

DAFTAR PUSTAKA

- Aleksić, J. M., Stojanović, D., Banović, B., & Jančić, R. (2012). A simple and efficient DNA isolation method for *Salvia officinalis*. *Biochemical Genetics*, 50, 881–892. <https://doi.org/10.1007/s10528-012-9528-y>
- Altschul, S. F., Gish, W., Miller, W., Myers, E. W., & Lipman, D. J. (1990). Basic local alignment search tool. *Journal of Molecular Biology*, 215(3), 403–410. [https://doi.org/10.1016/S0022-2836\(05\)80360-2](https://doi.org/10.1016/S0022-2836(05)80360-2)
- Altschul, S. F., Madden, T. L., Schäffer, A. A., Zhang, J., Zhang, Z., Miller, W., & Lipman, D. J. (1997). Gapped BLAST and PSI-BLAST: A new generation of protein database search programs. *Nucleic Acids Research*, 25(17), 3389–3402. <https://doi.org/10.1093/nar/25.17.3389>
- Amalraj, V. A., & Balasundaram, N. (2006). On the taxonomy of the members of 'Saccharum Complex'. *Genetic Resources and Crop Evolution*, 53(1), 35–41. <https://doi.org/10.1007/s10722-004-0581-1>
- Amarasinghe, S. L., Su, S., Dong, X., Zappia, L., Ritchie, M. E., & Gouil, Q. (2020). Opportunities and challenges in long-read sequencing data analysis. *Genome Biology*, 21(30), 1-16. <https://doi.org/10.1186/s13059-020-1935-5>
- Amunts, A., & Nelson, N. (2009). Plant photosystem I design in the light of evolution. *Structure*, 17(5), 637–650. <https://doi.org/10.1016/j.str.2009.03.006>
- Aristya, G. R., Nabillah, S. A. A., Kasiamdari, R. S., Damaiyani, J. & Prabowo, H. (2024). Phylogenetic and genetic variation of sugarcane (*Saccharum* spp.) from island of Java, Indonesia based on trnK chloroplast gene. *International Journal of Agriculture and Biosciences*, 13(2), 157-166.
- Asaf, S., Waqas, M., Khan, A. L., Khan, M. A., Kang, S.-M., Imran, Q. M., Shahzad, R., Bilal, S., Yun, B.-W., & Lee, I. J. (2017). The complete chloroplast genome of wild rice (*Oryza minuta*) and its comparison to related species. *Frontiers in Plant Science*, 8, 1-15. <https://doi.org/10.3389/fpls.2017.00304>
- Babu & Ethirajan. (1962). A note on use of *Saccharum spontaneum* L. in sugarcane breeding. *Proceedings of the 11th Congress of the International Society of Sugar Cane Technologists (ISSCT)*, 11, 464–469.
- Babu, K. S. D., Janakiraman, V., Palaniswamy, H., Kasirajan, L., Gomathi, R., & Ramkumar, T. R. (2022). A short review on sugarcane: Its domestication, molecular manipulations and future perspectives. *Genetic Resources and Crop Evolution*, 69(8), 2623–2643. <https://doi.org/10.1007/s10722-022-01430-6>
- Badan Pusat Statistik. (2025). *Statistik Tanaman Perkebunan Semusim Indonesia 2024*. Badan Pusat Statistik, 1-94.
- Bailey, T. L., Boden, M., Buske, F. A., Frith, M., Grant, C. E., Clementi, L., Ren, J., Li, W. W., & Noble, W. S. (2009). MEME SUITE: Tools for motif

- discovery and searching. *Nucleic Acids Research*, 37(Web Server), W202–W208. <https://doi.org/10.1093/nar/gkp335>
- Bailey, T. L., Boden, M., Buske, F. A., Frith, M., Grant, C. E., Clementi, L., Ren, J., Li, W. W., & Noble, W. S. (2009). MEME SUITE: Tools for motif discovery and searching. *Nucleic Acids Research*, 37, W202–W208. <https://doi.org/10.1093/nar/gkp335>
- Bailey, T.L., & Elkan, C. (1994). Fitting a mixture model by expectation maximization to discover motifs in biopolymers. *Proceedings International Conference on Intelligent Systems for Molecular Biology*, 2, 28–36.
