```
Tecbh1-TrCBM-C  420 VPSDVESQSPNSYVTYSNIKFGPINSTFT---ASNP-----------PGGN 461
Tecbh1-CtCBM-C  420 VPSDVESQSPNSYVTYSNIKFGPIGSTVPGLDGSNPGNPTTTVVPPASTSTS 476
Tecbh1-HgCBM-C  420 VPSDVESQSPNSYVTYSNIKFGPIGSTVAGLPGAGNGGNN-------GGNPP 469
                    **********************.**..   .:.             .

Tecbh1-TrCBM-C  RGTTTTRRPATT-TGSSPGPTQSHYGQCGGIGYSGPTVCASGTTCQVLNPYYSQCL 516
Tecbh1-CtCBM-C  RPTSSTSSPVSTPTGQPGGCTTQKWGQCGGIGYTGCTNCVAGTTCTQLNPWYSQCL 532
TeCBH1-HgCBM-C  PPTTTTSSAPATTTTASAGPKAGRWQQCGGIGFTGPTQCEEPYICTKLNDWYSQCL 525
                  *::*  . :* *  . * .  :: ******::* * *     *  ** :*****
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Additional file 2. Partial amino acid sequence alignment of the C-terminal end of *T.e.*CBH1 fused to the *T. reesei*, *C. thermophilum* or *H. grisea* linker-CBM sequences. The last amino acid of the native *T.e.*CBH1, Ser455, is shown in **bold** type in the *Te*CBH1-CBM-C sequence. The cysteine residues in the CBM that take part in disulfide bridge formation are shown in **bold** type and the aromatic amino acids predicted to bind cellulose are underlined. The *T.e.*CBH1-*T.r.*CBM-C enzyme has an additional N-glycosylation target site (Asn449) lacking from the other two bi-modular enzymes.