

Figure S1. Sequence alignment of granulin and progranulin. (A) Alignment of the archetypal granulin from *Hirudo nipponia* and the progranulin identified from the *W. pigra* genome; (B) Alignment of the tandem repeats within the progranulin. Note: the archetypal granulin is a short partial segment that is located in the N-terminus of the protein.

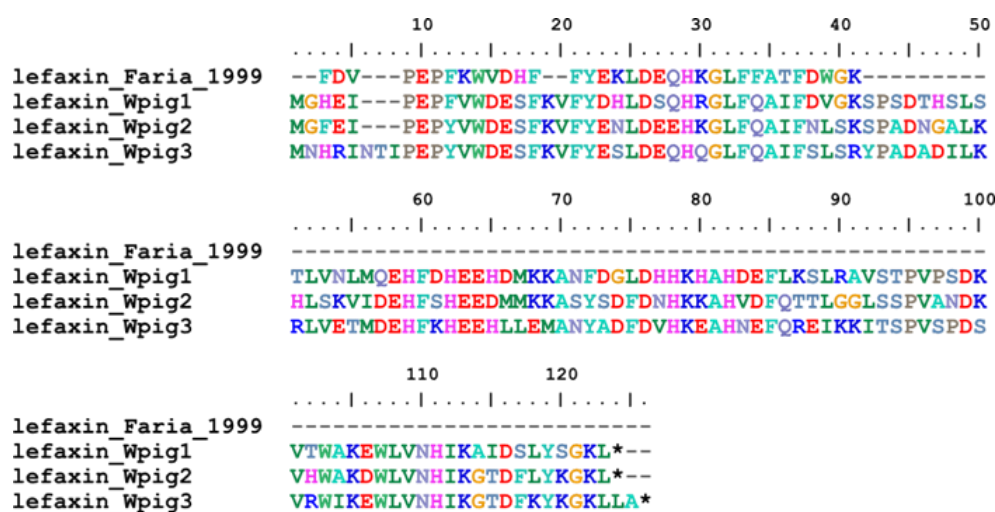


Figure S2. Sequence alignment of lefaxins. Alignment of the archetypal lefaxin first discovered from *Haementeria depressa* and the three lefaxins identified from the *W. pigra* genome.

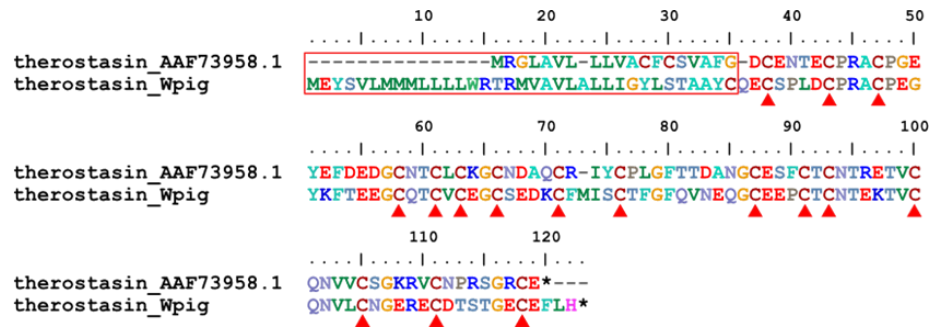


Figure S3. Sequence alignment therostasins. Alignment of the archetypal therostasin from *Theromyzon tessulatum* and the therostasin identified from the *W. pigra* genome.



Figure S4. Sequence alignment of eglins. Alignment of the archetypal eglin first discovered from *H. medicinalis* and two eglins identified from the *W. pigra* genome.

