http://dergipark.org.tr/tr/pub/anatolianbryology

DOI: 10.26672/anatolianbryology.1705249

Anatolian Bryology
Anadolu Briyoloji
Dergisi
Research Article
e-ISSN:2458-8474
Online

Detection of some phenolic content of *Grimmia ovalis* (Hedw.) Lindb. and investigation of its antimicrobial activity with molecular docking technique

Zafer Çambay[1]*, Harun USLU[2], Bünyamin GÖKTAŞ[2,3], Kevser ÖZDEMİR BAYÇINAR[4], Ümmügülsüm TÜKENMEZ EMRE[5], Mevlüt ALATAŞ[6]

[1] *Fırat University, Vocational School of Health Services, Department of Medical Services and Technique, Elazığ, TÜRKİYE*
[2] *Fırat University, Faculty of Pharmacy, Department of Pharmaceutical Chemistry, Elazığ, TÜRKİYE*
[3] *Anadolu University, Department of Pharmaceutical Chemistry, Graduate School, Eskisehir, TURKİYE*
[4] *Fırat University, Faculty of Pharmacy, Department of Pharmacognosy, Elazığ, TÜRKİYE*
[5] *Mardin Artuklu University, Vocational School of Health Services, Department of Medical Services and Technique, Mardin, TÜRKİYE*
[6] *Munzur University, Tunceli Vocational School, Tunceli, TÜRKİYE*

Received: 23 May 2025 **Revised: 17 June 2025** **Accepted: 18 June 2025**

Abstract

This study aims to investigate the phenolic compounds and pharmacological potential of *Grimmia ovalis* (Hedw.) Lindb. to understand their bioactive potential and to pioneer future research. It also aims to be one of the first studies on G. ovalis's in silico bioactivity. HPLC analysis revealed the detection of some phenolic compounds in *G. ovalis* extract. The study revealed the in silico antimicrobial potential of some phenolic compounds. We calculated that compounds of 2,5-dihydroxybenzoic acid and caffeic acid would inhibit Staphylococcus aureus UDP-N-acetylenolpyruvylglucosamine reductase (MurB) at micromolar levels. We concluded that they interacted with residues crucial for antimicrobial activity on the mentioned macromolecule.

Keywords: Bryophyte, Grimmiaceae, Antimicrobial Activity, Phenolic Compounds, Molecular Docking

Grimmia ovalis (Hedw.) Lindb. Türünün Bazı Fenolik Bileşiklerinin Belirlenmesi ve Moleküler Yerleştirme Tekniği ile Antimikrobiyal Aktivitesinin Araştırılması

Öz

Bu çalışma, *Grimmia ovalis* (Hedw.) Lindb.'in fenolik bileşenlerini ve farmakolojik potansiyelini araştırmayı, biyoaktif potansiyellerini anlamayı ve gelecekteki araştırmalara öncü olmayı amaçlamaktadır. Bununla beraber *in silico* biyoaktivite açısından *G. ovalis* üzerine yapılan ilk çalışmalardan biri olmayı hedeflemektedir. HPLC analizi, *G. ovalis* özütünün bazı fenolik bileşiklerinin tespitini ortaya koymuştur. Bazı fenolik bileşiklerin *in silico* antimikrobiyal potansiyeli ortaya çıkarılmıştır. 2,5-Dihidroksibenzoik asit ve Kafeik asit bileşiklerinin, *Staphylococcus aureus* UDP-N-asetilenolpiruvil glukozamin redüktaz (MurB) üzerinde mikromolar düzeyde inhibisyon yapacağı hesaplanmıştır. Bahsi geçen makromolekül üzerinde antimikrobiyal aktivite için önemli olan kalıntılar ile etkileşime girdiği sonucuna varılmıştır.

Anahtar kelimeler: Briyofit, Antimikrobiyal Aktivite, Fenolik Bileşikler, Moleküler Doklama.

