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Chemical Profiling of Lawsone and Computational Designing of its Mannich Base Derivatives for Potential Biological Activity

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Abstract

The purpose of this study was to explore the drug development potential of 15 newly synthesized Mannich base derivatives of Lawsone using in silico tools. The compounds were initially designed using ACD/ChemSketch, and their molecular properties were evaluated through Molinspiration, where all derivatives satisfied Lipinski's Rule of Five, indicating good drug-likeness. PASS online prediction revealed significant biological activity for several compounds, with Compound O identified as the strongest inhibitor of ubiquinol–cytochrome c reductase, and Compound E as the most potent inhibitor of gluconate 2-dehydrogenase. Compound K was predicted to be a CYP2J2 substrate, while Compound B exhibited the least predicted activity. Further, Swiss Target Prediction indicated that kinases were the most probable targets, followed by enzymes, proteases, nuclear receptors, and ligand-gated ion channels. The study successfully identified several Lawsone derivatives with promising drug-like and bioactive profiles, offering a strong foundation for future experimental validation and development of novel therapeutic agents.

Keywords: Lawsone, Mannich Reaction, Henna, Naphthoquinone, Chemsketch, Molinspiration, PASS, Swiss Target Prediction.

Introduction

Natural products are products that obtained from various natural sources which could be plants, microbesoranimals. Natural products can be an entire organism or a part of an organism or even an extract or an exudate, or pure compound isolated from plants, animals or microorganisms. Some of the examples are alkaloids, which are nitrogen-containing compounds derived from amino acids (e.g. morphine used as pain killer and vincristine used to treat cancers). Terpenoidsare formed from isoprene units (e.g. Taxol used in chemotherapy, Artemisinin used to treat malaria). Phenolic compounds are those having aromatic rings bonded to hydroxyl groups and glycosides are compounds having a sugar molecule linked to a non-sugar molecule frequently referred to as an aglycone. (eg. digoxin, a cardiac glycoside vital to heart function).

Lawsone, it is a Naphthoquinone derivative which is 2-hydroxy 1,4-naphthoquinone (or 2-hydroxy naphthalene 1,4-dione) can be found in the leaves of the plant Lawsonia inermis belonging to the family Lythraceae. It appears as yellow prims or crystals, melting point is195^0C, molecular weight is around 174.15g/mol and relatively insoluble in water. The biosynthesis of lawsone starts when phosphoenolpyruvate (PEP) and D- erythrose 4-phosphate (E4P) enter the shikimate pathway for conversion to shikimate which produces chorismite as its end product and this compound serves as a precursor for various aromatic compounds including 1, 4-naphthoquinones[1-4].

Chemistry of Lawsone: The compound contains a fused ring structure that consists of 1,4-naphthoquinone with a hydroxyl substituent at position 2 and biological activity depends on carbonyl groups at C1 and C4 together with a hydroxyl group at C2. Lawsone differs from juglone and plumbagin and menadione and other naphthoquinones by having a hydroxyl group attached to its 2-position. The hydroxyl group at 2-position enables lawsone to exhibit both enol and enone characteristics that other naphthoquinones possess. The hydroxyl group enables enol-keto tautomerism which reveals the 2- and 4- positions as possible reaction sites. Lawsone includes an enone functional group which enables chemical reactions at its 3-position. The functional groups present in lawsone enable its use as a foundation for creating naphthoquinone analogues. Various studies show that extending carbon chains and adding amines and aromatic rings and halides at the 3-position of lawsone improves its biological activity and medicinal properties. When comes to core structure, it is Naphthoquinone ring in which keto group at 1st and 4th position. On further elucidating, main component of Naphthoquinone was found to be Quinone[1-11].

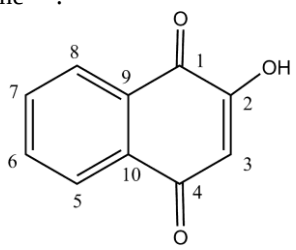
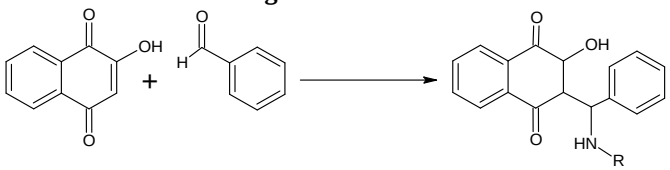


Figure-1: Lawsone.



Scheme-1: Reaction Scheme for Mannich Base Derivatives of Lawsone.

Table-1: Structure of Lawsone Derivatives.

Sl No.	CODE	R
1.	A	$C_6H_4(OH)_2$
2.	B	C_6H_5BrO
3.	C	C_7H_8
4.	D	C_7H_8
5.	E	C_7H_8O
6.	F	$C_8H_{10}O$
7.	G	C_8H_{10}
8.	H	$C_6H_4C_{l2}$
9.	I	C_6H_5F
10.	J	$C_8H_7F_3$
11.	K	C_6H_6
12.	L	C_6H_6O
13.	M	C_6H_5Cl
14.	N	$C_6H_4Cl_2$
15.	O	$C_6H_5NO_2$

Lawsone (2-hydroxy-1,4-naphthoquinone) undergoes a Mannich reaction in the presence of benzaldehyde and a primary amine to yield Mannich base derivatives.

