



Computational Chemistry in Plant Biology: Unraveling the Molecular Basis of Plant-Drug Interactions and Biochemical Pathways

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Abstract

Computational chemistry plays a crucial role in advancing our understanding of plant biology by unraveling the molecular basis of plant-drug interactions and biochemical pathways. This paper provides an overview of the applications of computational chemistry methods in plant biology research, focusing on the analysis of plant-drug interactions and biochemical pathways. In the introduction, the importance of understanding plant biology and chemistry is highlighted, emphasizing the significance of studying plant-drug interactions and biochemical pathways. Computational chemistry methods offer powerful tools to investigate these complex processes, providing insights that are challenging to obtain through traditional experimental approaches. The first section explores plant-drug interactions, discussing their relevance and showcasing case studies where computational chemistry techniques such as molecular docking and molecular

dynamics simulations have been employed to study these interactions. Examples of successful applications of computational chemistry in elucidating plant-drug interactions demonstrate the potential of these methods in advancing our knowledge in this area. In the second section, the focus shifts to biochemical pathways in plants. The significance of understanding these pathways is discussed, along with descriptions of computational chemistry methods such as quantum mechanics and molecular mechanics that are used to study biochemical pathways. Case studies illustrating the application of computational chemistry approaches in unraveling biochemical pathways in plants further underscore the utility of these methods. The final section delves into the applications and future directions of computational chemistry in plant biology, highlighting the potential for drug discovery and crop improvement. Future research directions, as well as challenges and limitations associated with computational chemistry approaches in plant biology, are also addressed. Overall, this paper underscores the valuable contributions of computational chemistry in elucidating plant-drug interactions and biochemical pathways, paving the way for innovative research and applications in plant biology.

Keywords: Computational chemistry, Plant biology, Plant-drug interactions, Biochemical pathways, Drug discovery

1-Introduction: -

Understanding plant biology and chemistry is essential for various reasons, from unraveling the biochemical pathways within plants to comprehending the interactions between plants and drugs. Plant biochemistry, as discussed by (Bate-Smith, 1959), explores the fundamental chemical processes occurring within plants, shedding light on how plants synthesize essential compounds and respond to environmental stimuli. This knowledge forms the basis for understanding how plants interact with their surroundings, including other organisms like microbes. The study by Foyer & Noctor (2003) emphasizes the significance of redox signaling in plants, showcasing how these signals regulate various aspects of plant biology, from gene expression to enzyme chemistry. Furthermore, exploring plant-drug interactions and biochemical pathways is crucial for applications in agriculture, medicine, and biotechnology. Chemical tools, such as those discussed by (Vivian, 2021), provide insights into plant-microbe interactions, enabling researchers to probe the signaling pathways between plants and microbes. Understanding these interactions is vital for developing strategies to enhance plant health, improve crop yields, and discover new bioactive compounds with potential pharmaceutical applications. Mhlongo et al. (2018) further elaborate on the chemistry of plant-microbe interactions in the rhizosphere, emphasizing the role of metabolomics in uncovering signaling mechanisms related to defense priming and induced systemic resistance.

In the realm of computational chemistry, methods are pivotal in advancing our understanding of plant biology. Häfner (2008) discusses the applications of *ab initio* simulations in materials science, highlighting how computational approaches elucidate the properties and behaviors of various substances relevant to plant biology. Computational chemistry techniques offer a powerful tool for studying complex biochemical pathways and interactions within plants. Boivin et al.

(2016) delve into how phytohormones like auxin and cytokinin modulate root-microbe interactions, showcasing how computational models help unravel the dynamics of these processes. The integration of synthetic biology with plant biology opens up new research and innovation avenues. Liu & Stewart (2015) discuss the emerging field of plant synthetic biology, which merges engineering principles with plant biology to design novel biological devices. This interdisciplinary approach holds promise for developing tailored solutions in agriculture, bioproduction, and environmental sustainability. Furthermore, Torii et al. (2018) highlight the role of synthetic chemistry in probing and manipulating auxin signaling, showcasing how chemical genetics can elucidate intricate plant signaling pathways.

In the realm of computational biology, systems bioinformatics plays a crucial role in enhancing our understanding of complex biological systems. Oulas et al. (2017) discuss how network-based approaches in systems biology can improve computational diagnostics and therapeutics, offering a holistic view of biological processes. By integrating various omics data, systems bioinformatics enables researchers to unravel intricate biological networks and identify potential biomarkers for precision medicine applications.

In conclusion, the synergy between plant biology, chemistry, and computational methods is essential for unraveling the complexities of plant biochemistry, understanding plant-drug interactions, and exploring biochemical pathways. By leveraging chemical tools, computational chemistry techniques, and systems bioinformatics, researchers can delve deeper into the molecular mechanisms governing plant biology, paving the way for innovative applications in agriculture, medicine, and biotechnology.

