

## DAFTAR PUSTAKA

- Abramson, J., Adler, J., Dunger, J., Evans, R., Green, T., Pritzel, A., ... & Jumper, J. M. (2024). Accurate structure prediction of biomolecular interactions with AlphaFold 3. *Nature*, *630*(8016), 493-500.
- Agustriana, E., Nuryana, I., Laksmi, F. A., Dewi, K. S., Wijaya, H., Rahmani, N., & Cameliawati Djohan, A. (2023). Optimized expression of large fragment DNA polimerase I from *Geobacillus stearothermophilus* in *Escherichia coli* expression system. *Preparative Biochemistry & Biotechnology*, *53*(4), 384-393.
- Akdel, M., Pires, D. E., Pardo, E. P., Jänes, J., Zalevsky, A. O., Mészáros, B., ... & Beltrao, P. (2022). A structural biology community assessment of AlphaFold2 applications. *Nature Structural & Molecular Biology*, *29*(11), 1056-1067.
- Ali, S. F., Rashid, N., Imanaka, T., & Akhtar, M. (2011). Family B DNA polimerase from a hyperthermophilic archaeon *Pyrobaculum calidifontis*: cloning, characterization and PCR application. *Journal of bioscience and bioengineering*, *112*(2), 118-123.
- Ausili, A., Cobucci-Ponzano, B., Di Lauro, B., D'Avino, R., Scirè, A., Rossi, M., ... & Moracci, M. (2006). Structural basis of the destabilization produced by an amino-terminal tag in the  $\beta$ -glycosidase from the hyperthermophilic archeon *Sulfolobus solfataricus*. *Biochimie*, *88*(7), 807-817.
- Baranovskiy, A. G., Lisova, A. E., Morstadt, L. M., Babayeva, N. D., & Tahirov, T. H. (2022). Insight into RNA–DNA primer length counting by human primosome. *Nucleic acids research*, *50*(11), 6264-6270.
- Bauer, R. J., Begley, M. T., & Trakselis, M. A. (2012). Kinetics and fidelity of polymerization by DNA polimerase III from *Sulfolobus solfataricus*. *Biochemistry*, *51*(9), 1996-2007.
- Bhatwa, A., Wang, W., Hassan, Y. I., Abraham, N., Li, X. Z., & Zhou, T. (2021). Challenges associated with the formation of recombinant protein inclusion bodies in *Escherichia coli* and strategies to address them for industrial applications. *Frontiers in bioengineering and*

*biotechnology*, 9, 630551.

- Bębenek, A., & Ziuzia-Graczyk, I. (2018). Fidelity of DNA replication—a matter of proofreading. *Current genetics*, 64(5), 985-996.
- Bedi, A. K., Sharma, M., & Sharma, S. (2025). Immuno-PCR: Advancements, and applications for infectious diseases diagnosis. *Clinica Chimica Acta*, 120409.
- Benedikter, B. J., Bouwman, F. G., Vajen, T., Heinzmann, A. C., Grauls, G., Mariman, E. C., ... & Stassen, F. R. (2017). Ultrafiltration combined with size exclusion chromatography efficiently isolates extracellular vesicles from cell culture media for compositional and functional studies. *Scientific reports*, 7(1), 15297.
- Bergkessel, M., & Guthrie, C. (2013). Colony PCR. In *Methods in enzymology* (Vol. 529, pp. 299-309). Academic Press.
- Beygmoradi, A., Homaei, A., Hemmati, R., & Fernandes, P. (2023). Recombinant protein expression: challenges in production and folding related matters. *International journal of biological macromolecules*, 233, 123407.
- Bhatwa, A., Wang, W., Hassan, Y. I., Abraham, N., Li, X. Z., & Zhou, T. (2021). Challenges associated with the formation of recombinant protein inclusion bodies in *Escherichia coli* and strategies to address them for industrial applications. *Frontiers in bioengineering and biotechnology*, 9, 630551.
- Böhlke, K., Pisani, F. M., Vorgias, C. E., Frey, B., Sobek, H., Rossi, M., & Antranikian, G. (2000). PCR performance of the B-type DNA polymerase from the thermophilic euryarchaeon *Thermococcus aggregans* improved by mutations in the Y-GG/A motif. *Nucleic Acids Research*, 28(20), 3910- 3917.
- Brenkman, A. B., Heideman, M. R., Truniger, V., Salas, M., & van der Vliet, P.C. (2001). The (I/Y) XGG motif of adenovirus DNA polymerase affects template DNA binding and the transition from initiation to elongation. *Journal of Biological Chemistry*, 276(32), 29846-29853.
- Cha, R. S., & Thilly, W. G. (1993). Specificity, efficiency, and fidelity of PCR. *Genome Research*, 3(3), S18-S29.

