

DAFTAR PUSTAKA

- Aanen, D. K., Van 'T Padje, A., & Auxier, B. (2023). Longevity of Fungal Mycelia and Nuclear Quality Checks: A New Hypothesis for the Role of Clamp Connections in Dikaryons. *Microbiology and Molecular Biology Reviews*, 87(3), e00022-21. <https://doi.org/10.1128/mmmbr.00022-21>
- Abbas, Q., Wilhelm, M., Kuster, B., Poppenberger, B., & Frishman, D. (2024). Exploring crop genomes: Assembly features, gene prediction accuracy, and implications for proteomics studies. *BMC Genomics*, 25(1), 619. <https://doi.org/10.1186/s12864-024-10521-w>
- Abramson, J., Adler, J., Dunger, J., Evans, R., Green, T., Pritzel, A., Ronneberger, O., Willmore, L., Ballard, A. J., Bambrick, J., Bodenstein, S. W., Evans, D. A., Hung, C.-C., O'Neill, M., Reiman, D., Tunyasuvunakool, K., Wu, Z., Žemgulytė, A., Arvaniti, E., ... Jumper, J. M. (2024). Accurate structure prediction of biomolecular interactions with AlphaFold 3. *Nature*, 630(8016), 493–500. <https://doi.org/10.1038/s41586-024-07487-w>
- Afonina, I. (1997). Efficient priming of PCR with short oligonucleotides conjugated to a minor groove binder. *Nucleic Acids Research*, 25(13), 2657–2660. <https://doi.org/10.1093/nar/25.13.2657>
- Agarwal, V., & McShan, A. C. (2024). The power and pitfalls of AlphaFold2 for structure prediction beyond rigid globular proteins. *Nature Chemical Biology*, 20(8), 950–959. <https://doi.org/10.1038/s41589-024-01638-w>
- Agilent Technologies. (2022). *Agilent 4200 TapeStation System-System Manual* (10th ed.). https://www.agilent.com/cs/library/usermanuals/public/4200-TapeStation_SystemManual.pdf?srltid=AfmBOooWIkY4tKMzFndVXg8nMz1p24AyU5r-B6dJ0dlCPStP4hx92O0K (Original work published Agilent)
- Ait Benkhali, J., Coppin, E., Brun, S., Peraza-Reyes, L., Martin, T., Dixelius, C., Lazar, N., Van Tilbeurgh, H., & Debuchy, R. (2013). A Network of HMG-box Transcription Factors Regulates Sexual Cycle in the Fungus *Podospora anserina*. *PLoS Genetics*, 9(7), e1003642. <https://doi.org/10.1371/journal.pgen.1003642>
- Allen, A. G., Barthelson, K., & Lardelli, M. (2023). pHAPE: A plasmid for production of DNA size marker ladders for gel electrophoresis. *Biology Methods and Protocols*, 8(1), bpad015. <https://doi.org/10.1093/biomethods/bpad015>

- Alsaedi, A. K. (2025). Utilizing Semi-Empirical Miedema's Model for Gibbs Free Energy Calculations in Fe-Al-Cr and Fe-Al-Cu Alloys. *Jordan Journal of Physics*, 18(2), 157. <https://doi.org/10.47011/18.2.5>
- Armstrong, J. A., & Schulz, J. R. (2015). Agarose Gel Electrophoresis. *Current Protocols Essential Laboratory Techniques*, 10(1). <https://doi.org/10.1002/9780470089941.et0702s10>
- Auxier, B., Scholtmeijer, K., Van Peer, A. F., Baars, J. J. P., Debets, A. J. M., & Aanen, D. K. (2021). Cytoplasmic Mixing, Not Nuclear Coexistence, Can Explain Somatic Incompatibility in Basidiomycetes. *Microorganisms*, 9(6), 1248. <https://doi.org/10.3390/microorganisms9061248>
- Badalyan, S., Gharibyan, N., Gianchino, C., Iotti, M., & Zambonelli, A. (2023). Morphological observation and biomass formation in different edible medicinal Morchella collections (Pezizomycetes, Ascomycota). *Italian Journal of Mycology*, 50-61 Pages. <https://doi.org/10.6092/ISSN.2531-7342/16112>
- Banuett, F. (2015). From dikaryon to diploid. *Fungal Biology Reviews*, 29(3–4), 194–208. <https://doi.org/10.1016/j.fbr.2015.08.001>
- Benitez, M., & Aguirre, V. (Eds.). (2012). *Protein purification*. Nova Science Publishers.
- Bennett, R. J., & Turgeon, B. G. (2016). Fungal Sex: The Ascomycota. *Microbiology Spectrum*, 4(5), 4.5.20. <https://doi.org/10.1128/microbiolspec.FUNK-0005-2016>
- Böhm, J., Dahlmann, T. A., Gümüşer, H., & Kück, U. (2015). A *MAT1*–2 wild-type strain from *Penicillium chrysogenum*: Functional mating-type locus characterization, genome sequencing and mating with an industrial penicillin-producing strain. *Molecular Microbiology*, 95(5), 859–874. <https://doi.org/10.1111/mmi.12909>
- Bowden, K. E., Joseph, S. J., Cartee, J. C., Ziklo, N., Danavall, D., Raphael, B. H., Read, T. D., & Dean, D. (2021). Whole-Genome Enrichment and Sequencing of Chlamydia trachomatis Directly from Patient Clinical Vaginal and Rectal Swabs. *mSphere*, 6(2), e01302-20. <https://doi.org/10.1128/mSphere.01302-20>
- Brúna, T., Lomsadze, A., & Borodovsky, M. (2020). GeneMark-EP+: Eukaryotic gene prediction with self-training in the space of genes and proteins. *NAR Genomics and Bioinformatics*, 2(2), lqaa026. <https://doi.org/10.1093/nargab/lqaa026>

