

Resource Summary Report

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ClusPro

RRID:SCR_018248

Type: Tool

Proper Citation

ClusPro (RRID:SCR_018248)

Resource Information

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

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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, service resource, software resource, web service

Defining Citation: [PMID:28079879](#)

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

Funding: NIGMS R01 GM061867;
NIGMS R35 GM118078

Availability: Free, Freely available

Resource Name: ClusPro

Resource ID: SCR_018248

Record Creation Time: 20220129T080339+0000

Record Last Update: 20260919T195518+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 979 mentions in open access literature.

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

Zhao J, et al. (2026) Extracellular Vesicle-Mediated O-GlcNAcase Transfer Drives Neuronal Necroptosis to Facilitate Gallbladder Cancer Perineural Invasion. *Cancer research*, 86(6), 1392.

Bhatt TC, et al. (2026) Discovery of age and blood group associated variability in nattokinase mediated thrombolysis and its relevance to cardiovascular management. *Scientific reports*, 16(1).

Santos RM, et al. (2026) Decoding Allosteric Inhibition in MALT1: The Hidden Role of Conformational Plasticity in Metastable States via Biased MD and Deep Learning. *The journal of physical chemistry. B*, 130(4), 1182.

Dos Santos MJM, et al. (2026) In Silico Analysis and Expression Profiling of Adhesin-Like Flocculins in *Trichosporon asahii*. *Mycopathologia*, 191(1), 28.

Shi X, et al. (2026) Secreted RCN3 acts as an early epithelial-fibroblast mediator via TGF β 1-Smad signaling in post-ALI pulmonary fibrosis. *Cell communication and signaling : CCS*, 24(1).

Xia Y, et al. (2026) NLK facilitates Caspase-8 activation to drive macrophage PANoptosis in sepsis. *Clinical and translational medicine*, 16(2), e70616.

Wang P, et al. (2026) DNA Polymerase Gamma Acetylation Governs Mitochondrial Homeostasis and Vascular Cell Senescence. *International journal of biological sciences*, 22(5), 2435.

Naveed M, et al. (2026) Multi-epitope vaccine against nucleoprotein and envelopment polyprotein of Batai orthobunyavirus using molecular docking and molecular dynamics studies. *Scientific reports*, 16(1).

Stolarik E, et al. (2026) Inhibition of cell surface GRP78 on brain tumors reverses drug resistance and stops cancer stem cell expansion. *The Journal of biological chemistry*, 111146.

Khan A, et al. (2026) Immunoinformatics-driven design of multi-epitope vaccine targeting antibiotic-resistant *Salmonella typhimurium*. *PloS one*, 21(2), e0342426.

Chundru D, et al. (2026) In silico design of a multiepitope subunit vaccine targeting *Salmonella enterica* serovar Infantis: an immunoinformatics and reverse vaccinology approach. *Frontiers in immunology*, 17, 1717278.

Guan B, et al. (2026) TRIM21-Mediated ubiquitination of FBL suppresses PI3K/AKT signaling and tumor progression in clear cell renal cell carcinoma. *Cellular and molecular life sciences : CMLS*, 83(1).

Cheng J, et al. (2026) Exploring Trop-2-Nanobody PPI Interactions through Molecular Dynamics Simulations and Biovalidations. *ACS omega*, 11(10), 16209.

Yakobi SH, et al. (2026) In Silico Design and Characterization of the Essential Outer-Membrane Lipoprotein LolB-Derived Multi-Epitope Vaccine Candidate Against *Pseudomonas aeruginosa*. *Methods and protocols*, 9(2).

Baniasadi Nejad N, et al. (2026) Computational design of a multi-epitope vaccine against *Helicobacter pylori* targeting CagA, FliD, urease, and OipA with cholera toxin B subunit (CTB) adjuvant. *BMC microbiology*, 26(1).

Seifi N, et al. (2026) Design and in silico evaluation of an mRNA vaccine against HTLV-1 using AI-driven reverse vaccinology approaches. *PloS one*, 21(5), e0340201.

Naveed M, et al. (2026) Immunoinformatics-driven design of a multi-epitope vaccine against Seoul Virus: Structural, dynamic, and immunogenic profiling. *Clinics (Sao Paulo, Brazil)*, 81, 100991.

Akwelle RN, et al. (2026) In Silico Design and Computational Characterization of Novel Chimeric Multiepitope Antigens for Mpox Serosurveillance: An Immunoinformatics Approach. *Health science reports*, 9(6), e72702.

Lawaetz AC, et al. (2026) Genome mining of amylases and amylase inhibitors from *Streptomyces*. *Microbial genomics*, 12(6).

Tomisch J, et al. (2026) A novel SadP-scFv UCHT1 lectibody activates T cells and mediates lysis of Burkitt's lymphoma cells. *RSC chemical biology*, 7(1), 81.