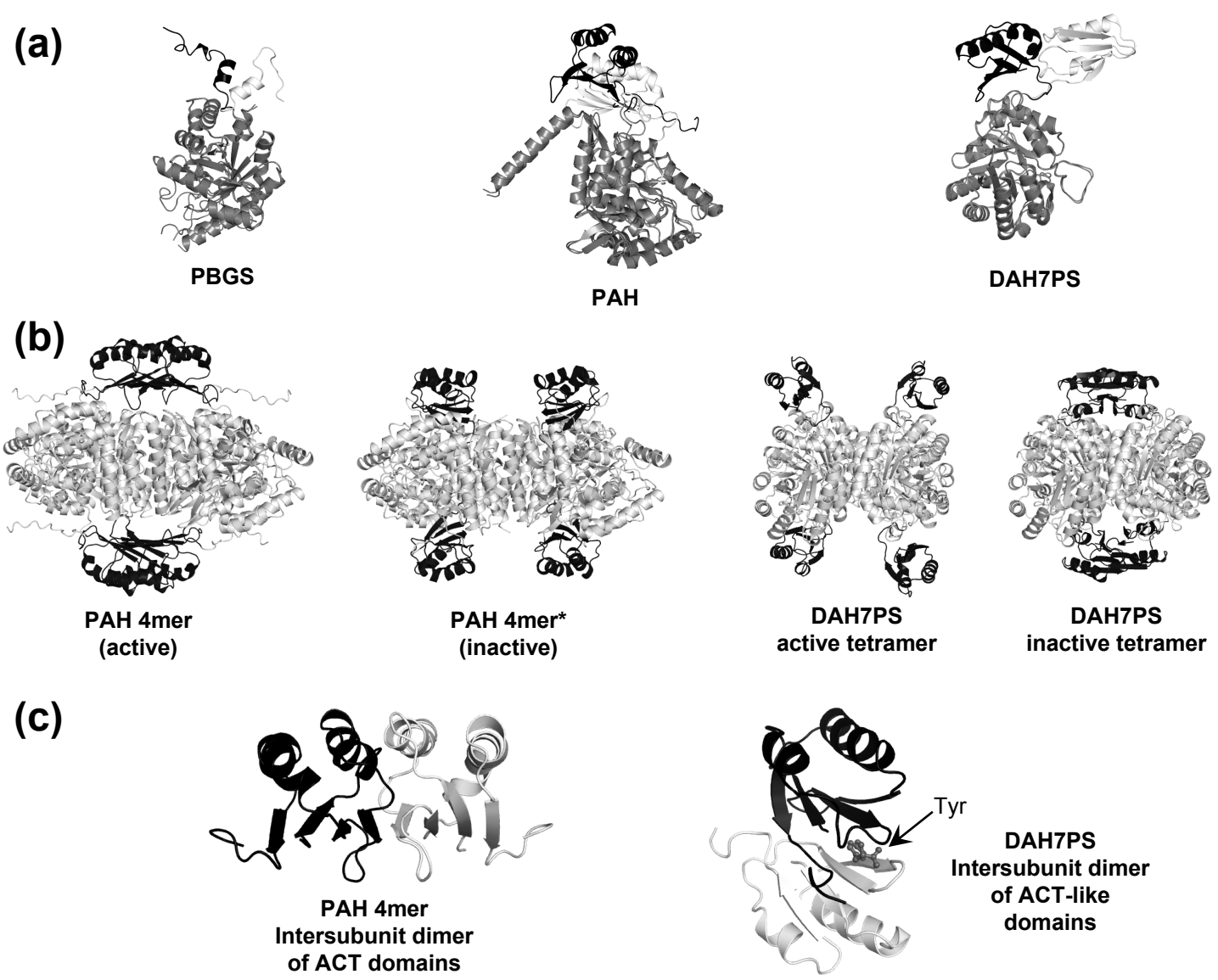

Supplemental Figure S1 – *Domain motions related to allosteric regulation*. **(a)** Shown are domain reorientations at the level of the subunit for PBGS [31], PAH, and DAH7PS [67]. For each protein, the superimposable catalytic domain is colored grey, while the mobile domain is colored black (active conformation) or white (inactive conformation). For PBGS, the orientation shown in grey/black (PDB id 1E51) assembles into an active octamer which can have an inter-subunit allosteric magnesium binding site. Shown in grey/white (PDBid 1PV8) is the orientation that assembles into a low activity hexamer, in which there is no allosteric magnesium binding site. For PAH the orientation shown in grey/black assembles into the high activity tetramer (4mer of this paper), which is posited to contain an intersubunit allosteric Phe binding site. The PAH orientation shown in grey/white is the form that assembles into the low activity tetramer (4mer* of this paper); it does not have the allosteric Phe binding site. For DAH7PS, the domain orientation shown in grey/white (PDB id 3PG9) is part of the feedback inhibited tetramer, which contains an allosteric tyrosine binding site at a subunit interface. The active form in grey/black (PDBid 1RZM) does not contain this allosteric tyrosine binding site. In all three cases, allosteric ligand binding pulls an equilibrium of structures toward the one with the allosteric ligand binding site. **(b)** The reorientation of regulatory domains is illustrated for the active and inactive conformations of PAH (left) and DAH7PS (right) tetramers. Each protein is colored light grey. For PAH the ACT domain portion of the regulatory domain is colored black. For DAH7PS, the ACT-like regulatory domain is colored black. **(c)** Alternate dimerization modes for ACT domain of PAH and the ACT-like domain of DAH7PS. In both cases, one chain is colored white and the other colored black. To prepare this figure, the black subunits were superimposed and their orientations are the same in both panels. For PAH, the allosteric phenylalanine is proposed Ito bind at the subunit interface (not shown). For DAH7PS, the allosteric tyrosine is shown bound is at the subunit interface.