Scopus

Documents

Johari, N.A.[a] , Azmihan, A.[a] , Abdullah, M.Z.[b] , Bakar, L.M.[a]

Molecular Docking Studies of Phytochemicals from Curcuma longa against Trehalose-6-Phosphate Phosphatases of Pathogenic Microbes

(2024) *Malaysian Journal of Chemistry*, 26 (5), pp. 273-293.

DOI: 10.55373/mjchem.v26i5.273

[a] School of Biology, Faculty of Applied Sciences, Universiti Teknologi MARA, Shah Alam, Shah Alam, Selangor40450, Malaysia
[b] Department of Fundamental Dental and Medical Sciences, Kulliyyah of Dentistry, International Islamic University Malaysia, Pahang, Kuantan, 25200, Malaysia

Abstract
Trehalose-6-phosphate phosphatases (TPP) are crucial enzymes used by pathogenic microbes for trehalose sugar biosynthesis, which is later beneficial for infection and proliferation. Therefore, inhibition of TPP proteins becomes the main focus for combating pathogenic microbial infection. This study aims to investigate the binding interactions between selected phytochemicals from Curcuma longa against TPP enzymes regarding the binding affinities and the presence of non-covalent interactions using molecular docking software. Molecular docking of C. longa phytochemicals against TPP was performed utilizing various software, including PyMol, Discovery Studio Biovia 2021, AutoDock Vina, and AutoDock Tools version 1.5.7. In silico molecular docking analysis using AutoDock Vina was done to predict the binding energy and interactions of 30 ligands that belong to C. longa with TPP proteins from Cryptococcus neoformans (PDB: 5DX9), Candida albicans TPP C-terminal domain (PDB: 5DXI) and TPP from Salmonella typhimurium in complex with trehalose (PDB: 6UPD), whereas ampicillin, fluconazole and isoniazid act as the drugs control. The three-dimensional (3D) models of TPP docked with 30 phytochemicals revealed that most of them have good binding affinities to the TPP enzyme. Interestingly, anthraquinones exhibited among the highest binding affinities, ΔG: -8.4, -8.1 and -7.5 kcal/mol. In addition, quercetin is one of the ligands that exhibit the strongest binding affinity, which is -9.3 kcal/mol interaction between TPP from C. neoformans, and affinity binding of -7.3 and -6.2 kcal/mol interaction with TPP from C. albicans and S. typhimurium respectively. These findings suggest that turmeric phytochemicals have some potential to act as TPP inhibitors, which could contribute toward the future development of new drugs against TPP-producing pathogenic microbes. The data presented warrant validation using in vitro and in vivo assays.

Author Keywords
binding affinity; Curcuma longa; new generation drugs; phytochemicals, molecular docking; Trehalose-6-phosphate phosphatases

References

- Umesh, H. R., Ramesh, K. V., Devaraju, K. S.
  Molecular Docking Studies of Phytochemicals Against Trehalose-6-Phosphate Phosphatases of Pathogenic Microbes
  (2020) *Beni-Suef University Journal of Basic and Applied Sciences*, 9 (1).
- Li, J., Fu, A., Zhang, L.
  An Overview of Scoring Functions Used for Protein– Ligand Interactions in Molecular Docking
  (2019) *Interdisciplinary Sciences: Computational Life Sciences*, 11 (2), pp. 320-328.
- Chen, X., Abubakar, Y. S., Yang, C., Wang, X., Miao, P., Lin, M., Wen, Y., Zheng, W.
  Trehalose Phosphate Synthase Complex-Mediated Regulation of Trehalose-6Phosphate Homeostasis Is Critical for Development and Pathogenesis in Magnaporthe oryzae
  (2021) *MSystems*, 6 (5).
- Yuan, S., Wei, X., Wang, S., Wang, J.
  Characterization of Trehalose-6-Phosphate Phosphatase in Trehalose Biosynthesis, Asexual Development, Stress Resistance and Virulence of An Insect Mycopathogen
  (2020) *Pesticide Biochemistry and Physiology*, 163, pp. 185-192.

- Micoli, F., Bagnoli, F., Rappuoli, R., Serruto, D.
The Role of Vaccines in Combatting Antimicrobial Resistance
(2021) *Nature Reviews Microbiology*, 19 (5), pp. 287-302.

- Adamczak, A., Ożarowski, M., Karpiński, T. M.
Curcumin, A Natural Antimicrobial Agent with Strain-Specific Activity
(2020) *Pharmaceuticals*, 13 (7), p. 153.

- Hussain, Y., Alam, W., Ullah, H., Dacrema, M., Daglia, M., Khan, H., Arciola, C. R.
Antimicrobial Potential of Curcumin: Therapeutic Potential and Challenges to Clinical Applications
(2022) *Antibiotics (Basel, Switzerland)*, 11 (3), p. 322.

- Oyinloye, B. E., Adekiya, T. A., Aruleba, R. T., Ojo, O. A., Ajiboye, B. O.
Structure-Based Docking Studies of GLUT4 Towards Exploring Selected Phytochemicals from Solanum xanthocarpum As a Therapeutic Target for The Treatment of Cancer
(2019) *Current Drug Discovery Technologies*, 16 (4), pp. 406-416.

- Tutumlu, G., Dogan, B., Avsar, T., Orhan, M. D., Calis, S., Durdagi, S.
Integrating Ligand and Target-Driven Based Virtual Screening Approaches With In Vitro Human Cell Line Models and Time-Resolved Fluorescence Resonance Energy Transfer Assay to Identify Novel Hit Compounds Against TPP
(2020) *Frontiers in Chemistry*, 8, p. 167.

