

Figure 5C – fit C-ter peptide

Nonlin fit		A
		dC E1174 (C-ter)
		Y
1	log(inhibitor) vs. response -- Variable slope (four parameters)	
2	Best-fit values	
3	Bottom	15.76
4	Top	95.62
5	LogIC50	-7.091
6	HillSlope	-0.9289
7	IC50	8.116e-008
8	Span	79.86
9	Std. Error	
10	Bottom	2.894
11	Top	2.804
12	LogIC50	0.06927
13	HillSlope	0.1349
14	Span	4.709
15	95% Confidence Intervals	
16	Bottom	9.848 to 21.67
17	Top	89.90 to 101.3
18	LogIC50	-7.232 to -6.949
19	HillSlope	-1.204 to -0.6534
20	IC50	5.860e-008 to 1.124e-007
21	Span	70.25 to 89.48
22	Goodness of Fit	
23	Degrees of Freedom	30
24	R square	0.9697
25	Absolute Sum of Squares	963.6
26	Sy,x	5.667
27		
28	Number of points	
29	Analyzed	34

Figure 5C – fit phosphorylated C-ter peptide

Nonlin fit		A
		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