

P.tricornutum	1	LSNLVDRCRSNTSTRIHFTLPHTHSTMKFSLATLSSLTLLVAPWAVAAASAACPYLEAAAP
Chlamydomonas	1	MEKSP-----FFAAL-----AL
P.multistriata	1	MASATTT---SCSSRNIRSVASFALLFALACLNGSYTAAQ-PSNPSTPPCRFLDDAPP
P.tricornutum	61	VEYELPASALTNPLVDLPVKFVGKSVITRSQVPFGSKPRVVVQRYSSKPTIAYDPTDGS
Chlamydomonas	13	V-----MLAGATAVHATAM-----
P.multistriata	57	LDVEIPS-VLT----HKKLSFLGVAAKVHRKATASGSKPRIRFLRYSSTPTV--DVTRGG
P.tricornutum	121	VTISSAACSGGVS---SEE-GSGATSSTKNSLMTMASTLAMYPALGGEIG--AGLALAGA
Chlamydomonas	27	-----
P.multistriata	110	ILVSAEGSGCDVSVDVSILSSSAPSRSTPRRLLAASAVAAGFLSSHKLGMLIAVLCLSSP
P.tricornutum	174	ALTNLPT--AHAQDESCMPSEVVMVEAPAAAYRGAVETCLA EVTQSQCPLPFPTEPTC--
Chlamydomonas	27	-----EKVGNYLIPVE-----SGE--TEGA
P.multistriata	170	SLVPGSAFAEAASSSTCTPSMEIVLEAPPYYLGSVEECLRSVSNPDHCPEPFPEFPICGA
P.tricornutum	230	---S-TPSPTCGVAVVGAGAGGLYTALRMVDERATEASDVCIFETTERVGGRLFSLRGLG
Chlamydomonas	45	---ETVMPKKCDVVVGCGCGGIYSAYRLSGTTLKP-SVCTFEATNRVGGRIFSIRGLG
P.multistriata	230	DDRE-LAAPACKLAVVGAGTGGLYTAYRLVEEGVFEGSDICIFEATDRVGGRIYSLRGFG
P.tricornutum	286	PDNDLSVDAGGYRTWPEFTPTLHALITEYLNIPMDCYDPSEVPCQKF-NIVDENGNGKAGF
Chlamydomonas	101	KLADMTVDLGAIRYVDGRHTLVQGLVENLLKLYVLYDPAS---TQERKIVDDKGGDLGF
P.multistriata	289	PEGDISVDAGAYRTWPDYPTTHALITEVLGFDVECYDEDD-PCTKF-NIVGETGEKIGF
P.tricornutum	345	ATFVEEMRRLTDAGACFYPFHEVRSIAKIEAPSDTATARNADGTAT-ELHFTNG-ATAV
Chlamydomonas	158	VTFVEELTKLSMSLGMKLFNLSPVTKVDRM--PSTSAD---AQYAVSVM-GPNGKIMKV
P.multistriata	347	ASFVEELMSRLIEKGACFFPRHNLVSAHN--NDDAET---DGYASNTLTFSNG-VKTR
P.tricornutum	403	ATFTTILGVPQRPLLNILRNSNFANSIM-----TAAKWD-AVHSV
Chlamydomonas	211	VAKHVI FNTQQRPLMRILQNSNLARVT-----EWSSALDMP
P.multistriata	400	ATHGTILNVPQRALLEILRESKDLFSSSSSSPSSIASGTNLDRSAREEEKRTYD-SLHSV
P.tricornutum	442	QTVIASKLYLYYPRGQVFWRKLNLAGDGFELDGD-----ARNMLLAGRYHDGHV
Chlamydomonas	247	FPLMAAKMYLYYDD--AWWVYMNRTTGSLNDPNTNNATTFNSSSLFTTPPLRGYHDGDW
P.multistriata	459	QTEIVTKLYLYYED--AWWYKLGTLTGDFSLPGD-----ARSMLLEGYHDGHV
P.tricornutum	491	ECEDENDP-DTCRGFLLAVYANDLSGNKAQFF-----RRYQDRPEP
Chlamydomonas	305	KCNADN---TKCHGMFMYTYASDNGGTYNRGGQGLDISPYNGVVPRIYWNVAVNPDPSKP
P.multistriata	506	KCEATDDGDEKCYGFLAVYAHDFSGTKAQYF-----RRFQDRPEP
P.tricornutum	532	VTILSNSDLESAEFLKHAHAQLEQYHLYENPGANYTGSEALAAFR-----NVNPPPEFAV
Chlamydomonas	362	YVVLDMTSSGGKNLIMEAHKKVVDYHISINAS-----IPEPY-----ASTYPSQAV
P.multistriata	548	VTILSDTNPEEEDFLRHAHERLVVDYHVYGEDNARLLNASAYSPPQFRKIIESPPPTFAV
P.tricornutum	586	LSTWNEAVPWAGGAHW-----TDIDNID--LAQKPLADSNIFVVNEAFSL
Chlamydomonas	408	VVWWDPOIQWTGGAWHSYKNGIYGSQVSTNYTDPRNAVPVASIKPFAGENVVVANEAFSA
P.multistriata	608	LANWNTAAFGAGGWHHW-----TDTANAE--KAMKPLNPLGIHVNEAFSK
P.tricornutum	631	LHGWAEGSIKLADSILEDYFNIA RPWNFEVSDFVQFVQQTNSRECVEGEGGSSGGGTDGG
Chlamydomonas	468	VQGWAEGLLMAENVVTQ-LGAARPTFIS-----TQRHDCVLYPSY--NY----
P.multistriata	653	IQGWAEGLLLADEILEEHYGVARPWSFEVPQSIFYLAQTSSEECVAGDDA--GSGQSGG

P.tricornutum	691	SSGGGGGDTSSGGGG-GASNPALCFTEDALVTMADGSLKRIVDVQLGDRVVTGTGKGNGLV
Chlamydomonas	510	-----NATL-----CGLS
P.multistriata	711	S-----SSGGAGPVAGELDLCAAGSLVEMANGNLVPIEDVVEEGDSVATGVGGKIGLV
P.tricornutum	750	TEKLIHPVKKT-----VPVAILATKDGDLTGTPHPIY--HQGEWIEMG
Chlamydomonas	518	LNPLVQGVTRR-----RAAAVSAS-----
P.multistriata	765	TEKLVHPVRMKEAKKTAWGAPYRTRRWSDVVVVPTTEHGDLVGTDPDHPVLLGNSSSEWMELG
P.tricornutum	792	D-LTSDLLTLT----EAHVEAFYNLEIDGD-----QAGTSSHSYVVNGIVASGLGDN
Chlamydomonas	537	-----ASIASETL-KAAAAGLSGG
P.multistriata	825	DALERNLLAVGARRVSRDVIDIFYNLEIDGKVKYKDDGRQAQQSPHSYVVNGVVASGLGDN
P.tricornutum	839	EDLNKLSPRQKIWKDEV-----IDVISQ-----
Chlamydomonas	555	RKLGAY-----
P.multistriata	885	PLLNRLFPRQRVFLEEQSKHHHDIDLISATSIVDKT

**Supplemental Figure S2.** Sequence alignment of the *Chlamydomonas reinhardtii* LAO1 protein (AAB97101.1) and putative orthologs identified in the diatoms *Phaeodactylum tricornutum* (Phatr3\_EG00033) and *Pseudo-nitzschia multistriata* (VEU40048.1).