- Buchfink, B., Reuter, K., & Drost, H.-G. (2021). Sensitive protein alignments at tree-of-life scale using DIAMOND. *Nature Methods*, 18(4), 366–368. <https://doi.org/10.1038/s41592-021-01101-x>
- BUSCO. (2026, March 25). BUSCO User Guide. *Interpreting the Results*. https://busco.ezlab.org/busco_userguide.html#complete
- Cacho, A., Smirnova, E., Huzurbazar, S., & Cui, X. (2016). A Comparison of Base-calling Algorithms for Illumina Sequencing Technology. *Briefings in Bioinformatics*, 17(5), 786–795. <https://doi.org/10.1093/bib/bbv088>
- Cassago, A., Panepucci, R. A., Baião, A. M. T., & Henrique-Silva, F. (2002). Cellophane based mini-prep method for DNA extraction from the filamentous fungus *Trichoderma reesei*. *BMC Microbiology*, 2(1), 14. <https://doi.org/10.1186/1471-2180-2-14>
- Catez, F., & Hock, R. (2010). Binding and interplay of HMG proteins on chromatin: Lessons from live cell imaging. *Biochimica et Biophysica Acta (BBA) - Gene Regulatory Mechanisms*, 1799(1–2), 15–27. <https://doi.org/10.1016/j.bbagr.2009.11.001>
- Chai, H., Liu, P., Ma, Y., Chen, W., Tao, N., & Zhao, Y. (2022). Organization and Unconventional Integration of the Mating-Type Loci in *Morchella* Species. *Journal of Fungi*, 8(7), 746. <https://doi.org/10.3390/jof8070746>
- Christita, M., Arini, D., Kinho, J., Halawane, J., Kafiar, J., & Diwi, M. (2017). Keragaman dan Potensi Makrofungi di Obyek Ekowisata Kaki Dian, Gunung Klabat-Minahasa Utara. *Jurnal Mikologi Indonesia*, 1(2), 82. <https://doi.org/10.46638/jmi.v1i2.22>
- Cock, P. J. A., Fields, C. J., Goto, N., Heuer, M. L., & Rice, P. M. (2010). The Sanger FASTQ file format for sequences with quality scores, and the Solexa/Illumina FASTQ variants. *Nucleic Acids Research*, 38(6), 1767–1771. <https://doi.org/10.1093/nar/gkp1137>
- Cooke, R. F., Cardoso, R. C., Cerri, R. L. A., Lamb, G. C., Pohler, K. G., Riley, D. G., & Vasconcelos, J. L. M. (2020). Cattle adapted to tropical and subtropical environments: Genetic and reproductive considerations. *Journal of Animal Science*, 98(2), skaa015. <https://doi.org/10.1093/jas/skaa015>
- Coppin, E., Berteaux-Lecellier, V., Bidard, F., Brun, S., Ruprich-Robert, G., Espagne, E., Aït-Benkhalil, J., Goarin, A., Nesseir, A., Planamente, S., Debuchy, R., & Silar, P. (2012). Systematic Deletion of Homeobox Genes in *Podospora anserina* Uncovers Their Roles in Shaping the Fruiting Body. *PLoS ONE*, 7(5), e37488. <https://doi.org/10.1371/journal.pone.0037488>

- Cravero, M., Robinson, A. J., Hilpisch, P., Chain, P. S., Bindschedler, S., & Junier, P. (2022). Importance of appropriate genome information for the design of mating type primers in black and yellow morel populations. *IMA Fungus*, 13(1), 14. <https://doi.org/10.1186/s43008-022-00101-6>
- Cseke, L. J. (2004). *Handbook of molecular and cellular methods in biology and medicine* (2nd ed). CRC Press.
- Cunha, E. N., De Souza, M. F. B., Lanza, D. C. F., & Lima, J. P. M. S. (2020). A low-cost smart system for electrophoresis-based nucleic acids detection at the visible spectrum. *PLOS ONE*, 15(10), e0240536. <https://doi.org/10.1371/journal.pone.0240536>
- Das, J. (2004). Comparison of Diverse Protein Sequences of the Nuclear-Encoded Subunits of Cytochrome C Oxidase Suggests Conservation of Structure Underlies Evolving Functional Sites. *Molecular Biology and Evolution*, 21(8), 1572–1582. <https://doi.org/10.1093/molbev/msh161>
- Del Fabbro, C., Scalabrin, S., Morgante, M., & Giorgi, F. M. (2013). An Extensive Evaluation of Read Trimming Effects on Illumina NGS Data Analysis. *PLoS ONE*, 8(12), e85024. <https://doi.org/10.1371/journal.pone.0085024>
- Ding, Y., Owen, M., Le, J., Batalov, S., Chau, K., Kwon, Y. H., Van Der Kraan, L., Bezares-Orin, Z., Zhu, Z., Veeraraghavan, N., Nahas, S., Bainbridge, M., Gleeson, J., Baer, R. J., Bandoli, G., Chambers, C., & Kingsmore, S. F. (2023). Scalable, high quality, whole genome sequencing from archived, newborn, dried blood spots. *Npj Genomic Medicine*, 8(1), 5. <https://doi.org/10.1038/s41525-023-00349-w>
- Du, X.-H., & Yang, Z. L. (2021). Mating Systems in True Morels (*Morchella*). *Microbiology and Molecular Biology Reviews*, 85(3), e00220-20. <https://doi.org/10.1128/MMBR.00220-20>
- Duintjer, A. J., Imholz, S., Pico-Knijnenburg, I., Heuperman, A., Hodemaekers, H., Deutekom, E. S., Voorhoeve, E., Dollé, M. E. T., & Van Der Burg, M. (2025). Comparing DNA Isolation and Preparation Protocols for Dried Blood Spots in the Context of Genomic Newborn Screening. *International Journal of Neonatal Screening*, 11(3), 75. <https://doi.org/10.3390/ijns11030075>
- Expasy. (2025). *UniProtKB/Swiss-Prot. Expasy (Swiss Bioinformatics Resource Portal)-SIB (Swiss Institute of Bioinformatics)*. <https://www.expasy.org/resources/uniprotkb-swiss-prot>
- Fangman, W. L. (1978). Separation of very large DNA molecules by gel electrophoresis. *Nucleic Acids Research*, 5(3), 653–665. <https://doi.org/10.1093/nar/5.3.653>

