

Resource Summary Report

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PretextMap

RRID:SCR_022023

Type: Tool

Proper Citation

PretextMap (RRID:SCR_022023)

Resource Information

URL: <https://github.com/wtsi-hpag/PretextMap>

Proper Citation: PretextMap (RRID:SCR_022023)

Description: Software tool to convert SAM formatted read pairs into genome contact maps. Prepares alignments for visualization with PretextView.

Synonyms: Paired REad TEXTure Mapper, Wellcome Sanger Institute's High Performance Assembly Group's Paired REad TEXTure Mapper

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

Keywords: convert SAM formatted read pairs, genome contact maps, prepare alignments for visualization

Availability: Free, Available for download, Freely available

Resource Name: PretextMap

Resource ID: SCR_022023

Record Creation Time: 20220421T050138+0000

Record Last Update: 20260811T043701+0000

Ratings and Alerts

No rating or validation information has been found for PretextMap.

No alerts have been found for PretextMap.

Data and Source Information

Usage and Citation Metrics

We found 88 mentions in open access literature.

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

Payne CY, et al. (2026) A genome assembly for Lahontan Cutthroat Trout, *Oncorhynchus clarkii henshawi*. The Journal of heredity, 117(1), 159.

El Idrissi H, et al. (2026) A phased, near-telomere-to-telomere chromosome-scale reference genome of the Moroccan argan tree. Scientific data, 13(1).

Kozak KM, et al. (2026) A highly contiguous genome assembly for the California vole, *Microtus californicus*, provides insight into phylogenetic relationships and patterns of synteny among voles. The Journal of heredity, 117(2), 347.

Chen SH, et al. (2026) Genome Assembly of *Spinifex sericeus* Provides Insights into Repetitive Content and Haplotype Variation in a Dioecious Coastal Grass. Genome biology and evolution, 18(3).

Helmy M, et al. (2026) High-quality mouse reference genomes reveal the structural complexity of the murine protein-coding landscape. Cell genomics, 6(2), 101074.

Pennington LK, et al. (2026) A reference genome for Colusa grass, *Neostapfia colusana*, a threatened and endangered California vernal pool plant. The Journal of heredity, 117(3), 459.

Nguyen PT, et al. (2026) A genome assembly of the California poppy, *Eschscholzia californica*. The Journal of heredity, 117(2), 309.

Martínez-Gómez J, et al. (2026) The reference genome of a Sierra Nevada endemic, the cut-leaved monkeyflower, *Mimulus laciniatus* (syn. *Erythranthe lacinata*). The Journal of heredity, 117(2), 318.

Richmond JQ, et al. (2026) A chromosome-level reference genome assembly for Gilbert's skink *Plestiodon gilberti*. The Journal of heredity, 117(1), 115.

Johns J, et al. (2026) A near chromosome-level assembly of the serpentine endemic columbine, *Aquilegia eximia*. The Journal of heredity, 117(1), 85.

Linn IJ, et al. (2026) A high-quality reference genome for the ornate shrew (*Sorex ornatus*). The Journal of heredity, 117(3), 450.

Dorsey BL, et al. (2026) A genome assembly of Douglas' meadowfoam, *Limnanthes douglasii* R. BR. The Journal of heredity, 117(3), 592.

Ballare KM, et al. (2026) Genome assemblies of two bumble bee species: *Bombus sonorus* and *Bombus vosnesenskii*. The Journal of heredity, 117(3), 611.

Cash EI, et al. (2025) Genome assembly of the winter ant, *Prenolepis imparis*. The Journal of heredity, 116(3), 354.

Supple MA, et al. (2025) A chromosome-level genome assembly of the mountain lion, *Puma concolor*. The Journal of heredity, 116(4), 479.

Francis BA, et al. (2025) Complete genome assemblies of two mouse subspecies reveal structural diversity of telomeres and centromeres. Nature genetics, 57(11), 2852.

Chrysostomakis I, et al. (2025) A high-quality reference genome for the Ural Owl (*Strix uralensis*) enables investigations of cell cultures as a genomic resource for endangered species. GigaScience, 14.

MacDonald ZG, et al. (2025) A genome assembly for the Chryxus Arctic (*Oeneis chryxus*), the highest butterfly in North America. The Journal of heredity, 116(3), 324.

Jacobs DK, et al. (2025) Reference genome for the endangered, genetically subdivided, northern tidewater goby, *Eucyclogobius newberryi*. The Journal of heredity, 116(2), 170.

Heaven T, et al. (2025) Chromosome-Level Assemblies of Three Candidatus *Liberibacter solanacearum* Vectors: *Dyspersa apicalis* (Förster, 1848), *Dyspersa pallida* (Burckhardt, 1986), and *Trioza urticae* (Linnaeus, 1758) (Hemiptera: Psylloidea). Genome biology and evolution, 17(6).