- Ceylan, H. K. (2023). Enhanced biomass production of recombinant pfu DNA polymerase producer *Escherichia coli* BL21 (DE3) by optimization of induction variables using response surface methodology. *The Protein Journal*, 42(4), 451-462.
- Chang, C., Luo, C. L., Eleraky, S., Lin, A., Zhou, G., & Gao, Y. (2023). Primer terminal ribonucleotide alters the active site dynamics of DNA polymerase  $\eta$  and reduces DNA synthesis fidelity. *Journal of Biological Chemistry*, 299(3).
- Chan, R. C. H., Lam, S. S. W., Fong, F. L. Y., Chan, D. T. W., Lee, F. W. F., & Sze, E. T. P. (2018). Optimization of protein extraction and two-dimensional gel electrophoresis profiles for the identification of *Cordyceps sinensis* and other similar species. *Plos one*, 13(8), e0202779.
- Chen, Y., Li, Q., Yang, J., & Xie, H. (2017). Promoting tag removal of a MBP- fused integral membrane protein by TEV protease. *Applied biochemistry and biotechnology*, 181(3), 939-947.
- Cho, S. S., Kim, K. P., Lee, K. K., Youn, M. H., & Kwon, S. T. (2012). Characterization and PCR application of a new high-fidelity DNA polymerase from *Thermococcus waiotapuensis*. *Enzyme and Microbial Technology*, 51(6-7), 334-341.
- Daimon, K., Ishino, S., Imai, N., Nagumo, S., Yamagami, T., Matsukawa, H., & Ishino, Y. (2018). Two family B DNA polymerases from *Aeropyrum pernix*, based on revised translational frames. *Frontiers in Molecular Biosciences*, 5, 37.
- de Marco, A., Deuerling, E., Mogk, A., Tomoyasu, T., & Bukau, B. (2007). Chaperone-based procedure to increase yields of soluble recombinant proteins produced in *E. coli*. *BMC biotechnology*, 7(1), 32.
- Del Prado, A., Rodríguez, I., Lázaro, J. M., Moreno-Morcillo, M., de Vega, M., & Salas, M. (2019). New insights into the coordination between the polymerization and 3'-5' exonuclease activities in  $\phi$ 29 DNA polymerase. *Scientific Reports*, 9(1), 923.
- Desai, D., Kantliwala, S. V., Vybhavi, J., Ravi, R., Patel, H., & Patel, J. (2024). Review of AlphaFold 3: transformative advances in drug design and therapeutics. *Cureus*, 16(7), e63646.

- Din, R. U., Khan, M. I., Jan, A., Khan, S. A., & Ali, I. (2020). A novel approach for high-level expression and purification of GST-fused highly thermostable Taq DNA polimerase in *Escherichia coli*. *Archives of Microbiology*, 202(6), 1449-1458.
- Du, Y., Wang, M., Sun, C. C., & Yu, H. (2022). Construction of an ultra-strong PtacM promoter via engineering the core-element spacer and 5' untranslated region for versatile applications in *Corynebacterium glutamicum*. *Biotechnology Notes*, 3, 88-96.
- Einsfeldt, K., Júnior, J. B. S., Argondizzo, A. P. C., Medeiros, M. A., Alves, T. L. M., Almeida, R. V., & Larentis, A. L. (2011). Cloning and expression of protease ClpP from *Streptococcus pneumoniae* in *Escherichia coli*: study of the influence of kanamycin and IPTG concentration on cell growth, recombinant protein production and plasmid stability. *Vaccine*, 29(41), 7136-7143.
- Eisenbrandt, R., Lázaro, J. M., Salas, M., & Vega, M. D. (2002).  $\Phi$ 29 DNA polimerase residues Tyr59, His61 and Phe69 of the highly conserved ExoII motif are essential for interaction with the terminal protein. *Nucleic acids research*, 30(6), 1379-1386.
- Eliseev, R., Alexandrov, A., & Gunter, T. (2004). High-yield expression and purification of p18 form of Bax as an MBP-fusion protein. *Protein expression and purification*, 35(2), 206-209.
- Elleuche, S., Schröder, C., Sahm, K., & Antranikian, G. (2014). Extremozymes—biocatalysts with unique properties from extremophilic microorganisms. *Current opinion in biotechnology*, 29, 116-123.
- Fan, Q., Neubauer, P., & Gimpel, M. (2021). Production of soluble regulatory hydrogenase from *Ralstonia eutropha* in *Escherichia coli* using a fed-batch-based autoinduction system. *Microbial Cell Factories*, 20(1), 201.
- Farrar, J. S., & Wittwer, C. T. (2015). Extreme PCR: efficient and specific DNA amplification in 15–60 seconds. *Clinical chemistry*, 61(1), 145-153.
- Feng, X., Liu, X., Xu, R., Zhao, R., Feng, W., Liao, J., ... & She, Q. (2020). A unique B-Family DNA polymerase facilitating error-prone DNA damage tolerance in crenarchaeota. *Frontiers in microbiology*, 11,

1585.

