

Resource Summary Report

Generated by [kravitz2](#) on Sep 17, 2026

HAPLOBUILD

RRID:SCR_009224

Type: Tool

Proper Citation

HAPLOBUILD (RRID:SCR_009224)

Resource Information

URL: <http://snp.bumc.bu.edu/modules.php?name=HaploBuild>

Proper Citation: HAPLOBUILD (RRID:SCR_009224)

Description: Software application for constructing and testing haplotypes for SNPs in close physical proximity to one another but which are not necessarily contiguous. Furthermore, the number of SNPs contained in the haplotype is not restricted, thereby permitting the evaluation of complex haplotype structures. The analysis of large amounts of SNP data creates difficulties for the analysis of haplotypes and their association to traits of interest. Commonly fairly simple methods, such as two- or three-SNP sliding windows are used to create haplotypes across large regions, but these may be of limited value when adjacent SNPs are in strong LD and provide redundant information. This program alleviates these difficulties. (entry from Genetic Analysis Software)

Abbreviations: HAPLOBUILD

Resource Type: software application, software resource

Keywords: gene, genetic, genomic, perl, linux, ms-windows, macos

Resource Name: HAPLOBUILD

Resource ID: SCR_009224

Alternate IDs: nlx_154381

Record Creation Time: 20220129T080251+0000

Record Last Update: 20260912T200242+0000

Ratings and Alerts

No rating or validation information has been found for HAPLOBUILD.

No alerts have been found for HAPLOBUILD.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We have not found any literature mentions for this resource.