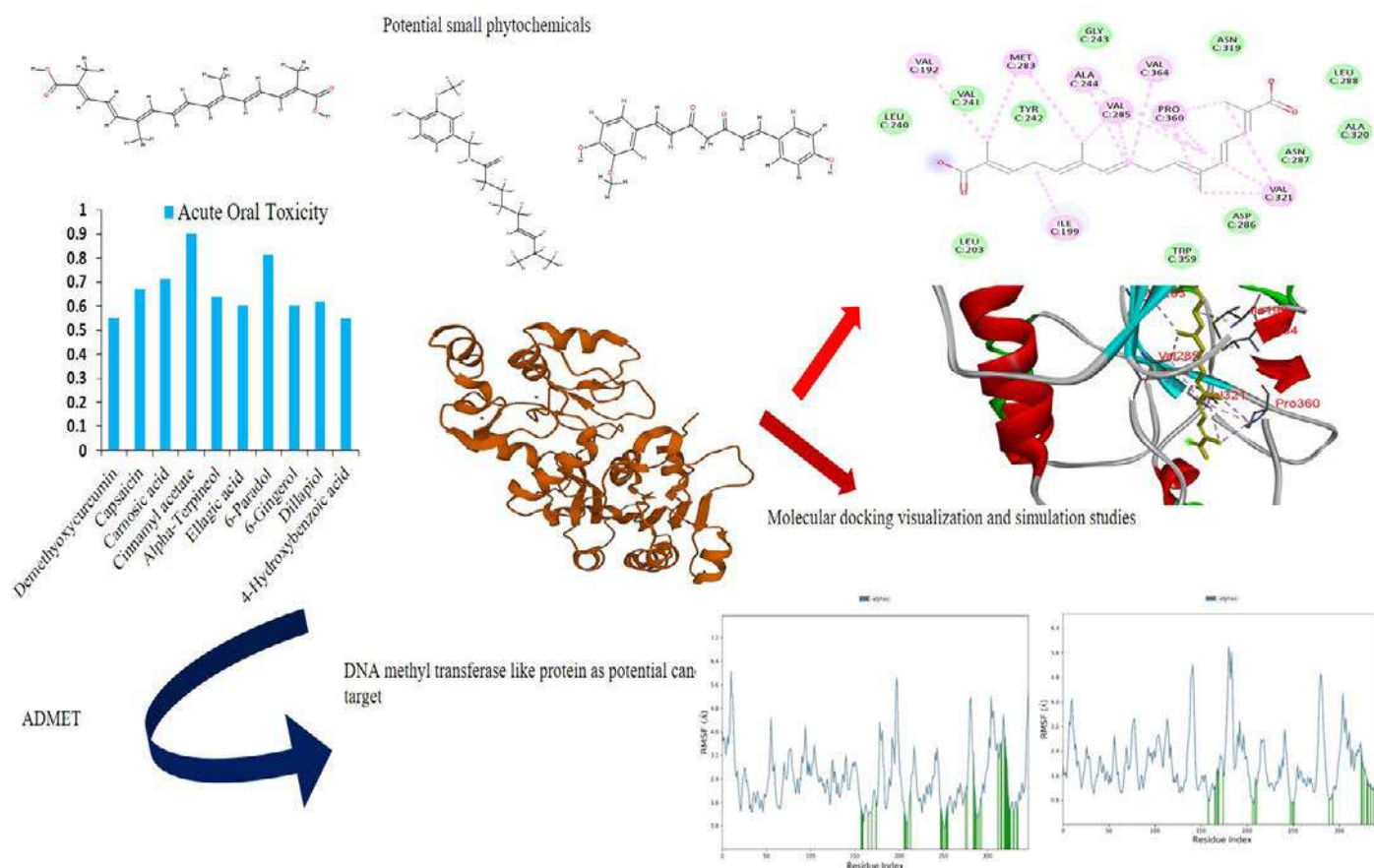


2023

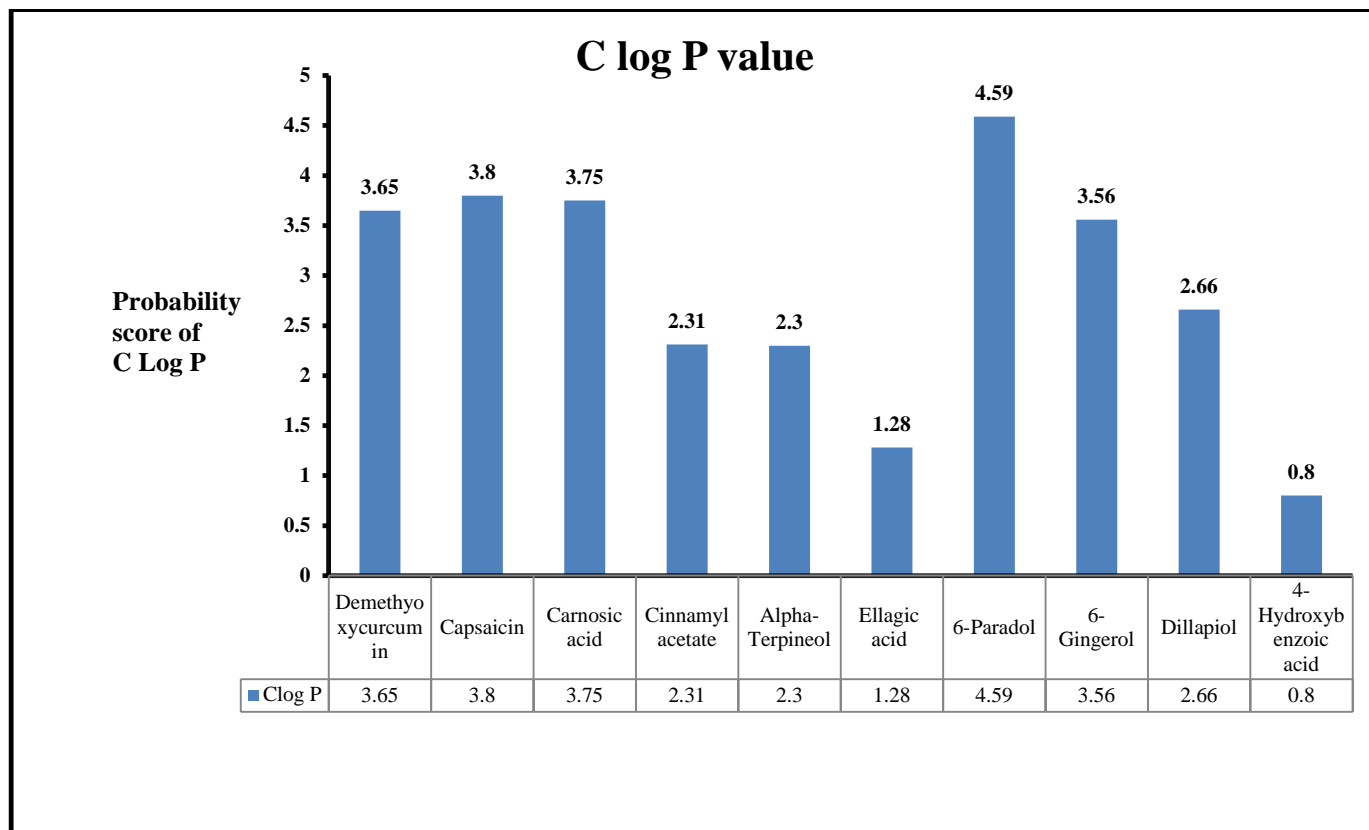
10(2), 537

Chemical Biology  
LETTERS**In silico identification of small natural inhibitors against DNA methyl transferase 3-like protein by integrative molecular docking and molecular dynamics approach**Paratpar Sarkar<sup>1</sup>, Niraj Niraj<sup>2</sup> and Vivek Srivastava<sup>1\*</sup><sup>1</sup>Department of Chemistry & Biochemistry, Sharda School of Basic Sciences & Research, Sharda University, Greater Noida-201308, UP, India, <sup>2</sup>Dr. R.P. Centre, All India Institute of Medical Sciences, Delhi, India.**Supplementary Information file****Article cover image:**

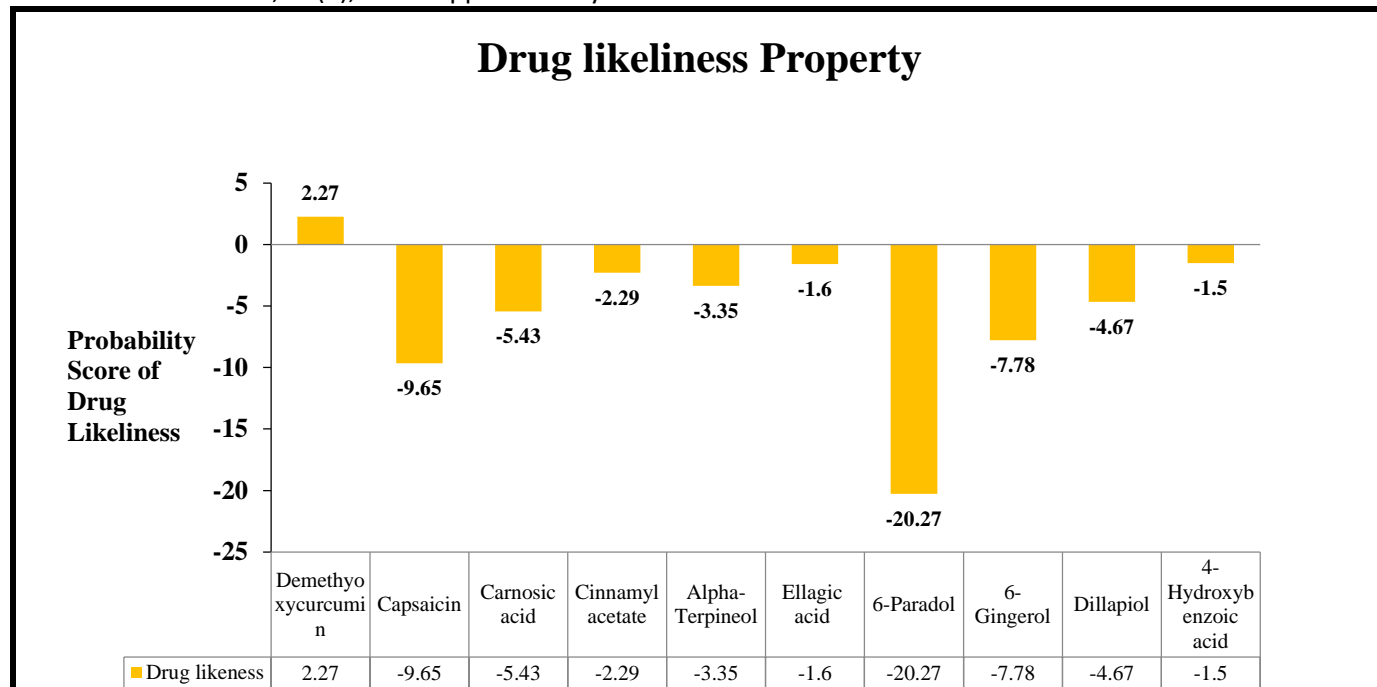
**Table 1:** Small phytochemicals from different plant species with their SMILE notation

Small phytochemicals	Comp (CID)	SMILE notation	Sources
Ferulic acid	445858	<chem>CC(C)(C)[Si](C)(C)OC1=C(C=C(C=C1)C=CC(=O)O[Si](C)(C)C(C)(C)OC</chem>	<i>Syzygium Aomaticum</i>
Crocetin	528123 2	<chem>CC(=CC=CC=C(C)C=CC=C(C)C(=O)O)C=CC=C(C)C(=O)O</chem>	<i>Crocus sativus</i>
Cinnamic acid	444539	<chem>C1=CC=C(C=C1)C=CC(=O)O</chem>	<i>Cinnamon</i>
Eugenol	3314	<chem>COC1=C(C=CC(=C1)CC=C)O</chem>	<i>Cinnamon</i>
Cinnamaldehyde	637511	<chem>C1=CC=C(C=C1)C=CC=O</chem>	<i>Cinnamon</i>
Allicin	65036	<chem>C=CCSS(=O)CC=C</chem>	<i>Allium sativum</i>
Alpha tumerone	558173	<chem>CC1=CC=C(CC1)C(C)CC(=O)C=C(C)C</chem>	<i>Curcumin Longa</i>
Curcumin	101341 351	<chem>CC1=C(C=C(C=C1)C=CC(=O)CC(=O)C=CC2=CC(=C(C=C2)O)O</chem> <chem>C)[N+](=O)[O-])[N+](=O)[O-]</chem>	<i>Curcumin Longa</i>
Estragole	8815	<chem>COC1=CC=C(C=C1)CC=C</chem>	<i>Ocimum basilicum</i>
Shogaol	528179 4	<chem>CCCCC=CC(=O)CCC1=CC(=C(C=C1)O)OC</chem>	<i>Ginger officinale</i>
Demethoxy curcumin	546942 4	<chem>COC1=C(C=CC(=C1)C=CC(=O)CC(=O)C=CC2=CC=C(C=C2)O)O</chem>	<i>Curcumin longa</i>
Capsaicin	154894 3	<chem>CC(C)/C=C/CCCCC(=O)NCC1=CC(=C(C=C1)O)OC</chem>	<i>Piper nigrum</i>
Cinnamyl acetate	528211 0	<chem>CC(=O)OC/C=C/C1=CC=CC=C1</chem>	<i>Curcumin Longa</i>
Alpha terpineol	17100	<chem>CC1=CCC(CC1)C(C)(C)O</chem>	<i>Elettaria cardamomum</i>
Ellagic acid	528185 5	<chem>C1=C2C3=C(C(=C1O)O)OC(=O)C4=CC(=C(C(=C43)OC2=O)O)O</chem>	<i>Syzygium aromaticum</i>
6-Paradol	94378	<chem>CCCCCCCC(=O)CCC1=CC(=C(C=C1)O)OC</chem>	<i>Ginger officinale</i>
6-Gingerol	442793	<chem>CCCCC(CC(=O)CCC1=CC(=C(C=C1)O)OC)O</chem>	<i>Ginger officinale</i>
Dillapiol(Di)	10231	<chem>COC1=C(C2=C(C=C1CC=C)OCO2)OC</chem>	<i>Foeniculum vulgare</i>
4-Hydroxybenzoic acid	135	<chem>C1=CC(=CC=C1C(=O)O)O</chem>	<i>Coriandrum sativum plant</i>

