

## DAFTAR PUSTAKA

- A'ayun, N. Q., Perdana, T. A., Pramono, P. A., & Laily, A. N. (2015). Identifikasi fitoplankton di perairan yang tercemar Lumpur Lapindo, Porong Sidoarjo. *Bioedukasi: Jurnal Pendidikan Biologi*, 8(1), 48–51.
- Afifah, N., Mariza, S. S. R., Pakarti, T. I., & Masitoh, F. (2022). *Analisis Kebutuhan Irigasi Lahan Pertanian Kanal Porong Di Kabupaten Sidoarjo Menggunakan Cropwat 8.0. 1.*
- Aghapour, A., Moussavi, G., & Yaghmaeian, K. (2013). Biological Degradation of Catechol in Wastewater using the Sequencing Continuous-inflow Reactor (SCR). *Journal of Environmental Health Science and Engineering*, 11. <https://doi.org/10.1186/2052-336X-11-3>
- Ali, S. S., Elsamahy, T., Al-Tohamy, R., Zhu, D., Mahmoud, Y. A.-G., Koutra, E., Metwally, M. A., Kornaros, M., & Sun, J. (2021). Plastic wastes biodegradation: Mechanisms, challenges and future prospects. *Science of The Total Environment*, 780, 146590. <https://doi.org/10.1016/j.scitotenv.2021.146590>
- Allocati, N., Masulli, M., Di Ilio, C., & Federici, L. (2018). Glutathione transferases: Substrates, inhibitors and pro-drugs in cancer and neurodegenerative diseases. *Oncogenesis*, 7(1), 8. <https://doi.org/10.1038/s41389-017-0025-3>
- Al-Turaiki, I. M., Mathkour, H., Touir, A., & Hammami, S. (2011). Computational Approaches for Gene Prediction: A Comparative Survey. In A. Abd Manaf, A. Zeki, M. Zamani, S. Chuprat, & E. El-Qawasmeh (Eds.), *Informatics Engineering and Information Science* (pp. 14–25). Springer Berlin Heidelberg.
- Andermann, T., Antonelli, A., Barrett, R. L., & Silvestro, D. (2022). Estimating Alpha, Beta, and Gamma Diversity Through Deep Learning. *Front Plant Sci*, 13, 839407. <https://doi.org/10.3389/fpls.2022.839407>
- Andika, N. (2021). *Propagation of the Sidoardjo Mud in the Porong River, East Java, Indonesia*. Colorado State University.
- Anteneh, Y. S., Yang, Q., Brown, M. H., & Franco, C. M. M. (2021). Antimicrobial Activities of Marine Sponge-Associated Bacteria. *Microorganisms*, 9(1). <https://doi.org/10.3390/microorganisms9010171>
- Arora, P. K. (2015). Bacterial degradation of monocyclic aromatic amines. *Frontiers in Microbiology*, 6. <https://www.frontiersin.org/articles/10.3389/fmicb.2015.00820>
- Barathi, S., J. G., Rathinasamy, G., Sabapathi, N., Aruljothi, K. N., Lee, J., & Kandasamy, S. (2023). Recent trends in polycyclic aromatic hydrocarbons pollution distribution and counteracting bio-remediation strategies. *Chemosphere*, 337, 139396. <https://doi.org/10.1016/j.chemosphere.2023.139396>

- Behjati, S., & Tarpey, P. S. (2013). What is next generation sequencing? *Archives of Disease in Childhood - Education & Practice Edition*, 98(6), 236. <https://doi.org/10.1136/archdischild-2013-304340>
- Beilen, J. B. van, & Li, Z. (2002). Enzyme technology: An overview. *Current Opinion in Biotechnology*, 13(4), 338–344. [https://doi.org/10.1016/S0958-1669\(02\)00334-8](https://doi.org/10.1016/S0958-1669(02)00334-8)
- Bhatt, P., Bhatt, K., Huang, Y., Li, J., Wu, S., & Chen, S. (2023). Biofilm formation in xenobiotic-degrading microorganisms. *Critical Reviews in Biotechnology*, 43(8), 1129–1149. <https://doi.org/10.1080/07388551.2022.2106417>
- Bhatt, P., Kumar, M. S., Mudliar, S., & Chakrabarti, T. (2007). Biodegradation of Chlorinated Compounds—A Review. *Critical Reviews in Environmental Science and Technology*, 37(2), 165–198. <https://doi.org/10.1080/10643380600776130>
- Bolyen, E., Rideout, J. R., Dillon, M. R., Bokulich, N. A., Abnet, C. C., Al-Ghalith, G. A., Alexander, H., Alm, E. J., Arumugam, M., Asnicar, F., Bai, Y., Bisanz, J. E., Bittinger, K., Brejnrod, A., Brislawn, C. J., Brown, C. T., Callahan, B. J., Caraballo-Rodríguez, A. M., Chase, J., ... Caporaso, J. G. (2019). Reproducible, interactive, scalable and extensible microbiome data science using QIIME 2. *Nat Biotechnol*, 37(8), 852–857. <https://doi.org/10.1038/s41587-019-0209-9>
- Brinkmann, C. M., Kearns, P. S., Evans-Illidge, E., & Kurtböke, D. Í. (2017). Diversity and Bioactivity of Marine Bacteria Associated with the Sponges *Candidaspongia flabellata* and *Rhopaloeides odorabile* from the Great Barrier Reef in Australia. *Diversity*, 9(3). <https://doi.org/10.3390/d9030039>
- Buchfink, B., Xie, C., & Huson, D. H. (2015). Fast and sensitive protein alignment using DIAMOND. *Nature Methods*, 12(1), 59–60. <https://doi.org/10.1038/nmeth.3176>
- Butina, T. V., Petrushin, I. S., Khanaev, I. V., & Bukin, Y. S. (2022). Metagenomic Assessment of DNA Viral Diversity in Freshwater Sponges, *Baikalospongia bacillifera*. *Microorganisms*, 10(2). <https://doi.org/10.3390/microorganisms10020480>
- Calheira, L., Lanna, E., & Pinheiro, U. (2019). Tropical freshwater sponges develop from gemmules faster than their temperate-region counterparts. *Zoomorphology*, 138(4), 425–436. <https://doi.org/10.1007/s00435-019-00458-0>
- Calle, M. L. (2019). Statistical Analysis of Metagenomics Data. *Genomics & Informatics*, 17(1), e6–e6. PubMed. <https://doi.org/10.5808/GI.2019.17.1.e6>
- Canellas, A. L. B., & Laport, M. S. (2022). The biotechnological potential of *Aeromonas*: A bird's eye view. *Critical Reviews in Microbiology*, 1–13. <https://doi.org/10.1080/1040841X.2022.2083940>
- Cao, B., Geng, A., & Loh, K.-C. (2008). Induction of ortho- and meta-cleavage pathways in *Pseudomonas* in biodegradation of high benzoate concentration: MS identification of catabolic enzymes. *Applied*