- Balsalobre, T. W. A., Da Silva Pereira, G., Margarido, G. R. A., Gazaffi, R., Barreto, F. Z., Anoni, C. O., Cardoso-Silva, C. B., Costa, E. A., Mancini, M. C., Hoffmann, H. P., De Souza, A. P., Garcia, A. A. F., & Carneiro, M. S. (2017). GBS-based single dosage markers for linkage and QTL mapping allow gene mining for yield-related traits in sugarcane. *BMC Genomics*, 18(1), 1-19. <https://doi.org/10.1186/s12864-016-3383-x>
- Bánki, O., Roskov, Y., Döring, M., Ower, G., Hernández Robles, D. R., Plata Corredor, C. A., Stjernegaard Jeppesen, T., Örn, A., Pape, T., Hobern, D., Garnett, S., Little, H., DeWalt, R. E., Miller, J., & Orrell, T. (2025). *Catalogue of Life* (Annual Checklist 2025). Catalogue of Life Foundation. <https://doi.org/10.48580/DGR6N>
- Begum, G., Albanna, A., Bankapur, A., Nassir, N., Tambi, R., Berdiev, B. K., Akter, H., Karuvantevida, N., Kellam, B., Alhashmi, D., Sung, W. W. L., Thiruvahindrapuram, B., Alsheikh-Ali, A., Scherer, S. W., & Uddin, M. (2021). Long-read sequencing improves the detection of structural variations impacting complex non-coding elements of the genome. *International Journal of Molecular Sciences*, 22(4), 1-14. <https://doi.org/10.3390/ijms22042060>
- Ben-Shem, A., Frolov, F., & Nelson, N. (2003). Crystal structure of plant photosystem I. *Nature*, 426(6967), 630–635. <https://doi.org/10.1038/nature02200>
- Bi, C., Paterson, A. H., Wang, X., Xu, Y., Wu, D., Qu, Y., Jiang, A., Ye, Q., & Ye, N. (2016). Analysis of the complete mitochondrial genome sequence of the diploid cotton *Gossypium raimondii* by comparative genomics approaches. *BioMed Research International*, 2016, 1–18. <https://doi.org/10.1155/2016/5040598>
- Brozynska, M., Furtado, A., & Henry, R. J. (2016). Genomics of crop wild relatives: Expanding the gene pool for crop improvement. *Plant Biotechnology Journal*, 14(5), 1070–1085. <https://doi.org/10.1111/pbi.12454>
- Caspy, I., & Nelson, N. (2018). Structure of the plant photosystem I. *Biochemical Society Transactions*, 46(2), 285–294. <https://doi.org/10.1042/BST20170299>

- Chan, C. X., Gross, J., Yoon, H. S., & Bhattacharya, D. (2011). Plastid origin and evolution: New models provide insights into old problems. *Plant Physiology*, 155(4), 1552–1560. <https://doi.org/10.1104/pp.111.173500>
- Cheavegatti-Gianotto, A., De Abreu, H. M. C., Arruda, P., Besspalhok Filho, J. C., Burnquist, W. L., Creste, S., Di Ciero, L., Ferro, J. A., De Oliveira Figueira, A. V., De Sousa Filgueiras, T., Grossi-de-Sá, M. D. F., Guzzo, E. C., Hoffmann, H. P., De Andrade Landell, M. G., Macedo, N., Matsuoka, S., De Castro Reinach, F., Romano, E., Da Silva, W. J., Silva Filho, M. de C., & César Ulian, E. (2011). Sugarcane (*Saccharum × officinarum*): A reference study for the regulation of genetically modified cultivars in Brazil. *Tropical Plant Biology*, 4(1), 62–89. <https://doi.org/10.1007/s12042-011-9068-3>
- Chitnis, P. R. (2001). Photosystem I: Function and physiology. *Annual Review of Plant Physiology and Plant Molecular Biology*, 52(1), 593–626. <https://doi.org/10.1146/annurev.arplant.52.1.593>
- Chothia, C., & Lesk, A. M. (1986). The relation between the divergence of sequence and structure in proteins. *The EMBO Journal*, 5(4), 823–826. <https://doi.org/10.1002/j.1460-2075.1986.tb04288.x>
- Cornejo-Corona, I., Boland, D. J., & Devarenne, T. P. (2024). Method for isolation of high molecular weight genomic DNA from *Botryococcus* biomass. *PLOS ONE*, 19(7), 1–12. <https://doi.org/10.1371/journal.pone.0301680>
- Coster, W., Weissensteiner, M. H., & Sedlazeck, F. J. (2021). Towards population-scale long-read sequencing. *Nature Reviews Genetics*, 22(9), 572–587. <https://doi.org/10.1038/s41576-021-00367-3>
- D'Hont, A., Ison, D., Alix, K., Roux, C., & Glaszmann, J. C. (1998). Determination of basic chromosome numbers in the genus *Saccharum* by physical mapping of ribosomal RNA genes. *Genome*, 41(2), 221–225. <https://doi.org/10.1139/g98-023>
- Zhu, J. R., Zhou, H., Pan, Y. B., & Lu, X. (2014). Genetic variability among the chloroplast genomes of sugarcane (*Saccharum* spp) and its wild progenitor species *Saccharum spontaneum* L. *Genetics and Molecular Research*, 13(2), 3037–3047. <https://doi.org/10.4238/2014.January.24.3>
- Daniell, H., Lin, C.-S., Yu, M., & Chang, W.-J. (2016). Chloroplast genomes: Diversity, evolution, and applications in genetic engineering. *Genome Biology*, 17(1), 1–29. <https://doi.org/10.1186/s13059-016-1004-2>
- Daniels, J., & Roach, B. T. (1987). Taxonomy and evolution. In D. J. Heinz (Ed.), *Sugarcane Improvement Through Breeding*. Elsevier, 7–84.