- Feng, X., Zhang, B., Gao, Z., Xu, R., Liu, X., Ishino, S., ... & She, Q. (2022). A well-conserved archaeal B-family polymerase functions as an extender in translesion synthesis. *Mbio*, *13*(1), e02659-21.
- Fernández-Rhodes, M., Adlou, B., Williams, S., Lees, R., Peacock, B., Aubert, D., & Davies, O. G. (2023). Defining the influence of size-exclusion chromatography fraction window and ultrafiltration column choice on extracellular vesicle recovery in a skeletal muscle model. *Journal of Extracellular Biology*, *2*(4), e85.
- Finn, Robert D., Teresa K. Attwood, Patricia C. Babbitt, Alex Bateman, Peer Bork, Alan J. Bridge, Hsin-Yu Chang et al. "InterPro in 2017—beyond protein family and domain annotations." *Nucleic acids research* 45, no. D1 (2017): D190-D199.
- Francis, D. M., & Page, R. (2010). Strategies to optimize protein expression in *E. coli*. *Current protocols in protein science*, *61*(1), 5-24.
- Freudenthal, B. D., Beard, W. A., & Wilson, S. H. (2012). Structures of dNTP intermediate states during DNA polymerase active site assembly. *Structure*, *20*(11), 1829-1837.
- Froger, A., & Hall, J. E. (2007). Transformation of plasmid DNA into *E. coli* using the heat shock method. *Journal of Visualized Experiments (JoVE)*, (6), e253.
- Fronza, F., Verardo, R., & Schneider, C. (2025). A streamlined tandem affinity purification of His-MBP-SpyCas9, without buffer exchange, suitable for in vitro cleavage applications. *MethodsX*, 103368.
- Gasteiger, E., Hoogland, C., Gattiker, A., Duvaud, S. E., Wilkins, M. R., Appel, R. D., & Bairoch, A. (2005). Protein identification and analysis tools on the ExpASY server. In *The proteomics protocols handbook* (pp. 571-607). Totowa, NJ: Humana press.
- Gong, P., Lei, P., Wang, S., Zeng, A., & Lou, H. (2020). Post-translational modifications aid archaeal survival. *Biomolecules*, *10*(4), 584.
- Gong, S., Kirmizialtin, S., Chang, A., Mayfield, J. E., Zhang, Y. J., & Johnson, K.A. (2021). Kinetic and thermodynamic analysis defines roles for two

- metal ions in DNA polymerase specificity and catalysis. *Journal of Biological Chemistry*, 296.
- Goyon, A., Tang, S., Fekete, S., Nguyen, D., Hofmann, K., Wang, S., ... & Zhang, K. (2023). Separation of plasmid DNA topological forms, messenger RNA, and lipid nanoparticle aggregates using an ultrawide pore size exclusion chromatography column. *Analytical Chemistry*, 95(40), 15017-15024.
- Greenough, L., Menin, J. F., Desai, N. S., Kelman, Z., & Gardner, A. F. (2014). Characterization of family D DNA polymerase from *Thermococcus* sp. 9N. *Extremophiles*, 18(4), 653-664.
- Guo, H. B., Perminov, A., Bekele, S., Kedziora, G., Farajollahi, S., Varaljay, V., ... & Berry, R. (2022). AlphaFold2 models indicate that protein sequence determines both structure and dynamics. *Scientific reports*, 12(1), 10696.
- Güssow, D., & Clackson, T. (1989). Direct clone characterization from plaques and colonies by the polymerase chain reaction. *Nucleic acids research*, 17(10), 4000.
- Han, P., Fan, H., & Tong, Y. (2023). Identifikasi DNA polimerase keluarga B baru dari *Enterococcus* phage IME199 dan produksi berlebihnya di *Escherichia coli* BL21 (DE3). *Pabrik Sel Mikroba*, 22 (1), 217.
- Harmalkar, A., Lyskov, S., & Gray, J. J. (2025). Reliable protein-protein docking with AlphaFold, Rosetta, and replica exchange. *Elife*, 13, RP94029.
- Harper, S., & Speicher, D. W. (2010). Purification of proteins fused to glutathione S-transferase. In *Protein chromatography: Methods and protocols* (pp. 259-280). Totowa, NJ: Humana Press.
- HEA-JIN, S. H. I. N., JIN, C. J., SUK-HOON, K. O. H., & SUK-TAE, K. W. O. N. (2005). Cloning, expression, and characterization of a family B-type DNA polymerase from the hyperthermophilic crenarchaeon *Pyrobaculum arsenaticum* and its application to PCR. *Journal of microbiology and biotechnology*, 15(6), 1359-1367.
- Hillis, D. M., & Bull, J. J. (1993). An empirical test of bootstrapping as a method for assessing confidence in phylogenetic analysis. *Systematic biology*, 42(2), 182-192.

