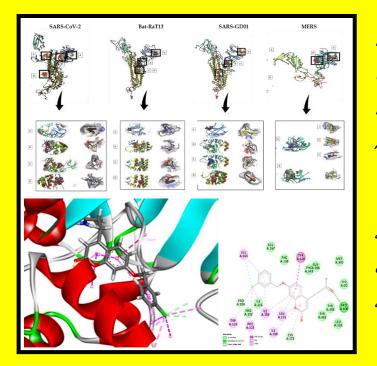
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Volume 1 Issue 1 June 2021



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Suitable Docking Protocol for the Design of Novel Coumarin Derivatives with Selective MAO-B Effects



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Department of Pharmacy

Faculty of Health Sciences Universitas Muhammadiyah Palangkaraya, Indonesia

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EDITORIAL WORDS

apt. Mohammad Rizki Fadhil Pratama, S.Farm., M.Si. Editor in Chief J Mol Docking

Assalamu'alaikum Wr. Wb.

Alhamdulillahirabbil 'alamin. After a long wait for almost 1 years from the first planned, finally the new scientific journal of the Department of Pharmacy Universitas Muhammadiyah Palangkaraya can be published. This scientifc journal was named **Journal of Molecular Docking** (*J Mol Docking*), inspired by one of the most popular *in silico* methods in computer-aided drug design. Journal of Molecular Docking published every 6 months (2 issues/year) every June and December.

This edition contains five articles consisting of writings from four countries including Indonesia, India, Bulgaria, and Egypt. The authors come from several institutions, including Bio Search Research Institution, Sekolah Tinggi Farmasi Muhammadiyah Tangerang, Sri Ramachandra Institute of Higher Education and Research, Siddha Central Research Institute – Central Council for Research in Siddha, Chhattisgarh Swami Vivekanand Technical University, Universitas Mataram, and Medical University – Sofia.

Editorial boards are fully aware that there are still room for improvement in this edition, hence with all humility willing to accept constructive suggestions and feedback for improvements to the publication for the next editions. The editorial board would like to thank all editors and reviewers, and contributors of the scientific articles who have provided the repetoire in this issue. We hope that all parties, especially the contributors of the articles, could re-participate for the the publication in the next edition on December 2021.

Wassalamu'alaikum Wr. Wb.

Palangka Raya, June 2021

Editor-in-Chief

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Author Guidelines JOURNAL OF MOLECULAR DOCKING

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- 1. Writing is the result of original research and literature review in the field of pharmacy, chemistry, bioinformatics, and others using *Molecular Docking Simulation* as its main analysis method which have never been published in other scientific publication media.
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