DAFTAR PUSTAKA

Aravindan, P. (2019). Host genetics and tuberculosis: Theory of genetic polymorphism and tuberculosis. *Lung India*, *36*(3), 244–252. https://doi.org/10.4103/lungindia.lungindia_146_15

Ates, L. S., Houben, E. N. G., & Bitter, W. (2016). Type VII Secretion: A Highly Versatile Secretion System. *Microbiology Spectrum*, *4*(1). https://doi.org/10.1128/microbiolspec.vmbf-0011-2015

Burcham, L. R., Le Breton, Y., Radin, J. N., Spencer, B. L., Deng, L., Hiron, A., Ransom, M. R., Mendonça, J. da C., Belew, A. T., El-Sayed, N. M., McIver, K. S., Kehl-Fie, T. E., & Doran, K. S. (2020). Identification of zinc-dependent mechanisms used by group b streptococcus to overcome calprotectin-mediated stress. *MBio*, *11*(6), 1–18. https://doi.org/10.1128/mBio.02302-20

Carey, A. F., Wang, X., Cicchetti, N., Spaulding, C. N., Liu, Q., Hopkins, F., Brown, J., Sixsmith, J., Sutiwisesak, R., Behar, S. M., Ioerger, T. R., & Fortune, S. M. (2022). Multiplexed Strain Phenotyping Defines Consequences of Genetic Diversity in Mycobacterium tuberculosis for Infection and Vaccination Outcomes. *MSystems*, *7*(3). https://doi.org/10.1128/msystems.00110-22

de Martino, M., Lodi, L., Galli, L., & Chiappini, E. (2019). Immune Response to Mycobacterium tuberculosis: A Narrative Review. *Frontiers in Pediatrics*, *7*. https://doi.org/10.3389/fped.2019.00350

Eom, H., & Song, W. J. (2019). Emergence of metal selectivity and promiscuity in metalloenzymes. In *Journal of Biological Inorganic Chemistry* (Vol. 24, Issue 4, pp. 517–531). Springer Verlag. https://doi.org/10.1007/s00775-019-01667-0

Felsenstein, J. (1985). Confidence limits on phylogenies: an approach using the bootstrap. evolution, 39(4), 783-791.

Gill, C. M., Dolan, L., Piggott, L. M., & McLaughlin, A. M. (2022). New developments in tuberculosis diagnosis and treatment. In *Breathe* (Vol. 18, Issue 1). European Respiratory Society. https://doi.org/10.1183/20734735.0149-2021

Hernández-Pando, R. (n.d.). *In silico EsxG·EsxH Rational Epitope Selection: Candidate Epitopes for Vaccine 2 Design against Pulmonary Tuberculosis 3 4 Constanza Estefania*. https://doi.org/10.1101/2022.06.19.496760

Kant Sharma, K., Singh, D., Vishwas Mohite, S., Williamson, P. R., & Kennedy, J. F. (2023). *Metal manipulators and regulators in human pathogens: A comprehensive review on microbial redox copper metalloenzymes "multicopper oxidases and superoxide dismutases."*

Kesehatan, J., Makassar, Y., Tahir, M., Farmasi, I., & Yamasi, A. F. (2024). TINGKAT KEPATUHAN PENGGUNAAN OBAT PADA PASIEN TB PARU DI KLINIK WIRAHUSADA MEDICAL CENTER KOTA MAKASSAR. *Jurnal Kesehatan Yamasi Makassar*, *8*(2), 52–60. http://journal.yamasi.ac.id

Ly, A., & Liu, J. (2020). Mycobacterial virulence factors: Surface-exposed lipids and secreted proteins. In *International Journal of Molecular Sciences* (Vol. 21, Issue 11). MDPI AG. https://doi.org/10.3390/ijms21113985

Machová, M. (2021). Phylogenetic trees and other evolutionary diagrams in biology textbooks and their importance in secondary science education. *Scientia in Educatione*, *12*(1), 16–36. https://doi.org/10.14712/18047106.1923

