

In Silico Pharmacokinetic Profiling, ADMET Prediction, and Drug-Likeness Evaluation of Phenolic Constituents Identified in Honey: Implications for Asthma and Inflammatory Disorders

Eda Sonmez Gurer¹, Sevgi Durna Dastan^{2,3}, Zeliha Selamoglu^{4,5,6*}, Taner Dastan⁷, Ainash Oshibayeva⁸, Nurdana Salybekova⁴

¹Department of Pharmacognosy, Faculty of Pharmacy, Sivas Cumhuriyet University, Sivas, Türkiye

ORCID: <https://orcid.org/0000-0003-0319-6312>

E-mail: edagurer@cumhuriyet.edu.tr

²Department of Biology, Faculty of Science, Sivas Cumhuriyet University, Sivas, Türkiye

³Department of Beekeeping, Beekeeping Development, Application and Research Center, Sivas Cumhuriyet University, Sivas, Türkiye

ORCID: <https://orcid.org/0000-0003-4946-5602>

E-mail: sdurna@cumhuriyet.edu.tr

⁴Department of Biology, Faculty of Sciences, Khoja Akhmet Yassawi International Kazakh- Turkish University, Turkestan, Kazakhstan

⁵Department of Biology, Faculty of Sciences, Western Caspian University, Baku, Azerbaijan

⁶Department of Medical Biology, Medicine Faculty, Nigde Omer Halisdemir University, Nigde, Türkiye

ORCID: <https://orcid.org/0000-0001-9056-6435>

*Corresponding Author's E-mail: zselamoglu@ohu.edu.tr

⁷Department of Biochemistry, Faculty of Science, Sivas Cumhuriyet University, Sivas, Türkiye

ORCID: <https://orcid.org/0000-0003-0296-6979>

E-Mail: tdastan@cumhuriyet.edu.tr

⁸Department of Public Health and Scientific Research, Faculty of Medicine, Khoja Akhmet Yassawi International KazakhTurkish University, Turkestan, Kazakhstan

ORCID: <https://orcid.org/0000-0002-5655-5465>

E-mail: ainash.oshibayeva@ayu.edu.kz

⁴Department of Biology, Faculty of Sciences, Khoja Akhmet Yassawi International Kazakh- Turkish University, Turkestan, Kazakhstan

ORCID: <https://orcid.org/0000-0002-3750-1023>

E-mail: nurdana.salybekova@ayu.edu.kz

44 Abstract

45 **Introduction:** Honey is a natural product of considerable medicinal interest owing to its diverse
46 phenolic composition and reported therapeutic properties. The honey samples contain a variety of
47 biologically active phenolic compounds; however, the drug-likeness and pharmacokinetic suitability of
48 these constituents have not been systematically characterized.

49 **Materials and Methods:** In the present study, five phenolic compounds commonly identified honey
50 samples, namely fumaric acid, p-hydroxybenzoic acid, p-coumaric acid, trans-2-hydroxycinnamic acid,
51 and chrysin, were evaluated using the SwissADMET computational platform. Physicochemical
52 properties, lipophilicity, aqueous solubility, pharmacokinetic parameters, drug-likeness compliance,
53 and medicinal chemistry attributes were assessed for each compound. The BOILED-Egg model was
54 employed to predict gastrointestinal absorption and blood-brain barrier permeability.

55 **Results:** All five compounds demonstrated high predicted gastrointestinal absorption and satisfied
56 Lipinski's Rule of Five without violations. Among the investigated molecules, chrysin exhibited the
57 highest lipophilicity (consensus Log P = 2.55) and molar refractivity, suggesting enhanced membrane
58 permeability and protein-binding potential. p-Coumaric acid and trans-2-hydroxycinnamic acid
59 displayed the most balanced physicochemical profiles with respect to oral bioavailability. None of the
60 compounds were predicted to be P-glycoprotein substrates or cytochrome P450 inhibitors.

61 **Conclusion:** Given the established anti-inflammatory and immunomodulatory properties attributed to
62 these compound classes in the literature, the present findings support their consideration as candidate
63 molecules for further experimental investigation in the context of inflammatory disorders.

64 **Keywords:** ADMET; BOILED-Egg model; Drug-likeness; Honey; In silico; Pharmacokinetics.

65

66 1. Introduction

67 Honey is one of the oldest natural products used for medicinal purposes, with therapeutic applications
68 spanning several millennia across diverse civilizations [1,2]. Beyond its nutritional value, honey has
69 traditionally been employed in the management of wounds, gastrointestinal disorders, respiratory
70 conditions, and infections [1]. Its antioxidant, antimicrobial, anti-inflammatory, and antiproliferative
71 properties are primarily attributed to phytochemical constituents, particularly flavonoids and phenolic
72 acids [2,3]. The composition of these bioactive compounds varies considerably with botanical and
73 geographical origin, thereby influencing therapeutic potential [4,6]. Honey phenolics comprise two
74 major groups: phenolic acids and flavonoids. Phenolic acids include hydroxybenzoic acid derivatives,
75 such as gallic acid, p-hydroxybenzoic acid, and vanillic acid, and hydroxycinnamic acid derivatives,
76 including caffeic, p-coumaric, ferulic, and cinnamic acids. Flavonoids include flavones (chrysin,
77 apigenin), flavonols (quercetin, kaempferol, galangin), flavanones (pinocembrin, naringenin,
78 hesperetin), and flavanonols (pinobanksin). Their relative abundance depends on nectar sources and is
79 influenced by geographical, climatic, and seasonal factors [3-6]. These compounds can modulate
80 oxidative stress, inflammatory signaling, and immune responses through multiple mechanisms [2,3].

