

Title of Research

**Molecular Docking and Pharmacokinetic Studies of
Punica granatum peel Phytochemicals to explore
potential Antibacterial Activity**

Author's Name and Affiliation

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Background and Objective

- The continuous emergence of novel antibiotic resistance strains of bacteria make serious problem regarding management and treatment of infected individuals worldwide.
- One study estimated about 700,000 people yearly were death and this will be increased to touch 10 million in the next three decades
- The plant *Punica granatum* is more well-known because it contain diverse array of phytochemicals demonstrates their therapeutic properties
- The objective is to analyze ADME characterization and docking of bioactive compounds of studied plant with two target proteins viz. D-alanine-D ligase from gram positive bacteria and DNA gyrase from gram-negative bacteria

Methodology

In Silico Analysis

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graph TD; A[In Silico Analysis] --> B[Selection of Target Proteins]; B --> C[Selection of Ligands from studied plant]; C --> D[Prediction of Active Site on studied Target Proteins]; B --> B1[D Ala-D Ala Ligase(PDB ID: 3N8D)]; B --> B2[DNA Gyrase (PDB ID: 4Z2D)]; C --> C1[17 phytocompounds selected]; D --> D1[CASTp];
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The flowchart illustrates the methodology for in silico analysis. It begins with 'In Silico Analysis', which leads to 'Selection of Target Proteins'. From this step, two specific proteins are identified: D Ala-D Ala Ligase (PDB ID: 3N8D) and DNA Gyrase (PDB ID: 4Z2D). The process then moves to 'Selection of Ligands from studied plant', where 17 phytocompounds are selected. Finally, the 'Prediction of Active Site on studied Target Proteins' is performed using the CASTp tool.

Selection of Target Proteins

D Ala-D Ala Ligase(PDB ID: 3N8D)

DNA Gyrase (PDB ID: 4Z2D)