- Microbiology and Biotechnology*, 81(1), 99–107.  
<https://doi.org/10.1007/s00253-008-1728-3>
- Cao, B., & Loh, K.-C. (2008). Catabolic pathways and cellular responses of *Pseudomonas putida* P8 during growth on benzoate with a proteomics approach. *Biotechnology and Bioengineering*, 101(6), 1297–1312.  
<https://doi.org/10.1002/bit.21997>
- Caporaso, J. G., Kuczynski, J., Stombaugh, J., Bittinger, K., Bushman, F. D., Costello, E. K., Fierer, N., Peña, A. G., Goodrich, J. K., Gordon, J. I., Huttley, G. A., Kelley, S. T., Knights, D., Koenig, J. E., Ley, R. E., Lozupone, C. A., McDonald, D., Muegge, B. D., Pirrung, M., ... Knight, R. (2010). QIIME allows analysis of high-throughput community sequencing data. *Nature Methods*, 7(5), 335–336.  
<https://doi.org/10.1038/nmeth.f.303>
- Casquilho, J. P. (2016). A methodology to determine the maximum value of weighted Gini–Simpson index. *SpringerPlus*, 5(1), 1143.  
<https://doi.org/10.1186/s40064-016-2754-8>
- Cassier-Chauvat, C., Marceau, F., Farci, S., Ouchane, S., & Chauvat, F. (2023). The Glutathione System: A Journey from Cyanobacteria to Higher Eukaryotes. *Antioxidants*, 12(6). <https://doi.org/10.3390/antiox12061199>
- Christensen, H., Andersson, A. J., Jørgensen, S. L., & Vogt, J. K. (2018). 16S rRNA Amplicon Sequencing for Metagenomics. In H. Christensen (Ed.), *Introduction to Bioinformatics in Microbiology* (pp. 135–161). Springer International Publishing. [https://doi.org/10.1007/978-3-319-99280-8\\_8](https://doi.org/10.1007/978-3-319-99280-8_8)
- Clark, C. M., Hernandez, A., Mallowney, M. W., Fitz-Henley, J., Li, E., Romanowski, S. B., Pronzato, R., Manconi, R., Sanchez, L. M., & Murphy, B. T. (2022). Relationship between bacterial phylotype and specialized metabolite production in the culturable microbiome of two freshwater sponges. *ISME Communications*, 2(1), 22.  
<https://doi.org/10.1038/s43705-022-00105-8>
- Cruaud, P., Vigneron, A., Dorea, C. C., Rodriguez, M. J., & Charette, S. J. (2020). Rapid Changes in Microbial Community Structures along a Meandering River. *Microorganisms*, 8(11).  
<https://doi.org/10.3390/microorganisms8111631>
- Cuvelier, M. L., Blake, E., Mulheron, R., McCarthy, P. J., Blackwelder, P., Thurber, R. L. V., & Lopez, J. V. (2014). Two distinct microbial communities revealed in the sponge *Cinachyrella*. *Frontiers in Microbiology*, 5.  
<https://www.frontiersin.org/articles/10.3389/fmicb.2014.00581>
- Das, N., & Chandran, P. (2011). Microbial degradation of petroleum hydrocarbon contaminants: An overview. *Biotechnology Research International*, 2011.
- de Jong, A., In T Zandt, M., Fiandi, L., Zaan, B., Geerling, G., Roosmini, D., Luke, C., Ariesyady, H., & Jetten, M. (2018). *Decrease in Microbial Diversity Along a Pollution Gradient in Citarum River Sediment*. <https://doi.org/10.1101/357111>
- Edgar, R. C., Haas, B. J., Clemente, J. C., Quince, C., & Knight, R. (2011). UCHIME improves sensitivity and speed of chimera detection.

- Bioinformatics*, 27(16), 2194–2200.  
<https://doi.org/10.1093/bioinformatics/btr381>
- Edwin, S., Ahmad, Y., Hermanto, M. E., Catur, R., Adi, P. F., & Anto, B. (2023). Revisit Study of Freshwater Sponges *Eunapius carteri* (Bowerbank, 1863) and a New Record of *Oncosclera asiatica* Manconi and Ruengsawang, 2012 (Porifera: Spongillida) in Porong River, East Java, Indonesia. *HAYATI Journal of Biosciences*, 30(2), 232–245.
- Eskander, S., & Saleh, H. E. D. (2017). Biodegradation: Process mechanism. *Environ. Sci. & Eng*, 8(8), 1–31.
- Fakhar, A., Gul, B., Gurmani, A. R., Khan, S. M., Ali, S., Sultan, T., Chaudhary, H. J., Rafique, M., & Rizwan, M. (2022). Heavy metal remediation and resistance mechanism of *Aeromonas*, *Bacillus*, and *Pseudomonas*: A review. *Critical Reviews in Environmental Science and Technology*, 52(11), 1868–1914. <https://doi.org/10.1080/10643389.2020.1863112>
- Figueira, V., Vaz-Moreira, I., Silva, M., & Manaia, C. M. (2011). Diversity and antibiotic resistance of *Aeromonas* spp. In drinking and waste water treatment plants. *Water Research*, 45(17), 5599–5611. <https://doi.org/10.1016/j.watres.2011.08.021>
- Fitrianto, A. R. (2019). *The Socio-Economic Impacts of the Porong Mud Volcano on the Shrimp Fisheries Sector in Sidoarjo District, East Java Province, Indonesia*. Curtin University.
- Flicek, P. (2007). Gene prediction: Compare and CONTRAST. *Genome Biology*, 8(12), 233. <https://doi.org/10.1186/gb-2007-8-12-233>
- Frey, K. G., Herrera-Galeano, J. E., Redden, C. L., Luu, T. V., Servetas, S. L., Mateczun, A. J., Mokashi, V. P., & Bishop-Lilly, K. A. (2014). Comparison of three next-generation sequencing platforms for metagenomic sequencing and identification of pathogens in blood. *BMC Genomics*, 15(1), 96. <https://doi.org/10.1186/1471-2164-15-96>
- Fukuyama, J., McMurdie, P. J., Dethlefsen, L., Relman, D. A., & Holmes, S. (2012). Comparisons of distance methods for combining covariates and abundances in microbiome studies. *Pac Symp Biocomput*, 213–224.
- Gaikwad, S., Shouche, Y. S., & Gade, W. N. (2016). Microbial community structure of two freshwater sponges using Illumina MiSeq sequencing revealed high microbial diversity. *AMB Express*, 6(1), 40. <https://doi.org/10.1186/s13568-016-0211-2>
- Gonçalves Pessoa, R. B., de Oliveira, W. F., Marques, D. S. C., dos Santos Correia, M. T., de Carvalho, E. V. M. M., & Coelho, L. C. B. B. (2019). The genus *Aeromonas*: A general approach. *Microbial Pathogenesis*, 130, 81–94. <https://doi.org/10.1016/j.micpath.2019.02.036>
- Gower, J. C. (2015). Principal Coordinates Analysis. In *Wiley StatsRef: Statistics Reference Online* (pp. 1–7). <https://doi.org/10.1002/9781118445112.stat05670.pub2>
- Gregorius, H.-R., & Gillet, E. M. (2008). Generalized Simpson-diversity. *Ecological Modelling*, 211(1), 90–96. <https://doi.org/10.1016/j.ecolmodel.2007.08.026>