Mertaniasih, N. M., Handijatno, D., Perwitasari, A. D. S., Dewi, D. N. S. S., Fanani, M. Z., & Afifah, I. Q. (2016). Sequence Analysis of the Gene Region Encoding ESAT-6, Ag85B, and Ag85C Proteins from Clinical Isolates of Mycobacterium tuberculosis. *Procedia Chemistry*, *18*, 225–230. https://doi.org/10.1016/j.proche.2016.01.035

Portal-Celhay, C., Tufariello, J. M., Srivastava, S., Zahra, A., Klevorn, T., Grace, P. S., Mehra, A., Park, H. S., Ernst, J. D., Jacobs, W. R., & Philips, J. A. (2016). Mycobacterium tuberculosis EsxH inhibits ESCRT-dependent CD4+ T-cell activation. *Nature Microbiology*, *2*. https://doi.org/10.1038/nmicrobiol.2016.232

Prihantika S., S., Kurniati, N., Rahadiyanto, K. Y., Saleh, M. I., Hafy, Z., Tanoerahardjo, F. S., Nugraha, J., & Salim, E. M. (2019). IFN-Gamma Secretion and IL-10 after Stimulation of ESAT-6-CFP-10 (EC610) Fusion Antigen in Patients with Active Tuberculosis and Latent Tuberculosis. *Biomedical Journal of Indonesia*, *5*(3), 106–115. https://doi.org/10.32539/bji.v5i3.8897

Schaible, U. E., Weiss, unter, & Weiss, G. (2015). *G€ unter Weiss Macrophage defense mechanisms against intracellular bacteria*. www.immunologicalreviews.com

Sukkhu, M., & Naidoo, Y. (2015). Evaluation of ESX Sequence Variations within Mycobacterium tuber-culosis Clinical and Laboratory Isolates. *Asian J. Adv. Basic Sci*, *3*(2), 117-141.

Sutiwisesak, R., Hicks, N. D., Boyce, S., Murphy, K. C., Papavinasasundaram, K., Carpenter, S. M., Boucau, J., Joshi, N., Le Gall, S., Fortune, S. M., Sassetti, C. M., & Behar, S. M. (2020). A natural polymorphism of Mycobacterium tuberculosis in the esxH gene disrupts immunodomination by the TB10.4-specific CD8 T cell response. *PLoS Pathogens*, *16*(10). https://doi.org/10.1371/journal.ppat.1009000

Turner, R. D., Chiu, C., Churchyard, G. J., Esmail, H., Lewinsohn, D. M., Gandhi, N. R., & Fennelly, K. P. (2017). Tuberculosis Infectiousness and Host Susceptibility. *Journal of Infectious Diseases*, *216*, S636–S643. https://doi.org/10.1093/infdis/jix361

Uplekar, S., Heym, B., Friocourt, V., Rougemont, J., & Cole, S. T. (2011). Comparative genomics of ESX genes from clinical isolates of Mycobacterium tuberculosis provides evidence for gene conversion and epitope variation. *Infection and Immunity*, *79*(10), 4042–4049. https://doi.org/10.1128/IAI.05344-11

Who. (n.d.). *Tuberculosis Country Profile 2021 Indonesia*. https://www.who.int/teams/global-tuberculosis-programme/data

Yang, Z., Davila, J., Zhang, L., Marrs, C. F., & Durmaz, R. (2010). Assessment of the genetic diversity of mycobacterium tuberculosis esxA, esxH, and fbpB genes among clinical isolates and its implication for the future immunization by new tuberculosis subunit vaccines Ag85B-ESAT-6 and Ag85B-TB10.4. *Journal of Biomedicine and Biotechnology*, *2010*. https://doi.org/10.1155/2010/208371

Yruela, I., Contreras-Moreira, B., Magalhã es, C., Osó Rio, N. S., & Gonzalo-Asensio, J. (2016). Mycobacterium tuberculosis complex exhibits lineage-specific variations affecting protein ductility and epitope recognition. *Genome Biology and Evolution*, *8*(12), 3751–3764. https://doi.org/10.1093/gbe/evw279

