

DAFTAR PUSTAKA

- A. Toropov, A., P. Toropova, A., Benfenati, E., & Fanelli, R. (2016). QSAR as a Random Event: Selecting of the Molecular Structure for Potential Anti-tuberculosis Agents. *Anti-Infective Agents*, 14(1), 3–10.
- Abdelli, I., Hassani, F., Bekkel Brikci, S., & Ghalem, S. (2021). In silico Study The Inhibition of Angiotensin Converting Enzyme 2 Receptor of COVID-19 By Ammoides Verticillata Components Harvested From Western Algeria. *Journal of Biomolecular Structure and Dynamics*, 39(9), 3263–3276.
- Abdullahi, M., Adeniji, S. E., Arthur, D. E., & Musa, S. (2020). Quantitative Structure-activity Relationship (QSAR) Modelling Study of Some Novel Carboxamide Series as New Anti-tubercular Agents. *Bulletin of the National Research Centre*, 44(136), 1–13.
- Adeniji, S. E., Uba, S., & Uzairu, A. (2018). QSAR Modeling and Molecular Docking Analysis of Some Active Compounds against *Mycobacterium tuberculosis* Receptor (Mtb CYP121). *Journal of Pathogens*, 2018(5), 1–24.
- Adeniji, S. E., Uba, S., Uzairu, A., & Arthur, D. E. (2019). A Derived QSAR Model for Predicting Some Compounds as Potent Antagonist against *Mycobacterium tuberculosis*: A Theoretical Approach. *Advances in Preventive Medicine*, 10(5), 1–18.
- Aggarwal, A., Parai, M. K., Shetty, N., Wallis, D., Woolhiser, L., Hastings, C., Dutta, N. K., Galaviz, S., Dhakal, R. C., Shrestha, R., Wakabayashi, S., Walpole, C., Matthews, D., Floyd, D., Scullion, P., Riley, J., Epemolu, O., Norval, S., Snavely, T., ... Sacchettini, J. C. (2017). Development of a Novel Lead that Targets *M. tuberculosis* Polyketide Synthase 13. *Cell*, 170(2), 249–259.
- Aini, N., Ramadiani, R., & Hatta, H. R. (2017). Sistem Pakar Pendiagnosa Penyakit Tuberkulosis. *Informatika Mulawarman : Jurnal Ilmiah Ilmu Komputer*, 12(1), 56–68.
- Aini, N. S., Ansori, A. N. M., Kharisma, V. D., Murtadlo, A. A. A., Tamam, M. B., Sucipto, T. H., Jakhmola, V., Rebezov, M., Saklani, T., & Zainul, R. (2023). An In Silico Study: Phytochemical Compounds Screening of *Garcinia atroviridis Griff. ex T. Anders* as Anti-DENV. *Journal of Pure and Applied Microbiology*, 17(4), 2467–2478.
- Alsayed, S. S. R., Lun, S., Luna, G., Beh, C. C., Payne, A. D., Foster, N., Bishai, W. R., & Gunosewoyo, H. (2020). Design, Synthesis, and Biological Evaluation of Novel Arylcarboxamide Derivatives as Anti-tubercular Agents. *RSC Advances*, 10(13), 7523–7540.
- Ascher, D. B., Jubb, H. C., Pires, D. E. V., Ochi, T., Higuero, A., & Blundell, T. L. (2015). Protein-protein Interactions: Structures and Druggability. *Multifaceted Roles of Crystallography*, 4(6), 141–163.

- Azzam, K. AL. (2023). SwissADME and pkCSM Webservers Predictors: an Integrated Online Platform for Accurate and Comprehensive Predictions for In Silico ADME/T Properties of Artemisinin and its Derivatives. *Complex Use of Mineral Resources*, 325(2), 14–21.
- Bagchi, M. C., & Ghosh, P. (2015). Anti-Tubercular Drug Designing Using Structural Descriptors. *Advances in Mathematical Chemistry and Applications*, 2(3), 179–190.
