Supplementary Table 1. Data resource for synthetic peptides

Peptide Name	Amino Acid Sequence	Number of amino acids in peptide
n-T1	CRYSDTTDSDPENEG	15
4p-T2	CRYpSDpTpTDpSDPENEG	18
4p-T3	CYpSDpTpTDpSDPENEPFDED	18
F-4p-T4	CpSDpTpTDpSDPENEPFDEDK$_{fluorescein}$G	19
n-T5	CRYSDTTDSDPENEPFDEDQHTQITKV	27
3p-T6	CYSDpTpTDpSDPENEPFDED	18
3p-T7	CYpSDTpTDpSDPENEPFDED	18
3p-T8	CYpSDpTTDpSDPENEPFDED	18
3p-T9	CYpSDpTpTDSDPENEPFDED	18
1p-T10	CYpSDTTDSDPENEPFDED	18
1p-T11	CYSDpTTDSDPENEPFDED	18
1p-T12	CYSDTpTDSDPENEPFDED	18
1p-T13	CYSDTTDpSDPENEPFDED	18
3p-T14	YpSDpTpTDS	7
4p-T15	YpSDpTpTDpSDPENEG	13
4p-T16	CpSDpTpTDpSDPENEPFDED	17
4p-T17	CpSDpTpTDpSDPENEPFDEDQHTQITKV	25

Supplementary Table 2. Data collection and refinement statistics

	n-crPTEN-13_{sp}-T1 7JUL	4p-crPTEN-13_{sp}-T2 7JUK	4p-crPTEN-20_{sp}-T3 7JVX	4p-crPTEN-22sp-T3 7JTX
Data collection				
Beamline/ Detector	NSLSII-AMX/DECTRIS EIGER 9M	NSLSII-AMX/ DECTRIS EIGER 9M	NSLSII-FMX/DECTRIS EIGER 16M	APS NE-CAT 24E/ DECTRIS EIGER 16M
Space group	I_4	I_4	I_4	I_4
Cell dimensions				
a, *b*, *c* (Å)	113.1,113.1, 57.5	113.4, 113.4, 57.0,	113.4, 113.4, 57.9,	111.9, 111.9, 60.7
α, β, δ (°)	90.0, 90.0, 90.0	90.0, 90.0, 90.0	90.0, 90.0, 90.0	90.0, 90.0, 90.0
Resolution (Å)	28.79-2.53 (2.64-2.53)	80.21-3.15 (3.23-3.15)	19.8-2.90 (3.2-2.9)	53.37-3.05 (3.16-3.05)
Number of reflections	101,029 (10,279)	41,598 (2,447)	20,136 (2,393)	27,601(2,708)
Number of unique reflections	12,325 (1,479)	6,346 (413)	7,482 (1,632)	7,099(687)
Rmeas	0.081 (0.60)	-	0.25 (0.79)	0.1178(2.581)
Rmerge	0.076 (0.561)	0.13 (0.72)	0.21 (0.78)	0.1012(2.235))
Rpim	0.028 (0.22)	0.059 (0.306)	-	0.057 (1.245)
$<I/(\sigma I)>$	14.8 (2.6)	9.50 (2.90)	3.19 (0.81)	11.1 (1.1)
$CC_{1/2}$ (%)	0.99 (0.90)	99.6 (88.8)	97.3 (70.5)	99.7(28.3)
Completeness (%)	99.7 (97.9)	99.3 (91.6)	90.3(78.3)	95.7 (94.2)
Redundancy	8.2 (6.9)	6.6 (5.9)	2.6 (1.4)	3.9 (3.8)
Refinement				
Resolution (Å)	79.9-2.25	28.52-3.15	19.8-3.20	53.37 – 3.05
No. reflections	11,720	6,023	5,538	6,976
R_{work} / R_{free}	0.18/0.23 (0.34/0.45)	0.18/0.28 (0.28/0.30)	0.23/0.27 (0.40/0.40)	0.23/0.27 (0.37/0.44)
No. atoms	2,654	2,625	2,620	2338
B factors	68.4	97.3	92.0	118.9
R.m.s. deviations				
Bond lengths (Å)	0.007	0.007	0.008	0.005
Bond angles (°)	1.541	1.600	1.632	0.80
Ramachandran				
Pref. regions (%)	87.4	87.3	87.7	94.5
Allowed (%)	8.7	8.7	7.7	5.4
Outliers (%)	3.8	3.8	4.5	0

Number of crystals for each structure should be noted in footnote.

[a] Values in parentheses are for highest-resolution shell.