2- Plant-Drug Interactions

2.1 Overview Plant-Drug Interactions and Their Significance

Plant-drug interactions are significant in various aspects of health and medicine. Plants contain bioactive compounds that can interact with conventional drugs, influencing their efficacy and safety. Pezzani et al. (2019) emphasize the potential synergistic effects between plant derivatives and conventional chemotherapeutic agents, highlighting the importance of investigating positive interactions to enhance treatment outcomes and minimize adverse effects, particularly in cancer therapy.

Additionally, medicinal plants are rich sources of secondary metabolites with anti-parasitic properties, as discussed by (Wink, 2012). These bioactive compounds from plants can target central mechanisms in parasites, such as DNA, membrane integrity, and signal transduction, demonstrating the potential of plant-derived compounds in combating parasitic diseases.

Flavonoids, a class of phytochemicals found in plants, have been shown to influence drug metabolism and pharmacokinetics through local gastrointestinal mechanisms, as highlighted by (Cermak & Wolfram, 2006). These interactions can impact the bioavailability and metabolism of drugs, underscoring the importance of considering plant compounds in drug therapy.

The assessment of herb-drug interactions is crucial in clinical practice to ensure patient safety and treatment efficacy. Fugh-Berman & Ernst (2001) stress the need to review and assess the reliability

of reports on herb-drug interactions, recognizing the potential risks associated with such interactions and the importance of understanding their mechanisms.

Understanding the evidence and mechanisms of herb-drug interactions is essential for healthcare professionals and researchers. Fasinu et al. (2012) provide an overview of herb-drug interactions, highlighting the clinical consequences of these interactions and the need for comprehensive knowledge to mitigate potential risks and optimize therapeutic outcomes.

In conclusion, plant-drug interactions represent a complex yet significant area of study in healthcare and pharmacology. By exploring the synergistic effects of plant derivatives with conventional drugs, leveraging plant compounds for anti-parasitic activities, considering the influence of flavonoids on drug metabolism, and assessing the reliability of reports on herb-drug interactions, researchers and healthcare providers can navigate the complexities of plant-drug interactions to enhance patient care and treatment efficacy.

2.2 Case Studies of Computational Chemistry Approaches

To explore case studies of computational chemistry approaches applied to studying plant-drug interactions, researchers have utilized molecular docking and molecular dynamics simulations to elucidate the molecular mechanisms underlying these interactions. Roy et al. (2022) emphasize the significance of molecular docking in investigating the interactions between proteins and ligands at a molecular level, highlighting its utility in designing new drug molecules against disease-causing biological targets. Similarly, Kanagavalli et al. (2021) underscore the importance of *in silico* molecular docking simulations in drug development and phytochemical screening, showcasing its role in identifying potential therapeutic agents from natural sources like *Boerhavia diffusa* Linn.

Furthermore, computational techniques such as molecular docking and molecular dynamics have been crucial in studying the impact of mutations, as demonstrated by Poustforoosh et al. (2022) in their investigation of the D614G mutation of SARS-CoV-2 on the efficacy of antiviral drugs. By utilizing computational methods, researchers can address challenges associated with clinical trials and gain insights into the molecular interactions between drugs and their targets. Firdayani et al. (2022) further exemplify the utility of molecular docking simulations in inhibiting SARS-CoV-2 proteases using bioactive constituents from medicinal plants, showcasing the versatility of computational approaches in drug discovery.

In the context of plant-based compounds, computational methods like molecular docking and molecular dynamics simulations have been pivotal in identifying potential therapeutic agents. Wani et al. (2021) conducted binding and drug displacement studies using spectroscopic techniques and molecular dynamic simulations to evaluate the interactions between colchicine, azithromycin, and bovine serum albumin. This approach provides valuable insights into the binding mechanisms of these compounds, shedding light on their potential therapeutic applications.

Moreover, computational drug discovery approaches have been employed to identify novel drug candidates from plant-derived compounds. Borah et al. (2022) utilized molecular docking and molecular dynamics simulations to explore potential therapeutic agents for Alzheimer's disease,

focusing on cholinesterase inhibitors. By leveraging computational tools, researchers can screen a wide range of compounds efficiently and predict their interactions with biological targets, facilitating the discovery of new drug candidates.

In the study by (Taherkhani et al., 2023), a computational drug discovery approach was utilized to identify flavonoids as strong inhibitors of MAPK3, showcasing the power of molecular docking in identifying bioactive compounds from plants. Similarly, Nouadi et al. (2021) employed molecular docking to predict the anti-COVID-19 therapeutic potential of medicinal Moroccan plants, highlighting the growing impact of computational techniques in drug discovery and development.

In conclusion, computational chemistry approaches, including molecular docking and molecular dynamics simulations, play a crucial role in studying plant-drug interactions. These methods enable researchers to explore the molecular interactions between plant-derived compounds and biological targets, identify potential therapeutic agents, and optimize drug discovery processes. By leveraging computational tools, researchers can accelerate the discovery of novel drug candidates from natural sources and gain valuable insights into the mechanisms underlying plant-drug interactions.