- Banuls, A. L., Sanou, A., Van Anh, N. T., & Godreuil, S. (2015). *Mycobacterium tuberculosis*: Ecology and Evolution of a Human Bacterium. *Journal of Medical Microbiology*, 64(11), 1261–1269.
- Bastos, M. L., Lan, Z., & Menzies, D. (2017). An updated Systematic Review and Meta-analysis for Treatment of Multidrug-resistant Tuberculosis. *European Respiratory Journal*, 49(3), 1–15.
- Bon, C., Cabantous, S., Julien, S., Guillet, V., Chalut, C., Rima, J., Brison, Y., Malaga, W., Sanchez-Dafun, A., Gavalda, S., Quémard, A., Marcoux, J., Waldo, G. S., Guilhot, C., & Mourey, L. (2022). Solution Structure of the Type I Polyketide Synthase Pks13 from *Mycobacterium tuberculosis*. *BMC Biology*, 20(1), 1–19.
- Brandis, G., & Hughes, D. (2018). Mechanisms of Fitness Cost Eduction for Rifampicin-Resistant Strains With Deletion or Duplication Mutations in rpoB. *Scientific Reports*, 8(1), 1–6.
- Brites, D., & Gagneux, S. (2015). Co-evolution of *Mycobacterium tuberculosis* and *Homo sapiens*. *Immunological Reviews*, 264(1), 6–24.
- Camassa, S., Palucci, I., Iantomasi, R., Cubeddu, T., Minerva, M., De Maio, F., Jouny, S., Petruccioli, E., Goletti, D., Ria, F., Sali, M., Sanguinetti, M., Manganelli, R., Rocca, S., Brodin, P., & Delogu, G. (2017). Impact of pe_pgrs33 Gene Polymorphisms on *Mycobacterium tuberculosis* Infection and Pathogenesis. *Frontiers in Cellular and Infection Microbiology*, 7(3), 1–16.
- Chemaxon, 2014, Log P and Log D Calculation, <https://docs.chemaxon.com/display/docs/logp-and-logd-calculations.md>, 1 januari 2024.
- Chemical Computing Grup, 2017, Molecular Operating Environment, <https://www.chemcomp.com/>, 13 januari 2024.
- Choudhary, S., Kesavan, A. K., Juneja, V., & Thakur, S. (2023). Molecular Modeling, Simulation and Docking of Rv1250 Protein from *Mycobacterium tuberculosis*. *Frontiers in Bioinformatics*, 3(6), 1–12.
- Dearden, J. C. (2017). The History and Development of Quantitative Structure-Activity Relationships (QSARs). *International Journal of Quantitative Structure-Property Relationships*, 2(2), 36–46.

- Drwal, M. N., Banerjee, P., Dunkel, M., Wettig, M. R., & Preissner, R. (2014). ProTox: A Web Server for the In silico Prediction of Rodent Oral Toxicity. *Nucleic Acids Research*, 42(4), 53–58.
- Dwivedi, N., Mishra, B. N., & Katoch, V. M. (2014). 2D-QSAR Model Development and Analysis on Variant Groups of Anti-tuberculosis Drugs. *Bioinformation*, 7(1), 82–90.
- Eddabra, R., & Neffa, M. (2020). Mutations Associated with Rifampicin Resistance in *Mycobacterium tuberculosis* Isolates from Moroccan Patients: Systematic Review. *Interdisciplinary Perspectives on Infectious Diseases*, 23(4), 8–15.
- Erazua, E. A., Akintelu, S. A., Adelowo, J. M., Odoemene, S. N., Josiah, O. M., Raheem, S. F., Latona, D. F., Adeoye, M. D., Esan, A. O., & Oyebamiji, A. K. (2021). QSAR and Molecular Docking Studies on Nitro (Triazole/Imidazole)-Based Compounds as Anti-Tubercular Agents. *Tropical Journal of Natural Product Research*, 5(11), 2022–2029.
