

References

- Akyüz, E., Vorob'ev, M. M., & Güler, G. (2025). Biophysical assessment of protein stability in ethanol-stressed environments via UV absorption and fluorescence spectroscopies. *Biophysical Chemistry*, 329, 107538. <https://doi.org/10.1016/j.bpc.2025.107538>
- Aravind, L., Abhiman, S., & Iyer, L. M. (2011). Natural history of the eukaryotic chromatin protein methylation system. *Progress in Molecular Biology and Translational Science*, 105–176. <https://doi.org/10.1016/b978-0-12-387685-0.00004-4>
- Arumsari, S., Wanandi, S. I., Syahrani, R. A., Watanabe, Y., & Mizuno, S. (2024). Design of specific and efficient sgRNA for CRISPR/cas9 system to knockout superoxide dismutase 2 in breast cancer stem cells. *International Journal of Technology*, 15(2), 353. <https://doi.org/10.14716/ijtech.v15i2.6680>
- Athey, J., Alexaki, A., Osipova, E., Rostovtsev, A., Santana-Quintero, L. V., Katneni, U., Simonyan, V., & Kimchi-Sarfaty, C. (2017). A new and updated resource for codon usage tables. *BMC Bioinformatics*, 18(1). <https://doi.org/10.1186/s12859-017-1793-7>
- Auerbach, G., Ostendorp, R., Prade, L., Korndörfer, I., Dams, T., Huber, R., & Jaenicke, R. (1998). Lactate dehydrogenase from the hyperthermophilic bacterium *Thermotoga maritima*: the crystal structure at 2.1 Å resolution reveals strategies for intrinsic protein stabilization. *Structure*, 6(6).
- Àvila-Cabré, S., Pérez-Trujillo, M., Albiol, J., & Ferrer, P. (2023). Engineering the synthetic β-alanine pathway in *Komagataella phaffii* for conversion of methanol into 3-hydroxypropionic acid. *Microbial Cell Factories*, 22(1). <https://doi.org/10.1186/s12934-023-02241-9>
- Bachleitner, S., Severinsen, M. M., Lutz, G., & Mattanovich, D. (2024). Overexpression of the transcriptional activators Mxr1 and Mit1 enhances lactic acid production on methanol in *Komagataella phaffii*. *Metabolic Engineering*, 85, 133–144. <https://doi.org/10.1016/j.ymben.2024.07.013>
- Baek, S.-H., Kwon, E. Y., Kim, Y. H., & Hahn, J.-S. (2015). Metabolic engineering and adaptive evolution for efficient production of D-lactic acid in *Saccharomyces cerevisiae*. *Applied Microbiology and Biotechnology*, 100(6), 2737–2748. <https://doi.org/10.1007/s00253-015-7174-0>
- Bailey, T. L., Johnson, J., Grant, C. E., & Noble, W. S. (2015). The MEME suite. *Nucleic Acids Research*, 43(W1), W39–W49. <https://doi.org/10.1093/nar/gkv416>
- Barbosa, C., Nogueira, S., Gadanho, M., & Chaves, S. (2016). DNA extraction: finding the most suitable method. *Molecular Microbial Diagnostic Methods*, 135–154. <https://doi.org/10.1016/b978-0-12-416999-9.00007-1>

- Barros, A. K. M. O., Ribeiro, A. C. S., de Oliveira, G. R., Lima, D. V. C., Feitosa, P. L. F., Alves, T. V. S., Mota, L. M. P., Vasconcelos, B. M. F., Borsuk, S., & Bezerra, F. S. B. (2026). In silico characterization and heterologous expression of the recombinant YkuE protein from *Corynebacterium pseudotuberculosis* for immunobiological purpose. *Research Square*. <https://doi.org/10.21203/rs.3.rs-9012757/v1>
- Bernauer, L., Radkohl, A., Lehmayr, L. G. K., & Emmerstorfer-Augustin, A. (2021). *Komagataella phaffii* as emerging model organism in fundamental research. *Frontiers in Microbiology*, 11. <https://doi.org/10.3389/fmicb.2020.607028>
- Bertoni, M., Kiefer, F., Biasini, M., Bordoli, L., & Schwede, T. (2017). Modeling protein quaternary structure of homo- and hetero-oligomers beyond binary interactions by homology. *Scientific Reports*, 7(1). <https://doi.org/10.1038/s41598-017-09654-8>
- Biassoni, R., & Raso, A. (2014). *Quantitative real-time PCR : Methods and protocols*. Humana Press.
- Bibliotex. (2019). *Illustrated handbook of metabolic engineering* (A. Mratinković, H. S. Fouda, S. El Hajj, D. Piestun, F. Killings, F. Parveen, I. Kronic, T. Nur, Michelle, J. Pehcevski, & Stephen, Eds.). Bibliotex.
- Bienert, S., Waterhouse, A., de Beer, T. A. P., Tauriello, G., Studer, G., Bordoli, L., & Schwede, T. (2016). The SWISS-MODEL repository—new features and functionality. *Nucleic Acids Research*, 45(D1), D313–D319. <https://doi.org/10.1093/nar/gkw1132>
- Blum, M., Hobbs, E., Florentino, L., & Bateman, A. (2026). InterProScan 6: a modern large-scale protein function annotation pipeline. *Bioinformatics Advances*, 6(1).
