



Figure S1. Phylogenetic analysis of Osp amino acid sequence in multi-species. The evolutionary histories of Osp were inferred using the neighbor-joining method. Note: GenBank accession numbers are as follows: *B. mori* (NP_001037168.1), *H. armigera* (XP_021187246.1), *P. xylostella* (XP_011552048.1), *S. frugiperda* (XP_035438721.2), *D. melanogaster* (NM_079223.2), *O. abietinus* (XP_012280703.1), *C. cinctus* (XP_015603565.1), *N. vespilloides* (XP_017777496.1), *T. castaneum* (XP_015840900.1), *M. persicae* (XP_022174293.1). The OfOsp protein is tightly clustered in the lepidopteran clade (Figure S1), indicating its conserved domain and high sequence identity to OfOsp protein from lepidopteran species.