- Ferrari, I. V. (2023). Assessing Antibiotic Safety : A Comparative Study of Four Promising Candidates Using pKCSM Database. *Journal Clinical Physiology*, 4(1), 1–8.
- Firdasari D., (2021), Studi *In Silico* Aktivitas Senyawa Turunan Zerumbon Hasil Subtitusi Ekso-Metilen Sebagai Kandidat Antimalaria, *Skripsi*, Fakultas Ilmu Kesehatan Universitas Islam Negeri Alauddin Makassar.
- Gagneux, S. (2018). Ecology and Evolution of *Mycobacterium tuberculosis*. *Nature Reviews Microbiology*, 16(4), 202–213.
- Gomes, M. N., Braga, R. C., Grzelak, E. M., Neves, B. J., Muratov, E., Ma, R., Klein, L. L., Cho, S., Oliveira, G. R., Franzblau, S. G., & Andrade, C. H. (2017). QSAR-driven Design, Synthesis and Discovery of Potent Chalcone Derivatives With Antitubercular Activity. *European Journal of Medicinal Chemistry*, 137(6), 126–138.
- Gordon, S. V., & Parish, T. (2018). Microbe Profile: *Mycobacterium tuberculosis*: Humanity's Deadly Microbial Foe. *Microbiology (United Kingdom)*, 164(4), 437–439.
- Ha, N. X., Anh, H. T. N., Khanh, P. N., Ha, V. T., Ha, N. V., Huong, T. T., & Cuong, N. M. (2023). In silico and ADMET Study of *Morinda longissima* Phytochemicals Against TNF- α for Treatment of Inflammation-Mediated Diseases. *Vietnam Journal of Chemistry*, 61(S1), 57–63.
- Hayakawa, I., Shioda, S., Chinen, T., Usui, T., & Kigoshi, H. (2019). Structure-activity Relationship Study of Gatastatin Based on The TOPLISS Tree Approach. *Heterocycles*, 99(1), 238–247.
- Howard, N. C., & Khader, S. A. (2020). Immunometabolism During *Mycobacterium tuberculosis* Infection. *Trends in Microbiology*, 28(10), 832–850.

- Huang, L., Nazarova, E. V., & Russell, D. G. (2019). *Mycobacterium tuberculosis*: Bacterial Fitness within the Host Macrophage. *Microbiology Spectrum*, 7(2), 1–18.
- Iacobino, A., Fattorini, L., & Giannoni, F. (2020). Drug-resistant Tuberculosis 2020: Where We Stand. *Applied Sciences (Switzerland)*, 10(6), 1–17.
- Janardhan, S., John, L., Prasanthi, M., Poroikov, V., & Narahari Sastry, G. (2017). A QSAR and Molecular Modelling Study Towards New Lead Finding: Polypharmacological Approach to *Mycobacterium tuberculosis*. *SAR and QSAR in Environmental Research*, 28(10), 815–832.
- Jiao, J. Y., Mao, Y. J., Feng, A. W., Li, X. F., Li, M. T., & Zhang, X. H. (2017). The Regioselective C5 Halogenation of Quinolines Using Sodium Halides Under Transition Metal-free Conditions. *Tetrahedron*, 73(11), 1482–1488.
- Kapp, E., Malan, S. F., Joubert, J., & Sampson, S. L. (2017). Small Molecule Efflux Pump Inhibitors in *Mycobacterium tuberculosis*: A Rational Drug Design Perspective. *Mini-Reviews in Medicinal Chemistry*, 18(1), 72–86.
- Kartasasmita, C. B. (2016). Epidemiologi Tuberkulosis. *Sari Pediatri*, 11(2), 103–124.
- Kemenkes RI, (2022), *Laporan Program Penanggulangan Tuberkulosis Tahun 2022*. Cetakan Edisi 2022, 1-132, Kementerian Kesehatan RI, Jakarta.