81 Despite the growing literature on honey-derived phenolics, pharmacokinetic and drug-likeness
82 evaluations have primarily focused on compounds identified in European, Mediterranean, Asian, and
83 Australasian honey varieties [7]. Recent analyses of honey samples from southern Kazakhstan identified
84 fumaric acid, p-hydroxybenzoic acid, p-coumaric acid, trans-2-hydroxycinnamic acid, and chrysin as
85 commonly occurring phenolics across multiple sampling localities [7]. Plant-derived polyphenols have
86 attracted increasing attention because of their pleiotropic pharmacological activities, favorable
87 preclinical safety profiles, and long history of human consumption [1-5]. Their ability to interact with
88 multiple inflammatory pathways may be advantageous in complex multifactorial diseases. Phenolic
89 acids and flavonoids have been reported to suppress Th2 cytokine production, inhibit mast cell
90 degranulation, reduce eosinophil recruitment, and attenuate mucus hypersecretion in experimental
91 models of allergic airway inflammation and asthma [6,7].

92 Honey has traditionally been used for the symptomatic management of respiratory conditions, including
93 cough, bronchitis, and asthma [7,8]. Its demulcent properties may alleviate bronchial irritation, while
94 its phenolic constituents may modulate airway inflammation through antioxidant and anti-inflammatory
95 mechanisms [7,8]. Several honey-derived phenolics suppress *NF- κ B* and *MAPK* signaling, reduce pro-
96 inflammatory cytokine production, and attenuate oxidative stress in preclinical models [9-11]. For
97 example, chrysin attenuates IgE-mediated immune responses and airway hyperresponsiveness, whereas
98 p-coumaric acid inhibits cyclooxygenase-2 (*COX-2*) and inducible nitric oxide synthase (*iNOS*)
99 expression through *NF- κ B* pathway suppression [9-11].

100 In silico approaches have become indispensable in contemporary drug discovery by enabling rapid
101 assessment of absorption, distribution, metabolism, excretion, and toxicity (ADMET) properties before
102 experimental validation [12-15]. Computational platforms such as SwissADME facilitate prediction of
103 physicochemical characteristics, drug-likeness, and pharmacokinetic behavior, supporting the
104 identification of compounds with favorable pharmaceutical profiles [14,15]. Therefore, the present
105 study aimed to evaluate the drug-likeness potential and pharmacokinetic profiles of five phenolic
106 compounds commonly identified in honey in the context of inflammatory disorders.

107

108 **2. Materials and Methods**

109 **2.1. Honey Samples and Compound Selection**

110 Honey samples were collected from four distinct localities in southern Kazakhstan (Table 1). Based on
111 analytical findings and literature data, five biologically active compounds consistently detected across
112 the samples were selected for in silico evaluation: fumaric acid, p-hydroxybenzoic acid, p-coumaric
113 acid, trans-2-hydroxycinnamic acid, and chrysin. The phenolic profile of Kazakhstani honey varies with
114 nectar source, geographical origin, and climatic conditions. These compounds were selected because
115 they were repeatedly detected in honey samples from different locations in southern Kazakhstan [4,5].
116 Here, “commonly identified” refers to their recurrence across independent samples rather than relative
117 abundance. Other constituents were excluded because they were detected only in specific samples,
118 occurred at trace levels, or lacked sufficient consistency for comparative in silico analysis. The selected
119 compounds also represent major phenolic classes in honey, including hydroxybenzoic acids,
120 hydroxycinnamic acids, and flavonoids, providing a structurally diverse and representative subset for
121 preliminary pharmacokinetic and drug-likeness screening.

122 **Table 1.** Geographical origins of honey samples collected from Kazakhstan

Sample Code	Location
B17	Kogam Village, Otrar
B18	Kelintobe Village, Zhanakorgan
B19	Shymkent
B20	Shieli

123

124 **2.2. In Silico Pharmacokinetic and Drug-Likeness Assessment**

125 The Simplified Molecular Input Line Entry System (SMILES) notations for each compound were
126 retrieved from the PubChem database (National Center for Biotechnology Information, U.S. National
127 Library of Medicine) [15-16] and are presented in Table 2.

128 **Table 2.** SMILES notations of selected bioactive compounds.

