Supplementary materials

Insulin–mimetic dihydroxanthyletin-type coumarins from *Angelica decursiva* with protein tyrosine phosphatase 1B and α-glucosidase inhibitory activities and docking studies of their molecular mechanisms

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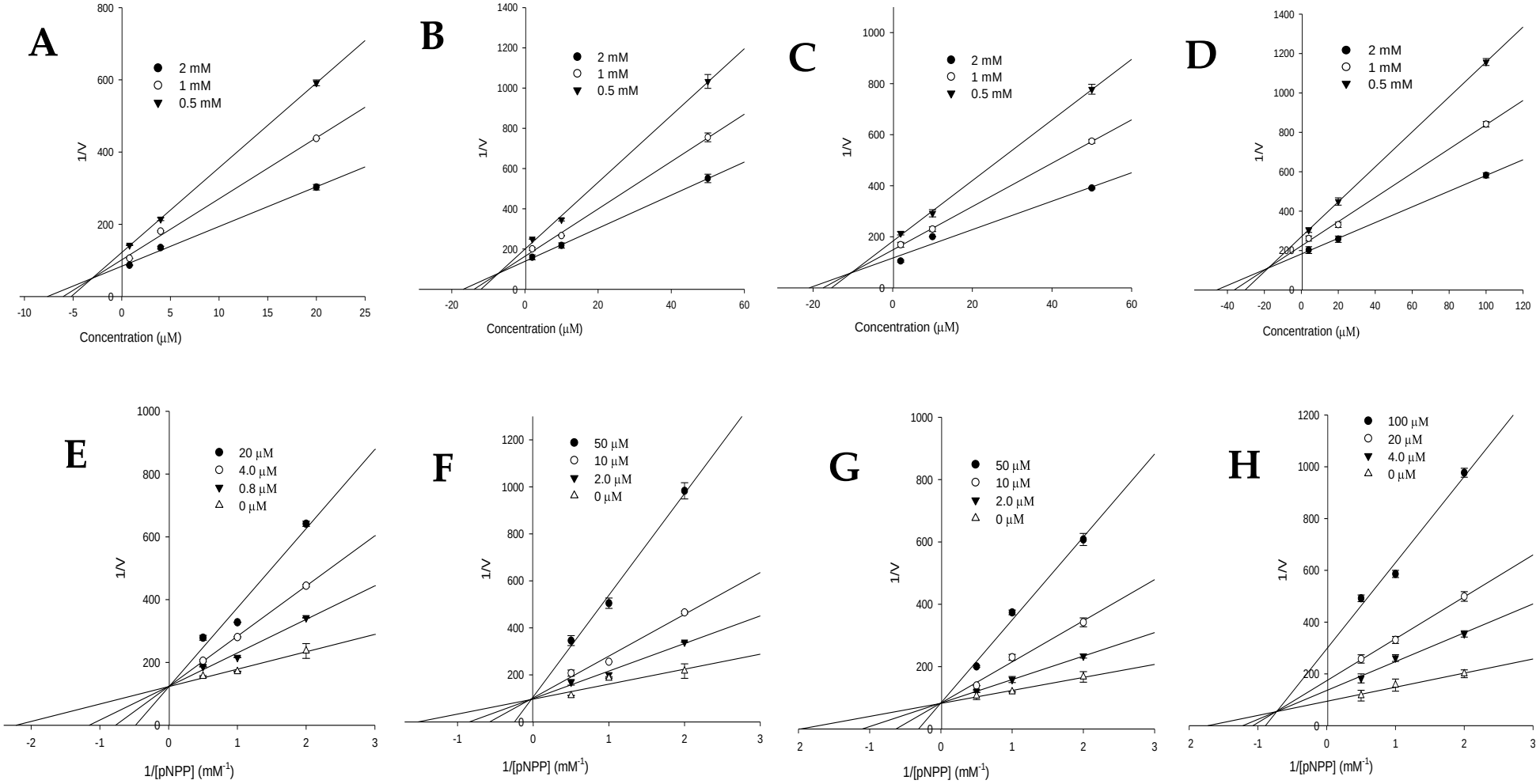

Figure S1. Dixon plots for PTP1B inhibition of dihydroxanthyletin-type coumarins. (+)-*trans*-decursidinol (A), Pd-C-I (B), Pd-C-II (C), Pd-C-III (D), were tested in the presence of different concentration of substrate (pNPP): 2mM (●); 1mM (○) and 0.5 mM (▼). Lineweaver-Burk plot for PTP1B inhibition of coumarins. PTP1B inhibition was analyzed in the presence of different concentration of sample as follows: 0 μM (Δ), 0.8 μM (▼), 4.0 μM (○) and 20 μM (●) for (+)-*trans*-decursidinol (E); 0 μM (Δ), 2 μM (▼), 10 μM (○) and 50 μM (●) for Pd-C-I (F); 0 μM (Δ), 2 μM (▼), 10 μM (○) and 50 μM (●) for Pd-C-II (G); 0 μM (Δ), 4 μM (▼), 20 μM (○) and 100 μM (●) for Pd-C-III (H).

