

Supplementary Information

Molecular Interactions of Cinnamil and Quinoxaline Derivatives by Bcl-2 Antiapoptotic Proteins: A Computational Study

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S1 Chemical reactivity descriptors

Table S1. Equations of the global and local descriptors used in the methodology.

Descriptor	Equation	Reference
Ionization potential	$I = E_{N-1} - E_N$	1
Electron affinity	$A = E_N - E_{N+1}$	1
Electrochemical potential	$\mu = -\frac{I + A}{2}$	1
Mulliken electronegativity	$\chi = -\mu$	2
Hardness	$\eta = I - A$	1
Electrophilicity	$\omega = \frac{\mu^2}{2\eta}$	1
Electroaccepting power	$\omega^+ = \frac{(I + 3A)^2}{16(I - A)}$	3
Electrodonating power	$\omega^- = \frac{(3I + A)^2}{16(I - A)}$	3
Fukui function electrophilic	$f^+(r) = \left(\frac{\partial \rho(r)}{\partial N} \right)_{v(r)}^+ = \rho_{N+1}(r) - \rho_N(r)$	4
Fukui function nucleophilic	$f^-(r) = \left(\frac{\partial \rho(r)}{\partial N} \right)_{v(r)}^- = \rho_N(r) - \rho_{N-1}(r)$	4
Dual Descriptor	$\Delta f = f^+(r) - f^-(r)$	5
Local electrochemical potential	$\mu_e(\mathbf{r}) = \begin{cases} \mu^-(\mathbf{r}) = -If^-(\mathbf{r}) & \text{para } \omega < 0 \\ \mu^+(\mathbf{r}) = -Af^+(\mathbf{r}) & \text{para } \omega > 0 \\ \mu^0(\mathbf{r}) = -\frac{1}{2}(If^-(\mathbf{r}) + Af^+(\mathbf{r})) & \text{para } \omega = 0 \end{cases}$	6-8
Local hardness	$\eta_\tau(\mathbf{r}) = \begin{cases} \eta_{PP}(\mathbf{r}) - \frac{1}{2}\eta\Delta f(\mathbf{r}) & \text{para } \omega = -1 \\ \eta_{PP}(\mathbf{r}) + \frac{1}{2}\eta\Delta f(\mathbf{r}) & \text{para } \omega = +0 \\ \eta(\mathbf{r}) & \text{para } \omega = 0 \end{cases}$	6-8