Materials and Methods

In silico analysis of the designed derivatives was carried out using the following computational tools.

Table-2: Software used in *In Silico* Study.

Software Used	Usage
ACD/ ChemSketch	To draw 2D Structure
Molinspiration	To calculate drug likeness property
PASS (Prediction of activity spectra for substances)	To Predict Bioactivity
Swiss Target Prediction	To Predict Target and activity

ACD/ChemSketch: ACD/ChemSketch is a molecular modelling application which enables users to build and edit chemical structure images. Through this program users can view molecules and molecular models both in two-dimensional and three-dimensional representations to study chemical bond structures and functional group characteristics.

The program provides users with sophisticated tools that enable molecular rotation and color application for enhanced visualization.

Mol inspiration: It provides an extensive selection of cheminformatics tools for molecule processing and manipulation which includes SMILES and SD file conversion and molecule normalization and tautomer generation and molecule fragmentation and various molecular property calculations essential for QSAR and molecular modelling and drug design and high-quality molecule depiction and molecular database tools with substructure and similarity search capabilities.

Pass online: It is used to analyse molecule biological capabilities through prediction of activity spectra of substances. The evaluation of new compounds against known biologically active substances enables researchers to determine if a compound will demonstrate specific effects.

Swiss target prediction: It is a web-based tool that implements ligand-based reverse screening through 2D (fingerprint) and 3D (shape/electrostatic) similarity analysis to forecast protein targets of small molecules.

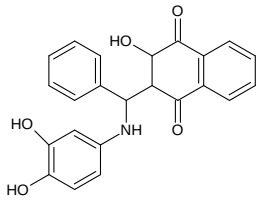
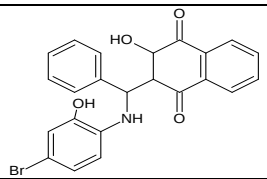
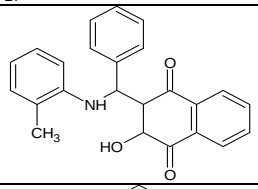
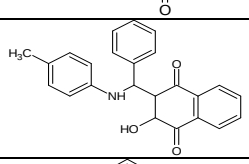
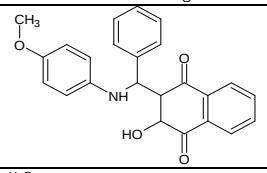
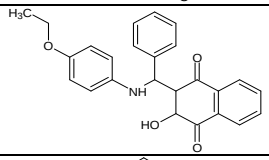
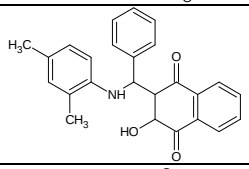
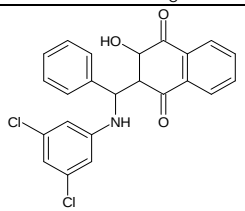
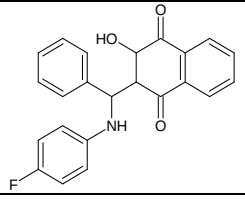
Results and Discussion

Using various Computational tools, following Results have been obtained and interpreted. 15 Mannich base Lawsone has been derived using ACD/ ChemSketch. By Performing Molinspiration, were able to detect lead like compounds and drug likeness. Using PASS online, predicted the potential bioactivity and at last, by using Swiss Target Prediction, able to predict possible Protein Target of the derived compounds.

ACD/ChemSketch: In this Section Table-3 shows that using ACD/Chemsketch, designed 15 Mannich base Lawsone derivatives including its Smiles notation and IUPAC name. All the compounds are labeled with specific Codes. Codes are A, B, C etc. with respective of each compound.

Molinspiration: By performing Molispiration, Table-4 and Table-5 shows all fifteen lawsone-derived compounds fully comply with Lipinski's Rule of Five, each with a molecular weight under 500 Da, $\log P \leq 5$, no more than 5 hydrogen bond donors, and no more than 10 hydrogen bond acceptors which results in zero violations.
This suggests for a strong potential for oral bioavailability and favourable ADME properties.

Table-3: Lawsone Derivatives with IUPAC names and Smile Notation.