* Corresponding author: zcambay@firat.edu.tr

To cite this article: *Çambay Z. Uslu H. Göktaş B. Özdemir Bayçınar K. Tükenmez Emre Ü. Alataş M. 2025. Detection of some phenolic content of Grimmia ovalis (Hedw.) Lindb. and investigation of its antimicrobial activity with molecular docking technique. Anatolian Bryology. 11:1, 52-58.*

1. Introduction

Bryophytes, or non-vascular plants, comprise a substantial and varied category that includes mosses, liverworts, and hornworts, and inhabit numerous ecological niches in terrestrial environments. The genus *Grimmia*, part of the family Grimmiaceae, is a significant ecological group of mosses, predominantly located on rocks and arid surfaces in temperate and hilly areas. However, despite their prevalence in ecosystems, studies on the phytochemical contents and pharmacological potential of *Grimmia* species are quite limited (Delgadillo Moya, 2015; Glime, 2007; Hardman, 2007).

Bryophytes have recently garnered significant scientific interest due to their unique secondary metabolites and resilience to extreme environmental conditions. The displayed features indicate a promising source of bioactive compounds with therapeutic applications (Asakawa and Ludwiczuk, 2018; Rios and Recio, 2005). Research focused on the *Grimmia* genus remains limited.

Initial research indicates that certain *Grimmia* species, including *Grimmia pilifera*, exhibit significant antibacterial and antioxidant properties, potentially attributable to the presence of flavonoids, diterpenes, and other phenolic chemicals (Barwant and Tripathi, 2023; Elibol et al., 2011; Peters et al., 2018). In addition, some species of this genus are considered to have the potential to be a source in the formulation of antibacterial drugs.

The aim of this study is to obtain information on the *in silico* antimicrobial activity of phenolic compounds obtained from the extract of *G. ovalis*. Furthermore, to our knowledge, this study is intended to be one of the first studies on the phytochemical and bioactivity of *G. ovalis*. This will help us understand how it can be used in pharmacology and open the door to future uses in natural product drug discovery.

2. Materials and Methods

2.1. Plant material and extraction process

The powdered plant was macerated with 70% ethanol for 3 days by rotating on a rotavapor for 1h. After filtering, it was evaporated to dryness on a rotavapor. The yield of the extract was determined as 6.15%.

The research materials were collected from Dolin Surroundings (Niğde), located in the C13 (Figure 1). Square in Turkey according to the Henderson (Henderson, 1961) grid system. It is a moss belonging to the Bryophyta division, Bryopsida class, Grimmiales order, Grimmiaceae family. It is one of the 33 taxa of the *Grimmia* genus in our country (Kürschner and Frey, 2011). *G. ovalis* is a taxon that generally spreads cosmopolitanly on rocks and loves semi-neutral, arid and open environments (Table 1). The bryophyte specimen (*G. ovalis*) used in the study is preserved in the bryophyte collection of ALATAŞ (Tunceli) with the Herbarium number ALT 4620.

