



Editorial

Molecular World Today and Tomorrow: Recent Trends in Biological Sciences

Wajid Zaman

Department of Life Sciences, Yeungnam University, Gyeongsan 38541, Republic of Korea; wajidzaman@yu.ac.kr

Introduction

Various molecular techniques based on omics (transcriptomics, proteomics, genomics) and phylogenetics have been applied in the field of biological sciences. Molecular dynamics and approaches have evolved into various quantitative tools that allow researchers from multiple disciplines to design different studies. The molecular-based techniques can be comprehensive and systematic, as they allow for the identification and resolution of genetic differences, molecular docking, and the construction of prediction models of ecological niches and taxonomic ranks [1,2]. The investigation of genomics, proteomics, and phylogenetic techniques requires the utilization of a novel class of DNA elements such as microsatellites from mitochondria and chloroplast and retrotransposons, resulting in genetic variations using molecular data [3]. In addition, the advantages and limitations of molecular approaches have been well studied and acknowledged. The combination of molecular phylogenetic and omics techniques as well as expression and pathway analyses may greatly increase our capacity to understand and develop new molecular mechanisms and stress responses in biological systems [4,5]. Furthermore, these techniques offer extensive opportunities for researchers to develop targeted therapy approaches and disease diagnoses using molecular data. It is necessary to evaluate and explore how data from diverse molecular techniques can be applied to different biological studies. The study and applications of molecular approaches hold significant potential for advancing genomics, proteomics, and phylogenetic techniques in biological sciences.

The molecular world is a fascinating field where scientists are constantly discovering new complex systems guiding life in the dynamic field of biological sciences. The topic of this Special Issue, “Molecular World Today and Tomorrow: Recent Trends in Biological Sciences,” explores the most recent advancements in this rapidly evolving subject while highlighting knowledge gaps and outlining a course for future research. The last ten years have seen incredible progress in our understanding of the molecular details of living things. Researchers have uncovered hitherto undiscovered information regarding cellular functions, signaling pathways, and the molecular causes of diseases thanks to developments in imaging technologies, genomics, and proteomics [6–8]. Our understanding of complicated biological phenomena has advanced even further with the combination of artificial intelligence and big data analytics [9,10]. Nevertheless, there remains a complex reality hidden behind these victories, and there are still many unanswered questions. New questions arise when we peel back the layers of intricacy, calling scientists to delve deeper and to continue learning.

Our Special Issue “Molecular World Today and Tomorrow” provides proof of the vitality and dynamism of the biological sciences today. The contributors shed light on the routes leading to the core of molecular biology through an extensive collection of research and review papers. As we read these pages, we are reminded that the molecular world is not only a field of study, but also a source of inspiration for the discoveries that will mold the sciences related to living things in the future.



Citation: Zaman, W. Molecular World Today and Tomorrow: Recent Trends in Biological Sciences. *Int. J. Mol. Sci.* **2024**, *25*, 3068. <https://doi.org/10.3390/ijms25053068>

Received: 26 January 2024

Accepted: 28 February 2024

Published: 6 March 2024



Copyright: © 2024 by the author. Licensee MDPI, Basel, Switzerland. This article is an open access article distributed under the terms and conditions of the Creative Commons Attribution (CC BY) license (<https://creativecommons.org/licenses/by/4.0/>).

Funding: This research received no external funding.

Acknowledgments: As Guest Editor of the Special Issue “Molecular World Today and Tomorrow: Recent Trends in Biological Sciences”, I would like to express my deep appreciation to all authors whose valuable work is published in this Special Issue and have thus contributed to the success of the edition.

Conflicts of Interest: The author declares no conflicts of interest.

List of Contributions: This special edition includes 17 carefully chosen papers, each adding a distinct viewpoint to the body of knowledge. Out of all of them, four thorough review articles give readers a broad picture of the state of the subject by delving deeply into critical advancements. These evaluations act as a compendium, assisting scholars and amateurs in navigating the intricate world of molecules. The collaborative character of the research featured in this Special Issue is one noteworthy feature. The publications included here demonstrate the growing multidisciplinary nature of the biological sciences. Scholars from diverse domains come together to investigate the molecular nuances that link biology to other sciences, like chemistry and computer science. These partnerships not only extend our comprehension, but also open new avenues for creative responses to challenging biological problems.

