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.