Figure 5C – source data

Table format:		× log[peptide]	Group A dC E1174 (C-ter)					Group B dC E1174 (Phos C-ter)				
1	Title	-9.0000	97	96	95	87		89	101			91
2	Title	-8.5240	93	106	83	86		91	81			82
3	Title	-8.0030	88	89	90	82		89	73	78	79	77
4	Title	-7.5270	74	64	81	68		77	77	84	65	77
5	Title	-7.0070	48	46	65	51		70	66	78	62	77
6	Title	-6.5310	28	36	39	34		65	58	69	58	75
7	Title	-6.0110	27	25	19	24		57	51	62	52	64
8	Title	-5.5350	18	17	13	21		45	41	49	43	60
9	Title	-5.0150				18		39	47	33	33	48
10	Title	-4.5440				17				27	21	33
11	Title	-4.0420								24	15	30
12	Title	-3.7440										
13	Title											

Figure 5C – fit C-ter peptide

	Nonlin fit	A dC E1174 (C-ter)	
-	922 H (M) 94 GON	dC E1174 (C-ter)	
1	log(inhibitor) vs. response Variable slope (four parameters)		
2	Best-fit values		
3	Bottom	15.76	
4	Тор	95.62	
5	LogIC50	-7.091	
3	HillSlope	-0.9289	
7	1C50	8.116e-008	
3	Span	79.86	
)	Std. Error		
0	Bottom	2.894	
1	Тор	2.804	
2	LogIC50	0.06927	
3	HillSlope	0.1349	
4	Span	4.709	
5	95% Confidence Intervals		
6	Bottom	9.848 to 21.67	
7	Тор	89.90 to 101.3	
8	LogIC50	-7.232 to -6.949	
9	HillSlope	-1.204 to -0.6534	
0	IC50	5.860e-008 to 1.124e-007	
1	Span	70.25 to 89.48	
2	Goodness of Fit		
3	Degrees of Freedom	30	
4	R square	0.9697	
5	Absolute Sum of Squares	963.6	
6	Sy.x	5.667	
7			
8	Number of points		
9	Analyzed	34	

Figure 5C – fit phosphorylated C-ter peptide

Newlin 54		A		
	Nonlin fit	dC E1174 (Phos C-ter)		
		Y		
1	log(inhibitor) vs. normalized response Variable slope			
2	Best-fit values			
3	LogIC50	-5.708		
4	HillSlope	-0.2911		
5	IC50	1.957e-006		
6	Std. Error			
7	LogIC50	0.07221		
8	HillSlope	0.01743		
9	95% Confidence Intervals			
10	LogIC50	-5.854 to -5.563		
11	HillSlope	-0.3262 to -0.2560		
12	IC50	1.400e-006 to 2.735e-006		
13	Goodness of Fit			
14	Degrees of Freedom	45		
15	R square	0.9107		
16	Absolute Sum of Squares	1859		
17	Sy.x	6.428		
18				
19	Number of points			
20	Analyzed	47		
04				