## **Resource Summary Report**

Generated by FDI Lab - SciCrunch.org on May 3, 2025

# **GraphRBF**

RRID:SCR\_025650

Type: Tool

### **Proper Citation**

GraphRBF (RRID:SCR\_025650)

#### **Resource Information**

URL: https://github.com/Wssduer/GraphRBF

**Proper Citation:** GraphRBF (RRID:SCR\_025650)

**Description:** Protein-protein and protein-nucleic acid binding site prediction via interpretable

hierarchical geometric deep learning.

Synonyms: Graph RBF

Resource Type: simulation software, software resource, software application

**Keywords:** Protein-protein, protein-nucleic acid, binding site, binding site prediction,

**Funding:** 

Availability: Free, Available for download, Freely available

Resource Name: GraphRBF

Resource ID: SCR\_025650

License: GNU GPL v3.0

**Record Creation Time:** 20240824T053240+0000

Record Last Update: 20250503T061248+0000

## Ratings and Alerts

No rating or validation information has been found for GraphRBF.

No alerts have been found for GraphRBF.

## 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 FDI Lab - SciCrunch.org.

Zhang S, et al. (2024) Protein-protein and protein-nucleic acid binding site prediction via interpretable hierarchical geometric deep learning. GigaScience, 13.