Figure S1

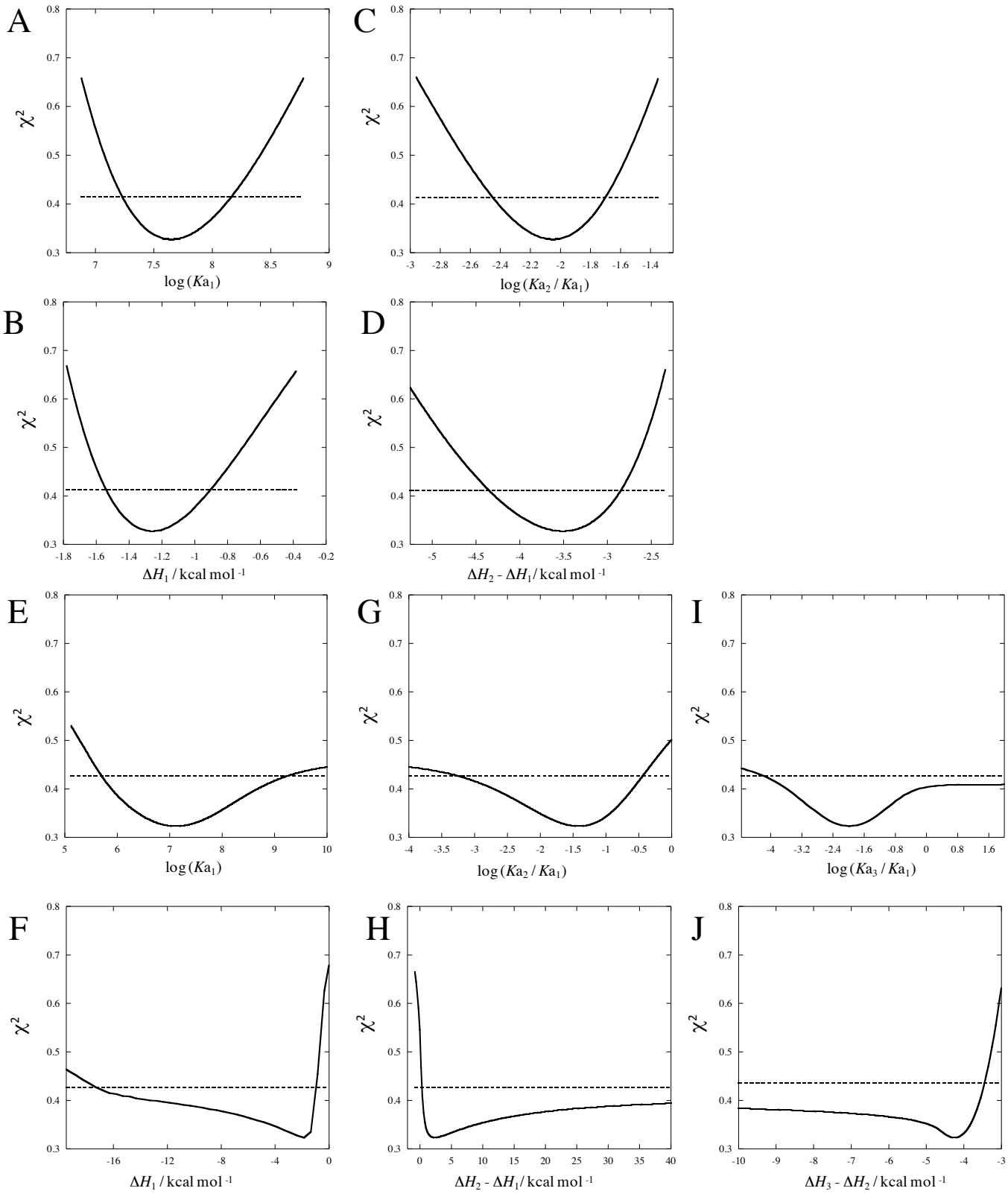

Figure S1. (A) - (D) show the error-surface projections of each fitting parameter for ABB model and (E) - (J) show those for ABBB model. The 68.3 % confidence intervals are shown as a dashed line.