- Deiner, K., Renshaw, M. A., Li, Y., Olds, B. P., Lodge, D. M., & Pfrender, M. E. (2017). Long-range PCR allows sequencing of mitochondrial genomes from environmental DNA. *Methods in Ecology and Evolution*, 8(12), 1888–1898. <https://doi.org/10.1111/2041-210X.12836>
- Desjardins, P., & Conklin, D. (2010). NanoDrop microvolume quantitation of nucleic acids. *Journal of Visualized Experiments*, 45, 2565, 1–5. <https://doi.org/10.3791/2565>

- Dilley, K., Pagan, F., & Chapman, B. (2021). Methods for ensuring the highest DNA concentration and yield in future and retrospective trace DNA extracts. *Science & Justice*, *61*(2), 193–197. <https://doi.org/10.1016/j.scijus.2020.11.005>
- Dillon, S. L., Shapter, F. M., Henry, R. J., Cordeiro, G., Izquierdo, L., & Lee, L. S. (2007). Domestication to crop improvement: Genetic resources for *Sorghum* and *Saccharum* (Andropogoneae). *Annals of Botany*, *100*(5), 975–989. <https://doi.org/10.1093/aob/mcm192>
- Doyle, J. J., & Doyle, J. L. (1987). A rapid DNA isolation procedure for small quantities of fresh leaf tissue. *Phytochemical Bulletin*, *19*(1), 11–15.
- Ewing, B., & Green, P. (1998). Base-Calling of automated sequencer traces using Phred. II. error probabilities. *Genome Research*, *8*(3), 186–194. <https://doi.org/10.1101/gr.8.3.186>
- Franco-Sierra, N. D., & Díaz-Nieto, J. F. (2020). Rapid mitochondrial genome sequencing based on Oxford Nanopore Sequencing and a proxy for vertebrate species identification. *Ecology and Evolution*, *10*(7), 3544–3560. <https://doi.org/10.1002/ece3.6151>
- Fromme, P., Jordan, P., & Krauß, N. (2001). Structure of photosystem I. *Biochimica et Biophysica Acta (BBA) - Bioenergetics*, *1507*(1–3), 5–31. [https://doi.org/10.1016/S0005-2728\(01\)00195-5](https://doi.org/10.1016/S0005-2728(01)00195-5)
- Gallagher, S. (1998). Quantitation of Nucleic Acids with Absorption Spectroscopy. *Current Protocols in Protein Science*, *13*(1), A.4K.1–A.4K.3. <https://doi.org/10.1002/0471140864.psa04ks13>
- Garsmeur, O., Droc, G., Antonise, R., Grimwood, J., Potier, B., Aitken, K., Jenkins, J., Martin, G., Charron, C., Hervouet, C., Cotset, L., Yahiaoui, N., Healey, A., Sims, D., Cherukuri, Y., Sreedasyam, A., Kilian, A., Chan, A., Van Sluys, M.-A., Swaminathan, K., Town, C., Bergès, H., Simmons, B., Glazsmann, J.-C., van der Vossen, E., Henry, R., Schmutz, J., & D'Hont, A. (2018). A mosaic monoploid reference sequence for the highly complex genome of sugarcane. *Nature Communications*, *9*, 2638, 1–10. <https://doi.org/10.1038/s41467-018-05051-5>
- Green, B. R. (2011). Chloroplast genomes of photosynthetic eukaryotes. *The Plant Journal*, *66*(1), 34–44. <https://doi.org/10.1111/j.1365-313X.2011.04541.x>
- Green, M. R., & Sambrook, J. (2012). *Molecular cloning: A laboratory manual* (4th ed). Cold Spring Harbor laboratory press.
- Greiner, S., Lehwark, P., & Bock, R. (2019). OrganellarGenomeDRAW (OGDRAW) version 1.3.1: Expanded toolkit for the graphical visualization of organellar genomes. *Nucleic Acids Research*, *47*(W1), W59–W64. <https://doi.org/10.1093/nar/gkz238>
- Grivet, L., & Arruda, P. (2002). Sugarcane genomics: Depicting the complex genome of an important tropical crop. *Current Opinion in Plant Biology*, *5*, 122–127. [https://doi.org/10.1016/S1369-5266\(02\)00255-9](https://doi.org/10.1016/S1369-5266(02)00255-9)
- Gu, W., Miller, S., & Chiu, C. Y. (2019). Clinical metagenomic next-generation sequencing for pathogen detection. *Annual Review of Pathology*:

- Mechanisms of Disease*, 14(1), 319–338. <https://doi.org/10.1146/annurev-pathmechdis-012418-012751>
- Gualberto, J. M., & Newton, K. J. (2017). Plant mitochondrial genomes: Dynamics and mechanisms of mutation. *Annual Review of Plant Biology*, 68(1), 225–252. <https://doi.org/10.1146/annurev-arplant-043015-112232>
- Guo, A.-Y., Zhu, Q.-H., Chen, X., & Luo, J.-C. (2007). GSDS: a gene structure display server. *Hereditas*, 29(8), 1023–1026. <https://doi.org/10.1360/yc-007-1023>
- Hapase, R. S., Sushir, K. V., Hapase, P. R., & Repale, J. M. (2010). Studies on variation in interspecific hybrids of *Saccharum*. *Sugar Tech*, 12(2), 155–159. <https://doi.org/10.1007/s12355-010-0029-7>
- Healey, A. L., Garsmeur, O., Lovell, J. T., Shengquiang, S., Sreedasyam, A., Jenkins, J., Plott, C. B., Piperidis, N., Pompidor, N., Llaca, V., Metcalfe, C. J., Doležel, J., Cápál, P., Carlson, J. W., Hoarau, J. Y., Hervouet, C., Zini, C., Dievart, A., Lipzen, A., Williams, M., Boston, L. B., Webber, J., Keymanesh, K., Tejomurthula, S., Rajasekar, S., Suchecki, R., Furtado, A., May, G., Parakkal, P., Simmons, B. A., Barry, K., Henry, R. J., Grimwood, J., Aitken, K. S., Schmutz, J., & D'Hont, A. (2024). The complex polyploid genome architecture of sugarcane. *Nature*, 628(8009), 804–810. <https://doi.org/10.1038/s41586-024-07231-4>