- Fraser, J. A., & Heitman, J. (2003). Fungal mating-type loci. *Current Biology*, 13(20), R792–R795. <https://doi.org/10.1016/j.cub.2003.09.046>
- Gannibal, P. B., & Kazartsev, I. A. (2013). Development of a PCR assay for amplification of mating-type loci of *Alternaria* spp. And related fungi. *Czech Mycology*, 65(1), 69–78. <https://doi.org/10.33585/cmy.65105>
- Gassmann, M., Schmidt, E., Inche, A., Pechtl, I., & McHoull, B. (2014). *The DNA Integrity Number (DIN): A novel Approach for Objective Integrity Classification of Genomic DNA Samples*. Agilent Technologies. https://www.agilent.com/cs/library/training/public/2014_ASHG_DIN_poster.PDF?srsId=AfmBOoqljSJLwsYAwFIEvY1BGU13aQgKuwxQgu_xEt_r_nbUzSL4hUtCS
- Ghafoori, S. M., Sethi, A., Petersen, G. F., Tanipour, M. H., Gooley, P. R., & Forwood, J. K. (2024). RNA Binding Properties of SOX Family Members. *Cells*, 13(14), 1202. <https://doi.org/10.3390/cells13141202>
- Gribskov, M. (2019). Identification of Sequence Patterns, Motifs and Domains. In *Encyclopedia of Bioinformatics and Computational Biology* (pp. 332–340). Elsevier. <https://doi.org/10.1016/B978-0-12-809633-8.20498-6>
- Guo, H.-B., Perminov, A., Bekele, S., Kedziora, G., Farajollahi, S., Varaljay, V., Hinkle, K., Molinero, V., Meister, K., Hung, C., Dennis, P., Kelley-Loughnane, N., & Berry, R. (2022). AlphaFold2 models indicate that protein sequence determines both structure and dynamics. *Scientific Reports*, 12(1), 10696. <https://doi.org/10.1038/s41598-022-14382-9>
- Gurevich, A., Saveliev, V., Vyahhi, N., & Tesler, G. (2013). QUAST: Quality assessment tool for genome assemblies. *Bioinformatics*, 29(8), 1072–1075. <https://doi.org/10.1093/bioinformatics/btt086>
- Hegemann, D., Navascués, P., & Snoeckx, R. (2025). Plasma gas conversion in non-equilibrium conditions. *International Journal of Hydrogen Energy*, 100, 548–555. <https://doi.org/10.1016/j.ijhydene.2024.12.351>
- Heitman, J., Kronstad, J., Taylor, J., & Casselton, L. (Eds.). (2007). *Sex in fungi: Molecular determination and evolutionary implications*. ASM Press. <https://doi.org/10.1128/9781555815837>
- Hilário, S., Gonçalves, M. F. M., & Alves, A. (2021). Using Genealogical Concordance and Coalescent-Based Species Delimitation to Assess Species Boundaries in the *Diaporthe* eres Complex. *Journal of Fungi*, 7(7), 507. <https://doi.org/10.3390/jof7070507>
- Hiramatsu, K., Matsuda, C., Masago, K., Toriyama, K., Sasaki, E., Fujita, Y., Haneda, M., Ebi, H., Shibata, N., & Hosoda, W. (2023). Diagnostic utility

- of DNA integrity number as an indicator of sufficient DNA quality in next-generation sequencing-based genomic profiling. *American Journal of Clinical Pathology*, 160(3), 261–267. <https://doi.org/10.1093/ajcp/aqad046>
- Hoff, K. J., Lange, S., Lomsadze, A., Borodovsky, M., & Stanke, M. (2016). BRAKER1: Unsupervised RNA-Seq-Based Genome Annotation with GeneMark-ET and AUGUSTUS. *Bioinformatics*, 32(5), 767–769. <https://doi.org/10.1093/bioinformatics/btv661>
- Hoff, K. J., Lomsadze, A., Borodovsky, M., & Stanke, M. (2019). Whole-Genome Annotation with BRAKER. In M. Kollmar (Ed.), *Gene Prediction* (Vol. 1962, pp. 65–95). Springer New York. https://doi.org/10.1007/978-1-4939-9173-0_5
- Hossain, M. S., Azimi, N., & Skiena, S. (2009). Crystallizing short-read assemblies around seeds. *BMC Bioinformatics*, 10(S1), S16. <https://doi.org/10.1186/1471-2105-10-S1-S16>
- Hussain, S., & Sher, H. (2021). Ecological characterization of Morel (*Morchella* spp.) habitats: A multivariate comparison from three forest types of district Swat, Pakistan. *Acta Ecologica Sinica*, 41(1), 1–9. <https://doi.org/10.1016/j.chnaes.2020.10.007>
- Illumina. (2014). *Estimating Sequencing Coverage*. Illumina. https://www.illumina.com/documents/products/techspotlights/techspotlight_sequencing.pdf
- Illumina. (2024). *XLEAP-SBS chemistry expands NextSeq 1000 and NextSeq 2000 system capabilities (Technical Note M-GL-02330 v1.0)*. <https://www.illumina.com/content/dam/illumina/gcs/assembled-assets/marketing-literature/nextseq-1000-2000-xleap-sbs-tech-note-m-gl-02330/nextseq-1000-2000-xleap-sbs-tech-note-m-gl-02330.pdf>
- Illumina. (2025). *Paired-End vs. Single-Read Sequencing Technology*. Advantages of Paired-End and Single-End Sequencing. <https://www.illumina.com/science/technology/next-generation-sequencing/plan-experiments/paired-end-vs-single-read.html>
- Integrated DNA Technology (IDT). (2023). *How to use the OligoAnalyzer Tool*. Determining the Physical Characteristics of Your Oligos. <https://www.idtdna.com/page/support-and-education/decoded-plus/using-the-oligoanalyzer-program/>
- Islam, S., Md Asif Hasan Mazumder Niloy, Sabina Yesmin, Mahiea Hossain Mahi, & Jebunnahar Khandakar. (2025). Establishment of a Simple and Efficient Single Spore Isolation Method for Gilled Mushroom. *Research in*

