**Table S1.** Codon usage of PCWDEs characterised in this study compared to those obtained from whole beetle transcriptomes, model insects (*T. castaneum* and *D. melanogaster*) and representatives of microbes (*Nocema Bombycis*, *Saccharomyces cerevisiae* and *Wolbachia*). The preferred codon(s) for each amino acid is highlighted in red.

| #Codon (amino acid) | PCWDEs | C.maculatus | C.tremulae | G.viridula | L.decemlineata | S.oryzae | T.castaneum | D.melanogaster | Nosema | S.cerevisiae | Wolbachia |
|---|---|---|---|---|---|---|---|---|---|---|---|
| GCA (A) | **0,287** | **0,346** | **0,352** | **0,361** | **0,348** | **0,322** | **0,329** | **0,314** | 0,27 | **0,29** | **0,387** |
| GCC (A) | 0,236 | 0,201 | 0,219 | 0,204 | 0,211 | 0,215 | 0,2 | 0,234 | 0,22 | 0,22 | 0,146 |
| GCG (A) | 0,161 | 0,132 | 0,116 | 0,128 | 0,127 | 0,145 | 0,197 | 0,187 | 0,15 | 0,11 | 0,11 |
| GCT (A) | **0,316** | **0,321** | **0,312** | **0,306** | **0,314** | **0,318** | **0,274** | **0,265** | **0,36** | **0,38** | **0,357** |
| TGC (C) | 0,414 | 0,392 | 0,38 | 0,362 | 0,376 | 0,351 | 0,361 | 0,483 | 0,26 | 0,37 | **0,503** |
| TGT (C) | **0,586** | **0,608** | **0,62** | **0,638** | **0,624** | **0,649** | **0,639** | **0,517** | **0,74** | **0,63** | 0,497 |
| GAC (D) | 0,433 | 0,381 | 0,346 | 0,347 | 0,366 | 0,373 | 0,407 | 0,416 | 0,26 | 0,35 | 0,273 |
| GAT (D) | **0,567** | **0,619** | **0,654** | **0,653** | **0,634** | **0,627** | **0,593** | **0,584** | **0,74** | **0,65** | **0,727** |
| GAA (E) | **0,65** | **0,66** | **0,68** | **0,682** | **0,678** | **0,689** | **0,698** | **0,611** | **0,72** | **0,7** | **0,668** |
| GAG (E) | 0,35 | 0,34 | 0,32 | 0,318 | 0,322 | 0,311 | 0,302 | 0,389 | 0,28 | 0,3 | 0,332 |
| TTC (F) | 0,477 | 0,358 | 0,386 | 0,41 | 0,387 | 0,315 | 0,251 | 0,327 | 0,26 | 0,41 | 0,316 |
| TTT (F) | **0,523** | **0,642** | **0,614** | **0,59** | **0,613** | **0,685** | **0,749** | **0,673** | **0,74** | **0,59** | **0,684** |
| GGA (G) | **0,376** | **0,337** | **0,356** | **0,364** | **0,359** | **0,341** | **0,305** | **0,286** | **0,4** | 0,22 | **0,33** |
| GGC (G) | 0,198 | 0,203 | 0,185 | 0,185 | 0,184 | 0,197 | 0,213 | 0,273 | 0,12 | 0,19 | 0,201 |
| GGG (G) | 0,178 | 0,167 | 0,186 | 0,169 | 0,177 | 0,17 | 0,192 | 0,214 | 0,22 | 0,12 | 0,145 |
| GGT (G) | 0,248 | 0,292 | 0,274 | 0,282 | 0,28 | 0,292 | 0,29 | 0,227 | 0,17 | **0,47** | **0,324** |
| CAC (H) | 0,44 | 0,387 | 0,372 | 0,366 | 0,378 | 0,377 | 0,43 | 0,443 | 0,31 | 0,36 | 0,366 |
| CAT (H) | **0,56** | **0,613** | **0,628** | **0,634** | **0,622** | **0,623** | **0,57** | **0,557** | **0,69** | **0,64** | **0,634** |
| ATA (I) | 0,312 | 0,358 | 0,339 | 0,355 | 0,335 | 0,366 | 0,314 | 0,337 | 0,33 | 0,27 | 0,377 |
| ATC (I) | 0,315 | 0,244 | 0,24 | 0,24 | 0,241 | 0,207 | 0,171 | 0,222 | 0,16 | 0,26 | 0,213 |
| ATT (I) | **0,373** | **0,398** | **0,421** | **0,405** | **0,424** | **0,427** | **0,515** | **0,441** | **0,51** | **0,46** | **0,41** |
| AAA (K) | **0,612** | **0,665** | **0,674** | **0,676** | **0,683** | **0,712** | **0,963** | **0,819** | **0,69** | **0,58** | **0,667** |
| AAG (K) | 0,388 | 0,335 | 0,326 | 0,324 | 0,317 | 0,288 | 0,037 | 0,181 | 0,31 | 0,42 | 0,333 |
| CTA (L) | 0,134 | 0,13 | 0,12 | 0,127 | 0,115 | 0,127 | 0,107 | 0,104 | 0,11 | 0,14 | 0,136 |
| CTC (L) | 0,14 | 0,107 | 0,117 | 0,12 | 0,121 | 0,093 | 0,086 | 0,124 | 0,06 | 0,06 | 0,095 |
| CTG (L) | 0,202 | 0,15 | 0,146 | 0,148 | 0,147 | 0,125 | 0,094 | 0,151 | 0,07 | 0,11 | 0,11 |
| CTT (L) | 0,158 | 0,187 | 0,184 | 0,179 | 0,19 | 0,182 | 0,165 | 0,175 | 0,21 | 0,13 | 0,205 |

| | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|
| TTA (L) | 0,161 | 0,207 | 0,195 | 0,188 | 0,196 | 0,27 | **0,325** | **0,223** | **0,38** | **0,28** | **0,259** |
| TTG (L) | **0,206** | **0,219** | **0,238** | **0,239** | **0,231** | **0,203** | 0,222 | **0,223** | 0,17 | **0,29** | 0,195 |
| ATG (M) | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 |
| AAC (N) | 0,435 | 0,398 | 0,362 | 0,356 | 0,382 | 0,367 | 0,334 | 0,373 | 0,27 | 0,41 | 0,338 |
| AAT (N) | **0,565** | **0,602** | **0,638** | **0,644** | **0,618** | **0,633** | **0,666** | **0,627** | **0,73** | **0,59** | **0,662** |
| CCA (P) | **0,398** | **0,389** | **0,405** | **0,401** | **0,39** | **0,379** | **0,345** | **0,354** | **0,33** | **0,42** | **0,398** |
| CCC (P) | 0,188 | 0,167 | 0,186 | 0,167 | 0,178 | 0,171 | 0,191 | 0,213 | 0,13 | 0,15 | 0,152 |
| CCG (P) | 0,16 | 0,13 | 0,117 | 0,131 | 0,135 | 0,15 | 0,207 | 0,202 | 0,16 | 0,12 | 0,104 |
| CCT (P) | 0,255 | 0,314 | 0,291 | 0,301 | 0,297 | 0,3 | 0,257 | 0,231 | **0,38** | 0,31 | 0,346 |
| CAA (Q) | **0,629** | **0,591** | **0,616** | **0,619** | **0,615** | **0,62** | **0,702** | **0,598** | **0,69** | **0,69** | **0,644** |
| CAG (Q) | 0,371 | 0,409 | 0,384 | 0,381 | 0,385 | 0,38 | 0,298 | 0,402 | 0,31 | 0,31 | 0,356 |
| AGA (R) | **0,252** | **0,342** | **0,372** | **0,359** | **0,346** | **0,339** | **0,261** | **0,225** | **0,48** | **0,48** | **0,406** |
| AGG (R) | 0,219 | 0,208 | 0,211 | 0,19 | 0,198 | 0,186 | 0,144 | 0,16 | 0,24 | 0,21 | 0,211 |
| CGA (R) | 0,167 | 0,146 | 0,151 | 0,175 | 0,165 | 0,158 | 0,192 | 0,182 | 0,1 | 0,07 | 0,104 |
| CGC (R) | 0,087 | 0,087 | 0,071 | 0,073 | 0,073 | 0,084 | 0,117 | 0,151 | 0,04 | 0,06 | 0,093 |
| CGG (R) | 0,134 | 0,084 | 0,086 | 0,081 | 0,09 | 0,093 | 0,115 | 0,14 | 0,06 | 0,04 | 0,066 |
| CGT (R) | 0,141 | 0,134 | 0,109 | 0,122 | 0,128 | 0,14 | 0,17 | 0,142 | 0,08 | 0,14 | 0,12 |
| | | | | | | | | | | | |
| **#Codon (amino acid)** | **PCWDEs** | **C.maculatus** | **C.tremulae** | **G.viridula** | **L.decemlineata** | **S.oryzae** | **T.castaneum** | **D.melanogaster** | **Nosema** | **S.cerevisiae** | **Wolbachia** |
| AGC (S) | 0,147 | 0,14 | 0,12 | 0,108 | 0,114 | 0,123 | 0,119 | 0,169 | 0,07 | 0,11 | 0,168 |
| AGT (S) | 0,17 | 0,185 | 0,177 | 0,181 | 0,178 | 0,193 | 0,2 | 0,171 | 0,25 | 0,16 | 0,195 |
| TCA (S) | **0,25** | **0,228** | **0,253** | **0,261** | **0,243** | **0,21** | **0,225** | **0,187** | 0,21 | **0,21** | 0,221 |
| TCC (S) | 0,15 | 0,139 | 0,146 | 0,133 | 0,149 | 0,142 | 0,125 | 0,156 | 0,08 | 0,16 | 0,121 |
| TCG (S) | 0,111 | 0,094 | 0,09 | 0,107 | 0,102 | 0,106 | 0,14 | 0,143 | 0,09 | 0,1 | 0,06 |
| TCT (S) | 0,172 | 0,214 | 0,214 | 0,211 | 0,214 | **0,226** | 0,191 | 0,174 | **0,3** | **0,26** | **0,235** |
| ACA (T) | **0,306** | **0,367** | **0,37** | **0,381** | **0,36** | **0,361** | **0,365** | **0,347** | 0,32 | 0,3 | 0,322 |
| ACC (T) | 0,222 | 0,2 | 0,212 | 0,184 | 0,198 | 0,192 | 0,17 | 0,199 | 0,14 | 0,22 | 0,204 |
| ACG (T) | 0,186 | 0,142 | 0,124 | 0,133 | 0,134 | 0,149 | 0,178 | 0,179 | 0,19 | 0,14 | 0,115 |
| ACT (T) | 0,287 | 0,291 | 0,294 | 0,302 | 0,308 | 0,298 | 0,287 | 0,275 | **0,35** | **0,35** | **0,359** |
| GTA (V) | 0,236 | 0,273 | 0,255 | 0,269 | 0,254 | 0,28 | 0,245 | 0,225 | 0,33 | 0,21 | 0,317 |
| GTC (V) | 0,215 | 0,187 | 0,18 | 0,183 | 0,186 | 0,178 | 0,172 | 0,196 | 0,14 | 0,21 | 0,131 |

| | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|
| GTG (V) | 0,23 | 0,213 | 0,224 | 0,222 | 0,205 | 0,186 | 0,205 | 0,257 | 0,18 | 0,19 | 0,201 |
| GTT (V) | **0,318** | **0,327** | **0,341** | **0,326** | **0,355** | **0,356** | **0,378** | **0,322** | **0,35** | **0,39** | **0,351** |
| TGG (W) | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 |
| TAC (Y) | 0,464 | 0,378 | 0,341 | 0,346 | 0,356 | 0,348 | 0,348 | 0,351 | 0,38 | 0,44 | 0,335 |
| TAT (Y) | **0,536** | **0,622** | **0,659** | **0,654** | **0,644** | **0,652** | **0,652** | **0,649** | **0,62** | **0,56** | **0,665** |
| TAA (*) | 0,385 | **0,384** | 0,355 | 0,333 | 0,37 | **0,479** | **0,544** | **0,458** | **0,7** | **0,47** | **0,466** |
| TAG (*) | 0,193 | 0,243 | 0,221 | 0,226 | 0,216 | 0,226 | 0,179 | 0,212 | 0,1 | 0,23 | 0,241 |
| TGA (*) | **0,422** | 0,373 | **0,424** | **0,441** | **0,413** | 0,295 | 0,277 | 0,33 | 0,2 | 0,3 | 0,293 |

**Table S2.** Codon usage of PCWDEs characterised in this study compared to those obtained from whole beetle transcriptomes, model insects (*T. castaneum* and *D. melanogaster*) and representatives of microbes (*Nocema Bombycis*, *Saccharomyces cerevisiae* and *Wolbachia*). The data are expressed in relative synonymous codon usage (RSCU) values. RSCU values lower than 1 indicate that a codon is avoided and values higher than 1 indicates the given codon is preferred. A higher RSCU value indicates a higher preference for the particular codon. The preferred codon(s) for each amino acid is highlighted in red.

| #Codon (amino acid) | PCWDEs | C.maculatus | C.tremulae | G.viridula | L.decemlineata | S.oryzae | T.castaneum | D.melanogaster | Nosema | S.cerevisiae | Wolbachia |
|---|---|---|---|---|---|---|---|---|---|---|---|
| GCA (A) | **4** | **4** | **5** | **5** | **5** | **3** | **2** | **5** | 3 | 5 | **7** |
| GCC (A) | 2 | 2 | 1 | 1 | 1 | 1 | 1 | 3 | 2 | 3 | 1 |
| GCG (A) | 1 | 1 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 |
| GCT (A) | **4** | **4** | 3 | 3 | 3 | **3** | **2** | 4 | **7** | **10** | **7** |
| TGC (C) | 6 | 6 | 5 | 5 | 5 | 5 | 3 | 8 | 1 | 2 | **15** |
| TGT (C) | **17** | **17** | **18** | **20** | **19** | **19** | **13** | **17** | **112** | **8** | 7 |
| GAC (D) | 7 | 7 | 4 | 5 | 4 | 4 | 3 | 4 | 4 | 10 | 2 |
| GAT (D) | **19** | **19** | **18** | **19** | **17** | **16** | **9** | **13** | **38** | **37** | **16** |
| GAA (E) | **24** | **24** | **25** | **26** | **25** | **22** | **14** | **18** | **55** | **45** | **20** |
| GAG (E) | 6 | 6 | 4 | 4 | 4 | 3 | 2 | 5 | 7 | 6 | 3 |
| TTC (F) | 9 | 9 | 12 | 12 | 12 | 7 | 4 | 6 | 4 | 9 | 7 |
| TTT (F) | **21** | **21** | **38** | **36** | **40** | **46** | **43** | **37** | **40** | **26** | **45** |
| GGA (G) | **11** | **11** | **7** | **6** | **6** | **6** | **2** | **4** | **9** | 2 | **3** |
| GGC (G) | 2 | 2 | 1 | 1 | 1 | 1 | 1 | 4 | 0 | 1 | 1 |
| GGG (G) | 2 | 2 | 1 | 1 | 1 | 1 | 0 | 2 | 2 | 0 | 0 |
| GGT (G) | 3 | 3 | 3 | 3 | 3 | 3 | **2** | 2 | 4 | **11** | **3** |
| CAC (H) | 6 | 6 | 5 | 5 | 5 | 4 | 3 | 6 | 1 | 3 | 5 |
| CAT (H) | **17** | **17** | **18** | **20** | **18** | **16** | **10** | **16** | **12** | **13** | **17** |
| ATA (I) | 6 | 6 | 12 | 13 | 12 | 14 | 5 | 10 | 9 | 5 | 15 |
| ATC (I) | 6 | 6 | 4 | 4 | 4 | 3 | 1 | 3 | 2 | 5 | 4 |
| ATT (I) | **11** | **11** | **15** | **15** | **15** | **16** | **28** | **13** | **42** | **15** | **16** |
| AAA (K) | **28** | **28** | **41** | **38** | **41** | **47** | **325** | **75** | **67** | **41** | **45** |
| AAG (K) | 9 | 9 | 6 | 6 | 6 | 6 | 0 | 3 | 10 | 15 | 11 |
| CTA (L) | 1 | 1 | 1 | 1 | 1 | 1 | 0 | 1 | 1 | 1 | 2 |

| | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|
| CTC (L) | 1 | 1 | 1 | 1 | 1 | 0 | 0 | 1 | 0 | 0 | 1 |
| CTG (L) | **3** | **3** | 2 | 2 | 2 | 1 | 0 | 2 | 0 | 1 | 1 |
| CTT (L) | 1 | 1 | 3 | 3 | 3 | 3 | 2 | 3 | 5 | 1 | 5 |
| TTA (L) | 1 | 1 | 3 | 3 | 3 | **9** | **8** | 5 | **18** | 8 | **9** |
| TTG (L) | **3** | **3** | **5** | **5** | **5** | 5 | 4 | **5** | 2 | **9** | 4 |
| ATG (M) | 18 | 18 | 19 | 20 | 18 | 16 | 10 | 16 | 22 | 20 | 16 |
| AAC (N) | 10 | 10 | 8 | 8 | 9 | 9 | 7 | 8 | 5 | 12 | 8 |
| AAT (N) | **27** | **27** | **31** | **31** | **30** | **32** | **28** | **27** | **43** | **35** | **33** |
| CCA (P) | **8** | **8** | **7** | **6** | **7** | **6** | **3** | **7** | 3 | **9** | **6** |
| CCC (P) | 1 | 1 | 1 | 1 | 1 | 1 | 0 | 2 | 0 | 1 | 0 |
| CCG (P) | 1 | 1 | 0 | 0 | 0 | 0 | 1 | 2 | 0 | 0 | 0 |
| CCT (P) | 3 | 3 | 3 | 3 | 3 | 3 | 1 | 2 | **6** | 4 | 5 |
| CAA (Q) | **27** | **27** | **24** | **23** | **23** | **21** | **16** | **21** | **18** | **13** | **22** |
| CAG (Q) | 8 | 8 | 7 | 7 | 7 | 6 | 2 | 7 | 2 | 2 | 6 |
| AGA (R) | **5** | **5** | **10** | **10** | **9** | **9** | **3** | **3** | **11** | **21** | **9** |
| AGG (R) | 3 | 3 | 2 | 2 | 2 | 2 | 0 | 1 | 2 | 4 | 2 |
| CGA (R) | 2 | 2 | 1 | 1 | 1 | 1 | 1 | 2 | 0 | 0 | 0 |
| CGC (R) | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 |
| CGG (R) | 1 | 1 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 |
| CGT (R) | 1 | 1 | 0 | 0 | 1 | 1 | 1 | 1 | 0 | 2 | 0 |

**Table S3.** Summary statistics for beetle EST datasets.

| Species | *Chrysomela tremulae* | *Leptinotarsa decemlineata* | *Gastrophysa viridula* | *Callosobruchus maculatus* | *Sitophilus oryzae* | *Diabrotica virgifera* | *Ips pini* | *Dendroctonus ponderosae* | *Diaprepes abbreviatus* | *Hypothenemus hampei* |
|---|---|---|---|---|---|---|---|---|---|---|
| Common name | Poplar leaf beetle | Colorado potato beetle | Green dock beetle | Cowpea weevil | Rice weevil | Western corn rootworm | Pine engraver | Mountain pine beetle | Diaprepes root weevil | Coffee berry borer |
| Food | Poplar leaves | Potato leaves | Dock leaves | Pulses/ beans | Rice grains | Maize roots | Pine xylem | Pine xylem | Citrus roots | Coffee beans |
| Tissue | Larval midgut | Larval midgut | Larval midgut | Whole larvae | Adult midgut | Larval midgut + adult head | Adult midgut | Adult midgut | Whole larvae | Larval midgut |
| Sequencing | 454 FLX | 454 Titanium | 454 Titanium | 454 Titanium | 454 Titanium | Sanger | Sanger | Sanger | Sanger | Sanger |
| Number of reads | 264,698 | 839,061 | 1,234,472 | 909,444 | 926,752 | 17,782 | 1,671 | 152,724 | 5,219 | 2,032 |
| Number of unique sequences after assembly | 10,910 | 21,692 | 20,817 | 32,584 | 22,989 | 7,686 | 618 | 17,528 | 1,987 | 854 |
| Number of contigs | - | - | - | - | - | 3,513 | 125 | 12,259 | 398 | 177 |
| Number of singletons | - | - | - | - | - | 4,173 | 493 | 5,269 | 1,589 | 677 |

