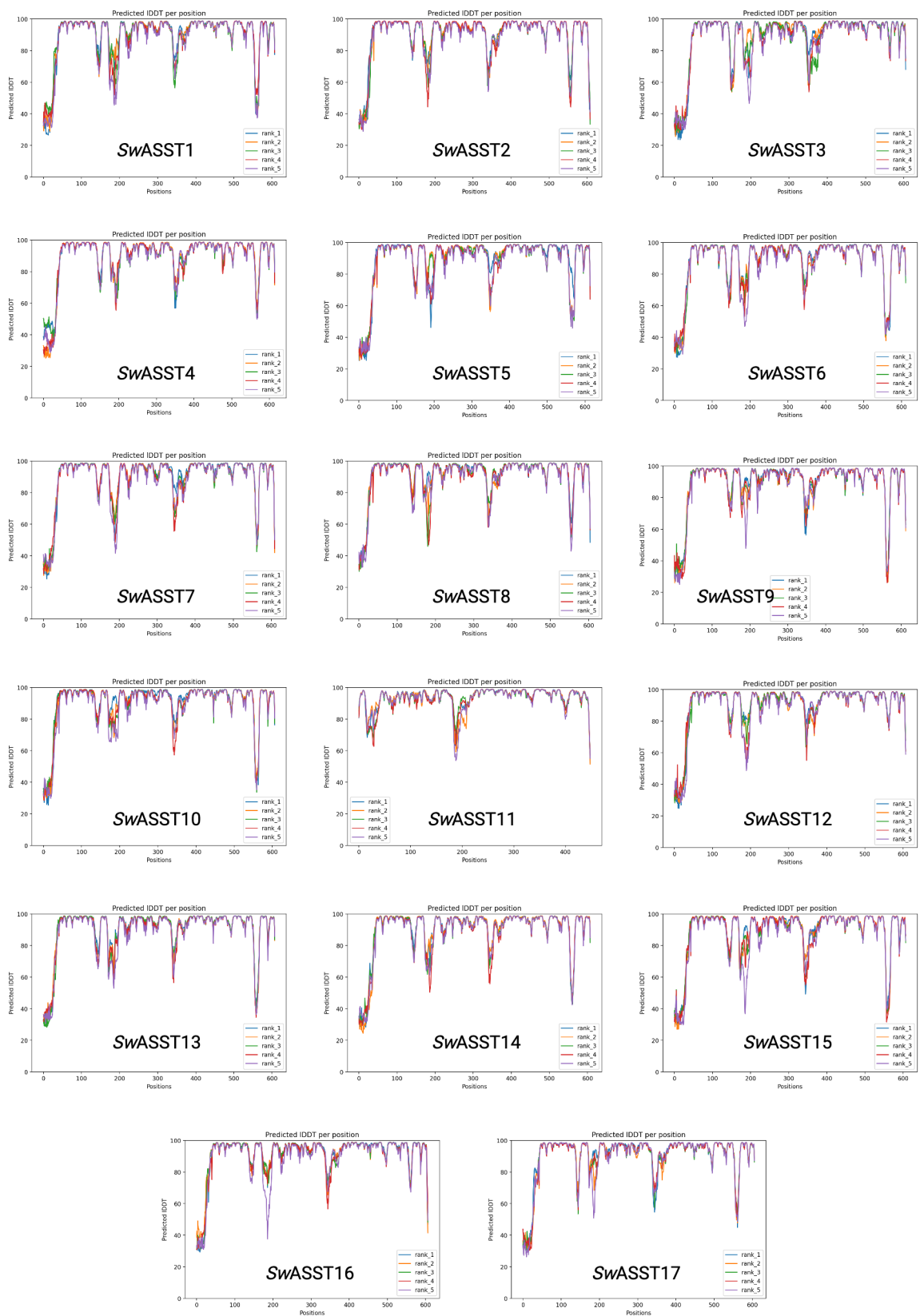
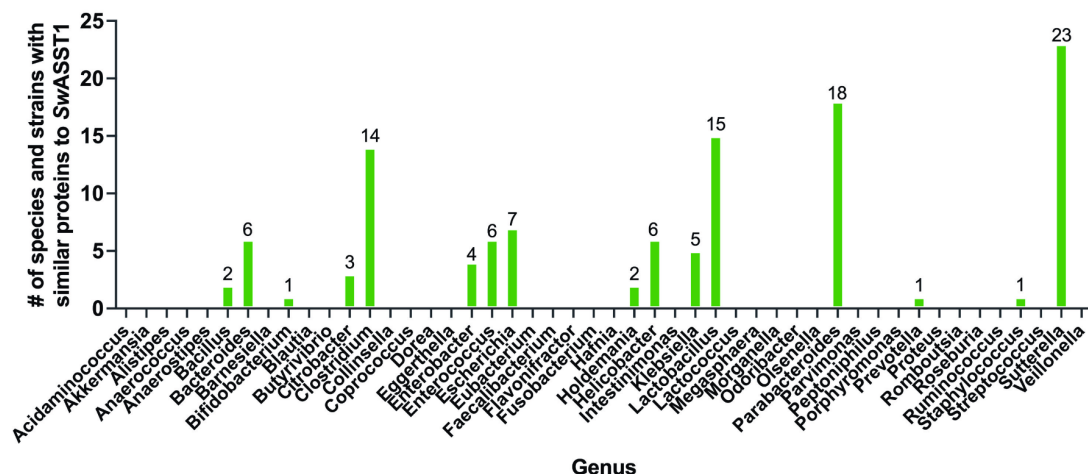


Figure S1. Partial multiple sequence alignment of all 17 *SwASSTs* with *EcASST*. Sequence alignment was performed on protein sequences without signal peptides. Color bar above aligned sequences shows the amino acid conservation at that position where dark red indicates highly conserved residues, while dark blue indicates little to no conservation.

