# **Resource Summary Report**

Generated by dkNET on Apr 18, 2025

# **CLUSTAG**

RRID:SCR\_001816

Type: Tool

### **Proper Citation**

CLUSTAG (RRID:SCR\_001816)

#### **Resource Information**

URL: http://www.math.hkbu.edu.hk/~mng/CLUSTAG/CLUSTAG.html

**Proper Citation:** CLUSTAG (RRID:SCR\_001816)

**Description:** Software application that uses hierarchical clustering and graph methods for selecting tag SNPs (single nucleotide polymorphisms). Cluster and set-cover algorithms are developed to obtain a set of tag SNPs that can represent all the known SNPs in a chromosomal region, subject to the constraint that all SNPs must have a squared correlation R2 > C with at least one tag SNP, where C is specified by the user. The program is implemented with Java, and it can run in Windows platform as well as the Unix environment.

**Abbreviations: CLUSTAG** 

Synonyms: CLUSTAG: Hierarchical Clustering and Graph Methods for Selecting Tag SNPs

Resource Type: software resource, software application

**Defining Citation: PMID:15585525** 

Keywords: gene, genetic, genomic, java, hierarchical clustering, single nucleotide

polymorphism, windows, unix

Funding:

Resource Name: CLUSTAG

Resource ID: SCR\_001816

Alternate IDs: nlx\_154273

Old URLs: http://hkumath.hku.hk/web/link/CLUSTAG/CLUSTAG.html

**Record Creation Time:** 20220129T080209+0000

Record Last Update: 20250416T063246+0000

## **Ratings and Alerts**

No rating or validation information has been found for CLUSTAG.

No alerts have been found for CLUSTAG.

### **Data and Source Information**

Source: SciCrunch Registry

## **Usage and Citation Metrics**

We found 1 mentions in open access literature.

**Listed below are recent publications.** The full list is available at dkNET.

Khvorykh G, et al. (2021) A Workflow for Selection of Single Nucleotide Polymorphic Markers for Studying of Genetics of Ischemic Stroke Outcomes. Genes, 12(3).