Abstract

The aryl hydrocarbon receptor (AhR) is a ligand-activated transcription factor; the AhR Per-AhR/Arnt-Sim (PAS) domain binds ligands. We developed homology models of the AhR PAS domain to characterize previously observed intra- and interspecies differences in ligand binding using molecular docking. In silico structure-based virtual ligand screening using our model resulted in the identification of pinocembrin and 5-hydroxy-7-methoxyflavone, which promoted nuclear translocation and transcriptional activation of AhR and AhR-dependent induction of endogenous target genes.