- Greule, A., Stok, J. E., De Voss, J. J., & Cryle, M. J. (2018). Unrivalled diversity: The many roles and reactions of bacterial cytochromes P450 in secondary metabolism. *Natural Product Reports*, 35(8), 757–791. <https://doi.org/10.1039/C7NP00063D>
- Guiasu, R. C., & Guiasu, S. (2012). The Weighted Gini-Simpson Index: Revitalizing an Old Index of Biodiversity. *International Journal of Ecology*, 2012, 478728. <https://doi.org/10.1155/2012/478728>
- Hahn, M. W. (2006). The microbial diversity of inland waters. *Environmental Biotechnology/Energy Biotechnology*, 17(3), 256–261. <https://doi.org/10.1016/j.copbio.2006.05.006>
- Hall, B. G. (2013). Building Phylogenetic Trees from Molecular Data with MEGA. *Molecular Biology and Evolution*, 30(5), 1229–1235. <https://doi.org/10.1093/molbev/mst012>
- Hardoim C. C. P., Costa R., Araújo F. V., Hajdu E., Peixoto R., Lins U., Rosado A. S., & van Elsas J. D. (2009). Diversity of Bacteria in the Marine Sponge *Aplysina fulva* in Brazilian Coastal Waters. *Applied and Environmental Microbiology*, 75(10), 3331–3343. <https://doi.org/10.1128/AEM.02101-08>
- He, Y., Caporaso, J. G., Jiang, X.-T., Sheng, H.-F., Huse, S. M., Rideout, J. R., Edgar, R. C., Kopylova, E., Walters, W. A., Knight, R., & Zhou, H.-W. (2015). Stability of operational taxonomic units: An important but neglected property for analyzing microbial diversity. *Microbiome*, 3(1), 20. <https://doi.org/10.1186/s40168-015-0081-x>
- Hentschel, U., Piel, J., Degan, S. M., & Taylor, M. W. (2012). Genomic insights into the marine sponge microbiome. *Nature Reviews Microbiology*, 10(9), 641–654. <https://doi.org/10.1038/nrmicro2839>
- Hernawan, U., & Budiono, K. (2016). Karakteristik dan distribusi lumpur Sidoarjo sepanjang Sungai, Estuari dan Perairan Porong. *Jurnal Geologi Kelautan*, 11(2), 91–99.
- Hu, T., Chitnis, N., Monos, D., & Dinh, A. (2021). Next-generation sequencing technologies: An overview. *Next Generation Sequencing and Its Application to Medical Laboratory Immunology*, 82(11), 801–811. <https://doi.org/10.1016/j.humimm.2021.02.012>
- IMPACTT investigators. (2022). Beta-diversity distance matrices for microbiome sample size and power calculations—How to obtain good estimates. *Computational and Structural Biotechnology Journal*, 20, 2259–2267. <https://doi.org/10.1016/j.csbj.2022.04.032>
- Jiang, X., Xu, S., Liu, Y., & Wang, X. (2015). River ecosystem assessment and application in ecological restorations: A mathematical approach based on evaluating its structure and function. *Ecological and Hydrological Responses to Changing Environmental Conditions in China's River Basins*, 76, 151–157. <https://doi.org/10.1016/j.ecoleng.2014.04.027>
- Johnson, J. S., Spakowicz, D. J., Hong, B.-Y., Petersen, L. M., Demkowicz, P., Chen, L., Leopold, S. R., Hanson, B. M., Agresta, H. O., Gerstein, M., Sodergren, E., & Weinstock, G. M. (2019). Evaluation of 16S rRNA gene sequencing for species and strain-level microbiome analysis. *Nature*

- Communications*, 10(1), 5029. <https://doi.org/10.1038/s41467-019-13036-1>
- Jun, L. Y., Yon, L. S., Mubarak, N. M., Bing, C. H., Pan, S., Danquah, M. K., Abdullah, E. C., & Khalid, M. (2019). An overview of immobilized enzyme technologies for dye and phenolic removal from wastewater. *Journal of Environmental Chemical Engineering*, 7(2), 102961. <https://doi.org/10.1016/j.jece.2019.102961>
- Jünemann, S., Kleinbölting, N., Jaenicke, S., Henke, C., Hassa, J., Nelkner, J., Stolze, Y., Albaum, S. P., Schlüter, A., Goesmann, A., Sczyrba, A., & Stoye, J. (2017). Bioinformatics for NGS-based metagenomics and the application to biogas research. *J Biotechnol*, 261, 10–23. <https://doi.org/10.1016/j.jbiotec.2017.08.012>
- Kameoka, S., Motooka, D., Watanabe, S., Kubo, R., Jung, N., Midorikawa, Y., Shinozaki, N. O., Sawai, Y., Takeda, A. K., & Nakamura, S. (2021). Benchmark of 16S rRNA gene amplicon sequencing using Japanese gut microbiome data from the V1–V2 and V3–V4 primer sets. *BMC Genomics*, 22(1), 527. <https://doi.org/10.1186/s12864-021-07746-4>
- Karlińska-Batres, K., & Wörheide, G. (2013). Microbial diversity in the coralline sponge *Vaceletia crypta*. *Antonie van Leeuwenhoek*, 103(5), 1041–1056. <https://doi.org/10.1007/s10482-013-9884-6>
- Keegan, K. P., Glass, E. M., & Meyer, F. (2016). MG-RAST, a Metagenomics Service for Analysis of Microbial Community Structure and Function. In F. Martin & S. Uroz (Eds.), *Microbial Environmental Genomics (MEG)* (Vol. 1399, pp. 207–233). Springer New York. [https://doi.org/10.1007/978-1-4939-3369-3\\_13](https://doi.org/10.1007/978-1-4939-3369-3_13)
- Keller-Costa, T., Jousset, A., van Overbeek, L., van Elsas, J. D., & Costa, R. (2014). The Freshwater Sponge *Ephydatia fluviatilis* Harbours Diverse *Pseudomonas* Species (Gammaproteobacteria, Pseudomonadales) with Broad-Spectrum Antimicrobial Activity. *PLOS ONE*, 9(2), e88429. <https://doi.org/10.1371/journal.pone.0088429>
- Kelly, S. L., & Kelly, D. E. (2013). Microbial cytochromes P450: Biodiversity and biotechnology. Where do cytochromes P450 come from, what do they do and what can they do for us? *Philos Trans R Soc Lond B Biol Sci*, 368(1612), 20120476. <https://doi.org/10.1098/rstb.2012.0476>
- Kennedy, J., Baker, P., Piper, C., Cotter, P. D., Walsh, M., Mooij, M. J., Bourke, M. B., Rea, M. C., O'Connor, P. M., Ross, R. P., Hill, C., O'Gara, F., Marchesi, J. R., & Dobson, A. D. W. (2009). Isolation and Analysis of Bacteria with Antimicrobial Activities from the Marine Sponge *Haliclona simulans* Collected from Irish Waters. *Marine Biotechnology*, 11(3), 384–396. <https://doi.org/10.1007/s10126-008-9154-1>
- Kers, J. G., & Saccetti, E. (2022). The Power of Microbiome Studies: Some Considerations on Which Alpha and Beta Metrics to Use and How to Report Results. *Frontiers in Microbiology*, 12. <https://www.frontiersin.org/articles/10.3389/fmicb.2021.796025>

