

Figure S1. 3D structure of modeled proteins with their Ramachandran plots (a, c) OBP1, (b, d) OR1 generated by Zlab server.

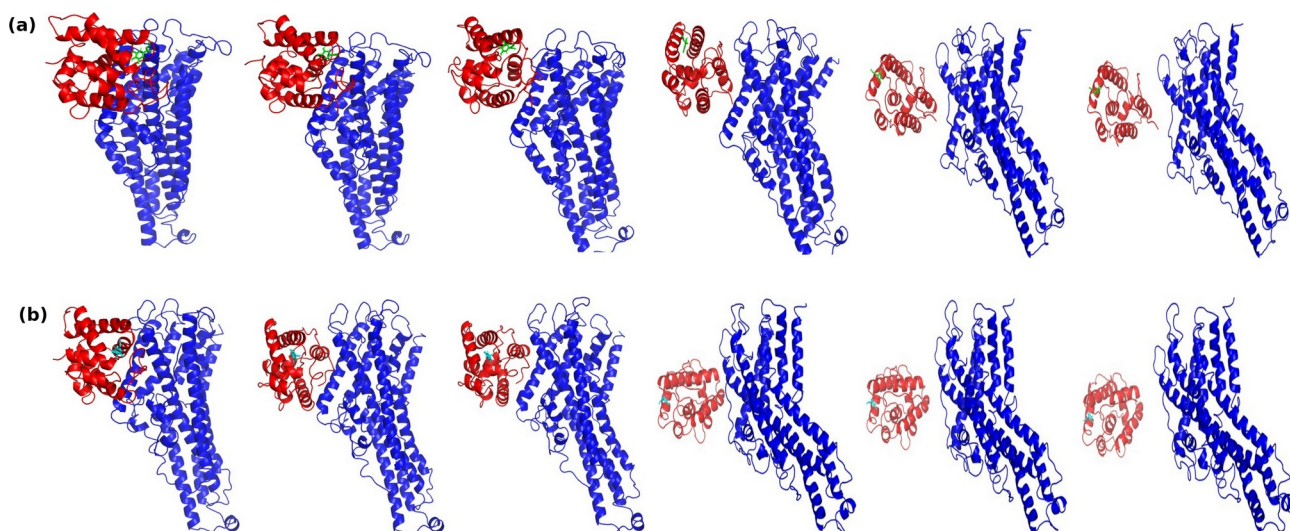


Figure S2. Different time interval snapshots from steered molecular dynamics analysis after applying an external pulling force, illustrating the position of the ligand in the active site throughout the simulation. (a) depicts the OBP1-Ethyl gallate (as ligand) and OR1 (receptor) complex, while (b) shows the OBP1-Methyl gallate (as ligand) and OR1 (receptor) complex.

Table S1. List of interaction energy generated from molecular docking analysis for the selected molecules.

S. No.	Protein-ligand complexes	CDOCKER Interaction energy (kcal/mol)
1	Quercetin	-24.7
2	Kaempferol	-20.9
3	IsoQuercetin	83.35
4	Catechin	-21.88
5	Fraxetin	-22.38
6	Etyhlbrovioflincarbo	-14.31
7	Ellagic acid	-23.24
8	Ethyl gallate	-33.72
9	6-O-galloyl	-23.11
10	Methyl gallate	-30.98
11	Gallic acid	-27.7
12	Blumenol C	750.9
13	Beta-D-glucose	6.45
14	2-formyl	-23.9
15	Shikimic acid	10.84
16	1-Naphthalenamine	8.21

Table S2. The mean and standard deviation of the various structural aspects of MD simulations analysis.

Complexes	Mean				Standard Deviation			
	H-BOND	RMSD	RMSF	Rg	H-BOND	RMSD	RMSF	Rg
OR1-OBP1	7.045	0.641	0.223	2.953	2.29	0.047	0.814	0.436
Ethyl gallate	7.781	0.951	0.182	2.878	2.419	0.142	0.634	0.278
Methyl gallate	10.333	0.686	0.170	2.885	2.744	0.051	0.674	0.272
Gallic acid	9.949	0.729	0.192	2.888	2.186	0.070	0.744	0.318
Quercetin	7.062	0.724	0.177	2.937	2.178	0.747	0.814	0.233

Table S3. List of protein-protein binding free energy components computed using MM-PBSA approach during the course of MD simulations.

Protein-protein complex	ΔE Van der Waal (kJ/mol)	SASA (kJ/mol)	ΔE Electrostatic (kJ/mol)	ΔE polar solvation (kJ/mol)	ΔE binding (kJ/mol)
OR1-OBP1	-513.521	-48.850	-1648.728	803.541	-1407.557

Table S4. List of protein-ligand binding free energy components calculated using MM-PBSA approach.

Protein-ligand complexes	ΔE Van der Waal (kJ/mol)	SASA (kJ/mol)	ΔE Electrostatic (kJ/mol)	ΔE polar solvation (kJ/mol)	ΔE binding (kJ/mol)
OBP1-ethyl gallate	-4.564	-7.315	-0.760	3.491	-9.148
OBP1-gallic acid	-6.201	1.073	222.392	-5.199	212.066
OBP1-methyl gallate	-41.548	-10.899	-7.211	8.008	-51.650
OBP1-Quercetin	-211.298	-24.947	-29.909	69.622	-196.531

Table S5. List of protein and protein-ligand binding free energy components computed using MM-PBSA technique.

Protein and Protein-ligand complexes	ΔE Van der Waal (kJ/mol)	SASA (kJ/mol)	ΔE Electrostatic (kJ/mol)	ΔE polar solvation (kJ/mol)	ΔE binding (kJ/mol)
OR1-OBP1-ethyl gallate	-794.872	-71.779	-2753.941	1341.120	-2279.473
OR1-OBP1-methyl gallate	-722.028	-66.748	-2433.139	1364.526	-1857.390
OR1-OBP1-Quercetin	-753.777	-67.388	-2217.591	1109.712	-1929.045

Table S6. Antifeedant activities of compounds against *P. xylostella*.

Feeding deterrence					
Compounds	DC₅₀ (mg L⁻¹)	Confidence limits (mg L⁻¹)	Slope ± SE	Chi square	p value
Ethyl gallate	865.88	663.35 – 1111.86	1.06 ± 0.14	3.22	0.36
Methyl gallate	648.92	328.62 – 1020.13	0.57 ± 0.13	0.65	0.88
*Neembaan (Azadirachtin 0.15% EC)	949.17	758.78 – 1181.52	1.23 ± 0.14	1.90	0.59
Growth inhibition					
	IC₅₀ (mg L⁻¹)	Confidence limits (mg L⁻¹)	Slope ± SE	Chi square	p value
Ethyl gallate	1103.72	808.62 – 1535.85	0.86 ± 0.14	0.79	0.85
Methyl gallate	991.29	801.43 – 1224.79	1.29 ± 0.14	0.42	0.94
*Neembaan (Azadirachtin 0.15% EC)	901.67	722.61 – 1115.05	1.27 ± 0.14	1.07	0.78

DC₅₀= Deterrence concentration to deter 50% of test population;

IC₅₀= Inhibition concentration to inhibit 50% of test population;

* The commercially available botanical insecticide (Neembaan®) in the market for the control of *P. xylostella* on cruciferous crops under field conditions was used as positive control for comparison.