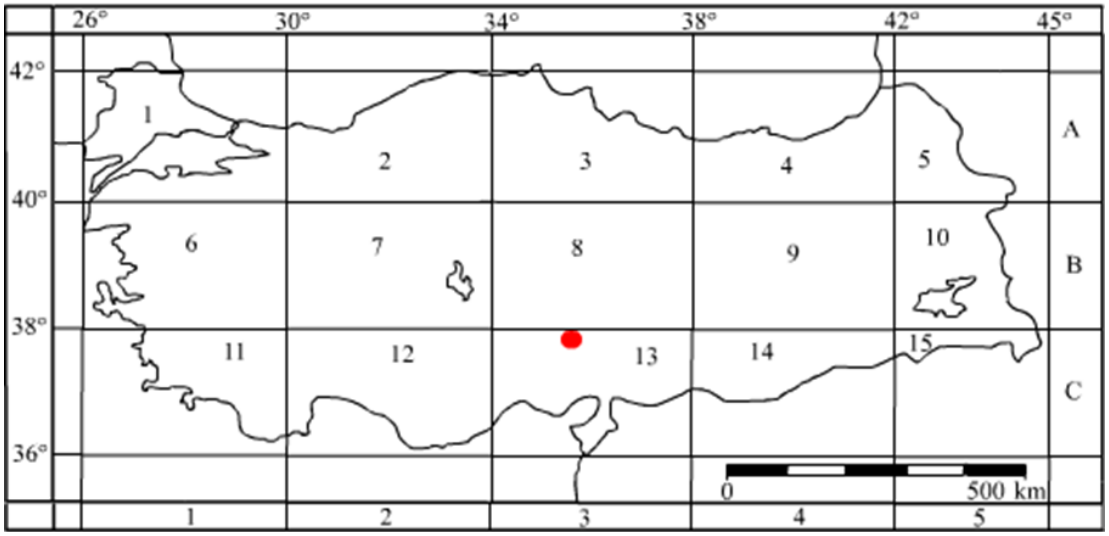


Figure 1. According to the Turkish grid system, the locality where the *Grimmia* sample was taken

Table 1. Locality information

Locality	Altitude (m)	Date	GPS Record
Dolin Surroundings, Niğde (Red Dot)	1690	14.09.2024	34°43'6.37"E, 37°53'40"N

2.2. Phenolic content

HPLC grade methanol was purchased from J.T. Baker, Acetonitrile was purchased from Isolab and all other chemicals were purchased from Merck. 8.0 mg (399.75 mg/ml) of the aboveground parts of *G. ovalis* was taken and closed in an airtight bottle. Alliance e2695 HPLC and C18 column (250 x 4.56mm. 5µ) was used to determine the phenolic compounds of the aboveground parts of *G. ovalis*. Phosphoric acid (pH 2) and Methanol:Acetonitrile (90:10) were used as mobile phases. The flow rate was set as 0.8 ml/min. The wavelength was determined as 280 nm and photodiode array (PDA) detector was used. The injection volume was 20 µL and the temperature was 30°C. The results were obtained with the Empower 3 program (Pirisi, Cabras, Cao, Migliorini, and Muggelli, 2000; Veneziani et al., 2018).

2.3. Molecular docking

The compounds detected in the phenolic components of *G. ovalis* were plotted to get SMILES from PubChem (https://pubchem.ncbi.nlm.nih.gov). The two substances found in the highest amounts (2,5-Dihydroxybenzoic acid and Caffeic acid) in the extract were identified and the molecular docking process was applied to these substances. Energy minimization of two components were performed with the ChemOffice software. To evaluate 1HSK-antimicrobial activity, molecular docking studies were performed using the standard procedure to determine the binding modes and docking scores of the two compounds detected in *G. ovalis* extract two phenolic components at the active sites of the 1HSK (Benson et al., 2001). The macromolecule crystal structures was retrieved from the Protein Data Bank server (https://www.rcsb.org/, accessed 20 May 2025) and optimized with Schrödinger Maestro (Maestro, 2024). Molecular docking was performed with both Autodock and Vina softwares (Eberhardt, Santos-Martins, Tillack, and Forli, 2021; Huey, Morris, Olson, and Goodsell, 2007). Since we had previously worked with this macromolecule for 1HSK, FAD was re-docked into the target site of the macromolecule to validate the docking program and the RMSD value was found to be appropriate (<2) (Unver, Uslu, Gurhan, and Goktas, 2024).

3. Results and Discussion

3.1. Phenolic content

According to the results of the applied HPLC analysis, 6 phenolic components were determined *G. ovalis* extract (Table 2). Two of these compounds were detected at very high concentrations compared to the others. 2,5-Dihydroxybenzoic acid was found at 1.219 ppm and Caffeic acid was found at 0.492 ppm and. Other compounds obtained were detected in the range of 0.251 ppm to 0.030 ppm.

3.2. Molecular docking

The active binding sites of the macromolecule (Pdb ID: 1HSK) have been previously determined in the protein data bank (Benson et al., 2001). Docking studies were performed to see the interaction modes of the two phenolic compounds (2,5-Dihydroxybenzoic acid and Caffeic acid) detected at the highest concentration in the *G. ovalis* extract with the active site of the macromolecule. Binding types and associated aminoacids were generated in detail by Maestro Software (Table 3-4, Figure 2-5). Some residues previously identified as important for the interaction Staphylococcus aureus UDP-N-acetylenolpyruvylglucosamine reductase (MurB) were described in detail in previous study (Benson et al., 2001; Unver et al., 2024). In the receptor, waters around the previously identified active site FAD (10Å) were left and all other water molecules were removed. The regular spacing of the grid boxes was determined to be 0.375 Å centered on FAD (40x40x40 $Å^3$). The interaction modes with 1HSK for 2,5-Dihydroxybenzoic acid and Caffeic acid were visualized in 2D and 3D with the Maestro program.