Figure S2

a

hSmc2H-CC30

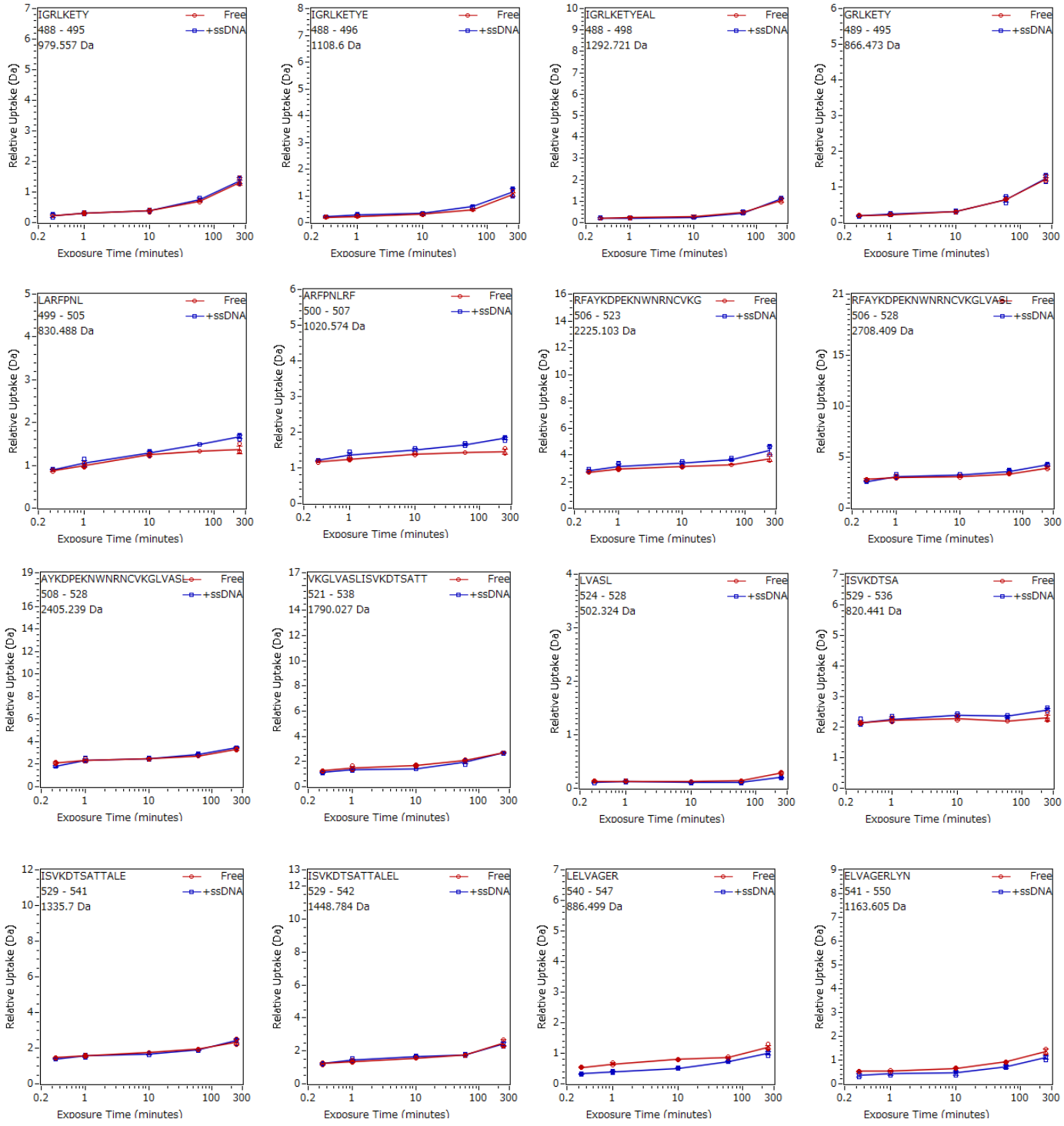

Figure S2. Relative deuterium incorporation curves for all hSmc2H-CC30 pepsin fragments. Both hSmc2H-CC30 alone (red) and hSmc2H-CC30-ssDNA complex (blue) are indicated.

