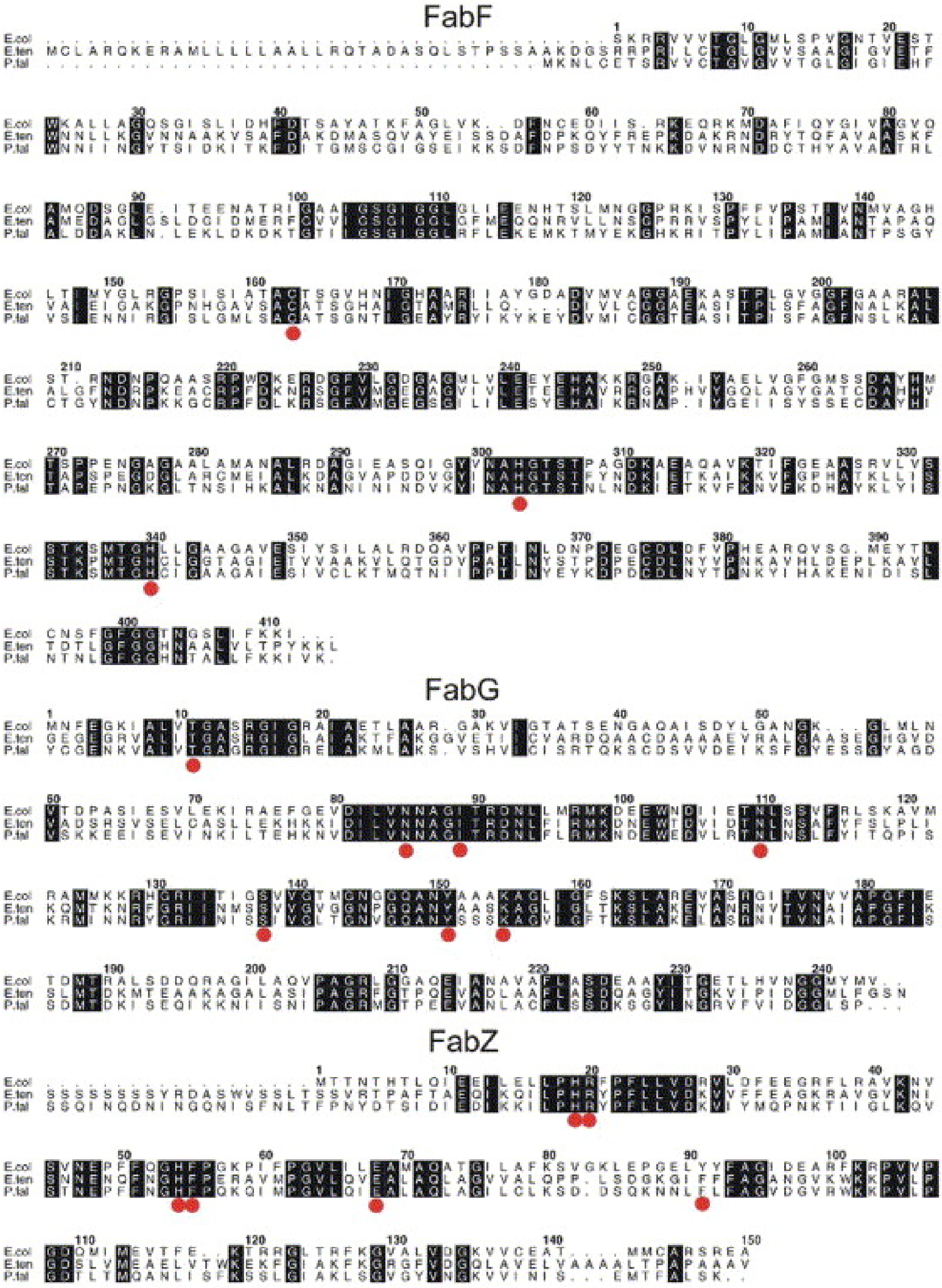
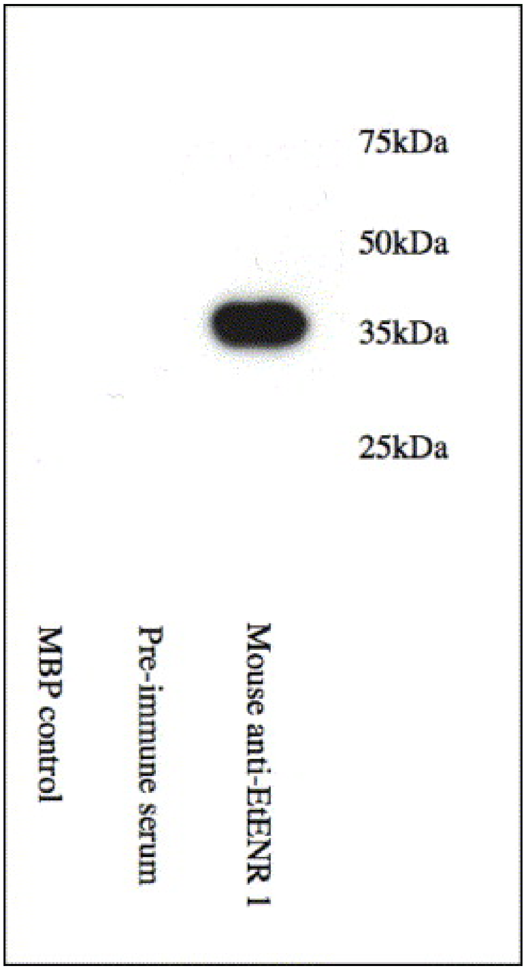
# Appendix A. Supplementary data



Supplementary Fig. 1. The primary structures of Pw-Vit20 and Pw-Vit36 isolated from *Paragonimus westermani*. The deduced amino acid (aa) sequences of Pw-Vit20 and Pw-Vit36 were aligned with those of *F. hepatica* (Fh-VitB1, **AAA29143** and Fh-

VitB2, **AAA29144**), *Clonorchis sinensis* (Cs-VitB1, **AAN64160** and Cs-VitB2, unpublished data) and *Opisthorchis viverrini* (Ov-VitB, **AAL23712**) using the ClustalX program. The identical aa in the alignment are highlighted in black, while similar residues are depicted in gray. The signal peptides predicted by the SignalP program are underlined. The boxed aa sequences indicate the conserved sequence motif, Gly-Gly-Gly-Tyr-Gly/Asp-Gly/Ser-Tyr-Gly-Lys, which has been detected in the trematode- specific eggshell proteins. The positions of the tyrosine residues converted into dihydroxyphenylalnine in the Fh-VitB proteins are marked with asterisks. The identity values of each of the eggshell proteins against Pw-Vit20 are shown at the end of each of the polypeptide sequences.



Supplementary data 2.