3. Biochemical Pathways

3.1 Overview of Biochemical Pathways In Plants And Their Importance

Biochemical pathways in plants are crucial for various physiological processes, including growth, development, stress responses, and defense mechanisms. Mithöfer & Boland (2012) discuss plant defense mechanisms against herbivores, emphasizing the diverse chemical defenses plants have evolved to deter herbivory. These defenses, such as glycosides and alkaloids, act as barriers against herbivores, with some being constitutive and others induced upon attack.

Furthermore, Sugawara et al. (2009) provide insights into the indole-3-acetaldoxime-dependent auxin biosynthesis pathway in Arabidopsis, highlighting the species-specific nature of this pathway. The biosynthesis of indole-3-acetic acid (IAA), a crucial plant hormone, involves intermediates like IAM and IAN, showcasing the complexity and specificity of auxin biosynthesis pathways across plant species.

Moreover, Fauteux et al. (2005) discuss the role of silicon in enhancing plant disease resistance against pathogenic fungi, emphasizing the need to elucidate the interactions between soluble silicon and plant biochemical pathways leading to disease resistance. Additionally, Nisbet et al. (2009) explore the emission of methane from plants, highlighting the existence of unknown biochemical pathways related to methanogenesis in plants. Understanding these pathways is crucial for comprehending the ecological implications of methane emission from plants and its impact on greenhouse gas dynamics.

In conclusion, biochemical pathways in plants are diverse and essential for various physiological functions, including defense mechanisms, hormone biosynthesis, disease resistance, and unique metabolic processes. Studying these pathways provides valuable insights into plant biology and opens avenues for further research into plant-microbe interactions, stress responses, and environmental adaptations.

3.2 Computational Chemistry Methods

Computational chemistry methods are essential in studying biochemical pathways, providing insights into the molecular mechanisms underlying complex biological processes. Quantum mechanics (QM) and molecular mechanics (MM) are two prominent computational approaches used for this purpose.

Quantum mechanics methods, as discussed by (Panitchayangkoon et al., 2010), offer a detailed understanding of quantum coherence in photosynthetic complexes, elucidating the efficiency of energy transfer processes. These methods enable researchers to explore the quantum aspects of biochemical reactions, such as photosynthesis, at a fundamental level.

On the other hand, molecular mechanics simulations, as highlighted by Avolio (Tao & Schlegel, 2010), are crucial for studying enzymatic reactions and biochemical pathways. By integrating quantum mechanics with molecular mechanics (QM/MM) methods, researchers can gain insights into the catalytic mechanisms of enzymes and the dynamics of biochemical reactions, facilitating the investigation of large biomolecular systems accurately and efficiently.

Furthermore, molecular dynamics simulations, a subset of molecular mechanics, are widely utilized to examine the dynamics and interactions of biomolecules in biochemical pathways. By simulating the movements of atoms and molecules over time, researchers can elucidate the structural changes and conformational dynamics involved in biological processes, as discussed by (Marchi et al., 2021).

In conclusion, computational chemistry methods, including quantum mechanics, molecular mechanics, and molecular dynamics simulations, provide powerful tools for studying biochemical pathways. These approaches offer a detailed understanding of the molecular interactions, energetics, and dynamics involved in biological processes, contributing to advancements in biochemistry, enzymology, and drug discovery.

3.3 Computational Chemistry Approaches

Case studies of computational chemistry approaches to understanding biochemical pathways in plants involve leveraging various computational tools to elucidate the intricate processes within plant biology. For instance, Sato et al. (2019) delve into the acceleration of mechanistic investigations of plant secondary metabolism using computational chemistry. By focusing on terpene/terpenoid, alkaloid, flavonoid, and lignin biosynthetic mechanisms, this study showcases how computational chemistry aids in unraveling the biosynthetic pathways of essential plant metabolites.

Moreover, Deshpande et al. (2016) explores the metal-dependent function of a mammalian Acireductone Dioxygenase, shedding light on the enzyme-ligand complexes' insights into substrate binding, metal coordination, and catalytic mechanisms. This case study exemplifies how computational chemistry elucidates the biochemical pathways involving metal-dependent enzymes, providing a deeper understanding of their functions.

Additionally, Faraji et al. (2015) utilizes computational inference to study the structure and regulation of the lignin pathway in *Panicum virgatum*. By analyzing the synthesis and translocation

of monolignols, the building blocks of lignin polymers, this study demonstrates how computational approaches can elucidate the intricate processes involved in lignin biosynthesis in plants.

These case studies highlight the diverse applications of computational chemistry in understanding biochemical pathways in plants, ranging from secondary metabolism to enzyme functions and regulatory networks. By integrating computational tools with biochemical knowledge, researchers can unravel the complexities of plant biochemistry, paving the way for advancements in plant biology, metabolic engineering, and biotechnological applications.

4. Potential Applications of Computational Chemistry in Plant Biology

Computational chemistry plays a crucial role in advancing plant biology by providing insights into biochemical pathways, plant-microbe interactions, and secondary metabolism. Through computational tools, researchers can explore plant biology at a molecular level, contributing to areas such as drug discovery, metabolic engineering, and understanding plant growth regulators.