- Keylock, C. J. (2005). Simpson diversity and the Shannon–Wiener index as special cases of a generalized entropy. *Oikos*, *109*(1), 203–207. <https://doi.org/10.1111/j.0030-1299.2005.13735.x>
- Kim, B.-R., Jiwon Shin, Robin B. Guevarra, Jun Hyung Lee, Doo Wan Kim, Kuk-Hwan Seol, Ju-Hoon Lee, & Hyeun Bum Kim. (2017). Deciphering Diversity Indices for a Better Understanding of Microbial Communities. *Journal of Microbiology and Biotechnology*, *27*(12), 2089–2093. <https://doi.org/10.4014/jmb.1709.09027>
- Konopiński, M. K. (2020). Shannon diversity index: A call to replace the original Shannon’s formula with unbiased estimator in the population genetics studies. *PeerJ*, *8*, e9391. <https://doi.org/10.7717/peerj.9391>
- Konopka, A. (2009). What is microbial community ecology? *The ISME Journal*, *3*(11), 1223–1230. <https://doi.org/10.1038/ismej.2009.88>
- Kooli, W. M., Junier Thomas, Shakya Migun, Monachon Mathilde, Davenport Karen W., Vaideeswaran Kaushik, Vernudachi Alexandre, Marozau Ivan, Monrouzeau Teddy, Gleasner Cheryl D., McMurry Kim, Lienhard Reto, Rufener Lucien, Perret Jean-Luc, Sereda Olha, Chain Patrick S., Joseph Edith, & Junier Pilar. (2019). Remedial Treatment of Corroded Iron Objects by Environmental Aeromonas Isolates. *Applied and Environmental Microbiology*, *85*(3), e02042-18. <https://doi.org/10.1128/AEM.02042-18>
- Kukurugya, M. A., Mendonca, C. M., Solhtalab, M., Wilkes, R. A., Thannhauser, T. W., & Aristilde, L. (2019). Multi-omics analysis unravels a segregated metabolic flux network that tunes co-utilization of sugar and aromatic carbons in *Pseudomonas putida*. *Journal of Biological Chemistry*, *294*(21), 8464–8479. <https://doi.org/10.1074/jbc.RA119.007885>
- Kunakom, S., Otani, H., Udway, D. W., Doering, D. T., & Mouncey, N. J. (2023). Cytochromes P450 involved in bacterial RiPP biosyntheses. *Journal of Industrial Microbiology and Biotechnology*, *50*(1), kuad005. <https://doi.org/10.1093/jimb/kuad005>
- Laurence, M., Hatzis, C., & Brash, D. E. (2014). Common Contaminants in Next-Generation Sequencing That Hinder Discovery of Low-Abundance Microbes. *PLOS ONE*, *9*(5), e97876. <https://doi.org/10.1371/journal.pone.0097876>
- Lee, S.-Y., & Eom, Y.-B. (2016). Analysis of microbial composition associated with freshwater and seawater. *Biomedical Science Letters*, *22*(4), 150–159. <https://doi.org/10.15616/BSL.2016.22.4.150>
- Liu, Y.-X., Qin, Y., Chen, T., Lu, M., Qian, X., Guo, X., & Bai, Y. (2021). A practical guide to amplicon and metagenomic analysis of microbiome data. *Protein & Cell*, *12*(5), 315–330. <https://doi.org/10.1007/s13238-020-00724-8>
- Loman, N. J., Misra, R. V., Dallman, T. J., Constantinidou, C., Gharbia, S. E., Wain, J., & Pallen, M. J. (2012). Performance comparison of benchtop high-throughput sequencing platforms. *Nature Biotechnology*, *30*(5), 434–439. <https://doi.org/10.1038/nbt.2198>

- Lozupone, C., Hamady Micah, Kelley Scott T., & Knight Rob. (2007). Quantitative and Qualitative  $\beta$  Diversity Measures Lead to Different Insights into Factors That Structure Microbial Communities. *Applied and Environmental Microbiology*, 73(5), 1576–1585. <https://doi.org/10.1128/AEM.01996-06>
- Lozupone, C., & Knight, R. (2005). UniFrac: A New Phylogenetic Method for Comparing Microbial Communities. *Applied and Environmental Microbiology*, 71(12), 8228–8235. <https://doi.org/10.1128/AEM.71.12.8228-8235.2005>
- Lozupone, C., Lladser, M. E., Knights, D., Stombaugh, J., & Knight, R. (2011). UniFrac: An effective distance metric for microbial community comparison. *The ISME Journal*, 5(2), 169–172. <https://doi.org/10.1038/ismej.2010.133>
- MacLean, A. M., MacPherson, G., Aneja Punita, & Finan Turlough M. (2006). Characterization of the  $\beta$ -Ketoadipate Pathway in *Sinorhizobium meliloti*. *Applied and Environmental Microbiology*, 72(8), 5403–5413. <https://doi.org/10.1128/AEM.00580-06>
- Magoč, T., & Salzberg, S. L. (2011). FLASH: fast length adjustment of short reads to improve genome assemblies. *Bioinformatics*, 27(21), 2957–2963. <https://doi.org/10.1093/bioinformatics/btr507>
- Manconi, R., Ruengsawang, N., Ledda, F. D., Hanjavanit, C., & Sangpradub, N. (2012). Biodiversity assessment in the Lower Mekong basin: First record of the genus *Oncosclera* (Porifera: Spongillina: Potamolepidae) from the Oriental Region. *Zootaxa*, 3544(1), 41–51.
- Manna, S. K., Das, B. K., Mohanty, B. P., Bandopadhyay, C., Das, N., Baitha, R., & Das, A. K. (2021). Exploration of heterotrophic bacterial diversity in sediments of the mud volcano in the Andaman and Nicobar Islands, India. *Environmental Nanotechnology, Monitoring & Management*, 16, 100465. <https://doi.org/10.1016/j.enmm.2021.100465>
- Margesin, R., & Schinner, F. (2001). Biodegradation and bioremediation of hydrocarbons in extreme environments. *Applied Microbiology and Biotechnology*, 56(5), 650–663. <https://doi.org/10.1007/s002530100701>
- Marzuki, I. (2021). *Eksplorasi spons indonesia: Seputar kepulauan spermonde*. Yayasan Kita Menulis.
- McLaughlin, J. E., McLaughlin, G. W., McLaughlin, J. S., & White, C. Y. (2016). Using Simpson's diversity index to examine multidimensional models of diversity in health professions education. *Int J Med Educ*, 7, 1–5. <https://doi.org/10.5116/ijme.565e.1112>
- Mishra, S., Lin, Z., Pang, S., Zhang, W., Bhatt, P., & Chen, S. (2021). Recent Advanced Technologies for the Characterization of Xenobiotic-Degrading Microorganisms and Microbial Communities. *Frontiers in Bioengineering and Biotechnology*, 9. <https://www.frontiersin.org/articles/10.3389/fbioe.2021.632059>
- Mongad, D. S., Chavan, N. S., Narwade, N. P., Dixit, K., Shouche, Y. S., & Dhotre, D. P. (2021). MicFunPred: A conserved approach to predict

