CLAIMS

1. An isolated polypeptide that is distinguished from a wild-type hydrolase enzyme by at least one amino acid substitution, wherein the at least one amino acid substitution is at a position corresponding to position 202, 247, 207, 210, 64, 90, 92, 154, 61 or 212 of SEQ ID NO: 1, wherein the wild-type hydrolase enzyme comprises an amino acid sequence having at least 85% sequence identity to an amino acid sequence in SEQ ID NO: 1–7, and wherein the polypeptide is capable of degrading a polyester.

2. The polypeptide of claim 1, wherein the polypeptide further comprises one or more amino acid substitutions at a position corresponding to position 4, 30, 31, 95, 136, 217, 220 or 246 of SEQ ID NO: 1; and/or
wherein the polypeptide comprises an amino acid substitution at positions corresponding to one of the following sets of positions of SEQ ID NO: 1:
   (a) 202 and 247;
   (b) 202, 207 and 247;
   (c) 202, 210 and 247;
   (d) 202, 207, 210 and 247;
   (e) 4, 202, 207, 210 and 247;
   (f) 30, 202, 207, 210 and 247;
   (g) 31, 202, 207, 210 and 247;
   (h) 61, 202, 207, 210 and 247;
   (i) 64, 202, 207, 210 and 247;
   (j) 90, 202, 207, 210 and 247;
   (k) 92, 202, 207, 210 and 247;
   (l) 95, 202, 207, 210 and 247;
   (m) 136, 202, 207, 210 and 247;
   (n) 154, 202, 207, 210 and 247;
   (o) 202, 207, 210, 212 and 247;
   (p) 202, 207, 210, 217 and 247;
   (q) 202, 207, 210, 220 and 247;
   (r) 202, 207, 210, 246 and 247;
   (s) 64, 90, 92, 136 and 154;

(t) 4, 64, 90, 92, 136 and 154;

(u) 30, 64, 90, 92, 136 and 154;

(v) 31, 64, 90, 92, 136 and 154;

(w) 61, 64, 90, 92, 136 and 154;

(x) 64, 90, 92, 95, 136 and 154;

(y) 64, 90, 92, 136, 154 and 212;

(z) 64, 90, 92, 136, 154 and 217;

(aa) 64, 90, 92, 136, 154 and 220;

(bb) 64, 90, 92, 136, 154 and 246;

(cc) 64, 90, 92, 136, 154, 202 and 247;

(dd) 64, 90, 92, 136, 154, 202, 207 and 247;

(ee) 64, 90, 92, 136, 154, 202, 210 and 247;

(ff) 64, 90, 92, 136, 154, 202, 207, 210 and 247;

(gg) 4, 30, 31, 61, 95, 212, 217, 220 and 246;

(hh) 4, 30, 31, 61, 64, 95, 212, 217, 220 and 246;

(ii) 4, 30, 31, 61, 90, 95, 212, 217, 220 and 246;

(jj) 4, 30, 31, 61, 92, 95, 212, 217, 220 and 246;

(kk) 4, 30, 31, 61, 95, 136, 212, 217, 220 and 246;

(ll) 4, 30, 31, 61, 95, 154, 212, 217, 220 and 246;

(mm) 4, 30, 31, 61, 95, 202, 212, 217, 220, 246 and 247;

(nn) 4, 30, 31, 61, 95, 207, 212, 217, 220 and 246;

(oo) 4, 30, 31, 61, 95, 210, 212, 217, 220 and 246;

(pp) 4, 64, 90, 92, 136, 154, 202, 207, 210 and 247;

(qq) 30, 64, 90, 92, 136, 154, 202, 207, 210 and 247;

(rr) 31, 64, 90, 92, 136, 154, 202, 207, 210 and 247;

(ss) 61, 64, 90, 92, 136, 154, 202, 207, 210 and 247;

(tt) 64, 90, 92, 95, 136, 154, 202, 207, 210 and 247;

(uu) 64, 90, 92, 136, 154, 202, 207, 210, 212 and 247;

(vv) 64, 90, 92, 136, 154, 202, 207, 210, 217 and 247;

(ww) 64, 90, 92, 136, 154, 202, 207, 210, 220 and 247;

(xx) 64, 90, 92, 136, 154, 202, 207, 210, 246 and 247;

(yy) 4, 30, 31, 61, 95, 202, 207, 210, 212, 217, 220, 246 and 247;

(zz) 4, 30, 31, 61, 64, 90, 92, 95, 136, 154, 212, 217, 220 and 246; and

(aaa) 4, 30, 31, 61, 64, 90, 92, 95, 136, 154, 202, 207, 210, 212, 217, 220, 246 and 247.

