CHAPTER VII
CONCLUSION

The full-length of DAR_Pem cDNA is 1,990 nucleotides long containing a 1,359 nucleotides ORF that can be translated into a putative DAR_Pem of 452 amino acids. Amino acid sequence analysis of DAR_Pem showed high homology to DAR type 1 of *Panulirus interruptus* ($D_{1\beta}$_Pan), *Bombyx mori* (BmDOP1), *Drosophila melanogaster*, and *Apis mellifera* at 70%, 58%, 46.6% and 46.1%, respectively. Characteristic of DAR_Pem was corresponded to seven transmembrane domains G-protein coupled receptors (GPCRs). It shared general consensus sequences of GPCR structure such as DRY sequence , ligand binding residues such as aspartic acid (D) in TM III, serine (S) in TM V and phenylalanine (F) in TM VI domains, and two cysteins that may form disulfide bond between e1 and e2. In addition, N-linked glycosylation site was predicted in the N-terminal extracellular loop and also several phosphorylation sites were located in i3 and intracellular C-terminal tail regions. A more diverse sequence between DAR_Pem and DAR type 1 in other species appeared in the C-terminal tail region. Therefore, C-tail region (15 kDa) was selected for polyclonal antibody production in rabbit. DAR_Pem mRNA was ubiquitously expressed in shrimp tissues with highest level in the brain, whereas low expression was found in the ovary. The high expression of DAR_Pem in the brain of shrimp at ovarian developmental stage I to III before declining in stage IV suggested that DAR_Pem may be involved in the inhibition of the release of GSH in the brain. Although DAR_Pem mRNA was expressed in diverse tissues, it could not be detected at protein level in these tissues by western blot with anti C-tail DAR antibody so far. To investigate functional activity of DAR_Pem in mediating cAMP level, recombinant DAR_Pem was expressed as a membrane protein in COS-1 cells. Activation by DA showed that DAR_Pem mediated an increase in cellular cAMP levels, which was in agreement with the functions of DAR_type1.