

# Resource Summary Report

Generated by [RRID](#) on Aug 8, 2026

## Feature Representation Enhancement End-to-end Protein Interaction Inference

RRID:SCR\_026316

Type: Tool

### Proper Citation

Feature Representation Enhancement End-to-end Protein Interaction Inference  
(RRID:SCR\_026316)

### Resource Information

**URL:** <https://github.com/qgpigass/FREEPII>

**Proper Citation:** Feature Representation Enhancement End-to-end Protein Interaction Inference (RRID:SCR\_026316)

**Description:** Software application encompassing autonomous feature extraction and feature representation enhancement for PPIs and protein complexes inference. FREEPII establishes feature maps that are consistent with model training, and emphasizes learning the feature representation of proteins rather than the feature representation of PPI, reducing the computational complexity from  $N^2$  to  $N$  ( $N$ : number of proteins). FREEPII uses protein sequences to expand the information available for calculating data similarity between proteins. Furthermore, it introduces network-level information into the final feature representation to rescale the strength of interactions present in CF-MS data.

**Abbreviations:** FREEPII

**Resource Type:** software resource, source code

**Keywords:** co-fractionation coupled with mass spectrometry analysis, protein-protein interactions, protein interactome inference,

**Availability:** Free, Available for download, Freely available,

**Resource Name:** Feature Representation Enhancement End-to-end Protein Interaction Inference

**Resource ID:** SCR\_026316

**License:** MIT license

**Record Creation Time:** 20250122T053336+0000

**Record Last Update:** 20260808T043037+0000

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## Ratings and Alerts

No rating or validation information has been found for Feature Representation Enhancement End-to-end Protein Interaction Inference.

No alerts have been found for Feature Representation Enhancement End-to-end Protein Interaction Inference.

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## Data and Source Information

**Source:** [SciCrunch Registry](#)

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## Usage and Citation Metrics

We found 1 mentions in open access literature.

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

Chen YH, et al. (2025) Complete end-to-end learning from protein feature representation to protein interactome inference. GigaScience, 14.