## CLAIMS

1. A variant of a parent cellulase, comprising an alteration at one or more positions corresponding to positions 292, 274, 266, 265, 255, 246, 237, 224 and 221 of the mature polypeptide of SEQ ID NO: 2, and the variant has cellulase activity.

2. The variant of claim 1, wherein the cellulase is GH45 cellulase.

3. The variant of claim 1 or 2, wherein the alteration is an insertion or deletion or substitution.

4. The variant of any of claims 1-3, comprising a catalytic domain and a cellulase binding domain, wherein the cellulase binding domain is heterologous to the catalytic domain.

5. The variant of any of claims 1-4, which is a variant of a parent cellulase selected from the group consisting of:

a. a polypeptide having at least 60% sequence identity to the mature polypeptide of SEQ ID NO: 2, SEQ ID NO: 4, SEQ ID NO: 8, SEQ ID NO: 12, SEQ ID NO: 13, SEQ ID NO: 14; or SEQ ID NO: 18;

b. a polypeptide encoded by a polynucleotide that hybridizes under low stringency conditions with (i) the mature polypeptide coding sequence of SEQ ID NO: 1, SEQ ID NO: 3, SEQ ID NO: 7, SEQ ID NO: 37, SEQ ID NO: 38, SEQ ID NO: 39 or SEQ ID NO: 17, (ii) the cDNA sequence thereof, or (iii) the full-length complement of (i) or (ii);

c. a polypeptide encoded by a polynucleotide having at least 60% identity to the mature polypeptide coding sequence of SEQ ID NO: 1, SEQ ID NO: 3, SEQ ID NO: 7, SEQ ID NO: 37, SEQ ID NO: 38, SEQ ID NO: 39 or SEQ ID NO: 17, or the cDNA sequence thereof; and

d. a fragment of the mature polypeptide of SEQ ID NO: 2, SEQ ID NO: 4, SEQ ID NO: 8, SEQ ID NO: 12, SEQ ID NO: 13, SEQ ID NO: 14; or SEQ ID NO: 18, which has cellulase activity.

6. The variant of any of claims 1-5, which has at least 60%, *e.g.*, at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95% identity, at least 96%, at least 97%, at least 98%, or at least 99%, but less than 100%, sequence identity to the amino acid sequence of the parent cellulase.

7. The variant of any of claims 1-6, which comprises one or more substitutions selected from the group consisting of W292Y, F274Y, W266Y, R265K, S255P, T246N, S224P, S224P and S221P.

8. The variant of claim 7, which comprises one or more substitutions selected from the group consisting of

W292Y
W266Y + W292Y
R265K + W292Y
R265K + W266Y + W292Y
F274Y + W292Y
W266Y + F274Y + W292Y
S221P + S224P + W292Y
S224P + T246N + W292Y
S255P + W292Y
W266Y + W292Y.

9. The variant of any of claims 1-8, which has an improved property relative to the parent, wherein the improved property is improved biofinishing performance, a reduced weight loss of cellulose-containing textile, and/or a reduced loss in cellulose-containing textile strength.

10. A variant of a parent GH45 cellulase, comprising a catalytic domain, and a cellulose binding domain, wherein the cellulase binding domain is heterologous to the catalytic domain, and wherein the variant has an improved biofinishing activity compared with the parent GH45 cellulase.

11. The variant of claim 10, wherein the catalytic domain is selected from the group consisting of:

a. a polypeptide having at least 60% sequence identity to the catalytic domain of SEQ ID NO: 12, SEQ ID NO: 13, or SEQ ID NO: 14;

b. a polypeptide encoded by a polynucleotide that hybridizes under low stringency conditions with (i) the catalytic domain coding sequence of SEQ ID NO: 37, SEQ ID NO: 38, or SEQ ID NO: 39, (ii) the cDNA sequence thereof, or (iii) the full-length complement of (i) or (ii);

c. a polypeptide encoded by a polynucleotide having at least 60% identity to the catalytic domain coding sequence of SEQ ID NO: 37, SEQ ID NO: 38, SEQ ID NO: 39, or the cDNA sequence thereof; and

d. a fragment of the catalytic domain of SEQ ID NO: 12, SEQ ID NO: 13, or SEQ ID NO: 14, which has cellulase activity.

12. The variant of claim 10 or 11, wherein the cellulose binding domain is selected from the group consisting of:

a. a polypeptide having at least 60% sequence identity to the cellulose binding domain of SEQ ID NO: 12, SEQ ID NO: 13, SEQ ID NO: 14 or SEQ ID NO: 8;

b. a polypeptide encoded by a polynucleotide that hybridizes under low stringency conditions with (i) the cellulose binding domain coding sequence of SEQ ID NO: 37, SEQ ID NO: 38, SEQ ID NO: 39 or SEQ ID NO: 7, (ii) the cDNA sequence thereof, or (iii) the full-length complement of (i) or (ii);

c. a polypeptide encoded by a polynucleotide having at least 60% identity to the cellulose binding domain coding sequence of SEQ ID NO: 37, SEQ ID NO: 38, SEQ ID NO: 39 or SEQ ID NO: 7, or the cDNA sequence thereof; and

d. a fragment of the cellulose binding domain of SEQ ID NO: 12, SEQ ID NO: 13, SEQ ID NO: 14 or SEQ ID NO: 8, which has the cellulose binding activity.

13. The variant of any of claims 10-12, wherein linker is selected from the group consisting of:

a. a polypeptide having at least 60% sequence identity to the linker of SEQ ID NO: 12, SEQ ID NO: 13, SEQ ID NO: 14 or SEQ ID NO: 8;

b. a polypeptide encoded by a polynucleotide that hybridizes under low stringency conditions with (i) the linker coding sequence of SEQ ID NO: 37, SEQ ID NO: 38, SEQ ID NO: 39 or SEQ ID NO: 7, (ii) the cDNA sequence thereof, or (iii) the full-length complement of (i) or (ii);

c. a polypeptide encoded by a polynucleotide having at least 60% identity to the linker coding sequence of SEQ ID NO: 37, SEQ ID NO: 38, SEQ ID NO: 39 or SEQ ID NO: 7, or the cDNA sequence thereof; and

d. a fragment of the linker of SEQ ID NO: 12, SEQ ID NO: 13, SEQ ID NO: 14 or SEQ ID NO: 8, which has the cellulose binding activity.

14. An polynucleotide encoding the variant of any of claims 1-13.

15. A nucleic acid construct, an expression vector, or a host cell comprising the polynucleotide of claim 14.

16. A process for biofinishing, comprising treating a cellulose-containing textile with the variant of any of claims 1-13.