Figure S2

b

hSmc2H-CC30

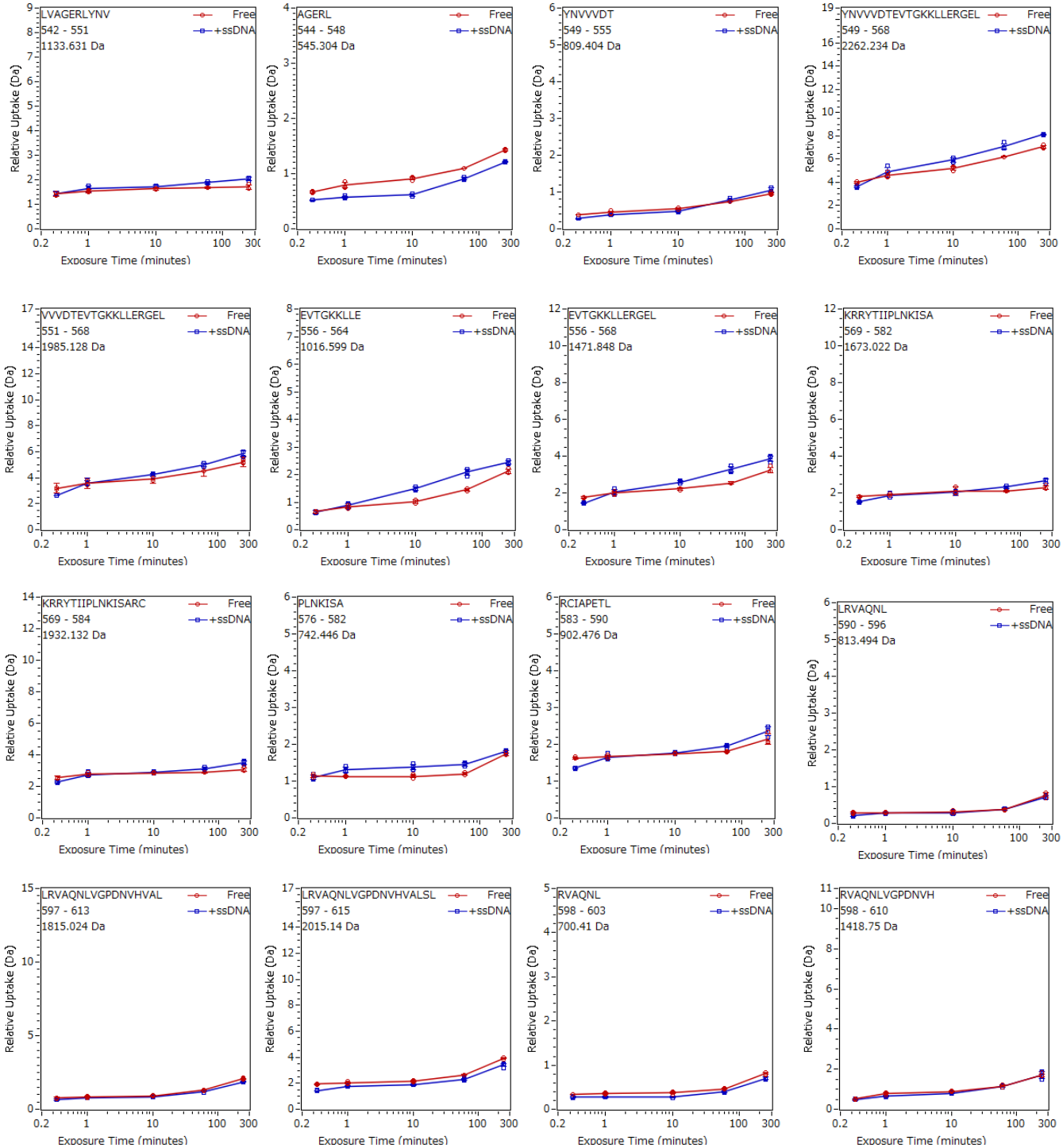

Figure S2

c

hSmc2H-CC30

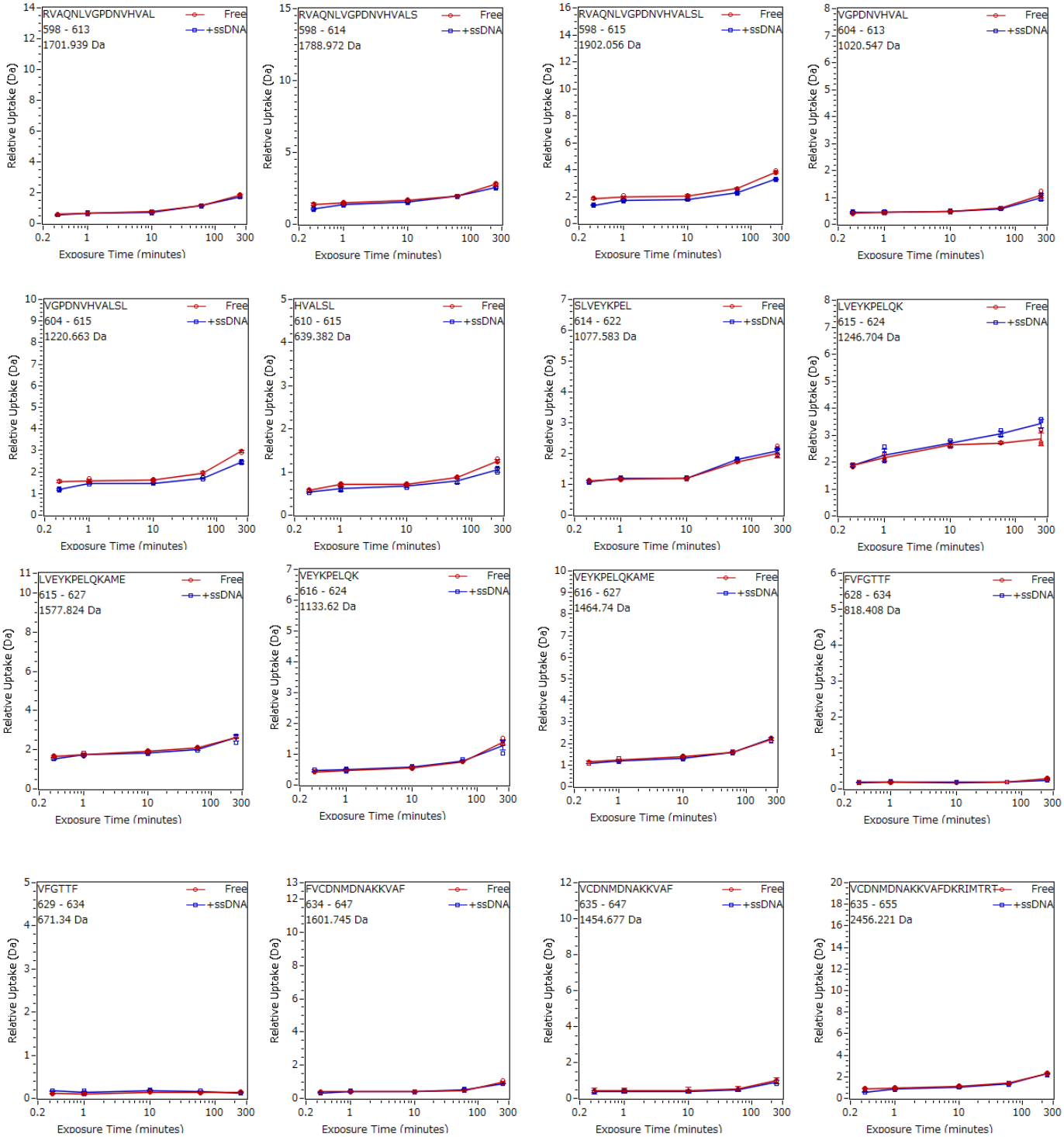