- Healey, A., Furtado, A., Cooper, T., & Henry, R. J. (2014). Protocol: A simple method for extracting next-generation sequencing quality genomic DNA from recalcitrant plant species. *Plant Methods*, 10(1), 1-8. <https://doi.org/10.1186/1746-4811-10-21>
- 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>
- Hollingsworth, P. M., Li, D.-Z., Van Der Bank, M., & Twyford, A. D. (2016). Telling plant species apart with DNA: From barcodes to genomes. *Philosophical Transactions of the Royal Society B: Biological Sciences*, 371(1702), 1-9. <https://doi.org/10.1098/rstb.2015.0338>
- Hu, B., Jin, J., Guo, A.-Y., Zhang, H., Luo, J.-C., & Gao, G. (2015). GSDS 2.0: An upgraded gene feature visualization server. *Bioinformatics*, 31(8), 1296–1297. <https://doi.org/10.1093/bioinformatics/btu817>
- Irvine, J. E. (1999). *Saccharum* species as horticultural classes: *Theoretical and Applied Genetics*, 98(2), 186–194. <https://doi.org/10.1007/s001220051057>
- Jain, M., Koren, S., Miga, K. H., Quick, J., Rand, A. C., Sasani, T. A., Tyson, J. R., Beggs, A. D., Dilthey, A. T., Fiddes, I. T., Malla, S., Marriott, H., Nieto, T., O'Grady, J., Olsen, H. E., Pedersen, B. S., Rhie, A., Richardson, H., Quinlan, A. R., Loman, N. J., & Loose, M. (2018). Nanopore sequencing and assembly of a human genome with ultra-long reads. *Nature Biotechnology*, 36(4), 338–345. <https://doi.org/10.1038/nbt.4060>

- Jaudou, S., Tran, M.-L., Vorimore, F., Fach, P., & Delannoy, S. (2022). Evaluation of high molecular weight DNA extraction methods for long-read sequencing of Shiga toxin-producing *Escherichia coli*. *PLOS ONE*, *17*(7), 1-12. <https://doi.org/10.1371/journal.pone.0270751>
- Jensen, P. E., Bassi, R., Boekema, E. J., Dekker, J. P., Jansson, S., Leister, D., Robinson, C., & Scheller, H. V. (2007). Structure, function and regulation of plant photosystem I. *Biochimica et Biophysica Acta (BBA) - Bioenergetics*, *1767*(5), 335–352. <https://doi.org/10.1016/j.bbabi.2007.03.004>
- Jin, J.-J., Yu, W.-B., Yang, J.-B., Song, Y., dePamphilis, C. W., Yi, T.-S., & Li, D.-Z. (2020). GetOrganelle: A fast and versatile toolkit for accurate de novo assembly of organelle genomes. *Genome Biology*, *21*(1), 1-31. <https://doi.org/10.1186/s13059-020-02154-5>
- Jordan, P., Fromme, P., Witt, H. T., Klukas, O., Saenger, W., & Krauß, N. (2001). Three-dimensional structure of Cyanobacterial photosystem I at 2.5 Å resolution. *Nature*, *411*(6840), 909–917. <https://doi.org/10.1038/35082000>
- Jumper, J., Evans, R., Pritzel, A., Green, T., Figurnov, M., Ronneberger, O., Tunyasuvunakool, K., Bates, R., Židek, A., Potapenko, A., Bridgland, A., Meyer, C., Kohl, S. A. A., Ballard, A. J., Cowie, A., Romera-Paredes, B., Nikolov, S., Jain, R., Adler, J., Back, T., Petersen, S., Reiman, D., Clancy, E., Zielinski, M., Steinegger, M., Pacholska, M., Berghammer, T., Bodenstein, S., Silver, D., Vinyals, O., Senior, A.W., Kavukcuoglu, K., Kohli, P., & Hassabis, D. (2021). Highly accurate protein structure prediction with AlphaFold. *Nature*, *596*(7873), 583–589. <https://doi.org/10.1038/s41586-021-03819-2>
- Karlin, S., & Altschul, S. F. (1990). Methods for assessing the statistical significance of molecular sequence features by using general scoring schemes. *Proceedings of the National Academy of Sciences of the United States of America*, *87*(6), 2264–2268. <https://doi.org/10.1073/pnas.87.6.2264>
- Kasiamdari, R. S., Aristya, G. R., Prabowo, H., Ariesta, C., & Arif, M. F. (2019). Genetic diversity of Indonesian's sugarcane varieties (*Saccharum officinarum*) based on RAPD molecular markers. *Biodiversitas: Journal of Biological Diversity*, *20*(10), 3005–3010. <https://doi.org/10.13057/biodiv/d201032>
- Krech, K., Fu, H.-Y., Thiele, W., Ruf, S., Schöttler, M. A., & Bock, R. (2012). The plastid genome-encoded Ycf4 protein functions as a nonessential assembly factor for photosystem I in higher plants. *PLoS ONE*, *7*(3), 1-6. <https://doi.org/10.1371/journal.pone.0032630>
- Kufareva, I., & Abagyan, R. (2011). Methods of protein structure comparison. In A. J. W. Orry & R. Abagyan (Eds), *Homology Modeling* (Vol. 857, pp. 231–257). Humana Press. https://doi.org/10.1007/978-1-61779-588-6_10
- Kusumawati, A. (2023). Potensi peningkatan produktivitas tebu di lahan pasiran dengan pemberian blotong basah. *Agrifor*, *22*(2), 223-232. <https://doi.org/10.31293/agrifor.v22i2.6702>

