

DAFTAR PUSTAKA

1. WHO. Noncommunicable diseases. 2023.
2. Indonesia KKR. Laporan Nasional Riskesdas 2018.
3. Roshandel G, Ghasemia-Kebria F, Malekzadeh R. Colorectal cancer: epidemiology, risk factors, and prevention. *Cancers (Basel)*. 2024;16.
4. Yusuf I, Pardamean B, Baurley JW, Budiarto A, Suriapranata I, Kusuma R, et al. Genetic risk factors for colorectal cancer in multiethnic Indonesians. 2021;1–9.
5. Morgan E, Arnold M, Gini A, Lorenzoni V, Cabasag CJ, Laversanne, Mathieu Vignat J, et al. Global burden of colorectal cancer in 2020 and 2040: incidence and mortality estimates from GLOBOCAN. 2022;72(2).
6. Alinia S, Asghari-jafarabadi M, Mahmoudi L. Predicting mortality and recurrence in colorectal cancer: Comparative assessment of predictive models. *Heliyon*. 2024;10(6).
7. Adiyasa MR. Pemanfaatan obat tradisional di Indonesia: distribusi dan faktor demografis yang berpengaruh. 2021;4(3):130–8.
8. Almeida M, Salam S, Rahmadani A, Narsa AC, Agung S, Kusuma F. The potency of the genus *Uncaria* from east borneo for herbal medicine purposes: A mini-review. *J Trop Pharm Chem*. 2022;6(2):167–76.
9. Oliveira LZ De, Farias ILG, Rigo ML, Glanzner WG, Gonçalves PBD, Cadoná FC, et al. Effect of *Uncaria tomentosa* extract on apoptosis triggered by oxaliplatin exposure on HT29 cells. 2014;(5).
10. Chu K, Miao M. Mechanism and target spot of burn and burn treatment based on network pharmacology mechanism and target spot of burn and burn treatment based on network pharmacology. 2019;
11. Thakur P, Kumar R, Choudhary N, Sharma R, Ashun C. Network pharmacology on mechanistic role of *Thymus linearis* Benth. against gastrointestinal and neurological diseases. *Phytomedicine*. 2023;121.
12. Hasibuan LS, Fariqi A, Prayitno L, Bangun MB. Integrasi data protein-protein interactions dan pathway untuk menentukan score pada pathway menggunakan analisis graf. 2023;3(6):719–27.
13. Hamim M, Al Z, Fadhilah HN, Hartanta F. Identifikasi interaksi protein-protein meningitis menggunakan clusterONE dan analisis jaringan. 2022;4(1):17–28.
14. Blake JA, Christie KR, Dolan ME, Drabkin HI, Hill DP. Gene ontology consortium: going forward. 2015;43:1049–56.
15. Shen J, Shalom J, Cock IE. The antiproliferative properties of *Uncaria*