3. The polypeptide of claim 1 or 2, wherein the polypeptide comprises one or more amino acid substitutions selected from the following:

(a) a substitution to K, L or I at a position corresponding to position 4 of SEQ ID NO: 1;

(b) a substitution to G, A, V or S at a position corresponding to position 30 of SEQ ID NO: 1;

(c) a substitution to G, A, V, S or T at a position corresponding to position 31 of SEQ ID NO: 1;

(d) a substitution to G, A, V, I or S at a position corresponding to position 61 of SEQ ID NO: 1;

(e) a substitution to G, A, V, I, L or S at a position corresponding to position 64 of SEQ ID NO: 1;

(f) a substitution to M, S, T, F, Y, W, D or E at a position corresponding to position 90 of SEQ ID NO: 1;

(g) a substitution to G, A, V, I, L, S, M, P, F, Y, W or N at a position corresponding to position 92 of SEQ ID NO: 1;

(h) a substitution to G, A, V, I or T at a position corresponding to position 95 of SEQ ID NO: 1;

(i) a substitution to G, A, V, S, H, R or K at a position corresponding to position 136 of SEQ ID NO: 1;

(j) a substitution to G, A, S, T or H at a position corresponding to position 154 of SEQ ID NO: 1;

(k) a substitution to C or A at a position corresponding to position 202 of SEQ ID NO: 1;

(l) a substitution to G, A, V, I, L, S, M, T, P, F, Y or W at a position corresponding to position 207 of SEQ ID NO: 1;

(m) a substitution to G, A, V, I, L, S or M at a position corresponding to position 210 of SEQ ID NO: 1;

(n) a substitution to G, A, V, I, L or S at a position corresponding to position 212 of SEQ ID NO: 1;

(o) a substitution to A, V, I, S or T at a position corresponding to position 217 of SEQ

ID NO: 1;

(p) a substitution to V, I, L, S or T at a position corresponding to position 220 of SEQ ID NO: 1;

(q) a substitution to G, A, V or S at a position corresponding to position 246 of SEQ ID NO: 1; and

(r) a substitution to C or A at a position corresponding to position 247 of SEQ ID NO: 1; optionally

wherein the polypeptide comprises one or more amino acid substitutions selected from the following:

(a) a K substitution at a position corresponding to position 4 of SEQ ID NO: 1;

(b) a A substitution at a position corresponding to position 30 of SEQ ID NO: 1;

(c) a A substitution at a position corresponding to position 31 of SEQ ID NO: 1;

(d) a G substitution at a position corresponding to position 61 of SEQ ID NO: 1;

(e) a A substitution at a position corresponding to position 64 of SEQ ID NO: 1;

(f) a F substitution at a position corresponding to position 90 of SEQ ID NO: 1;

(g) a Y or G substitution at a position corresponding to position 92 of SEQ ID NO: 1;

(h) a A substitution at a position corresponding to position 95 of SEQ ID NO: 1;

(i) a R substitution at a position corresponding to position 136 of SEQ ID NO: 1;

(j) a H substitution at a position corresponding to position 154 of SEQ ID NO: 1;

(k) a C substitution at positions corresponding to positions 202 and 247 of SEQ ID NO: 1;

(l) a I substitution at a position corresponding to position 207 of SEQ ID NO: 1;

(m) a M substitution at a position corresponding to position 210 of SEQ ID NO: 1;

(n) a A substitution at a position corresponding to position 212 of SEQ ID NO: 1;

(o) a A substitution at a position corresponding to position 217 of SEQ ID NO: 1;

(p) a V substitution at a position corresponding to position 220 of SEQ ID NO: 1; and

(q) a A substitution at a position corresponding to position 246 of SEQ ID NO: 1.

