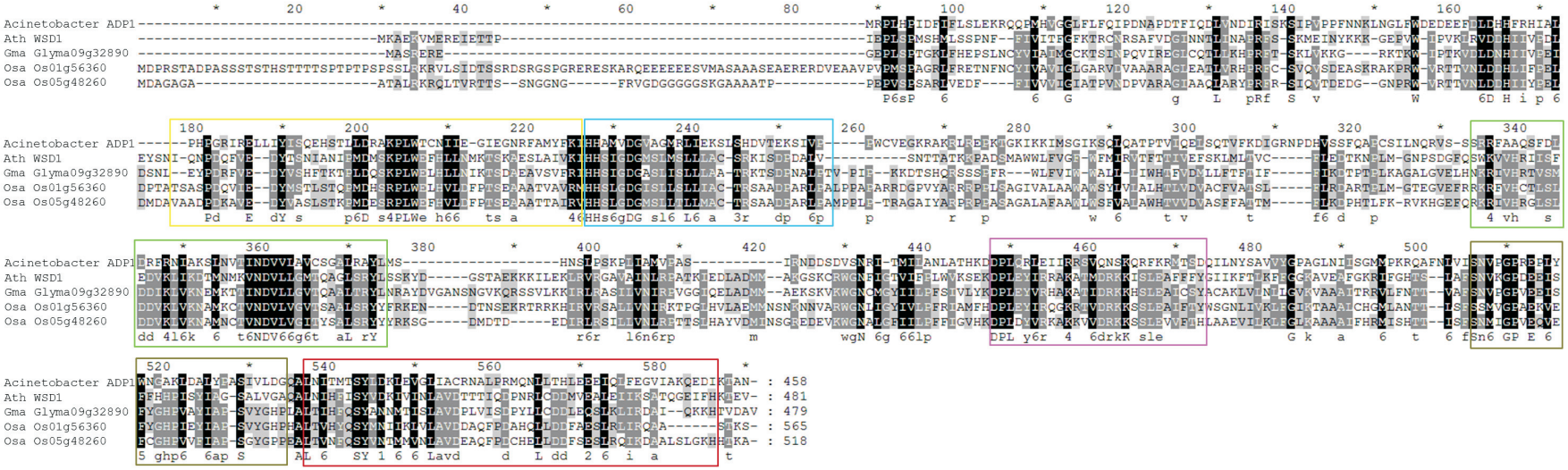

Figure S4 - Multiple sequence alignment of predicted amino acid sequences of WS/DGAT proteins. The WS/DGAT sequences from *G. max* (Gma), *A. thaliana* (Ath) and *O. sativa* (Osa) were aligned. Identical residues are shaded black, and similar residues are shaded gray. The color boxes indicate the conserved motifs on protein sequences shown in Figure 4A and 4B.