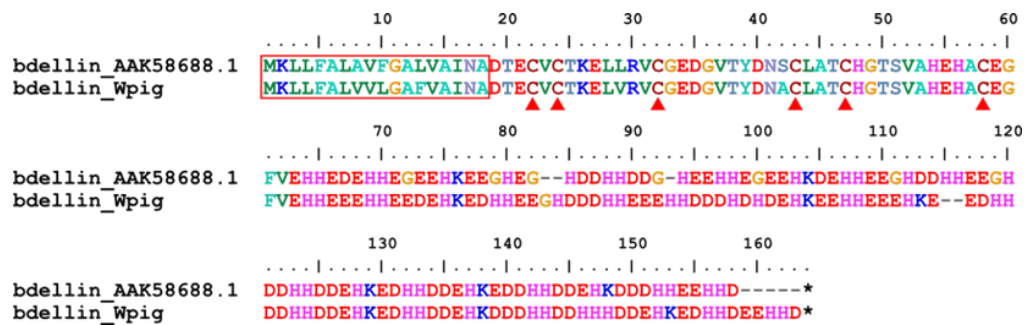


Figure S5. Sequence alignment of bdellins. Alignment of the archetypal bdellin from *H. medicinalis* and the bdellin from the *W. pigra* genome.

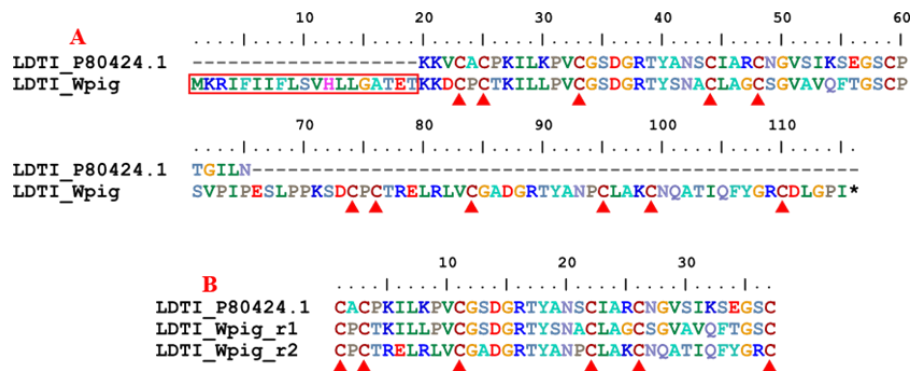


Figure S6. Sequence alignment of LDTIs. (A) Alignment of the LDTI from *H. medicinalis* and that from the *W. pigra* genome; (B) Alignment of the internal tandem repeats of the *W. pigra* LDTI.