**Table S4.** Families of beetle plant cell wall degrading enzymes identified in coleopteran-derived EST datasets.

| Family | Chrysomelidae | | | | | Curculionidae | | | | |
|---|---|---|---|---|---|---|---|---|---|---|
| Species | *Chrysomela tremulae* | *Leptinotarsa decemlineata* | *Gastrophysa viridula* | *Callosobruchus maculatus* | *Diabrotica virgifera* | *Sitophilus oryzae* | *Ips pini* | *Dendroctonus ponderosae* | *Diaprepes abbreviatus* | *Hypothenemus hampei* |
| Number of unique sequences | 23,238 | 21,692 | 20,817 | 32,584 | 7,686 | 22,989 | 618 | 17,528 | 1,987 | 854 |
| **Cellulolytic enzymes:** | | | | | | | | | | |
| Endo-β-1,4-glucanase (GH45) | **2** | **7** | **1** | - | **4** | **5** | **6** | **9** | **5** | **2** |
| Cellulose 1,4-β-cellobiosidase (GH48) | **2** | **3** | **3** | - | **1** | **2** | **3** | **6** | **1** | **2** |
| **Pectolytic enzymes:** | | | | | | | | | | |
| Endopolygalacturonase (GH28 subfamily A) | **9** | **10** | **7** | - | **3** | **7** | **2** | **19** | **4** | **2** |
| Endopolygalacturonase (GH28 subfamily B) | - | - | - | **7** | - | - | - | - | - | - |
| Pectin methylesterase (CE8) | - | - | - | - | - | **5** | **4** | **7** | **2** | - |
| Rhamnogalacturonate lyase (PL4) | - | - | - | - | - | - | **3** | **5** | - | - |
| **Other PCWDEs:** | | | | | | | | | | |
| β-mannanase (GH5 undefined subfamily) | - | - | **1** | **4** | - | - | - | - | - | - |
| β-mannanase (GH5 subfamily 7) | - | - | - | - | - | - | - | - | - | **2** |
| **Total** | **13** | **20** | **12** | **11** | **8** | **19** | **18** | **46** | **12** | **8** |

**Table S5.** cDNAs encoding beetle plant cell wall degrading enzymes identified from public databases. Genbank accession numbers are provided for each sequence.

| Super-family | **Chrysomeloidea** | | | | | **Curculionoidea** | | |
|---|---|---|---|---|---|---|---|---|
| Family | **Chrysomelidae** | | **Cerambycidae** | | | **Curculionidae** | | |
| Species | *Phaedon cochleariae* | *Gastrophysa atrocyanea* | *Apriona germari* | *Psacothea hilaris* | *Oncideres albomarginata chamela* | *Otiorhynchus sulcatus* | *Hypothenemus hampei* | *Sitophilus oryzae* |
| Common name | Mustard leaf beetle | Unknown | Mulberry longicorn beetle | Yellow-spotted longicorn beetle | Unknown | Black vine weevil | Coffee berry borer | Rice weevil |
| **Cellulolytic enzymes:** | | | | | | | | |
| Endo-β-1,4-glucanase (GH5 subfamily 2) | - | - | AAX18655.1 | BAB86867.1 | ADI24131.1 | - | - | - |
| Endo-β-1,4-glucanase (GH45) | CAA76931.1 | - | AAR22385.1<br>AAU44973.1 | - | ADI24132.1 | - | - | - |
| Cellulose 1,4-β-cellobiosidase (GH48) | - | BAE94320.1<br>BAE94321.1 | - | - | - | CAH25542.1 | - | - |
| **Pectolytic enzymes:** | | | | | | | | |
| Endopolygalacturonase (GH28) | CAA76930.1 | - | - | - | - | - | - | AAG35693.1 |
| Pectin methylesterase (CE8) | - | - | - | - | - | - | - | AAW28928.1 |
| **Other PCW degrading enzymes:** | | | | | | | | |
| β-mannanase (GH5 subfamily7) | - | - | - | - | - | - | ACU52527.1 | - |
| Xylanase (GH11) | CAA76932.1 | - | - | - | - | - | - | - |

**Figure S1.** Predicted amino acid alignment of GH48 beetle enzymes. The amino acid sequence of the cellulose Cell48F from the bacterium *Clostridium cellulolyticum*, for which the crystal structure has been resolved, is used as a reference sequence (1). The catalytic residues (predicted from the *C cellulolyticum* sequence) are marked with arrows. Glu44 (numbering according to the *C. cellulolyticum* sequence) acts as the catalytic nucleophile/base, and Glu55 is the catalytic proton donor. Note that, in *G. viridula* Cellbio-3, the residue corresponding to the catalytic nucleophile/base is an Asp residue rather than a Glu.