Compound	SMILES Notation
Fumaric acid	<chem>C(=C/C(=O)O)\C(=O)O</chem>
p-Hydroxybenzoic acid	<chem>C1=CC(=CC=C1C(=O)O)O</chem>
p-Coumaric acid	<chem>C1=CC(=CC=C1/C=C/C(=O)O)O</chem>
trans-2-Hydroxycinnamic acid	<chem>C1=CC=C(C(=C1)/C=C/C(=O)O)O</chem>
Chrysin	<chem>C1=CC=C(C=C1)C2=CC(=O)C3=C(C=C(C=C3O2)O)O</chem>

129
130 The physicochemical, pharmacokinetic, and drug-likeness properties of the selected compounds were
131 evaluated using the SwissADME web platform (<http://www.swissadme.ch>), a freely accessible
132 computational tool developed by the Swiss Institute of Bioinformatics [15,16]. Toxicity parameters,
133 including LD₅₀ values and toxicity classes, were determined using the ProTox-3.0 online server [15,16].
134 Bioavailability radar plots were generated to provide a graphical overview of oral bioavailability-related
135 properties across six dimensions: lipophilicity (LIPO), molecular size (SIZE), polarity (POLAR),
136 solubility (INSOLU), saturation (INSATU), and flexibility (FLEX) [15-19]. The BOILED-Egg (Brain
137 or Intestinal Estimated permeation) model was used to visualize predicted passive GI absorption and
138 BBB permeation based on WLOGP and TPSA coordinates [16,17].

139
140 **2.3 Molecular Docking Studies**

141 The potential binding modes and intermolecular interactions of the bioactive compounds with the target
142 protein were investigated using Maestro 14.5 (Schrödinger, 2025–3). The three-dimensional crystal
143 structure was retrieved from the Protein Data Bank (PDB) under accession code 5KIR. Prior to docking,
144 the protein was prepared using the Protein Preparation Wizard in Schrödinger Maestro 14.5, including
145 addition of missing hydrogen atoms, assignment of partial charges, completion of missing side chains,
146 and modeling of absent loop regions. Water molecules located more than 3 Å from the binding site were
147 removed. The prepared structure was energy-minimized at pH 7.0 using the OPLS4e force field.
148 Ligands were prepared with LigPrep by optimizing ionization states within pH 7.0 ± 2.0, verifying
149 stereochemistry, and performing energy minimization using the OPLS3e force field. The receptor grid
150 was generated around the protein active site, with standardized dimensions of 20 × 20 × 20 Å. For 5KIR,
151 grid-center coordinates were defined according to the active site, and docking simulations were
152 performed around these coordinates [18-20].

3. Results

3.1. Physicochemical Properties

The physicochemical properties of the five bioactive compounds are summarized in Table 3. Molecular weights ranged from 116.07 g/mol (fumaric acid) to 254.24 g/mol (chrysin), with all compounds below the Lipinski threshold of 500 g/mol [21]. Chrysin exhibited the highest number of aromatic heavy atoms (16 of 19), greatest molar refractivity (71.97), and most extensive ring system, indicating substantial potential for van der Waals and π - π stacking interactions with biological targets. TPSA values ranged from 57.53 Å² (p-hydroxybenzoic acid, p-coumaric acid, and trans-2-hydroxycinnamic acid) to 74.60 Å² (fumaric acid), remaining below the 140 Å² threshold associated with poor intestinal absorption [22]. All compounds had two hydrogen-bond donors and 3–4 acceptors, satisfying Lipinski criteria and indicating favorable intermolecular interaction potential [21]. Fsp3 was 0.00 for all compounds, reflecting their predominantly aromatic or unsaturated character and falling below the recommended 0.25 saturation threshold of the SwissADME bioavailability radar [14].

p-Coumaric acid and trans-2-hydroxycinnamic acid shared the molecular formula C₉H₈O₃ and molecular weight (164.16 g/mol) but differed in hydroxyl position. Although this isomerism does not alter the global physicochemical descriptors calculated by SwissADME, it may affect intramolecular hydrogen bonding, conformation, and biological activity [14,21-23]. Overall, chrysin and the hydroxycinnamic acid derivatives showed the most favorable profiles for biological target engagement.

These differences reflect the structural characteristics of the compounds. Fumaric acid, a non-aromatic dicarboxylic acid, has high polarity and hydrogen-bonding capacity but limited hydrophobic and π -stacking interactions. p-Hydroxybenzoic acid contains one aromatic ring with carboxylic acid and phenolic hydroxyl groups, resulting in moderate aromaticity and lipophilicity. The hydroxycinnamic acids, p-coumaric acid and trans-2-hydroxycinnamic acid, contain a propenoic acid side chain that increases conjugation and conformational rigidity. Chrysin is the most structurally complex compound, comprising three fused rings and two phenolic hydroxyl groups at C-5 and C-7 that may facilitate specific hydrogen-bonding interactions with molecular targets. These structural differences are reflected in their physicochemical profiles in molecular weight, molar refractivity (Table 3).

188 **Table 3.** Physicochemical properties of bioactive compounds.

