

DAFTAR PUSTAKA

- Acharya, B, Acharya, A, Gautam, S, Ghimire, S, P, Mishra, G, Parajuli, *et al* 2020, ‘Advances in diagnosis of Tuberculosis: an update into molecular diagnosis of Mycobacterium tuberculosis’, *Molecular biology reports*, Vol. 47, hal. 4065-4075.
- Alberts, B, Heald, R, Johnson, A, Morgan, D, Raff, M, Roberts, *et al* 2022, *Molecular Biology of the Cell*, 7th edn, W.W.Norton, New York
- Allué-Guardia, A, García, J, I & Torrelles, J, B 2021, ‘Evolution of drug-resistant Mycobacterium tuberculosis strains and their adaptation to the human lung environment’, *Frontiers in Microbiology*, Vol. 12, hal. 612675.
- Alsayed, S, S & Gunosewoyo, H 2023, ‘Tuberculosis: pathogenesis, current treatment regimens and new drug targets. *International journal of molecular sciences*’, Vol. 24, No.6, hal. 5202.
- Auganova, D, Atavliyeva, S, Amirkazin, A, Akisheva, A, Tsepke, A & Tarlykov, P 2023, ‘Genomic Characterization of Drug-Resistant Mycobacterium tuberculosis L2/Beijing Isolates from Astana, Kazakhstan’, *Antibiotics*, Vol. 12, No. 10, hal. 1523.
- Brooks, G, Carol, K, Butel, J 2013 *Jawetz, Melnick & Adelberg Medical Microbiology: Bacteriology*, The McGraw-Hill Companies, Inc, New York.
- Campos, P, F, Craig, O, E, Turner-Walker, G & Gilbert, M, T, P 2021, ‘DNA degradation in human remains over time: A review’, *Molecular Ecology Resources*, Vol. 21, No. 3, hal. 703–715.
- Centers for Disease Control and Prevention 2024, *Public Health Image Library*, dilihat 6 Desember 2024, <<https://phil.cdc.gov/details.aspx?pid=4428>>.
- Chandra, P, Grigsby, S, J & Philips, J, A 2022, ‘Immune evasion and provocation by Mycobacterium tuberculosis’, *Nature Reviews Microbiology*, Vol. 20, No.12, hal.750-766.
- Coddington, M 2020, *Missense, nonsense and frameshift mutations: A genetic guide*, Technology Networks, dilihat 27 Februari 2025, <<https://www.technologynetworks.com/genomics/articles/missense-nonsense-and-frameshift-mutations-a-genetic-guide-329274>>.
- Cole, S, Brosch, R, Parkhill, J, Garnier, T, Churcher, C, Harris, D *et al* 1998, ‘Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence’, *Nature* Vol. 393, hal. 537–544 (1998).

- Coll, F, Phelan, J, Hill-Cawthrone, G, A, Nair, M, B, Mallard, K, Ali, S 2018, ‘Genome-wide analysis of multi- and extensively drug-resistant *Mycobacterium tuberculosis*’, *nature genetics*, Vol. 50, hal. 307-216.
- Dartois, V, A, & Rubin, E, J 2022, ‘Anti-tuberculosis treatment strategies and drug development: challenges and priorities’, *Nature Reviews Microbiology*, Vol. 20, No. 11, hal. 685-701.
- Delogu, G, Sali, M & Fadda, G 2013, ‘The biology of mycobacterium tuberculosis infection’, *Mediterranean journal of hematology and infectious diseases*, Vol. 5, hal. 1.
- Gandhi, N, R, Nunn, P, Dheda, K, Schaaf, H, S, Zignol, M, Sooligen, D, V 2010, ‘Multidrug-resistant and extensively drug-resistant tuberculosis: a threat to global control of tuberculosis’, *The Lancet Respiratory Medicine*, Vol. 375, No. 9728, hal. 1830-1843.
- Geneious Prime 2025.0.3, *Manual User for Geneious Prime*, dilihat 23 Februari 2025, <<http://www.geneious.com/>>.
- Ghannam, M. G & Varacallo, M, A 2023, *Biochemistry, Polymerase Chain Reaction*, In StatPearls. StatPearls Publishing.
- Goossens, S, N, Sampson, S, L & Van Rie, A 2020, ‘Mechanisms of drug-induced tolerance in *Mycobacterium tuberculosis*’, *Clinical microbiology reviews*, Vol. 34, No. 1, hal. 10-1128.
- Gordon, S, V & Parish, T 2018, ‘Microbe Profile: *Mycobacterium tuberculosis*: Humanity’s deadly microbial foe’, *Microbiology*, Vol. 164, hal. 437-439.
- Green, M. R & Sambrook, J 2019, ‘Polymerase Chain Reaction’, *Cold Spring Harbor protocols*, Vol. 6. <https://doi.org/10.1101/pdb.top095109>
- Griffiths, A, J, F, Wessler, S, R, Carroll, S, B, Doebley, J 2020, *Introduction to Genetic Analysis*, 12th edn. W.H. Freeman, New York.
- Heather, J, M & Chain, B 2016, ‘The sequence of sequencers: The history of sequencing DNA’, *Genomics*, Vol. 107, No. 1, hal. 1-8.
- International Society for Biological and Environmental Repositories (ISBER) 2012, ‘Best practices for repositories: Collection, storage, retrieval, and distribution of biological materials for research’, *Biopreservation and Biobanking*, Vol. 10, No. 2, hal. 79–161.
- Iskandar, D, Suwantika, A, A, Pradipta, I, S, Postma, M, J & van Boven, J, F 2023, ‘Clinical and economic burden of drug-susceptible tuberculosis in Indonesia: national trends 2017–19’, *The Lancet Global Health*, Vol. 11, No. 1, hal. e117-e125.
- Kaaffah, S, Kusuma, I, Y, Renaldi, F, S, Lestari, Y, E, Pratiwi, A, D, E & Bahar, M, A 2023, ‘Knowledge, Attitudes, and Perceptions of Tuberculosis in