Sl. No	Code	Structure	Smiles Notation	IUPAC Name
1.	A		OC1C(=O)c2ccccc2C(=O)C1C(Nc1cc(O)c(O)cc1)c1ccccc1	2-[(3,4-dihydroxyanilino)(phenyl)methyl]-3-hydroxy-2,3-dihydronaphthalene-1,4-dione
2.	B		OC1C(=O)c2ccccc2C(=O)C1C(Nc1ccc(Br)cc1O)c1ccccc1	2-[(4-bromo-2-hydroxyanilino)(phenyl)methyl]-3-hydroxy-2,3-dihydronaphthalene-1,4-dione
3.	C		OC1C(=O)c2ccccc2C(=O)C1C(Nc1ccccc1C)c1ccccc1	2-hydroxy-3-[(2-methylanilino)(phenyl)methyl]-2,3-dihydronaphthalene-1,4-dione
4.	D		OC1C(=O)c2ccccc2C(=O)C1C(Nc1ccc(C)cc1)c1ccccc1	2-hydroxy-3-[(4-methylanilino)(phenyl)methyl]-2,3-dihydronaphthalene-1,4-dione
5.	E		OC1C(=O)c2ccccc2C(=O)C1C(Nc1ccc(OC)cc1)c1ccccc1	2-hydroxy-3-[(4-methoxyanilino)(phenyl)methyl]-2,3-dihydronaphthalene-1,4-dione
6.	F		OC1C(=O)c2ccccc2C(=O)C1C(Nc1ccc(OCC)cc1)c1ccccc1	2-hydroxy-3-[(4-ethoxyanilino)(phenyl)methyl]-2,3-dihydronaphthalene-1,4-dione
7.	G		OC1C(=O)c2ccccc2C(=O)C1C(Nc1ccc(C)cc1C)c1ccccc1	2-hydroxy-3-[(4,6-methylanilino)(phenyl)methyl]-2,3-dihydronaphthalene-1,4-dione
8.	H		OC1C(=O)c2ccccc2C(=O)C1C(Nc1cc(Cl)cc(Cl)c1)c1ccccc1	2-[(3,5-dichloroanilino)(phenyl)methyl]-3-hydroxy-2,3-dihydronaphthalene-1,4-dione
9.	I		OC1C(=O)c2ccccc2C(=O)C1C(Nc1ccc(F)cc1)c1ccccc1	2-[(4-fluoroanilino)(phenyl)methyl]-3-hydroxy-2,3-dihydronaphthalene-1,4-dione

