

Resource Summary Report

Generated by [RRID](#) on Aug 15, 2026

ChromoPainter

RRID:SCR_026062

Type: Tool

Proper Citation

ChromoPainter (RRID:SCR_026062)

Resource Information

URL: <https://github.com/sahwa/ChromoPainterV2>

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Description: Software tool to discover haplotypes in sequenced data. Colors each individual as hybrid of all other sequences. The "coancestry matrix" exposes ancestral associations among individuals. ChromoPainter algorithm uses Hidden Markov Model and outputs range of features, such as expected number of recombination events and sample haplotypes.

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

Defining Citation: [DOI:10.1371/journal.pgen.1002453](https://doi.org/10.1371/journal.pgen.1002453)

Keywords: discover haplotypes in sequenced data, discover haplotypes, sequenced data,

Availability: Free, Available for download, Freely available

Resource Name: ChromoPainter

Resource ID: SCR_026062

Alternate URLs: <http://www.paintmychromosomes.com/>

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Record Creation Time: 20241121T053249+0000

Record Last Update: 20260815T042922+0000

Ratings and Alerts

No rating or validation information has been found for ChromoPainter.

No alerts have been found for ChromoPainter.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 7 mentions in open access literature.

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

Borda V, et al. (2026) Unraveling the genetic landscape and admixture dynamics of urban populations across Peru. Communications biology, 9(1).

Thygesen VFDF, et al. (2026) The genomic history of Streptococcus mutans from the Mesolithic until modern times. Genome biology, 27(1).

Zhang X, et al. (2025) Protocol for reconstructing ancestral genomes from present-day samples by applying local ancestry inference. STAR protocols, 6(1), 103580.

Borda V, et al. (2025) Peruvian Population Genomics: Unraveling the Genetic Landscape and Admixture Dynamics of Urban Populations. bioRxiv : the preprint server for biology.

Suzuki R, et al. (2022) Helicobacter pylori genomes reveal Paleolithic human migration to the east end of Asia. iScience, 25(7), 104477.

Zhao Z, et al. (2022) Protocol to analyze population structure and migration history based on human genome variation data. STAR protocols, 4(1), 101928.

Brucato N, et al. (2017) Genomic admixture tracks pulses of economic activity over 2,000 years in the Indian Ocean trading network. Scientific reports, 7(1), 2919.