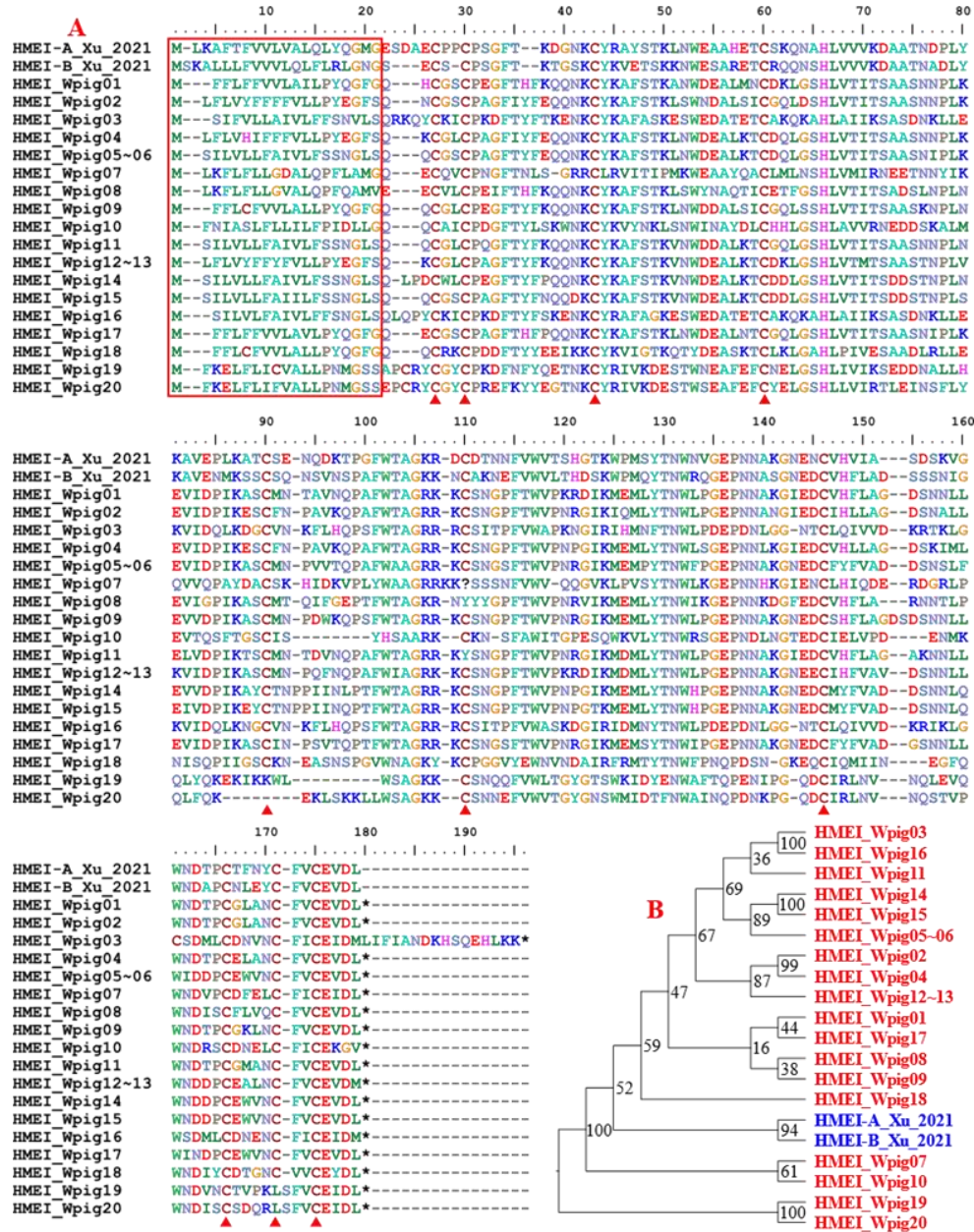
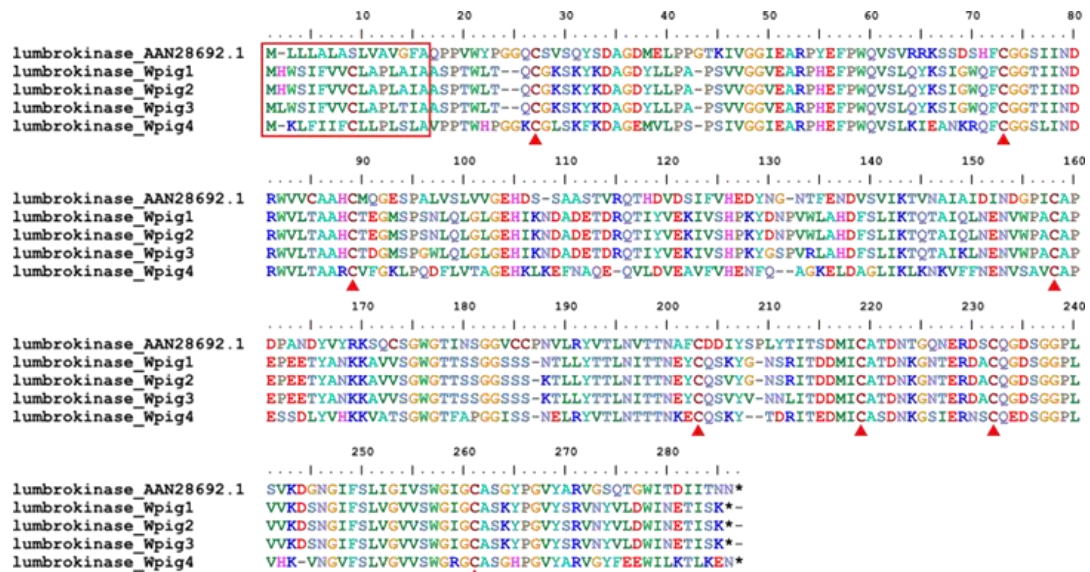
