

Resource Summary Report

Generated by [nidm-terms](#) on Jul 28, 2026

kruX

RRID:SCR_012076

Type: Tool

Proper Citation

kruX (RRID:SCR_012076)

Resource Information

URL: <https://code.google.com/p/kruX/>

Proper Citation: kruX (RRID:SCR_012076)

Description: An algorithm implemented in Matlab, Python and R that uses matrix multiplications to simultaneously calculate the Kruskal-Wallis test statistic for several millions of marker-trait combinations at once.

Resource Type: software resource

Defining Citation: [PMID:24423115](#)

Keywords: standalone software, matlab, python, r

Availability: GNU General Public License

Resource Name: kruX

Resource ID: SCR_012076

Alternate IDs: OMICS_04593

Record Creation Time: 20220129T080308+0000

Record Last Update: 20260725T190728+0000

Ratings and Alerts

No rating or validation information has been found for kruX.

No alerts have been found for kruX.

Data and Source Information

Usage and Citation Metrics

We found 5 mentions in open access literature.

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

Ramos-??lvarez I, et al. (2026) Role of serine/threonine phosphatases 1 and 2A in pancreatic acinar fluid and electrolyte secretion. American journal of physiology. Gastrointestinal and liver physiology.

Crawford AA, et al. (2021) Variation in the SERPINA6/SERPINA1 locus alters morning plasma cortisol, hepatic corticosteroid binding globulin expression, gene expression in peripheral tissues, and risk of cardiovascular disease. Journal of human genetics, 66(6), 625.

Wang L, et al. (2017) Efficient and accurate causal inference with hidden confounders from genome-transcriptome variation data. PLoS computational biology, 13(8), e1005703.

Sun Y, et al. (2016) Fine-mapping analysis revealed complex pleiotropic effect and tissue-specific regulatory mechanism of TNFSF15 in primary biliary cholangitis, Crohn's disease and leprosy. Scientific reports, 6, 31429.

van der Laan SW, et al. (2015) Variants in ALOX5, ALOX5AP and LTA4H are not associated with atherosclerotic plaque phenotypes: the Athero-Express Genomics Study. Atherosclerosis, 239(2), 528.