

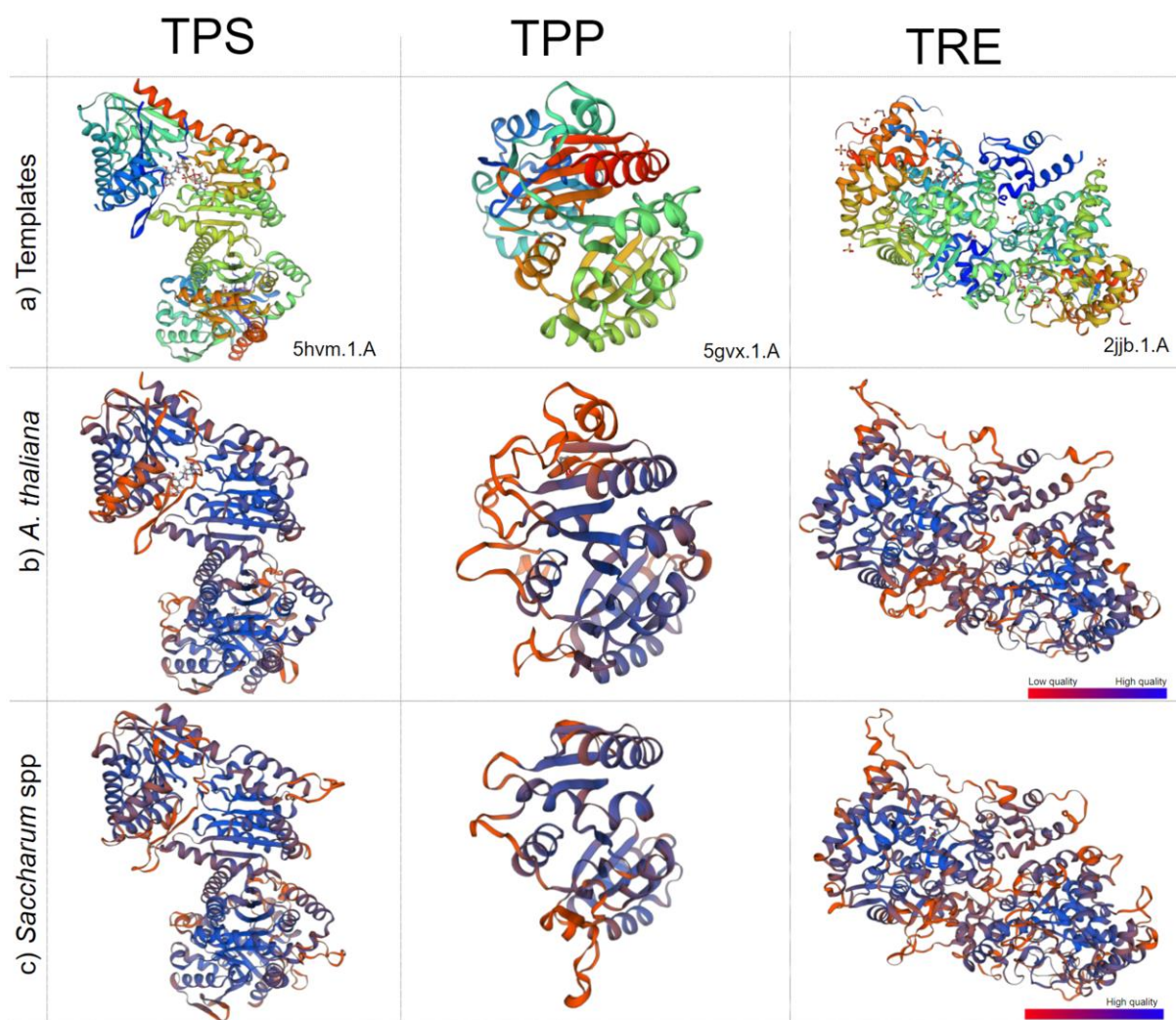


Figure S2. Three-dimensional (3D) structures of trehalose-6-phosphate synthase (TPS), trehalose-6-phosphate phosphatase (TPP), and trehalase (TRE) proteins. (a) 3D template structures of *A. fumigatus* TPS (ID model 5hvm.1.A), *M. tuberculosis* TPP (ID model 5gvx.1.A), and *E. coli* TRE (ID model 2jyb.1.A) from SWISS-MODEL (<http://swissmodel.expasy.org>) were used to predict protein quaternary structures of (b) *A. thaliana*, and (c) *Saccharum* spp. Sequences showed high conservation with the models indicated by colors from red (low quality) to blue (high quality). ID models, coverage, global model quality estimation (GMQE), quaternary structure quality estimate (QSQE), and identity are listed in Supplementary table S1.