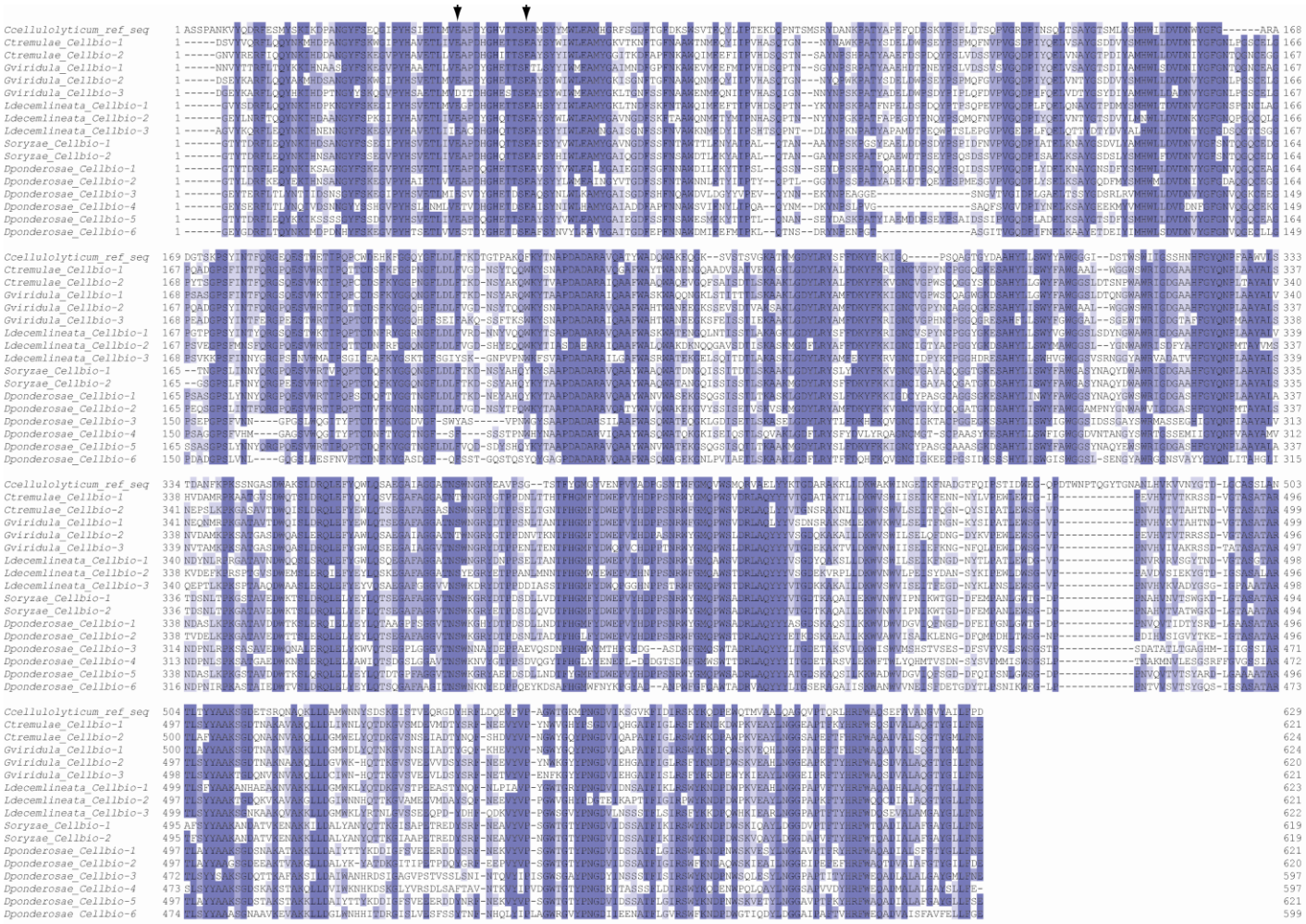


**Figure S2.** Predicted amino acid alignments of the beetle pectin methylesterases (CE8). The amino acid sequence of the pectin methylesterase from the fungus *Erwinia chrysanthemi*, for which the crystal structure has been resolved, is used as a reference sequence (2). The catalytic residues (predicted from the *E. chrysanthemi* sequence) are marked with arrows. Asp199 (numbering according to the *E. chrysanthemi* sequence) acts as the catalytic nucleophile/base, and Asp178 is the catalytic proton donor. Note that the catalytic nucleophile/base in *S. oryzae* Pectinesterase-5 is replaced by an Asn residue, suggesting a potential lack of catalytic activity for this protein.