One significant application of computational chemistry in plant biology is the investigation of plant secondary metabolism mechanisms. Studies, such as the work by (Sato et al., 2019), demonstrate how computational chemistry can expedite the exploration of terpene/terpenoid, alkaloid, flavonoid, and lignin biosynthetic pathways. By simulating these processes, researchers can uncover the molecular intricacies of plant secondary metabolites, potentially leading to the discovery of novel bioactive compounds with applications in pharmaceuticals and agriculture.

Furthermore, computational chemistry is valuable for studying plant growth regulators like auxins, which are essential for plant development and responses to environmental cues. Torii et al. (2018) emphasize the use of synthetic chemistry to investigate and manipulate auxin signaling pathways in plants. Computational approaches aid in understanding the molecular interactions between auxins and plant proteins, shedding light on the regulatory networks involved in plant growth and development.

Moreover, computational chemistry methods, such as molecular dynamics simulations and quantum mechanics calculations, can be utilized to explore the reactivity of plant metabolites, enzyme functions, and biochemical pathways' dynamics. Integrating computational systems biology with structural biology enables researchers to comprehend the molecular underpinnings of plant-microbe interactions, disease resistance mechanisms, and specialized metabolic pathways in medicinal plants.

In summary, computational chemistry offers diverse and extensive applications in plant biology, from unraveling biochemical pathways to designing innovative plant-based therapeutics. By harnessing computational tools, researchers can decode the complexities of plant biology, leading to groundbreaking discoveries and advancements in agriculture, medicine, and biotechnology.

4.1 Drug Discovery

Computational chemistry is a crucial tool in drug discovery within plant biology, enabling researchers to efficiently explore natural product libraries, identify bioactive compounds, and optimize drug candidates. By integrating computational approaches with traditional drug discovery methods, researchers can harness the vast potential of plant-based compounds for

developing novel therapeutics. Several studies support the significance of computational chemistry in drug discovery within plant biology: Thomford et al. (2018) emphasize the importance of plant-based natural product drug discovery and the contributions of computational approaches to this field. Macalino et al. (2015) highlights the role of computer-aided drug design (CADD) in modern drug discovery, emphasizing its ability to expedite drug development and minimize failures.

Galvis et al. (2013) showcase the potential of cantharidin-based small molecules as therapeutic agents, underlining the importance of natural substances, including those derived from plants, in drug discovery. Li & Lou (2017) discuss strategies to diversify natural products for drug discovery, emphasizing the structural diversity and biological activities of natural product libraries derived from plants, animals, and microorganisms. In conclusion, computational chemistry is a powerful tool that accelerates drug discovery within plant biology by facilitating the identification and optimization of bioactive compounds from natural sources.

4.2 Metabolic Engineering

Metabolic engineering, a field that involves modifying metabolic pathways in organisms to produce valuable compounds, has seen significant advancements through the integration of computational chemistry in plant biology. By leveraging computational tools, researchers can design and optimize metabolic pathways in plants to enhance the production of bioactive compounds, pharmaceuticals, and industrial chemicals. Several studies highlight the potential applications of computational chemistry in metabolic engineering within plant biology:

Verpoorte & Alfermann (2000) discuss the principles of metabolic engineering of plant secondary metabolism, emphasizing the role of computational approaches in optimizing biosynthetic pathways for the production of specialized metabolites. Kiss et al. (2013) focus on computational enzyme design, showcasing how biochemical building blocks can be utilized in the rational design of enzymes for metabolic engineering applications, enabling the creation of novel catalytic activities for targeted metabolic pathways.

Mintz-Oron et al. (2011) presents a study on the reconstruction of metabolic network models in *Arabidopsis*, accounting for subcellular compartmentalization and tissue-specificity. This work demonstrates how computational modeling can provide insights into plant metabolism and guide metabolic engineering strategies. Biggs et al. (2016) highlight the importance of overcoming heterologous protein interdependency in optimizing P450-mediated synthesis of complex molecules in *Escherichia coli*. This study exemplifies how metabolic engineering, coupled with computational chemistry, can be used to engineer microbial systems for the production of valuable compounds.

Sato et al. (2019) describe the acceleration of mechanistic investigations of plant secondary metabolism based on computational chemistry. This review underscores the application of computational chemistry in elucidating the biosynthetic mechanisms of various plant metabolites, such as terpenes, alkaloids, flavonoids, and lignin. In conclusion, computational chemistry plays a pivotal role in metabolic engineering within plant biology, offering tools to design, model, and optimize metabolic pathways for enhanced production of valuable compounds. By integrating

computational approaches with experimental techniques, researchers can drive innovations in plant biotechnology, pharmaceutical development, and sustainable chemical production.

4.3 Nutrition and Health

Computational chemistry is a valuable tool in plant biology, particularly in the areas of nutrition and health. Researchers use computational tools to explore the complex biochemical pathways of plants, uncovering essential nutrients and bioactive compounds that are beneficial for human health. Plants are rich sources of therapeutic phytochemicals, including pharmaceuticals and nutraceuticals, which are challenging to synthesize chemically, making plant extracts a crucial source of these compounds Barnum et al. (2021).