- Abdullah, M. Z., Bakar, L. M., Arief Ichwan, S. J., Othman, N., Taher, M.
Molecular Docking Study of Naturally Derived β-mangostin with Antiapoptotic TPP Proteins Toward Oral Cancer Treatment
(2022) *ESTEEM Academic Journal*, 18, pp. 128-138.

- Afriza, D., Suriyah, W. H., Ichwan, S. J. A.
In Silico Analysis of Molecular Interactions Between the Anti-Apoptotic Protein Survivin and Dentatin, Nordentatin, and Quercetin
(2018) *Journal of Physics: Conference Series*, 1073 (3), p. 032001.

- Vanaporn, M., Titball, R. W.
Trehalose and Bacterial Virulence
(2020) *Virulence*, 11 (1), pp. 1192-1202.

- Assoni, G., Frapporti, G., Colombo, E., Gornati, D., Posadas, I., Polito, L., Seneci, P., Arosio, D.
Trehalose-Based Neuroprotective Autophagy Inducers
(2021) *Bioorganic & Medicinal Chemistry Letters*, 40, pp. 127929-127929.

- Schwarz, S., Van Dijck, P.
Trehalose Metabolism: A Sweet Spot for Burkholderia pseudomallei Virulence
(2016) *Virulence*, 8 (1), pp. 5-7.

- MacIntyre, A. M., Barth, J. X., Pellitteri, M. C., Scarlett, C. O., Genin, S., Allen, C.
Trehalose Synthesis Contributes to Osmotic Stress Tolerance and Virulence of the Bacterial Wilt Pathogen Ralstonia solanacearum
(2020) *Molecular Plant-Microbe Interactions*, 33 (3), pp. 462-473.

- Pinzi, L., Rastelli, G.
Molecular docking: shifting paradigms in drug discovery
(2019) *International Journal of Molecular Sciences*, 20 (18), p. 4331.

- Wang, Z., Zhang, P., Ding, X., Wang, J., Sun, Y., Yin, C., Wang, W., Sun, D.
Co-Delivery of Ampicillin and B-Lactamase Inhibitor by Selenium Nanocomposite to Achieve Synergistic Anti-Infective Efficiency Through Overcoming Multidrug

Resistance
(2021) *Chemical Engineering Journal*, 414, p. 128908.

- Cavassin, F. B., Baú-Carneiro, J. L., Vilas-Boas, R. R., Queiroz-Telles, F.
Sixty years of Amphotericin B: An Overview of the Main Antifungal Agent Used to Treat Invasive Fungal Infections
(2021) *Infectious Diseases and Therapy*, 10 (1), pp. 115-147.

- Bhardwaj, P., Biswas, G. P., Mahata, Nibedita, Ghanta, Susanta, Bhunia, Biswanath
Exploration of Binding Mechanism of Triclosan Towards Cancer Markers Using Molecular Docking and Molecular Dynamics
(2022) *Chemosphere*, 293, pp. 133550-133550.

- Dasgupta, S., Bandyopadhyay, M.
Molecular Docking of SARS-COV-2 Spike Epitope Sequences Identifies Heterodimeric Peptide-Protein Complex Formation with Human Zo-1, TLR8 and Brain Specific Glial Proteins
(2021) *Medical Hypotheses*, 157, p. 110706.

- Bender, B. J., Gahbauer, S., Luttens, A., Lyu, J., Webb, C. M., Stein, R. M., Fink, E. A., Shoichet, B. K.
A Practical Guide to Large-Scale Docking
(2021) *Nature Protocols*, 16 (10), pp. 4799-4832.

- Gu, Y. -Y., Zhang, M., Cen, H., Wu, Y. -F., Lu, Z., Lu, F., Liu, X. -S., Lan, H. -Y.
Quercetin as a Potential Treatment for COVID-19-Induced Acute Kidney Injury: Based on Network Pharmacology and Molecular Docking Study
(2021) *PLOS ONE*, 16 (1), p. e0245209.

- Zeng, H., Sun, D., Chu, S., Zhang, J., Hu, G., Yang, R.
Inhibitory Effects of Four Anthraquinones on Tyrosinase Activity: Insight from Spectroscopic Analysis and Molecular Docking
(2020) *International Journal of Biological Macromolecules*, 160, pp. 153-163.

- Nordin, N., Abd Ghani, M. F., Othman, R.
Molecular Docking Study of Naturally Derived Flavonoids with Antiapoptotic BCL-2 and BCL-XL Proteins Toward Ovarian Cancer Treatment
(2020) *Journal of Pharmacy and Bioallied Sciences*, 12 (6), p. 676.

- Jakhar, R., Dangi, M., Khichi, A., Chhillar, A. K.
Relevance of Molecular Docking Studies in Drug Designing
(2020) *Current Bioinformatics*, 15 (4), pp. 270-278.

Correspondence Address
Bakar L.M.; School of Biology, Shah Alam, Selangor, Malaysia; email: latifahmunirah@uitm.edu.my

Publisher: Malaysian Institute of Chemistry

ISSN: 15112292
Language of Original Document: English
Abbreviated Source Title: Malays. J. Chem.
2-s2.0-85206163940
Document Type: Article
Publication Stage: Final
Source: Scopus