

Resource Summary Report

Generated by [PRECISE-TBI](#) on Jul 31, 2026

ConPlot

RRID:SCR_019216

Type: Tool

Proper Citation

ConPlot (RRID:SCR_019216)

Resource Information

URL: <http://www.conplot.org/>

Proper Citation: ConPlot (RRID:SCR_019216)

Description: Web application for visualisation of information derived from residue contact predictions in combination with other sources of information, such as secondary structure predictions, transmembrane helical topology, sequence conservation. Provides interactive interface for researchers in field of protein bioinformatics that are interested in analysing data on given protein.

Resource Type: service resource, data access protocol, software resource, web service, production service resource, analysis service resource

Keywords: Residue contact predictions, protein, secondary structure predictions, transmembrane helical topology, sequence conservation, protein bioinformatics, analysing data

Availability: Restricted

Resource Name: ConPlot

Resource ID: SCR_019216

Record Creation Time: 20220129T080344+0000

Record Last Update: 20260731T043043+0000

Ratings and Alerts

No rating or validation information has been found for ConPlot.

No alerts have been found for ConPlot.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 2 mentions in open access literature.

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

Sánchez Rodríguez F, et al. (2021) ConPlot: web-based application for the visualization of protein contact maps integrated with other data. *Bioinformatics* (Oxford, England), 37(17), 2763.

Mesdaghi S, et al. (2020) In silico prediction of structure and function for a large family of transmembrane proteins that includes human Tmem41b. *F1000Research*, 9, 1395.