Figure S2

d

hSmc2H-CC30

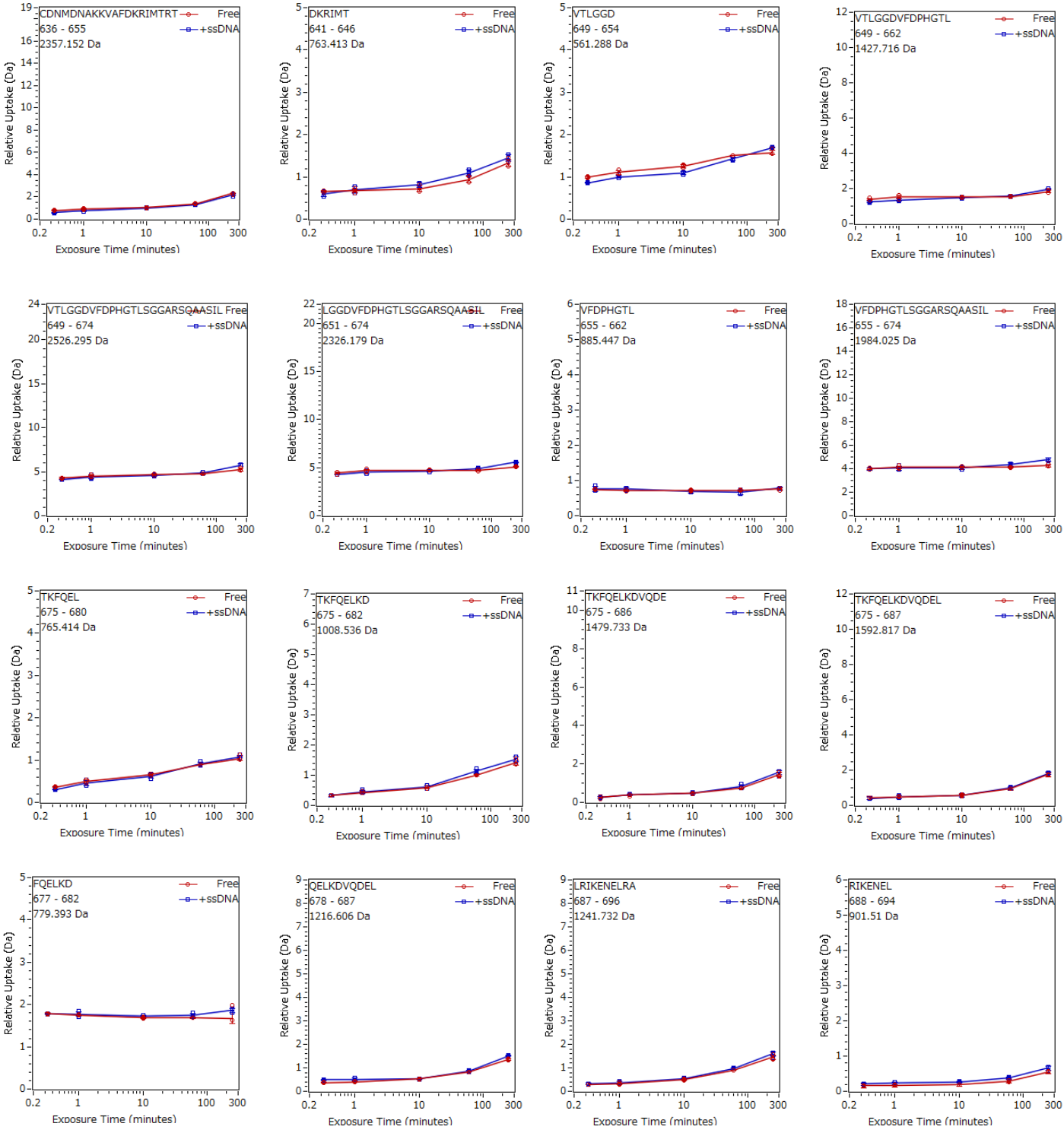

Figure S2

e

hSmc2H-CC30

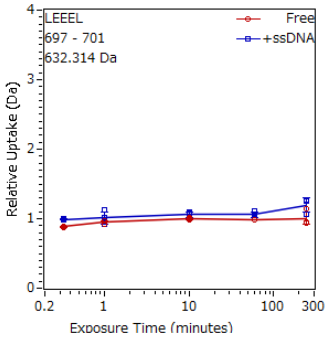