- Li, S., Duan, W., Zhao, J., Jing, Y., Feng, M., Kuang, B., Wei, N., Chen, B., & Yang, X. (2022). Comparative analysis of chloroplast genome in *Saccharum* spp. and related members of 'Saccharum Complex'. *International Journal of Molecular Sciences*, 23(14), 1-19. <https://doi.org/10.3390/ijms23147661>
- Li, Z., Parris, S., & Saski, C. A. (2020). A simple plant high-molecular-weight DNA extraction method suitable for single-molecule technologies. *Plant Methods*, 16(1), 1-6. <https://doi.org/10.1186/s13007-020-00579-4>
- Lima-Melo, Y., Alencar, V. T. C. B., Lobo, A. K. M., Sousa, R. H. V., Tikkanen, M., Aro, E.-M., Silveira, J. A. G., & Gollan, P. J. (2019). Photoinhibition of photosystem i provides oxidative protection during imbalanced photosynthetic electron transport in *Arabidopsis thaliana*. *Frontiers in Plant Science*, 10, 1-13. <https://doi.org/10.3389/fpls.2019.00916>
- Lin, B., Hui, J., & Mao, H. (2021). Nanopore technology and its applications in gene sequencing. *Biosensors*, 11(7), 1-17. <https://doi.org/10.3390/bios11070214>
- Linnaeus, C. (1753). *Species Plantarum*. Laurentii Salvii, 1-1200.
- Liu, P.-F., Avramova, L. V., & Park, C. (2009). Revisiting absorbance at 230 nm as a protein unfolding probe. *Analytical Biochemistry*, 389(2), 165–170. <https://doi.org/10.1016/j.ab.2009.03.028>
- Logsdon, G. A., Vollger, M. R., & Eichler, E. E. (2020). Long-read human genome sequencing and its applications. *Nature Reviews Genetics*, 21(10), 597–614. <https://doi.org/10.1038/s41576-020-0236-x>
- Lowe, T. M., & Eddy, S. R. (2010). tRNAscan-SE: Search and contextual analysis of transfer RNA genes. *Nucleic Acids Research*, 38, W88–W90. <https://doi.org/10.1093/nar/gkq519>
- Lu, G., Liu, P., Wu, Q., Zhang, S., Zhao, P., Zhang, Y., & Que, Y. (2024). Sugarcane breeding: A fantastic past and promising future driven by technology and methods. *Frontiers in Plant Science*, 15, 1-10. <https://doi.org/10.3389/fpls.2024.1375934>
- 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>
- Ma, M., Zhong, M., Zhang, Q., Zhao, W., Wang, M., Luo, C., & Xu, B. (2022). A genome-wide analysis of the chloroplast NADH dehydrogenase-like genes in *Zostera marina*. *Journal of Oceanology and Limnology*, 40(2), 656–677. <https://doi.org/10.1007/s00343-021-0027-z>
- Masago, K., Fujita, S., Oya, Y., Takahashi, Y., Matsushita, H., Sasaki, E., & Kuroda, H. (2021). Comparison between fluorimetry (Qubit) and spectrophotometry (NanoDrop) in the quantification of DNA and RNA extracted from frozen and FFPE tissues from lung cancer patients: A Real-World Use of Genomic Tests. *Medicina*, 57(12), 1-9. <https://doi.org/10.3390/medicina57121375>

- Mayjonade, B., Gouzy, J., Donnadieu, C., Pouilly, N., Marande, W., Callot, C., Langlade, N., & Muños, S. (2016). Extraction of high-molecular-weight genomic DNA for long-read sequencing of single molecules. *BioTechniques*, *61*(4), 203–205. <https://doi.org/10.2144/000114460>
- Miller, J. R., Koren, S., & Sutton, G. (2010). Assembly algorithms for next-generation sequencing data. *Genomics*, *95*(6), 315–327. <https://doi.org/10.1016/j.ygeno.2010.03.001>
- Mirajkar, S. J., Devarumath, R. M., Nikam, A. A., Sushir, K. V., Babu, H., & Suprasanna, P. (2019). Sugarcane (*Saccharum* spp.): Breeding and genomics. In J. M. Al-Khayri, S. M. Jain, & D. V. Johnson. *Advances in Plant Breeding Strategies: Industrial and Food Crops*, *6*, 363–406. https://doi.org/10.1007/978-3-030-23265-8_11
- Mohanta, T. K., Mishra, A. K., Khan, A., Hashem, A., Abd_Allah, E. F., & Al-Harrasi, A. (2020). Gene loss and evolution of the plastome. *Genes*, *11*(10), 1-23. <https://doi.org/10.3390/genes11101133>
- Mukherjee, S. K. (1957). Origin and distribution of *Saccharum*. *Botanical Gazette*, *119*(1), 55–61. <https://doi.org/10.1086/335958>
- Nestor, B. J., Bayer, P. E., Fernandez, C. G. T., Edwards, D., & Finnegan, P. M. (2023). Approaches to increase the validity of gene family identification using manual homology search tools. *Genetica*, *151*, 325–338. <https://doi.org/10.1007/s10709-023-00196-8>
- Okonechnikov, K., Golosova, O., Fursov, M., & the UGENE team. (2012). Unipro UGENE: A unified bioinformatics toolkit. *Bioinformatics*, *28*(8), 1166–1167. <https://doi.org/10.1093/bioinformatics/bts091>
- Olejniczak, S. A., Łojewska, E., Kowalczyk, T., & Sakowicz, T. (2016). Chloroplasts: State of research and practical applications of plastome sequencing. *Planta*, *244*(3), 517–527. <https://doi.org/10.1007/s00425-016-2551-1>
- P3GI (2025). *Varietas komersial di Indonesia*. <https://www.varietasp3gi.com/>
- Pan, L.-L., Wang, Y., Hu, J.-H., Ding, Z.-T., & Li, C. (2013). Analysis of codon use features of stearoyl-acyl carrier protein desaturase gene in *Camellia sinensis*. *Journal of Theoretical Biology*, *334*, 80–86.