- Khani-Meinagh, H., Mostafavi, H., Reiling, N., Mahdavi, M., & Zarrini, G. (2019). Design, Synthesis and Evaluation of Biological Activities of Some Novel Anti-TB Agents with Bio-reducible Functional Group. *BioImpacts*, 9(4), 199–209.
- Khawbung, J. L., Nath, D., & Chakraborty, S. (2021). Drug Resistant Tuberculosis: A Review. *Comparative Immunology, Microbiology and Infectious Diseases*, 74(4), 147–571.
- Loerger, T. R., O'Malley, T., Liao, R., Guinn, K. M., Hickey, M. J., Mohaideen, N., Murphy, K. C., Boshoff, H. I. M., Mizrahi, V., Rubin, E. J., Sassetti, C. M., Barry, C. E., Sherman, D. R., Parish, T., & Sacchettini, J. C. (2013). Identification of New Drug Targets and Resistance Mechanisms in *Mycobacterium tuberculosis*. *PLOS ONE*, 8(9), 1–13.
- Luijs, L., & Preez, I. du. (2020). The Echo of Pulmonary Tuberculosis: Mechanisms of Clinical Symptoms and other Disease-induced Systemic Complications. *Clinical Microbiology Reviews*, 33(4), 1–19.
- Madhulata Kumari. (2018). Comparative Analysis of Machine Learning Based QSAR Models and Molecular Docking Studies to Screen Potential Anti-tubercular Inhibitors Against InhA of *Mycobacterium tuberculosis*. *Int. J. Computational Biology and Drug Design*, 11(3), 210–235.
- Mar'iyah, K., & Zulkarnain. (2021). Patofisiologi Penyakit Infeksi Tuberkulosis.

- In Prosiding Seminar Nasional Biologi*, 7(1), 88–92.
- Marpaung, F. R., & Simorangkir, M. (2021). *Seminar Nasional Kimia Dan Pendidikan Kimia 2021*. 5(2), 275–279.
- Marrakchi, H., Lanéelle, M. A., & Daffé, M. (2014). Mycolic Acids: Structures, Biosynthesis, and Beyond. *Chemistry and Biology*, 21(1), 67–85.
- Mashabela, G. T., De Wet, T. J., & Warner, D. F. (2019). *Mycobacterium tuberculosis* Metabolism. *Microbiology Spectrum*, 2(5), 1107–1128.
- Meisoindigo, T., Inhibitor, S., Arba, M., Ardiansyah, R., & Leonita, M. (2016). Studi Hubungan Kuantitatif Struktur-aktivitas Senyawa Turunan Meisoindigo Sebagai Inhibitor CDK4. *Journal Kimia Riset*, 1(2), 129–136.
- Mody, V., Ho, J., Wills, S., Mawri, A., Lawson, L., Ebert, M. C. C. J. C., Fortin, G. M., Rayalam, S., & Taval, S. (2021). Identification of 3-chymotrypsin Like Protease (3CLPro) Inhibitors as Potential Anti-SARS-CoV-2 Agents. *Communications Biology*, 4(1), 10.
- Muhammad, U., Uzairu, A., & Ebuka Arthur, D. (2018). Review on: Quantitative Structure Activity Relationship (QSAR) Modeling. *Journal of Analytical & Pharmaceutical Research*, 7(2), 1–9.
- Muscia, G. C., Carnevale, J. P., Luczywo, A., Victoria Peláez, M., Rodríguez Ó Toole, A., Buldain, G. Y., Casal, J. J., & Asis, S. E. (2019). Synthesis, Anti-tuberculosis Activity and QSAR Study of 2,4-diarylquinolines and Analogous Polycyclic Derivatives. *Arabian Journal of Chemistry*, 12(7), 932–945.
