Aquaporins (AQP) are integral membrane proteins, whose function is to facilitate the passive transport of water across the plasma membrane of the cell. These proteins have been proven to be over-expressed in tumors, when compared to normal tissues. They can work as potential diagnostic and therapeutic targets in anticancer treatment.

In this project, we are developing a new computational workflow based on several methods that combine innovative ligand and structure-based approaches to identify new AQP-1 modulators. The growth of structure-function knowledge on AQP, makes them promising therapeutic target to be used in future computational drug discovery campaigns.

The hit rate for the identification of small-molecule AQP modulators appears to be very low. The use of additional conformations is what distinguishes our work. The use of MD snapshots allowed us to identify additional probable binding pockets in AQP-1 not found in the crystallographic structure. The results obtained with Automated pocket detection approach are not yet conclusive.

Ligand-based: identification of new AQP modulators based on the chemical characteristics of the available ones. Structure-based: pharmacophore and molecular docking, together with virtual screening.

Our goal is the identification of the most promising binding pockets of the protein for future drug discovery campaigns.

References
1. Verkman et al. (2014). NRDD, 13(4), 259
2. Wang et al. (2015). J/M, 13(96)
5. Morris et al. (2009). JCC, 30(16), 2785
6. Trott et al. (2010). JCC, 31(2), 455
7. Harris et al. (2007). PSFB, 70(4), 1506
8. Volkamer et al. (2012). B, 28(15), 2074