In conclusion, this study was carried out to reveal the *in silico* antimicrobial potential of phenolic components of *G. ovalis* extract. HPLC analysis revealed the detection of some phenolic compounds. Molecular docking study revealed dock scores and interacting residues. Molecular docking scores were good with 1HSK, which was selected for the antimicrobial activity study. In addition, some of the interactions observed and reported to be important between 1HSK and the cofactor (FAD) in previous studies were also observed in the two phenolic compounds we obtained and used in molecular docking studies. These interactions were hydrogen bonding with ASN80 and GLY146 for 2,5-Dihydroxbenzoic acid, and hydrogen bonding with TYR77, ASN80 and SER143 for Caffeic acid.

Consequently, this study, in which some phenolic contents of *G. ovalis* were determined and its antimicrobial activity was investigated by molecular docking technique, will constitute a resource for such studies on bryophytes in the future.

Table 2. Chemical compositions of the phenolic components of *G. ovalis* extract.

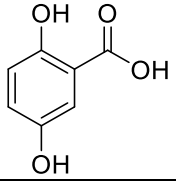
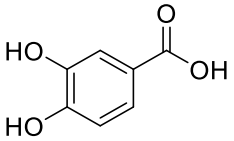
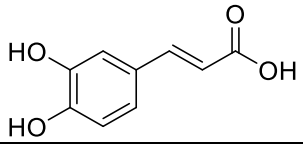
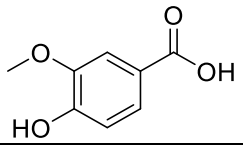
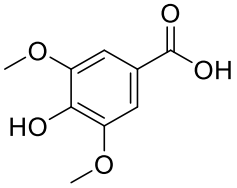
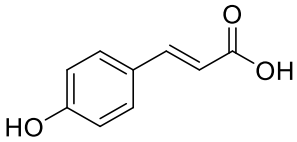
No	Compound	Chemical Structure	ppm	R^2
1	2,5-Dihydroxybenzoic acid		1.219	0.999979
2	3,4-Dihydroxybenzoic acid		0.251	0.997677
3	Caffeic acid		0.492	0.999713
4	Vanillic acid		0.161	0.999671
5	Syringic acid		0.071	0.983057
6	*p*-Qumaric acid		0.03	0.999736

Table 3. Molecular docking scores and estimated inhibition constants of Chemical compositions of phenolic components of *G. ovalis* and 1HSK.

Compounds	Autodock Results		Vina Results
	Estimated Inhibition Constant, Ki	Best Docking Score	Best Docking Score
2,5- Dihydroxybenzoic acid	24.63 µM	-6.29	-6.8
Caffeic acid	5.94 µM	-7.13	-7.5

µM: micromolar, Docking Score: Estimated Free Energy of Binding (kcal/mol)

Table 4. Interacting residues and interaction types of two phenolic components of *G. ovalis* with 1HSK.

Compounds	Autodock Results	
	Interacting Residues	Interaction Types
2,5- Dihydroxybenzoic acid	ASN80	Hydrogen Bond
	GLY146	Hydrogen Bond
	SER143	Hydrogen Bond
Caffeic acid	TYR77	Hydrogen Bond
	ASN80	Hydrogen Bond
	SER143	Hydrogen Bond