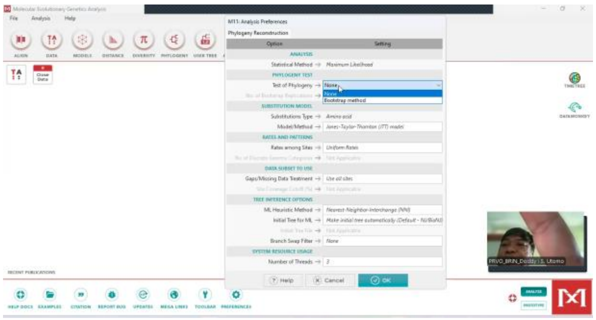
Zhang, Z., Guo, K., Pan, G., Tang, J., & Guo, F. (2017). Improvement of phylogenetic method to analyze compositional heterogeneity. *BMC Systems Biology*, *11*. https://doi.org/10.1186/s12918-017-0453-x

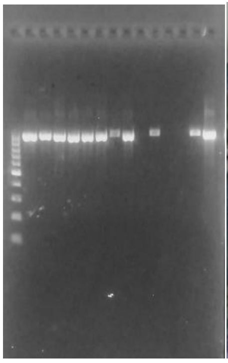
Lampiran 1 List Sampel

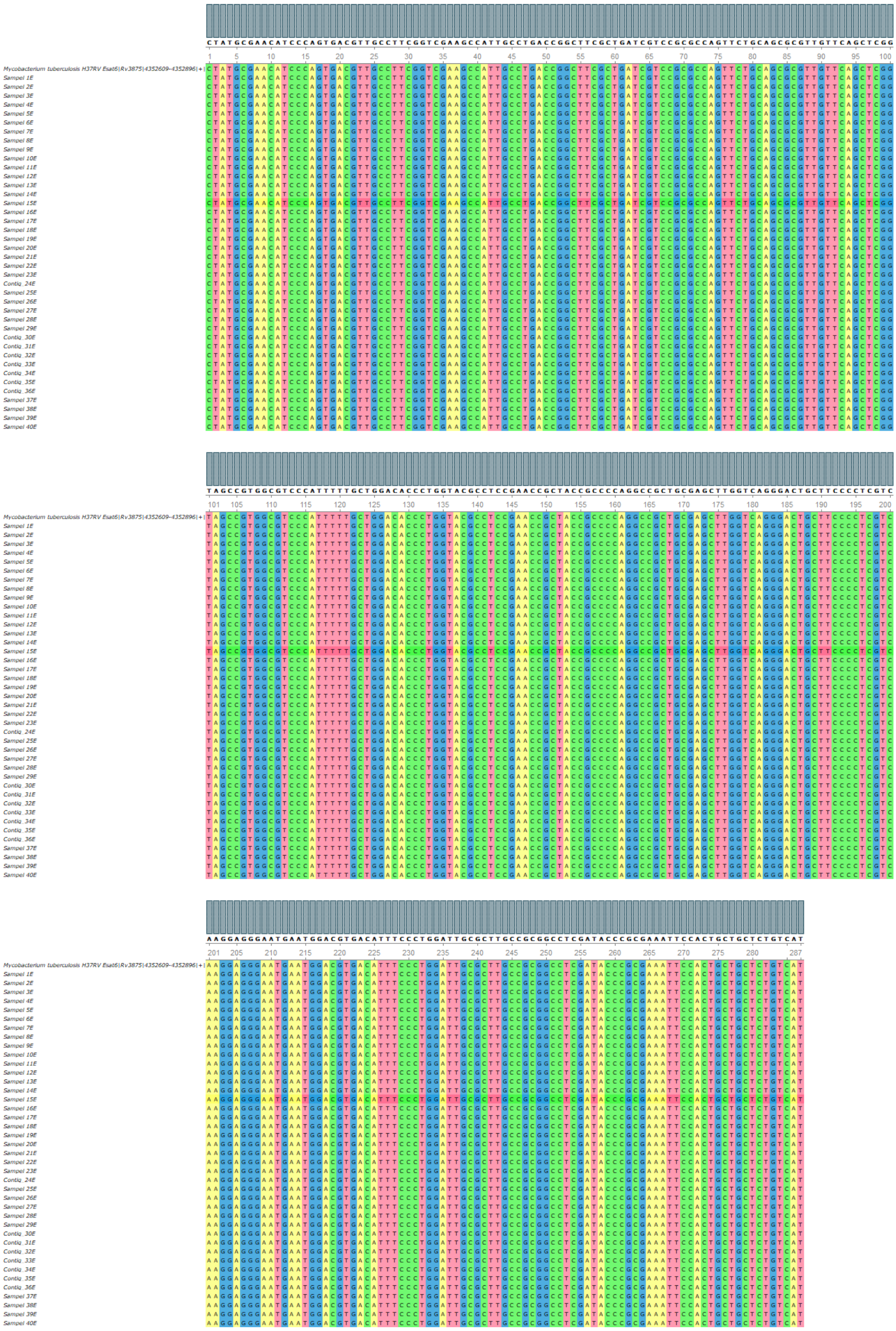
No	EsxH	ESAT-6
1	MDR 333	X7227
2	MDR 101	X7622
3	MDR 349	X6995
4	R017 SUS	MDR 2115
5	MDR 342 R	PL 123
6	R042 SUS	MDR 148A
7	MDR 313	MDR 054R
8	MDR 274	PL152
9	MDR 281	MDR 284
10	X7227	MDR 004 X
11	X7622	PL141
12	MDR 2115	R042
13	PL 123	MDR 332
14	MDR 2119	MDR 335
15	MDR 054 R	R028 SUS
16	PL 141	R007 R
17	MDR 2116	MDR 173 M
18	PL155	MDR 108 M
19	X7254	MDR 278 M
20	PL107	MDR 168
21	PL156	MDR 287 R
22	MDR 151 X	MDR 375
23	MDR 092 X	MDR 301 R
24	PL 089	MDR 141 M
25	MDR 274 R	MDR 151 X
26	MDR 301 R	MDR 374 R
27	X 6975	MDR 175 R
28	MDR 164 M	MDR 162 R
29	MDR 117 M	MDR 2116
30	X 6897	X7141
31	PL 114	PL 114
32	MDR 334	PL 089
33	X 7141	PL155
34	MDR 336	X 7254
35	MDR 175 R	PL 107