- Agriculture Livestock and Fisheries*, 11(3), 383–388.
<https://doi.org/10.3329/ralf.v11i3.78896>
- Jauhal, A. A., & Newcomb, R. D. (2021). Assessing genome assembly quality prior to downstream analysis: N50 versus BUSCO. *Molecular Ecology Resources*, 21(5), 1416–1421. <https://doi.org/10.1111/1755-0998.13364>
- Jayakumar, V., & Sakakibara, Y. (2019). Comprehensive evaluation of non-hybrid genome assembly tools for third-generation PacBio long-read sequence data. *Briefings in Bioinformatics*, 20(3), 866–876.
<https://doi.org/10.1093/bib/bbx147>
- Jiang, Z., Peng, Z., Wei, Z., Sun, J., Luo, Y., Bie, L., Zhang, G., & Wang, Y. (2024). A deep learning-based method enables the automatic and accurate assembly of chromosome-level genomes. *Nucleic Acids Research*, 52(19), e92–e92.
<https://doi.org/10.1093/nar/gkae789>
- Kaeoniwong, N., Sotome, K., Ichiyanagi, T., Shimomura, N., & Aimi, T. (2024). Life cycle and mating compatibility in the Japanese white jelly mushroom, *Tremella yokohamensis*. *Mycoscience*, 65(4), 208–215.
<https://doi.org/10.47371/mycosci.2024.05.003>
- Kalle, E., Kubista, M., & Rensing, C. (2014). Multi-template polymerase chain reaction. *Biomolecular Detection and Quantification*, 2, 11–29.
<https://doi.org/10.1016/j.bdq.2014.11.002>
- Kannan, S., & Zacharias, M. (2007). Folding of a DNA Hairpin Loop Structure in Explicit Solvent Using Replica-Exchange Molecular Dynamics Simulations. *Biophysical Journal*, 93(9), 3218–3228.
<https://doi.org/10.1529/biophysj.107.108019>
- Kong, N., Ng, W., Cai, L., Leonardo, A., Weimer, B. C., Kelly, L., & Clara, S. (2014). Integrating the DNA Integrity Number (DIN) to Assess Genomic DNA (gDNA) Quality Control Using the Agilent 2200 TapeStation System.
- Lan, L., Hu, H., Jia, Y., Zhang, X., Jia, M., Li, C., & Wu, Z. (2025). Tips for improving genome annotation quality. *Genomics Communications*, 2(1), 0–0. <https://doi.org/10.48130/gcomm-0025-0006>
- Li, Y., Yang, T., Qiao, J., Liang, J., Li, Z., Sa, W., & Shang, Q. (2024). Whole-genome sequencing and evolutionary analysis of the wild edible mushroom, *Morchella esculenta*. *Frontiers in Microbiology*, 14, 1309703.
<https://doi.org/10.3389/fmicb.2023.1309703>
- Liu, W., He, P., Shi, X., Zhang, Y., Perez-Moreno, J., & Yu, F. (2023). Large-Scale Field Cultivation of *Morchella* and Relevance of Basic Knowledge for Its

- Steady Production. *Journal of Fungi*, 9(8), 855. <https://doi.org/10.3390/jof9080855>
- Lu, Y., Li, M., Gao, Z., Ma, H., Chong, Y., Hong, J., Wu, J., Wu, D., Xi, D., & Deng, W. (2025). Advances in Whole Genome Sequencing: Methods, Tools, and Applications in Population Genomics. *International Journal of Molecular Sciences*, 26(1), 372. <https://doi.org/10.3390/ijms26010372>
- Lucena-Aguilar, G., Sánchez-López, A. M., Barberán-Aceituno, C., Carrillo-Ávila, J. A., López-Guerrero, J. A., & Aguilar-Quesada, R. (2016). DNA Source Selection for Downstream Applications Based on DNA Quality Indicators Analysis. *Biopreservation and Biobanking*, 14(4), 264–270. <https://doi.org/10.1089/bio.2015.0064>
- Luo, J., Wei, Y., Lyu, M., Wu, Z., Liu, X., Luo, H., & Yan, C. (2021). A comprehensive review of scaffolding methods in genome assembly. *Briefings in Bioinformatics*, 22(5), bbab033. <https://doi.org/10.1093/bib/bbab033>
- Luscombe, N. M., Austin, S. E., Berman, H. M., & Thornton, J. M. (2000). An overview of the structures of protein-DNA complexes. *Genome Biology*, 1(1), reviews001.1. <https://doi.org/10.1186/gb-2000-1-1-reviews001>
- Mäkinen, V., Salmela, L., & Ylinen, J. (2012). Normalized N50 assembly metric using gap-restricted co-linear chaining. *BMC Bioinformatics*, 13(1), 255. <https://doi.org/10.1186/1471-2105-13-255>
- Malarkey, C. S., & Churchill, M. E. A. (2012). The high mobility group box: The ultimate utility player of a cell. *Trends in Biochemical Sciences*, 37(12), 553–562. <https://doi.org/10.1016/j.tibs.2012.09.003>
- Manchanda, N., Portwood, J. L., Woodhouse, M. R., Seetharam, A. S., Lawrence-Dill, C. J., Andorf, C. M., & Hufford, M. B. (2020). GenomeQC: A quality assessment tool for genome assemblies and gene structure annotations. *BMC Genomics*, 21(1), 193. <https://doi.org/10.1186/s12864-020-6568-2>
- Marketshare.com. (2026). *Morel Mushroom Market—Forecasts from 2025 to 2030*. <https://www.marketresearch.com/Knowledge-Sourcing-Intelligence-LLP-v4221/Morel-Mushroom-Forecasts-43107558/>
- Martin, T., Lu, S.-W., Van Tilbeurgh, H., Ripoll, D. R., Dixelius, C., Turgeon, B. G., & Debuchy, R. (2010). Tracing the Origin of the Fungal α 1 Domain Places Its Ancestor in the HMG-Box Superfamily: Implication for Fungal Mating-Type Evolution. *PLoS ONE*, 5(12), e15199. <https://doi.org/10.1371/journal.pone.0015199>

