

Phytochemical Investigation of Plant-Derived Rutin Analogues

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Abstract: *This study focuses on the phytochemical investigation of plant-derived rutin analogues, highlighting their chemical diversity, structural characteristics, and pharmacological significance. Rutin, a flavonoid glycoside widely distributed among plant species, is recognized for its roles in plant defense and its potent antioxidant, anti-inflammatory, and vasoprotective effects. The work characterizes rutin as quercetin-3-O-rutinoside and examines how its molecular structure serves as a template to discover analogues with potentially enhanced bioactivity and stability. Advanced analytical techniques, including chromatographic profiling and mass spectrometric analysis, were applied to isolate and identify structurally related compounds from various plant sources. The results expand the understanding of flavonoid biosynthesis, molecular function, and structure-activity relationship, while computational target prediction reveals a spectrum of predicted biological targets, indicating potential applications in drug discovery. The outcomes aid in identifying plant species rich in novel bioactive flavonoids, fostering natural antioxidant resource development and the sustainable utilization of phytochemicals in pharmaceutical and nutraceutical spheres.*

Keywords: Rutin analogues, Phytochemical investigation, Flavonoids, Antioxidant activity, Drug discovery

I. INTRODUCTION

Rutin, a naturally occurring flavonoid glycoside widely distributed in plant species, plays a crucial role in plant defense mechanisms and contributes to various pharmacological properties. [3,4] Structurally characterized as quercetin-3-O-rutinoside, rutin exhibits potent antioxidant, anti-inflammatory, and vasoprotective activities that have attracted significant attention in phytochemical and pharmacological research [7&9]. Its chemical structure, consisting of a flavonol backbone conjugated with disaccharide moieties, serves as a model for investigating structural analogues with potentially enhanced bioactivity and stability. The occurrence of rutin and its analogues across different plant taxa presents an excellent opportunity to explore the structural diversity and metabolic adaptations underlying flavonoid biosynthesis [15 & 16].

Phytochemical studies focused on rutin analogues are essential for understanding the relationship between molecular structure and biological function. Such investigations employ modern analytical techniques, including chromatographic profiling, spectroscopic characterization, and mass spectrometric analysis, to isolate, identify, and compare structurally related compounds from various plant sources. Insights gained from these studies not only expand the chemical knowledge of flavonoids but also facilitate the discovery of novel bioactive molecules with therapeutic potential. Moreover, identifying plant species rich in rutin analogues contributes to the development of natural antioxidant resources and supports the sustainable utilization of phytochemicals in pharmaceutical and nutraceutical applications [5, 6 & 8].

II. METHODS

Target prediction is a fundamental step in modern drug discovery, encompassing the identification of biological targets (such as proteins or enzymes) that a particular compound might interact with. Computational tools like Swiss Target Prediction method by Bugnon M, and Zoete V [1,2] utilize chemical structure similarity, bioactivity data, and machine



learning models to systematically predict potential molecular targets based on input ligands. This accelerates the process of hypothesis generation for possible mechanisms of action and helps prioritize experimental validation, especially for novel or uncharacterized molecules.

III. RESULTS

The table 1: summarizes key chemical and physicochemical properties of a compound, including its formula (C₂₇H₃₀O₁₅), molecular weight (594.52 g/mol), and atom counts. It details structural features such as the number of heavy atoms (42), aromatic heavy atoms (16), and rotatable bonds (6). The compound also possesses a substantial number of hydrogen bond acceptors (15) and donors (9), which influence solubility and interaction with biological targets. Molar refractivity (139.36) and topological polar surface area (TPSA 249.20) are provided, reflecting its molecular size and capability for polar interactions.