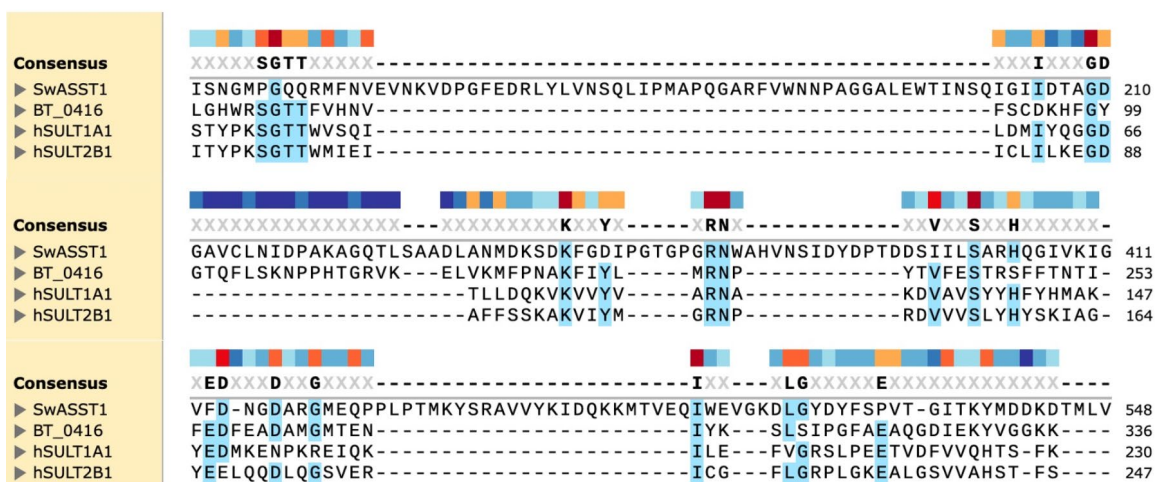


**Figure S2. IDDT plots for all predicted structures of *SwASST* proteins generated by AlphaFold2.** Each plot has confidence percentage on the y-axis and the amino acid position on the X-axis.

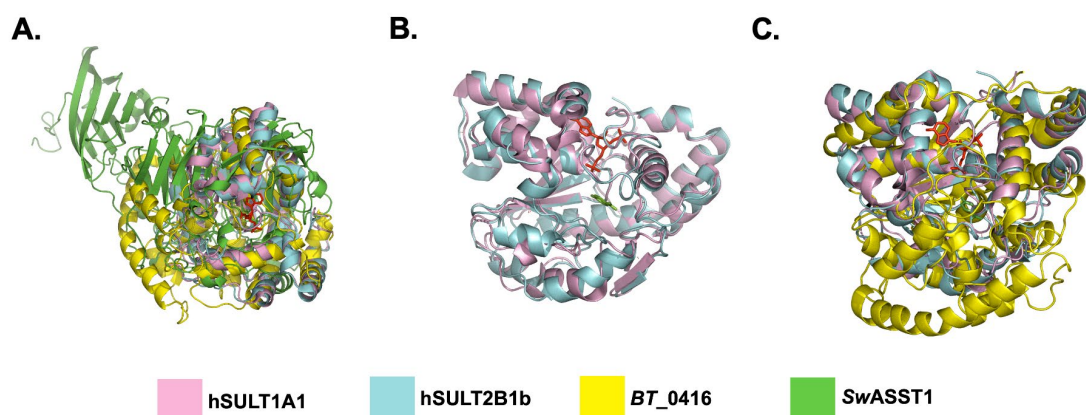




**Figure S6. Human gut microbial genera with sulfotransferases similar to *SwASST1*.** The bar graph represents total number of annotated sulfotransferases similar to *SwASST1* in species and strains from each genus.



**Figure S7. Multiple sequence alignment of *SwASST1* with *Bacteroides BT\_0416*, hSULT1A1, and hSULT2B1b.** Light blue highlighted regions are well conserved regions and regions that share a high percentage of similarity. Color bar above the sequences show the amino acid conservation at that position, where dark red is the most conserved and dark blue is the least conserved position.



**Figure S8. Structural alignments of *SwASST1* with *BT\_0416*, hSULT1A1, and hSULT2B1b.** A) Alignment of all four sulfotransferases. B) Alignment of both human sulfotransferases, hSULT1A1 and hSULT2B1b. C) Alignment of three PAPS-dependent sulfotransferases (*BT\_0416*, hSULT1A1, and hSULT2B1b). PAPS is shown in red and pNP is in lime green (visible in alignment B).