- McDonnell, E., Strasser, K., & Tsang, A. (2018). Manual Gene Curation and Functional Annotation. In R. P. De Vries, A. Tsang, & I. V. Grigoriev (Eds.), *Fungal Genomics* (Vol. 1775, pp. 185–208). Springer New York. https://doi.org/10.1007/978-1-4939-7804-5_16
- Mei-Han, Qingshan-Wang, Baiyintala, & Wuhanqimuge. (2019). The whole-genome sequence analysis of *Morchella sextelata*. *Scientific Reports*, 9(1), 15376. <https://doi.org/10.1038/s41598-019-51831-4>
- Meng, G., Li, J., Cao, Y., Li, F., Liu, M., Li, R., & Dong, C. (2025). Haplotype-resolved genomes of *Phlebotopus portentosus* reveal nuclear differentiation, TE-mediated variation, and saprotrophic potential. *IMA Fungus*, 16, e161411. <https://doi.org/10.3897/ima fungus.16.161411>
- Mergny, J.-L., & Lacroix, L. (2003). Analysis of Thermal Melting Curves. *Oligonucleotides*, 13(6), 515–537. <https://doi.org/10.1089/154545703322860825>
- Mertin, S., McDowall, S., & Harl, V. (1999). The DNA-binding specificity of SOX9 and other SOX proteins. *Nucleic Acids Research*, 27(5), 1359–1364. <https://doi.org/10.1093/nar/27.5.1359>
- Meurer, F., Bobrownik, M., Sadowski, G., & Held, C. (2016). Standard Gibbs Energy of Metabolic Reactions: I. Hexokinase Reaction. *Biochemistry*, 55(40), 5665–5674. <https://doi.org/10.1021/acs.biochem.6b00471>
- Mira-Jover, A., Graciá, E., Giménez, A., Fritz, U., Rodríguez-Caro, R. C., & Bourgeois, Y. (2024). Taking advantage of reference-guided assembly in a slowly-evolving lineage: Application to *Testudo graeca*. *PLOS ONE*, 19(8), e0303408. <https://doi.org/10.1371/journal.pone.0303408>
- Mizuno, G. P., Crispim, C. M., & Pizzinga, A. (2022). Independent events and their complements. Part II. *International Journal of Mathematical Education in Science and Technology*, 53(12), 3470–3483. <https://doi.org/10.1080/0020739X.2021.1985176>
- Montoliu-Nerin, M., Sánchez-García, M., Bergin, C., Grabherr, M., Ellis, B., Kutschera, V. E., Kierczak, M., Johannesson, H., & Rosling, A. (2020). Building de novo reference genome assemblies of complex eukaryotic microorganisms from single nuclei. *Scientific Reports*, 10(1), 1303. <https://doi.org/10.1038/s41598-020-58025-3>
- Nakayama, Y., Yamaguchi, H., Einaga, N., & Esumi, M. (2016). Pitfalls of DNA quantification using dnabinding fluorescent dyes and suggested solutions. *PLoS ONE*, 11(3). <https://doi.org/10.1371/journal.pone.0150528>

- Ningsih, S. S., Septiasari, A., Stujanna, E. N., Avissa, R., Ujianti, I., Permatasari, S. D., & Sukarya, W. S. (2024). Specific Primer Design to Detect Connexin-36 Gene in *Rattus Norvegicus* Brain. *THE JOURNAL OF MUHAMMADIYAH MEDICAL LABORATORY TECHNOLOGIST*, 7(1). <https://doi.org/10.30651/jmlt.v7i1.17985>
- Noman, E., Al-Gheethi, A., Rahman, N. K., Talip, B., Mohamed, R., & Kadir, O. A. (2018). Single Spore Isolation as a Simple and Efficient Technique to obtain fungal pure culture. *IOP Conference Series: Earth and Environmental Science*, 140, 012055. <https://doi.org/10.1088/1755-1315/140/1/012055>
- Pérez-Martín, J., & De Sena-Tomás, C. (2011). Dikaryotic cell cycle in the phytopathogenic fungus *Ustilago maydis* is controlled by the DNA damage response cascade. *Plant Signaling & Behavior*, 6(10), 1574–1577. <https://doi.org/10.4161/psb.6.10.17055>
- Peris, D., Lu, D. S., Kinneberg, V. B., Methlie, I.-S., Dahl, M. S., James, T. Y., Kauserud, H., & Skrede, I. (2022). Large-scale fungal strain sequencing unravels the molecular diversity in mating loci maintained by long-term balancing selection. *PLOS Genetics*, 18(3), e1010097. <https://doi.org/10.1371/journal.pgen.1010097>
- Perkel, J. (2012). Overcoming the Challenges of Multiplex Polymerase Chain Reaction. *American Laboratory*, 44, 32–34.
- Popovic, M., & Minceva, M. (2020). A thermodynamic insight into viral infections: Do viruses in a lytic cycle hijack cell metabolism due to their low Gibbs energy? *Heliyon*, 6(5), e03933. <https://doi.org/10.1016/j.heliyon.2020.e03933>
- Pradnyaniti, D. G., Wirajana, I. N., & Yowani, S. C. (2013). DESAIN PRIMER SECARA IN SILICO UNTUK AMPLIFIKASI FRAGMEN GEN *rpoB* *Mycobacterium tuberculosis* DENGAN POLYMERASE CHAIN REACTION (PCR). *Jurnal Farmasi Udayana*. <https://ojs.unud.ac.id/index.php/jfu/article/view/7387>
- Prhashanna, A., & Jayaraman, A. (2019). Melting thermodynamics of oligonucleic acids conjugated with relatively solvophobic linear polymers: A coarse-grained molecular simulation study. *Journal of Polymer Science Part B: Polymer Physics*, 57(18), 1196–1208. <https://doi.org/10.1002/polb.24780>
- Putra, I. P. (2021). MORELS OF WEST JAVA: DESCRIPTION AND POTENTIAL UTILIZATION. *Indonesian Journal of Science and Education*, 5(1), 49. <https://doi.org/10.31002/ijose.v5i1.3508>