- tomentosa Willd. DC. extracts against Caco2 and HeLa cancer cell lines. *Pharmacogn Nat Prod.* 2018;10(3):408–15.
16. Nazhand A, Durazzo A, Lucarini M, Silva AM, Souto SB, Severino P, et al. *Uncaria tomentosa* (Willd. ex Schult.): focus on nutraceutical aspects. *Curr Bioact Compd.* 2021;18(4).
 17. Batiha E-SG, Beshbishy MA, Wasef L, Elewa YH, El-Hack MEA, Taha AE, et al. *Uncaria tomentosa* (Willd. ex Schult.) DC.: a review on chemical constituents and biological activities. 2020;20(8).
 18. Zari A, Alfarteesh H, Buckner C, Lafrenie R. Treatment with *Uncaria tomentosa* promotes apoptosis in B16-BL6 mouse melanoma cells and inhibits the growth of B16-BL6 tumours. 2021;26(4).
 19. De Jong W, Melnyk M, Lozano LA, Rosales M, Garcia M. Una de gato: fate and future of a peruvian forest resource. *Occas Pap.* 1999;62(22).
 20. Lima RC De, Maria L, Valente M, Macedo F, Maria L, Barreto F, et al. Antiviral and virucidal activities of *Uncaria tomentosa* (cat's claw) against the chikungunya virus. 2024;16.
 21. Galliford C V, Scheidt KA. Pyrrolidinyl-spirooxindole natural products as inspirations for the development of potential therapeutic agents. 2007;46.
 22. Medicines AE. Assessment report on *Uncaria tomentosa* (Willd. ex Schult.) DC., cortex. 2015.
 23. Yayik N, Perez M, Molins E, Bosch J, Amat M. Studies on the enantioselective synthesis of e-ethylidene-bearing spiro{indolizidine-1,3'-oxindole} alkaloids. *Molecules.* 2021;26(2):428.
 24. Reis SRIN, Valente LMM, Sampaio AL, Siani AC, Gandini M, Azeredo EL, et al. Immunomodulating and antiviral activities of *Uncaria tomentosa* on human monocytes infected with dengue virus-2. *Int Immunopharmacol.* 2008;8(3):468–76.
 25. Wurm M, Kacani L, Laus G, Keplinger K, Dierich MP. Pentacyclic oxindole alkaloids from *uncaria tomentosa* induce human endothelial cells to release a lymphocyte-proliferation-regulating factor. *Planta Med.* 1998;64(8):701–4.
 26. Kosmider A, Czepielewska E, Kuras M, Gulewicz K, Pietrzak W, Nowak R, et al. *Uncaria tomentosa* leaves decoction modulates differently ROS production in cancer and normal cells, and effects cisplatin cytotoxicity. *Molecules.* 2017;22(4):620.
 27. Miftahussurur M. Buku ajar aspek diagnosis dan terapi terkini kanker kolorektal. Airlangga University Press; 2021.
 28. Sayuti M. Kanker kolorektal. 5(2):76–88.
 29. Dewi NNA, Widya Suksmarini NMP. Metilasi DNA dalam perkembangan kanker kolorektal. *Intisari Sains Medis.* 2018;9(2):124–30.

30. Macdonald JS, Woolley P V, Smythe T, Ueno W, Hoth D, Schein PS. 5-fluorouracil, adriamycin, and mitomycin-c (fam) combination chemotherapy in the treatment of advanced gastric cancer. *Am Cancer Soc.* 2007;44(1):42–7.
31. Putri PVP, Susanti NM., Laksmiani NP. Senyawa kuersetin sebagai agen antikanker kolorektal secara in silico. *J Kim.* 2019;13(2):166–71.
32. Ismail NE, Ramadhani D. Diagnosis dan terapi kanker kolorektal dengan HSP90. *J Farmaka.* 2019;17(2):87–93.
33. Sativa NO, Putri AO, Natasya Z, Rislia RA. Penambatan molekul senyawa aktif Curcuma xanthorrhiza Roxb. kandidat antikanker kolorektal terhadap reseptor lymphocyte-specific protein tyrosine kinase. *J Ilm Farm.* 2024;9(2):115–27.
34. Kola I, Landis J. Can the pharmaceutical industry reduce attrition rates? *Nat Rev Drugs Discov.* 2004;3(8):711–5.
35. Zhang W. Network pharmacology: A further description. *Netw Pharmacol.* 2016;1(1):1–14.
36. Zhang WJ. Network chemistry, network toxicology, network informatics, and network behavioristics: A scientific outline. *Netw Biol.* 2016;6(1):37–9.
37. Li S, Zhang B. Traditional chinese medicine network pharmacology: theory, methodology and application. *Chin J Nat Med.* 2013;11(2):110–20.
38. Sarker SD, Nahar L. Computational phytochemistry. Elsevier Science; 2024.
39. Rivas JD Las. Protein-protein interactions essentials: key concepts to building and analyzing interactome networks. *PLoS Comput Biol.* 2010;24(6).
40. Bultinck J, Lievens S, Tavernier J. Protein-protein interactions: network analysis and applications in drug discovery. *Curr Pharm Des.* 2012;18(30):4619–29.
41. Feng Y, Wang Q, Wang T. Drug target protein-protein interaction networks: a systematic perspective. *Biomed Res Int.* 2017;
42. Kanehisa M, Sato Y, Kawashima M, Furumichi M, Tanabe M. KEGG as a reference resource for gene and protein annotation. *Nucleic Acid Res.* 2016;44:457–62.
43. Chen L, Zhang Y-H, Wang S, Zhang Y, Huang T, Cai Y-D. Prediction and analysis of essential genes using the enrichments of gene ontology and KEGG pathways. *PLoS One.* 2017;12(9).
44. Xing Z, Chu C, Lei C, Xiangyin K. The use of gene ontology terms and KEGG pathways for analysis and prediction of oncogenes. *Biochim Biophys Acta.* 2016;1860(11):2725–34.

