Figure S1. Protein homology modeling of maize *p*CAT and rice PMT1 against sorghum HCT1. Stereo image of the crystal structure model for the sorghum HCT1 (blue with white labels) with bound catalytic products *p*CA-shikimate (magenta) and CoA (dark purple) with best-fit protein homology models of maize *p*CAT (green) and rice PMT1 (orange) putative active site residues are presented. Panels represent composite models turned counterclockwise in 45-degree increments (total of 180 degrees) around a vertical axis running the length of the page.