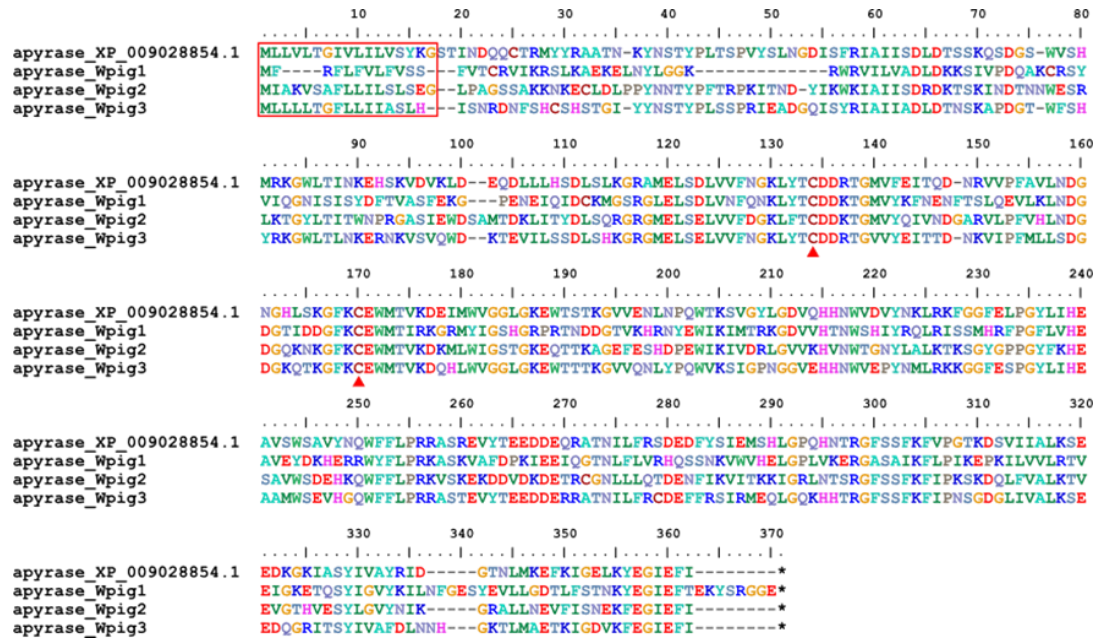