Property	Fumaric Acid	PHBA	p-Coumaric Acid	t2HCA	Chrysin
Formula	C ₄ H ₄ O ₄	C ₇ H ₆ O ₃	C ₉ H ₈ O ₃	C ₉ H ₈ O ₃	C ₁₅ H ₁₀ O ₄
MW (g/mol)	116.07	138.12	164.16	164.16	254.24
Heavy atoms	8	10	12	12	19
Aromatic heavy atoms	0	6	6	6	16
Fsp3	0.00	0.00	0.00	0.00	0.00
Rotatable bonds	2	1	2	2	1
H-bond acceptors	4	3	3	3	4
H-bond donors	2	2	2	2	2
Molar refractivity	24.41	35.42	45.13	45.13	71.97
TPSA (A2)	74.60	57.53	57.53	57.53	70.67

PHBA, p-hydroxybenzoic acid; t2HCA, trans-2-hydroxycinnamic acid; MW, molecular weight; Fsp3, fraction of sp³-hybridized carbon atoms; TPSA, topological polar surface area.

189

190 **3.2. Lipophilicity Analysis**

191 Lipophilicity is a key determinant of membrane permeability and oral bioavailability [22,23].
192 Consensus Log P values, calculated from five computational models, are presented in Table 4 and
193 Figure 1. Chrysin showed the highest value (2.55), consistent with its extended aromatic system and
194 relatively low polar surface area, suggesting favorable passive membrane permeation and hydrophobic
195 protein interactions [21-23]. Trans-2-Hydroxycinnamic acid (1.40) and p-coumaric acid (1.26) fell
196 within the optimal range for oral drug candidates (1.0–3.0), indicating balanced hydrophilic-lipophilic
197 properties [23-25]. p-Hydroxybenzoic acid showed moderate lipophilicity (1.05), whereas fumaric acid
198 had a negative Log P (-0.35), reflecting its highly hydrophilic character. Although all compounds fell
199 within the broadly acceptable range (-0.7 to +5.0), fumaric acid may exhibit limited passive diffusion
200 across lipid bilayers [15].

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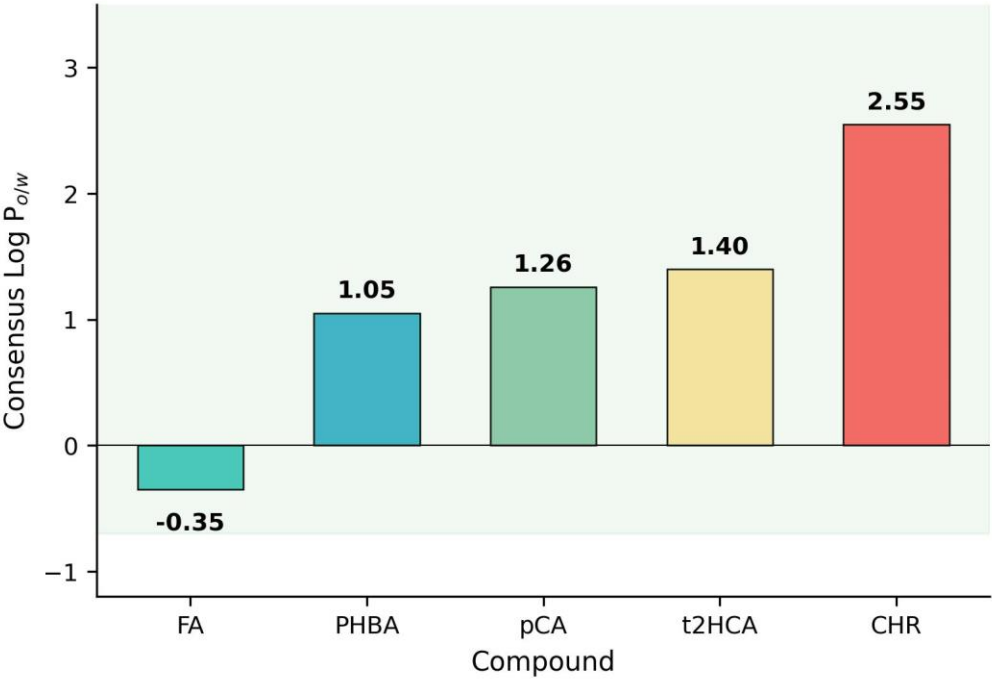
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205 **Table 4.** Lipophilicity and Aqueous Solubility parameters of bioactive compounds.

Compound	iLOGP	XLOGP3	WLOGP	MLOGP	SILICOS-IT	Consensus Log P
Fumaric acid	0.32	-0.34	-0.29	-0.64	-0.81	-0.35
PHBA	0.85	1.58	1.09	0.99	0.74	1.05
p-Coumaric acid	0.95	1.46	1.38	1.28	1.22	1.26
t2HCA	1.09	2.03	1.38	1.28	1.22	1.40
Chrysin	2.27	3.52	2.87	1.08	3.02	2.55

Compound	Log S (ESOL)	Class	Log S (Ali)	Class	Log S (SILICOS-IT)	Class
Fumaric acid	-0.21	Very soluble	-0.76	Very soluble	1.34	Soluble
PHBA	-2.07	Soluble	-2.40	Soluble	-1.17	Soluble
p-Coumaric acid	-2.02	Soluble	-2.27	Soluble	-1.28	Soluble
t2HCA	-2.37	Soluble	-2.87	Soluble	-1.28	Soluble
Chrysin	-4.19	Mod. soluble	-4.69	Mod. soluble	-4.98	Mod. Soluble