- functional profiles from 16S rRNA gene sequence data. *Genomics*, *113*(6), 3635–3643. <https://doi.org/10.1016/j.ygeno.2021.08.016>
- Mousavi, S. M., Hashemi, S. A., Iman Moezzi, S. M., Ravan, N., Gholami, A., Lai, C. W., Chiang, W.-H., Omidifar, N., Yousefi, K., & Behbudi, G. (2021). Recent Advances in Enzymes for the Bioremediation of Pollutants. *Biochemistry Research International*, *2021*, 5599204. <https://doi.org/10.1155/2021/5599204>
- Mubarok, I. D., Rifardi Rifardi, & Afrizal Tanjung. (2019). Temporal Study of TSS (Total Suspended Solid) Around Porong River Estuary Due to the Influence of Lapindo Mud Based on Landsat 8 OLI Satellite Imagery. *Jurnal Perikanan Dan Kelautan*, *24*(2), 119–129.
- Mukherjee, S., Ray, M., & Ray, S. (2015). Phagocytic efficiency and cytotoxic responses of Indian freshwater sponge (*Eunapius carteri*) cells isolated by density gradient centrifugation and flow cytometry: A morphofunctional analysis. *Zoology*, *118*(1), 8–18. <https://doi.org/10.1016/j.zool.2014.07.002>
- Mulla, S. I., Bharagava, R. N., Belhaj, D., Saratale, G. D., Bagewadi, Z. K., Saxena, G., Kumar, A., Mohan, H., Yu, C.-P., & Ninnekar, H. Z. (2019). An Overview of Nitro Group-Containing Compounds and Herbicides Degradation in Microorganisms. In P. K. Arora (Ed.), *Microbial Metabolism of Xenobiotic Compounds* (pp. 319–335). Springer Singapore. [https://doi.org/10.1007/978-981-13-7462-3\\_16](https://doi.org/10.1007/978-981-13-7462-3_16)
- Müller, W. E. G., Grebenjuk, V. A., Le Pennec, G., Schröder, H.-C., Brümmer, F., Hentschel, U., Müller, I. M., & Breter, H.-J. (2004). Sustainable Production of Bioactive Compounds by Sponges—Cell Culture and Gene Cluster Approach: A Review. *Marine Biotechnology*, *6*(2), 105–117. <https://doi.org/10.1007/s10126-002-0098-6>
- Muñoz-García, A., Mestanza, O., Isaza, J. P., Figueroa-Galvis, I., & Vanegas, J. (2019). Influence of salinity on the degradation of xenobiotic compounds in rhizospheric mangrove soil. *Environmental Pollution*, *249*, 750–757. <https://doi.org/10.1016/j.envpol.2019.03.056>
- Murphy, C. D. (2016). Microbial degradation of fluorinated drugs: Biochemical pathways, impacts on the environment and potential applications. *Applied Microbiology and Biotechnology*, *100*(6), 2617–2627. <https://doi.org/10.1007/s00253-016-7304-3>
- Nanjani, S., Patel, Z., Sharma, S., Pandita, P. R., Pandit, R., Joshi, M. N., Patel, A. K., & Joshi, C. (2022). Transcriptome profiling reveals upregulation of benzoate degradation and related genes in *Pseudomonas aeruginosa* D6 during textile dye degradation. *Environmental Research*, *212*, 113288. <https://doi.org/10.1016/j.envres.2022.113288>
- Narainsamy, K., Marteyn, B., Sakr, S., Cassier-Chauvat, C., & Chauvat, F. (2013). Chapter Five—Genomics of the Pleiotropic Glutathione System in Cyanobacteria. In F. Chauvat & C. Cassier-Chauvat (Eds.), *Advances in Botanical Research* (Vol. 65, pp. 157–188). Academic Press. <https://doi.org/10.1016/B978-0-12-394313-2.00005-6>

- Navas-Molina, J. A., Peralta-Sánchez, J. M., González, A., McMurdie, P. J., Vázquez-Baeza, Y., Xu, Z., Ursell, L. K., Lauber, C., Zhou, H., Song, S. J., Huntley, J., Ackermann, G. L., Berg-Lyons, D., Holmes, S., Caporaso, J. G., & Knight, R. (2013). Chapter Nineteen—Advancing Our Understanding of the Human Microbiome Using QIIME. In E. F. DeLong (Ed.), *Methods in Enzymology* (Vol. 531, pp. 371–444). Academic Press. <https://doi.org/10.1016/B978-0-12-407863-5.00019-8>
- Nurhatika, S., ERMAVITALINI, D., SAPUTRO, T. B., & APRIYATMOKO, Y. (2018). Biodiversity and characterization of high lipid content microalgae in Porong River Estuary East Java, Indonesia. *BIODIVERSITAS*, *19*(2), 627–632.
- Nurry, A., & Anjasmara, I. M. (2014). Kajian Perubahan Tutupan Lahan Daerah Aliran Sungai Brantas Bagian Hilir Menggunakan Citra Satelit Multi Temporal (Studi Kasus: Kali Porong, Kabupaten Sidoarjo). *Geoid*, *10*(1), 70–74.
- Ostroumov, S. A. (2005). Some aspects of water filtering activity of filter-feeders. *Hydrobiologia*, *542*(1), 275–286. <https://doi.org/10.1007/s10750-004-1875-1>
- Ouyang, L., Liu, X., Chen, H., Yang, X., Li, S., & Li, S. (2022). Comparison of the Microbial Communities Affected by Different Environmental Factors in a Polluted River. *Water*, *14*(23). <https://doi.org/10.3390/w14233844>
- Parfenova, V. V., Terkina, I. A., Kostornova, T. Ya., Nikulina, I. G., Chernykh, V. I., & Maksimova, E. A. (2008). Microbial community of freshwater sponges in Lake Baikal. *Biology Bulletin*, *35*(4), 374–379. <https://doi.org/10.1134/S1062359008040079>
- Patel, T., Chaudhari, H. G., Prajapati, V., Patel, S., Mehta, V., & Soni, N. (2022). A brief account on enzyme mining using metagenomic approach. *Frontiers in Systems Biology*, *2*. <https://www.frontiersin.org/articles/10.3389/fsysb.2022.1046230>
- Peng, X., Urso, M., & Pumera, M. (2023). Metal oxide single-component light-powered micromotors for photocatalytic degradation of nitroaromatic pollutants. *Npj Clean Water*, *6*(1), 21. <https://doi.org/10.1038/s41545-023-00235-z>
- Peterson, D., Bonham, K. S., Rowland, S., Pattanayak, C. W., RESONANCE Consortium, Klepac-Ceraj, V., Deoni, S. C. L., D'Sa, V., Bruchhage, M., Volpe, A., Beauchemin, J., Wallace, C., Rogers, J., Cano, R., Fernandes, J., Walsh, E., Rhodes, B., Huentelman, M., Lewis, C., ... Braun, J. (2021). Comparative Analysis of 16S rRNA Gene and Metagenome Sequencing in Pediatric Gut Microbiomes. *Frontiers in Microbiology*, *12*. <https://www.frontiersin.org/articles/10.3389/fmicb.2021.670336>
- Porter, A. W., & Young, L. Y. (2014). Chapter Five—Benzoyl-CoA, a Universal Biomarker for Anaerobic Degradation of Aromatic Compounds. In S. Sariaslani & G. M. Gadd (Eds.), *Advances in Applied Microbiology* (Vol. 88, pp. 167–203). Academic Press. <https://doi.org/10.1016/B978-0-12-800260-5.00005-X>