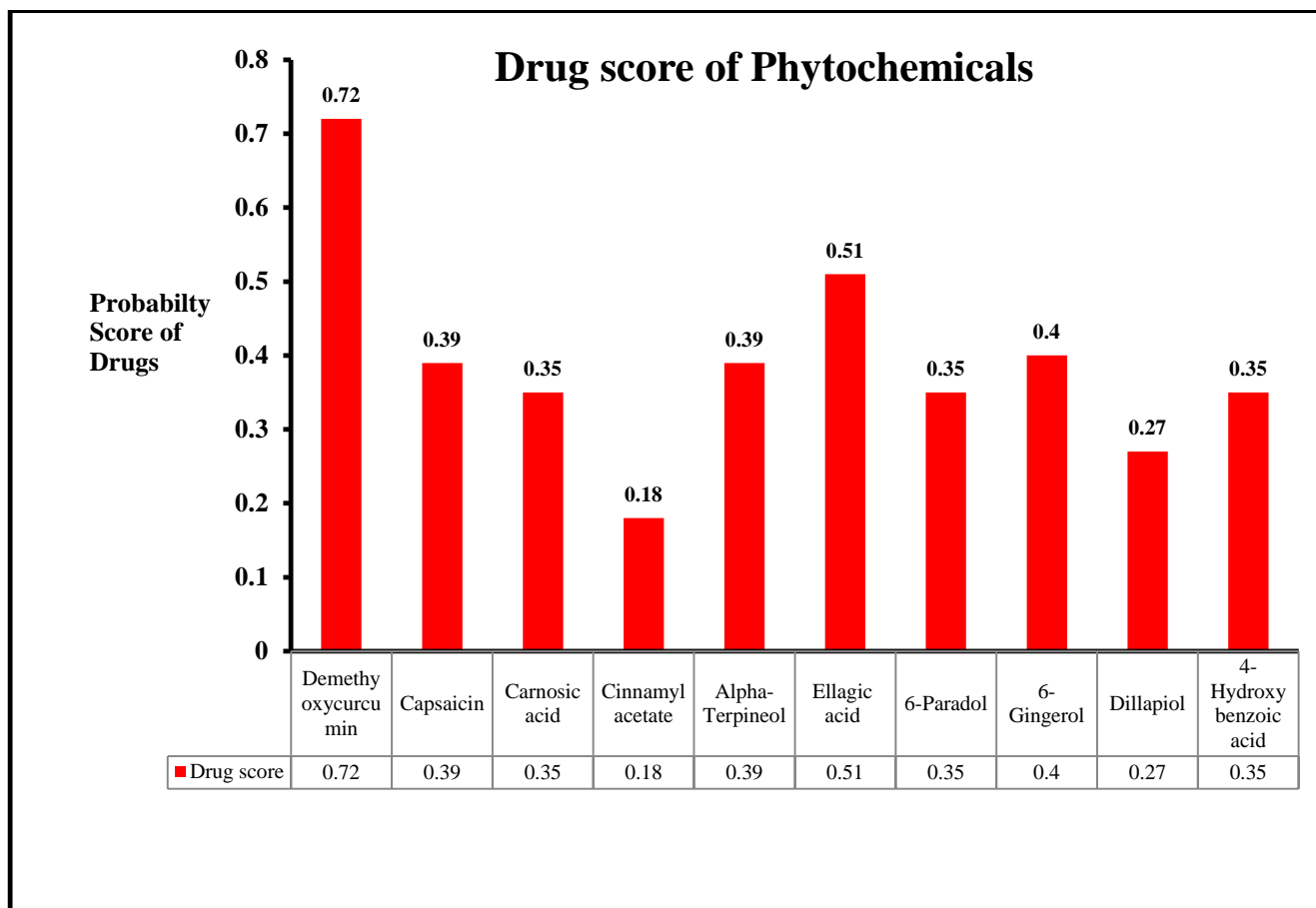
Carnosic acid      65126      CC(C)C1=C(C(=C2C(=C1)CCC3C2(CCCC3(C)C)C(=O)O)O)O      *Rosmarinus officinalis*



