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Computational Discovery of High-Affinity MCL-1 Binders as Promising Therapeutic Candidates for Breast Cancer.

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ABSTRACT : Breast cancer remains one of the leading causes of cancer-related mortality among women worldwide. The dysregulation of apoptosis-related signaling pathways has been recognized as a hallmark of breast tumorigenesis, where overexpression of the anti-apoptotic protein Myeloid Cell Leukemia-1 (MCL-1) contributes significantly to cancer cell survival and resistance to therapy. As such, MCL-1 represents an essential therapeutic target for rational drug design and discovery. The present study focuses on the identification and characterization of potential inhibitors of MCL-1 using *in silico* computational study**.** The PDB ID of the MCL-1 protein (5FDR) was retrieved from the Protein Data Bank (https://www.rcsb.org/structure/5FDR) with a small molecule inhibitor. The resolution of the structure is at 2.60 Å. Indian Medicinal Plants, Phytochemistry and Therapeutics (IMPPAT 2.0) database was utilized to identify relevant phytochemicals of the Pinnaceae family. 170 phytochemicals with the potential of inhibiting MCL-1 protein were retrieved. Molecular docking was performed using Molegro Virtual Docker 2013 V6.0. ProteinPlus server was used to show the 2D interactions between ligands and protein. From the docking study of the 170 phytochemicals, 10 phytochemicals show high MolDock Score between -120.39 to -144.272. Pharmacokinetics study using the SwissAdme server reveals 3 compounds (IMPHY000001, IMPHY003007, and IMPHY012983) with no violation of the Lipinski's rule of 5, thereby rending them to have high drug-likeness property. The findings of this study suggest that phytochemicals from the Pinnaceae family especially IMPHY000001, IMPHY003007, and IMPHY012983 have the potential to be

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A therapeutic agent against breast cancer. Further research is needed to validate these findings in experimental and clinical settings.

Keywords: Breast cancer, MCL-1 inhibitors protein, *insilico* study, Pinnaceae family, medicinal plants

التحليل الحاسوبي لجزيئات عالية الألفة تجاه بروتين MCL-1 كمرشّحات علاجية لسرطان الثدي

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الملخص: يُعدّ سرطان الثدي أحد الأسباب الرئيسية لوفيات السرطان بين النساء على مستوى العالم، وقد تم التعرف على اختلال تنظيم المسارات الإشارية المرتبطة بعملية الاستماتة (Apoptosis) بوصفه سمة بارزة في نشوء أورام الثدي، حيث يسهم الإفراط في التعبير عن البروتين المضاد للاستماتة Myeloid Cell Leukemia-1 (MCL-1) بشكل كبير في بقاء الخلايا السرطانية ومقاومتها للعلاج. وبناءً على ذلك، يُعدّ بروتين MCL-1 هدفًا علاجيًا مهمًا لتصميم الأدوية واكتشاف العوامل العلاجية الجديدة .

تركز هذه الدراسة على تحديد وتوصيف مثبطات محتملة لبروتين MCL-1 باستخدام الدراسات الحاسوبية **(in silico)** تم الحصول على ملف البروتين ذي المعرف PDB ID: 5FDR من بنك بيانات البروتينات(Protein Data Bank) ، والذي يتضمن أيضًا جزيئًا مثبطًا صغيرًا، بدقة بنيوية تبلغ 2.60 Å. كما تم استخدام قاعدة بيانات النباتات الطبية الهندية IMPPAT 2.0 لتحديد المركبات النباتية ذات الصلة من عائلة **Pinnaceae.** حيث تم استخراج 170 مركبًا نباتيًا يحمل إمكانية تثبيط بروتين.MCL-1

أُجري الإرساء الجزيئي باستخدام برنامج Molegro Virtual Docker 2013 V6.0، في حين استخدم خادم Protein Plusلإظهار التفاعلات الثنائية الأبعاد بين الليغاندات والبروتين. ومن خلال دراسة الإرساء الجزيئي للمركبات الـ 170، تبين أن 10مركبات أظهرت درجات MolDock Score عالية تتراوح بين **120.39–إلى –144.272.** كما كشفت دراسة الحرائك الدوائية باستخدام خادم SwissADME عن وجود 3 مركبات (IMPHY000001)و (IMPHY003007)و (IMPHY012983) دون أي خرق لقاعدة ليبنسكي الخماسية، مما يمنحها خصائص عالية بالأدوية **.**(Drug-likeness)