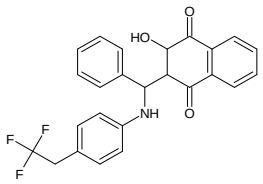
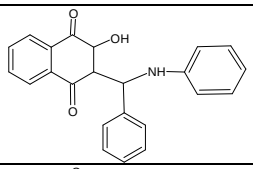
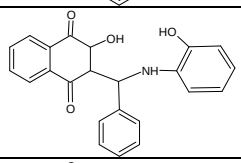
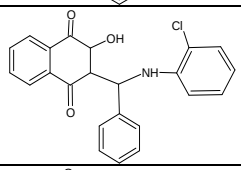
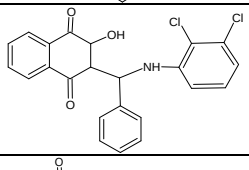
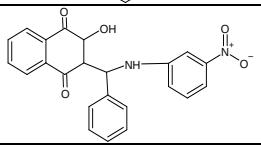
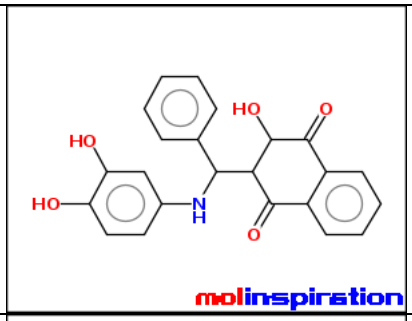
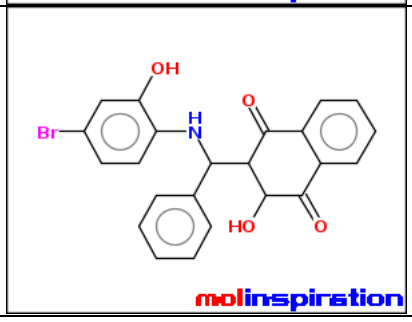
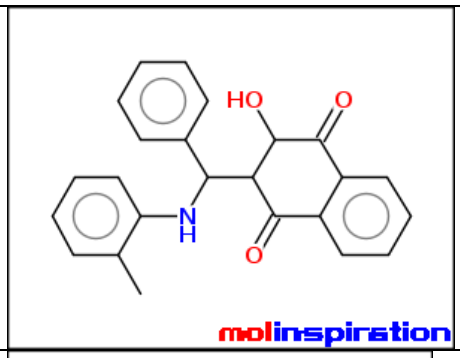
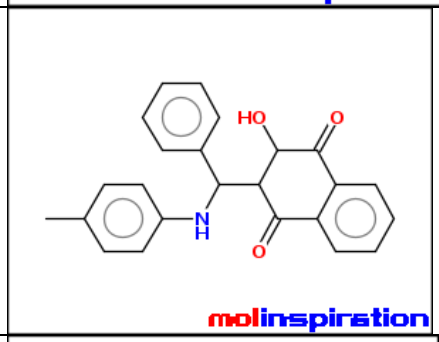
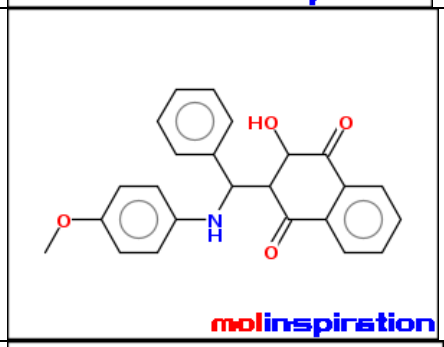
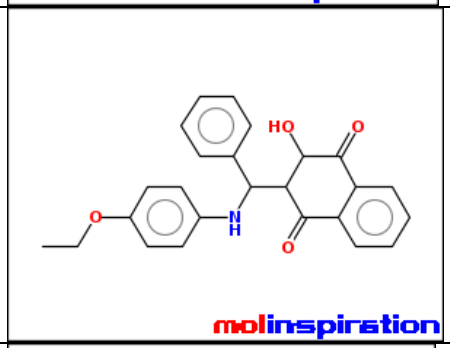
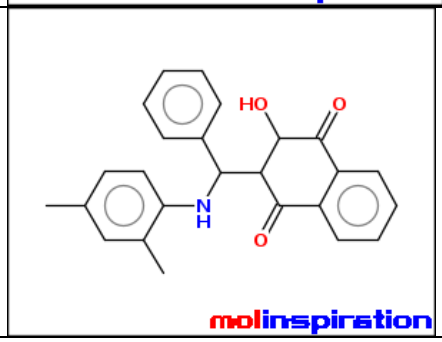
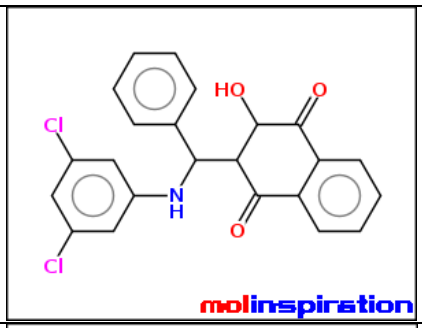
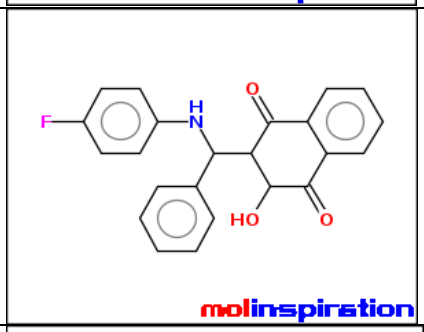
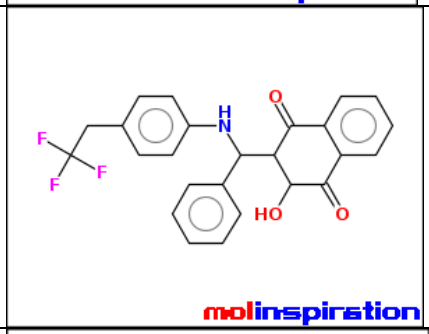
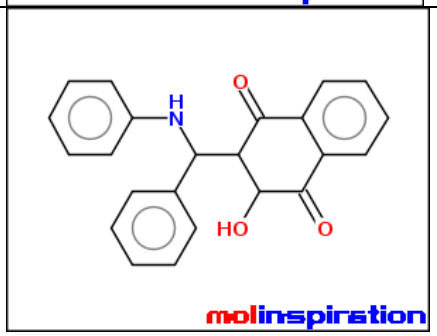
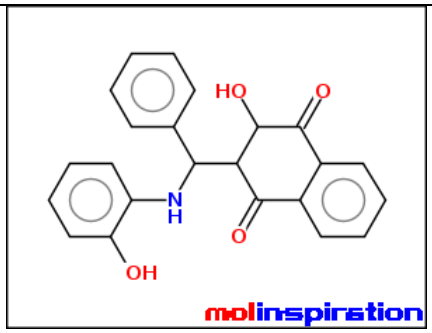
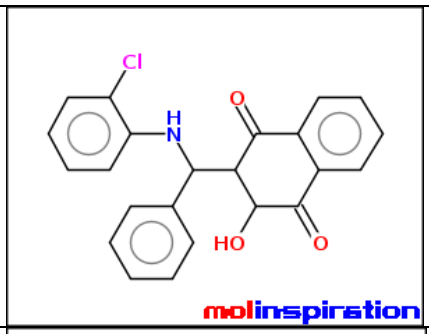
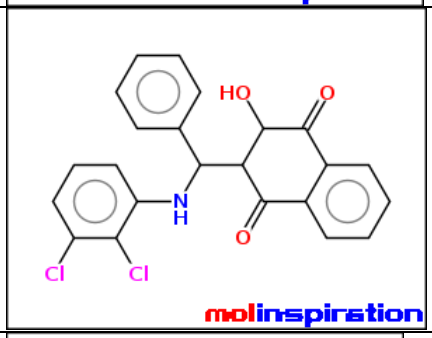
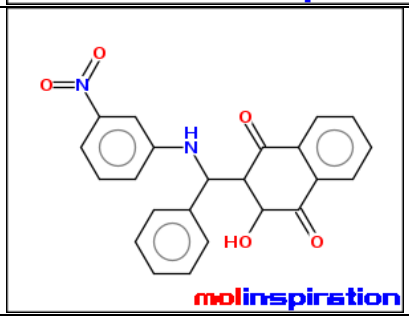
10.	J		OC1C(=O)c2ccccc2C(=O)C1C(Nc1ccc(CC(F)(F)F)cc1)c1ccccc1	2-[(4-trifluoromethylanilino)(phenyl)methyl]-3-hydroxy-2,3-dihydronaphthalene-1,4-dione
11.	K		OC1C(=O)c2ccccc2C(=O)C1C(Nc1ccccc1)c1ccccc1	2-[anilino(phenyl)methyl]-3-hydroxy-2,3-dihydronaphthalene-1,4-dione
12.	L		OC1C(=O)c2ccccc2C(=O)C1C(Nc1ccccc1O)c1ccccc1	2-hydroxy-3-[(2-hydroxyanilino)(phenyl)methyl]-2,3-dihydronaphthalene-1,4-dione
13.	M		OC1C(=O)c2ccccc2C(=O)C1C(Nc1ccccc1Cl)c1ccccc1	2-[(2-chloroanilino)(phenyl)methyl]-3-hydroxy-2,3-dihydronaphthalene-1,4-dione
14.	N		OC1C(=O)c2ccccc2C(=O)C1C(Nc1cccc(Cl)c1Cl)c1ccccc1	2-[(2,3-dichloroanilino)(phenyl)methyl]-3-hydroxy-2,3-dihydronaphthalene-1,4-dione
15.	O		O=[N+]([O-])c1cc(ccc1)NC(C1C(O)C(=O)c2ccccc2C1=O)c1ccccc1	2-hydroxy-3-[(3-nitroanilino)(phenyl)methyl]-2,3-dihydronaphthalene-1,4-dione

