		β3	β4	β6
Type I	PKCα	NGLSDP**Y**V**K**LKLIP	---------KNES**K**Q**K**TKTIRST	RRLSVEI**W**DWDRTTR--
	PKCβ	NGLSDP**Y**V**K**LKLIP	---------KSES**K**Q**K**TKTIKCS	RRLSVEI**W**DWDLTSR--
	PKCγ	NGLSDP**Y**V**K**LKLIP	---------RNLT**K**Q**K**TRTVKAT	RRLSVEV**W**DWDRTSR--
	synI C2A	GGTSDP**Y**V**K**VFLLP	----------DKKK**K**F**E**TKVHRK	KTLVMAV**Y**DFDRFSK--
	syn I C2B	GGLSDP**Y**V**K**IHLMQ	--------KRLK**K**K**K**RRIKKQ	VQVVVTV**L**DYDKIGK--
	Rabphilin 3A C2A	NGLADP**Y**V**K**LHHLP	--------SKSN**K**L**R**TKTLRN	KTLRISV**C**DEDKFGH--
	Rabphilin 3A C2B	NGYSDP**F**V**K**LWLKP	--------GKKA**K**H**K**TQIKKKT	KSLDISV**W**DYDIGKS--
	Doc2alpha C2A	NGLADP**Y**V**K**LHLLP	--------CKAN**K**L**K**TKTQRNT	KVLRISV**C**DEDKLSH--
	Doc2alpha C2B	NGYSDP**Y**V**K**TYLRP	--------DKKS**K**H**K**TCVKKKT	KTLEVTV**W**DYDIGKS--
	RIM1 C2A	GRPRNP**Y**V**K**MYFLPD----	---DKS**K**R**R**TKTVKKLL	RMLEITV**W**DQPRVQDEE
	RIM1 C2B	KSTPAP**Y**V**K**VYLLEN	--------CIA**K**K**K**TRIARKTL	KVLQVIV**W**GDYGRMDH-
Type II	cPLA$_2$α	-DTPDP**Y**V**E**LFISTTP	---------DS**RKRTRH**FNNDI	-NVLEIT**L**MDANYVM--
		β2	β3	β5

Fig. S1. **Sequence alignment of the β-groove region from various C2 domains including type I and II topologies.** The C2 domain of PKCα was used to perform the sequence alignment. Residues for Type I topology C2 domains that have been shown to bind phosphoinositides, particularly PI(4,5)P$_2$ are shown in bold. For cPLA$_2$α residues that are conserved with the purported PI(4,5)P$_2$ binding residues are shown in bold, residues that are distinct from PI(4,5)P$_2$ binding residues are highlighted in red, and C1P binding residues including those involved in nonspecific electrostatics are shown in blue.