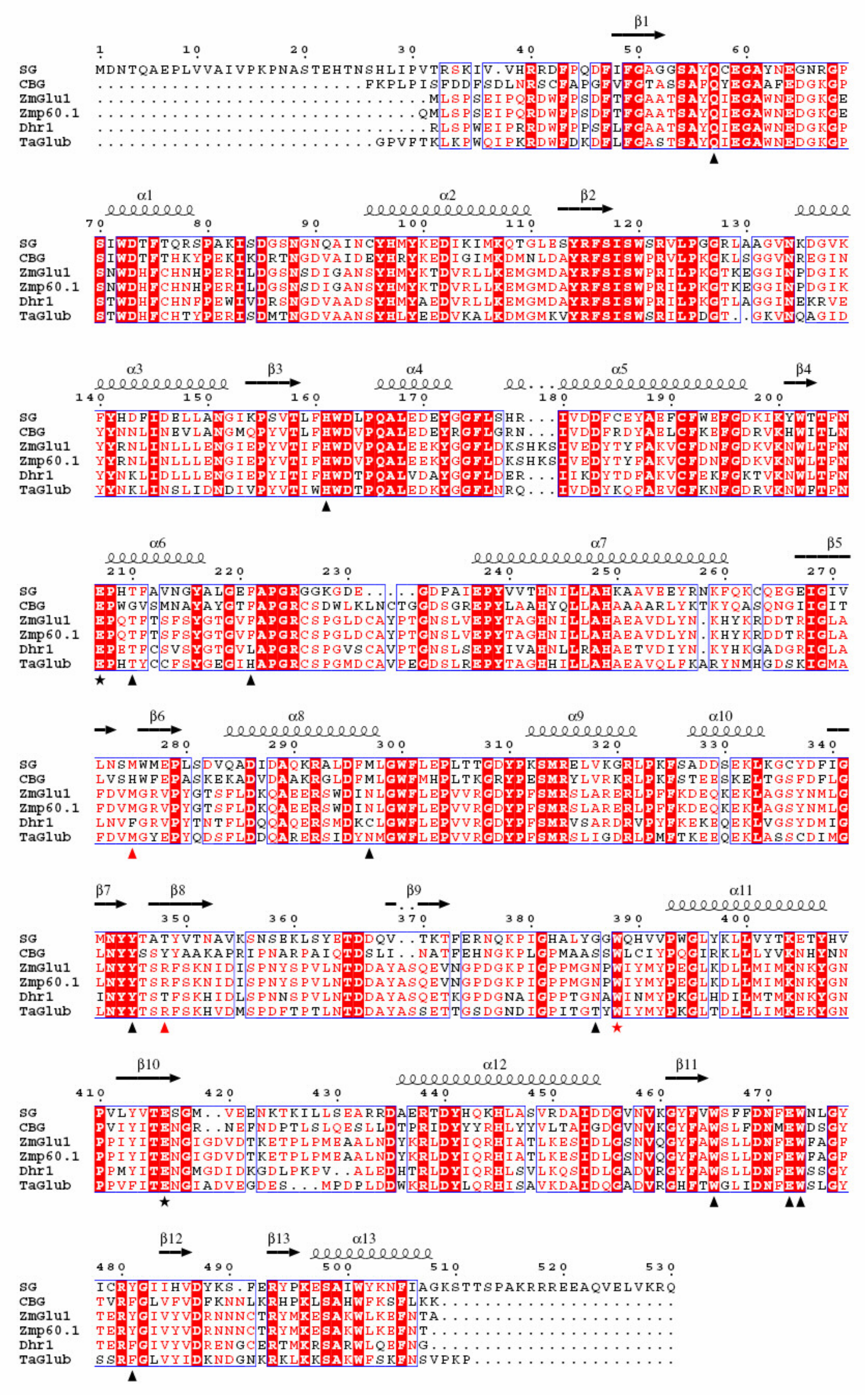
SG
CBG
ZmGlu1
Zmp60.1
Dhr1
TaGlub
β1
α1
α2
β2
α3
β3
α4
α5
β4
α6
α7
β5
β6
α8
α9
α10
β7
β8
β9
α11
β10
α12
β11
β12
β13
α13

Supplemental Figure 1. Structure Based Alignment of β-Glucosidases of Family 1 from Higher Plants.

SG, strictosidine glucosidase from *Rauvolfia serpentina*; CBG, cyanogenic β-glucosidase from *Trifolium repens*; ZmGlu1, ZmGlu1 from *Zea maize*; Zmp60.1, Zmp60.1 from *Z. maize*; DHR1, Dhurrinase 1 from *Sorghum bicolor*; TaGlub, TaGlu1b from *Triticum aestivum*. The red asterisk indicates the conserved Trp388 and the two residues influencing its conformation are marked by red triangles. The two black asterisks show the conservation of the catalytic residues and eleven additional residues which are involved in binding strictosidine are marked by black triangles. Horizontal arrows above the sequences indicate β-strands (labeled β1–β13); helical segments indicate α-helices (labeled α1- α13). The sequence numbering is shown according to SG amino acid sequence.

Table 1 supplementary

Overall comparison of plant glucosidases to SG.

PDB	Identity (%)	Similarity (%)	r.m.s.d. (Å)	Cα
1CBG	54	68	0.79	448
1E1E	45	67	0.87	437
1HXJ	46	62	0.86	437
1V02	45	61	0.87	441
2DGA	43	62	0.90	441

1CBG, cyanogenic β-glucosidase from *Trifolium repens*; 1E1E, ZmGlu1 from *Zea mays*; 1HXJ, Zmp60.1 from *Zea mays*; 1V02, Dhurrinase1 from *Sorghum bicolor*; 2DGA, TaGlu1b from *Triticum aestivum*.