- Boone, M., Eeckhaut, H., & Callewaert, N. (2025). High-Efficiency transformation of integrative libraries under zeocin selection in *Pichia pastoris*. *Methods in Molecular Biology*, 2697, 329–343. https://doi.org/10.1007/978-1-0716-4779-0_23
- Bustin, S. A., & Nolan, T. (2020). RT-qPCR testing of SARS-CoV-2: A primer. *International Journal of Molecular Sciences*, 21(8), 3004. <https://doi.org/10.3390/ijms21083004>
- Bustos, C., Quezada, J., Veas, R., Altamirano, C., Braun-Galleani, S., Fickers, P., & Berrios, J. (2022). Advances in cell engineering of the *Komagataella phaffii* platform for recombinant protein production. *Metabolites*, 12(4), 346–346. <https://doi.org/10.3390/metabo12040346>
- Cai, P., Wu, X., Deng, J., Gao, L., Shen, Y., Yao, L., & Zhou, Y. J. (2022). Methanol biotransformation toward high-level production of fatty acid derivatives by engineering the industrial yeast *Pichia pastoris*. *PNAS*, 119(29). <https://doi.org/10.1073/pnas.2201711119>
- Chatterjee, Y., Bhowal, B., Gupta, K. J., Pareek, A., & Singla-Pareek, S. L. (2023). Lactate dehydrogenase superfamily in rice and Arabidopsis: Understanding the molecular evolution and structural diversity. *International Journal of Molecular Sciences*, 24(6), 5900. <https://doi.org/10.3390/ijms24065900>

- Christensen, H., & Bisgaard, M. (2024). Pasteurella. *Molecular Medical Microbiology*, 1637–1656.
<https://doi.org/10.1016/b978-0-12-818619-0.00094-0>
- Combet, C., Blanchet, C., Geourjon, C., & Deléage, G. (2000). NPS@: Network protein sequence analysis. *Trends in Biochemical Sciences*, 25(3), 147–150.
[https://doi.org/10.1016/s0968-0004\(99\)01540-6](https://doi.org/10.1016/s0968-0004(99)01540-6)
- Cristescu, M. E., Innes, D. J., Stillman, J. H., & Crease, T. J. (2008). D- and L-lactate dehydrogenases during invertebrate evolution. *BMC Evolutionary Biology*, 8(1), 268.
<https://doi.org/10.1186/1471-2148-8-268>
- Cui, Y., Xu, J., Cheng, M., Liao, X., & Peng, S. (2018). Review of CRISPR/Cas9 sgRNA design tools. *Interdisciplinary Sciences, Computational Life Sciences*, 10(2), 455–465.
<https://doi.org/10.1007/s12539-018-0298-z>
- de França, J. O. C., da Silva Valadares, D., Paiva, M. F., Dias, S. C. L., & Dias, J. A. (2022). Polymers based on PLA from synthesis using D,L-Lactic acid (or racemic lactide) and some biomedical applications: A short review. *Polymers*, 14(12), 2317.
<https://doi.org/10.3390/polym14122317>
- de Lima, P. B. A., Mulder, K. C. L., Melo, N. T. M., Carvalho, L. S., Menino, G. S., Mulinari, E., de Castro, V. H., dos Reis, T. F., Goldman, G. H., Magalhães, B. S., & Parachin, N. S. (2016). Novel homologous lactate transporter improves L-lactic acid production from glycerol in recombinant strains of *Pichia pastoris*. *Microbial Cell Factories*, 15(1).
<https://doi.org/10.1186/s12934-016-0557-9>
- Deng, H., Zhadin, N., & Callender, R. (2001). Dynamics of protein ligand binding on multiple time scales: NADH binding to lactate dehydrogenase. *Biochemistry*, 40(13), 3767–3773.
<https://doi.org/10.1021/bi0026268>
- Desguin, B., Soumilion, P., Hausinger, R. P., & Hols, P. (2017). Unexpected complexity in the lactate racemization system of lactic acid bacteria. *FEMS Microbiology Reviews*, 41.
- Doench, J. G., Hartenian, E., Graham, D. B., Tothova, Z., Hegde, M., Smith, I., Sullender, M., Ebert, B. L., Xavier, R. J., & Root, D. E. (2014). Rational design of highly active sgRNAs for CRISPR-Cas9-mediated gene inactivation. *Nature Biotechnology*, 32(12), 1262–1267.
<https://doi.org/10.1038/nbt.3026>
- Dong, L., Wang, J., & Xia, Q. (2025). Chemically modified tRNA enhances the translation capacity of mRNA rich in cognate codons. *Nature Communications*, 16(1).
<https://doi.org/10.1038/s41467-025-62981-7>
- Gamage, D. G., Gunaratne, A., Periyannan, G. R., & Russell, T. G. (2019). Applicability of instability index for in vitro protein stability prediction. *Protein and Peptide Letters*, 26(5), 339–347.