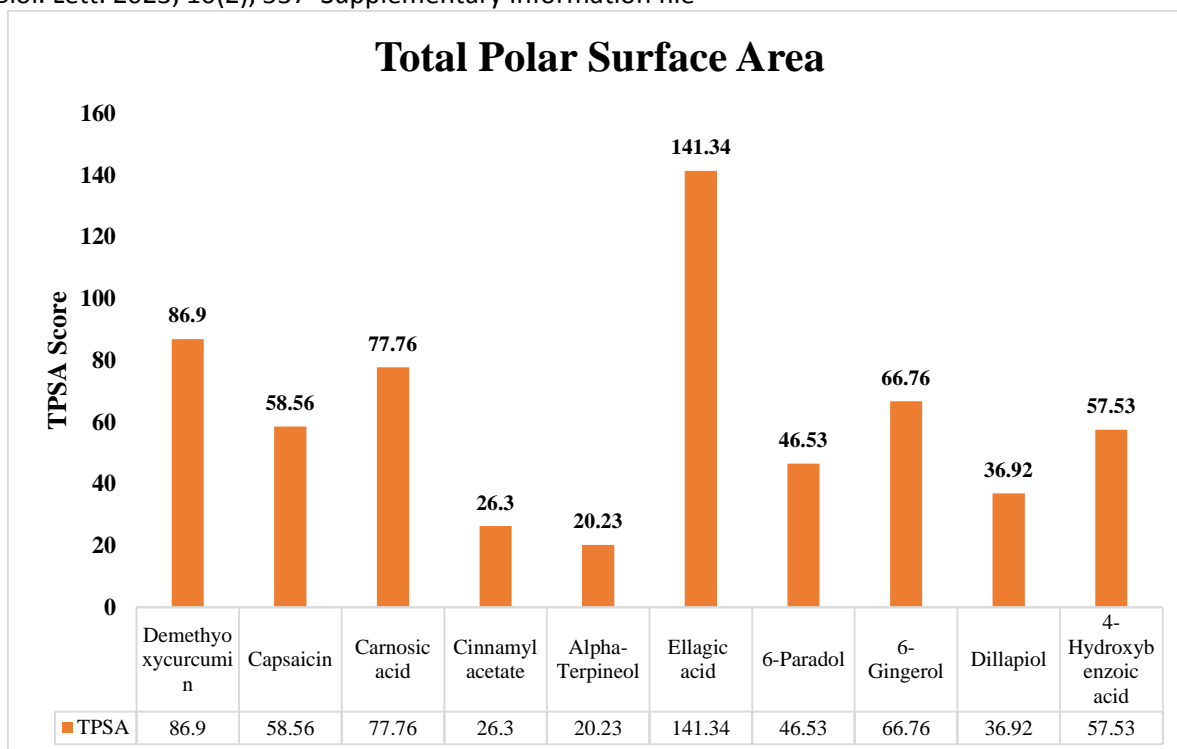
A



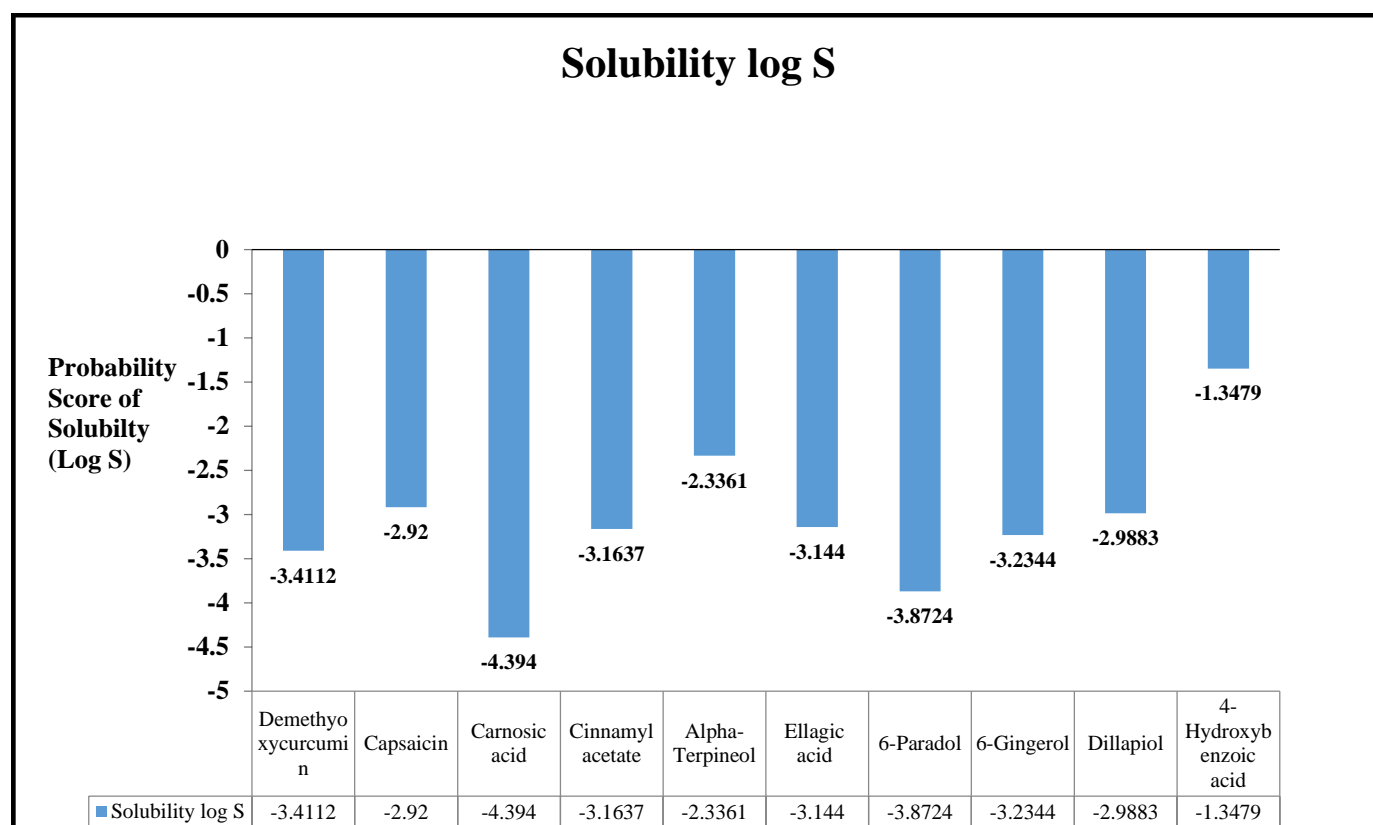
b



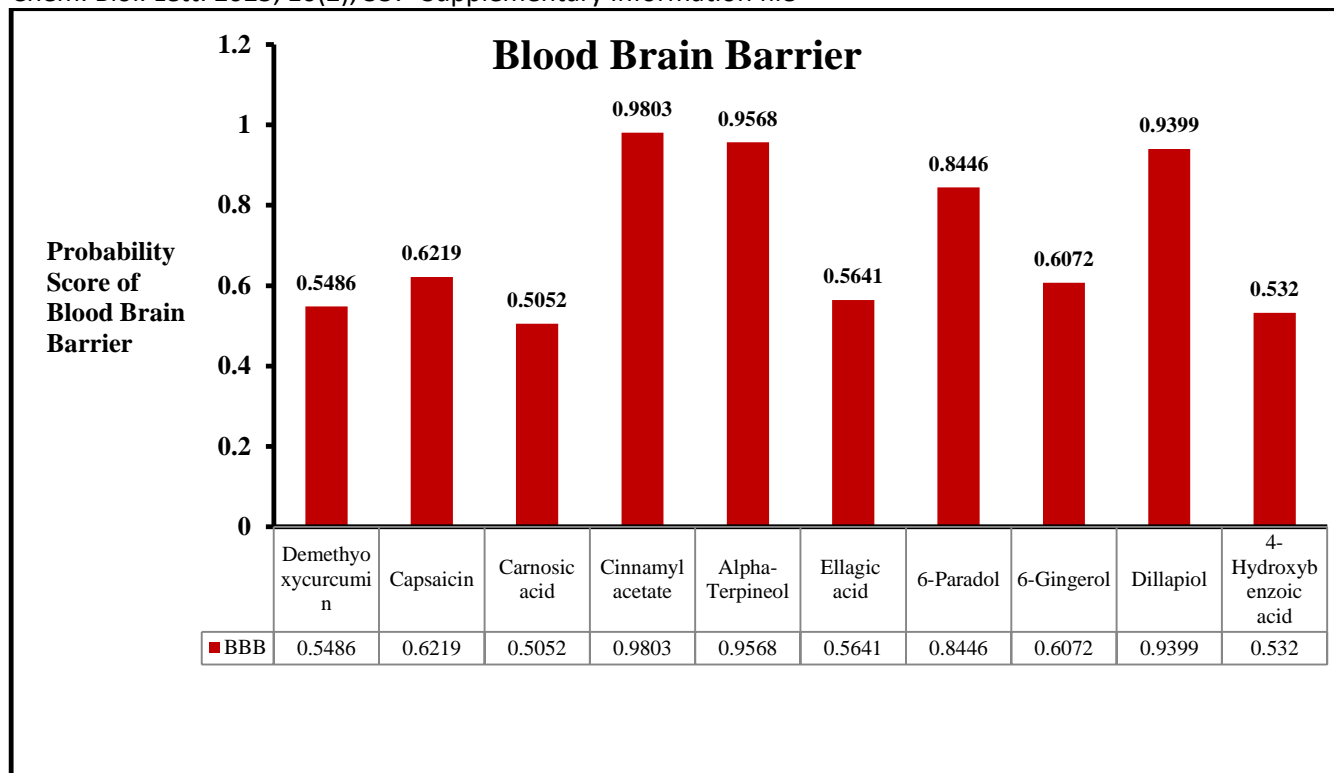
c



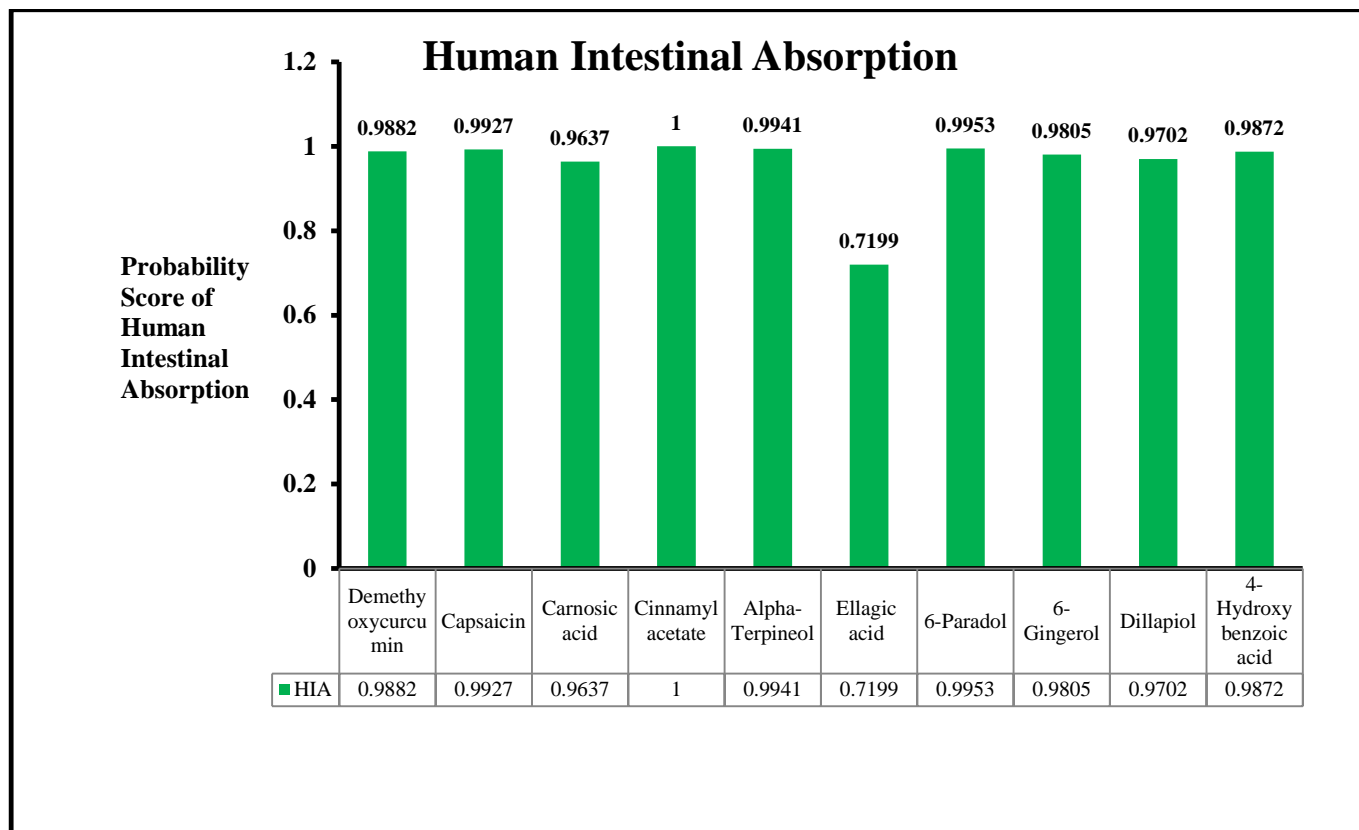
d



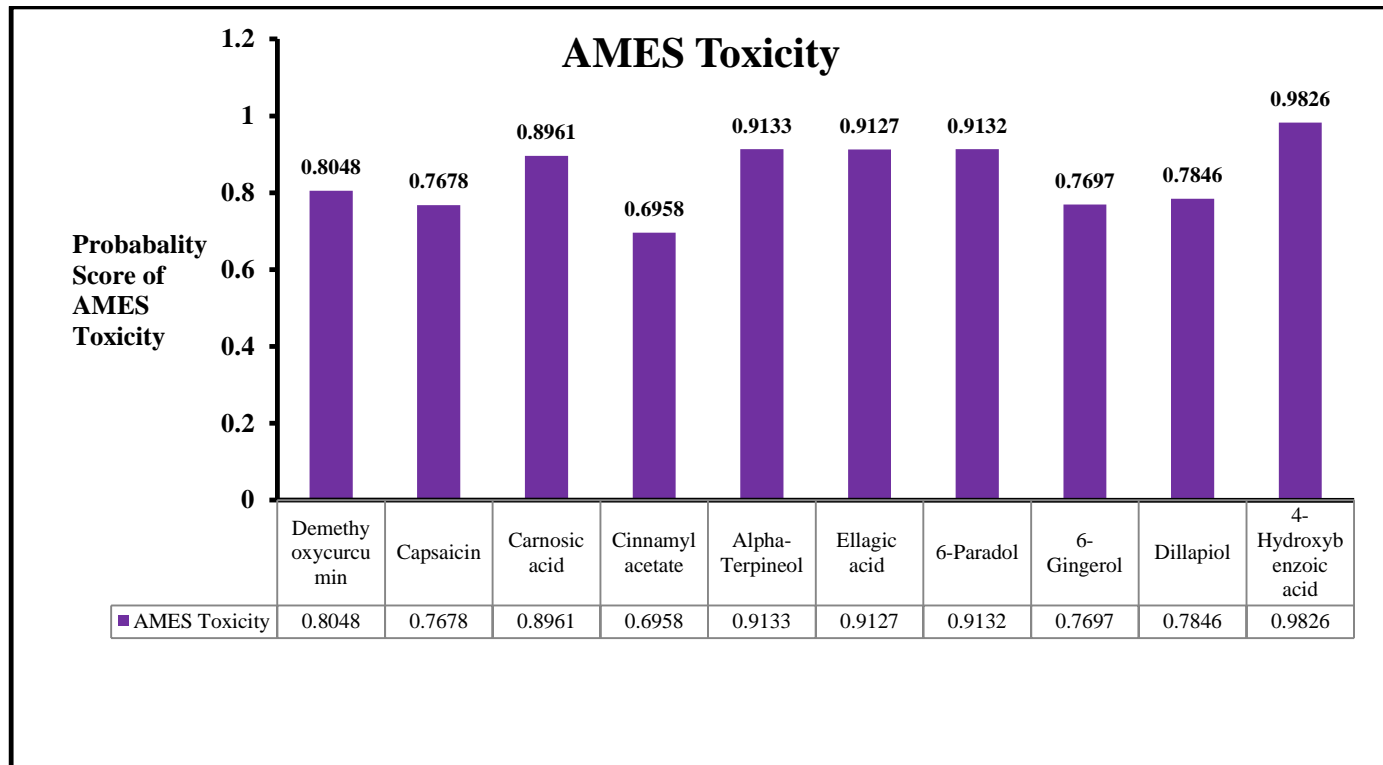
e



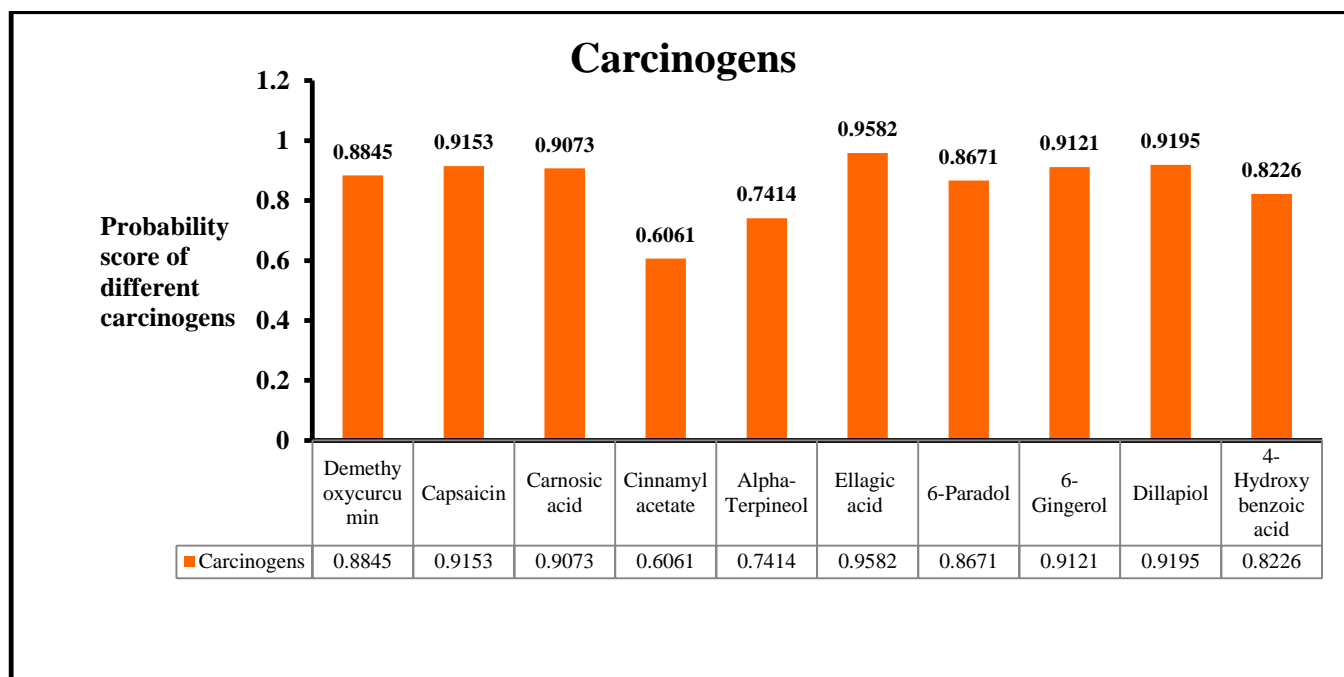
f



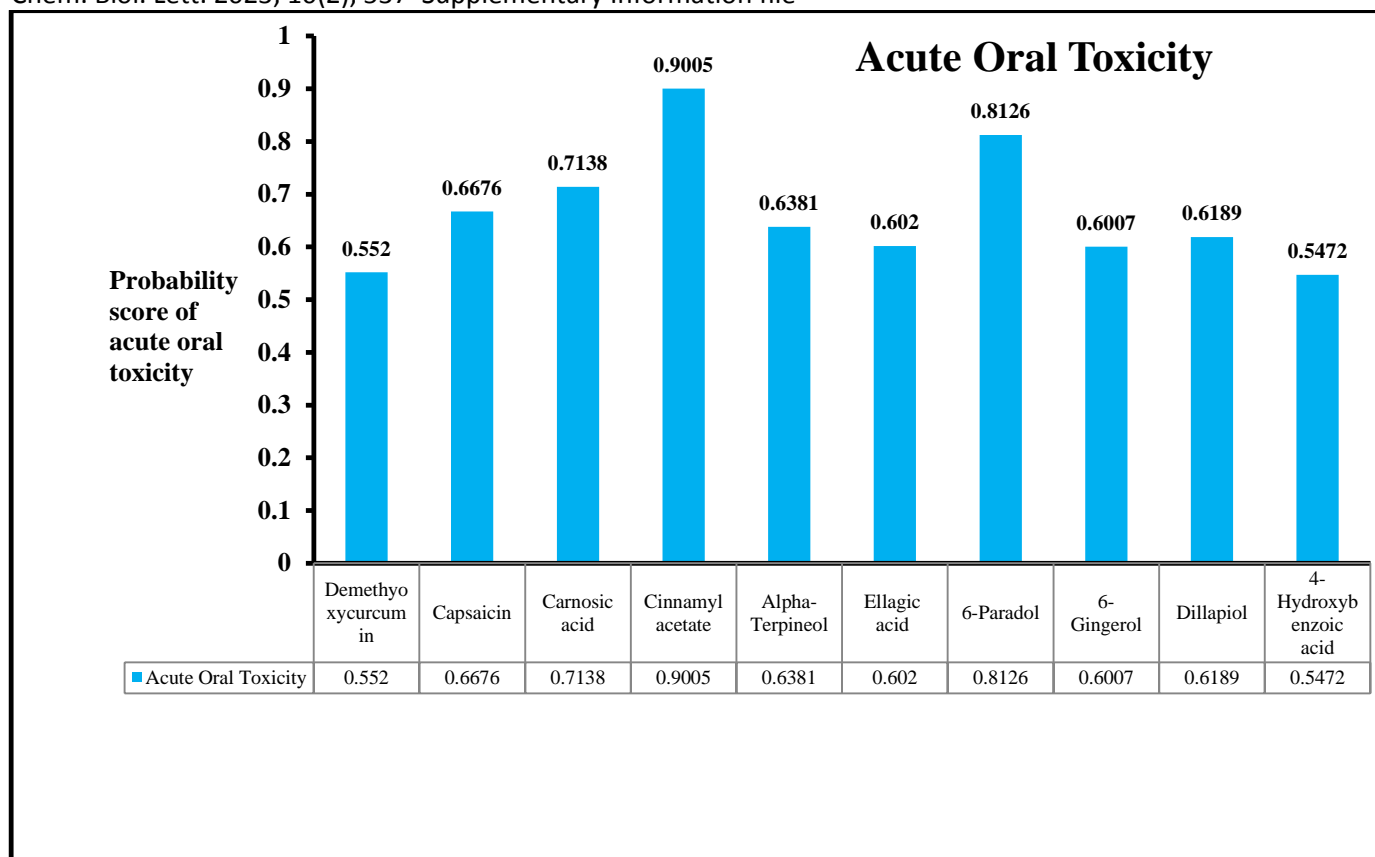
g



h



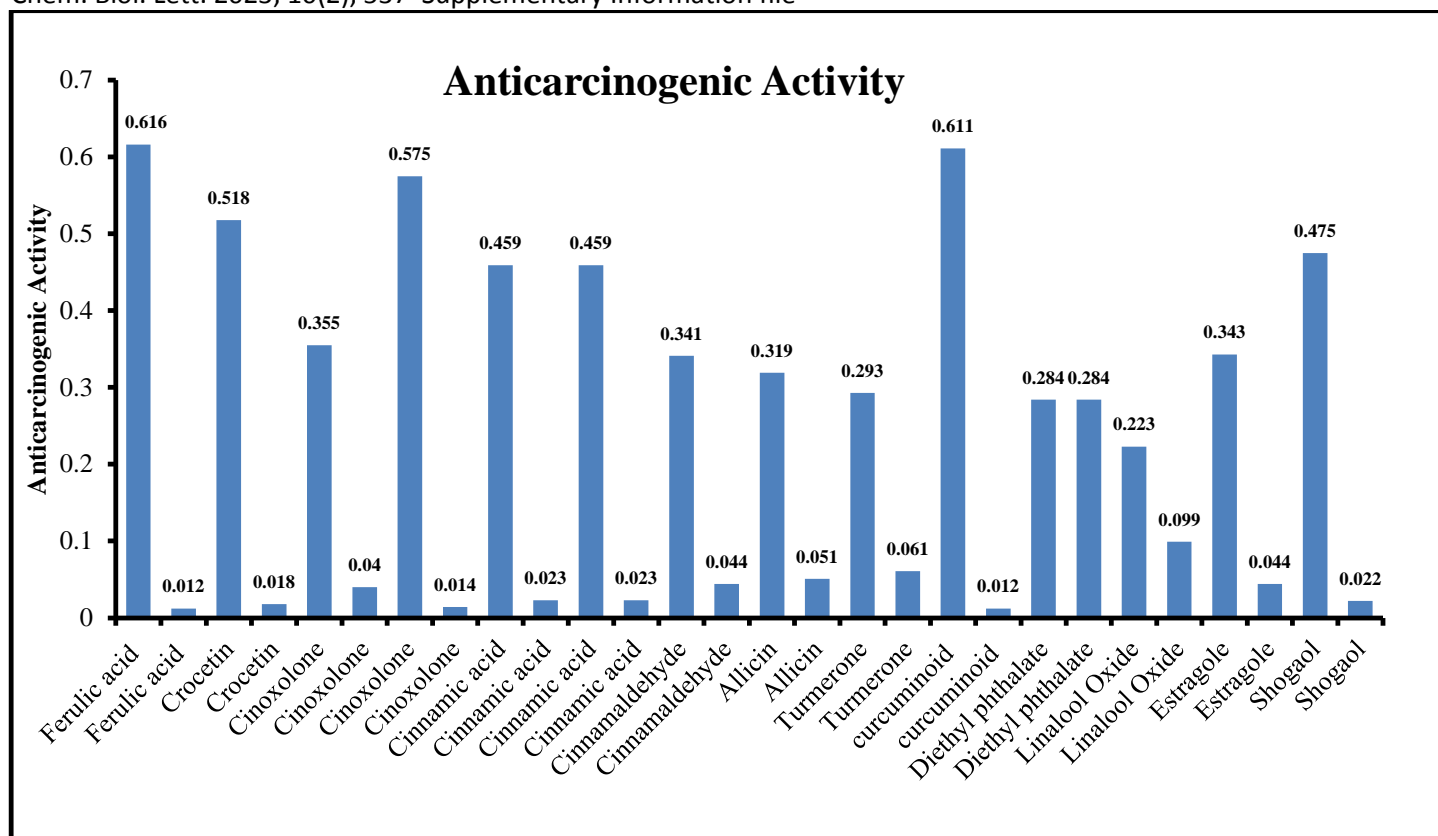
j



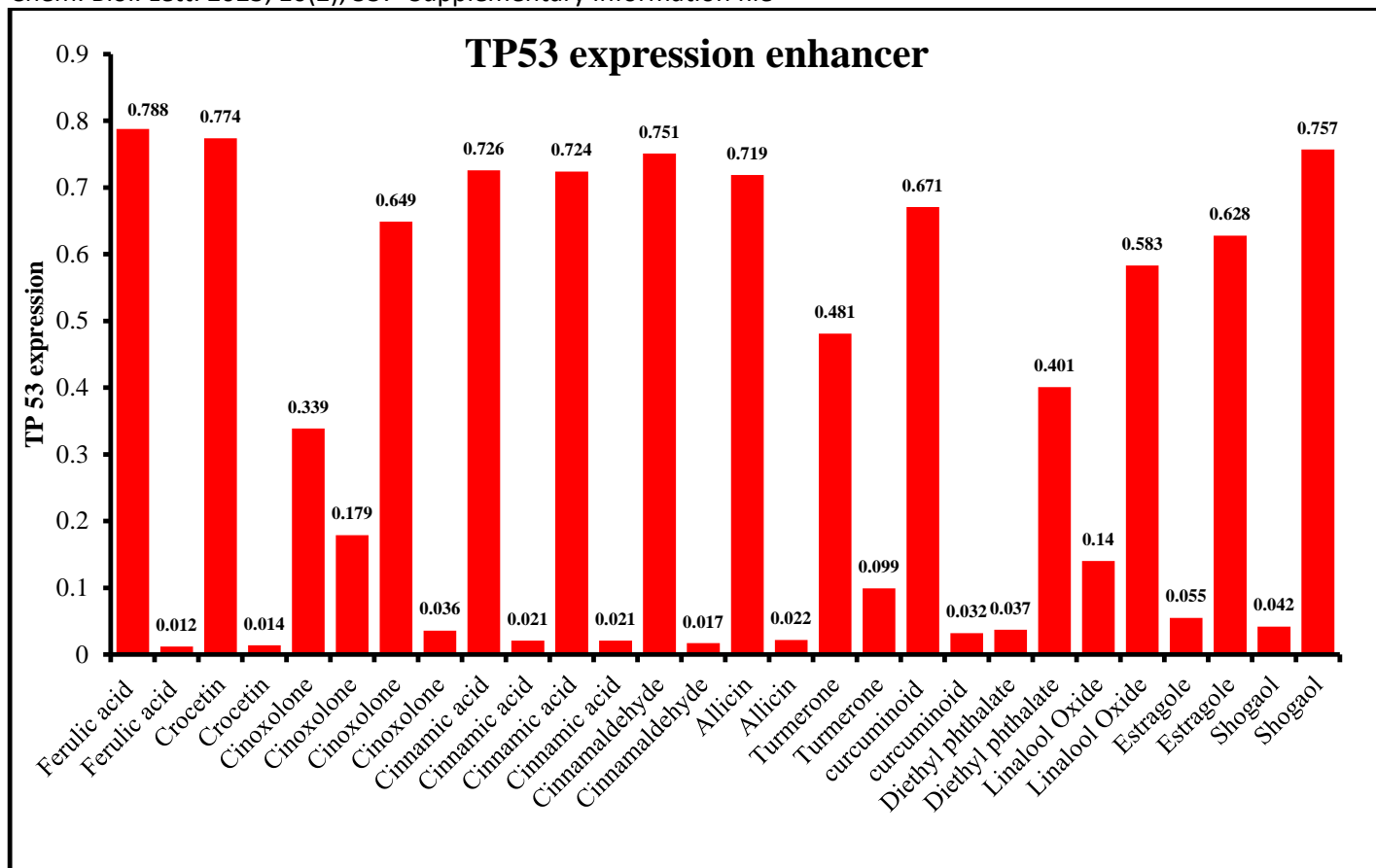
**j**

**Figure 1 : a to j** SWISS ADMET analysis of the studied phytochemicals using SWISS ADME software **a.** Calculated Log P prediction **b.** drug likeliness studies **c.** drug score **d.** total polar surface area **e.** aqueous solubility Log S **f.** Blood-brain barrier **g.** human intestinal absorption **h** AMES toxicity assay **i.** carcinogens **j.** acute oral toxicity

