Resource Summary Report

Generated by RRID on Aug 2, 2026

HPEPDOCK Server

RRID:SCR_018561
Type: Tool

Proper Citation

HPEPDOCK Server (RRID:SCR_018561)

Resource Information

URL: http://huanglab.phys.hust.edu.cn/hpepdock/

Proper Citation: HPEPDOCK Server (RRID:SCR_018561)

Description: Web server for blind peptide protein docking based on hierarchical algorithm. Blind peptide-protein docking by fast modeling of peptide conformations and global sampling of binding orientations.

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

Defining Citation: PMID:29746661

Keywords: Blind peptide protein docking, peptide conformation modeling, global sampling, blind orientation, protein, modeling, docking, bio.tools

Funding: National Key Research and Development Program of China ;
National Natural Science Foundation of China ;
Huazhong University of Science and Technology

Availability: Free, Freely available

Resource Name: HPEPDOCK Server

Resource ID: SCR_018561

Alternate IDs: biotools:hpepdock

Alternate URLs: https://bio.tools/hpepdock

Record Creation Time: 20220129T080340+0000

Record Last Update: 20260801T190600+0000

Ratings and Alerts

No rating or validation information has been found for HPEPDOCK Server.

No alerts have been found for HPEPDOCK Server.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 46 mentions in open access literature.

Listed below are recent publications. The full list is available at RRID .

Kim S, et al. (2026) Self-boosting targeted anticancer therapy via cancer cell self-reprogramming with GGT-targeting oxidative stress nanoamplifiers. Theranostics, 16(4), 1925.

Siddiki AZ, et al. (2025) Development of a multi-epitope chimeric vaccine in silico against Babesia bovis, Theileria annulata, and Anaplasma marginale using computational biology tools and reverse vaccinology approach. PloS one, 20(1), e0312262.

Ramalingam PS, et al. (2025) Unveiling reverse vaccinology and immunoinformatics toward Saint Louis encephalitis virus: a ray of hope for vaccine development. Frontiers in immunology, 16, 1576557.

Zahraei M, et al. (2025) In silico design of a multi-epitope vaccine against the triple negative breast cancer. Scientific reports, 15(1), 42425.

Atwal MS, et al. (2025) Accumulation of TDP-43 causes karyopherin-?4 pathology that characterises amyotrophic lateral sclerosis. Frontiers in neuroscience, 19, 1558227.

Souza-Silva TG, et al. (2025) Self and parasite-derived peptides selected upon DERAA-bearing HLA-DRB1 alleles activate CD4+ T cells from Chagas cardiomyopathy patients and are associated with ventricular dysfunction. Frontiers in immunology, 16, 1527115.

Mahafujul Alam SS, et al. (2025) Immunoinformatics based designing of a multi-epitope cancer vaccine targeting programmed cell death ligand 1. Scientific reports, 15(1), 12420.

Wang S, et al. (2025) AGDMP1 alleviates insulin resistance by modulating heat shock protein 60-mediated IRS-1/AKT/GLUT4 pathway and adipose inflammation: A potential therapeutic peptide for gestational diabetes mellitus. FASEB journal : official publication of the Federation of American Societies for Experimental Biology, 39(2), e70339.

Lietz S, et al. (2025) The antimicrobial peptide Angie 5 inhibits TcdA and TcdB from Clostridioides difficile. Cellular and molecular life sciences : CMLS, 82(1), 265.

Liao Z, et al. (2025) Involvement of interferon ?-producing mast cells in immune responses against melanocytes in vitiligo requires Mas-related G protein-coupled receptor X2 activation. Chinese medical journal, 138(11), 1367.

Nonog ZL, et al. (2025) Design and evaluation of a multi-epitope subunit vaccine against human norovirus using an immunoinformatics approach. Osong public health and research perspectives, 16(3), 236.

Wang F, et al. (2024) COSMIC-based mutation database enhances identification efficiency of HLA-I immunopeptidome. Journal of translational medicine, 22(1), 144.

Aslan A, et al. (2024) Therapeutic peptides for coronary artery diseases: in silico methods and current perspectives. Amino acids, 56(1), 37.

Ferreira JC, et al. (2024) Boosting immunity: synergistic antiviral effects of luteolin, vitamin C, magnesium and zinc against SARS-CoV-2 3CLpro. Bioscience reports, 44(8).

Banico EC, et al. (2024) Advancing one health vaccination: In silico design and evaluation of a multi-epitope subunit vaccine against Nipah virus for cross-species immunization using immunoinformatics and molecular modeling. PloS one, 19(9), e0310703.

Samman N, et al. (2024) Bioinformatics design of a peptide vaccine containing sarcoma antigen NY-SAR-35 epitopes against breast cancer and evaluation of its immunological function in BALB/c mouse model. PloS one, 19(6), e0306117.

Zhang TY, et al. (2024) Global fungal-host interactome mapping identifies host targets of candidalysin. Nature communications, 15(1), 1757.

Xu X, et al. (2024) Novel anti-inflammatory peptide alleviates liver ischemia-reperfusion injury. Journal of biomedical research, 39(1), 61.

Shetty S, et al. (2024) Immunoinformatics design of a multi-epitope vaccine for Chlamydia trachomatis major outer membrane proteins. Scientific reports, 14(1), 29919.

Cao X, et al. (2024) Antibiotics daptomycin interacts with S protein of SARS-CoV-2 to promote cell invasion of Omicron (B1.1.529) pseudovirus. Virulence, 15(1), 2339703.