206



207 **Figure 1.** Consensus Log P values of the investigated bioactive compounds

208

3.3. Aqueous Solubility

The predicted aqueous solubility values obtained using ESOL, Ali, and SILICOS-IT are summarized in Table 4. Fumaric acid showed the highest predicted solubility, classified as “very soluble” by ESOL ($\log S = -0.21$) and Ali ($\log S = -0.76$), consistent with its low molecular weight and high polarity. p-Hydroxybenzoic acid, p-coumaric acid, and trans-2-hydroxycinnamic acid were classified as “soluble” by all three models, indicating favorable dissolution properties for oral administration [22-24]. Chrysin exhibited the lowest predicted solubility and was classified as “moderately soluble” (ESOL $\log S = -4.19$; Ali $\log S = -4.69$; SILICOS-IT $\log S = -4.98$), likely reflecting its extended aromatic conjugation and higher lipophilicity. Thus, despite its favorable membrane-permeation and protein-binding characteristics, poor aqueous solubility may limit its oral bioavailability and require formulation strategies such as nanoencapsulation, cyclodextrin complexation, or solid dispersion [22-24]. The hydroxycinnamic acid derivatives showed a favorable balance between solubility and lipophilicity, suggesting potentially more predictable pharmacokinetic behavior (Table 4).

3.4. Pharmacokinetic Predictions

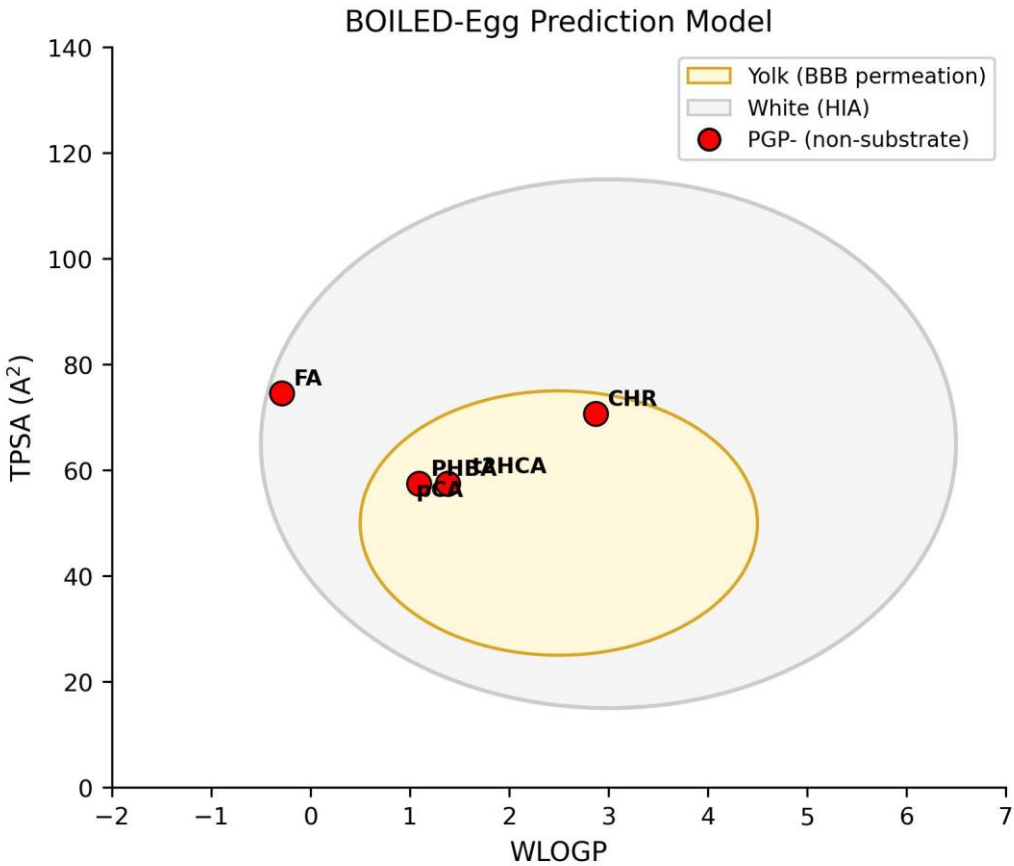
The predicted pharmacokinetic properties are presented in Table 5. All five compounds showed high predicted gastrointestinal (GI) absorption, consistent with their favorable Lipinski profiles and TPSA values [22-25]. Four compounds were predicted to cross the blood-brain barrier (BBB), whereas fumaric acid was not, consistent with its higher polarity ($\text{TPSA} = 74.60 \text{ \AA}^2$) and low lipophilicity in the BOILED-Egg model. None of the compounds were predicted to be P-glycoprotein (P-gp) substrates or inhibitors of CYP1A2, CYP2C19, CYP2C9, CYP2D6, or CYP3A4. These predictions suggest a low likelihood of active efflux and CYP-mediated pharmacokinetic interactions, although experimental validation is required [25]. Chrysin showed the highest predicted skin permeation coefficient ($\log K_p = -5.35 \text{ cm/s}$), whereas fumaric acid showed the lowest (-7.25 cm/s), consistent with their lipophilicity profiles (Figure 2) [25].