<https://doi.org/10.2174/0929866526666190228144219>

- Gassler, T., Heisteringer, L., Mattanovich, D., Gasser, B., & Prielhofer, R. (2019). CRISPR/Cas9-Mediated homology-directed genome editing in *Pichia pastoris*. *Methods in Molecular Biology*, 211–225. https://doi.org/10.1007/978-1-4939-9024-5_9
- Giguère, S., Wang, X., Huber, S., Xu, L., Warner, J., Weldon, S. R., Hu, J., Phan, Q. A., Tumang, K., Prum, T., Ma, D., Kirsch, K. H., Nair, U., Dedon, P., & Batista, F. D. (2024). Antibody production relies on the tRNA inosine wobble modification to meet biased codon demand. *Science*, 383(6679), 205–211. <https://doi.org/10.1126/science.adi1763>
- Goffin, P., Lorquet, F., Kleerebezem, M., & Hols, P. (2004). Major role of NAD-Dependent lactate dehydrogenases in aerobic lactate utilization in *Lactobacillus plantarum* during early stationary phase. *Journal of Bacteriology*, 186(19), 6661–6666. <https://doi.org/10.1128/jb.186.19.6661-6666.2004>
- Guex, N., Peitsch, M. C., & Schwede, T. (2009). Automated comparative protein structure modeling with SWISS-MODEL and Swiss-PdbViewer: A historical perspective. *Electrophoresis*, 30(S1), S162–S173. <https://doi.org/10.1002/elps.200900140>
- Gull, I., Aslam, M. S., Tipu, I., Mushtaq, R., & Athar, M. A. (2019). Reliable scarless fusion of genes through overlap extension PCR to develop chimeric genes. *Pakistan Journal of Zoology*, 51(4). <https://doi.org/10.17582/journal.pjz/2019.51.4.1561.1567>
- Guo, F., Dai, Z., Peng, W., Zhang, S., Zhou, J., Ma, J., Dong, W., Xin, F., Zhang, W., & Jiang, M. (2020). Metabolic engineering of *Pichia pastoris* for malic acid production from methanol. *Biotechnology and Bioengineering*, 118(1), 357–371. <https://doi.org/10.1002/bit.27575>
- Gupta, A., Krishna Rao, K., Sahu, U., & Rangarajan, P. N. (2021). Characterization of the transactivation and nuclear localization functions of *Pichia pastoris* zinc finger transcription factor Mxr1p. *Journal of Biological Chemistry*, 297(4), 101247. <https://doi.org/10.1016/j.jbc.2021.101247>
- Han, D., Churcher, S., & Nordman, J. T. (2023). PCR cloning intermediated gibbon assembly (PIG) for constructing DNA repair templates in CRISPR-Cas9 based gene editing. *microPublication Biology*. <https://doi.org/https://doi.org/10.17912/micropub.biology.000916>
- Hanukoglu, I. (2015). Proteopedia: Rossmann fold: A beta-alpha-beta fold at dinucleotide binding sites. *Biochemistry and Molecular Biology Education*, 43(3), 206–209. <https://doi.org/10.1002/bmb.20849>
- Hermantara, R. (2024). CRISPR-Cas9: A story of discovery, innovation, and revolution in genome editing. *Indonesian Journal of Life Sciences*, 6(1), 83–104. <https://doi.org/10.54250/ijls.v6i01.197>
- Hermantara, R., Richmond, L., Taqi, A. F., Chilaka, S., Jeantet, V., Guerrini, I., West, K., & West, A. (2024). Improving CRISPR–Cas9 directed faithful transgene integration outcomes by reducing

- unwanted random DNA integration. *Journal of Biomedical Science*, 31(1).
<https://doi.org/10.1186/s12929-024-01020-x>
- Hilgarth, R. S., & Lanigan, T. M. (2020). Optimization of overlap extension PCR for efficient transgene construction. *MethodsX*, 7, 100759. <https://doi.org/10.1016/j.mex.2019.12.001>
- Hillary, V. E., & Ceasar, S. A. (2022). A review on the mechanism and applications of CRISPR/cas9/cas12/cas13/cas14 proteins utilized for genome engineering. *Molecular Biotechnology*, 65(3). <https://doi.org/10.1007/s12033-022-00567-0>
- Ho, S. N., Hunt, H. D., Horton, R. M., Pullen, J. K., & Pease, L. R. (1989). Site-directed mutagenesis by overlap extension using the polymerase chain reaction. *Gene*, 77(1), 51–59.
[https://doi.org/10.1016/0378-1119\(89\)90358-2](https://doi.org/10.1016/0378-1119(89)90358-2)
- Hooft, R. W. W., Sander, C., & Vriend, G. (1997). Objectively judging the quality of a protein structure from a Ramachandran plot. *Bioinformatics*, 13(4), 425–430.
<https://doi.org/10.1093/bioinformatics/13.4.425>
- Hoorzook, K. B., & Barnard, T. G. (2022). DNA extraction of bacterial cells using a semi-automated filtration system. *MethodsX*, 9, 101785. <https://doi.org/10.1016/j.mex.2022.101785>
- Horton, R. M., Cai, Z., Ho, S. N., & Pease, L. R. (2013). Gene splicing by overlap extension: Tailor-Made genes using the polymerase chain reaction. *BioTechniques*, 54(3).
<https://doi.org/10.2144/000114017>
- Hossain, M. A. (2021). CRISPR-Cas9: A fascinating journey from bacterial immune system to human gene editing. *Progress in Molecular Biology and Translational Science*, 178, 63–83.
