

Resource Summary Report

Generated by [kravitz2](#) on Sep 4, 2026

DISENTANGLER

RRID:SCR_009161

Type: Tool

Proper Citation

DISENTANGLER (RRID:SCR_009161)

Resource Information

URL: <http://kumasakanatsuhiko.jp/projects/disentangler/>

Proper Citation: DISENTANGLER (RRID:SCR_009161)

Description: Software application that is a visualization technique for linkage disequilibrium mapping and haplotype analysis of multiple multi-allelic genetic markers. (entry from Genetic Analysis Software)

Abbreviations: DISENTANGLER

Resource Type: software application, software resource

Keywords: gene, genetic, genomic, java/jre1.5, bio.tools

Resource Name: DISENTANGLER

Resource ID: SCR_009161

Alternate IDs: nlx_154284, blotools:disentangler

Alternate URLs: <https://bio.tools/disentangler>

Record Creation Time: 20220129T080251+0000

Record Last Update: 20260904T000427+0000

Ratings and Alerts

No rating or validation information has been found for DISENTANGLER.

No alerts have been found for DISENTANGLER.

Data and Source Information

Usage and Citation Metrics

We found 6 mentions in open access literature.

Listed below are recent publications. The full list is available at [kravitz2](#) .

Kang B, et al. (2026) Recurrent connections facilitate occluded object recognition by explaining-away. Nature communications, 17(1).

Morita M, et al. (2026) Long-read KIR genotyping reveals donor KIR/HLA polymorphisms linked to posttransplant relapse in T-cell malignancies. Blood advances, 10(13), 4563.

Liu Z, et al. (2024) Human leukocyte antigen-DQA1*04:01 and rs2040406 variants are associated with elevated risk of childhood Burkitt lymphoma. Communications biology, 7(1), 41.

Valenzuela-Ponce H, et al. (2023) Honduras HIV cohort: HLA class I and CCR5-??32 profiles and their associations with HIV disease outcome. Microbiology spectrum, 11(6), e0161323.

Dallmann-Sauer M, et al. (2020) The complex pattern of genetic associations of leprosy with HLA class I and class II alleles can be reduced to four amino acid positions. PLoS pathogens, 16(8), e1008818.

Ferreiro-Iglesias A, et al. (2018) Fine mapping of MHC region in lung cancer highlights independent susceptibility loci by ethnicity. Nature communications, 9(1), 3927.