45. Du J, Li M, Yuan Z, Guo M, Song J, Xie X, et al. A decision analysis model for KEGG pathway analysis. *BMC Bioinformatics*. 2016;17(1):407.
46. Kanehisa M, Furumichi M, Tanabe M, Sato Y, Morishima K. KEGG: new perspectives on genomes, pathways, diseases and drugs. *Nucleic Acid Res*. 2017;45(1):353–61.
47. Du J, Yuan Z, Ma Z, Song J, Xie X, Chen Y. KEGG-PATH: Kyoto encyclopedia of genes and genomes-based pathway analysis using a path analysis model. *Mol Biosyst*. 2014;10(9):2441–7.
48. Monika G, Punam G, Sarbjot S, Gupta GD. An overview on molecular docking. *Int J Drug Dev Res*. 2010;2(2):219–31.
49. Jimenez-Luna J, Cuzzolin A, Bolcato G, Sturlese M, Moro S. A deep-learning approach toward rational molecular docking protocol selection. *Molecules*. 2020;25(11).
50. McNutt AT, Francoeur P, Aggarwal R, Masuda T, Meli R, Ragoza M, et al. GNINA 1.0: molecular docking with deep learning. *J Cheminform*. 2021;13(1):43.
51. Kitchen DB, Decornez H, Furr JR, Bajorath J. Docking and scoring in virtual screening for drug discovery: methods and applications. *Nat Rev Drugs Discov*. 2004;3(11):935–49.
52. Wang X, Shen Y, Wang S, Li S, Zhang W, Liu X, et al. PharmMapper 2017 update: a web server for potential drug target identification with a comprehensive target pharmacophore database. *Nucleic Acids Res*. 2017;45.
53. Daina A, Michielin O, Zoete V. Swiss target prediction: updated data and new features for efficient prediction of protein targets of small molecules. *Nucleic Acids Res*. 2019;47.
54. Afendi FM, Okada T, Yamazaki M, Hirai-Morita A, Nakamura Y, Nakamura K, et al. KNApSACk family databases: Integrated metabolite-plant species databases for multifaceted plant research. *Plant Cell Physiol*. 2012;53(2):1–12.
55. Murdiana HE, Murwanti R, Fakhrudin N, Ikawati Z. Multi-target mechanism of polyherbal extract to treat diabetic foot ulcer based on network pharmacology and molecular docking. *J Herbmed Pharmacol*. 2024;13(2):289–99.
56. Liu Z, Guo F, Wang Y, Li C, Zhang X, Li H. BATMAN-TCM: a bioinformatics analysis tool for molecular mechanism of traditional chinese medicine. *Nat Publ Gr*. 2016;
57. Heberle H, Meirelles GV, da Silva FR, Telles GP, Minghim R. InteractiVenn: a web-based tool for the analysis of sets through venn diagrams. *BMC Bioinformatics*. 2015 May;16(1):169.
58. Szklarczyk D, Franceschini A, Wyder S, Forslund K, Heller D, Huerta-