<https://doi.org/10.1016/bs.pmbts.2021.01.001>
- Huang, T. F., Purnomo, J. S., Rombot, A. B., Kowanda, I. A., Lorentz, R. T., Sugata, M., Jan, T. T., & Jo, J. (2025). Whole-Genome analysis and tolerance assessment on bifidobacteria-like bacteria isolated from breast milk and infant fecal samples in Indonesia. *Journal of Tropical Biodiversity and Biotechnology*, 10(2), jtbb15062. <https://doi.org/10.22146/jtbb.15062>
- Hwang, H. J., Kim, S. M., Chang, J. H., & Lee, S. B. (2011). Lactic acid production from seaweed hydrolysate of *Enteromorpha prolifera* (Chlorophyta). *Journal of Applied Phycology*, 24(4), 935–940. <https://doi.org/10.1007/s10811-011-9714-z>
- Inoue, Y., Nakamura, K., Yamada, R., Matsumoto, T., & Ogino, H. (2025). Improvement of D-lactic acid production from methanol by metabolically engineered *Komagataella phaffii* via ultra-violet mutagenesis. *Metabolic Engineering Communications*, 20, e00262.
<https://doi.org/10.1016/j.mec.2025.e00262>
- Jia, J., Mu, W., Zhang, T., & Jiang, B. (2009). Bioconversion of phenylpyruvate to phenyllactate: Gene cloning, expression, and enzymatic characterization of d- and l1-Lactate dehydrogenases from

- Lactobacillus plantarum* SK002. *Applied Biochemistry and Biotechnology*, 162(1), 242–251. <https://doi.org/10.1007/s12010-009-8767-9>
- Junqueira, A. C. de O., Melo, N. T. M., Parachin, N. S., & Paes, H. C. (2023). Loss of a functional mitochondrial pyruvate carrier in *Komagataella phaffii* does not improve lactic acid production from glycerol in aerobic cultivation. *Microorganisms*, 11(2).
- Karaoğlu, M., Erden-Karaoğlu, F., Yılmaz, S., & İnan, M. (2019). Identification of major ADH genes in ethanol metabolism of *Pichia pastoris*. *Yeast*, 37(2), 227–236. <https://doi.org/10.1002/yea.3443>
- Katoh, K., Rozewicki, J., & Yamada, K. D. (2017). MAFFT online service: multiple sequence alignment, interactive sequence choice and visualization. *Briefings in Bioinformatics*, 20(4). <https://doi.org/10.1093/bib/bbx108>
- Kavanagh, K. L., Elling, R. A., & Wilson, D. K. (2004). Structure of toxoplasma gondii LDH1: active-site differences from human lactate dehydrogenases and the structural basis for efficient APAD+ use. *Biochemistry*, 43(4), 879–889. <https://doi.org/10.1021/bi035108g>
- Khan, A. A., Allemailem, K. S., Alhumaydhi, F. A., Gowder, S. J. T., & Rahmani, A. H. (2020). The biochemical and clinical perspectives of lactate dehydrogenase: An enzyme of active metabolism. *Endocrine, Metabolic & Immune Disorders Drug Targets*, 20(6), 855–868. <https://doi.org/10.2174/1871530320666191230141110>
- Kleerebezem, M., Boekhorst, J., van Kranenburg, R., Molenaar, D., Kuipers, O. P., Leer, R., Turchini, R., Peters, S. A., Sandbrink, H. M., Fiers, M. W. E. J., Stiekema, W., Lankhorst, R. M. K., Bron, P. A., Hoffer, S. M., Groot, M. N. N., Kerkhoven, R., de Vries, M., Ursing, B., de Vos, W. M., & Siezen, R. J. (2003). Complete genome sequence of *Lactobacillus plantarum* WCFS1. *Proceedings of the National Academy of Sciences*, 100(4), 1990–1995. <https://doi.org/10.1073/pnas.0337704100>
- Kleiger, G., & Eisenberg, D. (2002). GXXXG and GXXXA motifs stabilize FAD and nad(p)-binding Rossmann folds through α -H $\cdots$ O hydrogen bonds and van der Waals interactions. *Journal of Molecular Biology*, 323(1), 69–76. [https://doi.org/10.1016/S0022-2836\(02\)00885-9](https://doi.org/10.1016/S0022-2836(02)00885-9)
- Kopperschlager, G., & Kirchberger, J. (1996). Methods for the separation of lactate dehydrogenases and clinical significance of the enzyme. *Journal of Chromatography B: Biomedical Sciences and Applications*, 684(1), 25–49. [https://doi.org/10.1016/0378-4347\(96\)00133-8](https://doi.org/10.1016/0378-4347(96)00133-8)
- Krishna, B. S., Nikhilesh, G. S. S., Tarun, B., V, N. S. K., & Gopinadh, R. (2018). Industrial production of lactic acid and its applications. *International Journal of Biotech Research*, 1(1).
