Appendix S3. Maximum likelihood tree of PLD homologs reconstructed from the multiple sequence alignment shown in Appendix S1. The tree was reconstructed using PhyML with all settings at default values, using the LG model of aminoacid substitution and 600 bootstrap replicates. Bootstrap support values are shown as percentages (from 0 to 100). The tree is visualized in Nexus format. For eukaryotic sequences, the sequence labels are the internal codes described in Table S1. For prokaryotic sequences, the labels correspond to UniProt IDs. For more details, see Methods.