1. Alam, I.; Batool, K.; Huang, Y.; Liu, J.; Ge, L. Developing Genetic Engineering Techniques for Control of Seed Size and Yield. *Int. J. Mol. Sci.* **2022**, *23*, 13256. <https://doi.org/10.3390/ijms232113256>.
2. Bobylev, A.G.; Yakupova, E.I.; Bobyleva, L.G.; Molochkov, N.V.; Timchenko, A.A.; Timchenko, M.A.; Kihara, H.; Nikulin, A.D.; Gabdulkhakov, A.G.; Melnik, T.N.; et al. Nonspecific Amyloid Aggregation of Chicken Smooth-Muscle Titin: In Vitro Investigations. *Int. J. Mol. Sci.* **2023**, *24*, 1056. <https://doi.org/10.3390/ijms24021056>.
3. Charoenwongpaiboon, T.; Oo, A.; Nasoontorn, S.; Rungrotmongkol, T.; Kanokmedhakul, S.; Mahalapbutr, P. Aurisin A Complexed with 2,6-Di-O-methyl- β -cyclodextrin Enhances Aqueous Solubility, Thermal Stability, and Antiproliferative Activity against Lung Cancer Cells. *Int. J. Mol. Sci.* **2022**, *23*, 9776. <https://doi.org/10.3390/ijms23179776>.
4. Chellappan, D.K.; Bhandare, R.R.; Shaik, A.B.; Prasad, K.; Suhaimi, N.A.A.; Yap, W.S.; Das, A.; Banerjee, P.; Ghosh, N.; Guith, T.; et al. Vaccine for Diabetes—Where Do We Stand? *Int. J. Mol. Sci.* **2022**, *23*, 9470. <https://doi.org/10.3390/ijms23169470>.
5. Di Sanzo, M.; Cozzolino, F.; Battaglia, A.M.; Aversa, I.; Monaco, V.; Sacco, A.; Biamonte, F.; Palmieri, C.; Procopio, F.; Santamaria, G.; et al. Ferritin Heavy Chain Binds Peroxiredoxin 6 and Inhibits Cell Proliferation and Migration. *Int. J. Mol. Sci.* **2022**, *23*, 12987. <https://doi.org/10.3390/ijms232112987>.
6. Kondratyev, M.; Rudnev, V.R.; Nikolsky, K.S.; Stepanov, A.A.; Petrovsky, D.V.; Kulikova, L.I.; Kopylov, A.T.; Malsagova, K.A.; Kaysheva, A.L. Atomic Simulation of the Binding of JAK1 and JAK2 with the Selective Inhibitor Ruxolitinib. *Int. J. Mol. Sci.* **2022**, *23*, 10466. <https://doi.org/10.3390/ijms231810466>.
7. Liang, Z.; Ali, Q.; Wang, Y.; Mu, G.; Kan, X.; Ren, Y.; Manghwar, H.; Gu, Q.; Wu, H.; Gao, X. Toxicity of *Bacillus thuringiensis* Strains Derived from the Novel Crystal Protein Cry31Aa with High Nematicidal Activity against Rice Parasitic Nematode *Aphelenchoides besseyi*. *Int. J. Mol. Sci.* **2022**, *23*, 8189. <https://doi.org/10.3390/ijms23158189>.
8. Liu, S.; Gong, W.; Liu, L.; Yan, R.; Wang, S.; Yuan, Z. Integrative Analysis of Transcriptome-Wide Association Study and Gene-Based Association Analysis Identifies In Silico Candidate Genes Associated with Juvenile Idiopathic Arthritis. *Int. J. Mol. Sci.* **2022**, *23*, 13555. <https://doi.org/10.3390/ijms232113555>.
9. Ma, M.; Liu, S.; Wang, Z.; Shao, R.; Ye, J.; Yan, W.; Lv, H.; Hasi, A.; Che, G. Genome-Wide Identification of the SUN Gene Family in Melon (*Cucumis melo*) and Functional Characterization of Two CmSUN Genes in Regulating Fruit Shape Variation. *Int. J. Mol. Sci.* **2022**, *23*, 16047. <https://doi.org/10.3390/ijms232416047>.
10. Nero, C.; Boldrini, L.; Lenkowicz, J.; Giudice, M.T.; Piermattei, A.; Inzani, F.; Pasciuto, T.; Minucci, A.; Fagotti, A.; Zannoni, G.; et al. Deep-Learning to Predict BRCA Mutation and Survival from Digital H & E Slides of Epithelial Ovarian Cancer. *Int. J. Mol. Sci.* **2022**, *23*, 11326. <https://doi.org/10.3390/ijms231911326>.
11. Park, H.; Miyano, S. Computational Tactics for Precision Cancer Network Biology. *Int. J. Mol. Sci.* **2022**, *23*, 14398. <https://doi.org/10.3390/ijms232214398>.