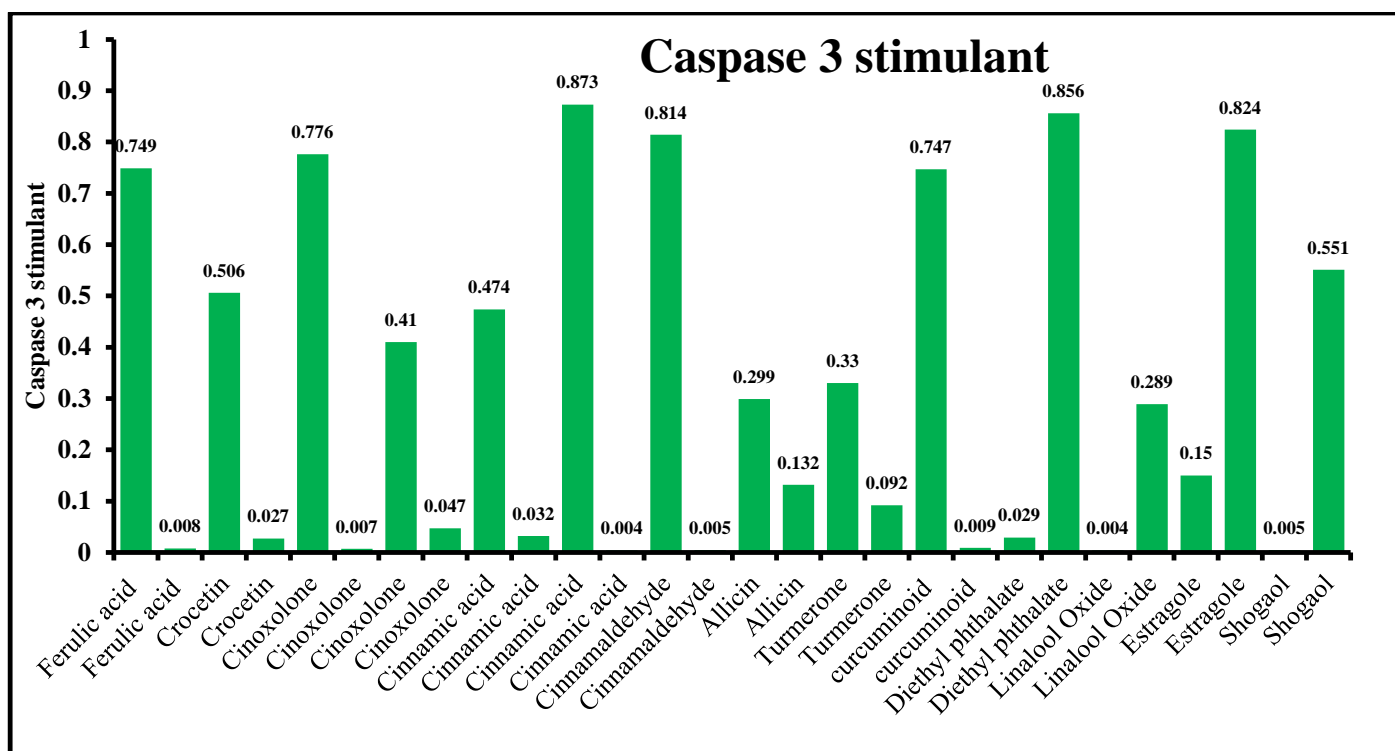




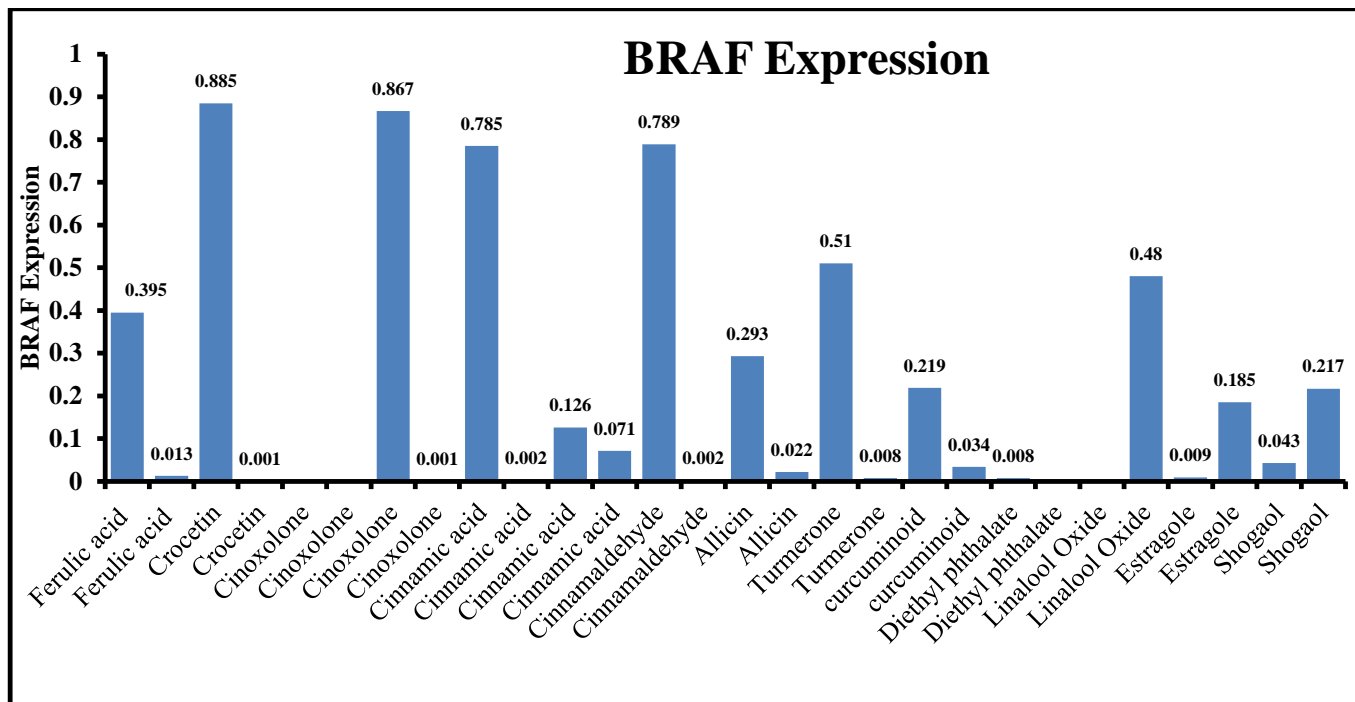
a



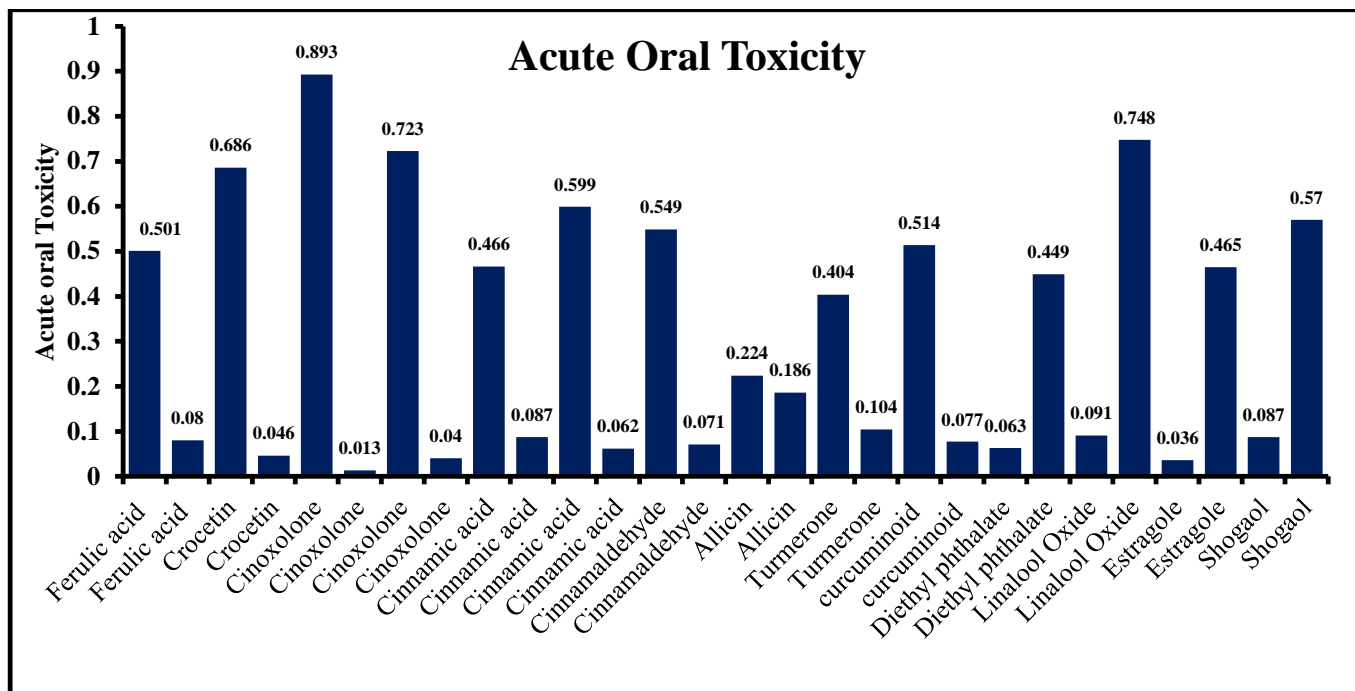
b



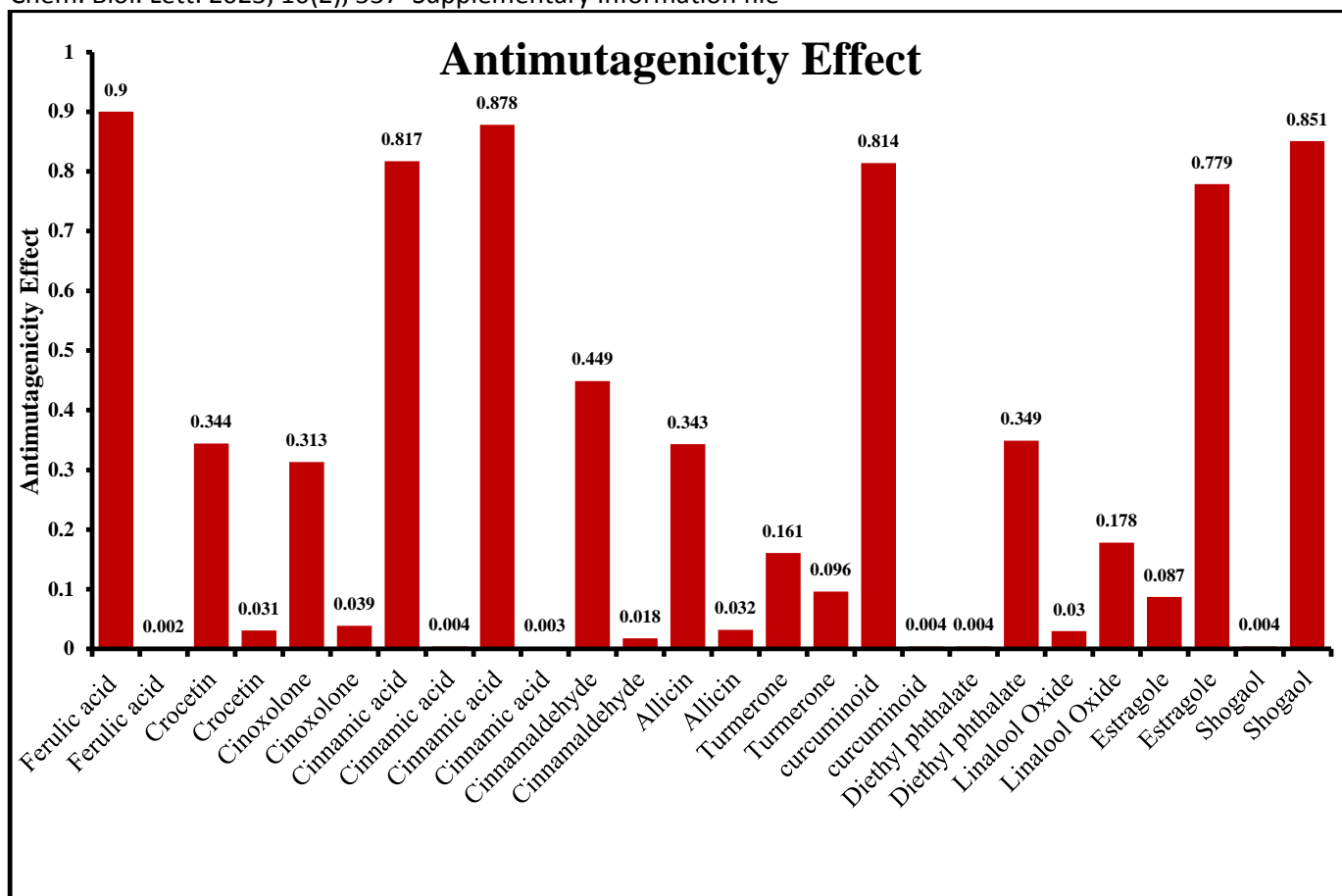
c



d



e



f

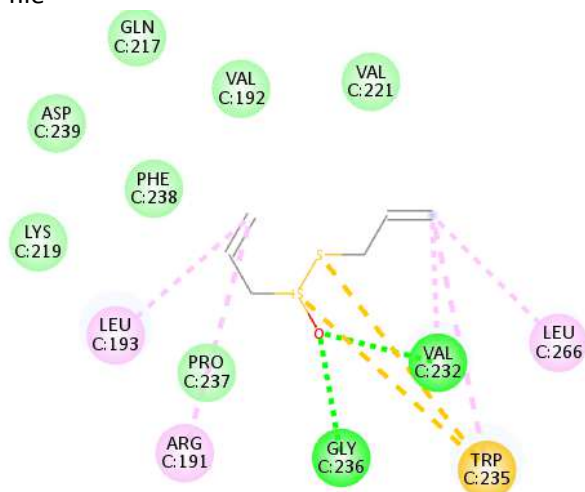
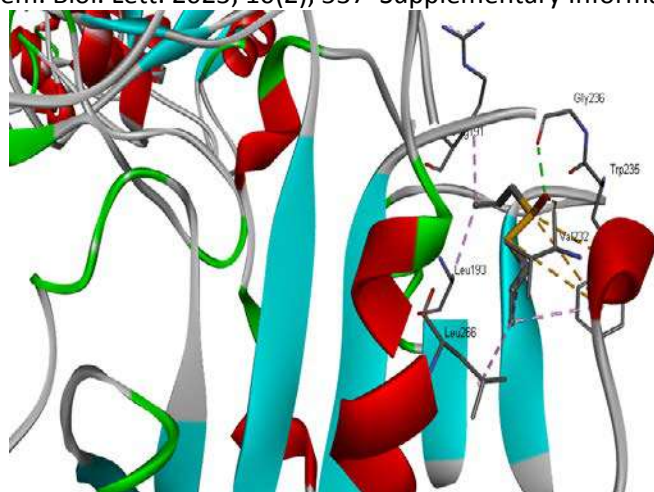
**Figure 2 a-f:** PASS (Prediction of Activity Spectra for Substances) analysis of studied phytochemicals

- a.** Anti-carcinogenic parameters **b.** TP53 expression pattern **c.** caspase 3 stimulant **d.** BRAF expression inhibitor **e.** toxicity studies **f.** antimutagenic studies

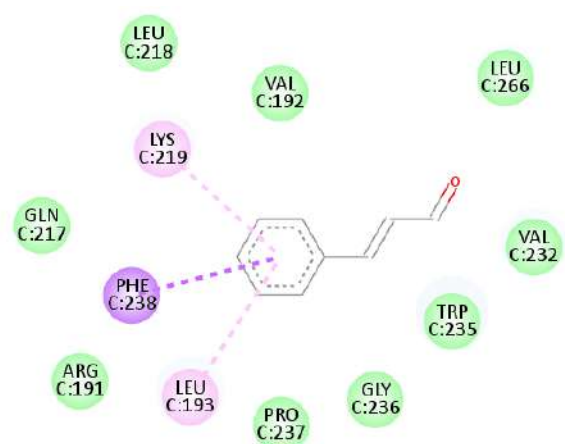
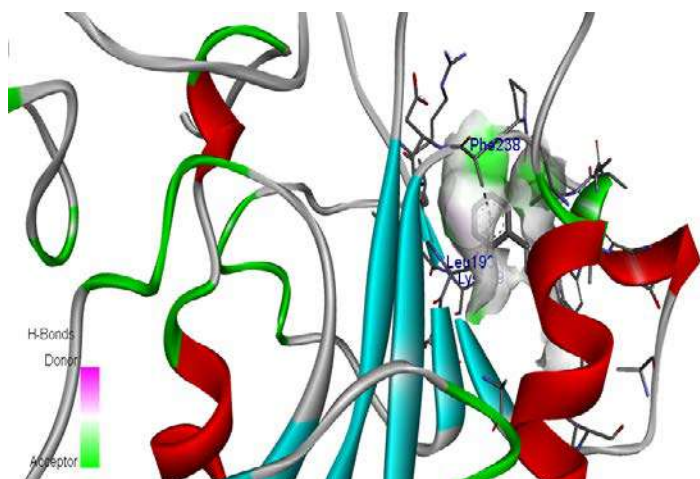
**Table 2:** Small phytochemicals with different binding energy released during interaction with 2PV0

