

Resource Summary Report

Generated by [RRID](#) on Aug 5, 2026

ClusPro

RRID:SCR_018248

Type: Tool

Proper Citation

ClusPro (RRID:SCR_018248)

Resource Information

URL: <https://cluspro.bu.edu/>

Proper Citation: ClusPro (RRID:SCR_018248)

Description: Web tool for protein-protein docking. Server provides removal of unstructured protein regions, application of attraction or repulsion, accounting for pairwise distance restraints, construction of homo-multimers, consideration of small-angle X-ray scattering data, and location of heparin-binding sites. Six different energy functions can be used, depending on protein type. This protocol describes use of various options, construction of auxiliary restraints files, selection of energy parameters, and analysis of results.

Synonyms: ClusPro 2.0

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

Defining Citation: [PMID:28079879](#)

Keywords: Protein-protein docking, protein structure, energy function, energy parameter selection, analysis, data

Funding: NIGMS R35 GM118078;
NIGMS R01 GM061867

Availability: Free, Freely available

Resource Name: ClusPro

Resource ID: SCR_018248

Record Creation Time: 20220129T080339+0000

Record Last Update: 20260805T044418+0000

Ratings and Alerts

No rating or validation information has been found for ClusPro.

No alerts have been found for ClusPro.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 858 mentions in open access literature.

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

Wang Y, et al. (2025) Homeodomain protein PRRX1 anchors the Ku heterodimers at DNA double-strand breaks to promote nonhomologous end-joining. Nucleic acids research, 53(6).

Panda S, et al. (2025) Designing a potent multivalent epitope vaccine candidate against *Orientia tsutsugamushi* via reverse vaccinology technique - bioinformatics and immunoinformatic approach. Frontiers in immunology, 16, 1513245.

Yang M, et al. (2025) S100P is a ferroptosis suppressor to facilitate hepatocellular carcinoma development by rewiring lipid metabolism. Nature communications, 16(1), 509.

Spanou CES, et al. (2025) Prodomain processing controls BMP-10 bioactivity and targeting to fibrillin-1 in latent conformation. FASEB journal : official publication of the Federation of American Societies for Experimental Biology, 39(3), e70373.

Ren X, et al. (2025) REG3A secreted by peritumoral acinar cells enhances pancreatic ductal adenocarcinoma progression via activation of EGFR signaling. Cell communication and signaling : CCS, 23(1), 96.

Shi C, et al. (2025) Comprehensive discovery and functional characterization of the noncanonical proteome. Cell research, 35(3), 186.

Fan S, et al. (2025) Pyridoxine dehydrogenase SePdx regulates photosynthesis via an association with the phycobilisome in a cyanobacterium. The Plant journal : for cell and molecular biology, 121(6), e70055.

Nie J, et al. (2025) A globular protein exhibits rare phase behavior and forms chemically regulated orthogonal condensates in cells. Nature communications, 16(1), 2449.

Iqbal MW, et al. (2025) Exploring deleterious non-synonymous SNPs in FUT2 gene, and implications for norovirus susceptibility and gut microbiota composition. Scientific reports, 15(1), 10395.

Zhu F, et al. (2025) Designing a multi-epitope vaccine against *Pseudomonas aeruginosa* via integrating reverse vaccinology with immunoinformatics approaches. Scientific reports, 15(1), 10425.

- Richard AC, et al. (2025) Using Short Molecular Dynamics Simulations to Determine the Important Features of Interactions in Antibody-Protein Complexes. *Proteins*, 93(4), 812.
- Nam J, et al. (2025) Blockade of ZMIZ1-GATA4 Axis Regulation Restores Youthfulness to Aged Cartilage. *Advanced science (Weinheim, Baden-Wurttemberg, Germany)*, 12(16), e2404311.
- Xue M, et al. (2025) Single amino acid mutations in histone H3.3 illuminate the functional significance of H3K4 methylation in plants. *Nature communications*, 16(1), 4408.
- Rashwan ME, et al. (2025) In silico prediction of GRP78-CRIPTO binding sites to improve therapeutic targeting in glioblastoma. *Scientific reports*, 15(1), 16660.
- Faruque M, et al. (2025) Deciphering Deleterious nsSNPs in MUC16's SEA Domain: Structural and Functional Implications in Cancer Metastasis via Computational Analysis. *Journal of cellular and molecular medicine*, 29(11), e70633.
- Sajjad A, et al. (2025) In-silico molecular analysis and blocking of the viral G protein of Nipah virus interacting with ephrin B2 and B3 receptor by using peptide mass fingerprinting. *Frontiers in bioinformatics*, 5, 1526566.
- Tombari W, et al. (2025) A novel mRNA-based multi-epitope vaccine for rabies virus computationally designed via reverse vaccinology and immunoinformatics. *Scientific reports*, 15(1), 30355.
- Ahmadi SF, et al. (2025) Computational and experimental discovery of peptide inhibitors targeting survivin for therapeutic potential in cancer. *Scientific reports*, 15(1), 30599.
- Nazeri N, et al. (2025) Engineering M13 bacteriophage to display HER2 mimotopes on pVIII for vaccine development. *Scientific reports*, 15(1), 22285.
- Zaman N, et al. (2025) Molecular insights into pangenome localization and constructs design for Hemophilus influenza vaccine. *Scientific reports*, 15(1), 22316.