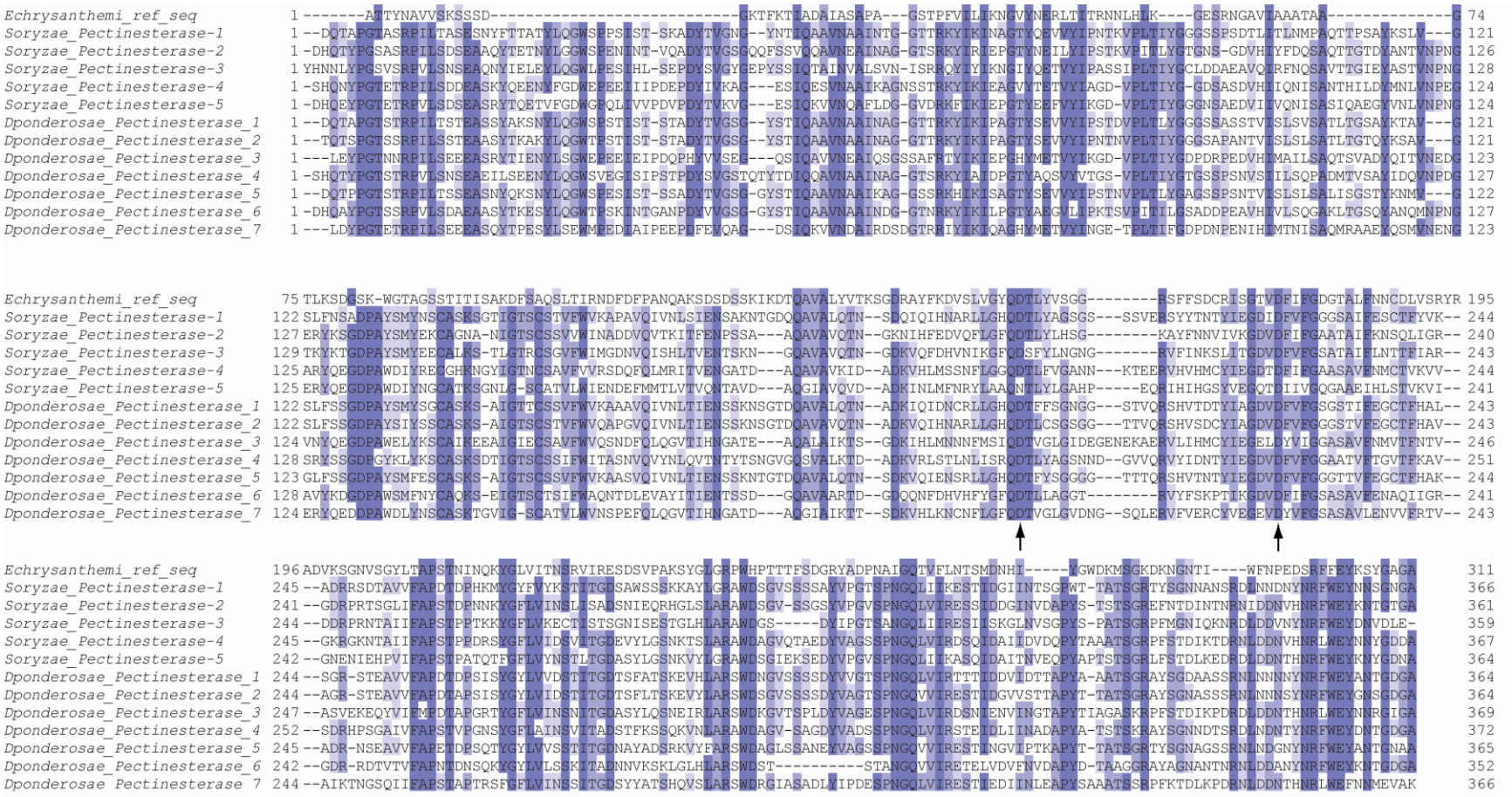


**Figure S3.** Predicted amino acid alignments of the beetle β-mannanase enzymes from a novel, unassigned, GH5 subfamily. The amino acid sequence of the β-mannanase from the Blue Mussel *Mytilus edulis*, for which the crystal structure has been resolved, is used as a reference sequence (3). The catalytic residues (predicted from *M. edulis*) are marked with arrows. Glu308 (numbering according to the *M. edulis* sequence) acts as the catalytic nucleophile/base, and Glu177 is the catalytic proton donor.