Figure S7. Sequence alignment and phylogenetic relationship of HMEIs. (A) Alignment of the HMEI-A and HMEI-B from *H. manillensis* and the HMEIs identified from the *W. pigra* genome; (B) phylogenetic relationships of the HMEIs.



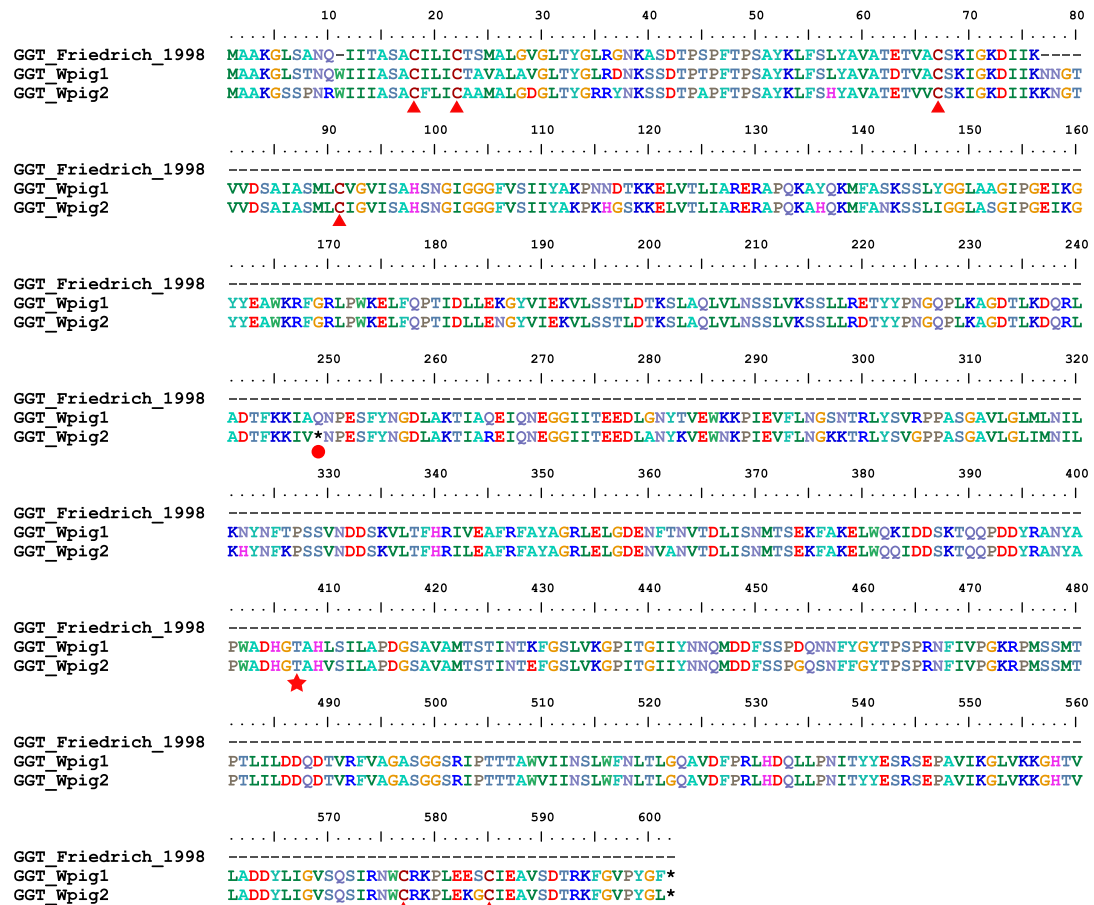


Figure S10. Sequence alignment of GGTs. Alignment of the archetypal GGT from *H. medicinalis* and those from *W. pigra* (the red dot shows the site of early termination; the red star shows the catalytic threonine).

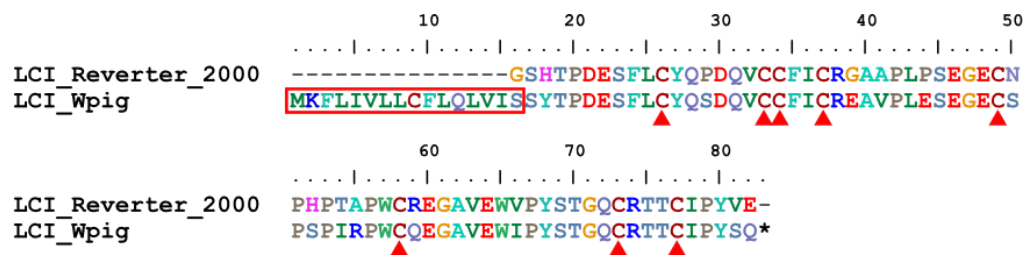


Figure S11. Sequence alignment of LCIs. Alignment of the archetypal LCI (from *H. medicinalis*) and the LCI identified from the *W. pigra* genome.