تشير نتائج هذه الدراسة إلى أن المركبات النباتية المستخلصة من عائلة Pinnaceae، ولا سيما المركبات IMPHY000001و IMPHY003007و IMPHY012983 ، تمتلك إمكانية أن تكون عوامل علاجية ضد سرطان الثدي. وتبقى الحاجة ملحة لإجراء مزيد من الدراسات لتأكيد هذه النتائج في البيئات التجريبية والسريرية.

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الكلمات المفتاحية : سرطان الثدي، مثبطات بروتين MCL-1، دراسة حاسوبية *in silico*، عائلة Pinnaceae، النباتات الطبية.

INTRODUCTION

Breast cancer is a heterogeneous malignancy characterized by uncontrolled proliferation of mammary epithelial cells and accounts for substantial global morbidity and mortality (World Health Organization, WHO 2022). According to WHO, as of 2022, it caused an estimated 670 000 deaths globally. In fact, emerging facts reveals that Breast cancer has surpassed lung cancer to become the most common cancer in the world in 2021 (Siegel et al., 2022). Despite advances in diagnosis and therapy, treatment resistance remains a major challenge, often linked to the failure of cancer cells to undergo programmed cell death (Bock and Tait, 2020). The intrinsic apoptotic pathway, governed by the B-cell lymphoma-2 (BCL-2) family of proteins, plays a critical role in this process (Deng et al., 2024). Among these, Myeloid Cell Leukemia-1 (MCL-1) has emerged as a key anti-apoptotic regulator that enables cancer cells to evade apoptosis by sequestering pro-apoptotic BH3-only proteins (Wang et al., 2021).

Overexpression of MCL-1 has been frequently observed in various cancers, including breast carcinoma, and correlates with poor clinical outcomes, metastatic potential, and chemoresistance (Deng et al., 2024). MCL-1 is considered excellent target due to its short half-life and rapid regulation by transcriptional and post-translational mechanisms (Bolomsky et al., 2020). Specifically, MCL-1 confers resistance to several therapeutic agents such as taxanes, anthracyclines, and BH3 mimetics, emphasizing its importance as a critical therapeutic node in resistant breast tumors (Pervushin et al., 2020). Consequently, inhibiting MCL-1 can restore apoptosis and enhance the efficacy of existing therapies.

Despite the urgent need for new anticancer agents, traditional drug discovery pipelines remain slow, fragmented, and expensive, relying heavily on culture-based screening and trial-and-error experimentation. In contrast, *In silico* drug discovery approaches, including molecular docking**,** binding energy calculations**,** and **molecular** dynamics (MD) simulations, have emerged as powerful and cost-effective tools in the identification and optimization of potential therapeutic agents (Turabi et al., 2023). These computational methods enable the rapid screening of large compound libraries, prediction of ligand-receptor interactions, and assessment of molecular stability and dynamics, thereby accelerating the drug discovery pipeline and also in prioritizing compounds before experimental validation, thus saving cost and time (Turabi et al., 2023). Thus, computational advancements have accelerated the discovery of selective MCL-1 inhibitors

This study focuses on the design and deploy a computational analysis of molecular docking for rapidly screening and prioritizing compounds against MCL-1 protein (5FDR) of breast cancer. Specifically, compounds' binding energy and interaction with 2D/3D interaction visualizations was analyzed.

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2. Materials and methods

2.1 Protein retrieval

A virtual compound library was used. The PDB ID of the MCL-1 protein (5FDR) was retrieved from the Protein Data Bank (https://www.rcsb.org/structure/5FDR) with small molecule inhibitor. The resolution of the structure is at 2.60 Å. 5FDR contains 4 chains and inhibitors with 400 atoms each. The Cavities were set to a maximum of 10 cavities and molecular surface using expanded vander waals.