- Hu, Y., An, Y., Fang, N., Li, Y., Jin, H., Nazarali, A., & Ji, S. (2015). The optimization of soluble PTEN expression in escherichia coli. *The Open Biochemistry Journal*, 9, 42.
- Hao, L., Zhang, Z. G., Shi, Z. D., Pang, K., Zhang, J. J., Dong, Y., & Han, C. H. (2015). Optimization Studies on Prokaryotic Cell Expression of the Human Tumor Necrosis Factor-Related Apoptosis-Inducing Ligand (TRAIL). *Cell biochemistry and biophysics*, 73(2), 275-279.
- Hussain, A., & Brooks III, C. L. (2024). Guiding discovery of protein sequence-structure-function modeling. *Bioinformatics*, 40(1), btae002.
- İncir, İ., & Kaplan, Ö. (2024). *Escherichia coli* as a versatile cell factory: Advances and challenges in recombinant protein production. *Protein Expression and Purification*, 219, 106463.
- Iwai, T., Kurosawa, N., Itoh, Y. H., Kimura, N., & Horiuchi, T. (2000). Sequence analysis of three family B DNA polymerases from the thermoacidophilic crenarchaeon *Sulfurisphaera ohwakuensis*. *DNA research*, 7(4), 243-251.
- Johnson, K. A. (2010). The kinetic and chemical mechanism of high-fidelity DNA polymerases. *Biochimica et Biophysica Acta (BBA)-Proteins and Proteomics*, 1804(5), 1041-1048.
- Jumper, J., Evans, R., Pritzel, A., Green, T., Figurnov, M., Ronneberger, O., ... & Hassabis, D. (2021). Highly accurate protein structure prediction with AlphaFold. *nature*, 596(7873), 583-589.
- Kähler, M., & Antranikian, G. (2000). Cloning and characterization of a family B DNA polymerase from the hyperthermophilic crenarchaeon *Pyrobaculum islandicum*. *Journal of Bacteriology*, 182(3), 655-663.
- Kakui, Y., Sunaga, T., Arai, K., Dodgson, J., Ji, L., Csikász-Nagy, A., ... & Sato, M. (2015). Module-based construction of plasmids for chromosomal integration of the fission yeast *Schizosaccharomyces pombe*. *Open Biology*, 5(6), 150054.
- Kaur, J., Kumar, A., & Kaur, J. (2018). Strategies for optimization of heterologous protein expression in *E. coli*: Roadblocks and reinforcements. *International journal of biological macromolecules*, 106, 803-822.
- Kazlauskas, D., Krupovic, M., Guglielmini, J., Forterre, P., & Venclovas, Č.

- (2020). Diversity and evolution of B-family DNA polymerases. *Nucleic acids research*, 48(18), 10142-10156.
- Kim, S., Jeong, H., Kim, E. Y., Kim, J. F., Lee, S. Y., & Yoon, S. H. (2018). Genomic and transcriptomic landscape of *Escherichia coli* BL21 (DE3). *Nucleic acids research*, 45(9), 5285-5293.
- Kim, H. J., Lee, J. H., Lee, K. B., Shin, J. W., Kwon, M. A., Lee, S., & Kim, I. G. (2021). Transglutaminase 2 crosslinks the glutathione S-transferase tag, impeding protein-protein interactions of the fused protein. *Experimental & molecular medicine*, 53(1), 115-124.
- Kobashigawa, Y., Namikawa, M., Sekiguchi, M., Inada, Y., Yamauchi, S., Kimoto, Y., & Morioka, H. (2021). Expression, purification and characterization of CAR/NCOA-1 tethered protein in *E. coli* using maltose-binding protein fusion tag and gelatinized corn starch. *Biological and Pharmaceutical Bulletin*, 44(1), 125-130.
- Kozlowski, L. P. (2022). Proteome-pI 2.0: proteome isoelectric point database update. *Nucleic acids research*, 50(D1), D1535-D1540.
- Kunkel, T. A., & Erie, D. A. (2015). Eukaryotic mismatch repair in relation to DNA replication. *Annual review of genetics*, 49(1), 291-313.
- Kurniasari, H., Noviannisa, F. A., Dzakiyyah, S. A., Zahrani, M., Habibi, M. R., Fauzia, K. A., & Alfaray, R. I. (2023). *Helicobacter pylori* Strain 26695 versus J99: Analysis on the Protein Structure and Physicochemical Characteristics. *Biomolecular and Health Science Journal*, 6(1), 20-24.
- Kuri, P. R., & Goswami, P. (2024). Unravelling aggregation propensity of rotavirus A VP6 expressed as *E. coli* inclusion bodies through in silico prediction. *Scientific Reports*, 14(1), 21464.
- Kazlauskas, D., Krupovic, M., Guglielmini, J., Forterre, P., & Venclovas, Č. (2020). Diversity and evolution of B-family DNA polymerases. *Nucleic acids research*, 48(18), 10142-10156.
- Kumar, S., Tsai, C. J., & Nussinov, R. (2000). Factors enhancing protein thermostability. *Protein engineering*, 13(3), 179-191.
- Kuznetsova, A. A., & Kuznetsov, N. A. (2023). Direct Enzyme Engineering of B Family DNA Polymerases for Biotechnological Approaches.

*Bioengineering*, 10(10), 1150.