Table-4: Molinspiration Data of Lawsone Derivatives.

Sl. No.	Structure	Result
1.		Molinspiration property engine v2022.08 miLogP 2.62 TPSA 106.85 n atoms 29 MW 389.41 n ON 6 n OHNH 4 n violations 0 nrotb 4 volume 340.93
2.		Molinspiration property engine v2022.08 miLogP 4.10 TPSA 86.62 natoms 29 MW 452.30 nON 5 nOHNH 3 nviolations 0 nrotb 4 volume 350.79

3.		Molinspiration property engine v2022.08 miLogP 3.99 TPSA 66.40 natoms 28 MW 371.44 nON 4 nOHNH 2 nviolations 0 nrotb 4 volume 341.45
4.		Molinspiration property engine v2022.08 miLogP 4.03 TPSA 66.40 natoms 28 MW 371.44 nON 4 nOHNH 2 nviolations 0 nrotb 4 volume 341.45
5.		Molinspiration property engine v2022.08 miLogP 3.64 TPSA 75.63 natoms 29 MW 387.44 nON 5 nOHNH 2 nviolations 0 nrotb 5 volume 350.44
6.		Molinspiration property engine v2022.08 miLogP 4.02 TPSA 75.63 natoms 30 MW 401.46 nON 5 nOHNH 2 nviolations 0 nrotb 6 volume 367.24
7.		Molinspiration property engine v2022.08 miLogP 4.41 TPSA 66.40 natoms 29 MW 385.46 nON 4 nOHNH 2 nviolations 0 nrotb 4 volume 358.01

8.		Molinspiration property engine v2022.08 miLogP 4.87 TPSA 66.40 natoms 29 MW 426.30 nON 4 nOHNH 2 nviolations 0 nrotb 4 volume 351.96
9.		Molinspiration property engine v2022.08 miLogP 3.75 TPSA 66.40 natoms 28 MW 375.40 nON 4 nOHNH 2 nviolations 0 nrotb 4 volume 329.82
10.		Molinspiration property engine v2022.08 miLogP 4.69 TPSA 66.40 natoms 32 MW 439.43 nON 4 nOHNH 2 nviolations 0 nrotb 6 volume 372.99
11.		Molinspiration property engine v2022.08 miLogP 3.59 TPSA 66.40 natoms 27 MW 357.41 nON 4 nOHNH 2 nviolations 0 nrotb 4 volume 324.89
12.		Molinspiration property engine v2022.08 miLogP 3.32 TPSA 86.62 natoms 28 MW 373.41 nON 5 nOHNH 3 nviolations 0 nrotb 4 volume 332.91

13.		Molinspiration property engine v2022.08 miLogP 4.22 TPSA 66.40 natoms 28 MW 391.85 nON 4 nOHNH 2 nviolations 0 nrotb 4 volume 338.43
14.		Molinspiration property engine v2022.08 miLogP 4.85 TPSA 66.40 natoms 29 MW 426.30 nON 4 nOHNH 2 nviolations 0 nrotb 4 volume 351.96
15.		Molinspiration property engine v2022.08 miLogP 3.52 TPSA 112.22 natoms 30 MW 402.41 nON 7 nOHNH 2 nviolations 0 nrotb 5 volume 348.22

Pass: Table-6 shows that 15 compounds' possible biological activities are revealed by the PASS (Prediction of Activity Spectra for Substances) analysis. Significant differences in biological activity between the compounds are found based on the predictions, especially with regard to CYP2J2 substrate affinity, gluconate 2-dehydrogenase (acceptor) inhibition, and ubiquinol-cytochrome c reductase inhibition. A thorough explanation of the best and worst-performing compounds for these targets can be found below.

As an inhibitor of ubiquinol-cytochrome c reductase, compound O shows the highest predicted activity. The nitro group on the aniline ring may be the cause of this high anticipated activity. Nitro groups may promote stronger interactions with the active site of the enzyme and are known to improve electron-withdrawing capacity. Furthermore, the naphthoquinone core structure may increase binding affinity to mitochondrial respiratory chain proteins by taking part in redox processes. Compound B exhibits the lowest anticipated inhibitory activity even though it contains a hydroxyl group and a bromine atom. Due to steric hindrance or improper placement within the binding pocket, the bromo substituent may not interact favourably with the enzyme target despite increasing molecular weight and lipophilicity.