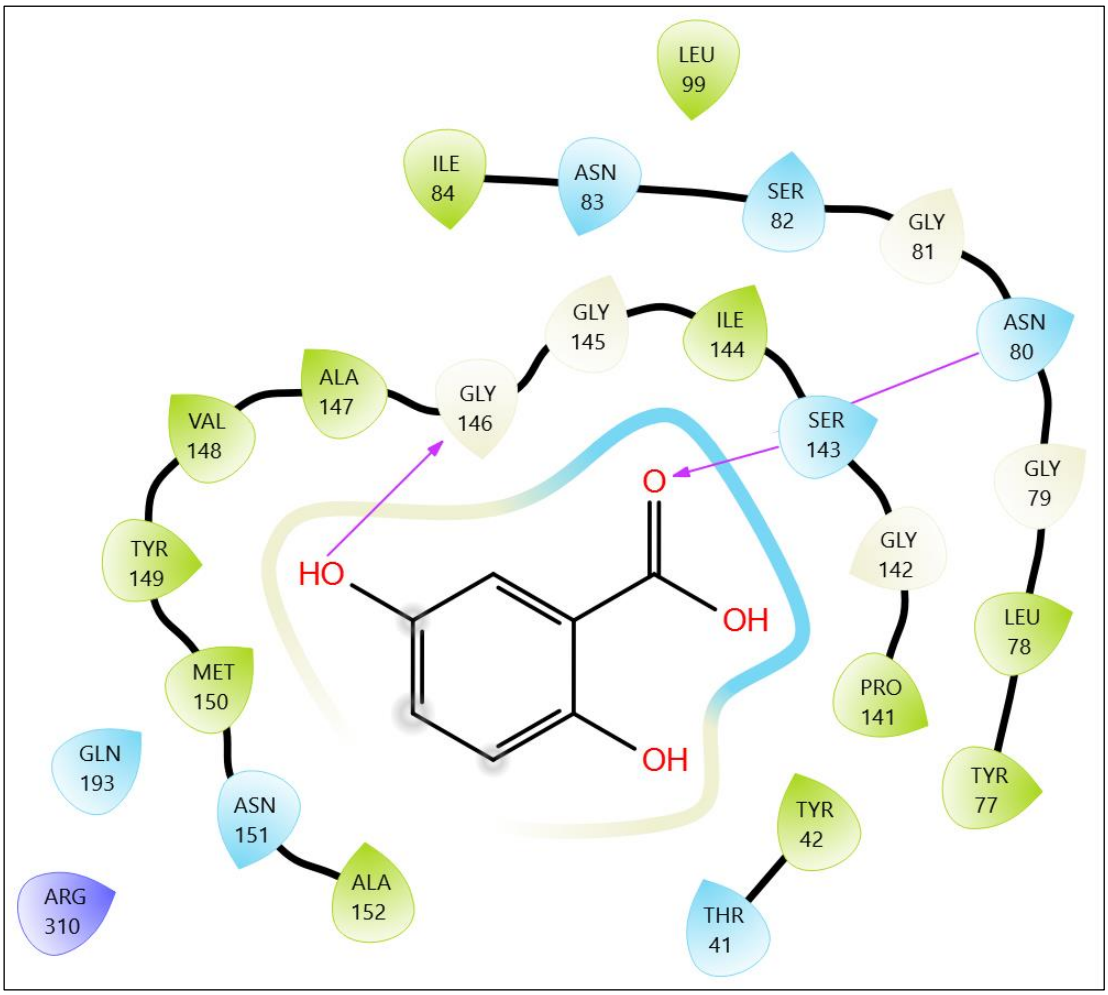


Figure 2. 2D interaction diagram with 1HSK for 2,5-Dihydroxbenzoic acid (Purple arrow: H-Bonds).