Figure S3

a

hSmc4H-CC30

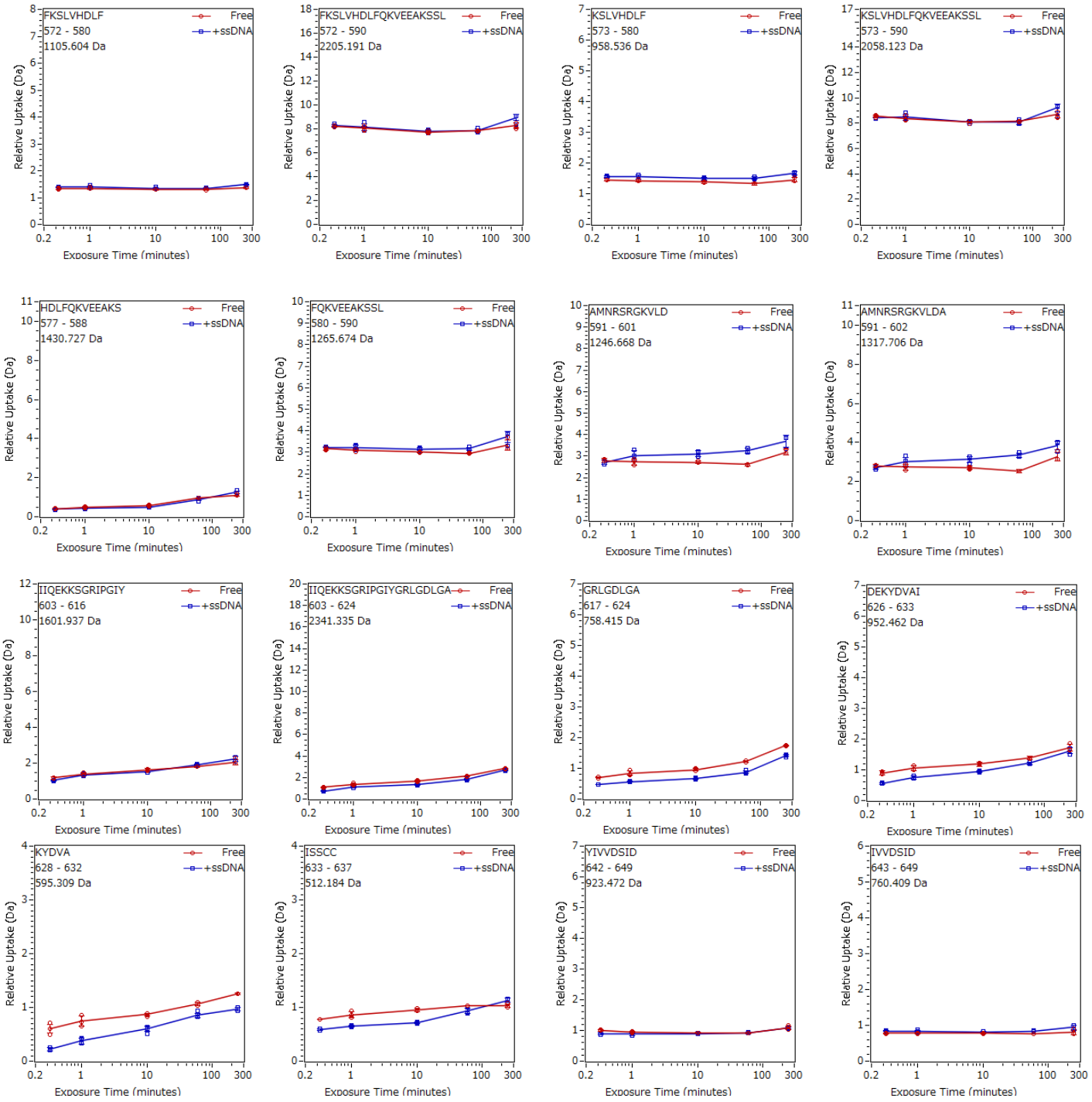

Figure S3. Relative deuterium incorporation curves for all hSmc4H-CC30 pepsin fragments. Both hSmc4H-CC30 alone (red) and hSmc4H-CC30-ssDNA complex (blue) are reported.

