

# Resource Summary Report

Generated by [nidm-terms](#) on Jul 29, 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:** software application, data access protocol, software resource, web service, simulation software

**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:** 20260729T044455+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 83 mentions in open access literature.

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

Ardini M, et al. (2025) Functional and structural characterization of the human indolethylamine N-methyltransferase through fluorometric, thermal and computational docking analyses. *Biology direct*, 20(1), 50.

Naz H, et al. (2025) Utilizing the subtractive proteomics approach to design ensemble vaccine against *Candida lusitanae* for immune response stimulation; a bioinformatics study. *PLoS one*, 20(2), e0316264.

Sattar A, et al. (2025) Computational screening and molecular modeling of probiotic-derived peptides targeting the conserved HR1 domain of SARS-CoV-2 spike protein. *Scientific reports*, 15(1), 44952.

Pape BF, et al. (2025) Unraveling the Binding Mode of TSC2-Rheb through Protein Docking and Simulations. *Biochemistry*, 64(5), 1006.

Dashti NR, et al. (2025) Circulating lncRNA HOTAIR is a biomarker for pediatric acute lymphoblastic leukemia and mediator of miR-326 exosomal export. *Scientific reports*, 15(1), 4901.

Wu L, et al. (2025) Viral protease binds to nucleosomal DNA and cleaves nuclear cGAS that attenuates type I interferon. *mBio*, 16(4), e0339524.

Li M, et al. (2025) LONP1 facilitates pulmonary artery smooth muscle cell glycolytic reprogramming by degrading MPC1 in pulmonary hypertension. *Clinical science (London, England : 1979)*, 139(10), 479.

Canny MD, et al. (2025) Dynamic conformations of the *P. furiosus* MR-DNA complex link Mre11 nuclease activity to DNA-stimulated Rad50 ATP hydrolysis. *Communications biology*, 8(1), 548.

Ali M, et al. (2025) A Computational Approach for Designing a Peptide-Based Acetyl-CoA Synthetase 2 Inhibitor: A New Horizon for Anticancer Development. *Cell biochemistry and biophysics*, 83(3), 3465.

Suksomboon P, et al. (2025) Construction, expression, and characterization of scFv fragment against *Fasciola gigantica* cathepsin L1H. *Parasitology research*, 124(5), 51.

Khan A, et al. (2025) Exploring the Dynamic Interplay of Deleterious Variants on the RAF1-RAP1A Binding in Cancer: Conformational Analysis, Binding Free Energy, and Essential Dynamics. *Proteins*, 93(3), 684.

Luo R, et al. (2025) CPZ promotes the proliferation of gastric cancer by activating the Wnt pathway through binding with DVL2. *Discover oncology*, 16(1), 2085.

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.

Ortega-Vallbona R, et al. (2025) Computational Characterization of the Interaction of CARD Domains in the Apoptosome. *Biochemistry*, 64(2), 401.

Plichta J, et al. (2025) In Silico-Designed TGF $\beta$ RI/TGF $\beta$ RII Receptor Complex Peptide Inhibitors Exhibit Biological Activity In Vitro. *Journal of cellular and molecular medicine*, 29(8), e70548.

Yin H, et al. (2025) Circovirus Rep evades immune restriction by disrupting cGAS oligomerization and phase separation. *PLoS pathogens*, 21(6), e1013244.

Zengin K, et al. (2025) The Function of TER94 of *Spodoptera frugiperda* 9 Cells When Infected With Invertebrate Iridescent Virus-6. *Journal of basic microbiology*, 65(8), e70045.

Gonzalez-Lozano MA, et al. (2025) EndoMAP.v1 charts the structural landscape of human early endosome complexes. *Nature*, 643(8070), 252.

Yang Y, et al. (2025) Structure and nucleic acid interactions of the S $\beta$ 60 domain of the hepatitis delta virus small antigen. *Proceedings of the National Academy of Sciences of the United States of America*, 122(19), e2411890122.

Chatterjee S, et al. (2025) Molecular dynamics reveal potential effects of novel VHL variants on VHL-Elongin C binding in ccRCC patients from Eastern India. *Scientific reports*, 15(1), 13022.