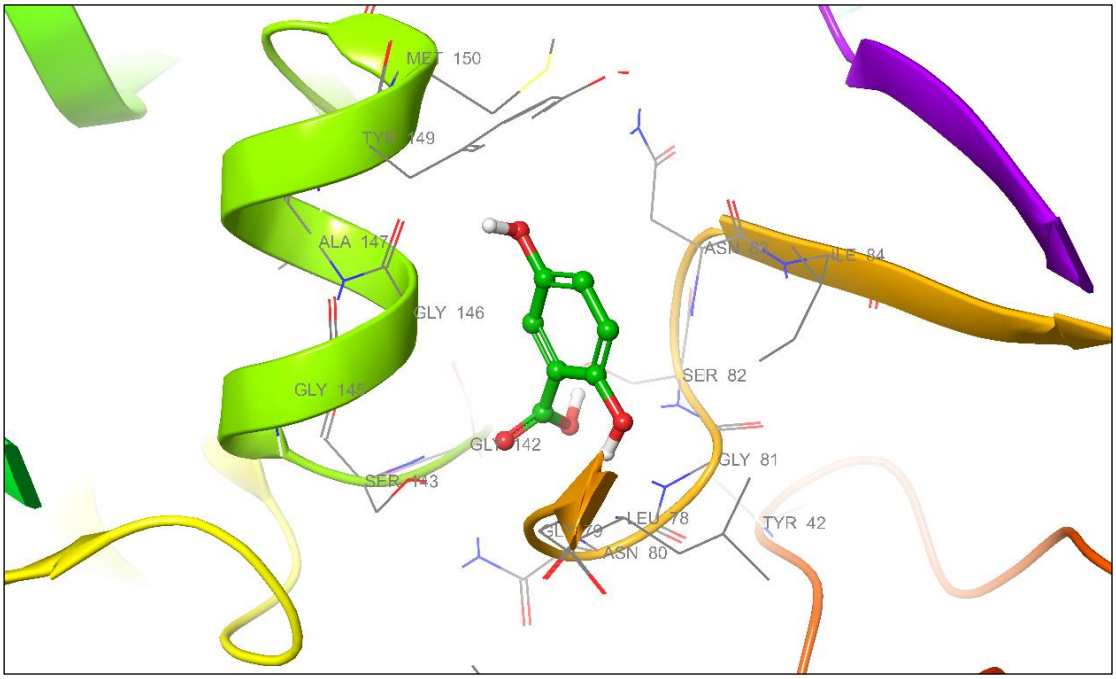


Figure 3. 3D interaction diagram with 1HSK for 2,5-Dihydroxbenzoic acid.

