

Resource Summary Report

Generated by [dkNET](#) on Sep 8, 2026

HADDOCK

RRID:SCR_019091

Type: Tool

Proper Citation

HADDOCK (RRID:SCR_019091)

Resource Information

URL: <https://alcazar.science.uu.nl/services/HADDOCK2.2/>

Proper Citation: HADDOCK (RRID:SCR_019091)

Description: Software tool as information driven flexible docking approach for modeling of biomolecular complexes. User friendly integrative modeling of biomolecular complexes. HADDOCK v 2.2 offers new features such as support for mixed molecule types, additional experimental restraints and improved protocols, all of this in user friendly interface.

Synonyms: HADDOCK2.2, HADDOCK2.4, High Ambiguity Driven protein-protein DOCKing

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

Defining Citation: [PMID:12580598](#), [PMID:26410586](#)

Keywords: Molecular docking, data driven, biomolecular complex, grid computing, hybrid modeling, protein complex

Availability: Restricted

Resource Name: HADDOCK

Resource ID: SCR_019091

Alternate URLs: <https://www.bonvinlab.org/software/haddock2.2/>,
<https://wenmr.science.uu.nl/haddock2.4/>

Record Creation Time: 20220129T080343+0000

Record Last Update: 20260905T132846+0000

Ratings and Alerts

No rating or validation information has been found for HADDOCK.

No alerts have been found for HADDOCK.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 168 mentions in open access literature.

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

Nath S, et al. (2026) Attenuated lamin A-prohibitin2 interaction leads to mitochondrial dysfunction in LMNA 289 A>G-mediated dilated cardiomyopathy. The Journal of biological chemistry, 302(4), 111274.

Zhao J, et al. (2026) Simultaneous inhibition of bacterial virulence and anti-phage defense systems by synergistic bacteriophage counter-defense proteins. The EMBO journal, 45(8), 2756.

Karaca Ocak ??, et al. (2026) Computational screening of AI-derived cyclotides as putative VEGFR2 binders for wound-site angiogenesis. Scientific reports, 16(1).

Fathi S, et al. (2026) Systems Vaccinology-Integrated Proteomics to Develop a Novel Prophylactic and Therapeutic Vaccine Against Human Papillomavirus 16. Bioinformatics and biology insights, 20, 11779322261437247.

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.

Dermawan D, et al. (2026) Integrative molecular simulations reveal NeuroAid II mechanisms in ischemic stroke through network pharmacology, molecular dynamics, and pharmacophore modeling. Scientific reports, 16(1), 6161.

Nde J, et al. (2026) Integrative Structural Modeling of Intrinsically Disordered Regions in a Human HDAC2 Chromatin Remodeling Complex. bioRxiv : the preprint server for biology.

Liu Y, et al. (2026) Characterization of a Goose-Origin Avian Orthoreovirus with Interferon Suppression Activity. Viruses, 18(4).

Rahimi-Farsi N, et al. (2026) Immunoinformatic-driven design of a multi-epitope vaccine against Helicobacter pylori. Biochemistry and biophysics reports, 45, 102498.

Nashed A, et al. (2026) An in vitro approach for simulating divergent Golgi O-glycosylation of tumor-associated MUC1 from normal MUC1. Nature communications, 17(1).

Elrashedy A, et al. (2026) Immunoinformatics-based design of artificial chimeric proteins as universal vaccine candidates against foot-and-mouth disease virus serotypes A, O, and SAT2. *Scientific reports*, 16(1).

Nandish V, et al. (2026) Comparative pangenomics of *Pasteurella multocida* uncovers adhesins specific to capsular serogroup B strains associated with bovine host tropism. *BMC microbiology*, 26(1).

Rasheed N, et al. (2026) Nanobody-based analysis of RhoGTPase stress response in *Schizosaccharomyces pombe*: Role of *mtl2*. *Biotechnology reports (Amsterdam, Netherlands)*, 51, e00963.

Yin H, et al. (2026) A designed peptide disrupting viral protease cleavage restores cGAS-DNA phase separation and type I interferon responses. *PLoS pathogens*, 22(6), e1014291.

Yang T, et al. (2026) Cell-Based Immunization Combined with Single-Round Cell Panning Enables Discovery of PSMA-Targeting Nanobodies from Phage Display Libraries. *Biomolecules*, 16(2).

Martins FG, et al. (2026) A Review of Current Computational Tools for Peptide-Protein Docking. *Journal of computational chemistry*, 47(5), e70328.

Sahu A, et al. (2026) Impairment of two non-essential *LytR-cpsA-psr* (*Lcp*) cell wall ligases decelerate cell wall assembly in *Mycobacterium smegmatis*. *BMC microbiology*, 26(1).

Lipskerov F, et al. (2026) Precise Mapping of the Proteasome Interaction Region (PIR) of p62/SQSTM1: Decoupling Condensate Formation from Proteasome Recruitment. *Cells*, 15(4).

Shuvo MN, et al. (2026) Computational and immunoinformatics approaches for designing phytocompound-based drugs and a multi-epitope vaccine targeting FemA, a cell wall protein of *Staphylococcus aureus*. *PloS one*, 21(4), e0346271.

Solanki G, et al. (2026) *Streptomyces koyangensis* L-asparaginase: computational prediction of dual-mechanism BCL-2 interaction in acute lymphoblastic leukemia. *Scientific reports*, 16(1).