutations between two groups of samples with Coselens. *STAR protocols*, 4(1), 102117.

Barros CP, et al. (2022) A new haplotype-resolved turkey genome to enable turkey genetics and genomics research. *GigaScience*, 12.

Kumagai A, et al. (2020) Binding of the Treslin-MTBP Complex to Specific Regions of the Human Genome Promotes the Initiation of DNA Replication. *Cell reports*, 32(12), 108178.

Kurmangaliyev YZ, et al. (2020) Transcriptional Programs of Circuit Assembly in the *Drosophila* Visual System. *Neuron*, 108(6), 1045.

van der Valk T, et al. (2019) Historical Genomes Reveal the Genomic Consequences of Recent Population Decline in Eastern Gorillas. *Current biology : CB*, 29(1), 165.

Tomassoni-Ardori F, et al. (2019) Rbfox1 up-regulation impairs BDNF-dependent hippocampal LTP by dysregulating TrkB isoform expression levels. *eLife*, 8.

Schwartzentruber J, et al. (2018) Molecular and functional variation in iPSC-derived sensory neurons. *Nature genetics*, 50(1), 54.

Aldiri I, et al. (2017) The Dynamic Epigenetic Landscape of the Retina During Development, Reprogramming, and Tumorigenesis. *Neuron*, 94(3), 550.

Samandi S, et al. (2017) Deep transcriptome annotation enables the discovery and functional characterization of cryptic small proteins. *eLife*, 6.

Guo T, et al. (2017) Genome-Wide Association Study to Find Modifiers for Tetralogy of Fallot in the 22q11.2 Deletion Syndrome Identifies Variants in the GPR98 Locus on 5q14.3. *Circulation. Cardiovascular genetics*, 10(5), e001690.

Davey JW, et al. (2016) Major Improvements to the *Heliconius melpomene* Genome Assembly Used to Confirm 10 Chromosome Fusion Events in 6 Million Years of Butterfly Evolution. *G3 (Bethesda, Md.)*, 6(3), 695.

Eising E, et al. (2016) Gene co-expression analysis identifies brain regions and cell types involved in migraine pathophysiology: a GWAS-based study using the Allen Human Brain Atlas. *Human genetics*, 135(4), 425.