

1. Supplementary Figures

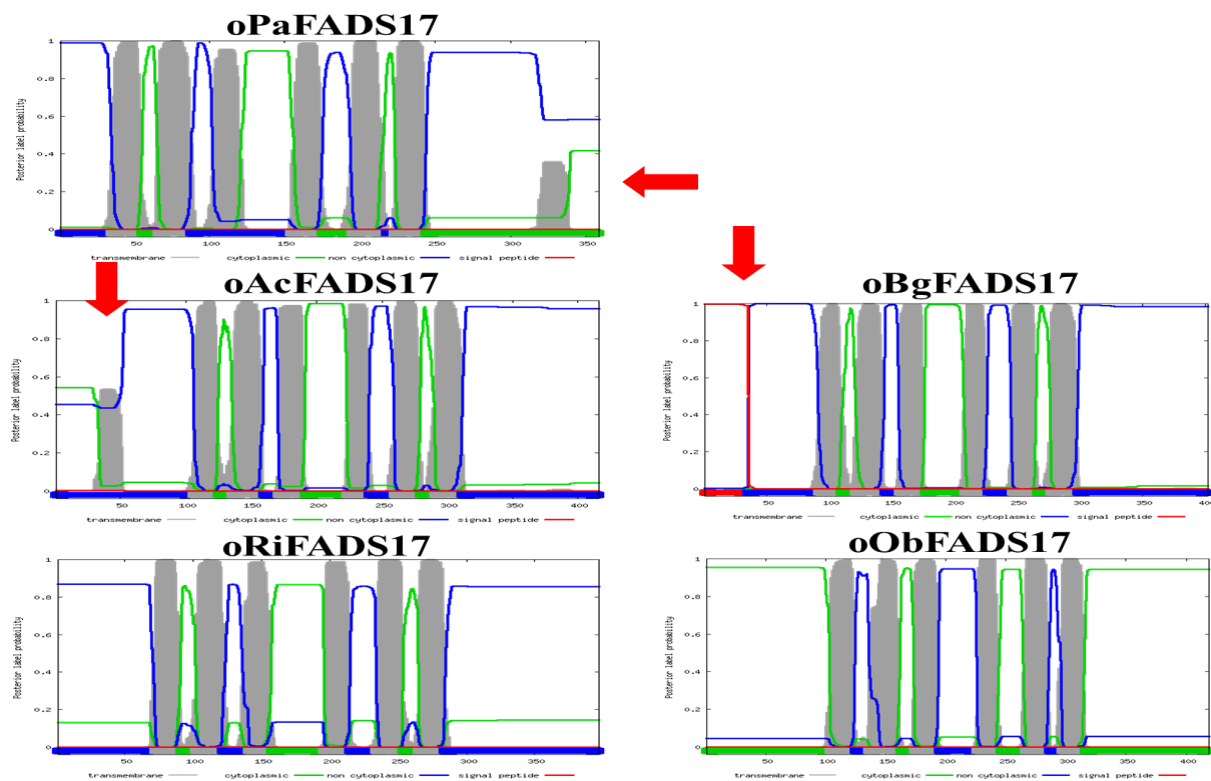


Fig. S1: Posterior probabilities for these oPaFADS17, oAcFADS17, oBgFADS17, oObFADS17 and oRiFADS17 proteins. Phobius, HMMTOP, and TMHMM online websites were used to perform bioinformatics analyses.

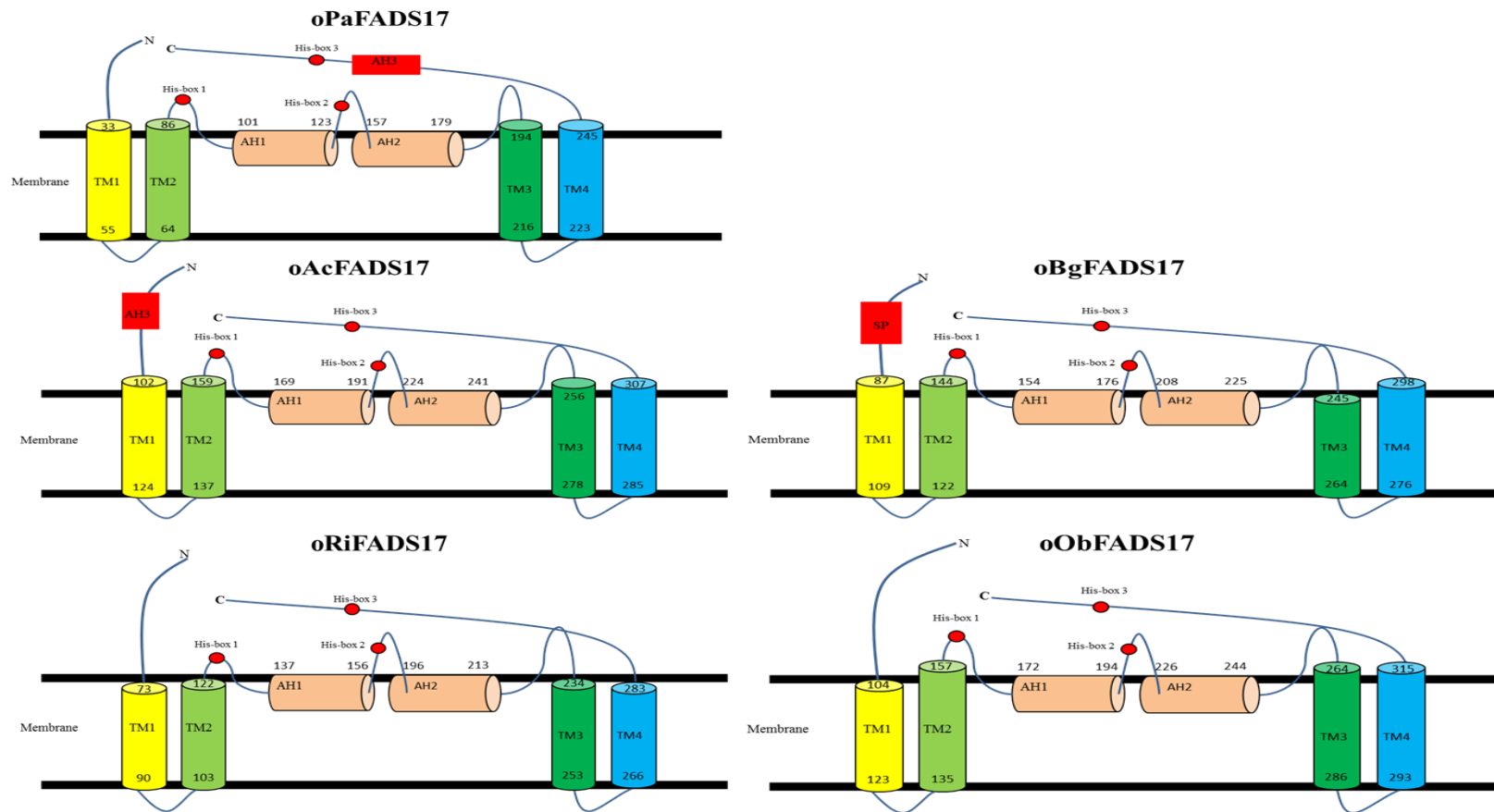


Fig. S2: Proposed topology model of these oPaFADS17, oAcFADS17, oBgFADS17, oObFADS17 and oRiFADS17 proteins. TM1~4 and AH1~2 were 6 transmembrane helix domains and the internal numbers indicated their probable locations. Pellets labeled in red denoted the three conserved histidine-rich motifs in the deduced primary amino acid sequences.