



**Fig S3.** Predictive 3D model of *CrtW*, *CrtZ*, and *DGAT1* protein modeling translated from *pWZg1-2A* plasmid and *psy1*, *crtYB*, and *lcyb* protein modeling translated from *pPYLG* plasmid. Prediction and analysis of enzymes were obtained using the Phyre2 web portal (Kelley et al., 2015). The multicistronic expression vector has resulted in a slight change in *crtZ* conformation near the P2A region. The first helix is very close to the N-terminal (12 amino acid) and this helix is predicted to be involved in the active site, and thus inhibit the enzyme from function correctly.