



Figure S3. Evolutionary tree of the newly proposed subfamily GH13_46. The tree is based on the alignment of all 108 sequences of the isolated N-terminal domain (the alignment can be inspected in Figure S1) preceding the catalytic TIM-barrel. The sequences are coloured according to four clusters seen in Figure 2 based on the alignment of entire sequences (Figure S1). The labels of protein sources consist of the UniProt accession number and the name of the organism (for details, see Table S1). The four experimentally characterized enzymes are marked by an asterisk.