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MOLECULAR DOCKING STUDY OF SOME ACTIVE PRINCIPLES FROM *SILYBUM MARIANUM, CHELIDONIUM MAJUS, GINKGO BILOBA, GELSEMIUM SEMPERVIRENS, ARTEMISIA ANNUA,* AND *TARAXACUM OFFICINALE*

Daniel Cord [a], Mirela Claudia Rimbu [a,*], Cristiana Tanase [b], Cristina Tablet [c], Gheorghe Duca [d]

[a] *Titu Maiorescu University of Bucharest, 22, Dambovnicului str. Sector 4, Bucharest 040317, Romania*
[b] *Victor Babes National Institute of Pathology, 99-101, Splaiul Independentei, Sector 5, Bucharest 050096, Romania*
[c] *Faculty of Pharmacy, Titu Maiorescu University, 16, Gheorghe Sincai blvd., Bucharest 040314, Romania*
[d] *Moldova State University, Institute of Chemistry, 3, Academiei str., Chisinau MD-2029, Republic of Moldova*
[*] *e-mail: mirela.rimbu@prof.utm.ro*

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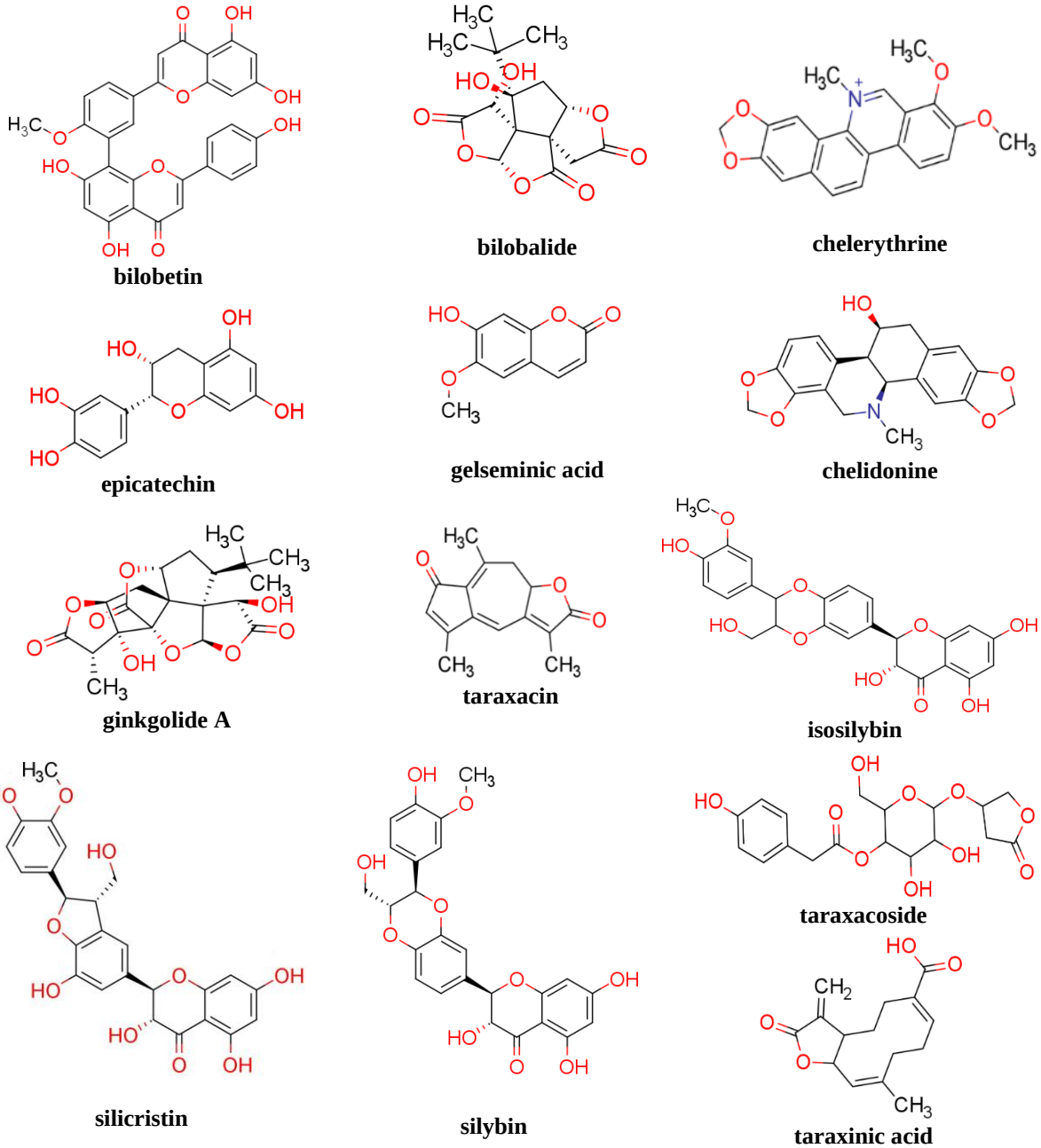