- Pearson, W. R. (2013). An introduction to sequence similarity (“Homology”) searching. *Current Protocols in Bioinformatics*, *42*(1), 1-8. <https://doi.org/10.1002/0471250953.bi0301s42>
- Phiri, T. M., Xiong, H., Pan, Y., Dickson, R. W., Joshi, N., Rojas, A., & Shi, A. (2024). Genomic association and prediction study for yield traits in a sugarcane (*Saccharum* spp. Hybrids) mapping population ‘lcp 85-384’. *Plant Breeding*, *144*(1), 56–69. <https://doi.org/10.1111/pbr.13214>
- Plotkin, J. B., & Kudla, G. (2011). Synonymous but not the same: The causes and consequences of codon bias. *Nature Reviews Genetics*, *12*(1), 32–42. <https://doi.org/10.1038/nrg2899>
- Porta-Pardo, E., Ruiz-Serra, V., Valentini, S., & Valencia, A. (2022). The structural coverage of the human proteome before and after AlphaFold.

- PLOS Computational Biology*, 18(1), 1-17.
<https://doi.org/10.1371/journal.pcbi.1009818>
- Priyono, D. S., Rafina, N., Arisuryanti, T., Lesmana, I., Yustian, I., & Setiawan, A. (2025). The first complete mitochondrial genome of Sumatran striped rabbit *Nesolagus netscheri* (Schlegel, 1880), and its phylogenetic relationship with other Leporidae. *Scientific Reports*, 15(1), 1-11.
<https://doi.org/10.1038/s41598-025-85212-x>
- Qian, W., Yang, J.-R., Pearson, N. M., Maclean, C., & Zhang, J. (2012). Balanced codon usage optimizes eukaryotic translational efficiency. *PLoS Genetics*, 8(3), 1-18. <https://doi.org/10.1371/journal.pgen.1002603>
- Ramadhan, I. C., Taryono, & Wulandari, R. (2014). Keragaan Pertumbuhan dan rendemen lima klon tebu (*Saccharum officinarum* L.) di ultisol, vertisol, dan inceptisol. *Vegetalika*, 3(4), 77-87. <https://doi.org/10.22146/veg.5763>
- Roach, B. T. (1977). Utilization of *Saccharum spontaneum* in sugarcane breeding. *Proceedings of the 16th Congress of the International Society of Sugar Cane Technologists (ISSCT)*, 16, 43-57.
- Rogers, S. O., & Bendich, A. J. (1985). Extraction of DNA from milligram amounts of fresh, herbarium and mummified plant tissues. *Plant Molecular Biology*, 5(2), 69-76. <https://doi.org/10.1007/BF00020088>
- Rokhman, Taryono, & Wulandari, R. (2014). Jumlah anakan dan rendemen enam klon tebu (*Saccharum officinarum* L.) asal bibit bagal, mata ruas tunggal, dan mata tunas tunggal. *Vegetalika*, 3(2), 1-12.
- Sahu, S. K., Thangaraj, M., & Kathiresan, K. (2012). DNA extraction protocol for plants with high levels of secondary metabolites and polysaccharides without using liquid nitrogen and phenol. *ISRN Molecular Biology*, 2012, 1-6. <https://doi.org/10.5402/2012/205049>
- Sambrook, J., & Russell, D. W. (2001). *Molecular cloning: A laboratory manual* (3rd ed). Cold Spring Harbor Laboratory Press.
- Sambrook, J., Fritsch, E. F., & Maniatis, T. (1989). *Molecular cloning: A laboratory manual* (2nd. ed). Cold Spring Harbor Laboratory Press.
- Sari, R., Taryono, & Wulandari, R. (2019). Indeks ketahanan salinitas 10 klon tebu (*Saccharum officinarum* L.). *Vegetalika*, 8(1), 1-10.
