What is claimed is:

1. An aglycosylated polypeptide having cellobiase activity comprising the amino acid sequence of SEQ ID NO: 1.

2. The aglycosylated polypeptide of claim 1, wherein the aglycosylated polypeptide:
i) has increased cellobiase activity as compared to glycosylated Cel3A enzyme from wild-type *T. reesei;*
ii) has increased substrate recognition, a more active substrate recognition site, or reduced steric hindrance as compared to glycosylated Cel3A enzyme from wild-type *T. reesei;* and/or
iii) hydrolyzes a carbohydrate such as cellobiose into one or more monosaccharides, e.g., glucose.

3. The aglycosylated polypeptide of any one of the preceding claims, wherein the cellobiase activity comprises hydrolysis of a beta 1,4 glycosidic linkage of cellobiose.

4. A nucleic acid sequence encoding the polypeptide of claims 1-3.

5. A nucleic acid sequence encoding a Cel3A enzyme, wherein the nucleic acid sequence comprises at least 85% identity to SEQ ID NO: 3.

6. A nucleic acid molecule comprising a nucleic acid sequence of any of claims 4 and 5.

7. The nucleic acid molecule of claim 6, further comprising a promoter, e.g., a promoter for prokaryotic cell expression, e.g., bacterial cell expression, e.g., expression in *E. coli,* wherein:

i) the promoter sequence is a constitutive promoter sequence, inducible promoter sequence, or a repressible promoter sequence; or

ii) the promoter is a T7 promoter.

8. The nucleic acid molecule of any one of claims 6-7, further comprising a nucleic acid sequence encoding:

i) a tag, e.g., a tag for detection and/or purification and/or for linkage to another molecule, e.g., a
His tag; or

ii) one or more signal sequences, e.g., a secretion signals sequence.

9. An expression vector comprising the nucleic acid sequence of claims 4-8, optionally wherein, the vector comprises a nucleic acid sequence encoding a selection marker, optionally wherein the selection marker comprises a kanamycin or an ampicillin marker.

10. A cell comprising the expression vector of claim 9, optionally wherein, the cell is a prokaryotic cell or bacterial cell.

11. A cell expressing a polypeptide of any one of claims 1-3, wherein, the cell is a prokaryotic cell or bacterial cell, and optionally wherein:

i) the cell is impaired for glycosylation; or

ii) the cell is an *E. coli* cell, wherein the *E. coli* cell is an origami *E. coli* cell.

12. A method for producing an aglycosylated polypeptide having cellobiase activity comprising the amino acid sequence of SEQ ID NO: 1 comprising culturing a cell comprising the nucleic acid of any one of claims 4-8 under conditions suitable for the expression of the polypeptide, wherein the cell does not glycosylate the polypeptide, e.g., a bacterial cell, e.g., an *E. coli* cell, e.g., an origami *E. coli* cell.

13. A method for producing an aglycosylated polypeptide having cellobiase activity comprising the amino acid sequence of SEQ ID NO: 1 comprising treating the polypeptide with a deglycosylating enzyme, optionally wherein, the deglycosylating enzyme is selected from PGNase and EndoH.

14. A method for producing an aglycosylated polypeptide having cellobiase activity comprising the amino acid sequence of SEQ ID NO: 1 comprising culturing a cell comprising the nucleic acid of any one of claims 4-8, wherein the nucleic acid sequence has one or more mutations which prevent glycosylation of the encoded polypeptide.

15. A method for culturing a cell expressing an aglycosylated polypeptide having cellobioase activity comprising the amino acid sequence of SEQ ID NO: 1 in the presence of a glycosylation inhibitor, e.g., tunicamycin.

16. An enzyme mixture comprising a glycosylated polypeptide comprising an amino acid sequence of SEQ ID NO: 1, and an aglycosylated polypeptide comprising an amino acid sequence of SEQ ID NO: 1, wherein both of the glycosylated polypeptide and the aglycosylated polypeptide have cellobiase activity.

17. The enzyme mixture of claim 16, wherein the aglycosylated polypeptide is the aglycosylated polypeptide of any one of claims 1-3.

18. The enzyme mixture of claim 16 or 17, wherein the glycosylated polypeptide and the aglycosylated polypeptide both comprise Cel3A enzyme from wild-type *T reesei.*

19. The enzyme mixture of any one of claims 16-18, further comprising at least one additional enzyme derived from a microorganism, wherein the additional enzyme has a biomass-degrading activity of a cellulose based material, and optionally wherein, the additional enzyme is selected from a ligninase, an endoglucanase, a cellobiohydrolase, xylanase, and a cellobiase.

20. The enzyme mixture of claim 16 or 17, wherein the mixture further comprises one or more ligninase, one or more endoglucanase, one or more cellobiohydrolase, one or more xylanase.

21. The enzyme mixture of any one of claims 16-20, wherein the ratio between the aglycosylated polypeptide to the remaining enzymes or to the glycosylated polypeptide in the mixture is at least 1:32.