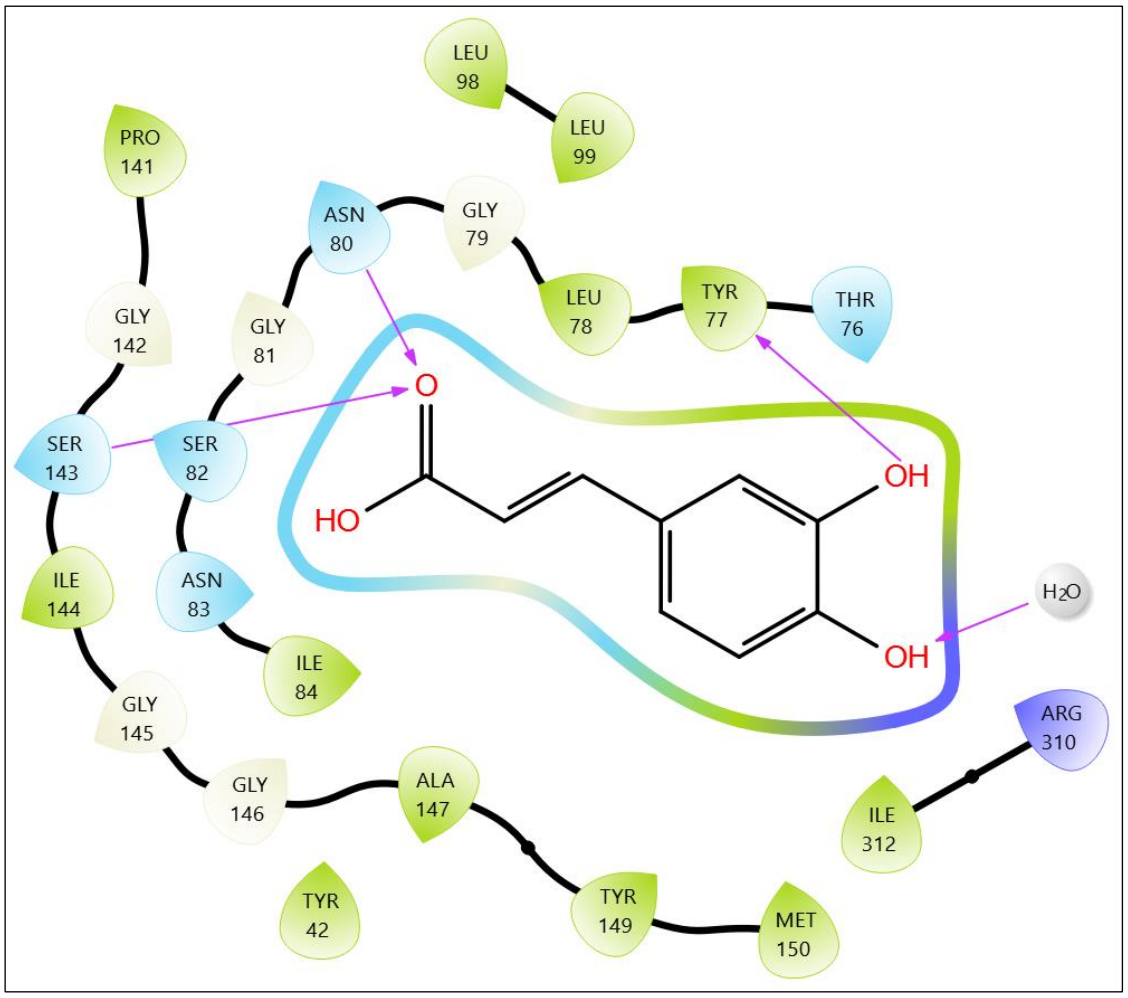


Figure 4. 2D interaction diagram with 1HSK for Caffeic acid (Purple arrow: H-Bonds).

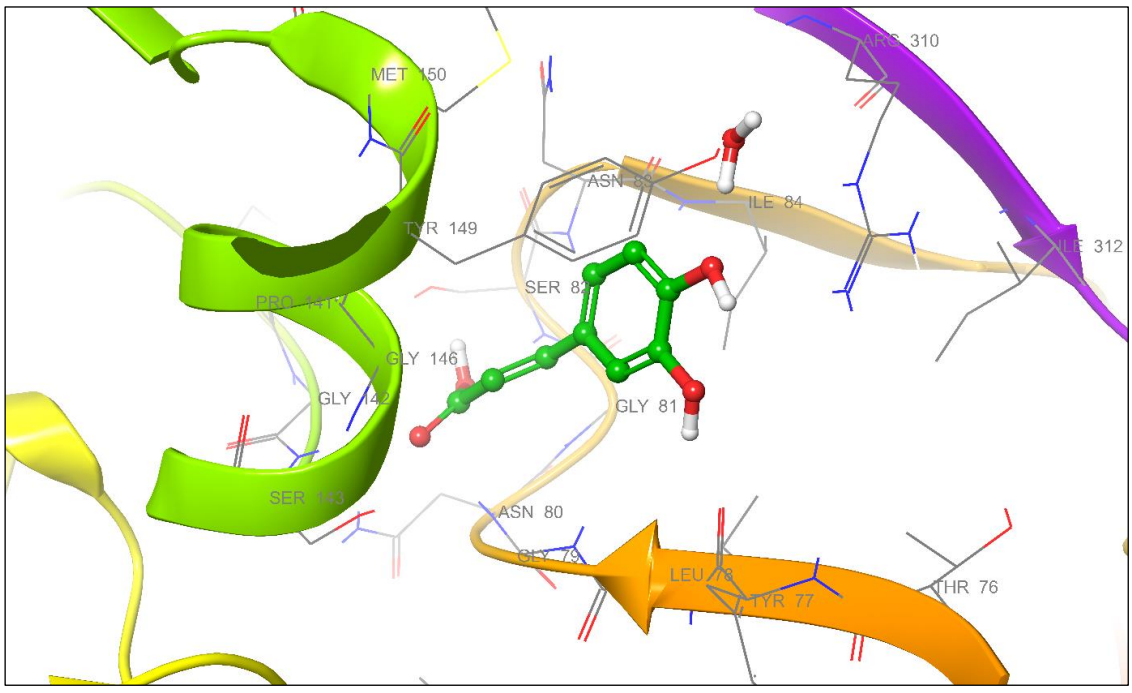


Figure 5. 3D interaction diagram with 1HSK for Caffeic acid.