Additionally, computational approaches are essential for designing and testing synthetic metabolic pathways in plants to improve their nutritional value and yield. Through in silico design, testing, and experimental validation of synthetic metabolic pathways, researchers can manipulate essential plant traits, leading to enhanced agronomic outcomes (Küken & Nikoloski, 2019).

Moreover, computational chemistry assists in optimizing plant metabolic networks to understand processes such as nutrient uptake, transport mechanisms, and mobilization. By reconstructing metabolic network models, researchers can gain insights into plant metabolism, subcellular compartmentalization, and tissue-specific metabolic activities, guiding strategies for metabolic engineering and enhancing plant nutrition (O'Sullivan et al., 2017).

In the realm of precision nutrition, computational biology tools have transformed the field by offering a modern toolkit for enhancing population health through personalized nutrition recommendations. By utilizing analytical chemistry and experimental biology, researchers can elucidate the molecular details of foods, essential nutrients, and their biological functions, paving the way for tailored nutrition interventions to prevent nutrient deficiencies and promote overall health (Nørskov et al., 2011).

In conclusion, computational chemistry in plant biology has significant potential for advancing our knowledge of plant metabolism, nutritional quality, and bioactive compound production. By combining computational approaches with experimental research, scientists can unlock the nutritional and health benefits of plants, contributing to the development of innovative strategies for personalized nutrition and wellness.

4.4 Synthetic Biology

Computational chemistry is a crucial tool in advancing plant biology through synthetic biology applications. Plant synthetic biology involves redesigning and engineering biological systems to utilize the natural capabilities of plants for novel purposes. Computational chemistry tools are essential for designing and optimizing synthetic metabolic pathways in plants, enabling the production of valuable compounds and enhancing plant traits for various applications Küken & Nikoloski (2019).

Researchers utilize computational approaches to predict and control the behavior of artificial biological pathways in plants. These predictive models assist in the rational design of enzymes, metabolic pathways, and genetic circuits, facilitating the creation of novel plant-based systems with tailored functionalities (McCarthy & Medford, 2020).

Furthermore, computational chemistry contributes to the development of synthetic gene networks and genetic circuits in plants. By modeling and simulating these engineered systems, researchers can predict the behavior of synthetic genetic elements, optimize their functions, and guide the construction of programmable plant genetic circuits for specific applications (DeNies et al., 2020). In the realm of drug discovery and production, synthetic biology-based approaches leverage computational tools to design de novo synthetic pathways for the biosynthesis of high-value compounds. By combining synthetic biology methodologies with computational chemistry, researchers can generate advanced natural product intermediates, overcome obstacles in drug discovery, and enhance the production of pharmaceuticals from plant sources (Barnum et al., 2021).

In summary, computational chemistry is a cornerstone in the field of plant synthetic biology, enabling the design, modeling, and optimization of synthetic metabolic pathways and genetic circuits in plants. The integration of computational approaches with experimental techniques drives innovations in plant biotechnology, pharmaceutical development, and sustainable chemical production.

4.5 Agricultural Sustainability

Computational chemistry is a valuable tool in advancing agricultural sustainability through its applications in plant biology. By utilizing computational tools, researchers can model and optimize metabolic pathways in plants to enhance crop productivity, nutrient content, and stress tolerance. Computational chemistry aids in the design of synthetic metabolic pathways, enabling the production of valuable compounds and the development of plant-based solutions for sustainable agriculture practices Yu (2024).

Additionally, computational approaches are crucial in studying plant-microbe interactions, which play a vital role in nutrient cycling, soil health, and plant growth. By analyzing the dynamics of plant-microbe interactions, researchers can identify beneficial microbial communities that promote plant health and sustainability in agricultural ecosystems (Shelake et al., 2019).

Moreover, computational chemistry contributes to the development of plant-based nanostructures with diverse applications in agriculture. By designing plant-derived nanostructures, researchers can create innovative materials for crop protection, nutrient delivery, and environmental remediation, fostering sustainable agricultural practices (Mohammadinejad et al., 2016). In summary, computational chemistry in plant biology provides a powerful toolkit for enhancing agricultural sustainability by optimizing metabolic pathways, studying plant-microbe interactions, and developing innovative plant-based materials for agricultural applications.

5. Summary

Computational chemistry plays a vital role in plant biology by unraveling the molecular basis of plant-drug interactions and biochemical pathways. Through computational tools, researchers can investigate the intricate mechanisms underlying how plants interact with drugs and synthesize essential compounds. By utilizing computational approaches, such as molecular docking and molecular dynamics simulations, scientists can gain insights into the molecular interactions within plants, optimize metabolic pathways, and design novel therapeutic agents derived from plant sources. This integration of computational chemistry in

plant biology enhances our understanding of plant biochemistry, facilitates drug discovery processes, and contributes to advancements in agriculture, medicine, and biotechnology.