22. A method of producing a product from a biomass or converting a biomass to a product comprising contacting a biomass, with an aglycosylated polypeptide having cellobiase activity comprising the amino acid sequence of SEQ ID NO: 1, and a microorganism that produces one or

more biomass-degrading enzyme or an enzyme mixture comprising biomass-degrading enzymes under conditions suitable for the production of the product.

23. A method of producing a product (e.g., a hydrogen, a sugar, an alcohol) from a biomass comprising contacting a biomass with an enzyme mixture of any one of claims 16-21 under conditions suitable for the production of the product.

24. The method of claim 22 or 23, wherein said product is a sugar product, optionally further comprising isolating the sugar product, wherein the isolating of the sugar product comprises precipitation, crystallization, chromatography, centrifugation, or extraction, and optionally wherein the sugar product is glucose and/or xylose.

25. The method of any one of claims 22-24, wherein the enzyme mixture comprises at least two of the enzymes selected from the group consisting of B2AF03, CIP1, CIP2, Cella, Cel3a, Cel5a, Cel6a, Cel7a, Cel7b, Cel12a, Cel45a, Cel74a, paMan5a, paMan26a, and Swollenin.

26. The method of any one of claims 22-25, wherein the biomass comprises one or more of an agricultural product or waste, a paper product or waste, a forestry product, or a general waste, or any combination thereof; wherein:

a) an agricultural product or waste comprises sugar cane, jute, hemp, flax, bamboo, sisal, alfalfa, hay, arracacha, buckwheat, banana, barley, cassava, kudzu, oca, sago, sorghum, potato, sweet potato, taro, yams, beans, favas, lentils, peas, grasses, switchgrass, miscanthus, cord grass, reed canary grass, grain residues, canola straw, wheat straw, barley straw, oat straw, rice straw, com cobs, com stover, com fiber, coconut hair, beet pulp, bagasse, soybean stover, grain residues, rice hulls, oat hulls, wheat chaff, barley hulls, or beeswing, or a combination thereof;

b) a paper product or waste comprises paper, pigmented papers, loaded papers, coated papers, filled papers, magazines, printed matter, printer paper, polycoated paper, cardstock, cardboard, paperboard, or paper pulp, or a combination thereof;

c) a forestry product comprises aspen wood, patticle board, wood chips, or sawdust, or a combination thereof; and

d) a general waste comprises manure, sewage, or offal, or a combination thereof.

27. The method of any one of claims 22-26, further comprising a step of treating the biomass prior to introducing the microorganism or the enzyme mixture to reduce the recalcitrance of the biomass, wherein the treating comprises bombardment with electrons, sonication, oxidation, pyrolysis, steam explosion, chemical treatment, mechanical treatment, or freeze grinding.

28. The method of any one of claims 22-27 wherein the microorganism that produces a biomass-degrading enzyme is from species in the genera selected from *Bacillus, Coprinus, Myceliophthora, Cephalosporium, Scytalidium, Penicillium, Aspergillus, Pseudomonas, Humicola, Fusarium, Thielavia, Acremonium, Chrysosporium* or *Trichoderma.*

29. The method of any one of claims 22-28, wherein the microorganism that produces a biomass-degrading enzyme is selected from *Aspergillus, Hwnicola insolens (Scytalidium thermophilum) Coprinus cinereus, Fusarium oxysporum, Myceliophthora thermophila, Meripilus giganteus, Thielavia terrestris, Acremonium persicinum, Acremonium acremonium, Acremonium brachypenium, Acremonium dichromosporum, Acremonium obclavatum, Acremonium pinkertoniae, Acremonium roseogriseum, Acremonium incoloratum, Acremoniumfitratum, Cluysosporium lucknowense, Trichoderma viride, Trichoderma reesei,* or *Trichoderma koningii.*

30. The method of any one of claims 22-29, wherein the microorganism has been induced to produce a biomass-degrading enzyme by combining the microorganism with an induction biomass sample under conditions suitable for increasing production of a biomass-degrading enzyme compared to an uninduced microorganism.

31. The method of claim 30, wherein said induction biomass sample comprises paper, paper products, paper waste, paper pulp, pigmented papers, loaded papers, coated papers, filled papers, magazines, printed matter, printer paper, polycoated paper, card stock, cardboard, paperboard, cotton, wood, particle board, forestry wastes, sawdust, aspen wood, wood chips, grasses, switchgrass, miscanthus, cord grass, reed canary grass, grain residues, rice hulls, oat hulls, wheat chaff, barley hulls, agricultural waste, silage, canola straw, wheat straw, barley straw, oat straw, rice straw, jute, hemp, flax, bamboo, sisal, abaca, com cobs, com stover, soybean stover, com fiber, alfalfa, hay,

coconut hair, sugar processing residues, bagasse, beet pulp, agave bagasse, algae, seaweed, manure, sewage, offal, agricultural or industrial waste, arracacha, buckwheat, banana, barley, cassava, kudzu, oca, sago, sorghum, potato, sweet potato, taro, yams, beans, favas, lentils, peas, or any combination thereof.