

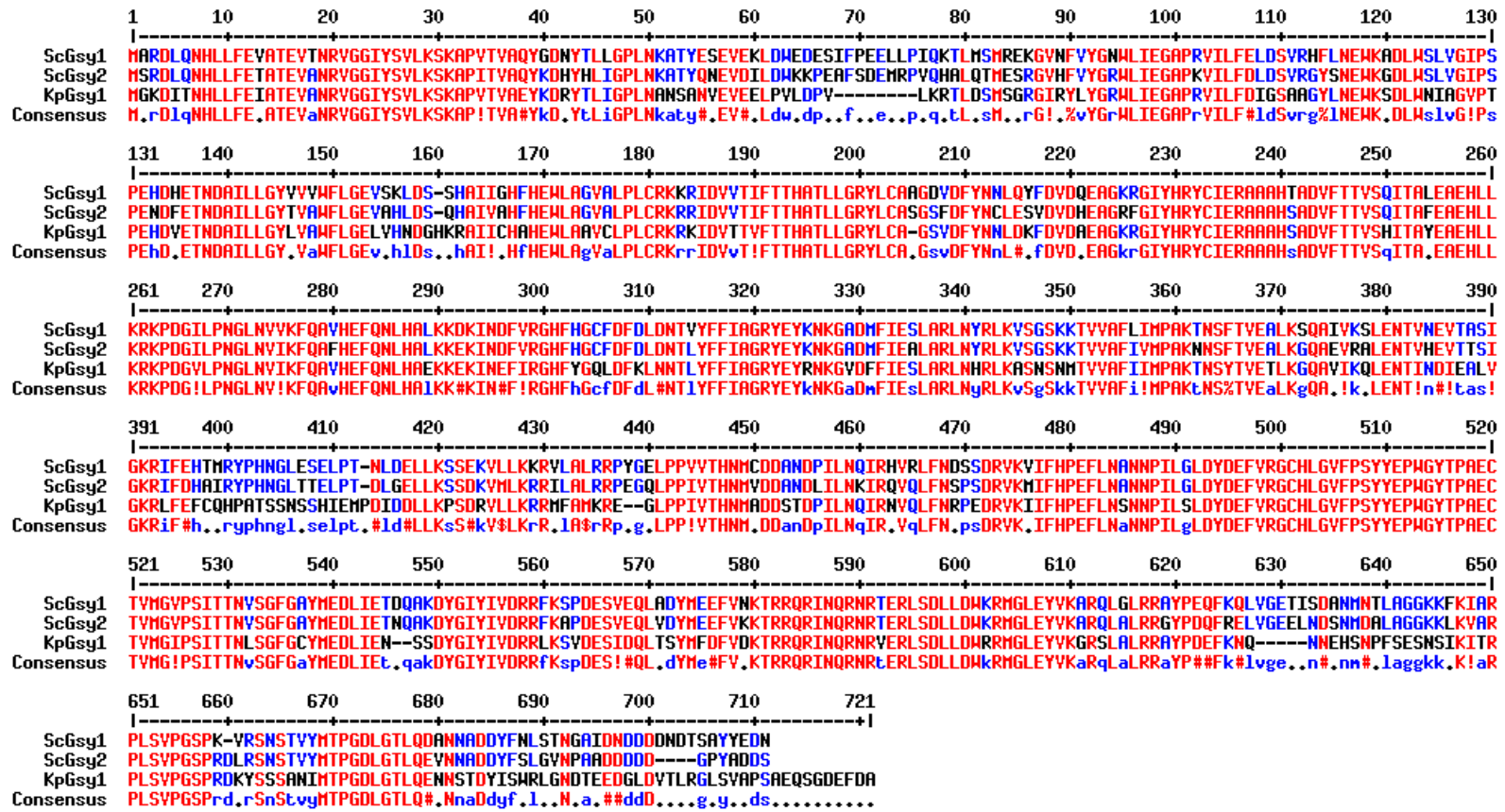


Figure S1. Multiple sequence alignment of *K. phaffii* Gsy1 and its orthologues in *S. cerevisiae*. ScGsy1, *S. cerevisiae* glycogen synthase 1 (YFR015C); ScGsy2, *S. cerevisiae* glycogen synthase 2 (YLR258W); KpGsy1, *K. phaffii* glycogen synthase 1 (XP_002493014.1). Color code of amino acid residues: red – high consensus, blue – low consensus, black – neutral. The alignment was generated using MultAlin software [32]. Alignment parameters: Blossum62 – 12 – 2 (symbol comparison table – gap penalty at opening – gap penalty at extension).