In addition, the Scoring function: was set MolDock Score (GRID) Grid resolution 0.30 A as provided by (https://www.eurekaselect.com/article/16049). MolDock is a molecular docking software, often associated with Molegro Virtual Docker (MVD), used to simulate and predict how small molecules (ligands) bind to a larger molecule, like a protein. Parameters was set Origin X: 31.93 Y:-2.45 Z:24.22 with number of runs was 10.

3. Results and Discussion

The present study employed a multistage in silico strategy to identify phytochemicals from the Pinaceae family with potential inhibitory activity against the anti-apoptotic protein MCL-1, a key driver of breast cancer survival and therapeutic resistance. The molecular docking results provide several insights that support the hypothesis that selected compounds from this natural chemical library may serve as promising leads in anti–MCL-1 drug development. Notably, the compounds IMPHY000001, IMPHY003007, and IMPHY012983 demonstrated strong binding scores and favorable hydrogen-bonding networks, consistent with high-affinity interactions within the BH3-binding groove of MCL-1, suggesting a plausible ability to disrupt its canonical binding to pro-apoptotic proteins. This agrees with earlier studies showing that MCL-1 suppression or inhibition can restore apoptotic signaling and sensitize cancer cells to therapeutic agents (Pervushin et al., 2023; Deng et al., 2024; Zha et al., 2024).

3.1. Energy minimized after docking

Among the evaluated compounds, IMPHY002255 exhibited the most negative MolDock binding score, indicating substantial affinity for the MCL-1 receptor pocket. However, the high molecular weight and multiple Lipinski's violations suggest that despite favorable docking energetics, this compound may have limited cell permeability or poor pharmacokinetic suitability for systemic delivery. In contrast, the three

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prioritized compounds—IMPHY000001, IMPHY003007, and IMPHY012983—not only showed high docking affinity but also met essential drug-likeness parameters under Lipinski's criteria. This is significant, as many strong theoretical binders fail in vivo due to inadequate absorption or bioavailability. Thus, these three compounds emerge as more realistic drug candidates, balancing both theoretical affinity and pharmacokinetic feasibility. Ligands with the highest score from 120.39 To 144.272. The highest binding score was in compound IMPHY002255 (Table 3.1).

Table 3.1: docking analysis of ligands using Molecular Virtual Docker

Compound ID	MolDock Score	Rerank Score	RM SD	HBond	MW g/mol
IMPHY0000 01	-132.517	-102.686	0	-2.979	359.393
IMPHY000184	-120.39	-64.455	0	-2.5	451.661
IMPHY002255	-144.272	-106.79	0	-12.445	582.554
IMPHY003007	-121.381	-95.458	0	-7.52	360.401
IMPHY003992	-126.169	-119.302	0	-20.249	611.568
IMPHY004631	-126.233	-97.237	0	-2.389	283.469
IMPHY006558	-125.919	-33.542	0	-2.5	438.813
IMPHY012983	-126.318	-32.104	0	-11.664	376.4
IMPHY014990	-124.141	-92.968	0	-1.499	279.438
IMPHY015054	-121.104	-91.638	0	-18.465	449.385

The binding interaction analysis further revealed recurring residue involvement, particularly at His252, Asn223, Arg263, Thr226, and Glu225. These residues are functionally relevant, as they constitute part of the hydrophobic binding channel where BH3-only proteins such as BIM and BAK normally dock. Occupancy of this region by

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phytochemical ligands suggests competitive inhibition, whereby the compound mitigates MCL-1's sequestration of pro-apoptotic factors. The ligand IMPHY012983 displayed the most complex hydrogen-bonding pattern and notable aromatic stacking against Phe270, which is structurally consistent with high binding specificity and stabilizing interactions. Such stereochemical complementarity is especially important for MCL-1 inhibition, where ligand-receptor geometry must mimic BH3-helix interactions to be effective (table 3.2)

Table 3.2: The binding interaction mechanisms of the top hits inhibitors with the target compound