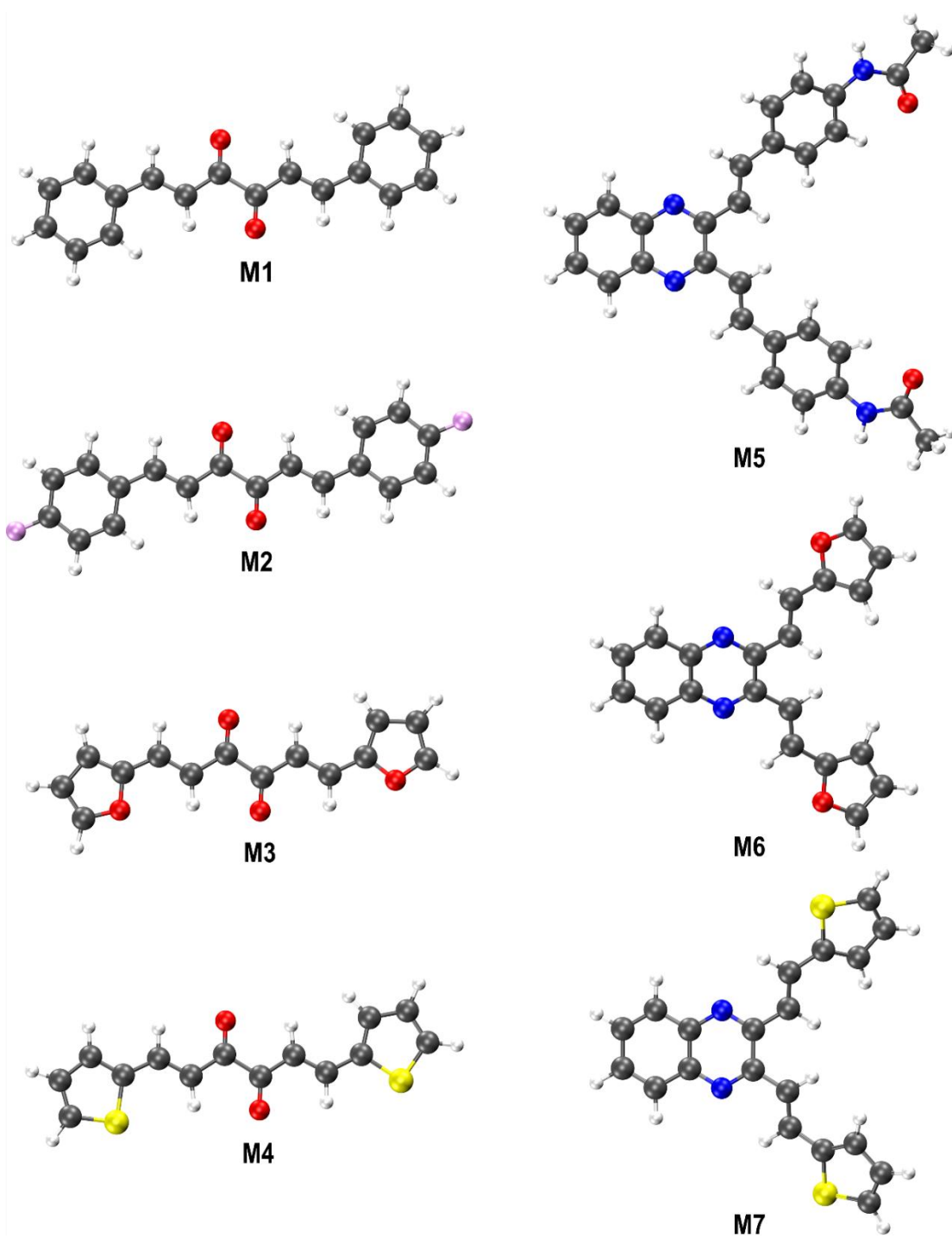


Figure S1. Optimized geometries of the cinnamil and quinoxaline derivatives under analysis.

S2 Molecular docking of the BCl-xl monomeric protein

Table S2. Results from molecular docking analysis, between ligands M1–M7 and in the monomeric protein Bcl-xl

Ligand	Binding sites	Binding energy (kcal/mol)	Inhibition constant (μM)	Binding distance ($\text{\AA}$)	Most significant interaction
M1	Leu108	−7.49	3.23	1.973	N-H...O _{lig}
M2	Ser106	−7.50	3.22	1.861	N-H...O _{lig}
M3	Ser106	−5.29	133.5	2.989	N-H...O _{lig}
M4	Leu108	−6.85	9.47	1.970	N-H...O _{lig}
M5	Ser106	−9.15	0.197	2.160	C-O...H-N _{lig}
M5	Gly138	−9.49	0.111	2.128	C=O...H-N _{lig}
M6	Leu108	−9.23	0.170	2.006	N-H...N-C _{lig}
M7	Leu108	−8.05	1.250	2.685	C=O...N-C _{lig}

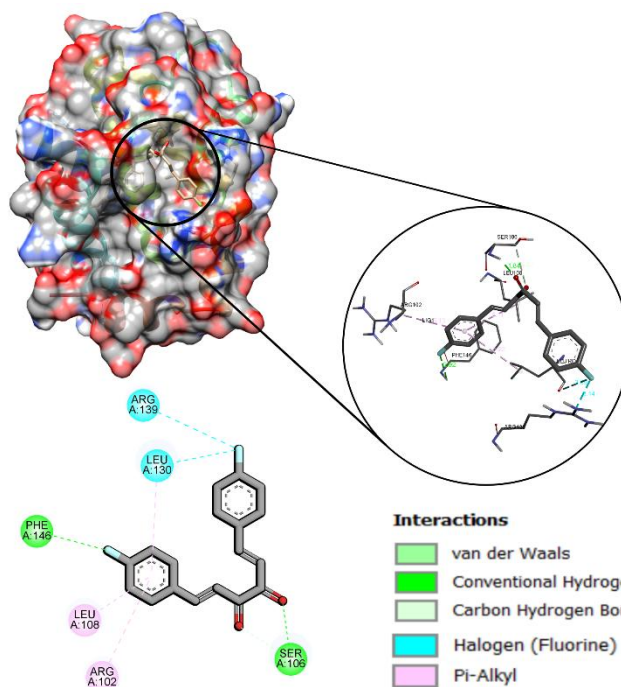


Figure S2. Relevant interactions identified in docking analysis between the ligand **M2** and the Bcl-xl protein.

S3 Chemical reactivity analysis

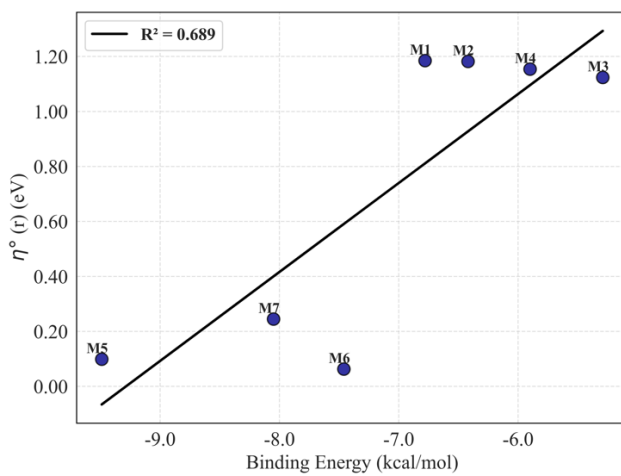


Figure S3. $\eta(r)$ vs BE profile for inhibitors binding to the Bcl-xl protein.

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