As an inhibitor of the enzyme gluconate 2-dehydrogenase, which is involved in the metabolism of carbohydrates, compound E exhibits superior activity. Its structure probably provides the best possible spatial arrangement and electrical characteristics to promote interaction with the active site of the enzyme. By strengthening hydrogen bonds or altering the molecule's electron distribution, the methoxy group at the para position may support this activity. Furthermore, the structure's functional groups and planar aromatic systems might promote stable binding in the active site, raising the expected inhibitory potential. However, in compound B Together with the hydroxyl, the bromo group may cause steric hindrance or lead to poor orientation inside the pockets of the enzyme. Its binding efficiency is probably decreased by these structural restrictions, resulting in consistently low activity.

The CYP2J2 enzyme, a cytochrome P450 isoform involved in drug metabolism, is expected to prefer compound K as its substrate. Aniline and phenyl groups, as well as the lack of large substituents like halogens or nitro groups, may encourage advantageous interactions with the hydrophobic pocket of the enzyme. This could improve binding efficiency or metabolic conversion. Once more, compound B is anticipated to have a low CYP2J2 substrate potential. Effective metabolism may be

hindered by the bromine substituent's introduction of steric bulk, which interferes with binding or appropriate orientation within the enzyme's active site.

Swiss target prediction: Table-7 shows that based on their chemical structures, we sought to determine the most likely macromolecular targets for the compounds we had chosen using Swiss Target Prediction. The compounds had the highest predicted binding affinity for the kinase family, according to the analysis, suggesting a high potential for interaction with proteins involved in cellular regulation and signal transduction pathways. Enzymes were the next most likely targets after kinases, indicating a potential impact on a range of biochemical processes. The third most likely target class was determined to be proteases, suggesting that they may play a part in regulating the activation or degradation of proteins. Furthermore, it was anticipated that ligand-gated ion channels and nuclear receptors would be less prominent but still significant targets, suggesting possible impacts on cellular signalling and gene expression, respectively. These results offer a fundamental comprehension of the pharmacological profiles and may guide further in vitro and in vivo validation studies.

Table-5: Results from Molinspiration. Lipinski's rule of lawsone derivatives.

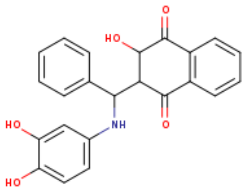
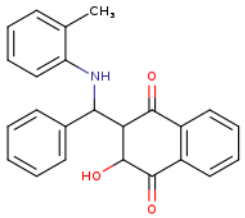
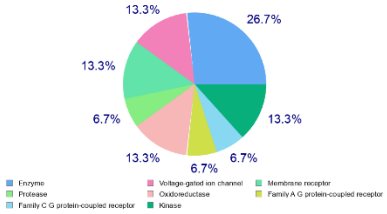
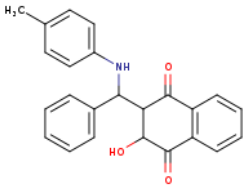
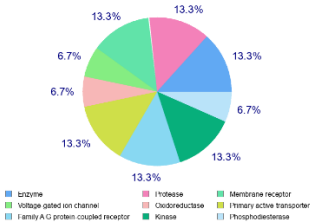
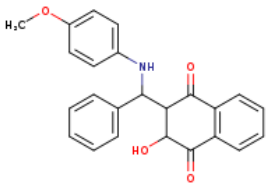
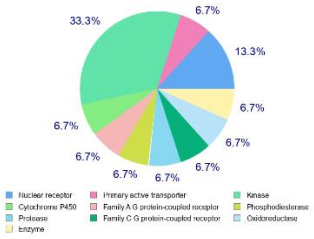
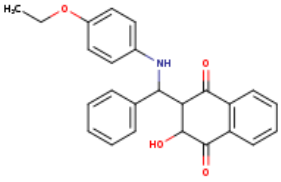
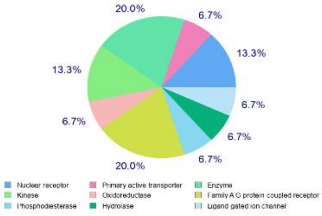
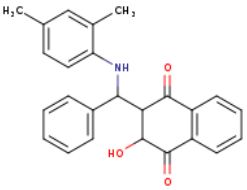
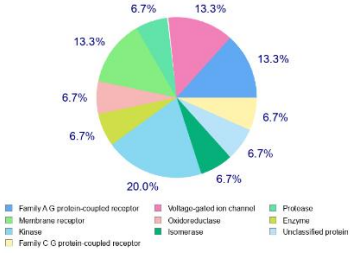
SL. No	Code	Molecular Weight	No. of h bond acceptor	No. of h bond Donor	log p Value	No. of Violations
1.	A	389.41	6	4	2.62	0
2.	B	452.30	5	3	4.10	0
3.	C	371.44	4	2	3.99	0
4.	D	371.44	4	2	4.03	0
5.	E	387.44	5	2	3.64	0
6.	F	401.46	5	2	4.02	0
7.	G	385.46	4	2	4.41	0
8.	H	456.30	4	2	4.87	0
9.	I	375.40	4	2	3.75	0
10.	J	439.43	4	2	4.69	0
11.	K	357.41	4	2	3.59	0
12.	L	373.41	5	3	3.32	0
13.	M	391.85	4	2	4.22	0
14.	N	426.30	4	2	4.85	0
15.	O	402.41	7	2	3.52	0

