

Resource Summary Report

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XP-CLR

RRID:SCR_004961

Type: Tool

Proper Citation

XP-CLR (RRID:SCR_004961)

Resource Information

URL: <https://reich.hms.harvard.edu/software>

Proper Citation: XP-CLR (RRID:SCR_004961)

Description: XP-CLR (Chen et al. 2010) uses allele frequency differentiation at linked loci to detect selective sweeps. Source code and documentation are available.

Synonyms: XP-CLR Software

Resource Type: software resource, source code

Funding:

Availability: Restricted

Resource Name: XP-CLR

Resource ID: SCR_004961

Alternate IDs: nlx_94751

Alternate URLs: <https://reich.hms.harvard.edu/software>

Old URLs: http://genetics.med.harvard.edu/reich/Reich_Lab/Software.html

Record Creation Time: 20220129T080227+0000

Record Last Update: 20250430T055329+0000

Ratings and Alerts

No rating or validation information has been found for XP-CLR.

No alerts have been found for XP-CLR.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 60 mentions in open access literature.

Listed below are recent publications. The full list is available at [FDI Lab - SciCrunch.org](#).

Zhou Y, et al. (2025) Telomere-to-telomere genome and resequencing of 254 individuals reveal evolution, genomic footprints in Asian icefish, *Protosalanx chinensis*. *GigaScience*, 14.

Guo N, et al. (2024) A graph-based pan-genome of *Brassica oleracea* provides new insights into its domestication and morphotype diversification. *Plant communications*, 5(2), 100791.

Li B, et al. (2024) Natural selection and genetic diversity maintenance in a parasitic wasp during continuous biological control application. *Nature communications*, 15(1), 1379.

Lin R, et al. (2024) Whole-genome selection signature differences between Chaohu and Ji'an red ducks. *BMC genomics*, 25(1), 522.

He Y, et al. (2024) Genomic insight into the origin, domestication, dispersal, diversification and human selection of Tartary buckwheat. *Genome biology*, 25(1), 61.

Qi L, et al. (2024) Genetic characteristics and selection signatures between Southern Chinese local and commercial chickens. *Poultry science*, 103(7), 103863.

Cho Y, et al. (2024) Whole-genome sequencing analysis of soybean diversity across different countries and selection signature of Korean soybean accession. *G3 (Bethesda, Md.)*, 14(8).

Lu XM, et al. (2024) Genome assembly of autotetraploid *Actinidia arguta* highlights adaptive evolution and enables dissection of important economic traits. *Plant communications*, 5(6), 100856.

Li T, et al. (2024) A comparative analysis reveals the genomic diversity among 8 Muscovy duck populations. *G3 (Bethesda, Md.)*, 14(7).

Li X, et al. (2024) Whole-genome resequencing to investigate the genetic diversity and mechanisms of plateau adaptation in Tibetan sheep. *Journal of animal science and biotechnology*, 15(1), 164.

Xu YX, et al. (2023) Whole-body adipose tissue multi-omic analyses in sheep reveal molecular mechanisms underlying local adaptation to extreme environments. *Communications biology*, 6(1), 159.

Chao J, et al. (2023) Genomic insight into domestication of rubber tree. *Nature communications*, 14(1), 4651.

Yin ZT, et al. (2023) Selection on the promoter regions plays an important role in complex traits during duck domestication. *BMC biology*, 21(1), 303.

Felkel S, et al. (2023) Genomic variation in the genus *Beta* based on 656 sequenced beet genomes. *Scientific reports*, 13(1), 8654.

Xu D, et al. (2023) Whole-genome sequencing revealed genetic diversity, structure and patterns of selection in Guizhou indigenous chickens. *BMC genomics*, 24(1), 570.

Coe K, et al. (2023) Population genomics identifies genetic signatures of carrot domestication and improvement and uncovers the origin of high-carotenoid orange carrots. *Nature plants*, 9(10), 1643.

Cho Y, et al. (2022) Comparative genomics and selection analysis of Yeonsan Ogye black chicken with whole-genome sequencing. *Genomics*, 114(2), 110298.

Yang L, et al. (2022) Evolutionary Conservation Genomics Reveals Recent Speciation and Local Adaptation in Threatened Takins. *Molecular biology and evolution*, 39(6).

Cui D, et al. (2022) Genomic insights on the contribution of introgressions from Xian/Indica to the genetic improvement of Geng/Japonica rice cultivars. *Plant communications*, 3(3), 100325.

Lv FH, et al. (2022) Whole-Genome Resequencing of Worldwide Wild and Domestic Sheep Elucidates Genetic Diversity, Introgression, and Agronomically Important Loci. *Molecular biology and evolution*, 39(2).