- Purnomo, T., Rachmadiarti, F., & Soegiyanto, S. (2018). *Impact of Lapindo Hot Mud Flowing on Macrozoobenthos Communities in Estuary Porong, East Java*. <https://doi.org/10.2991/icst-18.2018.11>
- Rai, R., Singh, S., Rai, K. K., Raj, A., Sriwastaw, S., & Rai, L. C. (2021). Regulation of antioxidant defense and glyoxalase systems in cyanobacteria. *Plant Physiology and Biochemistry*, *168*, 353–372. <https://doi.org/10.1016/j.plaphy.2021.09.037>
- Rajasabapathy, R., Ghadi, S. C., Manikandan, B., Mohandass, C., Surendran, A., Dastager, S. G., Meena, R. M., & James, R. A. (2020). Antimicrobial profiling of coral reef and sponge associated bacteria from southeast coast of India. *Microbial Pathogenesis*, *141*, 103972. <https://doi.org/10.1016/j.micpath.2020.103972>
- Ramya Sree, B., Sowjanya, B., & Divakar, K. (2019). Metagenomic bioprospecting of novel oxygen insensitive nitroreductase for degradation of nitro aromatic compounds. *International Biodeterioration & Biodegradation*, *143*, 104737. <https://doi.org/10.1016/j.ibiod.2019.104737>
- Romanenko, L. A., Uchino, M., Falsen, E., Frolova, G. M., Zhukova, N. V., & Mikhailov, V. V. (2005). *Pseudomonas pachastrellae* sp. Nov., isolated from a marine sponge. In *International Journal of Systematic and Evolutionary Microbiology* (Vol. 55, Issue 2, pp. 919–924). Microbiology Society. <https://doi.org/10.1099/ijs.0.63176-0>
- Salter, S., Cox, M., Turek, E., Calus, S., Cookson, W., Moffatt, M., Turner, P., Parkhill, J., Loman, N., & Walker, A. (2014). Reagent and laboratory contamination can critically impact sequence-based microbiome analyses. *BMC Biology*, *12*, 87. <https://doi.org/10.1186/s12915-014-0087-z>
- Sanabila, A. I., & Agustina, E. (2022). Identifikasi Kandungan Mikroplastik Pada Saluran Pencernaan Ikan di Kali Porong Sidoarjo. *Environmental Pollution Journal*, *2*(1). <http://ecotonjournal.id/index.php/epj/article/view/18>
- Sankara, S. H., Balachandran, K. R. S., Rangamaran, V. R., & Gopal, D. (2020). RemeDB: Tool for Rapid Prediction of Enzymes Involved in Bioremediation from High-Throughput Metagenome Data Sets. *Journal of Computational Biology*, *27*(7), 1020–1029. <https://doi.org/10.1089/cmb.2019.0345>
- Saravanan, A., Kumar, P. S., Vo, D.-V. N., Jeevanantham, S., Karishma, S., & Yaashikaa, P. R. (2021). A review on catalytic-enzyme degradation of toxic environmental pollutants: Microbial enzymes. *Journal of Hazardous Materials*, *419*, 126451. <https://doi.org/10.1016/j.jhazmat.2021.126451>
- Schellenberg, J., Reichert, J., Hardt, M., Klingelhöfer, I., Morlock, G., Schubert, P., Bižić, M., Grossart, H.-P., Kämpfer, P., Wilke, T., & Glaeser, S. P. (2020). The Bacterial Microbiome of the Long-Term Aquarium Cultured High-Microbial Abundance Sponge *Haliclona* cnidata – Sustained Bioactivity Despite Community Shifts Under Detrimental Conditions. *Frontiers in Marine Science*, *7*. <https://www.frontiersin.org/article/10.3389/fmars.2020.00266>

- Schuster, S. C. (2008). Next-generation sequencing transforms today's biology. *Nature Methods*, 5(1), 16–18. <https://doi.org/10.1038/nmeth1156>
- Senate, L. M., Tjatji, M. P., Pillay, K., Chen, W., Zondo, N. M., Syed, P. R., Mnguni, F. C., Chiliza, Z. E., Bamal, H. D., Karpoormath, R., Khoza, T., Mashele, S. S., Blackburn, J. M., Yu, J.-H., Nelson, D. R., & Syed, K. (2019). Similarities, variations, and evolution of cytochrome P450s in *Streptomyces* versus *Mycobacterium*. *Scientific Reports*, 9(1), 3962. <https://doi.org/10.1038/s41598-019-40646-y>
- Setiawan, E., Yanuar, A., Riani, C., Budiharjo, A., Firdaus, Y., Phontree, K., & Phuwapraisirisan, P. (2023). Phytochemical profile, free radical scavenging activity, and  $\alpha$ -glucosidase inhibitory activity of freshwater sponges *Oncosclera asiatica* and *Eunapius carteri* from East Java, Indonesia. *RASAYAN Journal of Chemistry*, 16, 2023. <https://doi.org/10.31788/RJC.2023.1648435>
- Shade, A., Jones, S. E., & McMahon, K. D. (2008). The influence of habitat heterogeneity on freshwater bacterial community composition and dynamics. *Environmental Microbiology*, 10(4), 1057–1067. <https://doi.org/10.1111/j.1462-2920.2007.01527.x>
- Shafi, S., Kamili, A. N., Shah, M. A., Parray, J. A., & Bandh, S. A. (2017). Aquatic bacterial diversity: Magnitude, dynamics, and controlling factors. *Microbial Pathogenesis*, 104, 39–47. <https://doi.org/10.1016/j.micpath.2017.01.016>
- Shahraki, M. F., Ariaeenejad, S., Fallah Atanaki, F., Zolfaghari, B., Koshiba, T., Kavousi, K., & Salekdeh, G. H. (2020). MCIC: Automated Identification of Cellulases From Metagenomic Data and Characterization Based on Temperature and pH Dependence. *Frontiers in Microbiology*, 11. <https://www.frontiersin.org/articles/10.3389/fmicb.2020.567863>
- Shannon, C. E. (1948). A mathematical theory of communication. *The Bell System Technical Journal*, 27(3), 379–423. <https://doi.org/10.1002/j.1538-7305.1948.tb01338.x>
- Sharma, P., & Kumar, S. (2021). Bioremediation of heavy metals from industrial effluents by endophytes and their metabolic activity: Recent advances. *Bioresource Technology*, 339, 125589. <https://doi.org/10.1016/j.biortech.2021.125589>
- Sharpton, T. J. (2014). An introduction to the analysis of shotgun metagenomic data. *Frontiers in Plant Science*, 5. <http://dx.doi.org/10.3389/fpls.2014.00209>
- Simpson, E. H. (1949). Measurement of Diversity. *Nature*, 163(4148), 688–688. <https://doi.org/10.1038/163688a0>
- Singh, A., & Ward, O. P. (2013). *Biodegradation and bioremediation* (Vol. 2). Springer Science & Business Media.
- Slatko, B. E., Gardner, A. F., & Ausubel, F. M. (2018). Overview of Next-Generation Sequencing Technologies. *Current Protocols in Molecular Biology*, 122(1), e59. <https://doi.org/10.1002/cpmb.59>