Figure S1. 2D structure of the natural compounds used in this study.

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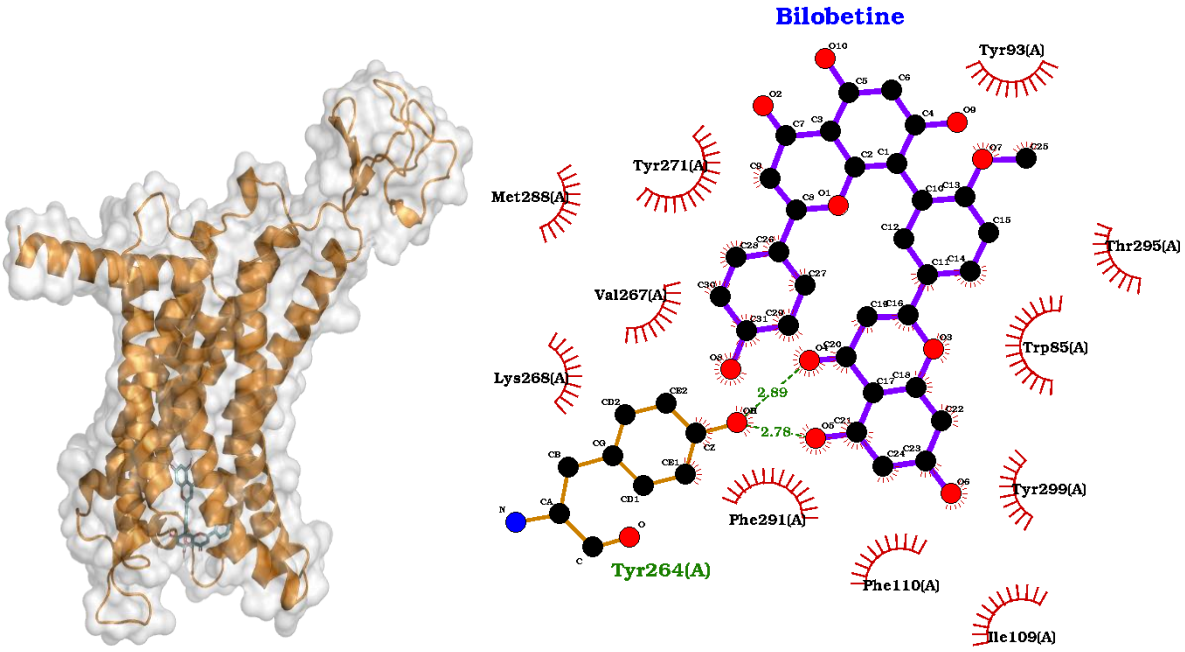

(a) ***(b)***

Figure S2. Structure of the most stable bilobetin–apelin receptor complex *(a)*. Interactions between bilobetin and the amino acid residues within the binding site (*b*)
(green indicates residues involved in hydrogen bonds with bilobetin, with distances shown in angstroms; red highlights hydrophobic interactions).