Figure S3

b

hSmc4H-CC30

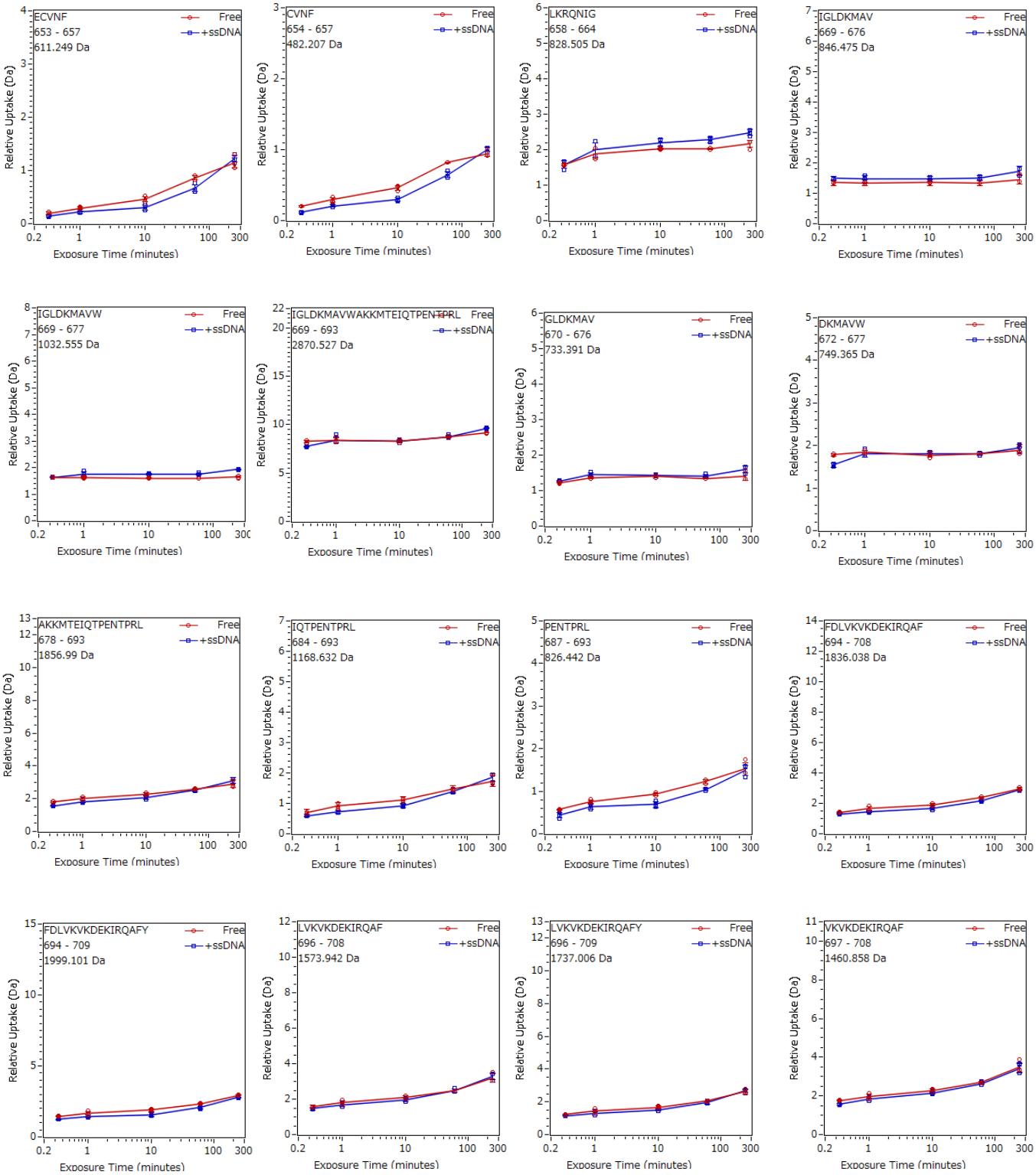

Figure S3

c