12. Petrovsky, D.V.; Rudnev, V.R.; Nikolsky, K.S.; Kulikova, L.I.; Malsagova, K.M.; Kopylov, A.T.; Kaysheva, A.L. PSSNet—An Accurate Super-Secondary Structure for Protein Segmentation. *Int. J. Mol. Sci.* **2022**, *23*, 14813. <https://doi.org/10.3390/ijms232314813>.
13. Rahim, W.; Khan, M.; Al Azzawi, T.N.; Pande, A.; Methela, N.J.; Ali, S.; Imran, M.; Lee, D.-S.; Lee, G.-M.; Mun, B.-G.; et al. Exogenously Applied Sodium Nitroprusside Mitigates Lead Toxicity in Rice by Regulating Antioxidants and Metal Stress-Related Transcripts. *Int. J. Mol. Sci.* **2022**, *23*, 9729. <https://doi.org/10.3390/ijms23179729>.
14. Rudnev, V.R.; Nikolsky, K.S.; Petrovsky, D.V.; Kulikova, L.I.; Kargatov, A.M.; Malsagova, K.A.; Stepanov, A.A.; Kopylov, A.T.; Kaysheva, A.L.; Efimov, A.V. 3 β -Corner Stability by Comparative Molecular Dynamics Simulations. *Int. J. Mol. Sci.* **2022**, *23*, 11674. <https://doi.org/10.3390/ijms231911674>.
15. Tai, J.; Park, J.; Han, M.; Kim, T.H. Screening Key Genes and Biological Pathways in Nasopharyngeal Carcinoma by Integrated Bioinformatics Analysis. *Int. J. Mol. Sci.* **2022**, *23*, 15701. <https://doi.org/10.3390/ijms232415701>.
16. Zhou, Y.; Manghwar, H.; Hu, W.; Liu, F. Degradation Mechanism of Autophagy-Related Proteins and Research Progress. *Int. J. Mol. Sci.* **2022**, *23*, 7301. <https://doi.org/10.3390/ijms23137301>.
17. Zhu, T.; Li, L.; Chang, H.; Zhan, J.; Ren, M. Target of Rapamycin Regulates Photosynthesis and Cell Growth in *Auxenochlorella pyrenoidosa*. *Int. J. Mol. Sci.* **2022**, *23*, 11309. <https://doi.org/10.3390/ijms231911309>.

References

1. Bhat, K.A.; Mir, R.A.; Farooq, A.; Manzoor, M.; Hami, A.; Allie, K.A.; Wani, S.M.; Khan, M.N.; Sayyed, R.Z.; Pocai, P. Advances in nematode identification: A journey from fundamentals to evolutionary aspects. *Diversity* **2022**, *14*, 536. [\[CrossRef\]](#)
2. Sawarkar, A.D.; Shrimankar, D.D.; Kumar, M.; Kumar, P.; Kumar, S.; Singh, L. Traditional system versus DNA barcoding in identification of bamboo species: A systematic review. *Mol. Biotechnol.* **2021**, *63*, 651–675. [\[CrossRef\]](#) [\[PubMed\]](#)
3. Genov, N.; Castellana, S.; Scholkmann, F.; Capocceffalo, D.; Truglio, M.; Rosati, J.; Turco, E.M.; Biagini, T.; Carbone, A.; Mazza, T.; et al. A Multi-Layered Study on Harmonic Oscillations in Mammalian Genomics and Proteomics. *Int. J. Mol. Sci.* **2019**, *20*, 4585. [\[CrossRef\]](#) [\[PubMed\]](#)
4. Vandereyken, K.; Sifrim, A.; Thienpont, B.; Voet, T. Methods and applications for single-cell and spatial multi-omics. *Nat. Rev. Genet.* **2023**, *24*, 494–515. [\[CrossRef\]](#) [\[PubMed\]](#)
5. Bludau, I.; Aebersold, R. Proteomic and interactomic insights into the molecular basis of cell functional diversity. *Nat. Rev. Mol. Cell Biol.* **2020**, *21*, 327–340. [\[CrossRef\]](#) [\[PubMed\]](#)
6. Chen, L.-L. The expanding regulatory mechanisms and cellular functions of circular RNAs. *Nat. Rev. Mol. Cell Biol.* **2020**, *21*, 475–490. [\[CrossRef\]](#) [\[PubMed\]](#)
7. Yue, J.; López, J.M. Understanding MAPK signaling pathways in apoptosis. *Int. J. Mol. Sci.* **2020**, *21*, 2346. [\[CrossRef\]](#) [\[PubMed\]](#)
8. Moujalled, D.; Strasser, A.; Liddell, J.R. Molecular mechanisms of cell death in neurological diseases. *Cell Death Differ.* **2021**, *28*, 2029–2044. [\[CrossRef\]](#) [\[PubMed\]](#)
9. Zhang, C.; Lu, Y. Study on artificial intelligence: The state of the art and future prospects. *J. Ind. Inf. Integr.* **2021**, *23*, 100224. [\[CrossRef\]](#)
10. Hassani, H.; Beneki, C.; Unger, S.; Mazinani, M.T.; Yeganegi, M.R. Text mining in big data analytics. *Big Data Cogn. Comput.* **2020**, *4*, 1. [\[CrossRef\]](#)

Disclaimer/Publisher’s Note: The statements, opinions and data contained in all publications are solely those of the individual author(s) and contributor(s) and not of MDPI and/or the editor(s). MDPI and/or the editor(s) disclaim responsibility for any injury to people or property resulting from any ideas, methods, instructions or products referred to in the content.