Small phytochemicals	Pub Chem Comp ID (CID)	Binding energy (Global energy) after docking with 2PV0 (kcal/mol)	Sources of these phytochemicals
Ferulic acid	445858		<i>Syzygium aomaticum</i>
		-37.44	
Crocetin	5281232		<i>Crocus sativus</i>
		<b>-49.27</b>	<i>Cinnamon</i>
Cinnamic acid	444539	-30.99	
Eugenol	3314	-29.72	<i>Cinnamon</i>

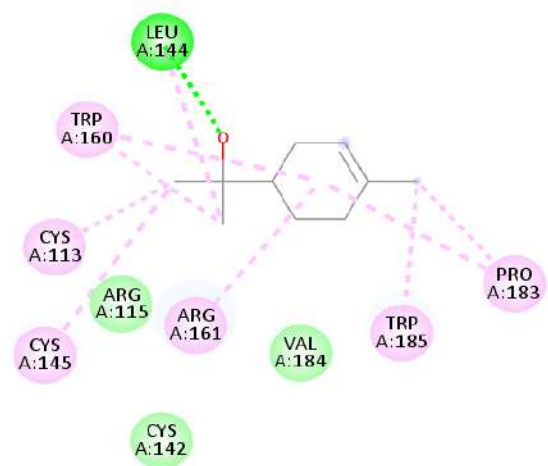
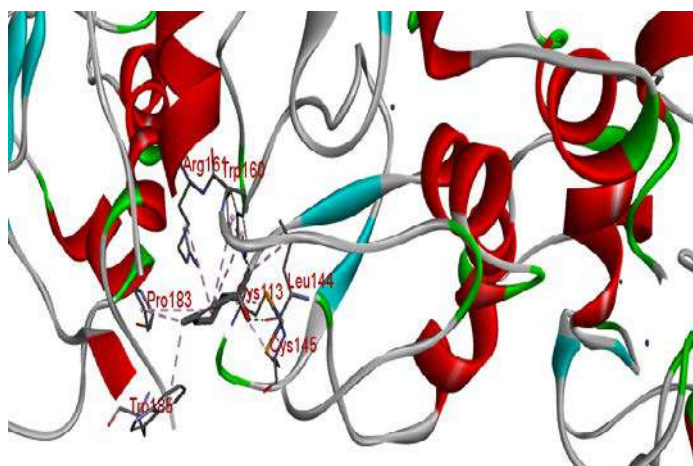
Cinnamaldehyde	637511		<i>Cinnamon</i>
		-27.60	
Allicin	65036		<i>Allium sativum</i>
		-33.27	
Curcumin	101341351		<i>Curcumin longa</i>
		-38.19	
Estragole	8815		<i>Ocimum basilicum</i>
	5469424	-29.69	
Demethoxy curcumin		<b>-48.27</b>	<i>Curcumin longa</i>
Capsaicin	1548943	<b>-42.85</b>	<i>Piper nigrum</i>
Cinnamyl acetate	5282110		<i>Curcumin longa</i>
		-36.53	
Alpha terpineol	17100		<i>Elettaria cardamomum</i>
		-27.65	
Carnosic acid	65126	<b>-44.72</b>	<i>Rosmarinus officinalis</i>



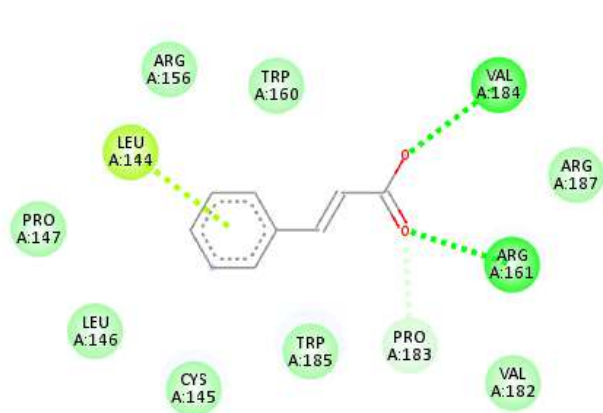
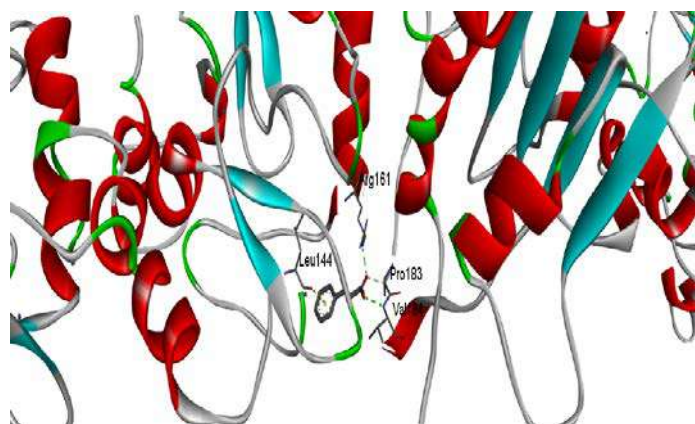
a



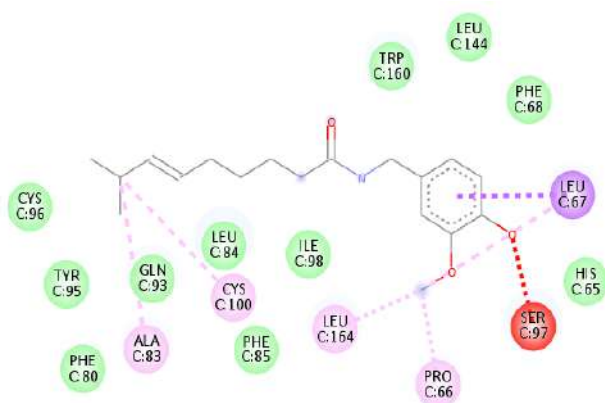
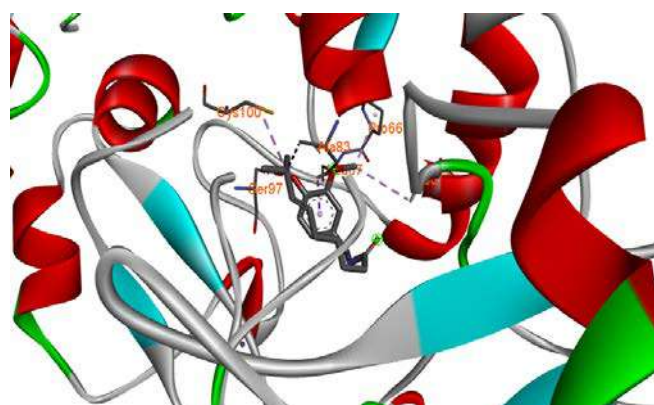
b



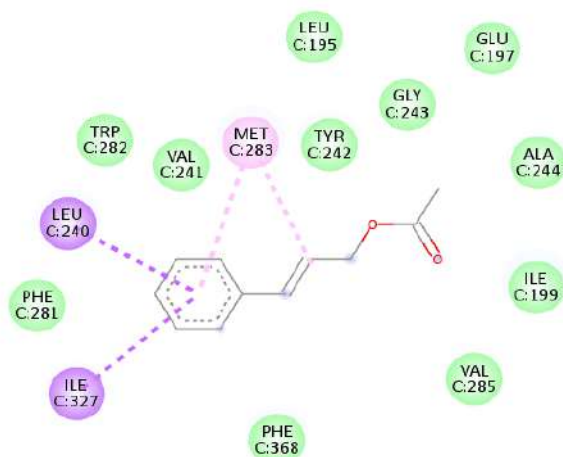
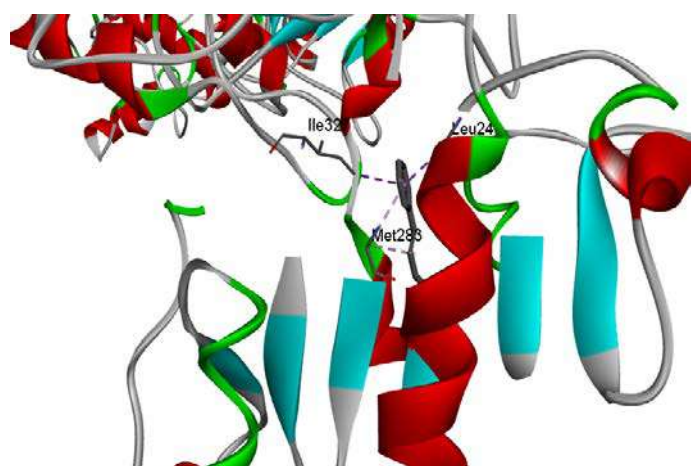
c



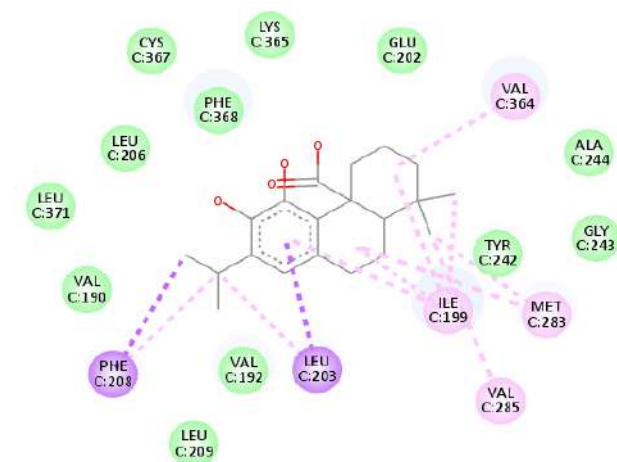
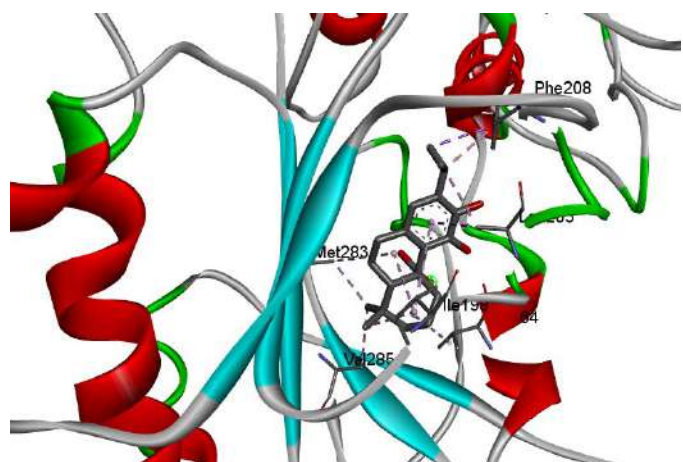
d



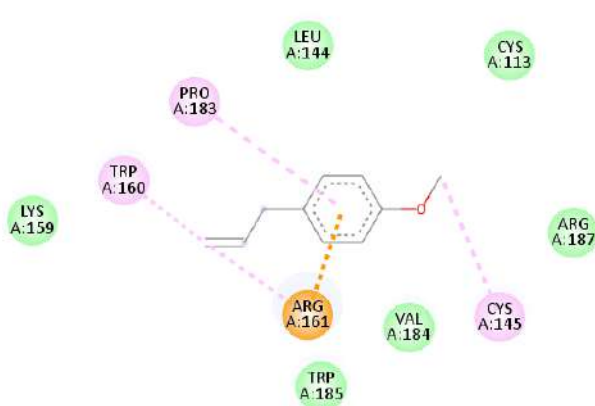
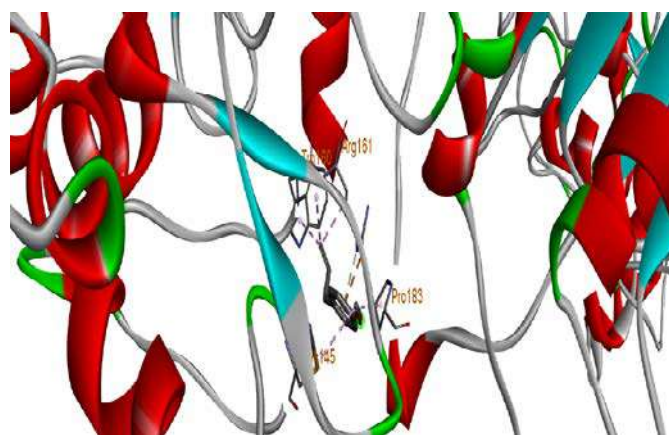
e