6. References

- Bate-Smith, E. (1959). *Plant biochemistry*, 100-123. <https://doi.org/10.1016/b978-0-08-009849-4.50008-1>
- Boivin, S., Fonouni-Farde, C., & Frugier, F. (2016). How auxin and cytokinin phytohormones modulate root microbe interactions. *Frontiers in Plant Science*, 7. <https://doi.org/10.3389/fpls.2016.01240>
- Foyer, C. and Noctor, G. (2003). Redox sensing and signalling associated with reactive oxygen in chloroplasts, peroxisomes and mitochondria. *Physiologia Plantarum*, 119(3), 355-364. <https://doi.org/10.1034/j.1399-3054.2003.00223.x>
- Häfner, J. (2008). ab-initio simulations of materials using vasp: density-functional theory and beyond. *Journal of Computational Chemistry*, 29(13), 2044-2078. <https://doi.org/10.1002/jcc.21057>
- Liu, W. and Stewart, C. (2015). Plant synthetic biology. *Trends in Plant Science*, 20(5), 309-317. <https://doi.org/10.1016/j.tplants.2015.02.004>
- Mhlongo, M., Piater, L., Madala, N., Labuschagne, N., & Dubery, I. (2018). The chemistry of plant-microbe interactions in the rhizosphere and the potential for metabolomics to reveal signaling related to defense priming and induced systemic resistance. *Frontiers in Plant Science*, 9. <https://doi.org/10.3389/fpls.2018.00112>
- Oulas, A., Minadakis, G., Zachariou, M., Sokratous, K., Bourdakou, M., & Spyrou, G. (2017). Systems bioinformatics: increasing precision of computational diagnostics and therapeutics through network-based approaches. *Briefings in Bioinformatics*, 20(3), 806-824. <https://doi.org/10.1093/bib/bbx151>
- Torii, K., Hagihara, S., Uchida, N., & Takahashi, K. (2018). Harnessing synthetic chemistry to probe and hijack auxin signaling. *New Phytologist*, 220(2), 417-424. <https://doi.org/10.1111/nph.15337>
- Vivian, L. (2021). Interrogating plant-microbe interactions with chemical tools: click chemistry reagents for metabolic labeling and activity-based probes. *Molecules*, 26(1), 243. <https://doi.org/10.3390/molecules26010243>
- Cermak, R. and Wolfram, S. (2006). The potential of flavonoids to influence drug metabolism and pharmacokinetics by local gastrointestinal mechanisms. *Current Drug Metabolism*, 7(7), 729-744. <https://doi.org/10.2174/138920006778520570>
- Fasinu, P., Bouic, P., & Rosenkranz, B. (2012). An overview of the evidence and mechanisms of herb-drug interactions. *Frontiers in Pharmacology*, 3. <https://doi.org/10.3389/fphar.2012.00069>
- Fugh-Berman, A. and Ernst, E. (2001). Herb-drug interactions: review and assessment of report reliability. *British Journal of Clinical Pharmacology*, 52(5), 587-595. <https://doi.org/10.1046/j.0306-5251.2001.01469.x>
- Pezzani, R., Salehi, B., Vitalini, S., Iriti, M., Zúñiga, F., Sharifi-Rad, J., ... & Martins, N. (2019). Synergistic effects of plant derivatives and conventional chemotherapeutic agents: an update on the cancer perspective. *Medicina*, 55(4), 110. <https://doi.org/10.3390/medicina55040110>
- Wink, M. (2012). Medicinal plants: a source of anti-parasitic secondary metabolites. *Molecules*, 17(11), 12771-12791. <https://doi.org/10.3390/molecules171112771>
- Borah, K., Bora, K., Mallik, S., & Zhao, Z. (2022). Potential therapeutic agents on alzheimer's disease through molecular docking and molecular dynamics simulation study of plant-based compounds. *Chemistry & Biodiversity*, 20(1). <https://doi.org/10.1002/cbdv.202200684>
- Kanagavalli, U., Deboral, E., Lakshmipriya, M., Sadiq, A., & Priya, A. (2021). In silico molecular docking of anthraquinone identified from boerhavia diffusa linn against bax and bcl-2 gene. *Journal of Pharmaceutical Research International*, 352-359. <https://doi.org/10.9734/jpri/2021/v33i57a34006>