4. The polypeptide of claim 3, wherein the polypeptide comprises one or more of the following amino acid substitutions:

(a) a C substitution at positions corresponding to positions 202 and 247 of SEQ ID NO: 1;

(b) a I substitution at a position corresponding to position 207 of SEQ ID NO: 1; and

(c) a M substitution at a position corresponding to position 210 of SEQ ID NO: 1; and/or wherein the polypeptide comprises one or more of the following amino acid substitutions:
(d) a A substitution at a position corresponding to position 64 of SEQ ID NO: 1;
(e) a F substitution at a position corresponding to position 90 of SEQ ID NO: 1;
(f) a Y or G substitution at a position corresponding to position 92 of SEQ ID NO: 1;
(g) a R substitution at a position corresponding to position 136 of SEQ ID NO: 1; and
(h) a H substitution at a position corresponding to position 154 of SEQ ID NO: 1; and/or wherein the polypeptide comprises one or more of the following amino acid substitutions:
(i) a K substitution at a position corresponding to position 4 of SEQ ID NO: 1;
(j) a A substitution at a position corresponding to position 30 of SEQ ID NO: 1;
(k) a A substitution at a position corresponding to position 31 of SEQ ID NO: 1;
(l) a G substitution at a position corresponding to position 61 of SEQ ID NO: 1;
(m) a A substitution at a position corresponding to position 95 of SEQ ID NO: 1;
(n) a A substitution at a position corresponding to position 212 of SEQ ID NO: 1;
(o) an A substitution at a position corresponding to position 217 of SEQ ID NO: 1;
(p) a V substitution at a position corresponding to position 220 of SEQ ID NO: 1; and
(q) an A substitution at a position corresponding to position 246 of SEQ ID NO: 1.

5. The polypeptide of any one of claims 1 to 4, wherein the polypeptide comprises an amino acid sequence with at least 85% sequence identity to an amino acid sequence set forth in SEQ ID NO: 14–30.

6. The polypeptide of any one of claims 1 to 5, wherein the polypeptide is capable of degrading PET.

7. The polypeptide of any one of claims 1 to 6, wherein the polypeptide comprises a fusion partner, optionally wherein the fusion partner comprises an amino acid sequence set forth in any one of SEQ ID NO: 31–37.

8. An isolated polypeptide comprising an amino acid sequence having at least 85% sequence identity to an amino acid sequence set forth in SEQ ID NO: 1, SEQ ID NO: 2, SEQ ID NO: 3 or SEQ ID NO: 4, SEQ ID NO: 5, SEQ ID NO: 6 or SEQ ID NO: 7, wherein the polypeptide has hydrolase activity.

9. The polypeptide of claim 8, wherein the polypeptide comprises an amino acid sequence set forth in SEQ ID NO: 1, SEQ ID NO: 2, SEQ ID NO: 3 or SEQ ID NO: 4, SEQ ID NO: 5, SEQ ID NO: 6, or SEQ ID NO: 7, and/or wherein the polypeptide further comprises an amino acid substitution at one or more positions corresponding to position 4, 30, 31, 61, 64, 90, 92, 95, 136, 154, 202, 207, 210, 212, 217, 220, 246 or 247 of SEQ ID NO: 1.
10. A polynucleotide encoding a polypeptide of any one of claims 1 to 9.

11. An expression vector comprising a polynucleotide of claim 10.

12. A host cell comprising a polynucleotide of claim 10 or an expression vector of claim 11.

13. A method of producing a polypeptide of any one of claims 1 to 9, comprising culturing a host cell of claim 12 under conditions suitable for expressing the polypeptide, optionally wherein the method further comprises recovering the polypeptide from the cell culture.

14. The method of claim 13, wherein the polypeptide is secreted extracellularly.

15. A method of degrading a product comprising at least one polyester, the method comprising contacting the product with a polypeptide of any one of claims 1 to 9 and/or with a cell expressing a polypeptide of any one of claims 1 to 9, under conditions suitable for degrading the at least one polyester, optionally wherein the polyester is selected from the group consisting of polyethylene terephthalate (PET), polytrimethylene terephthalate (PTT), polybutylene terephthalate (PBT), polyethylene isosorbide terephthalate (PEIT), polylactic acid (PLA), polyhydroxyalkanoate (PHA), polyethylene succinate (PES), polybutylene succinate (PBS), polybutylene succinate adipate (PBSA), polybutylene adipate terephthalate (PBAT), polyethylene furanoate (PEF), polycaprolactone (PCL), polyethylene adipate (PEA) and polyethylene naphthalate (PEN), polycyclohexylenedimethylene terephthalate (PCT), and co-polymers thereof, optionally wherein the polyester is PET.

16. A kit, comprising a polypeptide according to any one of claims 1 to 9.