241 **Table 5.** Predicted pharmacokinetic properties of bioactive compounds.

Parameter	Fumaric Acid	PHBA	p-Coumaric Acid	t2HCA	Chrysin
GI absorption	High	High	High	High	High
BBB permeant	No	Yes	Yes	Yes	Yes
P-gp substrate	No	No	No	No	No
CYP1A2 inhibitor	No	No	No	No	No
CYP2C19 inhibitor	No	No	No	No	No
CYP2C9 inhibitor	No	No	No	No	No
CYP2D6 inhibitor	No	No	No	No	No
CYP3A4 inhibitor	No	No	No	No	No
Log Kp (cm/s)	-7.25	-6.02	-6.26	-5.86	-5.35

GI, gastrointestinal; BBB, blood-brain barrier; P-gp, P-glycoprotein; CYP, cytochrome P450; Log Kp, skin permeation coefficient; PHBA, p-hydroxybenzoic acid; t2HCA, trans-2-hydroxycinnamic acid.

242



243 **Figure 2.** BOILED-Egg model predictions of compounds.

3.5. Drug-Likeness Assessment

Drug-likeness was evaluated using five complementary filters (Lipinski, Ghose, Veber, Egan, and Muegge), with results presented in Table 6. All five compounds satisfied the Lipinski, Veber, and Egan criteria without violations, supporting their basic suitability for oral drug development [22-25]. p-Coumaric acid and trans-2-hydroxycinnamic acid also passed the Ghose filter, whereas fumaric acid and p-hydroxybenzoic acid showed Ghose and Muegge violations, mainly due to their low molecular weights [23-25]. Chrysin was the only compound satisfying all five drug-likeness filters. However, its predicted bioavailability score (0.55) was lower than that of the other compounds (0.85), likely reflecting its lower aqueous solubility. This finding highlights the importance of the solubility–lipophilicity balance for oral bioavailability and the potential need for formulation optimization of chrysin [25].

Table 6. Drug-likeness evaluation and Medicinal chemistry attributes of bioactive compounds

Compound	Lipinski	Ghose	Veber	Egan	Muegge	BA Score
Fumaric acid	Yes; 0 viol.	No; 3 viol.	Yes	Yes	No; 2 viol.	0.85
PHBA	Yes; 0 viol.	No; 3 viol.	Yes	Yes	No; 1 viol.	0.85
p-Coumaric acid	Yes; 0 viol.	Yes	Yes	Yes	No; 1 viol.	0.85
t2HCA	Yes; 0 viol.	Yes	Yes	Yes	No; 1 viol.	0.85
Chrysin	Yes; 0 viol.	Yes	Yes	Yes	Yes	0.55

Compound	PAINS Alerts	Brenk Alerts	Leadlikeness	SA Score
Fumaric acid	0	1 (michael_acceptor_1)	No; MW < 250	1.80
PHBA	0	0	No; MW < 250	1.00
p-Coumaric acid	0	1 (michael_acceptor_1)	No; MW < 250	1.61
t2HCA	0	1 (michael_acceptor_1)	No; MW < 250	1.85
Chrysin	0	0	No; XLOGP3 > 3.5	2.93

BA, bioavailability; viol., violation(s); PHBA, p-hydroxybenzoic acid; t2HCA, trans-2-hydroxycinnamic acid.

PAINS, pan-assay interference compounds; SA, synthetic accessibility; MW, molecular weight; PHBA, p-hydroxybenzoic acid; t2HCA, trans-2-hydroxycinnamic acid.

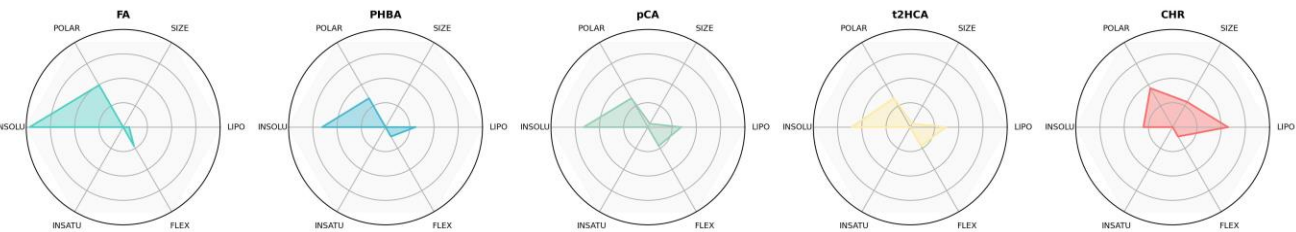


Figure 3. Bioavailability radar plots for bioactive compounds

3.6. Medicinal Chemistry Attributes

Medicinal chemistry assessment (Table 6) showed that none of the five compounds triggered PAINS alerts, suggesting a low likelihood of nonspecific reactivity [25]. Brenk michael_acceptor_1 alerts were identified for fumaric acid, p-coumaric acid, and trans-2-hydroxycinnamic acid due to their α,β -unsaturated carbonyl groups. Although this feature may indicate electrophilic reactivity, it is also common in approved drugs and natural products and does not preclude further development [25].