- Sleator, R. D., Shortall, C., & Hill, C. (2008). Metagenomics. *Letters in Applied Microbiology*, 47(5), 361–366. <https://doi.org/10.1111/j.1472-765X.2008.02444.x>
- Soon, W. W., Hariharan, M., & Snyder, M. P. (2013). High-throughput sequencing for biology and medicine. *Molecular Systems Biology*, 9(1), 640. <https://doi.org/10.1038/msb.2012.61>
- Spellerberg, I. F., & Fedor, P. J. (2003). A tribute to Claude Shannon (1916–2001) and a plea for more rigorous use of species richness, species diversity and the ‘Shannon–Wiener’ Index. *Global Ecology and Biogeography*, 12(3), 177–179. <https://doi.org/10.1046/j.1466-822X.2003.00015.x>
- Sukhanova, E. V., Shtykova, Yu. R., Suslova, M. Yu., Pestunova, O. S., Kostornova, T. Ya., Khanaev, I. V., Zimens, E. A., Podlesnaya, G. V., & Parfenova, V. V. (2019). Diversity and Physiological and Biochemical Properties of Heterotrophic Bacteria Isolated from Lake Baikal Epilithic Biofilms. *Microbiology*, 88(3), 324–334. <https://doi.org/10.1134/S0026261719030147>
- Suntoyo, Ikhwan, H., Zikra, M., Sukmasari, N. A., Angraeni, G., Tanaka, H., Umeda, M., & Kure, S. (2015). Modelling of the COD, TSS, Phosphate and Nitrate Distribution Due to the Sidoarjo Mud Flow into Porong River Estuary. *The 2nd International Seminar on Ocean and Coastal Engineering, Environment and Natural Disaster Management, 2014*, 14, 144–151. <https://doi.org/10.1016/j.proeps.2015.07.095>
- Susilowati, E., Rahmansyah, A., & Sudarto, S. (2017). Spatial Analysis and Risk Assessment of Heavy Metal in Aquaculture Sediment of Porong River Estuary. *Jurnal Pembangunan Dan Alam Lestari*, 8, 111–116. <https://doi.org/10.21776/ub.jp.al.2017.008.02.09>
- Swenson, N. G., Erickson, D. L., Mi, X., Bourg, N. A., Forero-Montaña, J., Ge, X., Howe, R., Lake, J. K., Liu, X., Ma, K., Pei, N., Thompson, J., Uriarte, M., Wolf, A., Wright, S. J., Ye, W., Zhang, J., Zimmerman, J. K., & Kress, W. J. (2012). Phylogenetic and functional alpha and beta diversity in temperate and tropical tree communities. *Ecology*, 93(sp8), S112–S125. <https://doi.org/10.1890/11-0402.1>
- Takeshi, K., Luciano, Dias, S.-J. C., Andrea, S.-C., Souza, de O. T. C., Pellon, de M. F., & Flávio, H.-S. (2016). Metagenomics Analysis of Microorganisms in Freshwater Lakes of the Amazon Basin. *Genome Announcements*, 4(6), e01440-16. <https://doi.org/10.1128/genomeA.01440-16>
- Tan, Z., Yang, X., Chen, L., Liu, Y., Xu, H.-J., Li, Y., & Gong, B. (2022). Biodegradation mechanism of chloramphenicol by *Aeromonas media* SZW3 and genome analysis. *Bioresour. Technol.*, 344, 126280. <https://doi.org/10.1016/j.biortech.2021.126280>
- Taniguchi, T., Okuno, M., Shinoda, T., Kobayashi, F., Takahashi, K., Yuasa, H., Nakamura, Y., Tanaka, H., Kajitani, R., & Itoh, T. (2023). GINGER: an integrated method for high-accuracy prediction of gene structure in higher