- Muslih, F. A., Kurniawati, E., Ma, B., Ilmu, I., Bhakti, K., Islam, U., Maulana, N., Brw, K. V., & Kadiri, U. (2023). ADMET Prediction of the Dominant Compound from Mangosteen (*Garcinia mangostana L.*) using pkCSM : A Computational Approach. *International Journal of Contemporary Sciences*, 1(1), 33–38.
- Mvondo, J. G. M., Matondo, A., Mawete, D. T., Bambi, S.-M. N., Mbala, B. M., & Lohohola, P. O. (2021). In Silico ADME/T Properties of Quinine Derivatives using SwissADME and pkCSM Webservers. *International Journal of TROPICAL DISEASE & Health*, 42(11), 1–12.
- Nidhi, & Siddiqi, M. I. (2014). Recent Advances in QSAR-based Identification and Design of Anti-Tubercular Agents. *Current Pharmaceutical Design*, 20(27), 4418–4426.
- Nugraha, R, (2023), Telaah in silico dan Uji Aktivitas Senyawa Sulfonyl-amidine Turunan Piperin Sebagai Kandidat Anti-TB MDR, *Tesis*, Fakultas Pascasarjana Universitas Hasanuddin, Makassar.
- Nurhajri, N. A., Kurniawan, E., & Mentari, I. N. (2022). Deteksi Resistensi *Mycobacterium tuberculosis* Terhadap Antibiotik Etambutol Dengan Teknik Polymerase Chain Reaction (PCR). *Media of Medical Laboratory Science*,

- 6(1), 16–22.
- Odingo, J. O., Early, J. V., Smith, J., Johnson, J., Bailey, M. A., Files, M., Guzman, J., Ollinger, J., Korkegian, A., Kumar, A., Ovechkina, Y., & Parish, T. (2019). 8-Hydroxyquinolines are Bactericidal Against *Mycobacterium tuberculosis*. *Drug Development Research*, 80(5), 566–572.
- Patel, K. D., Vekariya, R. H., Prajapati, N. P., Patel, D. B., Patel, H. D., Shaikh, T., Rajani, D. P., Rajani, S., Shah, N. S., & Jhala, D. (2020). Synthesis of N’-(Quinazolin-4-yl)isonicotinohydrazides and Their Biological Screening, Docking and ADME Studies. *Arabian Journal of Chemistry*, 13(1), 1986–2000.
- Patel, N., O’Malley, T., Zhang, Y. K., Xia, Y., Sunde, B., Flint, L., Korkegian, A., Ioerger, T. R., Sacchettini, J., Alley, M. R. K., & Parish, T. (2017). A Novel 6-benzyl Ether Benzoxaborole is Active Against *Mycobacterium tuberculosis* In Vitro. *Antimicrobial Agents and Chemotherapy*, 61(9), 1–39.
- Patel, S. R., Gangwal, R., Sangamwar, A. T., & Jain, R. (2015). Synthesis, Biological Evaluation and 3D QSAR Study of 2,4-Disubstituted Quinolines as Anti-tuberculosis Agents. *European Journal of Medicinal Chemistry*, 93(4), 511–522.
- Pathak, A., K. Singour, P., K. Srivastava, A., Gouda, P., Kumar, S., & K. Goutam, B. (2016). Hansch Analysis of Novel Acetamide Derivatives as Highly Potent and Specific MAO-A Inhibitors. *Central Nervous System Agents in Medicinal Chemistry*, 16(2), 143–151.
- Pires, D. E. V., & Ascher, D. B. (2016). CSM-lig: a Web Server for Assessing and Comparing Protein-small Molecule Affinities. *Nucleic Acids Research*, 44(3), 557–561.
- Pires, D. E. V., Blundell, T. L., & Ascher, D. B. (2015). pkCSM: Predicting Small-Molecule Pharmacokinetic and Toxicity Properties Using Graph-based Signatures. *Journal of Medicinal Chemistry*, 58(9), 4066–4072.
