# 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 liftover 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:** 20260801T190141+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 18 mentions in open access literature.

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


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

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.