Declaration

Author contributions: Concept, ZÇ; Conception and design, ZÇ, MA, HU; Supervision consultancy, MA; Resources, BG, KÖB, ÜTE; Materials, MA, ZÇ, ÜTE; Data collection and/or processing, ZÇ, KÖB, BG; Analysis and/or interpretation, ZÇ, HU, BG; Literature search, ZÇ, KÖB, MA; Writing stage, ZÇ; Critical review, MA, ZÇ.

Conflict of interest: The authors have no competing interest to declare regarding the content of this article.

Funding: The authors declare that no funding, grant or other support was received during the preparation of this article**.**

Ethical approval: This research did not involve human or animal subjects and therefore does not require ethical approval.

References

Asakawa Y. Ludwiczuk A. 2018. Chemical Constituents of Bryophytes: Structures and Biological Activity. J Nat Prod. 81:3, 641-660. doi:10.1021/acs.jnatprod.6b01046.

Barwant M. Tripathi S. 2023. Research in Mycology Series-II (Issue June). Blue Duck Publications. Srinagar.

Benson T. E. Harris M. S. Choi G. H. Cialdella J. I. Herberg J. T. Martin J. P. Baldwin E. T. 2001. A Structural Variation for MurB: X-ray Crystal Structure of Staphylococcus aureus UDP-N-Acetylenolpyruvylglucosamine Reductase (MurB). Biochemistry. 40:8, 2340-2350. doi:10.1021/bi002162d.

Delgadillo Moya C. 2015. *Grimmia* (Grimmiaceae, Bryophyta) in the Neotropics. Ciudad Universitaria, Delegación Coyoacán.

Eberhardt J. Santos-Martins D. Tillack A. F. Forli S. 2021. AutoDock Vina 1.2. 0: New docking methods, expanded force field, and python bindings. Journal of chemical information and modeling. 61:8, 3891-3898.

Elibol B. Ezer T. Kara R. Çelik G. Y. Çolak E. 2011. Antifungal and Antibacterial effects of some Acrocarpic Mosses. African Journal of Biotechnology. 10:6, 986-989.

Glime J. 2007. Bryophyte ecology. Volume 1: Physiological ecology. Michigan Technological University and the International Association of Bryologists. In: Houghton.

Hardman A. 2007. Terrestrial lichen and bryophyte communities of the Blue Mountains in Northeast Oregon.

Henderson D. M. 1961. Contribution to the bryophyte flora of Turkey. Notes from the Royal Botanic Garden Edinburgh. 10, 279-301.

Huey R. Morris G. M. Olson A. J. Goodsell D. S. 2007. A semiempirical free energy force field with charge-based desolvation. Journal of computational chemistry. 28:6, 1145-1152.

Kürschner H. Frey W. 2011. Liverworts, mosses and hornworts of southwest Asia (Marchantiophyta, Bryophyta, Anthocerotophyta). Nova Hedwigia. Beihefte, Beih. 139.

Maestro S. 2024. Schrödinger Release 2024-3: LLC, New York, NY.

Peters K. Gorzolka K. Bruelheide H. Neumann S. 2018. Seasonal variation of secondary metabolites in nine different bryophytes. Ecology and Evolution. 8:17, 9105-9117.

Pirisi F. M. Cabras P. Cao C. F. Migliorini M. Muggelli M. 2000. Phenolic compounds in virgin olive oil. 2. Reappraisal of the extraction, HPLC separation, and quantification procedures. Journal of agricultural and food chemistry. 48:4, 1191-1196.

Rios J.-L. Recio M. C. 2005. Medicinal plants and antimicrobial activity. Journal of ethnopharmacology, 100:1-2, 80-84.

Unver T. Uslu H. Gurhan I. Goktas B. 2024. Screening of phenolic components and antimicrobial properties of Iris persica L. subsp. persica extracts by in vitro and in silico methods. Food Science & Nutrition. 12:9, 6578-6594.

Veneziani G. Esposto S. Taticchi A. Urbani S. Selvaggini R. Sordini B. Servili M. 2018. Characterization of phenolic and volatile composition of extra virgin olive oil extracted from six Italian cultivars using a cooling treatment of olive paste. LWT. 87: 523-528.