Table 1: Physicochemical Properties of C₂₇H₃₀O₁₅:

Physicochemical Properties	
Formula	C ₂₇ H ₃₀ O ₁₅
Molecular weight	594.52 g/mol
Num. heavy atoms	42
Num. arom. heavy atoms	16
Fraction Csp ³	0.44
Num. rotatable bonds	6
Num. H-bond acceptors	15
Num. H-bond donors	9
Molar Refractivity	139.36
TPSA	249.20 Å ²

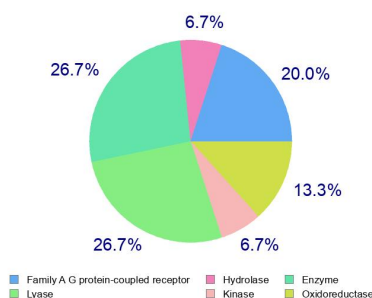


Fig 1. Target Prediction

Water solubility of the compound is shown using different prediction models. According to ESOL, the compound has a Log S of -3.42, indicating it is classified as "Soluble," with a calculated solubility of 2.24e-01 mg/mL (3.76e-04 mol/L). The Ali model gives a lower solubility (9.31e-03 mg/mL; 1.57e-05 mol/L), classifying the compound as "Moderately soluble." SILICOS-IT predicts a Log S of -0.88 and a higher solubility (7.77e01 mg/mL; 1.31e-01 mol/L), also labeling it "Soluble." Solubility estimates are important for assessing how the compound might behave in biological systems.

Drug-likeness assessments are provided via rule-based filters. The compound violates multiple criteria in Lipinski (3 violations), Ghose (4 violations), Veber (1 violation), Egan (1 violation), and Muegge (3 violations) rules, mostly due to its molecular weight, number of hydrogen bond donors/acceptors, TPSA, and atom counts, which may affect oral bioavailability. The calculated bioavailability score is relatively low (0.17), suggesting limited potential for successful oral drug development without further optimization. A figure summarizing target prediction is also referenced, which would further guide its potential applications in biological assays and drug discovery contexts [12 & 13].



The target prediction results for the compound in question reveal a diverse set of predicted protein targets, each annotated by common names, UniProt and ChEMBL IDs, target class, and their respective probability scores. High-confidence interactions (probability = 1.0) are noted with several G protein-coupled receptors (GPCRs) such as Neuromedin-U receptor 2 (NMUR2), Alpha-2a adrenergic receptor (ADRA2A), and Acetylcholinesterase (ACHE), among others. Additional targets include enzymes (like Aldose reductase and Carbonic anhydrases), kinases, oxidoreductases, and secreted proteins (like TNF-alpha and Interleukin-2), with varying degrees of prediction confidence. The presence of multiple predicted targets hints at potential polypharmacology, suggesting the compound could modulate several pathways in biological systems.

Table 2: Water Solubility

Water Solubility	
Log <i>S</i> (ESOL)	-3.42
Solubility	2.24e-01 mg/ml ; 3.76e-04 mol/l
Class	Soluble
Log <i>S</i> (Ali)	-4.81
Solubility	9.31e-03 mg/ml ; 1.57e-05 mol/l
Class	Moderately soluble
Log <i>S</i> (SILICOS-IT)	-0.88
Solubility	7.77e+01 mg/ml ; 1.31e-01 mol/l
Class	Soluble

Table 3; Drug likeliness

Drug likeliness	
Lipinski	No; 3 violations: MW>500, NorO>10, NHorOH>5
Ghose	No; 4 violations: MW>480, WLOGP<-0.4, MR>130, #atoms>70
Veber	No; 1 violation: TPSA>140
Egan	No; 1 violation: TPSA>131.6
Muegge	No; 3 violations: TPSA>150, H-acc>10, H-don>5
Bioavailability Score	0.17

These predictions are valuable for guiding subsequent laboratory studies, helping researchers focus on the most likely and therapeutically relevant targets. Furthermore, the data include the number of known actives (previously characterized compounds), providing a reference to gauge novelty and credibility. Overall, computational target prediction bridges the gap between chemical design and biological testing, increasing the efficiency of drug development by highlighting the biological roles and molecular interactions most pertinent to a compound's therapeutic potential.