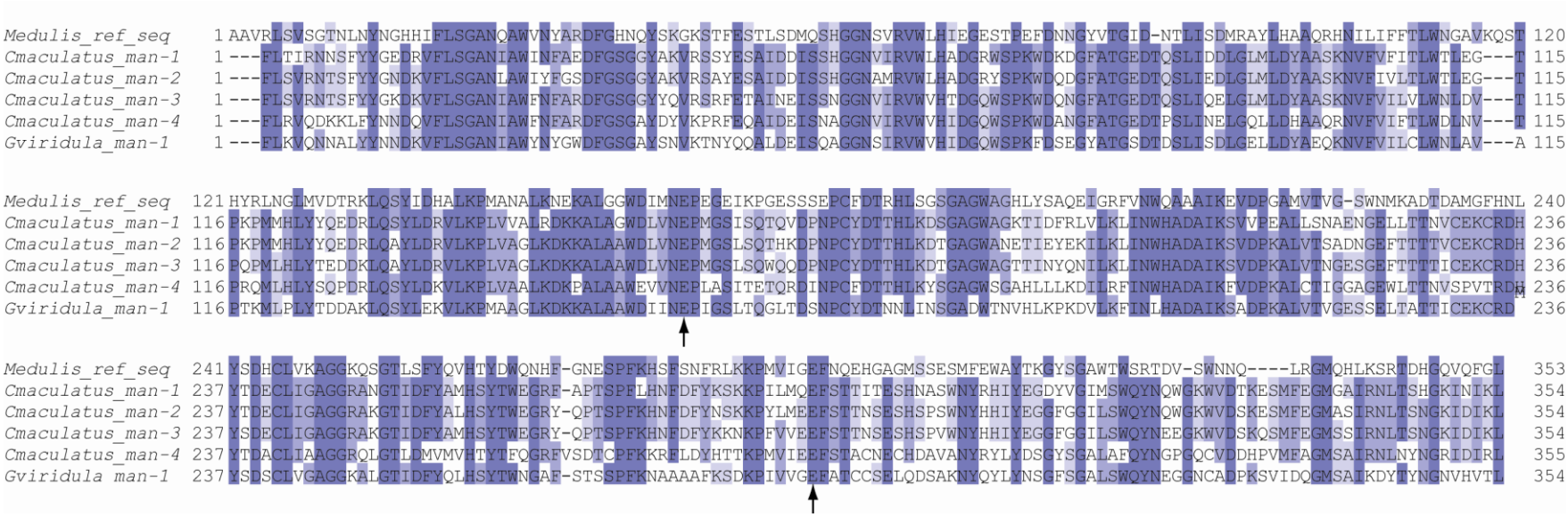
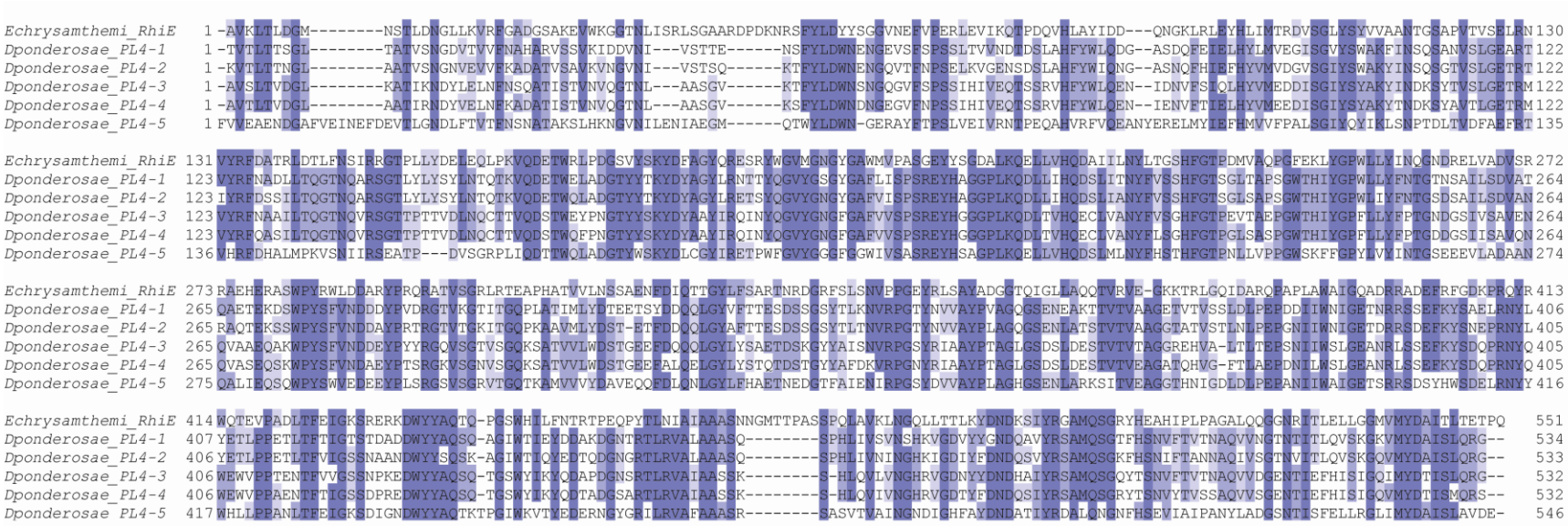


**Figure S4.** Predicted amino acid alignments of beetle-derived rhamnogalacturonate lyases (PL4). The amino acid sequence of RhiE, a rhamnose-induced protein from the plant pathogen *Erwinia chrysanthemi* harboring rhamnogalacturonate lyase activity on rhamnogalacturonan I, is used as a reference sequence (4).



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