- Kumar, P., Nagarajan, A., & Uchil, P. D. (2018). Analysis of cell viability by the lactate dehydrogenase assay. *Cold Spring Harbor Protocols*, 2018(6), pdb.prot095497. <https://doi.org/10.1101/pdb.prot095497>

- Kumar, S., & Deshpande, P. A. (2021). Structural and thermodynamic analysis of factors governing the stability and thermal folding/unfolding of SazCA. *PLOS ONE*, 16(4), e0249866. <https://doi.org/10.1371/journal.pone.0249866>
- Kyte, J., & Doolittle, R. F. (1982). A simple method for displaying the hydropathic character of a protein. *Journal of Molecular Biology*, 157(1), 105–132. [https://doi.org/10.1016/0022-2836\(82\)90515-0](https://doi.org/10.1016/0022-2836(82)90515-0)
- Labun, K., Montague, T. G., Krause, M., Torres Cleuren, Y. N., Tjeldnes, H., & Valen, E. (2019). CHOPCHOP v3: Expanding the CRISPR web toolbox beyond genome editing. *Nucleic Acids Research*, 47(W1), W171–W174. <https://doi.org/10.1093/nar/gkz365>
- Lee, J. J., Crook, N., Sun, J., & Alper, H. S. (2016). Improvement of lactic acid production in *Saccharomyces cerevisiae* by a deletion of *ssb1*. *Journal of Industrial Microbiology and Biotechnology*, 43(1), 87–96. <https://doi.org/10.1007/s10295-015-1713-7>
- Lee, J.-E., Hwang, G., Lee, J.-H., & Kim, G.-B. (2025). Overexpression and characterization of l-lactate dehydrogenase from *Lactocaseibacillus casei* HY2782 to control post-acidification in yogurt. *Food Science of Animal Resources*, 45(6), 1815–1828. <https://doi.org/10.5851/kosfa.2025.e25>
- Liao, H., Wu, J., VanDusen, N. J., Li, Y., & Zheng, Y. (2024). CRISPR/Cas9-Mediated homology-directed repair for precise gene editing. *Molecular Therapy — Nucleic Acids*, 35(4), 102344–102344. <https://doi.org/10.1016/j.omtn.2024.102344>
- Lin-Cereghino, J., Naranjo, C. A., & Lin-Cereghino, G. P. (2022). Competent Cell Preparation and Transformation of *Pichia pastoris*. *Methods in Molecular Biology*, 113–120. https://doi.org/10.1007/978-1-0716-2399-2_7
- Lu, S., Wang, J., Chitsaz, F., Derbyshire, M. K., Geer, R. C., Gonzales, N. R., Gwadz, M., Hurwitz, D. I., Marchler, G. H., Song, J. S., Thanki, N., Yamashita, R. A., Yang, M., Zhang, D., Zheng, C., Lanczycki, C. J., & Marchler-Bauer, A. (2019). CDD/SPARCLE: the conserved domain database in 2020. *Nucleic Acids Research*, 48(D1). <https://doi.org/10.1093/nar/gkz991>
- Lu, Y., Xiao, S., Yuan, M., Gao, Y., Sun, J., & Xue, C. (2018). Using overlap-extension PCR technique to fusing genes for constructing recombinant plasmids. *Journal of Basic Microbiology*, 58(3), 273–276. <https://doi.org/10.1002/jobm.201700455>
- Luo, M., Wang, J., Dong, Z., Wang, C., & Lu, G. (2022). CRISPR-Cas9 sgRNA design and outcome assessment: Bioinformatics tools and aquaculture applications. *Aquaculture and Fisheries*, 7(2), 121–130. <https://doi.org/10.1016/j.aaf.2021.10.002>
- Madern, D., Ebel, C., Mevarech, M., Richard, S. B., Pfister, C., & Zaccai, G. (2000). Insights into the molecular relationships between malate and lactate dehydrogenases: structural and biochemical properties of monomeric and dimeric intermediates of a mutant of tetrameric

- I-[LDH-like] malate dehydrogenase from the halophilic archaeon *Haloarcula marismortui*. *Biochemistry*, 39(5), 1001–1010. <https://doi.org/10.1021/bi9910023>
- Maldonado-Barragán, A., & West, S. A. (2019). The cost and benefit of quorum sensing-controlled bacteriocin production in *Lactobacillus plantarum*. *Journal of Evolutionary Biology*, 33(1), 101–111. <https://doi.org/10.1111/jeb.13551>
- Manghwar, H., Li, B., Ding, X., Hussain, A., Lindsey, K., Zhang, X., & Jin, S. (2020). CRISPR/Cas systems in genome editing: Methodologies and tools for sgRNA design, off-target evaluation, and strategies to mitigate off-target effects. *Advanced Science*, 7(6). <https://doi.org/10.1002/advs.201902312>
- Marchler-Bauer, A., Bo, Y., Han, L., He, J., Lanczycki, C. J., Lu, S., Chitsaz, F., Derbyshire, M. K., Geer, R. C., Gonzales, N. R., Gwadz, M., Hurwitz, D. I., Lu, F., Marchler, G. H., Song, J. S., Thanki, N., Wang, Z., Yamashita, R. A., Zhang, D., ... Bryant, S. H. (2017). CDD/SPARCLE: functional classification of proteins via subfamily domain architectures. *Nucleic Acids Research*, 45(D1), D200–D203. <https://doi.org/10.1093/nar/gkw1129>
- Martínez-Miranda, J. G., Chairez, I., & Durán-Páramo, E. (2022). Mannitol production by heterofermentative lactic acid bacteria: A review. *Applied Biochemistry and Biotechnology*, 194(6), 2762–2795. <https://doi.org/10.1007/s12010-022-03836-5>