- Nouadi, B., Ezaouine, A., Messal, M., Blaghen, M., Bennis, F., & Chegdani, F. (2021). Prediction of anti-covid 19 therapeutic power of medicinal moroccan plants using molecular docking. *Bioinformatics and Biology Insights*, 15, 117793222110091. <https://doi.org/10.1177/11779322211009199>
- Poustforoosh, A., Hashemipour, H., Tüzün, B., Azadpour, M., Faramarz, S., Pardakhty, A., ... & Nematollahi, M. (2022). The impact of d614g mutation of sars-cov-2 on the efficacy of anti-viral drugs: a comparative molecular docking and molecular dynamics study. *Current Microbiology*, 79(8). <https://doi.org/10.1007/s00284-022-02921-6>
- Riswoko, A. and Helianti, I. (2022). Inhibition of sars-cov-2 proteases by medicinal plant bioactive constituents: molecular docking simulation. *Iop Conference Series Earth and Environmental Science*, 976(1), 012054. <https://doi.org/10.1088/1755-1315/976/1/012054>
- Roy, M., Swargiary, A., & Daimari, M. (2022). Gas chromatography-mass spectrometry analysis and antihyperglycemic property of *lindernia crustacea* (L.) f. muell.. *IJPS*, 84(3). <https://doi.org/10.36468/pharmaceutical-sciences.972>
- Taherkhani, A., Khodadadi, P., Samie, L., Azadian, Z., & Bayat, Z. (2023). Flavonoids as strong inhibitors of mapk3: a computational drug discovery approach. *International Journal of Analytical Chemistry*, 2023, 1-16. <https://doi.org/10.1155/2023/8899240>
- Wani, T., Bakheit, A., Al-Majed, A., Altwaijry, N., Baquaysh, A., Aljuraissy, A., ... & Zargar, S. (2021). Binding and drug displacement study of colchicine and bovine serum albumin in presence of azithromycin using multispectroscopic techniques and molecular dynamic simulation. *Journal of Molecular Liquids*, 333, 115934. <https://doi.org/10.1016/j.molliq.2021.115934>
- Fauteux, F., Rémus-Borel, W., Menzies, J., & Bélanger, R. (2005). Silicon and plant disease resistance against pathogenic fungi. *Fems Microbiology Letters*, 249(1), 1-6. <https://doi.org/10.1016/j.femsle.2005.06.034>
- Mithöfer, A. and Boland, W. (2012). Plant defense against herbivores: chemical aspects. *Annual Review of Plant Biology*, 63(1), 431-450. <https://doi.org/10.1146/annurev-arplant-042110-103854>
- Nisbet, R., Fisher, R., Nimmo, R., Bendall, D., Crill, P., Gallego-Sala, A., ... & Nisbet, E. (2009). Emission of methane from plants. *Proceedings of the Royal Society B Biological Sciences*, 276(1660), 1347-1354. <https://doi.org/10.1098/rspb.2008.1731>
- Sugawara, S., Hishiyama, S., Jikumaru, Y., Hanada, A., Nishimura, T., Koshihara, T., ... & Kasahara, H. (2009). Biochemical analyses of indole-3-acetaldoxime-dependent auxin biosynthesis in arabidopsis. *Proceedings of the National Academy of Sciences*, 106(13), 5430-5435. <https://doi.org/10.1073/pnas.0811226106>
- Marchi, S., Zanella, M., Pinton, P., Crafa, S., & Boniolo, G. (2021). Mitopaths: a new logically-framed tool for visualizing multiple mitochondrial pathways. *Iscience*, 24(4), 102324. <https://doi.org/10.1016/j.isci.2021.102324>
- Panitchayangkoon, G., Hayes, D., Fransted, K., Caram, J., Harel, E., Wen, J., ... & Engel, G. (2010). Long-lived quantum coherence in photosynthetic complexes at physiological temperature. *Proceedings of the National Academy of Sciences*, 107(29), 12766-12770. <https://doi.org/10.1073/pnas.1005484107>
- Tao, P. and Schlegel, H. (2010). A toolkit to assist oniom calculations. *Journal of Computational Chemistry*, 31(12), 2363-2369. <https://doi.org/10.1002/jcc.21524>
- Marchi, S., Zanella, M., Pinton, P., Crafa, S., & Boniolo, G. (2021). Mitopaths: a new logically-framed tool for visualizing multiple mitochondrial pathways. *Iscience*, 24(4), 102324. <https://doi.org/10.1016/j.isci.2021.102324>