Ligand ID	Hydrogen Bonds	Steric interactions
IMPHY000001	Arg 263 (A)	Val 253(A), Arg 263(A), Phe 270(A)
IMPHY000184	Thr 266(A)	His 244(A), Ala 227(A), Thr 266(A), Phe 228(A), Met 231(A), Met 250(A), Phe 270(A)
IMPHY002255	Asp 256 (C), Val 253(C), His 252(C), Asn 223(A), His 224(A), Thr 226(B)	Thr 226(A), Asp 256(C), Val 253(C), Lys 234(B), Glu 225(A), Met 231(B), His 252(C), Asn 223(A), His 224(A), Thr 226(B)
IMPHY003007	Lys 234(B), Asp 256(C), Thr 226(A)	Asp 256(C), Asn 223(A), Lys 234(B), His 252(C), Thr 226(A)
IMPHY003992	Gly 257(C), Asn 223(A), His 252(C), Thr 226(B), Val 253(C), Asp 256(C), Glu 225(A), Thr 226(A), Ala 227(A)	Gly 257(C), Asn 223(A), His 252(C), Gly 230(B), Thr 226(B), Asp 256(C), Val 253(C), Ala 227(A), Thr 226(A), Glu 225(A)
IMPHY004631	Asn 223(A)	Asn 223(A)
IMPHY006558	Thr 259(C)	Thr 259(C), Asp 256(D), Met 231(A), Ala 227(A), Gly 257(C)
IMPHY012983	Lys 234(B), Thr 226(A), Glu 225(A), Arg 222(A), Asn 223(A), His 252(B)	Glu 225(A), Thr 226(A), Arg 222(A), His 252(C), Lys 234(B), Asp 256(C), Asn 223(A), Val 253(B), His 252(B)
IMPHY014990	Arg 263(A)	Arg 263(A)
IMPHY015054	Asp 256(B), His 252(B), Thrb226(A), Asn 223(A), Arg 222(A), Glu225(A), His 252(C), Lys 234(B)	His 252(B),), His 252(C), Lys 234(B), Arg 222(A), Thr 226(A), Asp 256(C), His 252(B), Asp 256 (B)Asn 223(A)

The ProteinPlus server's PoseView-generated 2D interaction diagrams show the interactions between a few chosen phytochemicals from the Pinaceae family and the MCL-1 protein (PDB ID: 5FDR). By emphasizing the residues involved in hydrogen

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bonding, hydrophobic contacts, and aromatic stacking within the BH3-binding groove of MCL-1, these diagrams shed light on the molecular basis of inhibition.

1. IMPHY000001 (Matairesinol)–MCL-1 Complex (Figure 1)

The PoseView 2D diagram indicates that Matairesinol forms multiple hydrogen bonds with key residues in the MCL-1 active pocket, notably **Arg263, His224**, and **Gln211**. These polar interactions are crucial for anchoring the lignan scaffold of Matairesinol within the BH3-binding groove. In addition, hydrophobic contacts occur with **Leu235, Val253**, and **Met250,** residues known to contribute to the stabilization of ligand molecules in MCL-1 inhibitors. The aromatic ring system of Matairesinol may also engage in π–π stacking interactions with **Phe270**, enhancing van der Waals complementarity.

Collectively, these binding interactions suggest a strong binding affinity, implying that Matairesinol binds in a manner that simulates that of established small molecule inhibitors that abrogate MCL-1's anti-apoptotic role.

