# **Resource Summary Report**

Generated by NIF on May 24, 2025

# **XP-CLR**

RRID:SCR\_004961

Type: Tool

## **Proper Citation**

XP-CLR (RRID:SCR\_004961)

#### **Resource Information**

**URL:** <a href="https://reich.hms.harvard.edu/software">https://reich.hms.harvard.edu/software</a>

**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:** 20250524T060026+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 NIF.

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).