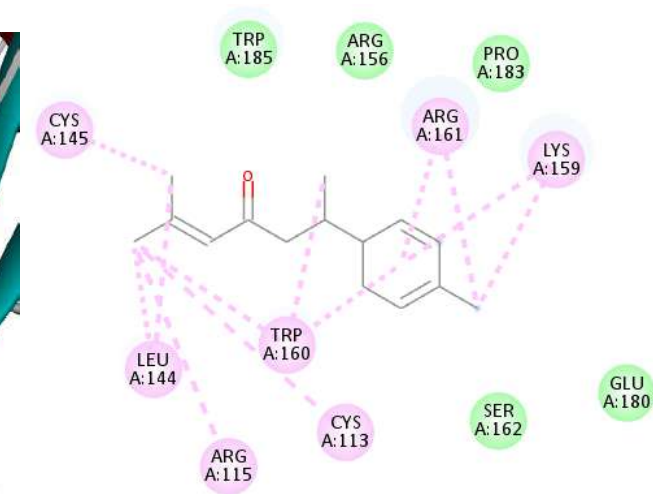
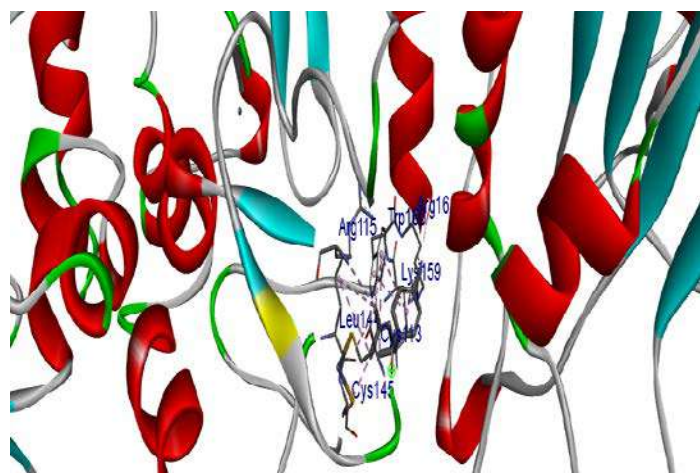
f



g

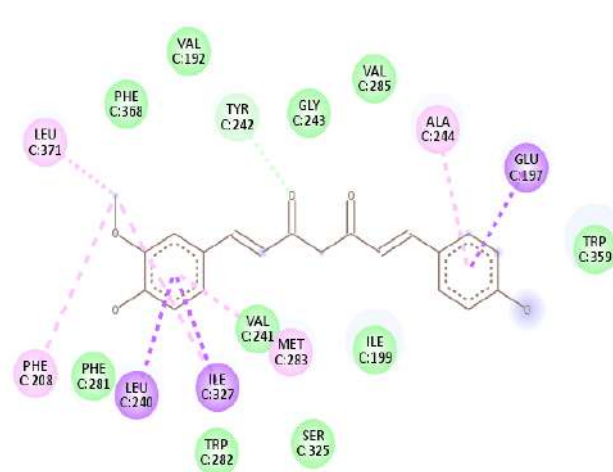
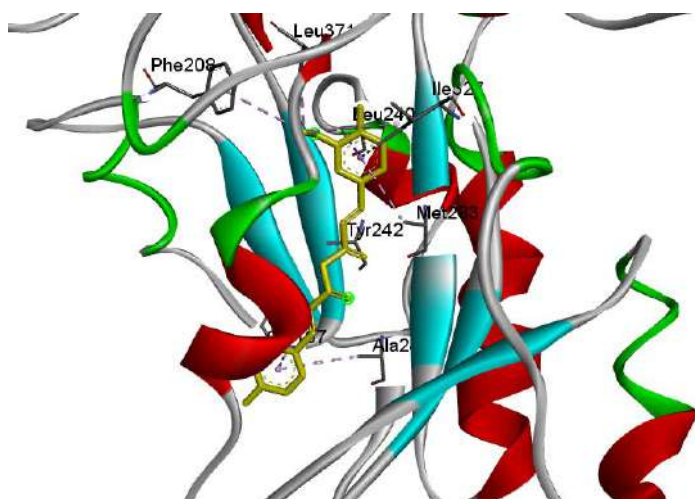


h

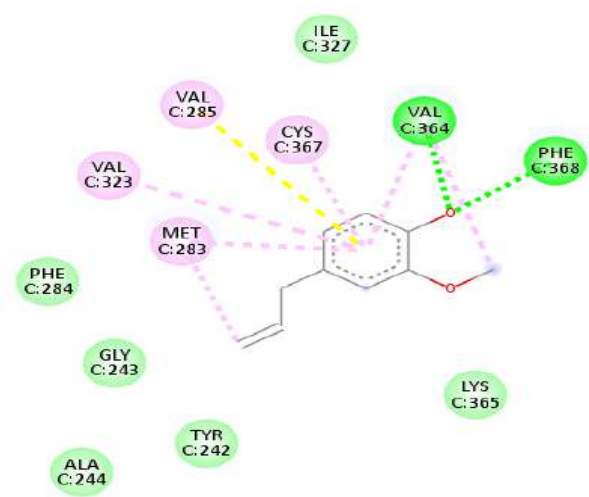
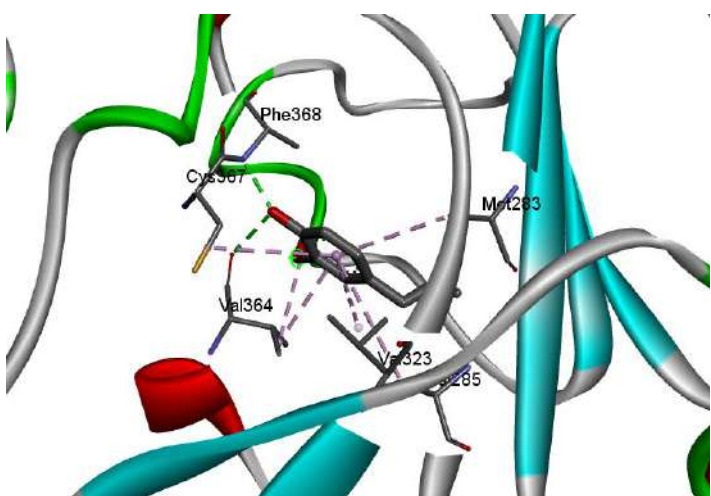


i

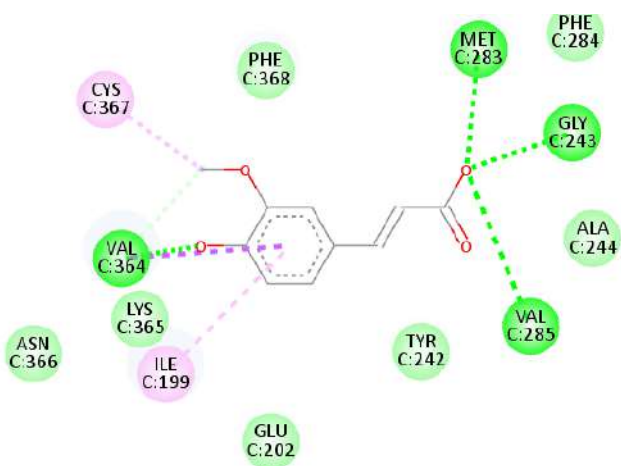
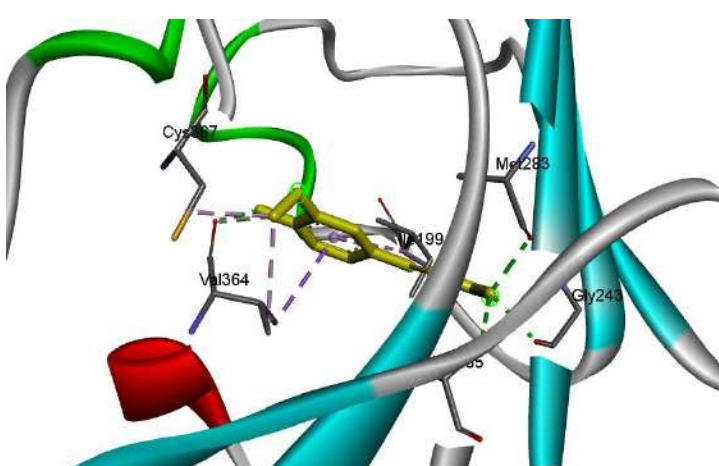




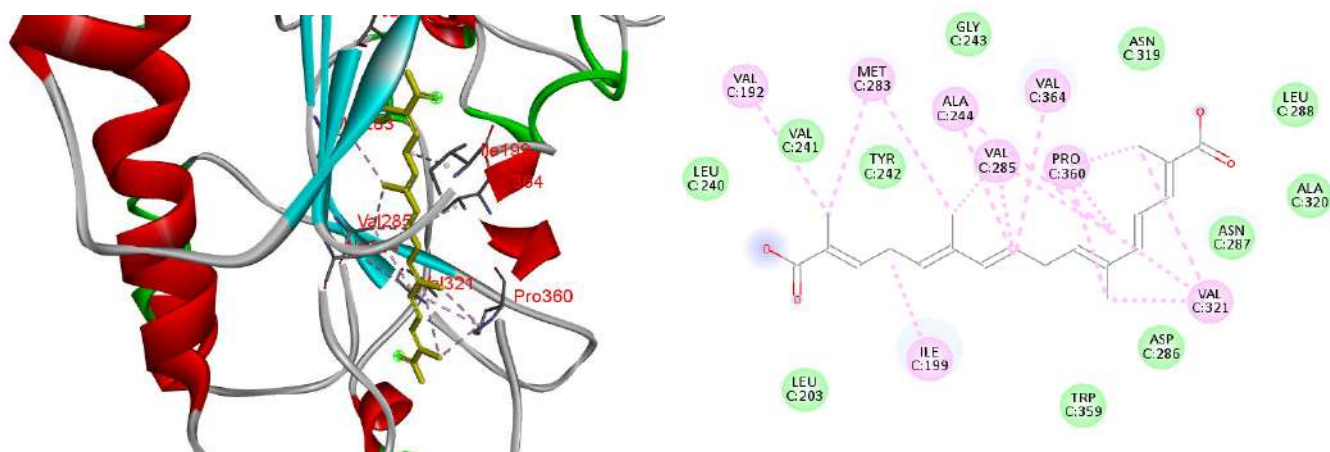
j



k



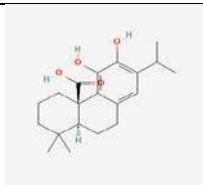
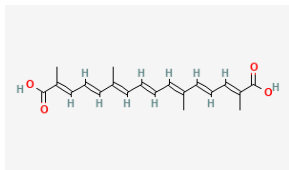
l

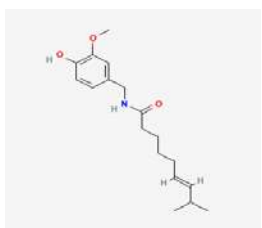
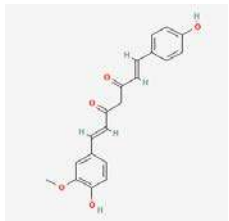


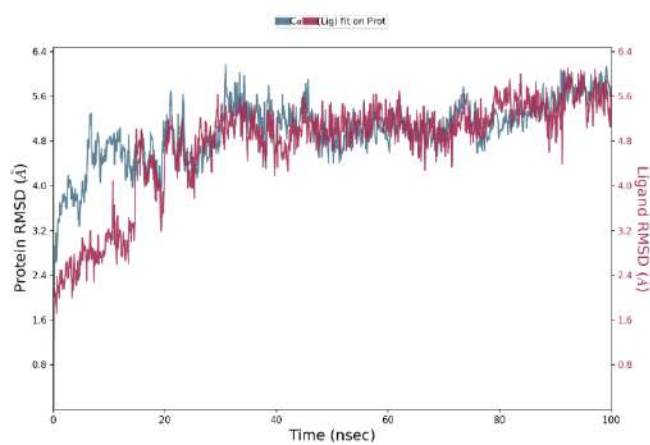
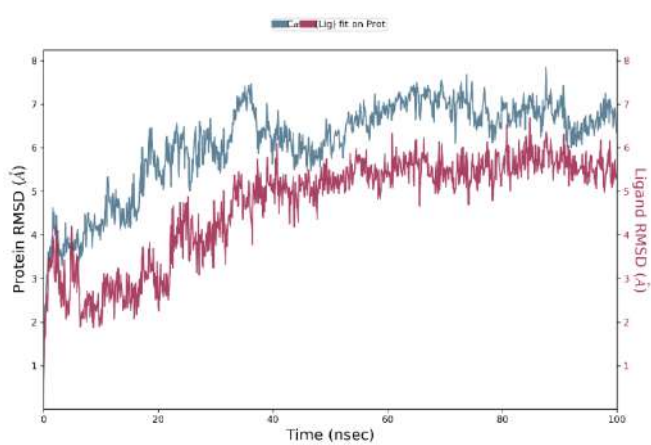
**m**

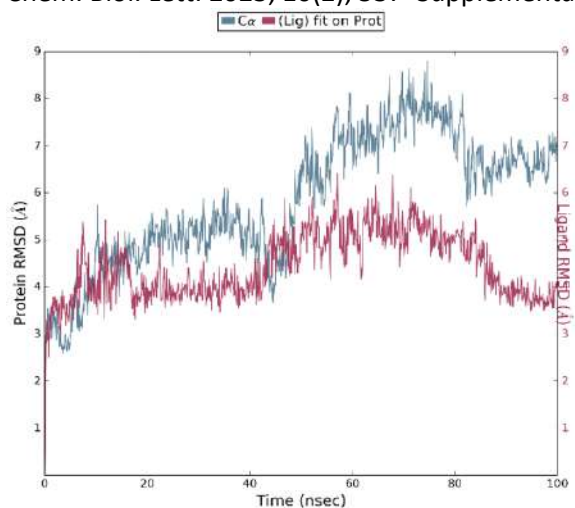
**Figure 3 a –m** 3D (Left panel) and 2D (right panel) representations of the binding modes of studied small phytochemicals against DNA methyl transferase 3-like protein (PDB ID: 2PV0). Also, hydrogen bonding interaction (shown in fluorescent green) and other types of non-covalent interaction (shown in dark and light purple) were also depicted throughout all figures **a.** allucin **b.** cinnamaldehyde **c.** alpha terpineol **d.** cinnamic acid **e.** capsaicin **f.** cinnamyl acetate **g.** carnosic acid **h.** estragole **i.** curcumin **j.** demethoxycurcumin **k.** eugenol **l.** ferulic acid **m.** crocetin