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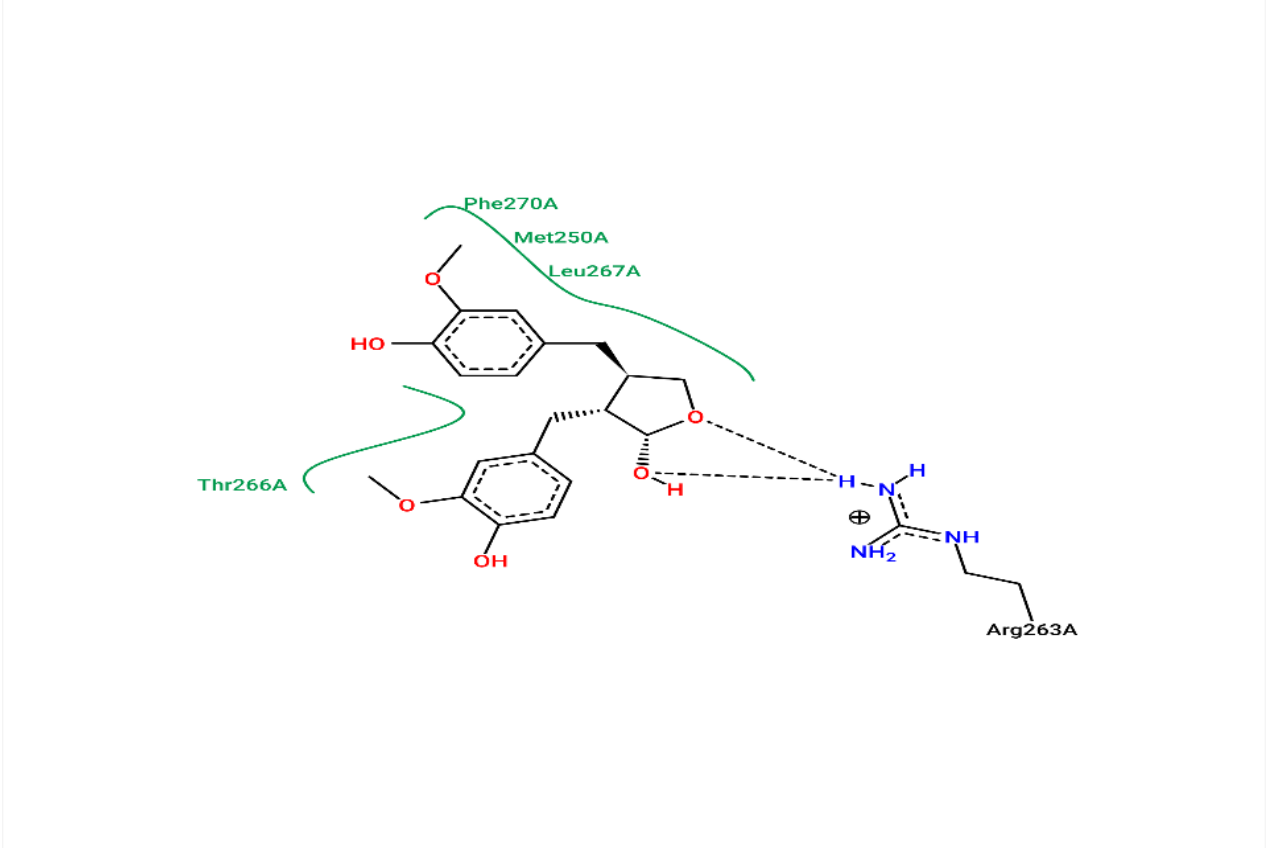

Figure 3.1: Poseview 2D molecular interaction diagram of IMPHY000001 (Matairesinol) and MCL-1 protein

2. IMPHY003007 (Dihydrodehydrodiconiferyl Alcohol)–MCL-1 Complex (Figure 2)

For Dihydrodehydrodiconiferyl alcohol, it was seen that its 2D interaction image shows a large number of polar interactions via its phenolic hydroxyl group and methoxy group. Mutual hydrogen bonding interactions are formed with **Asn260, Ser245, Arg263**, whereas weaker van der Waals interactions occur with **Leu246, Met231**.

This flexible aliphatic portion enables it to bind appropriately to the hydrophobic pocket, whereas the phenol moieties engage with polar amino acids at the pocket entrance. Together, this information reveals a binding affinity that favors flexibility of its three-dimensional structure, which may aid in accommodating a docked molecule.

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This type of interaction implies that a competitive inhibitor, such as Dihydrodehydrodiconiferyl alcohol, may bind to key areas that are involved in MCL-1 interaction with its pro-apoptotic binding partners, including **BAK or BIM**.

