

Resource Summary Report

Generated by [NIF](#) on Sep 12, 2026

Pairwise Conservation Scores - An Algorithm to Identify Conserved K-mers

RRID:SCR_013409

Type: Tool

Proper Citation

Pairwise Conservation Scores - An Algorithm to Identify Conserved K-mers
(RRID:SCR_013409)

Resource Information

URL: <http://bioinfo.au.tsinghua.edu.cn/software/pcs/>

Proper Citation: Pairwise Conservation Scores - An Algorithm to Identify Conserved K-mers (RRID:SCR_013409)

Description: A stand-alone package to identify and analyze conserved k-mers in pairwise alignment. This program shows high performance for identifying miRNA seed binding sites in 3'-UTRs.

Abbreviations: PCS

Synonyms: Pairwise Conservation Scores

Resource Type: software resource

Keywords: perl, perl script, bio.tools

Resource Name: Pairwise Conservation Scores - An Algorithm to Identify Conserved K-mers

Resource ID: SCR_013409

Alternate IDs: biotools:pcs, nlx_33020

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

Old URLs: <http://bioinfo.au.tsinghua.edu.cn/member/~gujin/pcs/>

Record Creation Time: 20220129T080316+0000

Record Last Update: 20260905T132735+0000

Ratings and Alerts

No rating or validation information has been found for Pairwise Conservation Scores - An Algorithm to Identify Conserved K-mers.

No alerts have been found for Pairwise Conservation Scores - An Algorithm to Identify Conserved K-mers.

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 [NIF](#) .

Pajic P, et al. (2024) Emergence of saliva protein genes in the secretory calcium-binding phosphoprotein (SCPP) locus and accelerated evolution in primates. bioRxiv : the preprint server for biology.

Schieferdecker A, et al. (2019) Structural Mapping of Missense Mutations in the Pex1/Pex6 Complex. International journal of molecular sciences, 20(15).

Fritsch C, et al. (2012) Genome-wide search for novel human uORFs and N-terminal protein extensions using ribosomal footprinting. Genome research, 22(11), 2208.