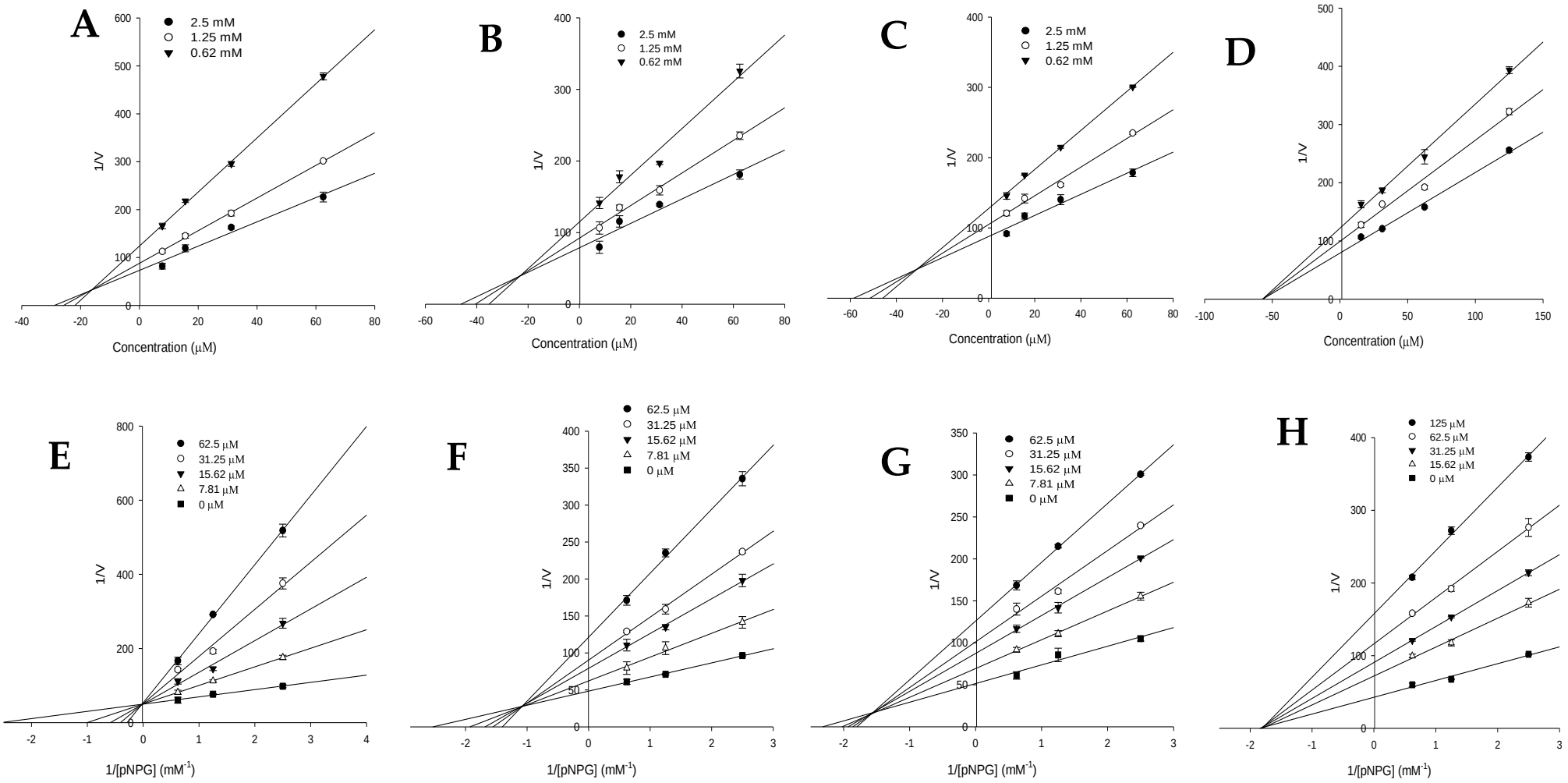

Figure S2. Dixon plots for α-glucosidase inhibition of dihydroxanthyletin-type coumarins. (+)-*trans*-decursidinol (A), Pd-C-I (B), Pd-C-II (C), Pd-C-III (D) were tested in the presence of different concentration of substrate (pNPG): 2.5mM (●); 1.25mM (○) and 0.625 mM (▼). Lineweaver-Burk plot for α-glucosidase inhibition of coumarins. α-Glucosidase inhibition was analyzed in the presence of different concentration of sample as follows: 0 μM (■), 7.81 μM (Δ), 15.62 μM (▼), 31.25 μM (○) and 62.5 μM (●) for (+)-*trans*-decursidinol (E); 0 μM (■), 7.81 μM (Δ), 15.62 μM (▼), 31.25 μM (○) and 62.5 μM (●) for Pd-C-I (F); 0 μM (■), 7.81 μM (Δ), 15.62 μM (▼), 31.25 μM (○) and 62.5 μM (●) for Pd-C-II (G); 0 μM (■), 15.62 μM (Δ), 31.25 μM (▼), 62.5 μM (○) and 125 μM (●) for Pd-C-III (H).

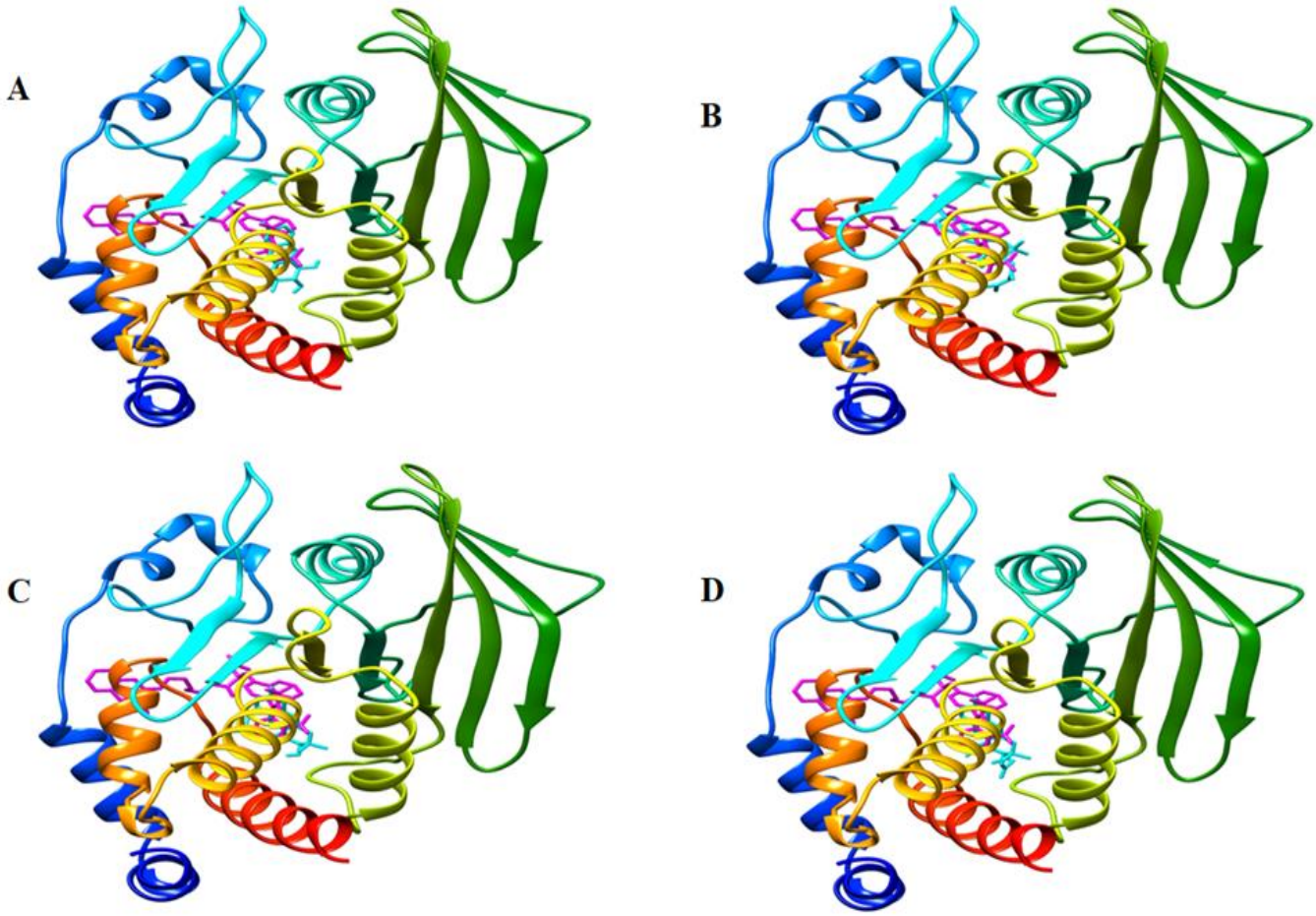

Figure S3. Molecular docking models for PTP1B inhibition of (+)-trans-decursidinol (A), Pd-C-I (B), Pd-C-II (C), and Pd-C-III (D). Compound 23 denote (magenta color) and dihydroxanthyletin-type coumarins (light blue color).