- Indonesia: A Multi-Center Cross-Sectional Study. *Infection and Drug Resistance*', hal.1787-1800.
- Kementerian Kesehatan Republik Indonesia 2023, *Program Penanggulangan Tuberkulosis Tahun 2022, Jakarta*
- Khan, A. S, Wilcox, A. S, Polymeropoulos, M, H, Hopkins, J, A, Stevens, T, J, Robinson, et al 1992, 'Single pass sequencing and physical and genetic mapping of human brain cDNAs', *Nature genetics*, Vol. 2, No. 3, hal. 180–185.
- Khawbung, J, L, Nath, D & Chakraborty, S 2021, 'Drug resistant Tuberculosis: A review', *Comparative immunology, microbiology and infectious diseases*, Vol. 74, hal. 101574.
- Kim, J, M, Oh, J, E, Kim, R, Heo, Y, J & Cho, J, H, 2023 'A novel approach of usage of Gram staining to indentify Mycobacterium tuberculosis from tissues', *예방수의 학회지*, Vol. 47, No. 1, hal. 1-6.
- Koch, Robert 1906, 'The Nobel Lecture On How The Fight Against Tuberculosis Now Stands', *The Lancet*. Vol. 167, No. 4317, hal. 1449–1451.
- Kumar, S & Jena, L 2014, 'Understanding rifampicin resistance in tuberculosis through a computational approach', *Genomics & Informatics*, Vol. 12, No. 4, hal. 276-282.
- Leung, A, N, 1999, 'Pulmonary tuberculosis: the essentials', *Radiology*, Vol. 210, No, 2, hal. 307-322.
- Lodish, H & Zipursky, S, L 2001, 'Molecular cell biology', *Biochem Mol Biol Educ*, Vol. 29, hal. 126–133.
- Loman, N, J, Quick, J & Simpson, J, T 2015, 'A complete bacterial genome recovered from a nanopore sequencer', *Nature*, Vol. 517, No. 7536, hal. 608-611.
- List of Prokaryotic names with Standing in Nomenclature (LPSN), 2024, 'Species Mycobacterium tuberculosis', DSMZ, dilihat 5 Desember 2024, <<https://lpsn.dsmz.de/species/mycobacterium-tuberculosis>>.
- Maladan, Y, Wahyuni, T & Krismawati, H 2021, 'Single nucleotide polymorphism in the rpoB gene Mycobacterium tuberculosis from Papua-Indonesia and its impact on rifampicin resistance: A whole genome sequencing analysis', *Microbiology Indonesia*, Vol. 15, No. 2, hal. 1.
- Marchais, A, Naville, M, Bohn, C, Bouloc, P & Gautheret, D 2009, 'Single-pass classification of all noncoding sequences in a bacterial genome using phylogenetic profiles', *Genome research*, Vol. 19, No. 6, hal. 1084–1092.