- eukaryotes at the gene and exon level. *DNA Research*, 30(4), dsad017. <https://doi.org/10.1093/dnares/dsad017>
- Tarawneh, K., AL-Quraishi, F., Qaralleh, H., Al Tarawneh, A., Al-limoun, M., & Khleifat, K. (2022). Biodegradation of Chlorobenzoic Acid Substitutes, Particularly, 2- Chlorobenzoic Acid by *Aeromonas hydrophila*. *Journal of Basic and Applied Research in Biomedicine*, 5(2), 124–135.
- Taylor, M. W., Radax Regina, Steger Doris, & Wagner Michael. (2007). Sponge-Associated Microorganisms: Evolution, Ecology, and Biotechnological Potential. *Microbiology and Molecular Biology Reviews*, 71(2), 295–347. <https://doi.org/10.1128/MMBR.00040-06>
- Thomas, T., Gilbert, J., & Meyer, F. (2012). Metagenomics—A guide from sampling to data analysis. *Microbial Informatics and Experimentation*, 2(1), 3. <https://doi.org/10.1186/2042-5783-2-3>
- Thomas, T., Moitinho-Silva, L., Lurgi, M., Björk, J. R., Easson, C., Astudillo-García, C., Olson, J. B., Erwin, P. M., López-Legentil, S., Luter, H., Chaves-Fonnegra, A., Costa, R., Schupp, P. J., Steindler, L., Erpenbeck, D., Gilbert, J., Knight, R., Ackermann, G., Victor Lopez, J., ... Webster, N. S. (2016). Diversity, structure and convergent evolution of the global sponge microbiome. *Nature Communications*, 7(1), 11870. <https://doi.org/10.1038/ncomms11870>
- Thukral, A. (2017). A review on measurement of Alpha diversity in biology. *Agricultural Research Journal*, 54, 1. <https://doi.org/10.5958/2395-146X.2017.00001.1>
- Ting, A. S. Y., Zoqratt, M. Z. H., Tan, H. S., Hermawan, A. A., Talei, A., & Khu, S. T. (2021). Bacterial and eukaryotic microbial communities in urban water systems profiled via Illumina MiSeq platform. *3 Biotech*, 11(2), 40. <https://doi.org/10.1007/s13205-020-02617-3>
- Tomei, M. C., Mosca Angelucci, D., Clagnan, E., & Brusetti, L. (2021). Anaerobic biodegradation of phenol in wastewater treatment: Achievements and limits. *Applied Microbiology and Biotechnology*, 105(6), 2195–2224. <https://doi.org/10.1007/s00253-021-11182-5>
- Triaji, M., Risjani, Y., & Mahmudi, M. (2017). Analysis of Water Quality Status in Porong River, Sidoarjo by Using NSF-WQI Index (Nasional Sanitation Foundation – Water Quality Index). *Jurnal Pembangunan Dan Alam Lestari*, 8, 117–119. <https://doi.org/10.21776/ub.jp.al.2017.008.02.10>
- Tringe, S. G., & Rubin, E. M. (2005). Metagenomics: DNA sequencing of environmental samples. *Nature Reviews Genetics*, 6(11), 805–814. <https://doi.org/10.1038/nrg1709>
- Tripathi, L. K., & Nailwal, T. K. (2020). Chapter 20—Metagenomics: Applications of functional and structural approaches and meta-omics. In S. De Mandal & P. Bhatt (Eds.), *Recent Advancements in Microbial Diversity* (pp. 471–505). Academic Press. <https://doi.org/10.1016/B978-0-12-821265-3.00020-7>
- Ufarté, L., Laville, É., Duquesne, S., & Potocki-Veronese, G. (2015). Metagenomics for the discovery of pollutant degrading enzymes.

- Biotechnology Advances*, 33(8), 1845–1854.  
<https://doi.org/10.1016/j.biotechadv.2015.10.009>
- Vega, L., Jaimes, J., Morales, D., Martínez, D., Cruz-Saavedra, L., Muñoz, M., & Ramírez, J. D. (2021). Microbial Communities' Characterization in Urban Recreational Surface Waters Using Next Generation Sequencing. *Microbial Ecology*, 81(4), 847–863. <https://doi.org/10.1007/s00248-020-01649-9>
- Vidali, M. (2001). *Bioremediation. An overview*. 73(7), 1163–1172.  
<https://doi.org/10.1351/pac200173071163>
- Wei, Z.-G., Zhang, X.-D., Cao, M., Liu, F., Qian, Y., & Zhang, S.-W. (2021). Comparison of Methods for Picking the Operational Taxonomic Units From Amplicon Sequences. *Frontiers in Microbiology*, 12.  
<https://www.frontiersin.org/articles/10.3389/fmicb.2021.644012>
- Weyrich, L. S., Farrer, A. G., Eisenhofer, R., Arriola, L. A., Young, J., Selway, C. A., Handsley-Davis, M., Adler, C. J., Breen, J., & Cooper, A. (2019). Laboratory contamination over time during low-biomass sample analysis. *Molecular Ecology Resources*, 19(4), 982–996.  
<https://doi.org/10.1111/1755-0998.13011>
- Whiteley, C. G., & Lee, D.-J. (2006). Enzyme technology and biological remediation. *Enzyme and Microbial Technology*, 38(3), 291–316.  
<https://doi.org/10.1016/j.enzmictec.2005.10.010>
- Whittaker, R. H. (1972). EVOLUTION AND MEASUREMENT OF SPECIES DIVERSITY. *TAXON*, 21(2–3), 213–251. <https://doi.org/10.2307/1218190>
- Willis, A. D. (2019). Rarefaction, Alpha Diversity, and Statistics. *Frontiers in Microbiology*, 10.  
<https://www.frontiersin.org/articles/10.3389/fmicb.2019.02407>
- Wulandari, D., Dewantoro, G., Lunggani, A. T., Supriyadi, A., Riani, C., Setiawan, E., Farikha, S. L., & Budiharjo, A. (2023). Antibacterial Activity of Freshwater Sponge *Oncosclera asiatica* Against *Escherichia coli* and *Staphylococcus aureus*. *Bioma : Berkala Ilmiah Biologi*, 24(2), 120–129. <https://doi.org/10.14710/bioma.24.2.120-129>
- Xu, X., Wang, H., Guo, D., Man, X., Jun, L., Li, J., Luo, C., Zhang, M., Zhen, L., & Liu, X. (2021). Curcumin modulates gut microbiota and improves renal function in rats with uric acid nephropathy. *Renal Failure*, 43, 1063–1075.  
<https://doi.org/10.1080/0886022X.2021.1944875>
- Yadav, R., Rajput, V., & Dharne, M. (2021). Functional metagenomic landscape of polluted river reveals potential genes involved in degradation of xenobiotic pollutants. *Environmental Research*, 192, 110332.  
<https://doi.org/10.1016/j.envres.2020.110332>
- Yilmaz, P., Parfrey, L. W., Yarza, P., Gerken, J., Pruesse, E., Quast, C., Schweer, T., Peplies, J., Ludwig, W., & Glöckner, F. O. (2014). The SILVA and “All-species Living Tree Project (LTP)” taxonomic frameworks. *Nucleic Acids Research*, 42(D1), D643–D648. <https://doi.org/10.1093/nar/gkt1209>
- Zar, J. H. (2014). Spearman Rank Correlation: Overview. In *Wiley StatsRef: Statistics Reference Online*. <https://doi.org/10.1002/x18445112.stat05964>

- Zhang, W., Fan Xiaoqian, Shi Haobo, Li Jian, Zhang Mingqian, Zhao Jin, & Su Xiaoquan. (2023). Comprehensive Assessment of 16S rRNA Gene Amplicon Sequencing for Microbiome Profiling across Multiple Habitats. *Microbiology Spectrum*, 11(3), e00563-23. <https://doi.org/10.1128/spectrum.00563-23>
- Zhang, X., Gu, Q., Long, X.-E., Li, Z.-L., Liu, D.-X., Ye, D.-H., He, C.-Q., Liu, X.-Y., Väänänen, K., & Chen, X.-P. (2016). Anthropogenic activities drive the microbial community and its function in urban river sediment. *Journal of Soils and Sediments*, 16(2), 716–725. <https://doi.org/10.1007/s11368-015-1246-8>
- Zylstra, G. J., & Gibson, D. T. (1989). Toluene Degradation by *Pseudomonas putida* F1: Nucleotide Sequence of the *todC1C2BADE* Genes and Their Expression in *Escherichia coli*. *Journal of Biological Chemistry*, 264(25), 14940–14946. [https://doi.org/10.1016/S0021-9258\(18\)63793-7](https://doi.org/10.1016/S0021-9258(18)63793-7)