Selection of Ligands from studied plant

17 phytocompounds selected

Prediction of Active Site on studied Target Proteins

CASTp

Molecular Docking



→ **AutoDock 4.2.6**

Evaluation of Drug Likelihood



→ **Lipinski's rule of five**

→ **BOILED Egg Model**

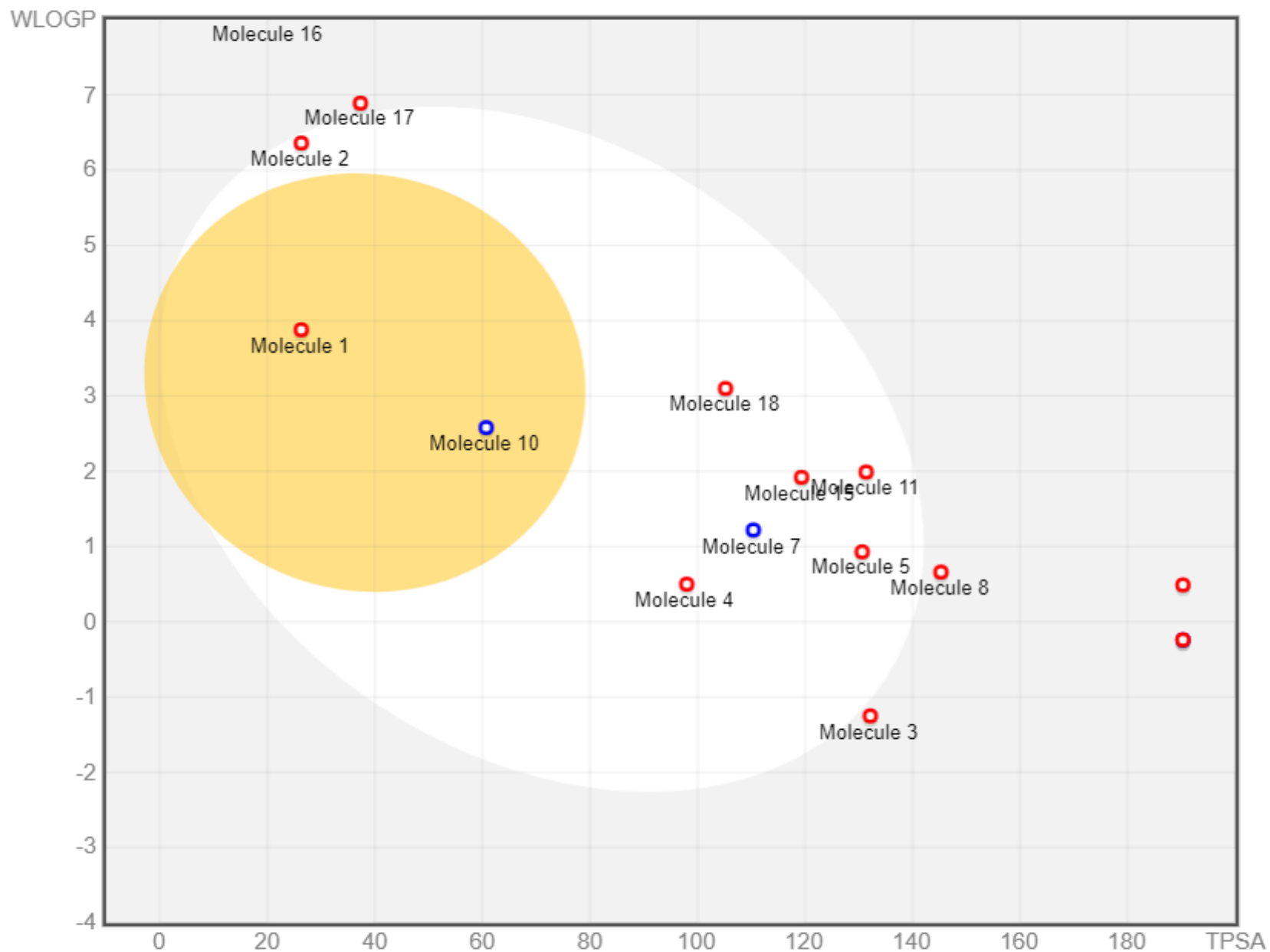
Results

➤ Docking Scores

S. No.	Ligands (Molecules)	Binding affinity (Kcal/mol)	
		3N8D	4Z2D
1.	Limonen -"6-ol", pivalate	-6	-5.5
2.	9-12-octadecadienoic acid, ethyl ester	-5.6	-5.1
3.	Citric acid	-5.8	-5.4
4.	Gallic acid	-5.9	-5.5
5.	Gallocatechin	-7.8	-7.4
6.	Granatin A	-9.9	-9.5
7.	Catechin	-8.7	-7.3
8.	Brevifolin carboxylic acid	-8.3	-7.1
9.	Dihydromyricetin 3-O-rhamnoside	-7.6	-7.7
10.	Estriol	-7.8	-7.3
11.	Quercetin	-8.5	-7.5
12.	Cynaroside	-8.2	-8.2
13.	Astragalin	-7.5	-8
14.	Quercitrin	-9.1	-7.7
15.	3,3'-Di-O-methylellagic acid	-8.1	-7.7
16.	Gamma sitosterol	-2.1	-1.6
17.	Gadoleic acid	-5	-3.6
18.	Tributyl acetyl citrate	-5	-5.6
19.	Vancomycin	8.7	-
20.	Levofloxacin	-	-7.6

➤ Lipinski properties of plant compounds analyzed by molinspiration

S. No.	Compound (Molecules)	Mol. Wt. (<500Da)	Log p (<5)	H-bond Donor (<5)	H-bond acceptor (<10)	TPSA <140
1	Limonen -"6-ol" ,pivalate	236	3.39	0	2	26.30
2	9-12 octadecadienoic acid,ethyl ester	308	5.03	0	2	26.30
3	Citric acid	192	-1.49	4	7	132.13
4	Gallic acid	170	0.21	4	5	97.99
5	Gallocatechin	306	0.98	6	7	130.61
6	Granatin A	800	0.56	12	23	383.49
7	Catechin	290	1.47	5	6	110.38
8	Brevifolin carboxylic acid	292	0.11	4	8	145.27
9	Dihydromyricetin 3-O-rhamnoside	466	1.30	8	12	206.60
10	Estriol	288	2.23	3	3	60.69
11	Quercetin	302	1.63	5	7	131.36
12	Cynaroside (Luteolin 7-O-glycoside)	448	1.83	7	12	190.28
13	Astragalin (Kaempferol 3-O-glucoside)	448	0.53	7	11	190.28
14	Quercetin 3-O-rhamnoside	448	1.27	7	11	190.28
15	3,3'-Di-O-methylellagic acid	330	1.90	2	8	119.34
16	Gamma sitosterol	414	4.79	1	1	20.23
17	Gadoleic acid	310	4.45	1	2	37.30
18	Tributyl acetylcitrate	402	4.58	0	8	105.20



Actions

☒ Show Molecules Name

Legends

- BBB
- HIA
- PGP+
- PGP-

Remarks

3 molecules out of range!

Conclusion

The several antibiotics available are become fail to treatment of infectious diseases caused by antibiotic resistant strains of bacteria which leads to search of novel drug sources. The drug potentials from *Punica granatum* peel were studied by use of molecular docking to D-alanine-D alanine ligase (3N8D) from gram positive bacteria and DNA gyrase (4Z2D) from gram negative bacteria. Among compounds, granatin A, quercitrin, astragalin and cymaroside showed great binding affinity with 3N8D and 4Z2D. As a result, these molecules can be examined in more detail for in vitro research, which is a valuable tool for developing new medications for the treatment of bacterial infections.



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