

Serotonin 5-HT₆ Receptor Antagonists for the Treatment of Cognitive Deficiency in Alzheimer's Disease

Bellinda Benhamú,[§] Mar Martín-Fontecha,[§] Henar Vázquez-Villa,[§] Leonardo Pardo,[†] and María L. López-Rodríguez^{,§}*

[§] Departamento de Química Orgánica I, Facultad de Ciencias Químicas, Universidad Complutense de Madrid, E-28040 Madrid, Spain

[†] Laboratori de Medicina Computacional, Unitat de Bioestadística, Facultat de Medicina, Universitat Autònoma de Barcelona, E-08193 Bellaterra, Barcelona, Spain

Supporting Information

Contents

1. Computational models of the complexes between representative compounds (4, 17, 27, 31, 50, 56, 65, 71, 75) and the 5-HT ₆ R	Page S2
2. References	Page S2

1. Computational models of the complexes between representative compounds (4, 17, 27, 31, 50, 56, 65, 71, 75) and the 5-HT₆R. MODELLER v9.7¹ was used to build a homology model of human 5-HT₆R (Uniprot code P50406) using the crystal structure of human 5-HT_{1B} (PDB code 4IAR)² as template. Compounds **4, 17, 27, 31, 50, 56, 65, 71, 75** were docked into the receptor model using the Autodock Vina tool.³ All docking solutions were visually inspected and the poses in which the protonated amine of the ring forms an ionic interaction with D3.32 and the HBA group hydrogen bonds N6.55 were energy minimized. Computer simulations were performed with the GROMACS 4.6.3 simulation package,⁴ using the AMBER99SB force field as implemented in GROMACS, and the general Amber force field (GAFF) and HF/6-31G*-derived RESP atomic charges for the ligands. This procedure has been previously validated.⁵

2. References

1. Marti-Renom, M. A.; Stuart, A. C.; Fiser, A.; Sanchez, R.; Melo, F.; Sali, A. Comparative protein structure modeling of genes and genomes. *Annu. Rev. Biophys. Biomol. Struct.* **2000**, 29, 291-325.
2. Wang, C.; Jiang, Y.; Ma, J.; Wu, H.; Wacker, D.; Katritch, V.; Han, G. W.; Liu, W.; Huang, X. P.; Vardy, E.; McCorvy, J. D.; Gao, X.; Zhou, E. X.; Melcher, K.; Zhang, C.; Bai, F.; Yang, H.; Yang, L.; Jiang, H.; Roth, B. L.; Cherezov, V.; Stevens, R. C.; Xu, H. E. Structural Basis for Molecular Recognition at Serotonin Receptors. *Science* **2013**, 340, 610-614.
3. Trott, O.; Olson, A. J. AutoDock Vina: improving the speed and accuracy of docking with a new scoring function, efficient optimization, and multithreading. *J. Comput. Chem.* **2010**, 31, 455-61.
4. Hess, B.; Kutzner, C.; van der Spoel, D.; Lindahl, E. GROMACS 4: Algorithms for highly efficient, load-balanced, and scalable molecular simulation. *J. Chem. Theory Comput.* **2008**, 4, 435-447.
5. Cordomi, A.; Caltabiano, G.; Pardo, L. Membrane Protein Simulations Using AMBER Force Field and Berger Lipid Parameters. *J. Chem. Theory Comput.* **2012**, 8, 948-958.