- Panitchayangkoon, G., Hayes, D., Fransted, K., Caram, J., Harel, E., Wen, J., ... & Engel, G. (2010). Long-lived quantum coherence in photosynthetic complexes at physiological temperature. *Proceedings of the National Academy of Sciences*, 107(29), 12766-12770. <https://doi.org/10.1073/pnas.1005484107>
- Tao, P. and Schlegel, H. (2010). A toolkit to assist oniom calculations. *Journal of Computational Chemistry*, 31(12), 2363-2369. <https://doi.org/10.1002/jcc.21524>
- Sato, H., Saito, K., & Yamazaki, M. (2019). Acceleration of mechanistic investigation of plant secondary metabolism based on computational chemistry. *Frontiers in Plant Science*, 10. <https://doi.org/10.3389/fpls.2019.00802>
- Torii, K., Hagihara, S., Uchida, N., & Takahashi, K. (2018). Harnessing synthetic chemistry to probe and hijack auxin signaling. *New Phytologist*, 220(2), 417-424. <https://doi.org/10.1111/nph.15337>
- Galvis, C., Méndez, L., & Kouznetsov, V. (2013). Cantharidin-based small molecules as potential therapeutic agents. *Chemical Biology & Drug Design*, 82(5), 477-499. <https://doi.org/10.1111/cbdd.12180>
- Li, G. and Lou, H. (2017). Strategies to diversify natural products for drug discovery. *Medicinal Research Reviews*, 38(4), 1255-1294. <https://doi.org/10.1002/med.21474>
- Macalino, S., Gosu, V., Hong, S., & Choi, S. (2015). Role of computer-aided drug design in modern drug discovery. *Archives of Pharmacal Research*, 38(9), 1686-1701. <https://doi.org/10.1007/s12272-015-0640-0>
- Thomford, N., Senthebane, D., Rowe, A., Munro, D., Seele, P., Maroyi, A., ... & Dzobo, K. (2018). Natural products for drug discovery in the 21st century: innovations for novel drug discovery. *International Journal of Molecular Sciences*, 19(6), 1578. <https://doi.org/10.3390/ijms19061578>
- Verpoorte, R. and Alfermann, A. (2000). Metabolic engineering of plant secondary metabolism.. <https://doi.org/10.1007/978-94-015-9423-3>
- Barnum, C., Endelman, B., & Shih, P. (2021). Utilizing plant synthetic biology to improve human health and wellness. *Frontiers in Plant Science*, 12. <https://doi.org/10.3389/fpls.2021.691462>
- Küken, A. and Nikoloski, Z. (2019). Computational approaches to design and test plant synthetic metabolic pathways. *Plant Physiology*, 179(3), 894-906. <https://doi.org/10.1104/pp.18.01273>
- Nørskov, J., Abild-Pedersen, F., Studt, F., & Bligaard, T. (2011). Density functional theory in surface chemistry and catalysis. *Proceedings of the National Academy of Sciences*, 108(3), 937-943. <https://doi.org/10.1073/pnas.1006652108>
- O'Sullivan, A., Henrick, B., Dixon, B., Zivkovic, A., Smilowitz, J., Lemay, D., ... & Schaefer, S. (2017). 21st century toolkit for optimizing population health through precision nutrition. *Critical Reviews in Food Science and Nutrition*, 58(17), 3004-3015. <https://doi.org/10.1080/10408398.2017.1348335>
- Barnum, C., Endelman, B., & Shih, P. (2021). Utilizing plant synthetic biology to improve human health and wellness. *Frontiers in Plant Science*, 12. <https://doi.org/10.3389/fpls.2021.691462>
- DeNies, M., Liu, A., & Schnell, S. (2020). Are the biomedical sciences ready for synthetic biology?. *Biomolecular Concepts*, 11(1), 23-31. <https://doi.org/10.1515/bmc-2020-0003>
- Küken, A. and Nikoloski, Z. (2019). Computational approaches to design and test plant synthetic metabolic pathways. *Plant Physiology*, 179(3), 894-906. <https://doi.org/10.1104/pp.18.01273>
- McCarthy, D. and Medford, J. (2020). Quantitative and predictive genetic parts for plant synthetic biology. *Frontiers in Plant Science*, 11. <https://doi.org/10.3389/fpls.2020.512526>
- Mohammadinejad, R., Karimi, S., Iravani, S., & Varma, R. (2016). Plant-derived nanostructures: types and applications. *Green Chemistry*, 18(1), 20-52. <https://doi.org/10.1039/c5gc01403d>
- Shelake, R., Pramanik, D., & Kim, J. (2019). Exploration of plant-microbe interactions for sustainable agriculture in crispr era. *Microorganisms*, 7(8), 269. <https://doi.org/10.3390/microorganisms7080269>

- Yu, P. (2024). Metal–organic framework-mediated delivery of nucleic acid across intact plant cells. *Acs Applied Materials & Interfaces*, 16(15), 18245-18251. <https://doi.org/10.1021/acsami.3c19571>
- Biggs, B., Lim, C., Sagliani, K., Shankar, S., Stephanopoulos, G., Mey, M., ... & Ajikumar, P. (2016). Overcoming heterologous protein interdependency to optimize p450-mediated taxol precursor synthesis in *Escherichia coli*. *Proceedings of the National Academy of Sciences*, 113(12), 3209-3214. <https://doi.org/10.1073/pnas.1515826113>
- Kiss, G., Çelebi-Ölçüm, N., Moretti, R., Baker, D., & Houk, K. (2013). Computational enzyme design. *Angewandte Chemie*, 52(22), 5700-5725. <https://doi.org/10.1002/anie.201204077>
- Mintz-Oron, S., Meir, S., Malitsky, S., Ruppin, E., Aharoni, A., & Shlomi, T. (2011). Reconstruction of *Arabidopsis* metabolic network models accounting for subcellular compartmentalization and tissue-specificity. *Proceedings of the National Academy of Sciences*, 109(1), 339-344. <https://doi.org/10.1073/pnas.1100358109>
- Sato, H., Saito, K., & Yamazaki, M. (2019). Acceleration of mechanistic investigation of plant secondary metabolism based on computational chemistry. *Frontiers in Plant Science*, 10. <https://doi.org/10.3389/fpls.2019.00802>