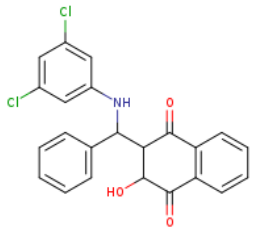
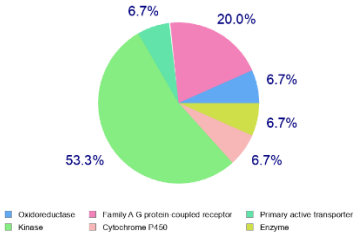
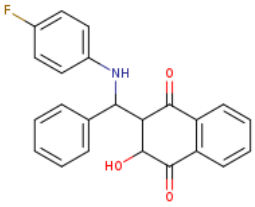
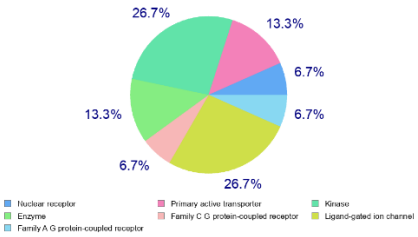
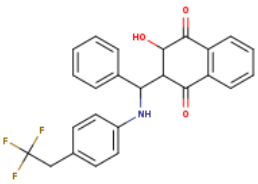
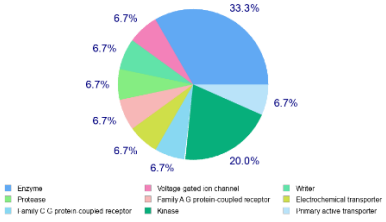
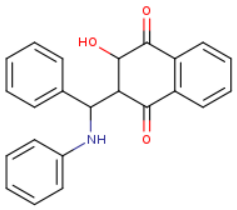
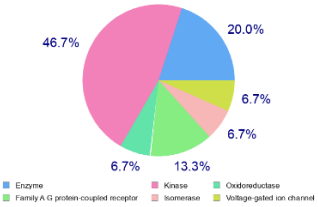
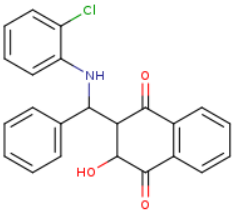
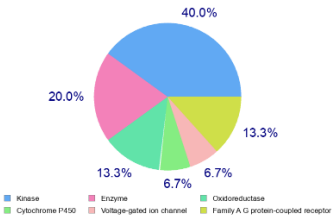
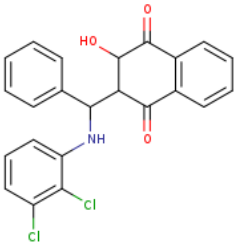
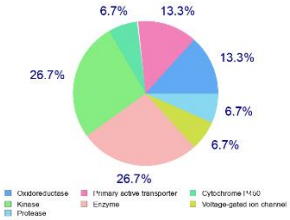
Table-6: PASS Value of Proposed Derivatives.

Ubiquinol- Cytochrome C Reductase Inhibitors			
Sl no.	Code	Pa	Pi
1	A	0,751	0,050
2	B	0,549	0,129
3	C	0,743	0,053
4	D	0,787	0,037
5	E	0,783	0,038
6	F	0,782	0,039
7	G	0,666	0,081
8	H	0,749	0,051
9	I	0,594	0,110
10	J	0,547	0,129
11	K	0,789	0,037
12	L	0,794	0,035
13	M	0,723	0,060
14	N	0,752	0,016
15	O	0,877	0,010
CYP2J2 Substrate			
Sl No.	Code	Pa	Pi
1	A	0,590	0,066
2	B	0,444	0,134
3	C	0,674	0,040
4	D	0,674	0,040
5	E	0,508	0,100
6	F	0,499	0,104
7	G	0,607	0,060

8	H	0,652	0,046
9	I	0,554	0,080
10	J	0,550	0,089
11	K	0,720	0,028
12	L	0,624	0,055
13	M	0,788	0,015
14	N	0,710	0,031
15	O	0,517	0,096
Gluconate -2-Dehydrogenase (Acceptor) Inhibitor			
Sl. No.	Code	Pa	Pi
1	A	0,654	0,085
2	B	0,458	0,238
3	C	0,619	0,109
4	D	0,619	0,109
5	E	0,776	0,023
6	F	0,679	0,068
7	G	0,569	0,145
8	H	0,698	0,057
9	I	0,544	0,165
10	J	0,493	0,207
11	K	0,670	0,074
12	L	0,674	0,071
13	M	0,694	0,060
14	N	0,676	0,071
15	O	0,517	0,187

Table-7: Results from SWISS target Prediction.