- Putriani, H. N. (2016). Hubungan Kuantitatif Struktur Aktivitas Senyawa 1-Benzene Acyl-2-(Methylindol-3-Yl)-Benzimidazole Sebagai Inhibitor Polimerisasi Tubulin dan Antiproliferasi Mcf-7 Serta Studi Farmakofor, *Virtual Screening, Docking Molekuler, Uji Toksisitas, dan Profil Farmakokinetik, Skripsi*, Fakultas Kedokteran dan Ilmu Kesehatan UIN Alaiiddin, Makassar.
- Rahman, N., Basharat, Z., Yousuf, M., Castaldo, G., Rastrelli, L., & Khan, H. (2020). Virtual Screening of Natural Products Against Type II Virtual Screening of Natural Products Against Yype II Transmembrane Serine Protease. *Molecules*, 25(10), 1–12.
- Ravimohan, S., Kornfeld, H., Weissman, D., & Bisson, G. P. (2018). Tuberculosis and Lung Damage: From Epidemiology to Pathophysiology. *European*

- Respiratory Review*, 27(147), 1–20.
- Ruswanto, R. (2015). Molecular Docking Empat Turunan Isonicotinohydrazide pada *Mycobacterium tuberculosis* Enoyl-Acyl Carrier Protein Reductase (InhA). *Jurnal Kesehatan Bakti Tunas Husada: Jurnal Ilmu-Ilmu Keperawatan*, 13(1), 135–141.
- Sabine Ehrt, Dirk Schnappinger, K. Y. R. (2017). Metabolic Principles of Persistence and Pathogenicity in *Mycobacterium tuberculosis*. *Nat Rev Microbiol*, 176(1), 139–148.
- Saleh, W, (2015), Studi Hubungan Kuantitatif Struktur-Studi Hubungan Kuantitatif Struktur-Aktivitas Anti-tuberkulosis Senyawa Amidasi Etil P-Metoksisinamat dengan Pendekatan Hansch dan Penambatan Molekuler Pada Enzim InhA, *Skripsi*, Fakultas Kedokteran dan Ilmu Kesehatan UIN Syarif Hidayatullah, Jakarta
- Saritha Jyostna, T., Anusha Reddy, K., Ashma, M., Anuradha Bai, S., & Jyothi, V. (2019). Molecular Properties Prediction of Phenothiazine Derivatives by Using Swiss ADME, PkCSM, Lazar and Protox. *World Journal of Pharmaceutical Sciences*, 7(11), 65–71.
- Sigurdardottir, A. G., Winter, A., Sobkowicz, A., Fragai, M., Chirgadze, D., Ascher, D. B., Blundell, T. L., & Gherardi, E. (2015). Exploring the Chemical Space of the Lysine-binding Pocket of the First Kringle Domain of Hepatocyte Growth Factor/scatter factor (HGF/SF) Yields a New Class of Inhibitors of HGF/SF-MET Binding. *Chemical Science*, 6(11), 6147–6157.
- Singh, N., Dalal, V., & Kumar, P. (2018). Structure Based Mimicking of Phthalic Acid Esters (PAEs) and Inhibition of hACMSD, an Important Enzyme of the Tryptophan Kynurenine Metabolism Pathway. *International Journal of Biological Macromolecules*, 108(12), 214–224.
- Siswandono, 2016, *Kimia Medisinal*, Cetakan Edisi II, 447-487, Airlangga University Press, Surabaya.
- Singh, R., Dwivedi, S. P., Gaharwar, U. S., Meena, R., Rajamani, P., & Prasad, T. (2020). Recent Updates on Drug Resistance in *Mycobacterium tuberculosis*. *Journal of Applied Microbiology*, 128(6), 1547–1567.
- Szumowsk, J. D., & Lynch, J. B. (2015). Profile of Delamanid for The Treatment of Multidrug-resistant Tuberculosis. *Drug Design, Development and Therapy*, 9(5), 677–682.
