



**Fig. 5. Wider FAD-access channels in LPMO-activating AADs compared with AAO.** The channels connecting the active-site cavity to solvent in *Pleurotus eryngii* AAO (PDB 3FIM) (A) and three AADs (AAQO1-AAQO3) from the *Pycnoporus cinnabarinus* genome and secretome (B-D, homology models) are shown. Channels were depicted by CAVER, with FAD as spheres and several active-site residues as sticks (CPK colored), including two catalytic histidines (green carbons) and other residues (cyan carbons) affecting the size and shape of the FAD access channel (see bottleneck in A). Adapted from Mathieu et al. (2016).