**Table 3:** Four best-optimized structure for MD simulation analysis

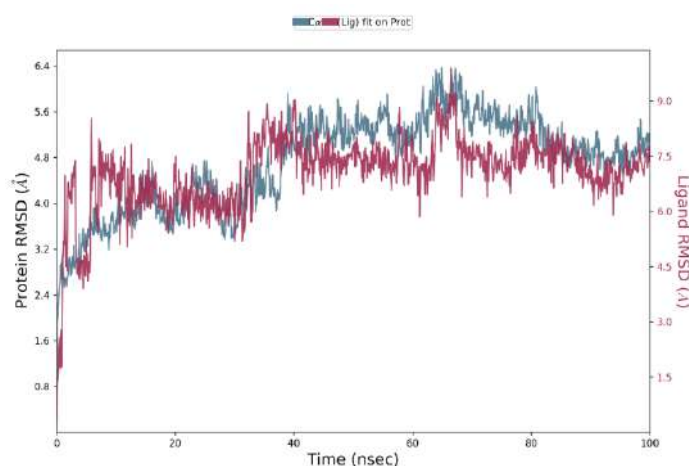
S.No	Compound name	RMSD	Interacting residues during MD simulation	MMGBSA ( $\Delta G$ -bind) post MD (kcal/mol)
1	 <b>Carnosic acid</b>	0.5-1.0 Å	Val192,Ile199,Leu203,Leu240,Tyr242,Thr361,Val364,and Tyr377	<b>-64.59±5</b>
2	 <b>Crocetin</b>	1.0-2.0 Å	Val192,Leu193,Ile199,Leu203,Leu240,Val241,Tyr242,Asn287,Lys358,Leu363,Val364,and Cys367	<b>-51.85±4</b>

	<b>Crocetin</b>			
<b>3</b>	 <b>Capsaicin</b>	<b>2.5-3.0 Å</b>	Leu84,Tyr87,Ser97,Leu164,Arg161,Thr181 and Tyr374	<b>-48.93±5</b>
<b>4</b>	 <b>Demethoxycurcumin</b>	<b>3.0-4.0 Å</b>	Asp89,Gly243,Ile199,Phe208,Thr361,Asn287,Phe368 and Thr380	<b>-41.85±4</b>

**a****b**

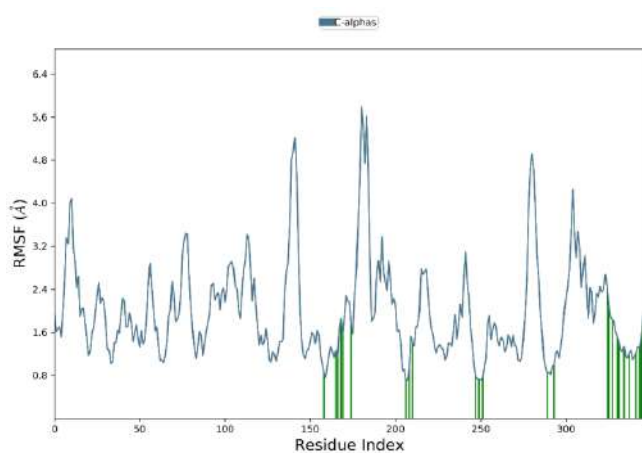


**c**

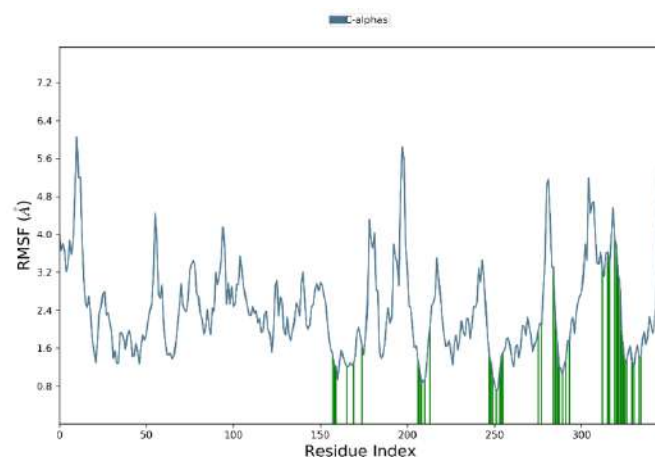


**d**

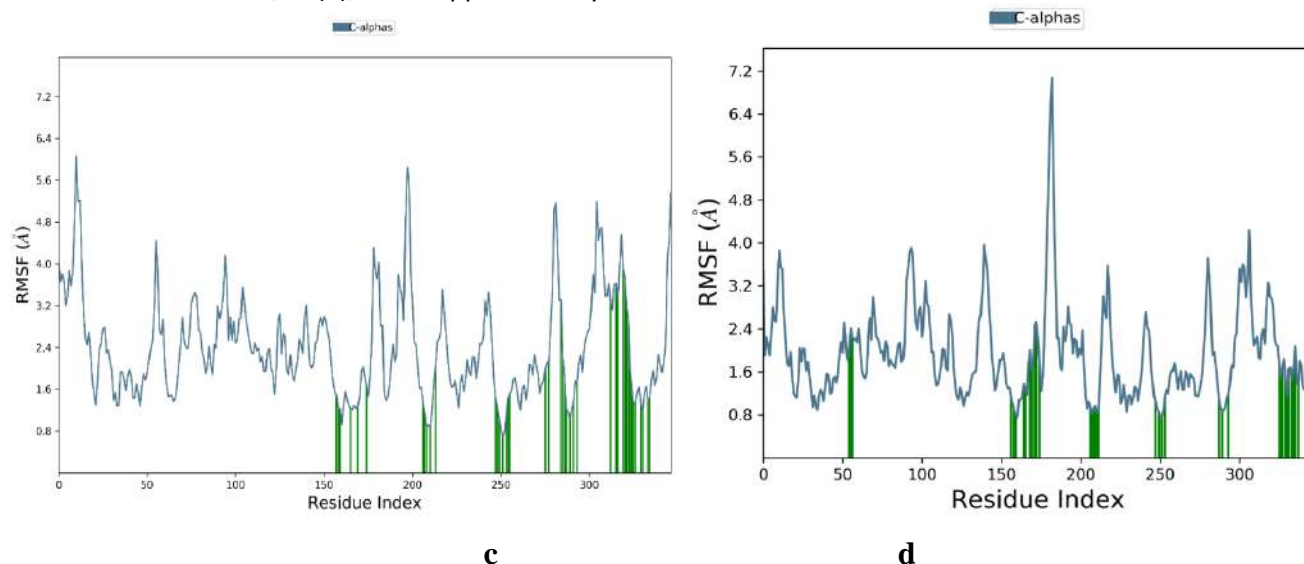
**Figure 4.** Representation of RMSD after MD simulation of the four top ranked compounds, X-axis represents simulation time in ns and the Y- axis represents the RMSD value. **a.** Carnosic acid **b.** Crocetin **c.** Capsaicin **d.** Demethoxycurcumin.



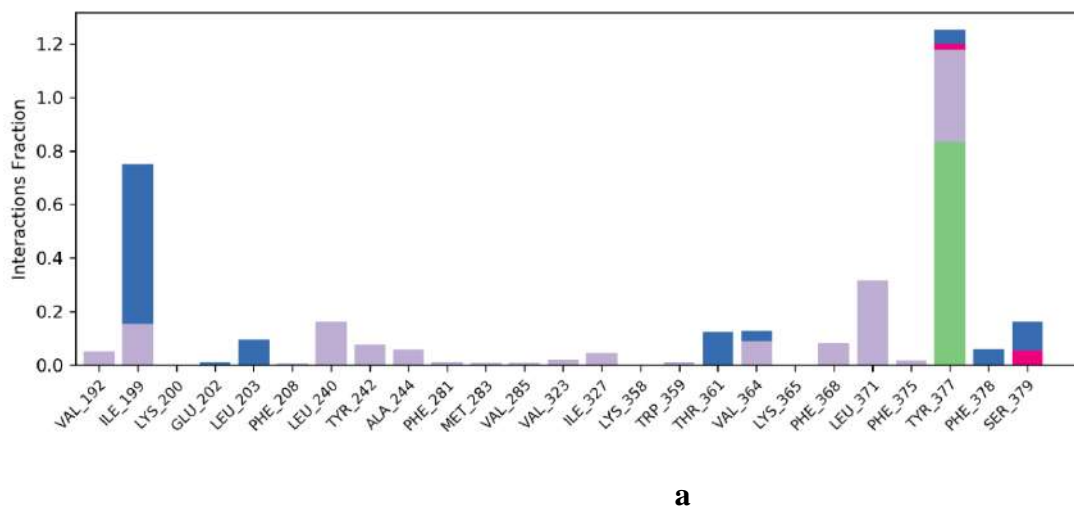
**a**



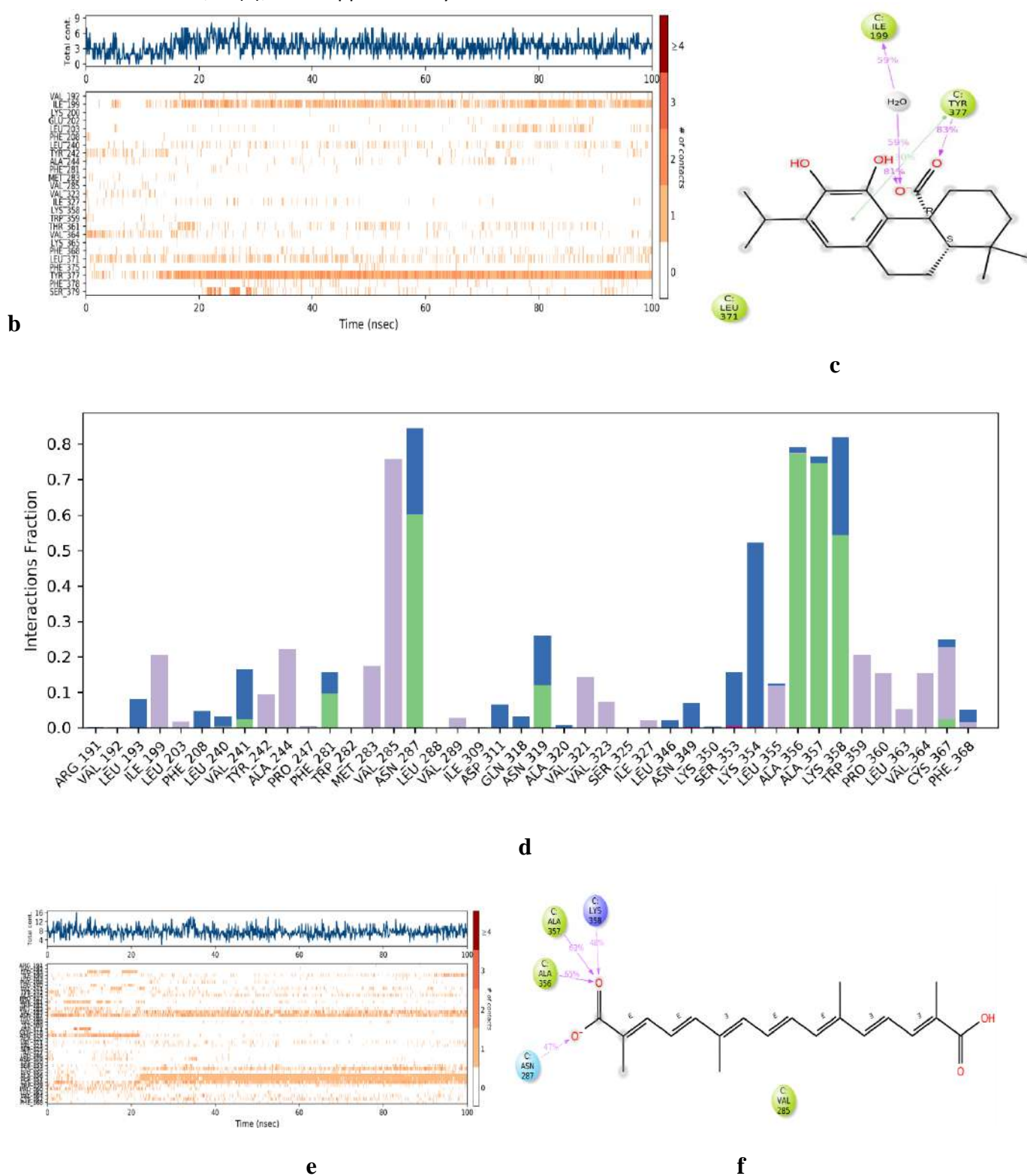
**b**



**Figure 5.** Representation of RMSF after MD simulation of the four top-ranked compounds. The X-axis represents residue numbers and the Y-axis represents RMSF values. **a.** Carnosic acid **b.** Crocetin **c.** Capsaicin **d.** Demethoxycurcumin. Blue color represents local changes along the protein chain, peaks indicate areas of the protein that fluctuate the most during the simulation, while green peaks show interactions of the residues with ligands.



**a**



**Figure 6.** Representation of protein-ligand contacts by MD simulation with compound Carnosic acid and Crocetin (**a**) and (**d**) stacked bar charts normalized over the course of the trajectory in which the X-axis shows residue name, Y-axis shows interaction fractions, (**b**) and (**e**) timeline of interactions and contacts (X-axis

Chem. Biol. Lett. 2023, 10(2), 537 Supplementary Information file  
simulation time in nanoseconds and Y-axis name of residue). (c) and (f) 2D interactions of protein in complex  
with Carnosic acid and Crocetin.