- Sereika, M., Kirkegaard, R. H., Karst, S. M., Michaelsen, T. Y., Sørensen, E. A., Wollenberg, R. D., & Albertsen, M. (2022). Oxford Nanopore R10.4 long-read sequencing enables the generation of near-finished bacterial genomes from pure cultures and metagenomes without short-read or reference polishing. *Nature Methods*, 19(7), 823-826.
<https://doi.org/10.1038/s41592-022-01539-7>
- Sharp, P. M., Stenico, M., Peden, J. F., & Lloyd, A. T. (1993). Codon usage: Mutational bias, translational selection, or both? *Biochemical Society Transactions*, 21(4), 835-841.
- Sharp, P. M., Tuohy, T. M., & Mosurski, K. R. (1986). Codon usage in yeast: Cluster analysis clearly differentiates highly and lowly expressed genes. *Nucleic Acids Research*, 14(13), 5125-5143.
<https://doi.org/10.1093/nar/14.13.5125>

- Sheng, J., She, X., Liu, X., Wang, J., & Hu, Z. (2021). Comparative analysis of codon usage patterns in chloroplast genomes of five *Miscanthus* species and related species. *PeerJ*, 9, 1-18. <https://doi.org/10.7717/peerj.12173>
- Slapnik, B., Šket, R., Črepinšek, K., Tesovnik, T., Bizjan, B. J., & Kovač, J. (2024). The quality and detection limits of mitochondrial heteroplasmy by long read nanopore sequencing. *Scientific Reports*, 14(1), 1-12. <https://doi.org/10.1038/s41598-024-78270-0>
- Souza, G. M., Berges, H., Bocs, S., Casu, R., D'Hont, A., Ferreira, J. E., Henry, R., Ming, R., Potier, B., Van Sluys, M.-A., Vincentz, M., & Paterson, A. H. (2011). The sugarcane genome challenge: Strategies for sequencing a highly complex genome. *Tropical Plant Biology*, 4(3), 145–156. <https://doi.org/10.1007/s12042-011-9069-8>
- Stevenson, G. C. (1965). *Genetics and Breeding of Sugar Cane*. Longmans.
- Sulaiman, A. A., Sulaeman, Y., Mustikasari, N., Nursyamsi, D., & Syakir, A. M. (2019). Increasing sugar production in Indonesia through land suitability analysis and sugar mill restructuring. *Land*, 8(4), 1-17. <https://doi.org/10.3390/land8040061>
- Sun, K., Liu, Y., Zhou, X., Yin, C., Zhang, P., Yang, Q., Mao, L., Shentu, X., & Yu, X. (2022). Nanopore sequencing technology and its application in plant virus diagnostics. *Frontiers in Microbiology*, 13, 1-12. <https://doi.org/10.3389/fmicb.2022.939666>
- Tillich, M., Lehwark, P., Pellizzer, T., Ulbricht-Jones, E. S., Fischer, A., Bock, R., & Greiner, S. (2017). GeSeq – versatile and accurate annotation of organelle genomes. *Nucleic Acids Research*, 45(W1), W6–W11. <https://doi.org/10.1093/nar/gkx391>
- Trigodet, F., Lolans, K., Fogarty, E., Shaiber, A., Morrison, H. G., Barreiro, L., Jabri, B., & Eren, A. M. (2022). High molecular weight DNA extraction strategies for long-read sequencing of complex metagenomes. *Molecular Ecology Resources*, 22(5), 1786–1802. <https://doi.org/10.1111/1755-0998.13588>
- Twyford, A. D., & Ness, R. W. (2017). Strategies for complete plastid genome sequencing. *Molecular Ecology Resources*, 17(5), 858–868. <https://doi.org/10.1111/1755-0998.12626>
- Usman, T., Yu, Y., Liu, C., Fan, Z., & Wang, Y. (2014). Comparison of methods for high quantity and quality genomic DNA extraction from raw cow milk. *Genetics and Molecular Research*, 13(2), 3319–3328. <https://doi.org/10.4238/2014.April.29.10>
- Vaillancourt, B., & Buell, C. R. (2019). *High molecular weight DNA isolation method from diverse plant species for use with Oxford Nanopore sequencing* (Preprint). bioRxiv. <https://doi.org/10.1101/783159>
- Varadi, M., Bertoni, D., Magana, P., Paramval, U., Pidruchna, I., Radhakrishnan, M., Tsenkov, M., Nair, S., Mirdita, M., Yeo, J., Kovalevskiy, O., Tunyasuvunakool, K., Laydon, A., Židek, A., Tomlinson, H., Hariharan, D., Abrahamson, J., Green, T., Jumper, J., Birney, E., Steinegger, M., Hassabis, D., & Velankar, S. (2024). AlphaFold protein structure database

- in 2024: Providing structure coverage for over 214 million protein sequences. *Nucleic Acids Research*, 52(D1), D368–D375. <https://doi.org/10.1093/nar/gkad1011>
- 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), 1-14. <https://doi.org/10.1371/journal.pone.0305650>
- Vidigal, P. M. P., Coelho, A. S. G., Novaes, E., Barbosa, M. H. P., & Peternelli, L. A. (2016). Complete chloroplast genome sequence and annotation of the *Saccharum hybrid* cultivar RB867515. *Genome Announcements*, 4(5), e01157-16. <https://doi.org/10.1128/genomeA.01157-16>
- Walker, D. I. T. (1971). Utilization of noble and *Saccharum spontaneum* germplasm in the West Indies. *Proceedings of the 14th Congress of the International Society of Sugar Cane Technologists (ISSCT)*, 14, 224–232.
