

Resource Summary Report

Generated by [kravitz2](#) on Aug 1, 2026

SuperDCA

RRID:SCR_018175

Type: Tool

Proper Citation

SuperDCA (RRID:SCR_018175)

Resource Information

URL: <https://github.com/santeripuranen/SuperDCA>

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Description: Software tool for global direct coupling analysis of input genome alignments. Implements variant of pseudolikelihood maximization direct coupling analysis, with emphasis on optimizations that enable its use on genome scale. May be used to discover co evolving pairs of loci.Used for genome wide epistasis analysis.

Synonyms: Super Direct Coupling Analysis

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

Defining Citation: [PMID:29813016](#)

Keywords: Protein, sequence, alignment, analysis, genome, loci, epistasis

Funding: Academy of Finland ;
Wellcome Trust ;
Royal Society ;
European Research Council

Availability: Free, Available for download, Freely available

Resource Name: SuperDCA

Resource ID: SCR_018175

Record Creation Time: 20220129T080339+0000

Record Last Update: 20260801T042813+0000

Ratings and Alerts

No rating or validation information has been found for SuperDCA.

No alerts have been found for SuperDCA.

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](#) .

Cui Y, et al. (2020) The landscape of coadaptation in *Vibrio parahaemolyticus*. eLife, 9.