Synthetic accessibility scores ranged from 1.00 (p-hydroxybenzoic acid) to 2.93 (chrysin) on a 1–10 scale, indicating relatively favorable synthetic accessibility for all compounds. Combined with their natural occurrence in honey, these findings support their potential for further development [25].

Figure 4. Comparative physicochemical heatmap of the compounds

Comparative Physicochemical Properties							
FA	116.07	74.60	-0.35	2	4	2	24.41
PHBA	138.12	57.53	1.05	2	3	1	35.42
pCA	164.16	57.53	1.26	2	3	2	45.13
t2HCA	164.16	57.53	1.40	2	3	2	45.13
CHR	254.24	70.67	2.55	2	4	1	71.97
	MW (g/mol)	TPSA (Å²)	Consensus Log P	H-bond Donors	H-bond Acceptors	Rotatable Bonds	Molar Refractivity

3.7. Integrated BOILED-Egg and Bioavailability Radar Interpretation

The BOILED-Egg model predicts gastrointestinal absorption and BBB permeation based on WLOGP and TPSA coordinates [23-25]. As shown in Figure 2, all five compounds were located in the white region, indicating high predicted human intestinal absorption, while four were also positioned in the yellow region (yolk), suggesting potential passive BBB permeation. Fumaric acid was outside the yolk, consistent with its high polarity and TPSA. All compounds were PGP-, indicating no predicted P-glycoprotein substrate activity.

Although BBB permeability may be relevant to neuroimmune interactions, its significance here should be interpreted cautiously because these findings are based solely on computational predictions. Accordingly, BBB permeability should be considered a general pharmacokinetic indicator rather than evidence of therapeutic central effects.

The bioavailability radar plots (Figure 3) showed that p-coumaric acid and trans-2-hydroxycinnamic acid had the most balanced profiles across the evaluated parameters. All compounds failed the saturation criterion ($F_{sp3} \geq 0.25$), reflecting their predominantly aromatic structures. Overall, integrated physicochemical, pharmacokinetic, and drug-likeness analyses identified p-coumaric acid and trans-2-hydroxycinnamic acid as the most favorable candidates, followed by p-hydroxybenzoic acid, chrysin, and fumaric acid.

3.8. Oral Toxicity Prediction and Molecular Docking Results

Toxicity was predicted using the ProTox-3.0 online server. Predicted LD₅₀ values ranged from 1350 to 3919 mg/kg (Table 7), with chrysin showing the highest (3919 mg/kg) and fumaric acid the lowest value (1350 mg/kg). Toxicity classes were additionally predicted using the ProTox-II model, which ranks compounds from class 1 (most toxic) to class 6 (least toxic). Overall, the investigated honey-derived compounds showed relatively low predicted toxicity.

303 **Table 7.** Predicted Toxicity Parameters

Compound	LD50(mg/kg)	Toxicity Class
Fumaric acid	1350	4
p-Hydroxybenzoic acid	2200	5
p-Coumaric acid	2850	5
trans-2-Hydroxycinnamic acid	2850	5
Chrysin	3919	5

Compound	Docking Score
Chrysin	-8.412
p-Hydroxybenzoic acid	-6.522
trans-2-Hydroxycinnamic acid	-5.794
p-Coumaric acid	-5.633
Fumaric acid	-3.331

304

305 Molecular docking revealed marked differences in binding affinities among the compounds (Table 7).

306 Chrysin showed the strongest predicted affinity (−8.412 kcal/mol), likely due to its extensive flavonoid

307 scaffold and favorable hydrophobic complementarity. Among the phenolic acids, p-hydroxybenzoic

308 acid (−6.522 kcal/mol) showed stronger binding than trans-2-hydroxycinnamic acid (−5.794 kcal/mol)

309 and p-coumaric acid (−5.633 kcal/mol), whereas fumaric acid exhibited the weakest affinity (−3.331

310 kcal/mol), consistent with its smaller size and limited interaction capacity.

311 Chrysin formed hydrophobic interactions with Val523, Ala527, and Leu352, while p-hydroxybenzoic

312 acid established polar contacts with Arg120 and Tyr355. Trans-2-Hydroxycinnamic acid and p-

313 coumaric acid interacted with Arg120 through their acrylate side chains, with p-coumaric acid

314 additionally interacting with Ser353. Fumaric acid interacted with Ser530 and Gly526 within a confined

315 region of the active site (Figure 5). Overall, the docking results indicate that complementary

316 hydrophobic and hydrogen-bonding interactions contribute to ligand stabilization within the target

317 binding site.