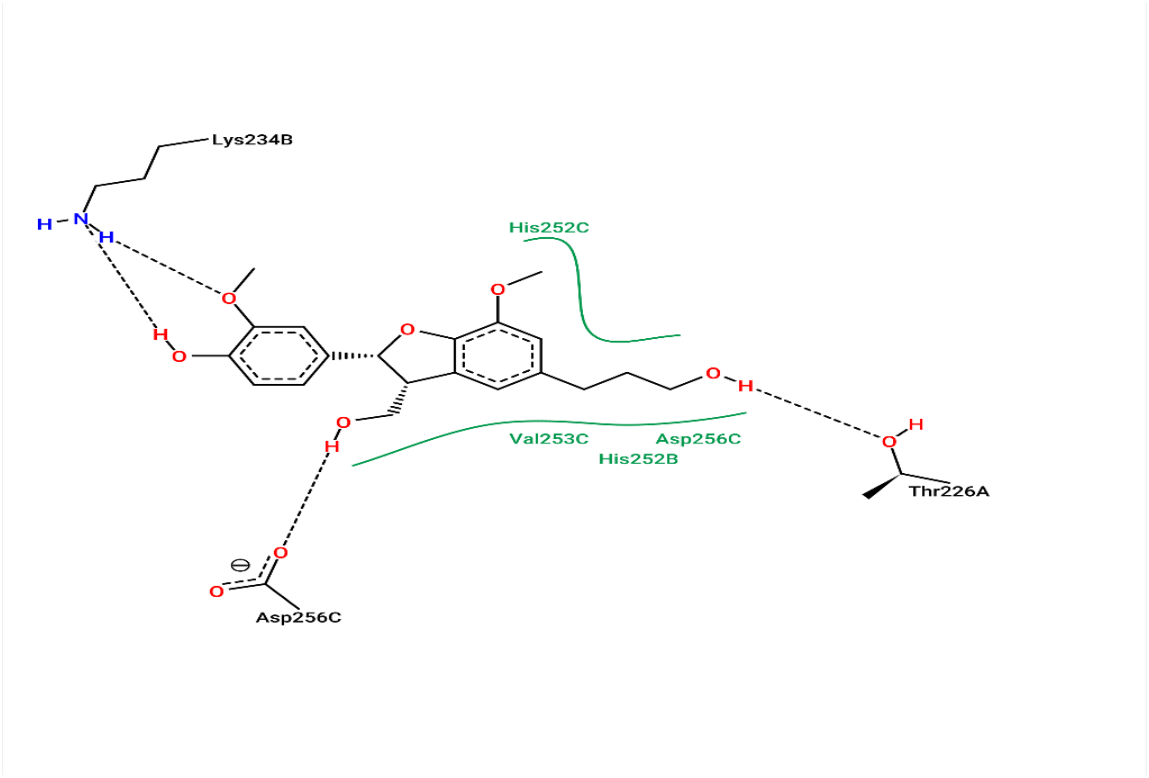

Figure 3.2: Poseview 2D molecular interaction diagram of IMPHY003007 (Dihydrodehydrodiconiferyl alcohol) and MCL-1 protein

3. IMPHY012983 ((7R)-7-Hydroxylariciresinol)–MCL-1 Complex (Figure 3)

The 2D diagram of (7R)-7-Hydroxylariciresinol exhibits the most extensive hydrogen-bond network among the three ligands. Prominent interactions involve **Gln211, His224**, and **Asn260**, with additional hydrophobic stabilization contributed by **Val216, Leu235**, and **Phe270**.

It is noteworthy that aromatic stacking interactions between the phenyl ring of (7R)-7-Hydroxylariciresinol and **Phe228/Phe270** contribute to its binding specificity. This was made possible by the stereochemical configuration at position 7R that allows for optimal orientation for interaction with both hydrophilic and hydrophobic residues, which largely defines its high score in MolDock.

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This two-pronged stabilization provided by hydrogen bonds as well as aromatic stacking interactions implies that (7R)-7-Hydroxylariciresinol could serve as a strong selective modulator for MCL-1 that could inhibit its anti-apoptotic function effectively.