- Kuznetsova, AA, Bedritskikh, KS, Bulygin, AA, & Kuznetsov, NA (2023). Kloning, Ekspresi, dan Karakterisasi Polimerase DNA Keluarga A dari *Massilia aurea*. *Fermentasi*, 9 (7), 650.
- Laemmli, U. K. (1970). Cleavage of structural proteins during the assembly of the head of bacteriophage T4. *nature*, 227(5259), 680-685.
- Laksmi, F. A., Dewi, K. S., Nuryana, I., Yulianti, S. E., Ramadhan, K. P., Hadi, M. I., & Nugraha, Y. (2024). High-level expression of codon-optimized Taq DNA polimerase under the control of rhaBAD promoter. *Analytical Biochemistry*, 692, 115581.
- Laskowski, R. A., MacArthur, M. W., Moss, D. S., & Thornton, J. M. (1993). PROCHECK: a program to check the stereochemical quality of protein structures. *Applied Crystallography*, 26(2), 283-291.
- Lee, H. R., Helquist, S. A., Kool, E. T., & Johnson, K. A. (2008). Importance of hydrogen bonding for efficiency and specificity of the human mitochondrial DNA polimerase. *Journal of Biological Chemistry*, 283(21), 14402-14410.
- Lee, J., Jeong, S., Ye, Y., Chen, V., Vigneswaran, S., Leiknes, T., & Liu, Z. (2017). Protein fouling in carbon nanotubes enhanced ultrafiltration membrane: fouling mechanism as a function of pH and ionic strength. *Separation and Purification Technology*, 176, 323-334.
- Lee, J. I., Kim, Y. J., Bae, H., Cho, S. S., Lee, J. H., & Kwon, S. T. (2010). Biochemical properties and PCR performance of a family B DNA polimerase from hyperthermophilic euryarchaeon *Thermococcus peptonophilus*. *Applied biochemistry and biotechnology*, 160(6), 1585-1599.
- Levy, M. S., Lotfian, P., O’Kennedy, R., Lo-Yim, M. Y., & Shamlou, P. A. (2000). Quantitation of supercoiled circular content in plasmid DNA solutions using a fluorescence-based method. *Nucleic Acids Research*, 28(12), e57-e57.
- Li, L., Li, H., Tian, Q., Ge, B., Xu, X., Chi, Y., ... & Zhou, Y. (2022). Expression

and purification of soluble recombinant  $\beta$ -lactamases using *Escherichia coli* as expression host and pET-28a as cloning vector. *Microbial Cell Factories*, 21(1), 244.

- Liu, B., Li, G., Sui, X., Yin, J., Wang, H., & Ren, X. (2009). Expression and functional analysis of porcine aminopeptidase N produced in prokaryotic expression system. *Journal of biotechnology*, 141(1-2), 91-96.
- Li, X., Jin, J., Guo, Z., & Liu, L. (2022). Evolution of plasmid- construction. *International Journal of Biological Macromolecules*, 209, 1319-1326.
- Lobb, R. J., Becker, M., Wen Wen, S., Wong, C. S., Wiegmans, A. P., Leimgruber, A., & Möller, A. (2015). Optimized exosome isolation protocol for cell culture supernatant and human plasma. *Journal of extracellular vesicles*, 4(1), 27031.
- Luis, I. M., Alexandre, B. M., Oliveira, M. M., & Abreu, I. A. (2016). Selection of an appropriate protein extraction method to study the phosphoproteome of maize photosynthetic tissue. *PloS one*, 11(10), e0164387.
- Makarova, K. S., Krupovic, M., & Koonin, E. V. (2014). Evolution of replicative DNA polymerases in archaea and their contributions to the eukaryotic replication machinery. *Frontiers in microbiology*, 5, 354.
- McInerney, P., Adams, P., & Hadi, M. Z. (2014). Error rate comparison during polymerase chain reaction by DNA polymerase. *Molecular biology international*, 2014(1), 287430.
- Menacho-Melgar, Romel, Zhixia Ye, Eirik A. Moreb, Tian Yang, John P. Efromson, John S. Decker, and Michael D. Lynch. "Improved, scalable, two-stage, autoinduction of recombinant protein expression in *E. coli* utilizing phosphate depletion." *bioRxiv* (2019): 820787.
- Miyabayashi, H., Sakai, H. D., & Kurosawa, N. (2021). DNA polymerase B1 binding protein 1 is important for DNA repair by holoenzyme PolB1 in the extremely thermophilic crenarchaeon *Sulfolobus acidocaldarius*. *Microorganisms*, 9(2), 439.
- Morra, R., Shankar, J., Robinson, C. J., Halliwell, S., Butler, L., Upton, M., ... & Dixon, N. (2016). Dual transcriptional-translational cascade permits cellular level tuneable expression control. *Nucleic acids research*,

44(3), e21-e21.

- Murat, P., GuiLbaud, G., & Sale, J. E. (2020). DNA polymerase stalling at structured DNA constrains the expansion of short tandem repeats. *Genome biology*, 21(1), 209.
- Nguyen, M. T., Krupa, M., Koo, B. K., Song, J. A., Vu, T. T. T., Do, B. H., & Choe, H. (2016). Prokaryotic soluble overexpression and purification of human VEGF165 by fusion to a maltose binding protein tag. *PloS one*, 11(5), e0156296.
- Nguyen, M. T., Heo, Y., Do, B. H., Baek, S., Kim, C. J., Jang, Y. J., & Choe, H. (2020). Bacterial overexpression and purification of soluble recombinant human serum albumin using maltose-binding protein and protein disulphide isomerase. *Protein Expression and Purification*, 167, 105530.
- Nuryana, I., Laksmi, FA, Dewi, KS, Akbar, FR, & Harmoko, R. (2023). Optimalisasi kodon gen yang mengkode DNA polimerase dari *Pyrococcus furiosus* dan ekspresinya pada *Escherichia coli*. *Jurnal Rekayasa Genetika dan Bioteknologi*, 21 (1), 129.
- Opendenstein, P., Clodt, J. I., Müschen, C. R., Filiz, V., & Buyel, J. F. (2019). A combined ultrafiltration/diafiltration step facilitates the purification of cyanovirin-N from transgenic tobacco extracts. *Frontiers in bioengineering and biotechnology*, 6, 206.
- Qing, R., Hao, S., Smorodina, E., Jin, D., Zalevsky, A., & Zhang, S. (2022). Protein design: From the aspect of water solubility and stability. *Chemical Reviews*, 122(18), 14085-14179.
- Paraskevopoulou, V., & Falcone, F. H. (2018). Polyionic tags as enhancers of protein solubility in recombinant protein expression. *Microorganisms*, 6(2), 47.
- Parida, P. P., Saraswathi, D., Mopidevi, S. M., & Raran-Kurussi, S. (2023). Advancing large-scale production of TEV protease through an innovative NT\* tag-based fusion construct. *Current Research in Structural Biology*, 6, 100106.
- Parkash, V., Kulkarni, Y., Bylund, G. O., Osterman, P., Kamerlin, S. C. L., &

