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[73] Pinf000096

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[74] Pirr002822

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[76] Dpur006360

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[77] Ngru000802

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[78] Ngru000879

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[79] Imul007111

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[81] Sagg004103

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[221] Ata26918041  
MDTLLLIQVYAHAWDGSSELFNVLKEAAGRKAHILLSLNAQT--NMMGSAHINHAKF  
WLVRTAILGGIDVDEEHDSGLAAVDNFTVPPMPQTAPHSYAAAWFKAVDYIDPL--DAL  
VDAERVRFIVIVSKAFRDH--YVHEKGLLIDQYALVGSMLCVRTG

[222] Aker004831  
FPAIYAIEILLEMVYWRAGKEVVSRLIEARERGV-KIIYDCIET---KELFVGVS-----  
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RR---GVKVEVV-----RAVLHAKVAIFDDVSVVGTYNFPIS

[223] Alim003592  
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LVVDVAITGGMNIP-E-RDVGPAVPAIF-TIRPSSALSTIRRGYLRAIHQINSY--RRA--  
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[224] Sagg004318  
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[225] D1B824\_THEAS  
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[226] CLS\_GE0SW  
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[227] CLS\_GEOTN  
FAAIFELEIHLEYEIEIGQKLKHLVMEKACQGVVRFVLYDAVGSYIEELRAAGVERNHRKI  
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[228] CLS\_BACHD  
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KIAALSGIDVRLRSYLEAGVFLHSKIIIVDEIASIGTSNMMS  
[229] CLS\_BACPE  
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[230] CLS2\_BACCR  
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[231] CLS2\_BACAN  
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[232] CLS1\_BACSU  
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[233] CLS1\_BACCR  
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[234] CLS1\_BACAN  
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[235] A7G6H0\_CLOBH  
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[236] A5I5A8\_CLOBH  
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[237] Q8YAV5\_LISMO  
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[238] CLS2\_STAES  
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[239] CLS2\_STAAR  
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[240] Q2FWG8\_STAA8  
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[241] CLS1\_STAEQ  
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[242] CLS1\_STAAR  
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[243] Q2FYW4\_STAA8  
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[244] CLS\_LISW6

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[245] CLS\_LISMO  
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[246] CLSA\_BACSU  
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[247] CLS\_OCEIH  
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[248] F9UTG6\_LACPL  
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[249] CLS\_CLOP1  
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[250] Q838D8\_ENTFA  
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[251] Q2FM09\_METHJ  
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[252] Q9CGC3\_LACLA  
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[253] Q834N6\_ENTFA  
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[254] Q8A0P3\_BACTN  
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[255] CLSA\_PSEPU  
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[256] CLSA\_PSEFS  
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[257] CLSA\_PSEFS  
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[258] CLSA\_PSESM  
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[259] CLSA\_PSEAB  
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[260] CLSA\_PSEAE  
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[261] Q63S27\_BURPS  
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[262] Q7NE04\_GLOVI  
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[263] Q9CGY2\_LACLA  
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[264] Q8R663\_FUSNN  
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[265] Q8A560\_BACTN  
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[266] Q8PEG6\_XANCP  
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[267] CLSB\_BACSU  
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[268] Q814S4\_BACCR  
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[269] Q81JV3\_BACAN  
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[270] Q81EE3\_BACCR  
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[271] Q81RJ0\_BACAN  
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[272] Q6HZR7\_BACAN  
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[273] Q81S74\_BACAN  
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[274] Q81F64\_BACCR  
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[275] Q8A640\_BACTN  
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[276] Y988\_STRMU  
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[277] Q8DRD9\_STRR6  
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[278] Q97E04\_CLOAB  
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[279] Q72EZ4\_DESVH



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[280] Q746Z5\_GEOSL  
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[281] Q74FX0\_GEOSL  
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[282] Q7VTL1\_BORPE  
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[283] CLSA\_CITK8  
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[284] CLSA\_SALTY  
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[285] CLSA\_SHIDS  
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[286] CLSA\_ECOLI  
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[287] CLSA\_YERP3  
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[288] CLSA\_YERPE  
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[289] CLSA\_SERP5  
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[290] CLSA\_PECCP  
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[291] CLSA\_EDWI9  
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[292] CLSA\_ERWT9  
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[293] CLSA\_SODGM  
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[294] CLSA\_PROMH  
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[298] CLSA\_BUCAP  
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[389] Ehux028152  
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[397] B1L3J9\_KORCO  
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[398] Q97II3\_CLOAB  
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[501] Q32D67\_SHIDS  
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[503] PPK\_SALTY  
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[505] PPK\_SYNY3  
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[506] PPK\_THEEB  
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[507] Q7NKH7\_GLOVI  
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LLVVYVHLATGNY ---YTDYPLDGLADDLFTHYRKLSPA-----PGRIIAKMNSLVDRAL  
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[509] PPK\_PROMM  
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[510] Q7V9H1\_PROMA  
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[512] PPK\_PROA2  
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[514] PPK\_STAES  
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[515] PPK\_STAS1  
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[521] PPK\_MYCGI  
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[527] A0QUZ3\_MYCS2  
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[535] PPK\_PSESM  
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IKKKPSRIRT -LVYINIIN - -SFHFKGIYFFNITTFGSSNYRS
[571] Q7NGA0_GLOVI
LPQHPILIRVYIAIHELNLPGIALAIGECDRRGVAVRVILEHTYHRDFASVAFANIMHMKF
LIIDRVVTGSTNFTTSDVEVGARIGVQFGPGE - - - -AGINALIALFVFSAPKIAKAI
QRAAGQGVRLWGM - - - - -LHHKFALLDNTVLTGSHNWSVA
[572] Q55769_SYNY3
LPQEEIQVYLAVQELRLPRIAQAALVEKQKTGVRVRLVLENTYNQTIKEAVETELMHHKF
MVLDTVIVTSANFTPSDQKVGETTIVTKFSPDRRAIPFPNTSNGLIALFVFSQALSNI
NRFQAGTEVKLLGVTLLE - - -LHHKFALVDDTVITGSHNWSVA
[573] Q8DGH8_THEEB
LPQHPQIKVHVAVQEFRLPNLAKALATROQAGVRVRLVMENTYTAPWAKYTAAQLMHHKF
IVIDQVIATTANFTLSDVAVGDAMVTVRFSPTPRSQPWTSTNGLIALFVFSQELSNVL
EERHNQGVKIRMMGVAMANTTQLHHKYGVVDDTVIVGSHNWSVA
;
END;

```

Appendix S1. Multiple Sequence Alignment of PLD Homologs from Selected Algae and Other Representative Taxa from the Eukaryotic and Prokaryotic Domains. Sequences coming from the HMMER iterative data-mining and the non-iterative search were aligned using hmalign and manually corrected. The resulting alignment was trimmed using BMGE (see Methods for full detail). The MSA, used for phylogenetic tree reconstruction, is visualized in Nexus format. For eukaryotic sequences, labels correspond to the internal codes described in Table S1. For prokaryotic sequences, labels are Uniprot IDs. Numbers at the top of the figure are: Number of taxa (NTAX=573), number of characters (NCHAR=164). Dashes indicate gaps.