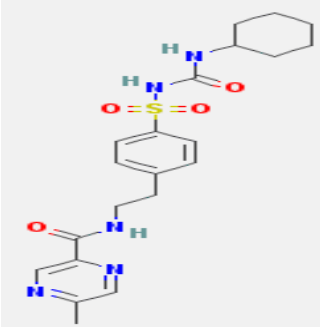
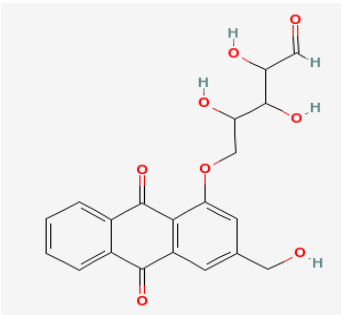
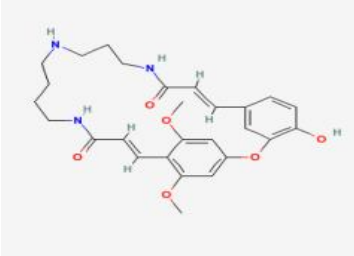
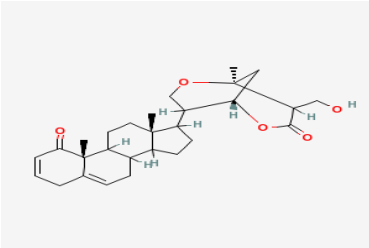


Supplementary material:

Table 1: Comparative study representation of drug likeness and biochemical properties, docking score (using Hex and Quantum) and binding pocket analysis for AhG compounds vs. bench mark drug satisfying Protein-Ligand Interaction study (Stage I and II).

Sl. No.	Name of the plant (the compound)	Chemical properties of the compound	Docking score	Binding Analysis	Pocket
Std Drug	Flax plant (Glipizide) Structure of the compound CID: 3478	 Canonical smile: <chem>CC1=NC=C(N=C1)C(=O)NCCCC=CC=C(C=C2)S(=O)(=O)NC(=O)NC3CCCCC3</chem>	Lipinski Rule: Molecular Weight : 445.53518 [g/mol] Molecular Formula : C ₂₁ H ₂₇ N ₅ O ₄ S XLogP3-AA : 1.9 H-Bond Donor : 3 H-Bond Acceptor : 6	Hex Score: Energy minimized (Kcal/mol) 151.85 Docking results (E-Total) -257.66 Quantum Score: Gibbs free energy (kcal/mol) -19.38 Root Mean Square Deviation (A°) 47.39	Amino acid base LEU 32 Rank: H-Bond distance (A°) 1.63
1.	Aloe barbadensis (Aloins) Structure of the compound CID: 221037	 Canonical smile: <chem>C1=CC=C2C(=C1)C(=O)C3=CC(=CC(=C3C2=O)OCC(C(C(=O)O)O)O)CO</chem>	Lipinski Rule: Molecular Weight : 386.35212 [g/mol] Molecular Formula : C ₂₆ H ₁₈ O ₈ XLogP3-AA : -0.4 H-Bond Donor : 4 H-Bond Acceptor : 8	Hex Score: Energy minimized (Kcal/mol) 50.12 Docking results (E-Total) -260.48 Quantum Score: Gibbs free energy (kcal/mol) -20.07 Root Mean Square Deviation (A°) 25.92	Amino acid base GLU 30 Rank: FOURTH H-Bond distance (A°) 2.50
2.	Capparis decidua (Capparisin-ine) Structure of the compound CID: 16058118	 Canonical smile: <chem>COC1=CC2=CC(=C1C=CC(=O)NCCCCNCCCNC(=O)C=CC3=CC(=C(C=O)O)O2)OC</chem>	Lipinski Rule: Molecular Weight : 495.56742 [g/mol] Molecular Formula : C ₂₇ H ₃₃ N ₃ O ₆ XlogP3-AA : 3 H-Bond Donor : 4 H-Bond Acceptor : 7	Hex Score: Energy minimized (Kcal/mol) 150.29 Docking results (E-Total) -283.00 Quantum Score: Gibbs free energy (kcal/mol) -20.40 Root Mean Square Deviation (A°) 32.96	Amino acid base GLY 59 Rank: THIRD H-Bond distance (A°) 1.73
3.	Desmodium Gangeticum (Daturilinol) Structure of the compound CID: 5316315	 Canonical smile: <chem>CC12CCC3C(C1CCC2C4COC5(CC4OC(=O)C5CO)C)CC=C6C3(C(=O)C=CC6)C</chem>	Lipinski Rule: Molecular Weight: 454.59832 [g/mol] Molecular Formula: C ₂₈ H ₃₈ O ₅ XLogP3-AA: 4.8 H-Bond Donor: 1 H-Bond Acceptor: 5	Hex Score: Energy minimized (Kcal/mol) 371.14 Docking results (E-Total) -267.19 Quantum Score: Gibbs free energy (kcal/mol) -11.16 Root Mean Square Deviation (A°) 26.69	Amino acid base LEU 32, GLY 59 Rank: SIXTH H-Bond distance (A°) 1.60, 1.70