- Johansson, E. (2023). A sensor complements the steric gate when DNA polymerase  $\epsilon$  discriminates ribonucleotides. *Nucleic Acids Research*, *51*(20), 11225-11238.
- Perdikari, T. M., Murthy, A. C., Ryan, V. H., Watters, S., Naik, M. T., & Fawzi, N. L. (2020). SARS-CoV-2 nucleocapsid protein phase-separates with RNA and with human hnRNPs. *The EMBO journal*, *39*(24), e106478.
- Ravitchandirane, G., Bandhu, S., & Chaudhuri, T. K. (2022). Multimodal approaches for the improvement of the cellular folding of a recombinant iron regulatory protein in *E. coli*. *Microbial Cell Factories*, *21*(1), 20.
- Ribeiro, C., Santos, E. T., Costa, L., Brazinha, C., Saraiva, P., & Crespo, J. G. (2022). Nannochloropsis sp. Biorefinery: recovery of soluble protein by membrane ultrafiltration/diafiltration. *Membranes*, *12*(4), 401.
- Rizki, W. O. S., Ratnaningsih, E., & Hertadi, R. (2025). Enhanced production of polyhydroxybutyrate in recombinant *Escherichia coli* for sustainable material. *Next Materials*, *9*, 101050.
- Rosano, G. L., & Ceccarelli, E. A. (2014). Recombinant protein expression in *Escherichia coli*: advances and challenges. *Frontiers in microbiology*, *5*, 172.
- Roske, J. J., & Yeeles, J. T. (2024). Structural basis for processive daughter-strand synthesis and proofreading by the human leading-strand DNA polymerase Pol  $\epsilon$ . *Nature Structural & Molecular Biology*, *31*(12), 1921-1931.
- Rasooli, F., & Hashemi, A. (2019). Efficient expression of EpEX in the cytoplasm of *Escherichia coli* using thioredoxin fusion protein. *Research in Pharmaceutical Sciences*, *14*(6), 554-565.
- Raran-Kurussi, S., Cherry, S., Zhang, D., & Waugh, D. S. (2017). Removal of affinity tags with TEV protease. In *Heterologous Gene Expression in E. coli: Methods and Protocols* (pp. 221-230). New York, NY: Springer New York.
- Raper, A. T., Reed, A. J., & Suo, Z. (2018). Kinetic mechanism of DNA polymerases: contributions of conformational dynamics and a third divalent metal ion. *Chemical reviews*, *118*(12), 6000-6025.
- Reuten, R., Nikodemus, D., Oliveira, M. B., Patel, T. R., Brachvogel, B., Breloy,

- I., ... & Koch, M. (2016). Maltose-binding protein (MBP), a secretion-enhancing tag for mammalian protein expression systems. *PloS one*, 11(3), e0152386.
- Robert, X., & Gouet, P. (2014). Deciphering key features in protein structures with the new ENDscript server. *Nucleic acids research*, 42(W1), W320-W324.
- Rogozin, I. B., Makarova, K. S., Pavlov, Y. I., & Koonin, E. V. (2008). A highly conserved family of inactivated archaeal B family DNA polymerases. *Biology Direct*, 3(1), 32.
- Rosano, G. L., & Ceccarelli, E. A. (2014). Recombinant protein expression in *Escherichia coli*: advances and challenges. *Frontiers in microbiology*, 5, 172.
- Rouches, M. V., Xu, Y., Cortes, L. B. G., & Lambert, G. (2022). A plasmid system with tunable copy number. *Nature communications*, 13(1), 3908.
- Rudinger, N. Z., Kranaster, R., & Marx, A. (2007). Hydrophobic amino acid and single-atom substitutions increase DNA polymerase selectivity. *Chemistry & biology*, 14(2), 185-194.
- Saghatelian, A., Panosyan, H., & Birkeland, N. K. (2021). The genus *Thermus*: A brief history of cosmopolitan extreme thermophiles: Diversity, distribution, biotechnological potential and applications. In *Microbial Communities and their Interactions in the Extreme Environment* (pp. 141-175). Singapore: Springer Singapore.
- Sakai, H. D., Nur, N., Suwanto, A., & Kurosawa, N. (2024). Complete genome sequence of strain KD-1T, the type strain of *Sulfurisphaera javensis*, isolated from an Indonesian hot spring. *Microbiology Resource Announcements*, 13(12), e00664-24.
- Samman, N., Al-Muhalhil, K., & Nehdi, A. (2023). A simple and efficient method for Taq DNA polymerase purification based on heat denaturation and affinity chromatography. *Journal of King Saud University-Science*, 35(3), 102565.
- Saraswat, M., Musante, L., Ravidá, A., Shortt, B., Byrne, B., & Holthofer, H. (2013). Preparative purification of recombinant proteins: current status

and future trends. *BioMed research international*, 2013(1), 312709.