- Taufiq M., 2021, Analisis Hubungan Kuantitatif Struktur dan Aktivitas Senyawa Turunan Aminoalkanol Xanton Sebagai Antikanker Menggunakan Metode Semiempiris Austin Model 1, *Skripsi*, Fakultas Sains dan Teknologi Universitas Islam Negeri Alauddin, Makassar.
- Volynets, G. P., Tukalo, M. A., Bdzhola, V. G., Derkach, N. M., Gumeniuk, M. I., Tarnavskiy, S. S., & Yarmoluk, S. M. (2020). Novel Isoniazid Derivative as

- Promising Antituberculosis Agent. *Future Microbiology*, 15(10), 869–879.
- Wang, S., Luan, J., Chen, L., Liu, H., Li, W., & Wang, J. (2023). Computational Characteristics of the Structure-activity Relationship of Inhibitors Targeting Pks13-TE Domain. *Computational Biology and Chemistry*, 104(4), 107–864.
- Wang, X., Zhao, W., Wang, B., Ding, W., Guo, H., Zhao, H., Meng, J., Liu, S., Lu, Y., Liu, Y., & Zhang, D. (2021). Identification of Inhibitors Targeting Polyketide Synthase 13 of *Mycobacterium tuberculosis* as Antituberculosis Drug Leads. *Bioorganic Chemistry*, 114(7), 2–11.
- WHO. (2020). *Global Tuberculosis Report 2020* (2020th ed.) dan (2023th ed.). World Health Organization, Geneva.
- Wilson, C., Ray, Wyatt, P. G. (2022). Optimization of TAM16, a Benzofuran That Inhibits the Thioesterase Activity of Pks13; Evaluation Toward a Preclinical Candidate for a Novel Antituberculosis Clinical Target. *Journal of Medicinal Chemistry*, 65(1), 409–423.
- Yadav, D. K., Ahmad, I., Shukla, A., Khan, F., Negi, A. S., & Gupta, A. (2014). QSAR and Docking Studies on Chalcone Derivatives for Antitubercular Activity Against M.tuberculosis H37Rv. *Journal of Chemometrics*, 28(6), 499–507.
- Yeni, Y., & Rachmania, R. A. (2022). The Prediction of Pharmacokinetic Properties of Compounds in Hemigraphis alternata (Burm.F.) T. Ander Leaves Using pkCSM. *Indonesian Journal of Chemistry*, 22(4), 1081–1089.
- Yuanita, E., Sudirman, Dharmayani, N. K. T., Ulfah, M., & Syahri, J. (2020). Quantitative Structure-activity Relationship (QSAR) and Molecular Docking of Xanthone Derivatives as Anti-tuberculosis Agents. *Journal of Clinical Tuberculosis and Other Mycobacterial Diseases*, 21(4), 100–203.
- Zhang, W., Liu, L. ling, Lun, S., Wang, S. S., Xiao, S., Gunosewoyo, H., Yang, F., Tang, J., Bishai, W. R., & Yu, L. F. (2021). Design and Synthesis of Mycobacterial Pks13 Inhibitors: Conformationally Rigid Tetracyclic Molecules. *European Journal of Medicinal Chemistry*, 213(5), 113–202.
- Zhang, W., Lun, S., Wang, S. H., Jiang, X. W., Yang, F., Tang, J., Manson, A. L., Earl, A. M., Gunosewoyo, H., Bishai, W. R., & Yu, L. F. (2018). Identification of Novel Coumestan Derivatives as Polyketide Synthase 13 Inhibitors Against *Mycobacterium tuberculosis*. *Journal of Medicinal Chemistry*, 61(3), 791–803.
- Zhao, W., Wang, B., Liu, Y., Fu, L., Sheng, L., Zhao, H., Lu, Y., & Zhang, D. (2020). Design, Synthesis, and Biological Evaluation of Novel 4H-chromen-4-one Derivatives as Antituberculosis Agents Against Multidrug-resistant Tuberculosis. *European Journal of Medicinal Chemistry*, 189(3), 112–275.