



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 $<10 \text{ \AA}$. 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.