322 4. Discussion

323 The pharmacokinetic and drug-likeness profiles established in the present study gain particular
324 significance when considered alongside the reported biological activities of these compounds. Fumaric
325 acid, through derivatives such as dimethyl fumarate (DMF), activates the nuclear factor erythroid 2-
326 related factor 2 (Nrf2) pathway, enhancing antioxidant defenses while suppressing NF- κ B-mediated
327 pro-inflammatory cytokine production [6-7]. This dual mechanism is highly relevant to oxidative stress-
328 related diseases, including inflammation and asthma. p-Coumaric acid suppresses COX-2 and iNOS
329 expression via inhibition of NF- κ B and MAPK signaling and reduces TNF- α and IL-6 production
330 in inflammatory models [6-8]. Its balanced lipophilicity and high predicted GI absorption support the
331 feasibility of these effects following oral administration. Similarly, trans-2-hydroxycinnamic acid
332 modulates inflammatory pathways and exhibits antioxidant activity, with a pharmacokinetic profile
333 comparable to that of p-coumaric acid [9-12]. Chrysin warrants particular attention due to its ability to
334 suppress NF- κ B, STAT3, and PI3K/Akt signaling, modulate mast cell activation, and attenuate IgE-
335 mediated immune responses [6-12]. Experimental asthma models have shown reductions in airway
336 hyperresponsiveness and eosinophilic infiltration [6-12]. Although its high molar refractivity and
337 lipophilicity suggest strong receptor-binding potential, limited aqueous solubility remains a key
338 pharmacokinetic challenge that may be overcome through nanocarrier systems or structural
339 modifications. p-Hydroxybenzoic acid exhibits free radical scavenging activity through its phenolic
340 hydroxyl group. Although related hydroxybenzoic acid derivatives reduce pro-inflammatory mediator
341 expression [5-12], direct evidence for p-hydroxybenzoic acid remains limited. The coexistence of these
342 five phenolics in honey suggests potential synergistic interactions. Multi-target modulation of the NF-
343 κ B, MAPK, and PI3K/Akt pathways may provide broader anti-inflammatory effects than single-target
344 approaches [5-12]. Their diverse physicochemical properties, ranging from hydrophilic fumaric acid to
345 lipophilic chrysin, indicate complementary biodistribution patterns that may contribute to the enhanced
346 biological activity often observed in whole honey compared with isolated constituents. Overall, the
347 ADMET and drug-likeness analyses indicate that p-coumaric acid, trans-2-hydroxycinnamic acid, and
348 chrysin possess favorable pharmacokinetic characteristics for modulating inflammatory signaling. Their
349 multi-target mechanisms, natural origin, and reported preclinical safety support further evaluation as
350 complementary therapeutic candidates for inflammatory diseases. Several limitations should be
351 acknowledged. SwissADMET predictions do not fully capture the complexity of in vivo
352 pharmacokinetics, including first-pass metabolism, microbiome-mediated biotransformation, and
353 tissue-specific accumulation. Likewise, the BOILED-Egg model predicts BBB permeability based
354 solely on passive diffusion and excludes several active transport mechanisms. In addition, commonly
355 used drug-likeness filters were developed primarily using synthetic compounds and may have limited
356 applicability to low-molecular-weight natural phenolics. Future studies should validate these findings

357 through experimental ADME approaches, including Caco-2 permeability, microsomal stability, and
358 plasma protein binding assays.

359 **5. Conclusions**

360 The present in silico investigation demonstrated that the five phenolic compounds commonly identified
361 in honey samples from the southern regions of Kazakhstan possess favorable physicochemical,
362 pharmacokinetic, and drug-likeness profiles that suggest their potential as candidates for further
363 experimental investigations. It should be emphasized that the present findings are based exclusively on
364 computational predictions and require experimental confirmation. Future studies incorporating
365 molecular docking simulations, in vitro cell culture models, and in vivo animal models are warranted to
366 validate the hypotheses generated in this study.

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372 **Authors' Contribution:**

373 Study concept and design: S.D.D and Z.S

374 Acquisition of data: E.S.G and T.D

375 Analysis and interpretation of data: E.S.G and S.D.D

376 Drafting of the manuscript: S.D.D, N.S, Z.S

377 Critical revision of the manuscript for important intellectual content: Z.S, A.O.

378 Administrative, technical, and material support: N.S, A.O, S.D.D, Z.S

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382 **Supplementary Materials**

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389 **Institutional Review Board Statement**

390 Not applicable.

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393 **Data Availability Statement**

394 All data generated or analyzed during this study are included in this published article. The SwissADME
395 platform is freely accessible at <http://www.swissadme.ch>. Compound SMILES notations were retrieved
396 from the PubChem database (<https://pubchem.ncbi.nlm.nih.gov/>).

397 **Conflicts of Interest**

398 The authors declare no conflicts of interest.

399 **Use of Artificial Intelligence Tools**

400 The authors declare that an artificial intelligence (AI) tool was utilized during the preparation of this
401 manuscript. Claude (Anthropic) was employed to assist with language editing and scientific writing
402 refinement. All AI-generated content was critically reviewed, verified, and revised by the authors, who
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