

FIGURE 2. Membrane protein simulation system. Top (A) and side view (B) of the simulation system of a mammalian AQP1 tetramer embedded in a pure POPE bilayer. In the side view, the front monomer is removed for clarity. Water molecules permeating water pores within individual AQP1 monomers are represented by a blue space-filling representation, whereas bulk water is shown in a light blue transparent box. The locations of the water pores and the central pore are indicated by arrows.

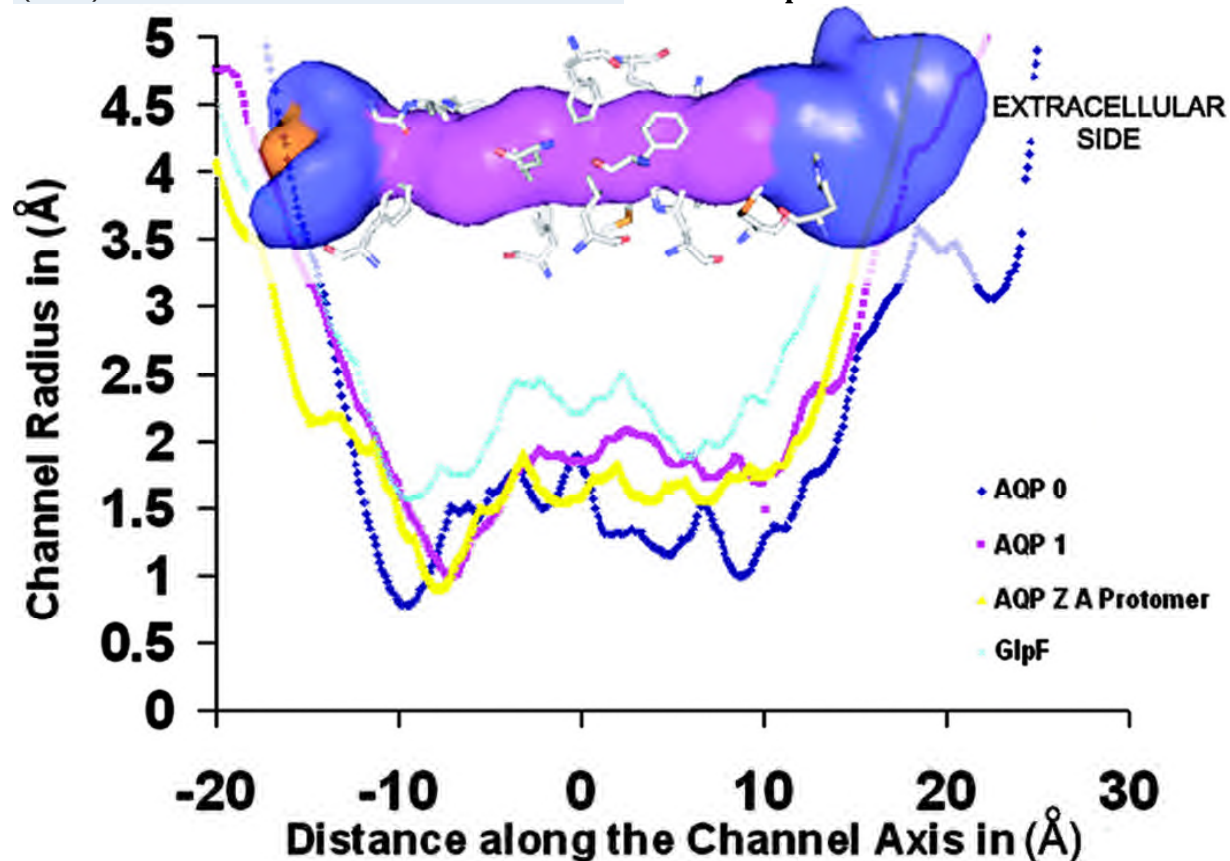


Fig. 3. **Channel radius profile plot.** Channel radius profiles of AQPs of known structure with corresponding structural elements are shown (22, 23). The AQPZ “A” protomer was used for radius calculations for AQPZ. The distance along the **channel axis** is calculated by using a point **midway** between the **Asn-Pro-Ala** sequences (NPAs) as the **zero ↓ point**. **Radii** were calculated with hole (39). **Channel volume** is shown in the background, with major **channel-forming residues**. The **pink central region** has a **diameter** of $<2.5 \text{ \AA}$, the **blue region** has a **diameter** of $>2.5 \text{ \AA}$ and $\leq 10 \text{ \AA}$. All images were made with pymol.

Tyr-149(Thr-149) points directly into the **channel** and, together with **Val-56(Ile-56)**, **Gly-64(64)**, **His-66(66)**, and **Phe-75(Leu-75)**, forms another **constriction** that is the **narrowest region** of the **channel**. It accepts a sphere with a **maximum diameter** of 1.5 \AA (as determined by using the program hole; ref. 21). In **AQP0**, it serves as a **cytoplasmic end** of the **narrow** part of the **channel**. Continuing in toward the **cytoplasmic side**, the **channel** widens slightly to accept a sphere with an **average diameter** of 3 \AA , which is significantly **narrower** than in other **AQP** structures (**AQP1**, $3.5\text{--}4.0 \text{ \AA}$; **GlpF**, $4.0\text{--}5.0 \text{ \AA}$) (22, 23). The **two residues Tyr-23(Leu-21)** and **Tyr-149(Thr-149)** are in quasi-2-fold related positions evoked by gene duplication, and in the other **AQPs**, **Tyr-23(Leu-21)** is either a **phenylalanine** or a **leucine** and **Tyr-149(Thr-149)** is either a **threonine** or **leucine**.