- Masnaini, M., Achyar, A., Chatri, M., Putri, D. H., Ahda, Y., & Irdawati. (2023). Primer design and optimization of PCR methods for detecting mixed rat meat in food samples. *Advances in Biological Sciences Research*, 282–289. https://doi.org/10.2991/978-94-6463-166-1_37
- Mohammadhassan, R., Tutunchi, S., Nasehi, N., Goudarziasl, F., & Mahya, L. (2023). The prominent characteristics of the effective sgRNA for a precise CRISPR genome editing. In *CRISPR Technology - Recent Advances*. IntechOpen. <https://doi.org/10.5772/intechopen.106711>
- Montague, T. G., Cruz, J. M., Gagnon, J. A., Church, G. M., & Valen, E. (2014). CHOPCHOP: a CRISPR/Cas9 and TALEN web tool for genome editing. *Nucleic Acids Research*, 42(W1), W401–W407. <https://doi.org/10.1093/nar/gku410>
- Murray-Nerger, L. A., & Gewurz, B. E. (2024). Efficient CRISPR/Cas9 knock-in approaches for manipulation of endogenous genes in human B lymphoma cells. *Current Protocols*, 4(11), e70041–e70041. <https://doi.org/10.1002/cpz1.70041>
- Najibi, S. M., Maadooliat, M., Zhou, L., Huang, J. Z., & Gao, X. (2017). Protein structure classification and loop modeling using multiple ramachandran distributions. *Computational and Structural Biotechnology Journal*, 15, 243–254. <https://doi.org/10.1016/j.csbj.2017.01.011>
- Nelson, M. N., & Fitch, D. H. A. (2011). Overlap extension PCR: An efficient method for transgene construction. *Methods in Molecular Biology*, 459–470. https://doi.org/10.1007/978-1-61779-228-1_27

- Niazvand, F., Fathinezhad, Z., Alfuraiji, N., Etajuri, E. A., Amini-Chermahini, F., Chehelgerdi, M., & Ranjbar, R. (2021). Clustered regularly interspaced short palindromic repeats system of genome engineering in embryos to repair genes. *Journal of Biomedical Nanotechnology*, 17(3), 331–356. <https://doi.org/10.1166/jbn.2021.3045>
- Niepmann, M. (2024). Importance of michaelis constants for cancer cell redox balance and lactate secretion—revisiting the warburg effect. *Cancers*, 16(13), 2290–2290. <https://doi.org/10.3390/cancers16132290>
- Njabon, E. N., Patouossa, I., Carlson, K. L., Lowe, S. L., Forlemu, N. Y., & Thomasson, K. A. (2020). Brownian dynamics simulations of the interactions between lactate dehydrogenase (LDH) and G- or f-actin. part I: Muscle and heart homo-isoforms. *Scientific African*, 9, e00510. <https://doi.org/10.1016/j.sciaf.2020.e00510>
- Obst, U., Lu, T. K., & Sieber, V. (2017). A modular toolkit for generating *Pichia pastoris* secretion libraries. *ACS Synthetic Biology*, 6(6), 1016–1025. <https://doi.org/10.1021/acssynbio.6b00337>
- Ojo, A. O., & de Smidt, O. (2023). Lactic acid: A comprehensive review of production to purification. *Processes*, 11(3), 688. <https://doi.org/10.3390/pr11030688>
- Okazaki, Y., Nguyen, T., Nishihara, A., Endo, H., Ogata, H., Nakano, S., & Tamaki, H. (2023). A fast and easy method to co-extract DNA and RNA from an environmental microbial sample. *Microbes and Environments*, 38(1). <https://doi.org/10.1264/jsme2.me22102>
- Othman, M., Ariff, A. B., Rios-Solis, L., & Halim, M. (2017). Extractive fermentation of lactic acid in lactic acid bacteria cultivation: A review. *Frontiers in Microbiology*, 8. <https://doi.org/10.3389/fmicb.2017.02285>
- Papaneophytou, C., Zervou, M.-E., & Theofanous, A. (2021). Optimization of a colorimetric assay to determine lactate dehydrogenase B activity using design of experiments. *SLAS Discovery*, 26(3), 383–399. <https://doi.org/10.1177/2472555220956589>
- Paremskaia, A. I., Kogan, A. A., Murashkina, A., Naumova, D. A., Satish, A., Abramov, I. S., Feoktistova, S. G., Mityaeva, O. N., Deviatkin, A. A., & Pavel Yu Volchkov. (2024). Codon-optimization in gene therapy: promises, prospects and challenges. *Frontiers in Bioengineering and Biotechnology*, 12. <https://doi.org/10.3389/fbioe.2024.1371596>
- Park, H. J., Bae, J. H., Ko, H. J., Lee, S. H., Sung, B. H., Han, J. I., & Sohn, J. H. (2018). Low-pH production of d-lactic acid using newly isolated acid tolerant yeast *Pichia kudriavzevii* NG7. *Biotechnology and Bioengineering*, 115(9), 2232–2242. <https://doi.org/10.1002/bit.26745>
- Payá, G., Bautista, V., Camacho, M., Esclapez, J., & Bonete, M.-J. (2023). Comprehensive bioinformatics analysis of the biodiversity of lsm proteins in the archaea domain. *Microorganisms*, 11(5), 1196. <https://doi.org/10.3390/microorganisms11051196>

