# **Resource Summary Report**

Generated by dkNET on May 12, 2025

# **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:** web service, analysis service resource, service resource, data access protocol, production service resource, software resource

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

**Funding:** 

Availability: Restricted

Resource Name: ConPlot

Resource ID: SCR\_019216

**Record Creation Time:** 20220129T080344+0000

Record Last Update: 20250509T060318+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 dkNET.

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.