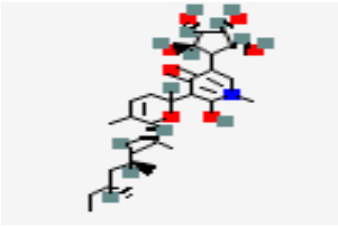
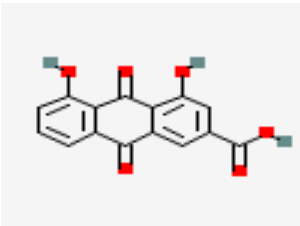
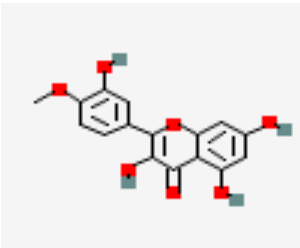
4.	Senna occidentalis (L.) (Funiculosin) Structure of the compound CID: 6444332		<p>Lipinski Rule: Molecular Weight : 491.61694 [g/mol] Molecular Formula : C₂₇H₄₁NO₇ XLogP3-AA: 2.1 H-Bond Donor: 5 H-Bond Acceptor: 8</p> <p>Chemical/Bio-activity miLogP: 2.323 GPCR ligand: 0.20 Ion channel Modulator: -0.03 Kinase inhibitor: -0.06 Nuclear receptor Ligand: 0.28</p>	<p>Hex Score:</p> <p>Energy minimized (Kcal/mol) 91.58</p> <p>Quantum Score:</p> <p>Gibbs free energy (kcal/mol) -37.52</p>	<p>Amino acid base</p> <p>Docking results (E-Total) -269.31</p> <p>Rank: FIRST</p> <p>Root Mean Square Deviation (A°) 38.95</p>	<p>H-Bond (A°) GLU 13</p>	<p>distance 1.21</p>
5.	Senna occidentalis (L.) (Rhein) Structure of the compound CID: 101168		<p>Lipinski Rule: Molecular Weight: 284.22042 [g/mol] Molecular Formula: C₁₅H₈O₅ XLogP3-AA: 2.2 H-Bond Donor: 3 H-Bond Acceptor: 6</p> <p>Chemical/Bio-activity miLogP: 2.997 GPCR ligand: -0.08 Ion channel Modulator: -0.10 Kinase inhibitor: 0.01 Nuclear receptor Ligand: 0.29</p>	<p>Hex Score:</p> <p>Energy minimized (Kcal/mol) 37.06</p> <p>Quantum Score:</p> <p>Gibbs free energy (kcal/mol) -27.32</p>	<p>Amino acid base</p> <p>Docking results (E-Total) -258.48</p> <p>Rank: SECOND</p> <p>Root Mean Square Deviation (A°) 39.09</p>	<p>H-Bond (A°) LEU 32, GLY 59</p>	<p>distance 1.56, 2.17</p>
6.	Costus spicatus (Tamarixetin) Structure of the compound CID: 5281699		<p>Lipinski Rule: Molecular Weight : 316.26228 [g/mol] Molecular Formula : C₁₆H₁₂O₇ XLogP3-AA : 1.9 H-Bond Donor : 4 H-Bond Acceptor : 7</p> <p>Chemical/Bio-activity miLogP: 1.99 GPCR ligand: -0.10 Ion channel Modulator: -0.26 Kinase inhibitor: 0.25 Nuclear receptor Ligand: 0.28</p>	<p>Hex Score:</p> <p>Energy minimized (Kcal/mol) -17.56</p> <p>Quantum Score:</p> <p>Gibbs free energy (kcal/mol) -15.65</p>	<p>Amino acid base</p> <p>Docking results (E-Total) -258.00</p> <p>Rank: FIFTH</p> <p>Root Mean Square Deviation (A°) 19.70</p>	<p>H-Bond (A°) ILE 25</p>	<p>distance 1 . 5 4</p>

Table 2: Pharmacokinetic and pharmodynamic studies for AhG compounds on various body organelles.

Sl. No.	Compound	ADME Properties					Toxicity Properties					
		Oral Availability	Solubility	Drug binding to plasma protein	Volume of Distribution	AMES	Health effect					
							B ^a	C ^a	G ^a	K ^a	Lj ^a	Lu ^a
Drug	Glipizide	%F(Oral) > 30%: 0.886	-3.15	%PPB: 99.13%	0.19 L/kg	0.000	0.46	0.92	0.97	0.31	0.28	0.23
1	Aloins	%F(Oral) > 70%: 0.732		LogKa HSA : 4.86								
		%F(Oral) > 30%: 0.086	-3.53	%PPB: 15.83%	1.29 L/kg	0.739	0.20	0.85	0.35	0.30	0.18	0.20
		%F(Oral) > 70%: 0.040		LogKa HSA: 2.94								
2	Capparisi-nine	%F(Oral) > 30%: 0.729	-2.13	%PPB: 61.93%	3.42 L/kg	0.207	0.00	0.02	0.92	0.18	0.14	0.00
		%F(Oral) > 70%: 0.521		LogKa HSA: 3.92								
3	Funiculosin	%F(Oral) > 30%: 0.773	-3.66	%PPB: 98.55%	0.36 L/kg	0.018	0.98	0.99	0.99	0.97	0.94	0.99
		%F(Oral) > 70%: 0.148		LogKa HSA: 4.04								
4	Rhein	%F(Oral) > 30%: 0.296	-2.99	%PPB: 97.49%	0.23 L/kg	0.977	0.15	0.34	0.23	0.09	0.06	0.41
		%F(Oral) > 70%: 0.080		LogKa HSA: 5.16								

B^a= Blood; C^a= Cardiovascular system; G^a= Gastrointestinal system; K^a= Kidney; Lj^a= Liver; Lu^a= Lungs