- Qiagen. (2023). *CLC Genomics Workbench 22.0.3 user manual (Windows, macOS and Linux)*. Qiagen. https://resources.qiagenbioinformatics.com/manuals/clcgenomicsworkbench/2203/index.php?manual=Introduction_CLC_Genomics_Workbench.html
- Qin, Q., Teng, Y.-F., Hu, W. S., Wei, J.-Y., Yu, Z.-D., Du, P., Zhang, X.-Y., Guo, X., Chen, M.-Q., Wei, W., & Du, X.-H. (2025). Unexpected richness and distinct patterns of *Morchella* (Ascomycota) species diversity in Chongqing, a notable “Furnace City”: Unveiling rich diversity in hot regions. *IMA Fungus*, 16, e152685. <https://doi.org/10.3897/ima fungus.16.152685>
- Ramšak, B., Markau, J., Pazen, T., Dahlmann, T. A., Krappmann, S., & Kück, U. (2021). The master regulator MAT1-1-1 of fungal mating binds to its targets via a conserved motif in the human pathogen *Aspergillus fumigatus*. *G3*, 11(2), jkaa012. <https://doi.org/10.1093/g3journal/jkaa012>
- Ranallo-Benavidez, T. R., Jaron, K. S., & Schatz, M. C. (2020). GenomeScope 2.0 and Smudgeplot for reference-free profiling of polyploid genomes. *Nature Communications*, 11(1), 1432. <https://doi.org/10.1038/s41467-020-14998-3>
- Ren, R., Tang, S., Yan, L., Fan, T., Lei, X., Shao, C., Yang, Y., Zhu, H., Yang, D., & Xu, J. (2024). Whole-Genome Resequencing and Evolutionary Analysis of Wild Morel Mushroom *Morchella* sp. *Horticulturae*, 10(12), 1287. <https://doi.org/10.3390/horticulturae10121287>
- Retnowati, A., Faulina, S. A., Helbert, H., Riffiani, R., Saskiawan, I., Hidayat, A., Turjaman, M., Surya Hakim, S., Rahayu, L. M., Aryanto, A., Ningrum, R. S., Girmansyah, D., Rianto, T., Soesmardi, B., Surahmat, I. L., Hidayat, I., Kuswanda, W., Alikodra, H. S., Silfariani, Y., & Nurlhida, F. A. H. (2025). *Morchella rinjaniensis*: A Novel Species of Tropical *Morchella* (Ascomycota, Pezizales, and Morchellaceae) Discovered in UNESCO Rinjani-Lombok Biosphere Reserve, Indonesia. *Mycobiology*, 53(4), 367–378. <https://doi.org/10.1080/12298093.2025.2505301>
- Rianto. (2012). *Ekologi Morel Rinjani (Morchella Aff. Deliciosa) Di Taman Nasional Gunung Rinjani Nusa Tenggara Barat* [Dissertation]. IPB University.
- Riffiani, R., Setiarto, R. H. B., & Khusniati, T. (2023). *Specific primer for rapid detection and identification of probiotic Lactiplantibacillus plantarum*. 060005. <https://doi.org/10.1063/5.0183361>
- Robbe, P., Popitsch, N., Knight, S. J. L., Antoniou, P., Becq, J., He, M., Kanapin, A., Samsonova, A., Vavoulis, D. V., Ross, M. T., Kingsbury, Z., Cabes, M., Ramos, S. D. C., Page, S., Dreau, H., Ridout, K., Jones, L. J., Tuff-Lacey,

- A., Henderson, S., ... Schuh, A. (2018). Clinical whole-genome sequencing from routine formalin-fixed, paraffin-embedded specimens: Pilot study for the 100,000 Genomes Project. *Genetics in Medicine*, 20(10), 1196–1205. <https://doi.org/10.1038/gim.2017.241>
- Rohs, R., Jin, X., West, S. M., Joshi, R., Honig, B., & Mann, R. S. (2010). Origins of Specificity in Protein-DNA Recognition. *Annual Review of Biochemistry*, 79(1), 233–269. <https://doi.org/10.1146/annurev-biochem-060408-091030>
- Sánchez Flores, M., Valenzuela, R., Hernández-Muñoz, M. A., García Jiménez, J., Martínez-Pineda, M., & Raymundo, T. (2020). Ascomicetos del bosque mesófilo de montaña de Honey, Puebla de los Ángeles, México. *Acta Botanica Mexicana*, (127). <https://doi.org/10.21829/abm127.2020.1719>
- Satam, H., Joshi, K., Mangrolia, U., Waghoo, S., Zaidi, G., Rawool, S., Thakare, R. P., Banday, S., Mishra, A. K., Das, G., & Malonia, S. K. (2023). Next-Generation Sequencing Technology: Current Trends and Advancements. *Biology*, 12(7), 997. <https://doi.org/10.3390/biology12070997>
- Setyawati, R., & Zubaidah, S. (2021). *Optimasi Konsentrasi Primer dan Suhu Annealing dalam Mendeteksi Gen Leptin pada Sapi Peranakan Ongole (PO) Menggunakan Polymerase Chain Reaction (PCR) | Setyawati | Indonesian Journal of Laboratory*. <https://jurnal.ugm.ac.id/ijl/article/view/65550>
- Shafer, D., & Zhang, Z. (2012). *Introductory Statistics (Kap. 3.3: Conditional Probability and Independent Events)*. https://stats.libretexts.org/Bookshelves/Introductory_Statistics/Introductory_Statistics_%28Shafer_and_Zhang%29/03%3A_Basic_Concepts_of_Probability/3.03%3A_Conditional_Probability_and_Independent_Events
- Shim, S.-M., Kim, J.-H., Jung, S.-E., Kim, D.-J., Oh, J.-H., Han, B.-G., & Jeon, J.-P. (2010). Multilaboratory Assessment of Variations in Spectrophotometry-Based DNA Quantity and Purity Indexes. *Biopreservation and Biobanking*, 8(4), 187–192. <https://doi.org/10.1089/bio.2010.0016>
- Shinoda, N., Yoshida, T., Kusama, T., Takagi, M., Hayakawa, T., Onodera, T., & Sugiura, K. (2009). High GC Contents of Primer 5'-End Increases Reaction Efficiency in Polymerase Chain Reaction. *Nucleosides, Nucleotides and Nucleic Acids*, 28(4), 324–330. <https://doi.org/10.1080/15257770902963400>
- Simão, F. A., Waterhouse, R. M., Ioannidis, P., Kriventseva, E. V., & Zdobnov, E. M. (2015). BUSCO: Assessing genome assembly and annotation completeness with single-copy orthologs. *Bioinformatics*, 31(19), 3210–3212. <https://doi.org/10.1093/bioinformatics/btv351>