- Shad, M., Liaqat, A., Nazir, A., Hussain, N., Yaqoob, K., Akhtar, M. W., & Sajjad, M. (2025). Exploration of Comprehensive Structural and Functional Potential of Recombinant Proteins Using Cutting-Edge Bioinformatics Tools. *Applied Biochemistry and Biotechnology*, 197(11), 7015-7043.
- Shendge, A. A., & D'Souza, J. S. (2022). Strategic optimization of conditions for the solubilization of GST-tagged amphipathic helix-containing ciliary proteins overexpressed as inclusion bodies in *E. coli*. *Microbial Cell Factories*, 21(1), 258.
- Shi, T., Zhang, L., Liang, M., Wang, W., Wang, K., Jiang, Y., ... & Tan, G. Y. (2021). Screening and engineering of high-activity promoter elements through transcriptomics and red fluorescent protein visualization in *Rhodobacter sphaeroides*. *Synthetic and Systems Biotechnology*, 6(4), 335- 342.
- Sievers, F., Wilm, A., Dineen, D., Gibson, T. J., Karplus, K., Li, W., ... & Higgins, D. G. (2011). Fast, scalable generation of high-quality protein multiple sequence alignments using Clustal Omega. *Molecular systems biology*, 7, 539.
- Silaban, S., Gaffar, S., Simorangkir, M., Maksum, I. P., & Subroto, T. (2018, December). Effect of IPTG concentration on recombinant human prethrombin-2 expression in *Escherichia coli* BL21 (DE3) ArcticExpress. In *IOP Conference Series: Earth and Environmental Science* (Vol. 217, No. 1, p. 012039). IOP Publishing.
- Simas, R. G., Pessoa Junior, A., & Long, P. F. (2023). Mechanistic aspects of IPTG (isopropylthio- $\beta$ -galactoside) transport across the cytoplasmic membrane of *Escherichia coli*—a rate limiting step in the induction of recombinant protein expression. *Journal of Industrial Microbiology and Biotechnology*, 50(1), kuad034.
- Singh, S. M., & Panda, A. K. (2005). Solubilization and refolding of bacterial inclusion body proteins. *Journal of bioscience and bioengineering*, 99(4), 303-310.
- Smith, M. A., & Bidochka, M. J. (1998). Bacterial fitness and plasmid loss: the importance of culture conditions and plasmid size. *Canadian journal of microbiology*, 44(4), 351-355.

- Subekti, D., Hidayat, S. H., & Damayanti, T. A. (2020). Quantitative polimerase chain reaction (Q-PCR) for detection of sugarcane streak mosaic virus. In *IOP conference series: earth and environmental science* (Vol. 418, No. 1, p. 012062). IOP Publishing.
- Taycher, E., Rolfs, A., Hu, Y., Zuo, D., Mohr, S. E., Williamson, J., & LaBaer, J. (2007). A novel approach to sequence validating protein expression clones with automated decision making. *BMC bioinformatics*, 8(1), 198.
- Taylor, S. C., Laperriere, G., & Germain, H. (2017). Droplet Digital PCR versus qPCR for gene expression analysis with low abundant targets: from variable nonsense to publication quality data. *Scientific reports*, 7(1), 2409.
- Tripathi, S., Srivastava, Y., Sangwan, R. S., & Sangwan, N. S. (2020). In silico mining and functional analysis of AP2/ERF gene in *Withania somnifera*. *Scientific reports*, 10(1), 4877.
- Tsuboi, K., Sakai, HD, Nur, N., Stedman, KM, Kurosawa, N., & Suwanto, A. (2018). *Sulfurisphaera javensis* sp. nov., archaeon hipertermofilik dan asidofilik yang diisolasi dari sumber air panas Indonesia, dan klasifikasi ulang *Sulfolobus tokodaii* Suzuki *et al.* 2002 sebagai sisir *Sulfurisphaera tokodaii*. November *Jurnal Internasional Mikrobiologi Sistematis dan Evolusioner* , 68 (6), 1907-1913.
- Vashishtha, A. K., Wang, J., & Konigsberg, W. H. (2016). Different divalent cations alter the kinetics and fidelity of DNA polimerases. *Journal of Biological Chemistry*, 291(40), 20869-20875.
- Veisi, K., Farajnia, S., Zarghami, N., Khorshid, H. R. K., Samadi, N., Khosroshahi, S. A., & Jaliani, H. Z. (2015). Chaperone-assisted soluble expression of a humanized anti-EGFR ScFv antibody in *E. Coli*. *Advanced pharmaceutical bulletin*, 5(Suppl 1), 621.
- Vera, A., González-MontaLbán, N., Arís, A., & Villaverde, A. (2007). The conformational quality of insoluble recombinant proteins is enhanced at low growth temperatures. *Biotechnology and bioengineering*, 96(6), 1101-1106.
- Vieira, D. D. S., Polveiro, R. C., Butler, T. J., Hackett, T. A., Braga, C. P., Puniya,

