Resource Summary Report

Generated by NIF on Apr 23, 2025

HADDOCK

RRID:SCR_019091
Type: Tool

Proper Citation

HADDOCK (RRID:SCR_019091)

Resource Information

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

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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 resource, data access protocol, software application, simulation software, web service

Defining Citation: PMID:12580598, PMID:26410586

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

Funding:

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: 20250422T060133+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 58 mentions in open access literature.

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

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

Helmold BR, et al. (2025) Spastin and alsin protein interactome analyses begin to reveal key canonical pathways and suggest novel druggable targets. Neural regeneration research, 20(3), 725.

Klössel S, et al. (2024) Yeast TLDc domain proteins regulate assembly state and subcellular localization of the V-ATPase. The EMBO journal, 43(9), 1870.

Yang K, et al. (2024) Molecular mechanism of specific HLA-A mRNA recognition by the RNA-binding-protein hMEX3B to promote tumor immune escape. Communications biology, 7(1), 158.

Williams ME, et al. (2024) HIV-1 Vif protein sequence variations in South African people living with HIV and their influence on Vif-APOBEC3G interaction. European journal of clinical microbiology & infectious diseases : official publication of the European Society of Clinical Microbiology, 43(2), 325.

Wang H, et al. (2024) Bacterial exonuclease III expands its enzymatic activities on single-stranded DNA. eLife, 13.

Masoumzadeh E, et al. (2024) Human CSTF2 RNA Recognition Motif Domain Binds to a U-Rich RNA Sequence through a Multistep Binding Process. Biochemistry, 63(19), 2449.

Sila T, et al. (2024) SARS-CoV-2 variant with the spike protein mutation F306L in the

southern border provinces of Thailand. Scientific reports, 14(1), 7729.

Xiao C, et al. (2024) Tailored UPRE2 variants for dynamic gene regulation in yeast. Proceedings of the National Academy of Sciences of the United States of America, 121(19), e2315729121.

Costa L, et al. (2024) Linking genotype to trophoblast phenotype in preeclampsia and HELLP syndrome associated with STOX1 genetic variants. iScience, 27(3), 109260.

Naveed M, et al. (2024) An in silico approach uncovering the competency of oncolytic human adenovirus 52 for targeted breast cancer virotherapy. Scientific reports, 14(1), 26405.

Iqbal MW, et al. (2024) Analysis of damaging non-synonymous SNPs in GPx1 gene associated with the progression of diverse cancers through a comprehensive in silico approach. Scientific reports, 14(1), 28690.

Jauhar MM, et al. (2024) Bioinformatics design of peptide binding to the human cardiac troponin I (cTnI) in biosensor development for myocardial infarction diagnosis. PloS one, 19(10), e0305770.

Sarvmeili J, et al. (2024) Immunoinformatics design of a structural proteins driven multi-epitope candidate vaccine against different SARS-CoV-2 variants based on fynomer. Scientific reports, 14(1), 10297.

Shang W, et al. (2024) Iterative In Silico Screening for Optimizing Stable Conformation of Anti-SARS-CoV-2 Nanobodies. Pharmaceuticals (Basel, Switzerland), 17(4).

Nugraha MF, et al. (2024) Novel prophylactic and therapeutic multi-epitope vaccine based on Ag85A, Ag85B, ESAT-6, and CFP-10 of Mycobacterium tuberculosis using an immunoinformatics approach. Osong public health and research perspectives, 15(4), 286.

Han J, et al. (2024) Tumor necrosis factor-inducible gene 6 protein and its derived peptide ameliorate liver fibrosis by repressing CD44 activation in mice with alcohol-related liver disease. Journal of biomedical science, 31(1), 54.

Taghizadeh MS, et al. (2024) Structure-guided design and cloning of peptide inhibitors targeting CDK9/cyclin T1 protein-protein interaction. Frontiers in pharmacology, 15, 1327820.

Cobe BL, et al. (2024) Bactericidal effectors of the Stenotrophomonas maltophilia type IV secretion system: functional definition of the nuclease TfdA and structural determination of TfcB. mBio, 15(7), e0119824.

Wang XT, et al. (2024) Zinc metalloprotease FgM35, which targets the wheat zinc-binding protein TaZnBP, contributes to the virulence of Fusarium graminearum. Stress biology, 4(1), 45.