36	MDR 139 M	X 7300
37	MDR 162 R	PL 156
38	MDR 2260	MDR041
39	PL 133	MDR058
40	R012 SUS	MDR 334 R

Lampiran 2






CTATGCGAACATCCCAGTGACGTTGCCTTCGGTCGAAGCCATTGCCTGACCGGCTTCGCTGATCGTCCGCGCCAGTTCTGCAGCGCGTTGTTCAGCTCGG
TAGCCGTGGCGTCCCATTTTTGCTGGACACCCTGGTACGCCTCCGAACCGCTACCGCCCCAGGCCGCTGCGAGCTTGGTCAGGGACTGCTTCCCCTCGTC
AAGGAGGGAATGAATGGACGTGACATTTCCCTGGATTGCGCTTGCCGCGGCCTCGATACCCGCGAAATTCCACTGCTGCTCTGTCAT
Mycobacterium tuberculosis H37RV Esat6|Rv3875|4352609-4352896|+|
Sampel 1E
Sampel 2E
Sampel 3E
Sampel 4E
Sampel 5E
Sampel 6E
Sampel 7E
Sampel 8E
Sampel 9E
Sampel 10E
Sampel 11E
Sampel 12E
Sampel 13E
Sampel 14E
Sampel 15E
Sampel 16E
Sampel 17E
Sampel 18E
Sampel 19E
Sampel 20E
Sampel 21E
Sampel 22E
Sampel 23E
Contig_24E
Sampel 25E
Sampel 26E
Sampel 27E
Sampel 28E
Sampel 29E
Contig_30E
Contig_31E
Contig_32E
Contig_33E
Contig_34E
Contig_35E
Contig_36E
Sampel 37E
Sampel 38E
Sampel 39E
Sampel 40E