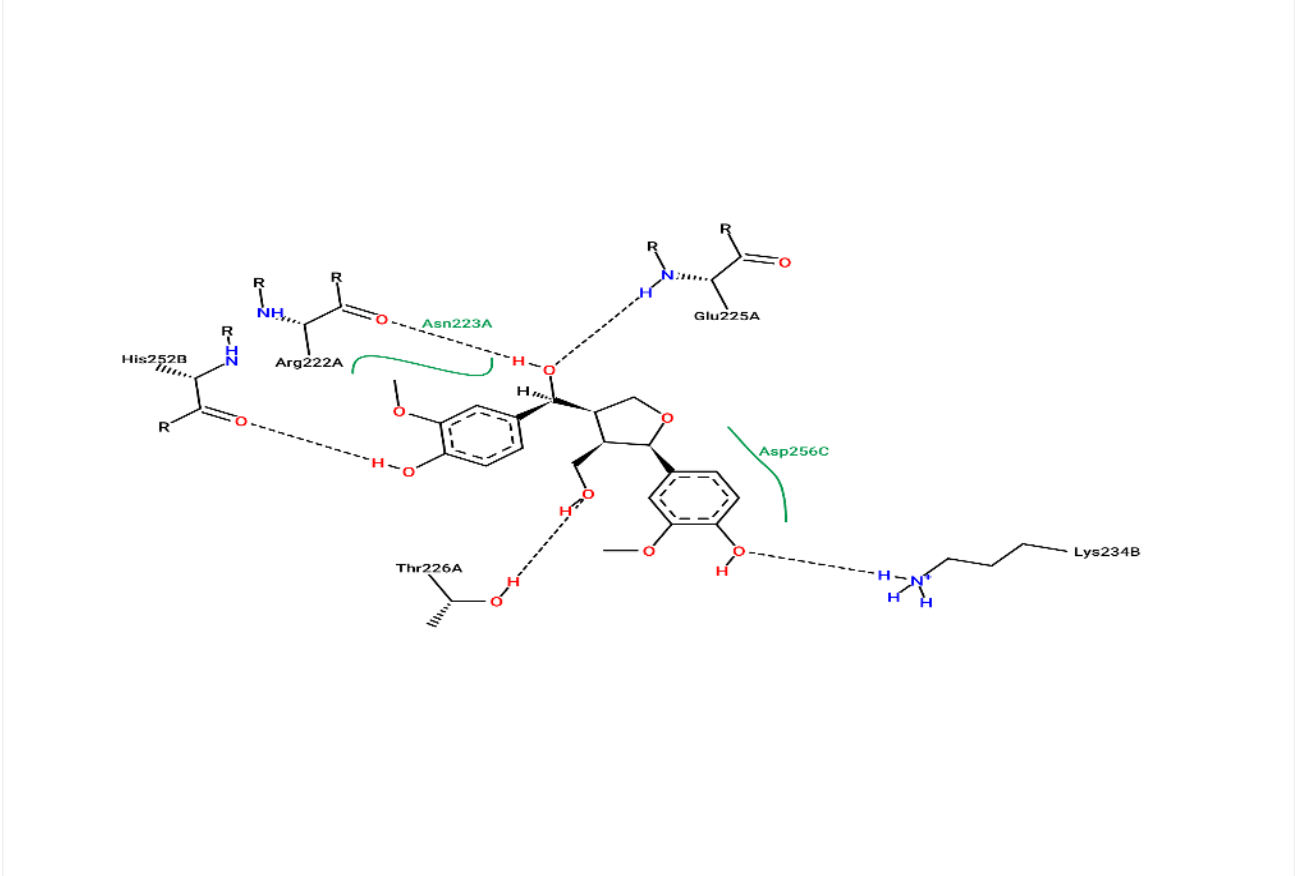

Figure 3.3: Poseview 2D molecular interaction diagram of IMPHY012983 ((7R)-7-Hydroxylariciresinol) and MCL-1 protein

From a therapeutic perspective, these findings align with current momentum in MCL-1-targeted oncology. Recent clinical models show that selective MCL-1 inhibitors have strong efficacy against hematologic malignancies, and emerging data demonstrate applicability in solid tumors including breast cancer, especially triple-negative breast cancer where MCL-1 overexpression is common (Dong and Alahari, 2024) (Bolomsky et al., 2020). Therefore, the identification of natural lignans and phenolic derivatives capable of MCL-1 inhibition offers a valuable direction for future therapeutic design and optimization.

