

Resource Summary Report

Generated by [Kravitz](#) on Sep 10, 2026

SpydrPick

RRID:SCR_018176

Type: Tool

Proper Citation

SpydrPick (RRID:SCR_018176)

Resource Information

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

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Description: Software command line tool for performing direct coupling analysis of aligned categorical datasets. Used for analysis at scale of pan genomes of many bacteria. Incorporates correction for population structure, which adjusts for phylogenetic signal in data without requiring explicit phylogenetic tree.

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

Defining Citation: [PMID:31361894](#)

Keywords: Direct coupling analysis, aligned categorical datasets, analysis, genome, bacteria, phylogenetic signal, correction, phylogenetic tree, data, bio.tools

Funding: COIN Center of Excellence ;
Academy of Finland ;
European Research Council ;
Wellcome Trust

Availability: Free, Available for download, Freely available

Resource Name: SpydrPick

Resource ID: SCR_018176

Alternate IDs: biotools:SpydrPick

Alternate URLs: <https://anaconda.org/bioconda/spydrpick>, <https://bio.tools/SpydrPick>

License: GNU Affero General Public License

Record Creation Time: 20220129T080339+0000

Record Last Update: 20260905T132832+0000

Ratings and Alerts

No rating or validation information has been found for SpydrPick.

No alerts have been found for SpydrPick.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 3 mentions in open access literature.

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

Posada-Reyes AB, et al. (2022) An Epistatic Network Describes oppA and glgB as Relevant Genes for Mycobacterium tuberculosis. Frontiers in molecular biosciences, 9, 856212.

Chewapreecha C, et al. (2022) Co-evolutionary Signals Identify Burkholderia pseudomallei Survival Strategies in a Hostile Environment. Molecular biology and evolution, 39(1).

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