- Cepas J, et al. STRING v10: protein–protein interaction networks, integrated over the tree of life. *Nucleic Acids Res.* 2015 Jan;43:447–52.
59. Bateman A, Martin M-J, Orchard S, Magrane M, Ahmad S, Alpi E, et al. UniProt: the universal protein knowledgebase in 2023. *Nucleic Acids Res.* 2023 Jan;51:523–31.
60. Alam MS, Rahaman MM, Sultana A, Wang G, Mollah MNH. Statistics and network-based approaches to identify molecular mechanisms that drive the progression of breast cancer. *Comput Biol Med.* 2022 Jun;
61. Halgren TA. Merck molecular force field. i. basis, form, scope, parameterization, and performance of MMFF94. *J Comput Chem.* 1996;17(5–6):490–519.
62. Hanwell MD, Curtis DE, Lonie DC, Vandermeersch T, Zurek E, Hutchison GR. Avogadro: An advanced semantic chemical editor, visualization, and analysis platform. *J Cheminform.* 2012;4(8).
63. Burley SK, Piehl DW, Vallat B, Zardecki C. RCSB protein data bank: supporting research and education worldwide through explorations of experimentally determined and computationally predicted atomic level 3D biostructures. *IUCrJ.* 2024 May 1;11(3):279–86.
64. U.S. Department of Agriculture. Dr. duke's phytochemical and ethnobotanical databases.
65. Kanehisa M. Linking databases and organisms: GenomeNet resources in Japan. *Comput corner.* 1997;442–6.
66. Consortium TU. UniProt: a hub for protein information. 2015;43:204–12.
67. Chicco D, Agapito G. Nine quick tips for pathway enrichment analysis. *PLoS Comput Biol.* 2022;18(8):1–15.
68. Francipane MG, Lagasse E. mTOR pathway in colorectal cancer: an update. 2013;5(1).
69. Moshawih S, Lim AF, Ardianto C, Goh KW, Kifli N, Goh HP, et al. Target-based small molecule drug discovery for colorectal cancer: A review of molecular pathways and in silico studies. *Biomolecules.* 2022;12(7).
70. Asano D, Takakusa H, Nakai D. Oral absorption of middle-to-large molecules and its improvement, with a focus on new modality drugs. *Pharmaceutics.* 2024;
71. Hakiki A, Andika A, Rahmawati R. Studi molecular docking dan prediksi ADMET senyawa turunan kurkumin sebagai inhibitor kasein kinase 2- α . *J Ilmu Kefarmasian.* 2024;5(2):195.
72. Katayama N. Quantitative analysis of aggregation-solubility relationship by in-silico solubility prediction. 2010;99–107.

73. Wulandari RP, Gabriel K, Nurdin HA, Pakhrul DHF, Harits S, Prameswari N, et al. In silico study of secondary metabolite compounds in parsley (*Petroselinum crispum*) as a drug therapy for blood cancer (Myeloproliferative Neoplasm (MPN)) targeting JAK-2. *Indones J Chem Sci.* 2023;12(2).
74. Deep-PK : Theory. 1998.
75. Abdullah SS, Putra PP, Antasionasti I, Suoth EJ, Putri R, Abdullah I. Analisis sifat fisikokimia, farmakokinetik dan toksikologi pada pericarpium pala (*Myristica fragrans*) secara artificial intelligence. 2021;14(2).
76. Smyth MS, Martin JHJ. Review xray crystallography. 2000;(53):8–14.
77. Panwar V, Singh A, Bhatt M, Tonk RK, Azizov S, Raza AS, et al. Multifaceted role of mTOR (mammalian target of rapamycin) signaling pathway in human health and disease. 2023;
78. Djinovic-carugo K, Carugo O, Djinovic-carugo K, Carugo O. Missing strings of residues in protein crystal structures. 2016;
79. Liao J, Wang Q, Wu F, Huang Z. In silico methods for identification of potential active sites of therapeutic targets. *Molecules.* 2022;27.