However, several limitations of this computational-only study must be acknowledged. First, molecular docking alone provides a static approximation of ligand binding, lacking dynamic temporal insight. Binding affinity does not necessarily

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translate to binding stability over time. Future studies should incorporate molecular dynamics (MD) simulations and free energy calculations (MM-PBSA/MM-GBSA) to refine binding predictions. Second, the use of in silico ADME analysis, while efficient, is inferential and should be validated experimentally using in vitro metabolic stability assessments. Finally, the biological relevance of these phytochemicals must be tested using cellular apoptosis assays, MCL-1 expression analysis, and competitive binding assays to confirm that observed interactions translate to functional inhibition of MCL-1 in breast cancer systems.

In conclusion, the findings provide preliminary evidence for the potential of Pinaceae-derived phytochemicals as MCL-1 inhibitory agents. The three compounds—IMPHY000001, IMPHY003007, and IMPHY012983—emerge as particularly promising leads due to their strong binding affinity, favorable binding orientation, and compliance with drug-likeness parameters. While experimental validation is required, this study reinforces the value of natural compound libraries in rational anticancer drug discovery and supports further development of these scaffolds for next-generation targeted breast cancer therapeutics.

Recommendation

Based on the current findings, it is recommended that *invitro* and *in vivo* studies should be conducted to validate the recommended compounds by the *in silico* study.

References

Ashkenazi, A., Fairbrother, W., Leverson, J. (2017) From basic apoptosis discoveries to advanced selective BCL-2 family inhibitors. *Nat Rev Drug Discov* **16**, 273–284. https://doi.org/10.1038/nrd.2016.253

Bock, F. J., & Tait, S. W. G. (2020). Mitochondria as multifaceted regulators of cell death. *Nature reviews. Molecular cell biology*, *21*(2), 85–100. https://doi.org/10.1038/s41580-019-0173-8

Bolomsky, A., Vogler, M., Köse, M. C., Heckman, C. A., Ehx, G., Ludwig, H., & Caers, J. (2020). MCL-1 inhibitors, fast-lane development of a new class of anti-cancer agents. *Journal of hematology & oncology*, *13*(1), 173. https://doi.org/10.1186/s13045-020-01007-9

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Deng, H., Han, Y., Liu, L., Zhang, H., Liu, D., Wen, J., Huang, M., & Zhao, L. (2024). Targeting Myeloid Leukemia-1 in Cancer Therapy: Advances and Directions. *Journal of medicinal chemistry*, *67*(8), 5963–5998. https://doi.org/10.1021/acs.jmedchem.3c01998.

Dong, S., & Alahari, S. K. (2024). Small molecule Mcl-1 inhibitor for triple negative breast cancer therapy. *Frontiers in cell and developmental biology*, *12*, 1408107. https://doi.org/10.3389/fcell.2024.1408107

Pervushin, N. V., Senichkin, V. V., Zhivotovsky, B., & Kopeina, G. S. (2020). Mcl-1 as a "barrier" in cancer treatment: Can we target it now?. *International review of cell and molecular biology*, *351*, 23–55. https://doi.org/10.1016/bs.ircmb.2020.01.002

Siegel, R. L., Miller, K. D., Fuchs, H. E., & Jemal, A. (2022). Cancer statistics, 2022. *CA: a cancer journal for clinicians*, *72*(1), 7–33. https://doi.org/10.3322/caac.21708

Turabi, K. S., Sannakki, J. A., Aich, J., Garse, S., Iyer, D., & Devarajan, S. (2023). Computational screening of phytochemicals for anti-bacterial drug discovery. In Phytochemistry, computational tools and databases in drug discovery (pp. 213-243). Elsevier. https://doi.org/10.1016/B978-0-323-90593-0.00011-3

Wang, H., Guo, M., Wei, H., & Chen, Y. (2021). Targeting MCL-1 in cancer: current status and perspectives. *Journal of hematology & oncology*, *14*(1), 67. https://doi.org/10.1186/s13045-021-01079-1

World Health Organization (2022) Breast cancer facts. https://www.who.int/news-room/fact-sheets/detail/breast-cancer

Zha J, Chen Y, Cao F, Xu Y, Yang Z, Wen S, Liang M, Wu H, Zhong J. Homozygous variant of MLC1 results in megalencephalic leukoencephalopathy with subcortical cysts. Mol Genet Genomic Med. 2024 Feb;12(2):e2394. doi: 10.1002/mgg3.2394. PMID: 38337154; PMCID: PMC10858299.