- Pineda, J. R. E. T., Callender, R., & Schwartz, S. D. (2007). Ligand binding and protein dynamics in lactate dehydrogenase. *Biophysical Journal*, 93(5), 1474–1483. <https://doi.org/10.1529/biophysj.107.106146>
- Prielhofer, R., Barrero, J. J., Steuer, S., Gassler, T., Zahrl, R., Baumann, K., Sauer, M., Mattanovich, D., Gasser, B., & Marx, H. (2017). GoldenPiCS: a golden gate-derived modular cloning system for applied synthetic biology in the yeast *Pichia pastoris*. *BMC Systems Biology*, 11(1). <https://doi.org/10.1186/s12918-017-0492-3>
- Rawoof, S. A. A., Kumar, P. S., Vo, D.-V. N., Devaraj, K., Mani, Y., Devaraj, T., & Subramanian, S. (2020). Production of optically pure lactic acid by microbial fermentation: a review. *Environmental Chemistry Letters*, 19(1), 539–556. <https://doi.org/10.1007/s10311-020-01083-w>
- Robergs, R., Nalos, M., Kelbich, P., Jizerová, A., Mervartová, I., Vostrý, M., Štengl, M., & Babuška, V. (2026). D- and L-lactate dehydrogenase reactions increase pH to lactate production and decrease pH to pyruvate production. *Frontiers in Molecular Biosciences*, 13. <https://doi.org/10.3389/fmolb.2026.1715499>
- Roche, D. B., & McGuffin, L. J. (2016). In silico identification and characterization of protein-ligand binding sites. *Methods in Molecular Biology (Clifton, N.J.)*, 1414, 1–21. https://doi.org/10.1007/978-1-4939-3569-7_1
- Roche, J., Girard, E., Mas, C., & Madern, D. (2019). The archaeal LDH-like malate dehydrogenase from *Ignicoccus islandicus* displays dual substrate recognition, hidden allostery and a non-canonical tetrameric oligomeric organization. *Journal of Structural Biology*, 208(1), 7–17. <https://doi.org/10.1016/j.jsb.2019.07.006>
- Rodwell, V. W., Bender, D., Botham, K. M., Kennelly, P. J., & P. Anthony Weil. (2018). *Harper's illustrated biochemistry thirty-first edition*. McGraw Hill Professional.
- Seddik, H. A., Bendali, F., Gancel, F., Fliss, I., Spano, G., & Drider, D. (2017). *Lactobacillus plantarum* and its probiotic and food potentialities. *Probiotics and Antimicrobial Proteins*, 9(2), 111–122. <https://doi.org/10.1007/s12602-017-9264-z>
- Siegumfeldt, H., Rechinger, K. B., & Jakobsen, M. (2000). Dynamic changes of intracellular pH in individual lactic acid bacterium cells in response to a rapid drop in extracellular pH. *Applied and Environmental Microbiology*, 66(6), 2330–2335. <https://doi.org/10.1128/aem.66.6.2330-2335.2000>
- Smirnov, K., Weiss, F., Hatzl, A.-M., Rieder, L., Olesen, K., Jensen, S., & Glieder, A. (2024). Comparison of CRISPR-MAD7 and CRISPR-Cas9 for gene disruptions in *Komagataella phaffii*. *Fungal Genomics, Genetics and Molecular Biology*, 10(3), 197. <https://doi.org/10.3390/jof10030197>

- Song, B., Yang, S., Hwang, G.-H., Yu, J., & Bae, S. (2021). Analysis of NHEJ-Based DNA repair after CRISPR-Mediated DNA cleavage. *International Journal of Molecular Sciences*, 22(12), 6397. <https://doi.org/10.3390/ijms22126397>
- Sophian, A. (2021). Short communication: Analysis of purity and concentration of extracted DNA on salted fish processed food products. *Asian Journal of Natural Product Biochemistry*, 19(1). <https://doi.org/10.13057/biofar/f190104>
- Studer, G., Rempfer, C., Waterhouse, A. M., Gumienny, R., Haas, J., & Schwede, T. (2019). QMEANDisCo – distance constraints applied on model quality estimation. *Bioinformatics*, 36(6). <https://doi.org/10.1093/bioinformatics/btz828>
- Suzuki, K., Maeda, S., & Morokuma, K. (2019). Roles of closed- and open-loop conformations in large-scale structural transitions of l-lactate dehydrogenase. *ACS Omega*, 4(1), 1178–1184. <https://doi.org/10.1021/acsomega.8b02813>
- Taguchi, H., & Ohta, T. (1991). D-lactate dehydrogenase is a member of the D-isomer-specific 2-hydroxyacid dehydrogenase family. cloning, sequencing, and expression in Escherichia coli of the D-lactate dehydrogenase gene of *Lactobacillus plantarum*. *Journal of Biological Chemistry*, 266(19), 12588–12594. [https://doi.org/10.1016/s0021-9258\(18\)98939-8](https://doi.org/10.1016/s0021-9258(18)98939-8)
- Thomson, J. M., Gaucher, E. A., Burgan, M. F., De Kee, D. W., Li, T., Aris, J. P., & Benner, S. A. (2005). Resurrecting ancestral alcohol dehydrogenases from yeast. *Nature Genetics*, 37(6), 630–635. <https://doi.org/10.1038/ng1553>