- Metzker, M, L 2010, ‘Sequencing technologies - the next generation’, *Nature Reviews Genetics*, Vol. 11, hal. 31-46.
- Miotto, P, Cabibbe, A, M, Borroni, E, Degano, M & Cirillo, D, M 2018, ‘Role of Disputed Mutations in the rpoB Gene in Interpretation of Automated Liquid MGIT Culture Results for Rifampin Susceptibility Testing of Mycobacterium tuberculosis’, *Journal of clinical microbiology*, Vol. 56, No.5, hal. e01599-17.
- Muzzey, D, Evans, E, A & Lieber, C 2015, ‘Understanding the Basics of NGS: From Mechanism to Variant Calling’, *Current genetic medicine reports*, Vol. 3, No. 4, hal. 158–165.
- Noviyani, A, Nopsopon, T & Pongpirul, K 2021, ‘Variation of tuberculosis prevalence across diagnostic approaches and geographical areas of Indonesia’, *Plos one*, Vol. 16, No. 10, hal.e0258809.
- Pankhurst, L, J, Del Ojo Elias, C, Votintseva, A, A, Walker, T, M, Cole, K, Davies, J, Crook, D, W 2016, ‘Rapid, comprehensive, and affordable mycobacterial diagnosis with whole-genome sequencing: a prospective study’, *The Lancet Respiratory Medicine*, Vol. 4, No. 1, hal. 49-58.
- Ramesh, R., Munshi, A & Panda, S, K 1992, ‘Polymerase chain reaction’. *The National medical journal of India*, Vol. 5, No. 3, hal. 115–119.
- Rana, B & Joshi, G, K 2023, ‘Electrophoresis: Basic principle, types, and applications’, *Basic Biotechniques for Bioprocess and Bioentrepreneurship*, Vol. 11, hal. 183-193.
- Sanger, F, Nicklen, S & Coulson, A, R 1977, ‘DNA sequencing with chain-terminating inhibitors’ *Proceedings of the National Academy of Sciences*, Vol. 74, No.12, hal. 5463-5467
- Sarwani, D, Nurlaela, S, Zahrotul, I 2012, ‘Faktor Risiko Multidrug Resistant Tuberculosis’, *Jurnal Kesehatan Masyarakat*, Vol. 8, No. 1. 60-66.
- Singh, A, Gupta, A, K & Singh, S 2020, ‘Molecular mechanisms of drug resistance in Mycobacterium tuberculosis: Role of nanoparticles against multi-drug-resistant tuberculosis (MDR-TB)’, *NanoBioMedicine*, hal. 285-314.
- Smith, L, M, Sanders, J, Z, Kaiser, R, J, Hughes, P, Dodd, C, Connell, C, R, et al 1986, ‘Fluorescence detection in automated DNA sequence analysis’, *Nature*, Vol. 321, No. 6071, hal. 674-679.
- Stoffels, K, Allix-Béguec, C, Groenen, G, Wanlin, M, Berkvens D, Mathys, V et al 2013, ‘From Multidrug- to Extensively Drug-Resistant Tuberculosis: Upward Trends as Seen from a 15-Year Nationwide Study’, *PLOS ONE*, Vol. 8, No. 5, hal. e63128.

- Tania, T, Sudarmono, P, Kusumawati, R, L, Rukmana, A, Pratama, W, A, Regmi, S, M, et al 2020, 'Whole-genome sequencing analysis of multidrug-resistant *Mycobacterium tuberculosis* from Java, Indonesia', *Journal of medical microbiology*, Vol. 69, No. 7, hal.1013-1019.
- Thawornwattana, Y, Mahasirimongkol, S, Yanai, H, Maung, H, M, W, Cui, Z, Chongsuvivatwong, V, et al 2021, 'Revised nomenclature and SNP barcode for *Mycobacterium tuberculosis* lineage 2', *Microbial genomics*, Vol. 7, No. 11, hal. 000697.
- Tortoli, E 2014, 'Microbiological features and clinical relevance of new species of the genus *Mycobacterium*', *Clinical Microbiology Reviews*, Vol. 27, No. 4, hal. 727-752.
- Tramini, J 2023, 'Electrophoresis in Molecular Biology: Principles and Applications', *Journal of Biomolecular Research & Therapeutics*, Vol. 12, hal. 335.
- Walker, T. M, Kohl, T, A, Omar, S, V, Hedge, J, Del Ojo Elias, C, Bradley, P & Niemann, S 2015, 'Whole-genome sequencing for prediction of *Mycobacterium tuberculosis* drug susceptibility and resistance: a retrospective cohort study', *The Lancet Infectious Diseases*, Vol. 15, No. 10, 1193-1202.
- World Health Organization, 2021, *Tuberculosis diagnostics*, dilihat 8 Juli 2024, <<https://www.who.int/teams/global-tuberculosis-programme/laboratory-strengthening>>.
- World Health Organization, 2023, *Global Tuberculosis Report 2023*, dilihat 8 Juli 2024, <<https://www.who.int/teams/global-tuberculosis-programme/tb-reports>>.
- World Health Organization 2023, 2nd edn, *Catalogue of mutations in *Mycobacterium tuberculosis* complex and their association with drug resistance*, Geneva.