- Siswanto, T., Sianipar, N. F., Warnars, H. L. H. S., & Prabowo, H. (2022). Algorithm Model Determination of DNA Primer Design For The Success PCR Process. *International Journal of Emerging Technology and Advanced Engineering*, 12(7), 101–107. https://doi.org/10.46338/ijetae0722_11
- Sorin, E. J., Rhee, Y. M., Nakatani, B. J., & Pande, V. S. (2003). Insights into Nucleic Acid Conformational Dynamics from Massively Parallel Stochastic Simulations. *Biophysical Journal*, 85(2), 790–803. [https://doi.org/10.1016/S0006-3495\(03\)74520-2](https://doi.org/10.1016/S0006-3495(03)74520-2)
- Stanke, M., Diekhans, M., Baertsch, R., & Haussler, D. (2008). Using native and syntenically mapped cDNA alignments to improve *de novo* gene finding. *Bioinformatics*, 24(5), 637–644. <https://doi.org/10.1093/bioinformatics/btn013>
- Stanke, M., Schöffmann, O., Morgenstern, B., & Waack, S. (2006). Gene prediction in eukaryotes with a generalized hidden Markov model that uses hints from external sources. *BMC Bioinformatics*, 7(1), 62. <https://doi.org/10.1186/1471-2105-7-62>
- Štros, M., Launholt, D., & Grasser, K. D. (2007). The HMG-box: A versatile protein domain occurring in a wide variety of DNA-binding proteins. *Cellular and Molecular Life Sciences*, 64(19–20), 2590–2606. <https://doi.org/10.1007/s00018-007-7162-3>
- Sun, S., Coelho, M. A., David-Palma, M., Huang, J., Bian, Z., & Heitman, J. (2025). Fungal sexual reproduction and mating-type loci. *Current Biology*, 35(11), R496–R503. <https://doi.org/10.1016/j.cub.2025.04.061>
- Tanabe, A. S., Nagai, S., Hongo, Y., Yasuike, M., Nakamura, Y., Fujiwara, A., & Katakura, S. (2019). Primer Design, Evaluation of Primer Universality, and Estimation of Identification Power of Amplicon Sequences In Silico. In T. Gojobori, T. Wada, T. Kobayashi, & K. Mineta (Eds.), *Marine Metagenomics* (pp. 21–36). Springer Singapore. https://doi.org/10.1007/978-981-13-8134-8_3
- Thaenkham, U., Chaisiri, K., & Hui En Chan, A. (2022). Implementation of Genetic Markers from Molecular Systematics to DNA Taxonomy and Field Application. In U. Thaenkham, K. Chaisiri, & A. Hui En Chan, *Molecular Systematics of Parasitic Helminths* (pp. 339–358). Springer Nature Singapore. https://doi.org/10.1007/978-981-19-1786-8_14
- Thapar, R. (2015). Structure-specific nucleic acid recognition by L-motifs and their diverse roles in expression and regulation of the genome. *Biochimica et Biophysica Acta (BBA) - Gene Regulatory Mechanisms*, 1849(6), 677–687. <https://doi.org/10.1016/j.bbagrm.2015.02.006>

- Thermo Fisher Scientific. (2024). *Thermo Scientific NanoDrop Spectrophotometers Nucleic acid measurements* (Version T104 08/24).
- Thermo Fisher Scientific. (2025a). *PCR Cycling Parameters—Six Key Considerations for Success | Thermo Fisher Scientific—ID*. <https://www.thermofisher.com/id/en/home/life-science/cloning/cloning-learning-center/invitrogen-school-of-molecular-biology/pcr-education/pcr-reagents-enzymes/pcr-cycling-considerations.html>
- Thermo Fisher Scientific. (2025b). *Steps in Nucleic Acid Gel Electrophoresis | Thermo Fisher Scientific—ID*. <https://www.thermofisher.com/id/en/home/life-science/cloning/cloning-learning-center/invitrogen-school-of-molecular-biology/na-electrophoresis-education/na-electrophoresis-workflow.html>
- Tjahjono, Y., Wedharga, I. G. P. A., Novita, B. D., Tahalele, P., Wijaya, H., Soediono, E. I., Hendrata, A. P., Dewi, S., Wijaya, S., Ervina, M., & Kuncorojakti, S. (2025). Optimized RT-qPCR Detection of Hepatic Lipopolysaccharide-Binding Protein in Diet-Induced Obese Mice. *Jurnal Medik Veteriner*, 8(2), 308–317. <https://doi.org/10.20473/jmv.vol8.iss2.2025.308-317>
- Van De Wetering, M., Oosterwegel, M., Van Norren, K., & Clevers, H. (1993). Sox-4, an Sry-like HMG box protein, is a transcriptional activator in lymphocytes. *The EMBO Journal*, 12(10), 3847–3854. <https://doi.org/10.1002/j.1460-2075.1993.tb06063.x>
- Van Pelt-Verkuil, E., & Te Witt, R. (2019). Principles of PCR. In E. Van Pelt-Verkuil, W. B. Van Leeuwen, & R. Te Witt (Eds.), *Molecular Diagnostics* (pp. 131–215). Springer Singapore. https://doi.org/10.1007/978-981-13-1604-3_5
- Van Wyk, J., Wang, X., Mathieu, D., Mills, G. L., Childs, K. L., & Bonito, G. (2026). Life cycle transcriptomics of the homothallic cultivated morel (*Morchella rufobrunnea*). *Fungal Genetics and Biology*, 182, 104056. <https://doi.org/10.1016/j.fgb.2025.104056>
- Vats, S., Kumar, V., Mandlik, R., Patil, G., Sonah, H., Roy, J., Sharma, T. R., & Deshmukh, R. (2023). Reference Guided De Novo Genome Assembly of Transformation Pliable *Solanum lycopersicum* cv. Pusa Ruby. *Genes*, 14(3), 570. <https://doi.org/10.3390/genes14030570>
- Ven, S., & Rani, A. (2012). Discriminatory Power of Agarose Gel Electrophoresis in DNA Fragments Analysis. In S. Magdeldin (Ed.), *Gel Electrophoresis—Principles and Basics*. InTech. <https://doi.org/10.5772/36891>

