

Resource Summary Report

Generated by [dkNET](#) on Sep 9, 2026

COACH

RRID:SCR_027684

Type: Tool

Proper Citation

COACH (RRID:SCR_027684)

Resource Information

URL: <https://aideepmed.com/COACH/>

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Description: Web application for protein-ligand binding site prediction. Starting from given structure of target proteins, COACH will generate complementray ligand binding site predictions using two comparative methods, TM-SITE and S-SITE, which recognize ligand-binding templates from the BioLiP protein function database by binding-specific substructure and sequence profile comparisons.

Synonyms: , COACH server

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

Defining Citation: [PMID:23975762](#)

Keywords: protein-ligand binding site prediction, protein, ligand, binding site prediction,

Funding: NIGMS GM083107;
NIGMS GM084222;
NSF Career Award

Availability: Free, Freely available

Resource Name: COACH

Resource ID: SCR_027684

Alternate URLs: <http://zhanglab.ccmb.med.umich.edu/COACH/>

Record Creation Time: 20251120T080608+0000

Record Last Update: 20260905T133555+0000

Ratings and Alerts

No rating or validation information has been found for COACH.

No alerts have been found for COACH.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 7 mentions in open access literature.

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

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).

Abdelazim AA, et al. (2025) In-silico screening and analysis of missense SNPs in human CYP3A4/5 affecting drug-enzyme interactions of FDA-approved COVID-19 antiviral drugs. Scientific reports, 15(1), 2153.

Van Norden M, et al. (2025) Strategies for robust, accurate, and generalizable benchmarking of drug discovery platforms. Bioinformatics (Oxford, England), 41(11).

Van Norden M, et al. (2024) Strategies for robust, accurate, and generalizable benchmarking of drug discovery platforms. bioRxiv : the preprint server for biology.

Bruggemann L, et al. (2023) Multiscale Analysis and Validation of Effective Drug Combinations Targeting Driver KRAS Mutations in Non-Small Cell Lung Cancer. International journal of molecular sciences, 24(2).

Shinwari K, et al. (2023) In-silico assessment of high-risk non-synonymous SNPs in ADAMTS3 gene associated with Hennekam syndrome and their impact on protein stability and function. BMC bioinformatics, 24(1), 251.

Ahmad HI, et al. (2021) In Silico Structural, Functional, and Phylogenetic Analysis of Cytochrome (CYPD) Protein Family. BioMed research international, 2021, 5574789.