

Resource Summary Report

Generated by [kravitz2](#) on Jul 31, 2026

fs-tool

RRID:SCR_018250

Type: Tool

Proper Citation

fs-tool (RRID:SCR_018250)

Resource Information

URL: <https://github.com/bjohnnyd/fs-tool>

Proper Citation: fs-tool (RRID:SCR_018250)

Description: Software tool to calculate fraction of shared bound peptides between HLA proteins. Command-line tool to calculate fraction of shared bound peptides between HLA alleles from NetMHCpan binding predictions. Compares fraction shared between HLA allele and individual taking into account HLA and KIR genotypes.

Synonyms: fraction shared tool

Resource Type: software resource, software application, data processing software

Keywords: calculate fraction of shared peptides, peptides between HLA proteins, HLA alleles, NetMHCpan binding prediction, genotype, data

Availability: Free, Available for download, Freely available

Resource Name: fs-tool

Resource ID: SCR_018250

License: MIT Licens

Record Creation Time: 20220129T080339+0000

Record Last Update: 20260731T043027+0000

Ratings and Alerts

No rating or validation information has been found for fs-tool.

No alerts have been found for fs-tool.

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 [kravitz2](#) .

Debebe BJ, et al. (2020) Identifying the immune interactions underlying HLA class I disease associations. eLife, 9.