- Thøgersen, J., Madzharova, F., Weidner, T., & Jensen, F. (2024). Aqueous pyruvate partly dissociates under deep ultraviolet irradiation but is resilient to near ultraviolet excitation. *Nature Communications*, 15(1). <https://doi.org/10.1038/s41467-024-46309-5>
- Tokmakov, A. A., Kurotani, A., & Sato, K.-I. (2021). Protein pl and intracellular localization. *Frontiers in Molecular Biosciences*, 8(775736). <https://doi.org/10.3389/fmolb.2021.775736>
- Tsaruk, A., Filip, K., Sibirny, A., & Ruchala, J. (2025). Native and recombinant yeast producers of lactic acid: Characteristics and perspectives. *International Journal of Molecular Sciences*, 26(5), 2007–2007. <https://doi.org/10.3390/ijms26052007>
- Tsuge, Y., & Yamaguchi, A. (2021). Physiological characteristics of *Corynebacterium glutamicum* as a cell factory under anaerobic conditions. *Applied Microbiology and Biotechnology*, 105(16–17), 6173–6181. <https://doi.org/10.1007/s00253-021-11474-w>
- Valvona, C. J., Fillmore, H. L., Nunn, P. B., & Pilkington, G. J. (2015). The regulation and function of lactate dehydrogenase A: Therapeutic potential in brain tumor. *Brain Pathology*, 26(1), 3–17. <https://doi.org/10.1111/bpa.12299>
- Wang, J., Chitsaz, F., Derbyshire, M. K., Gonzales, N. R., Gwadz, M., Lu, S., Marchler, G. H., Song, J., Thanki, N., Yamashita, R. A., Yang, M., Zhang, D., Zheng, C., Lanczycki, C. J., & Marchler-Bauer,

- A. (2022). The conserved domain database in 2023. *Nucleic Acids Res.*, 51(D1), D384–D388. <https://doi.org/10.1093/nar/gkac1096>
- Wang, Y., Li, R., Zhao, F., Wang, S., Zhang, Y., Fan, D., & Han, S. (2024). Metabolic engineering of *Komagataella phaffii* for the efficient utilization of methanol. *Microbial Cell Factories*, 23(1). <https://doi.org/10.1186/s12934-024-02475-1>
- Wang, Y., Wang, Y., Cui, J., Wu, C., Yu, B., & Wang, L. (2025). Non-conventional yeasts: promising cell factories for organic acid bioproduction. *Trends in Biotechnology*. <https://doi.org/10.1016/j.tibtech.2024.12.004>
- Wang, Y., Wu, J., Lv, M., Shao, Z., Hungwe, M., Wang, J., Bai, X., Xie, J., Wang, Y., & Geng, W. (2021). Metabolism characteristics of lactic acid bacteria and the expanding applications in food industry. *Frontiers in Bioengineering and Biotechnology*, 9(612285). <https://doi.org/10.3389/fbioe.2021.612285>
- Waterhouse, A., Bertoni, M., Bienert, S., Studer, G., Tauriello, G., Gumienny, R., Heer, F. T., de Beer, T. A. P., Rempfer, C., Bordoli, L., Lepore, R., & Schwede, T. (2018). SWISS-MODEL: homology modelling of protein structures and complexes. *Nucleic Acids Research*, 46(W1), W296–W303. <https://academic.oup.com/nar/article/46/W1/W296/5000024>
- Wu, J., Nuyt, A., Iwaki, M., Miki, S., & Asano, Y. (2025). Study on the asymmetric synthesis of chiral 3,3,3-trifluoro-2-hydroxypropanoic acids by lactate dehydrogenase. *ChemBioChem*, 26(11), e202500047–e202500047. <https://doi.org/10.1002/cbic.202500047>
- Xu, H., Xiao, T., Chen, C.-H., Li, W., Meyer, C. A., Wu, Q., Wu, D., Cong, L., Zhang, F., Liu, J. S., Brown, M., & Liu, X. S. (2015). Sequence determinants of improved CRISPR sgRNA design. *Genome Research*, 25(8), 1147–1157. <https://doi.org/10.1101/gr.191452.115>
- Xu, Q., Bai, C., Liu, Y., Song, L., Tian, L., Yan, Y., Zhou, J., Zhou, X., Zhang, Y., & Cai, M. (2019). Modulation of acetate utilization in *Komagataella phaffii* by metabolic engineering of tolerance and metabolism. *Biotechnology for Biofuels*, 12(1). <https://doi.org/10.1186/s13068-019-1404-0>
- Yamada, R., Ogura, K., Kimoto, Y., & Ogino, H. (2019). Toward the construction of a technology platform for chemicals production from methanol: d-lactic acid production from methanol by an engineered yeast *Pichia pastoris*. *World Journal of Microbiology and Biotechnology*, 35(2). <https://doi.org/10.1007/s11274-019-2610-4>
- Zavec, D., Troyer, C., Maresch, D., Altmann, F., Hann, S., Gasser, B., & Mattanovich, D. (2021). Beyond alcohol oxidase: The methylotrophic yeast *Komagataella phaffii* utilizes methanol also with its native alcohol dehydrogenase *Adh2*. *FEMS Yeast Research*, 21(2). <https://doi.org/10.1093/femsyr/foab009>

Zhang, Y., Vadhvani, P. V., Kumar, A., Hardwidge, P. R., Govind, R., Tanaka, T., & Kondo, A. (2015). Enhanced D-lactic acid production from renewable resources using engineered *Lactobacillus plantarum*. *Applied Microbiology and Biotechnology*, 100(1), 279–288. <https://doi.org/10.1007/s00253-015-7016-0>