

#NEXUS

BEGIN trees;

TREE '[1]con_all_compat' =

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((((Aano005865:0.752916,Pirr011769:0.2418198)0.611:0.1224197,Pinf011946:0.3826852)0.585:0.07520503,Alai013376:0.340936)0.683:0.1367885,(((Anig006882:0.3272198,
(Tlon003902:0.1766767,Scer005474:0.5250027)0.985:0.1316935)1.000:0.2088152,
(((Bflo026111:0.3672955,Nvec018540:0.3128689)0.998:0.1632713,
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END;

Appendix S2. Bayesian tree of PLD homologs from algae and other representative taxa reconstructed from the multiple sequence alignment shown in Appendix S1. The tree was reconstructed using Mr. Bayes (see Methods for setting details). For calculations, two MCMCMC runs with four chains each were run for 20,000,000 generations. The convergence of the runs was evaluated using AWTY online and the consensus was calculated using all compatible trees. 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.