

Supplementary

A

	10	20	30	40	50	60
pEGFR-cSH2	GSPIPHHDEK	TWNVGSS NRN	KAENLLRGKR	DGTFLVRESS	KQGCYACSVV	VDGEVK HCVI
C1	GSPIPHHDEK	TWNVGSS NRN	KAENLLRGKR	DGTFLVRESS	KQGCYACSVV	VDGEVK HCVI
C2	GSPIPHHDEK	TWNVGSS NRN	KAENLLRGKR	DGTFLVRESS	KQGCYACSVV	VDGEVK HCVI
C3	GSPIPHHDEK	TWNVGSS NRN	KAENLLRGKR	DGTFLVRESS	KQGCYACSVV	VDGEVK HCVI
C4	GSPIPHHDEK	TWNVGSSN RN	KAENLLRGKR	DGTFLVRESS	KQGCYACSVV	VDGEVK HCVI
	70	80	90	100	109	
pEGFR-cSH2	NKTATGYG FA	E ^P YNLYSSLK	ELVLHYQHTS	LVQH N DSLNV	TLAYPVYAQ	
C1	NKTATGYG FA	E ^P YNLYSSLK	ELVLHYQHTS	LVQHND S LNV	TLAYPVYAQ	PI3K p85 α
C2	NKTATGYG FA	E ^P YNLYSSLK	ELVLHYQHTS	LVQHND S LNV	TLAYPVYAQ	cSH2 domain
C3	NKTATGYG FA	E ^P YNLYSSLK	ELVL H YQHTS	LVQHND S LNV	TLAYPVYAQ	
C4	N KTATGYG FA	E ^P YNLYSSLK	ELVLHYQHTS	LVQHND S LNV	TLAYPVYAQ	

B

	10	20	30	40	50	60
pEGFR-nSH2	—MSLQNAEW	YWGDISREEV	NEKLRDTADG	TFLV R DASTK	MHGDYTLTLR	GGNNNK L IKI
N1	NNMSLQNAEW	YWGDISREEV	NEKLRDTADG	TFLV R DASTK	MHGDYTLTLR	GGNNNK L IKI
N2	—NMSLQNAEW	YWGDISREEV	NEKLRDTADG	TFLV R DASTK	MHGDYTLTLR	GGNNNK L IKI
N3	NNMSLQNAEW	YWGDISREEV	NE K LRDTADG	TFLV R DASTK	MHGDYTLTLR	GGNNNK L IKI
N4	—NMSLQNAEW	YWGDISREEV	NE K LRDTADG	TFLV R DASTK	MHGDYTLTLR	GGNNNK L IKI
	70	80	90	100	110	
pEGFR-nSH2	FHRDGKYGFS	DPLTFSSVVE	LINHYRNESL	AQYNP K L DVK	LLYPVSKYQQ	107
N1	FHRDGKYGFS	DPLTFSSVVE	LINHYRNESL	AQYNP K L DVK	LLYPVSKYQQ	110 PI3K p85 α
N2	FHRDGKYGFS	DPLTFSSVVE	LINHYRNESL	AQYNP K L DVK	LLYPVSKYQQ	115 nSH2 domain
N3	FHRDGKYGFS	DPLTFSSVVE	LINHYRNESL	AQYNP K L DVK	LLYPVSKYQQ	110
N4	FHRDGKYGFS	DPLTFSSVVE	LINHYRNESL	AQYNP K L DVK	LLYPVSKYQQ	115 DQVVKE

Figure S1. Sequence alignment of C1-C4 and N1-N4 to pEGFR-cSH2 and pEGFR-nSH2 to find the overlap of the residues important for CaM-p85 α and pEGFR-p85 α interactions. Important residues are in red.

A

	10	20	30	40	50	60	
pEGFR-cSH2	GSPIPHHDEK	TWNVGSSN RN	KAENLLRGKR	DGTFLV RESS	KQGCY ACSVV	VDGEV KHCVI	
C1	GSPIPHHDEK	TWNVGSSN RN	KAENLLRGKR	DGTFLV RESS	KQGCYACSVV	VDGEV KHCVI	
C2	GSPIPHHDEK	TWNVGSS RN	KAENLLRGKR	DGTFLV RESS	KQGCY ACSVV	VDGEV KHCVI	
C3	GSPIPHHDEK	TWNVGSSN RN	KAENLLRGKR	DGTFLV RESS	KQGCY ACSVV	VDGEV KHCVI	
C4	GSPIPHHDEK	TWNVGSSN RN	KAENLLRGKR	DGTFLV RESS	KQGCY ACSVV	VDGEV KHCVI	
	70	80	90	100	109		
pEGFR-cSH2	NKTATGYG FA	E PYNLYSSLK	ELVLHYQHTS	LVQ HNDLSNV	TLAYPVYAQ		
C1	NKTATGYGFA	E PYNLYSSLK	ELVLHYQHTS	LVQ HNDLSNV	TLAYPVYAQ	PI3K p85 α	
C2	NKTATGYGFA	E PYNLYSSLK	ELVLHYQHTS	LVQ HNDLSNV	TLAYPVYAQ	cSH2 domain	
C3	NKTATGYG FA	E PYNLYSSLK	ELVLHYQHTS	LVQ HNDLSNV	TLAYPVYAQ		
C4	NKTATGYG FA	E PYNLYSSLK	ELVLHYQHTS	LVQ HNDLSNV	TLAYPV YAQ		