The Query for Target Prediction

Query	<chem>C[C@@H]1O[C@@H](OC[C@H]2O[C@@H](Oc3c(oc4cc(O)cc(O)c4c3=O)-c3</chem>
Approach	MMFF-based

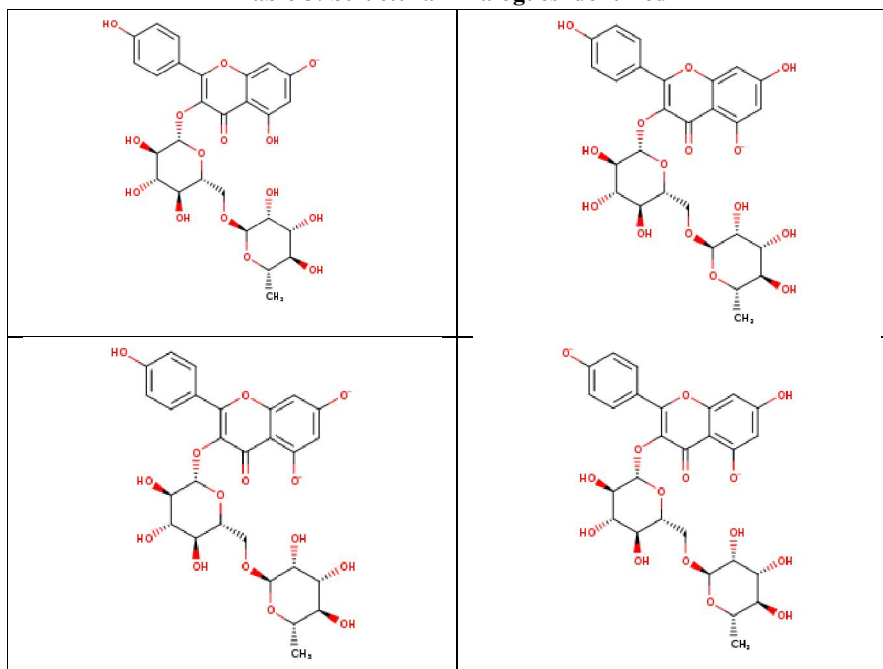


Table 4: Target Prediction

Target	Common name	Uniprot ID	ChEMBL ID	Target Class	Probability*	Known actives (3D/2D)
Neuromedin-U receptor 2	NMUR2	Q9GZQ4	CHEMBL1075144	Family A G protein-coupled receptor	1.0	1 / 1
Alpha-2a adrenergic receptor	ADRA2A	P08913	CHEMBL1867	Family A G protein-coupled receptor	1.0	1 / 1
Adrenergic receptor alpha-2	ADRA2C	P18825	CHEMBL1916	Family A G protein-coupled receptor	1.0	2 / 2
Acetylcholinesterase	ACHE	P22303	CHEMBL220	Hydrolase	1.0	2 / 19
Aldose reductase (by homology)	AKR1B1	P15121	CHEMBL1900	Enzyme	0.532	10 / 64
Carbonic anhydrase VII	CA7	P43166	CHEMBL2326	Lyase	0.343	5 / 13
Carbonic anhydrase XII	CA12	O43570	CHEMBL3242	Lyase	0.343	5 / 20
Carbonic anhydrase IV	CA4	P22748	CHEMBL3729	Lyase	0.343	4 / 10
Carbonic anhydrase II	CA2	P00918	CHEMBL205	Lyase	0.334	4 / 10
NADPH oxidase 4	NOX4	Q9NPH5	CHEMBL1250375	Enzyme	0.244	1 / 7
Quinone reductase 2	NQO2	P16083	CHEMBL3959	Enzyme	0.235	1 / 1
Ribosomal protein S6 kinase alpha 3	RPS6KA3	P51812	CHEMBL2345	Kinase	0.226	11 / 19
Xanthine dehydrogenase	XDH	P47989	CHEMBL1929	Oxidoreductase	0.118	2 / 18
Cyclooxygenase-2	PTGS2	P35354	CHEMBL230	Oxidoreductase	0.082	1 / 5
Phosphodiesterase 5A	PDE5A	O76074	CHEMBL1827	Phosphodiesterase	0.082	1 / 6
Adenosine A1 receptor (by homology)	ADORA1	P30542	CHEMBL226	Family A G protein-coupled receptor	0.082	0 / 14
TNF-alpha	TNF	P01375	CHEMBL1825	Secreted protein	0.082	0 / 3
Interleukin-2	IL2	P60568	CHEMBL5880	Secreted protein	0.082	0 / 4
Arachidonate 5-lipoxygenase	ALOX5	P09917	CHEMBL215	Oxidoreductase	0.082	0 / 29



Table 5: Structural Analogues identified



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