Code	Structure	Results
A		
C		
D		
E		
F		
G		

H		 6.7% 20.0% 6.7% 6.7% 53.3% 6.7% Oxidoreductase Family A G protein-coupled receptor Primary active transporter Kinase Cytochrome P450 Enzyme
I		 26.7% 13.3% 6.7% 13.3% 6.7% 26.7% Nuclear receptor Primary active transporter Kinase Enzyme Family C G protein-coupled receptor Ligand-gated ion channel Family A G protein-coupled receptor
J		 6.7% 33.3% 6.7% 6.7% 6.7% 6.7% 6.7% 20.0% Enzyme Voltage gated ion channel Writer Protease Family A G protein-coupled receptor Electrochemical transporter Family C G protein-coupled receptor Kinase Primary active transporter
K		 46.7% 20.0% 6.7% 6.7% 6.7% 13.3% Enzyme Kinase Oxidoreductase Family A G protein-coupled receptor Isomerase Voltage-gated ion channel
M		 40.0% 20.0% 13.3% 13.3% 6.7% 6.7% Kinase Enzyme Oxidoreductase Cytochrome P450 Voltage-gated ion channel Family A G protein-coupled receptor
N		 6.7% 13.3% 13.3% 26.7% 6.7% 6.7% 26.7% Oxidoreductase Primary active transporter Cytochrome P450 Kinase Enzyme Voltage-gated ion channel Protease

Conclusion

We started with the goal of exploring natural products for drug development and chose our compound Lawsone through a thorough literature review. Using ChemSketch, we designed 15 derivatives, carefully drawing each structure. We then used Molinspiration to quickly calculate key drug-like properties, including MiLogP, molecular weight, polar surface area, rotatable bonds, and the number of H-bond donors and acceptors. We confirmed that all 15 compounds met Lipinski's Rule of Five (LogP ≤ 5, MW ≤ 500 Da, H-bond donors ≤ 5, acceptors ≤ 10), showing their suitability as orally active candidates.

PASS analysis highlighted clear differences in predicted activity. Compound O, which has a nitro-substituted redox core, was expected to be the strongest inhibitor of ubiquinol–cytochrome c reductase. Compound E, which has a methoxy group, was expected to be the top inhibitor of gluconate 2-dehydrogenase. Compound K, because of its simple and flexible structure, was expected to be a CYP2J2 substrate. Compound B, featuring a bulky bromo substituent, was expected to be the weakest among all targets.

In summary, our streamlined workflow from selecting a natural scaffold to designing derivatives in ChemSketch, evaluating properties with Molinspiration, and predicting target-specific activities which show that structural modifications can create compounds with distinct and promising bioactivity profiles. Compounds O, E, and K clearly stand out as the top candidates for further experimental validation and therapeutic development.

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References

1. Nair, A. S., Sekar, M., Gan, S. H., Kumarasamy, V., Subramaniyan, V., Wu, Y. S., ... & Wong, L. S. (2024). Lawsone unleashed: A comprehensive review on chemistry, biosynthesis, and therapeutic potentials. *Drug Design, Development and Therapy*, 3295-3313.

2. Madaras, S. (2021). Towards Elucidation of the Reaction Mechanism Between Lawsone and Amino Acids. (Doctoral dissertation, Flinders University, College of Science and Engineering.).

3. Nariya, P., Shukla, F., Vyas, H., Devkar, R., & Thakore, S. (2020). Synthesis and characterization of Mannich bases of lawsone and their anticancer activity. *Synthetic Communications*, 50(11), 1724-1735.

4. Sánchez-Calvo, J. M., Barbero, G. R., Guerrero-Vásquez, G., Durán, A. G., Macías, M., Rodríguez-Iglesias, M. A., ... & Macías, F. A. (2016). Synthesis, antibacterial and antifungal activities of naphthoquinone derivatives: a structure–activity relationship study. *Medicinal Chemistry Research*, 25(6), 1274-1285.

5. PR, K. R., Fernandez, A., Laila, S. P., CS, S., & VS, V. (2017). Synthesis, spectral characterization, crystal structure, cytotoxicity and apoptosis—Inducing activity of two derivatives of 2-hydroxy-1, 4-naphthaquinone. *Photodiagnosis and Photodynamic Therapy*, 17, 250-259.

6. Ashnagar, A., & Shiri, A. (2011). Isolation and characterization of 2-hydroxy-1, 4-naphthoquinone (lawsone) from the powdered leaves of henna plant marketed in Ahwaz city of Iran. *IJ Chemtech Res*, 3(4), 1941-1944.

7. Rahmoun, N. M., Boucherit-Otmani, Z., Boucherit, K., Benabdallah, M., Villemin, D., & Choukchou-Braham, N. (2012). Antibacterial and antifungal activity of lawsone and novel naphthoquinone derivatives.3 *Medecine et maladies infectieuses*, 42(6), 270-275.

8. Bhasin, D., Chettiar, S. N., Etter, J. P., Mok, M., & Li, P. K. (2013). Anticancer activity and SAR studies of substituted 1, 4-naphthoquinones. *Bioorganic & medicinal chemistry*, 21(15), 4662-4669.

9. Kumar, K., Kumar, P., & Ahmed, S. (2024). Isolation and biological properties of Lawsone: a review. *Int J Pharm Sci Med*, 9, 13-25.

10. Roman, G. (2022). Anticancer activity of Mannich bases: a review of recent literature. *ChemMedChem*, 17(16), e202200258.

11. Kathawate, L., Joshi, P. V., Dash, T. K., Pal, S., Nikalje, M., Weyhermüller, T., ... & Salunke-Gawali, S. (2014). Reaction between lawsone and aminophenol derivatives: Synthesis, characterization, molecular structures and antiproliferative activity. *Journal of Molecular Structure*, 1075, 397-405.