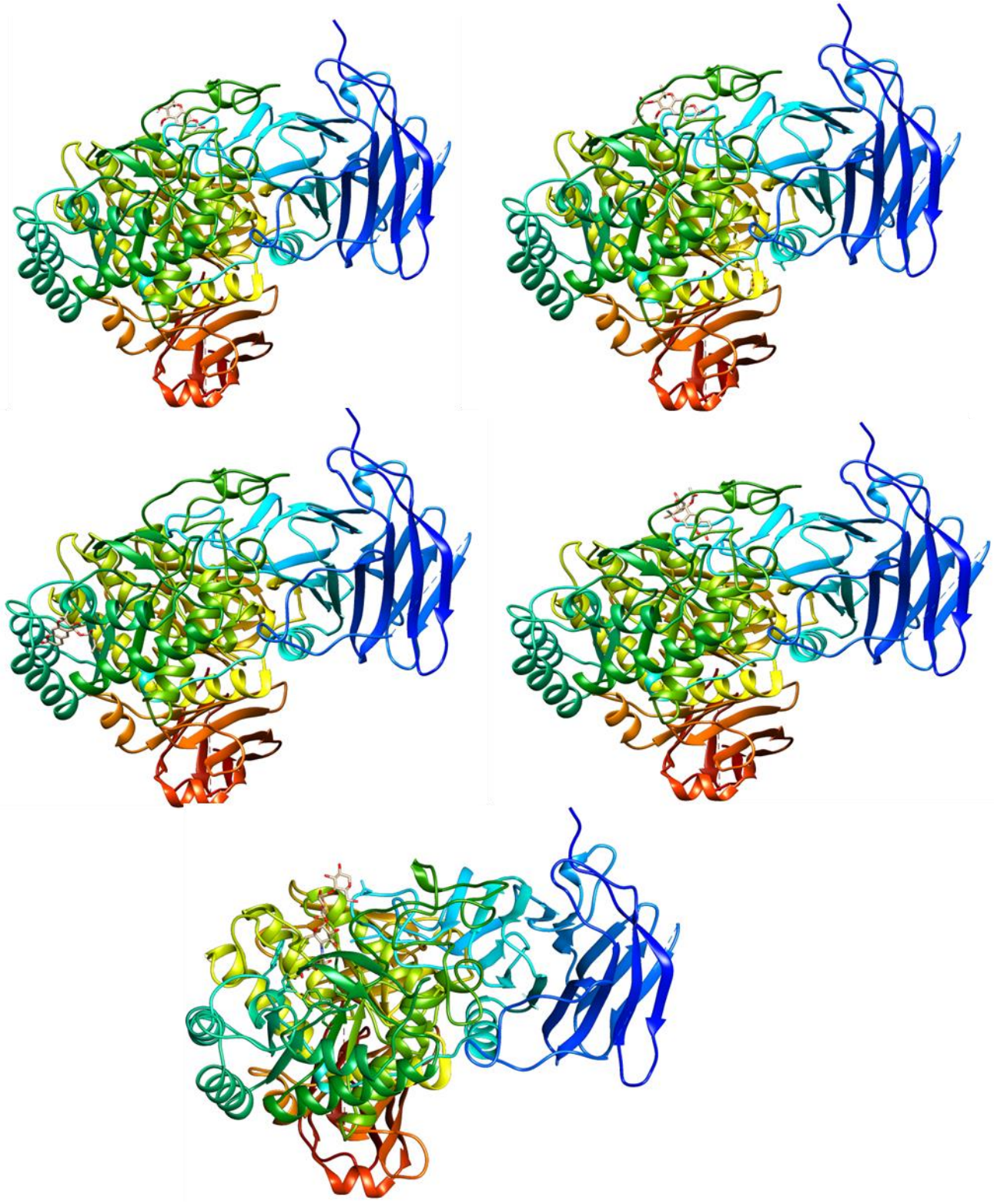

Figure S4. Molecular docking models for α-glucosidase inhibition of (+)-*trans*-decursidinol (A), Pd-C-I (B), Pd-C-II (C), Pd-C-III (D) and acarbose (E).