- Versmessen, N., Van Simaey, L., Negash, A. A., Vandekerckhove, M., Hulpiau, P., Vaneechoutte, M., & Cools, P. (2024). Comparison of DeNovix, NanoDrop and Qubit for DNA quantification and impurity detection of bacterial DNA extracts. *PLOS ONE*, 19(6), e0305650. <https://doi.org/10.1371/journal.pone.0305650>
- Wallen, R. M., & Perlin, M. H. (2018). An Overview of the Function and Maintenance of Sexual Reproduction in Dikaryotic Fungi. *Frontiers in Microbiology*, 9, 503. <https://doi.org/10.3389/fmicb.2018.00503>
- Waterhouse, R. M., Seppey, M., Simão, F. A., Manni, M., Ioannidis, P., Klioutchnikov, G., Kriventseva, E. V., & Zdobnov, E. M. (2018). BUSCO Applications from Quality Assessments to Gene Prediction and Phylogenomics. *Molecular Biology and Evolution*, 35(3), 543–548. <https://doi.org/10.1093/molbev/msx319>
- West, S. M., Rohs, R., Mann, R. S., & Honig, B. (2010). Electrostatic Interactions between Arginines and the Minor Groove in the Nucleosome. *Journal of Biomolecular Structure and Dynamics*, 27(6), 861–866. <https://doi.org/10.1080/07391102.2010.10508587>
- Whittle, C. A., Votintseva, A., Ridout, K., & Filatov, D. A. (2015). Recent and Massive Expansion of the Mating-Type-Specific Region in the Smut Fungus *Microbotryum*. *Genetics*, 199(3), 809–816. <https://doi.org/10.1534/genetics.114.171702>
- Wicaksono, A., Raihandhany, R., & Aryantha, I. N. P. (2021). Upaya Kultivasi Jamur Morel (*Morchella esculenta* (L.) Pers.) dari Kawasan Lembang, Jawa Barat dan Optimasi Pertumbuhannya dengan Menggunakan Media Pati. *Jurnal Mikologi Indonesia*, 5(1). <https://doi.org/10.46638/jmi.v5i1.165>
- Willis, A., Knudsen, T., & Askar, M. Z. (2018). P097 Quantity, integrity & purity: A comparative study of different genomic dna assessment methods. *Human Immunology*, 79, 133–134. <https://doi.org/10.1016/j.humimm.2018.07.156>
- Winston, C., Organick, L., Ward, D., Ceze, L., Strauss, K., & Chen, Y.-J. (2022). Combinatorial PCR Method for Efficient, Selective Oligo Retrieval from Complex Oligo Pools. *ACS Synthetic Biology*, 11(5), 1727–1734. <https://doi.org/10.1021/acssynbio.1c00482>
- Wittmeier, P., & Hummel, S. (2022). Agarose Gel Electrophoresis to Assess PCR Product Yield: Comparison with Spectrophotometry, Fluorometry and qPCR. *BioTechniques*, 72(4), 155–158. <https://doi.org/10.2144/btn-2021-0094>
- Wolfenbarger, S. N., Twomey, M. C., Gadoury, D. M., Knaus, B. J., Grünwald, N. J., & Gent, D. H. (2015). Identification and distribution of mating-type

idiomorphs in populations of *Podosphaera macularis* and development of chasmothecia of the fungus. *Plant Pathology*, 64(5), 1094–1102. <https://doi.org/10.1111/ppa.12344>

Wong, L.-P., Ong, R. T.-H., Poh, W.-T., Liu, X., Chen, P., Li, R., Lam, K. K.-Y., Pillai, N. E., Sim, K.-S., Xu, H., Sim, N.-L., Teo, S.-M., Foo, J.-N., Tan, L. W.-L., Lim, Y., Koo, S.-H., Gan, L. S.-H., Cheng, C.-Y., Wee, S., ... Teo, Y.-Y. (2013). Deep Whole-Genome Sequencing of 100 Southeast Asian Malays. *The American Journal of Human Genetics*, 92(1), 52–66. <https://doi.org/10.1016/j.ajhg.2012.12.005>

Yesudhas, D., Batool, M., Anwar, M., Panneerselvam, S., & Choi, S. (2017). Proteins Recognizing DNA: Structural Uniqueness and Versatility of DNA-Binding Domains in Stem Cell Transcription Factors. *Genes*, 8(8), 192. <https://doi.org/10.3390/genes8080192>

Yu, S., Wang, Y., Li, X., Yu, F., & Li, W. (2017). The factors affecting the reproducibility of micro-volume DNA mass quantification in Nanodrop 2000 spectrophotometer. *Optik*, 145, 555–560. <https://doi.org/10.1016/j.ijleo.2017.08.031>

Yuwono, T. (2005). *Biolog Molekuler*. Erlangga.

Zhu, X., Ma, K., Sun, M., Zhang, J., Liu, L., & Niu, S. (2023). Isolation and identification of pathogens of *Morchella sextelata* bacterial disease. *Frontiers in Microbiology*, 14, 1231353. <https://doi.org/10.3389/fmicb.2023.1231353>