B

	10	20	30	40	50	60	
pEGFR-nSH2	---MSLQNAEW	YWGDISREEV	NEKLRDTADG	TFLVRDASTK	MHGDYTLTLR	KGGNNKLI KI	
N1	NNMSLQNAEW	YWGDISREEV	NEKLRDTADG	TFLVRDASTK	MHGDYTLTLR	KGGNNKLI KI	
N2	-NMSLQNAEW	YWGDISREEV	NEKLRDTADG	TFLVRDASTK	MHGDYTLTLR	KGGNNKLI KI	
N3	NNMSLQNAEW	YWGDISREEV	NEKLRDTADG	TFLVRDASTK	MHGDYTLTLR	KGGNNKLI KI	
N4	--NMSLQNAEW	YWGDISREEV	NEKLRDTADG	TFLVRDASTK	MHGDYTLTLR	KGGNNKLI KI	
	70	80	90	100	110		
pEGFR-nSH2	FHRDG KYGF S	DPLTFSSVVE	LINHYRNE SL	AQYNPKLD VK	LLYPVSKY QQ	107	
N1	FHRDG KYGF S	DPLTF SSVVE	LINHYRNE SL	AQYNPKLD VK	LLYPV SKYQQ	110	PI3K p85 α
N2	FHRDGKYGFS	DPLTFSSVVE	LINHYRNE SL	AQYNPKLD VK	LLYPV SKYQQ	DQVVKE 115	nSH2 domain
N3	FHRDG KYGF S	DPLTF SSVVE	LINHYRNE SL	AQYNPKLD VK	LLYPV SKYQQ	110	
N4	FHRDG KYGF S	DPLTFSSVVE	LINHY RNE SL	AQYNPKLD VK	LLYPV SKYQQ	DQVVKE 115	

Figure S2. Sequence alignment of C1-C4 and N1-N4 to pEGFR-cSH2 and pEGFR-nSH2 to find the overlap of the interface residues (red) within CaM-p85 α and pEGFR-p85 α interactions.

Table S1. Summary of the hydrogen bonds and salt bridges formed between CaM and cSH2 in the C2

Number	H Bonds	Distance (Å)
Hb1	CaM-D47-OD1…cSH2-R37-NH1	3.20
Hb2	CaM-D47-OD1…cSH2-R37-NH2	2.83
Hb3	CaM-D47-OD2…cSH2-R37-NH1	2.98
Hb4	CaM-G56-O…cSH2-R19-NH1	3.66
Hb5	CaM-E79-OE1…cSH2-K41-HZ3	1.94
Number	Salt Bridge	Distance (Å)
Sb1	CaM-D47-OD1…cSH2-R37-NH1	3.20
Sb2	CaM-D47-OD1…cSH2-R37-NH2	2.83
Sb3	CaM-D47-OD2…cSH2-R37-NH1	2.98
Sb4	CaM-E79-OE1…cSH2-K41-NZ	2.87

Table S2. Summary of the hydrogen bonds formed between CaM and nSH2 in the N2

Number	H Bonds	Distance (Å)
Hb1	CaM-K26-HZ2···nSH2-E21-OE2	1.78
Hb2	CaM-N49-HD21···nSH2-N53-OD1	1.81
Hb3	CaM-Q139-HE22···nSH2-H61-O	2.24
Hb4	CaM-D54-O···nSH2-N20-HD21	2.35
Hb5	CaM-D54-OD1···nSH2-R24-HE	2.05
Hb6	CaM-D54-OD1···nSH2-R24-HH11	1.81
Hb7	CaM-E41-OE1···nSH2-R34-HH12	1.96
Hb8	CaM-E41-OE1···nSH2-R34-HH22	1.85
Hb9	CaM-E41-OE2···nSH2-S37-H	1.96
Hb10	CaM-E41-OE2···nSH2-T38-H	2.08
Hb11	CaM-Q45-OE1···nSH2-L56-H	2.28
Hb12	CaM-E41-OE2···nSH2-K58-HZ2	1.99
Hb13	CaM-Q139-O···nSH2-R62-HE	1.68
Hb14	CaM-Q139-O···nSH2-R62-HH11	2.23
Hb15	CaM-E123-OE2···nSH2-K65-HZ1	1.96
Number	Salt Bridge	Distance (Å)
Sb1	CaM-K26-NZ···nSH2-E21-OE1	3.57
Sb2	CaM-K26-NZ···nSH2-E21-OE2	2.76
Sb3	CaM-D54-OD1···nSH2-R24-NE	2.97
Sb4	CaM-D54-OD2···nSH2-R24-NE	3.37
Sb5	CaM-D54-OD1···nSH2-R24-NH1	2.76
Sb6	CaM-E41-OE1···nSH2-R34-NH1	2.85
Sb7	CaM-E41-OE1···nSH2-R34-NH2	2.71
Sb8	CaM-E41-OE2···nSH2-K58-NZ	2.90
Sb9	CaM-E123-OE2···nSH2-K65-NZ	2.83
Sb10	CaM-E123-OE1···nSH2-K65-NZ	3.33