



Figure S5. Evolutionary tree of the  $\alpha$ -amylase family GH13. The tree covers 253 sequences with focus on the novel subfamily GH13\_46 around the cyclomaltodextrinase from *Flavobacterium* sp. No. 92 (for details, see Table S1). The tree is based on the alignment shown in Figure S4, spanning the sequence segment from the beginning of the strand  $\beta$ 2 (CSR-VI) to the end of the strand  $\beta$ 8 (CSR-VII), i.e. the substantial part of the catalytic TIM-barrel including the domain B. The same but simplified tree without the leaves is presented in Figure 4.