

# Resource Summary Report

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## 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.

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## Data and Source Information

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

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## 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- $\beta$ 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 DERAAs bearing HLA-DRB1 alleles activate CD4<sup>+</sup> 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  $\gamma$ -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.

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.

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.

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 (B.1.1.529) pseudovirus. *Virulence*, 15(1), 2339703.