- B. L., ... & Feitosa, F. L. (2021). An in silico, structural, and biological analysis of lactoferrin of different mammals. *International journal of biological macromolecules*, 187, 119-126.
- Vieille, C., & Zeikus, G. J. (2001). Hyperthermophilic enzymes: sources, uses, and molecular mechanisms for thermostability. *Microbiology and molecular biology reviews*, 65(1), 1-43.
- Vu, T. T. T., Koo, B. K., Song, J. A., Chong, S. H., Park, C. R., Nguyen, M. T., & Choe, H. (2015). Soluble overexpression and purification of bioactive human CCL2 in *E. coli* by maltose-binding protein. *Molecular biology reports*, 42(3), 651-663.
- Wang, F., & Yang, W. (2009). Structural insight into translesion synthesis by DNA Pol II. *Cell*, 139(7), 1279-1289.
- Wang, M., Liu, J. K., Gao, T., Xu, L. L., Zhang, X. X., Nie, J. H., & Chen, H. X. (2022). A platform method for plasmid isoforms analysis by capillary gel electrophoresis. *Electrophoresis*, 43(11), 1174-1182.
- Wang, S., Wang, S., Shi, D., & Lv, R. (2025). Improving process robustness of cation exchange chromatography with cationic buffers for the reduction of aggregates. *Protein Expression and Purification*, 228, 106657.
- Wang, X., Gui, P., Li, X., Lu, F., Jing, W., Li, C., ... & Ma, F. (2025). A safety and absolute activity measurement method for Phi29 DNA polymerase based on chemiluminescent detection of dATP consumption. *Analytica Chimica Acta*, 1353, 343952.
- Wang, Y., Demir, B., Mohammad, H., Oren, E. E., & Anantram, M. P. (2023). Computational study of the role of counterions and solvent dielectric in determining the conductance of B-DNA. *Physical Review E*, 107(4), 044404.
- Wiederstein, M., & Sippl, M. J. (2007). ProSA-web: interactive web service for the recognition of errors in three-dimensional structures of proteins. *Nucleic acids research*, 35(suppl\_2), W407-W410.
- Yamashige, R., Kimoto, M., Takezawa, Y., Sato, A., Mitsui, T., Yokoyama, S., & Hirao, I. (2012). Highly specific unnatural base pair systems as a third base pair for PCR amplification. *Nucleic acids research*, 40(6), 2793-2806.

- Yılmaz, M., Ozic, C., & Gok, İ. (2012). Principles of nucleic acid separation by agarose gel electrophoresis. *Gel Electrophoresis–Principles and Basics*, 4, 33.
- Yoda, T., Tanabe, M., Tsuji, T., Yoda, T., Ishino, S., Shirai, T., & Nishida, H. (2017). Exonuclease processivity of archaeal replicative DNA polymerase in association with PCNA is expedited by mismatches in DNA. *Scientific reports*, 7(1), 44582.
- Yong, C., Zhou, Y., & Gyorgy, A. (2024, December). The impact of plasmid copy number on leaky gene expression and on the behavior of an activator-based genetic switch. In *2024 IEEE 63rd Conference on Decision and Control (CDC)* (pp. 5592-5597). IEEE.
- Yuan, H., Wang, Y., & Liu, X. P. (2022). The thumb subdomain of *Pyrococcus furiosus* DNA polimerase is responsible for deoxyuracil binding, hydrolysis and polymerization of nucleotides. *The International Journal of Biochemistry & Cell Biology*, 144, 106171.
- Zhang, L., Jiang, D., Shi, H., Wu, M., Gan, Q., Yang, Z., & Oger, P. (2020). Characterization and application of a family B DNA polimerase from the hyperthermophilic and radioresistant euryarchaeon *Thermococcus gammatolerans*. *International journal of biological macromolecules*, 156, 217-224.
- Zhang, L., Kang, M., Xu, J., & Huang, Y. (2015). Archaeal DNA polimerases in biotechnology. *Applied microbiology and biotechnology*, 99(16), 6585-6597.
- Zhang, L., Zhang, L., Liu, Y., Yang, S., Gao, C., Gong, H., ... & He, Z. G. (2009). Archaeal eukaryote-like Orc1/Cdc6 initiators physically interact with DNA polymerase B1 and regulate its functions. *Proceedings of the National Academy of Sciences*, 106(19), 7792-7797.
- Zhou, H. X., & Pang, X. (2018). Electrostatic interactions in protein structure, folding, binding, and condensation. *Chemical reviews*, 118(4), 1691-1741.
- Zhu, B., Cai, G., Hall, E. O., & Freeman, G. J. (2007). In-Fusion™ assembly: seamless engineering of multidomain fusion proteins, modular vectors, and mutations. *Biotechniques*, 43(3), 354-359.