- Wambugu, P., Brozynska, M., Furtado, A., Waters, D., & Henry, R. (2015). Relationships of wild and domesticated rices (*Oryza* AA genome species) based upon whole chloroplast genome sequences. *Scientific Reports*, 5, 1-9. <https://doi.org/10.1038/srep13957>
- Wen, H., Wang, L., Gong, Y., Zhang, Y., Zhao, T., Feng, C., Wang, J., & Lin, J. (2024). Genome-Wide identification and characterization of GRAS transcription factor family in cultivated hybrid sugarcane ZZ1 (*Saccharum officinarum*) and their role in development and stress. *International Journal of Molecular Sciences*, 25(24), 1-17. <https://doi.org/10.3390/ijms252413470>
- Wicke, S., Schneeweiss, G. M., dePamphilis, C. W., Müller, K. F., & Quandt, D. (2011). The evolution of the plastid chromosome in land plants: Gene content, gene order, gene function. *Plant Molecular Biology*, 76(3–5), 273–297. <https://doi.org/10.1007/s11103-011-9762-4>
- Widyasari, W. B., Putra, L. K., Ranomahera, M. R. R., & Puspitasari, A. R. (2022). Historical notes, germplasm development, and molecular approaches to support sugarcane breeding program in Indonesia. *Sugar Tech*, 24(1), 30–47. <https://doi.org/10.1007/s12355-021-01069-0>
- Yadav, S., Jackson, P., Wei, X., Ross, E. M., Aitken, K., Deomano, E., Atkin, F., Hayes, B. J., & Voss-Fels, K. P. (2020). Accelerating genetic gain in sugarcane breeding using genomic selection. *Agronomy*, 10(4), 1-21. <https://doi.org/10.3390/agronomy10040585>
- Yang, Q., Xin, C., Xiao, Q.-S., Lin, Y.-T., Li, L., & Zhao, J.-L. (2023). Codon usage bias in chloroplast genes implicate adaptive evolution of four ginger species. *Frontiers in Plant Science*, 14, 1-12. <https://doi.org/10.3389/fpls.2023.1304264>
- 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>

- Yuan, S., Cohen, D. B., Ravel, J., Abdo, Z., & Forney, L. J. (2012). Evaluation of Methods for the Extraction and Purification of DNA from the Human Microbiome. *PLoS ONE*, 7(3), 1-10. <https://doi.org/10.1371/journal.pone.0033865>
- Zhang, M., Zhang, Y., Scheuring, C. F., Wu, C.-C., Dong, J. J., & Zhang, H.-B. (2012). Preparation of megabase-sized DNA from a variety of organisms using the nuclei method for advanced genomics research. *Nature Protocols*, 7(3), 467–478. <https://doi.org/10.1038/nprot.2011.455>
- Zhang, Y., & Skolnick, J. (2004). Scoring function for automated assessment of protein structure template quality. *Proteins: Structure, Function, and Bioinformatics*, 57(4), 702–710. <https://doi.org/10.1002/prot.20264>
- Zhang, Y., Ji, M., Deng, L., Lian, L., Jian, L., & Zhang, R. (2025). Codon usage bias analysis of self-incompatibility genes BrSRK, BrSLG, and BrSP11/BrSCR in *Brassica rapa* reveals insights into their coevolution. *Genetic Resources and Crop Evolution*, 72(7), 8653–8674. <https://doi.org/10.1007/s10722-025-02473-1>
- Zhou, D., Yin, Z., Liu, X., Li, Z., Yan, M., Que, Y., & Xu, L. (2020). The complete mitochondrial genome sequence and phylogenetic analysis of sugarcane (*Saccharum* spp.) cultivar ROC22. *Mitochondrial DNA Part B*, 5(2), 1915–1916. <https://doi.org/10.1080/23802359.2020.1756492>
- Zhu, X.-G., Long, S. P., & Ort, D. R. (2010). Improving photosynthetic efficiency for greater yield. *Annual Review of Plant Biology*, 61(1), 235–261. <https://doi.org/10.1146/annurev-arplant-042809-112206>
- Zorz, J., Li, C., Chakraborty, A., Gittins, D. A., Surcon, T., Morrison, N., Bennett, R., MacDonald, A., & Hubert, C. R. J. (2023). *SituSeq*: An offline protocol for rapid and remote Nanopore 16S rRNA amplicon sequence analysis. *ISME Communications*, 3(1), 1-11. <https://doi.org/10.1038/s43705-023-00239-3>
- Zoschke, R., & Bock, R. (2018). Chloroplast translation: Structural and functional organization, operational control, and regulation. *The Plant Cell*, 30(4), 745–770. <https://doi.org/10.1105/tpc.18.00016>
- Zumroh, A., Budi, S., & Lailiyah, W. N. (2023). Genetic diversity, heritability, and productivity of new sugarcane (*Saccharum officinarum* L.) clones on paddy fields for enhanced sugar production in Indonesia. *Jurnal Ilmiah Pertanian*, 20(2), 189-199. <https://doi.org/10.31849/jip.v20i2.12533>