hSmc4H-CC30

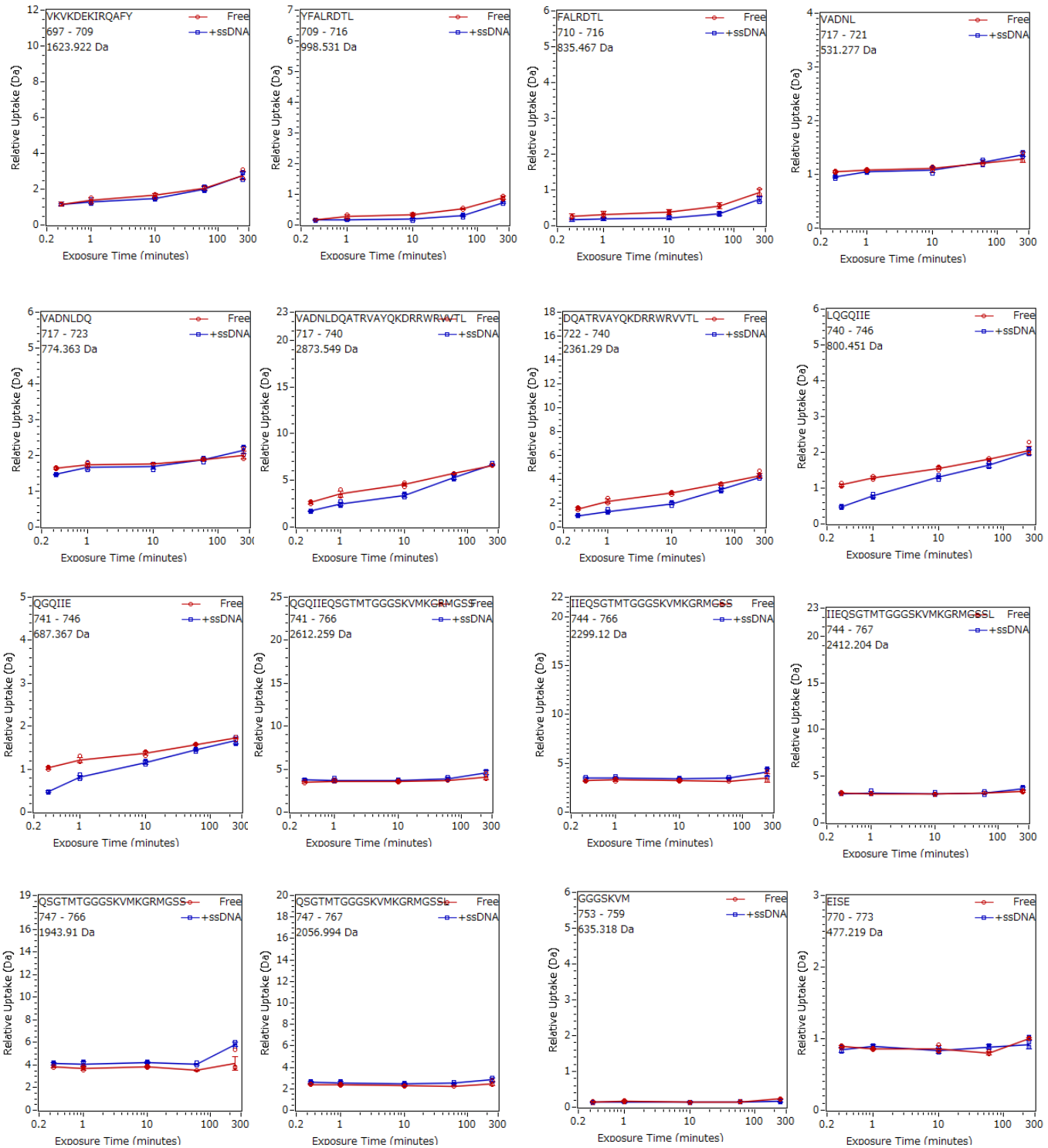

Figure S3

d

hSmc4H-CC30

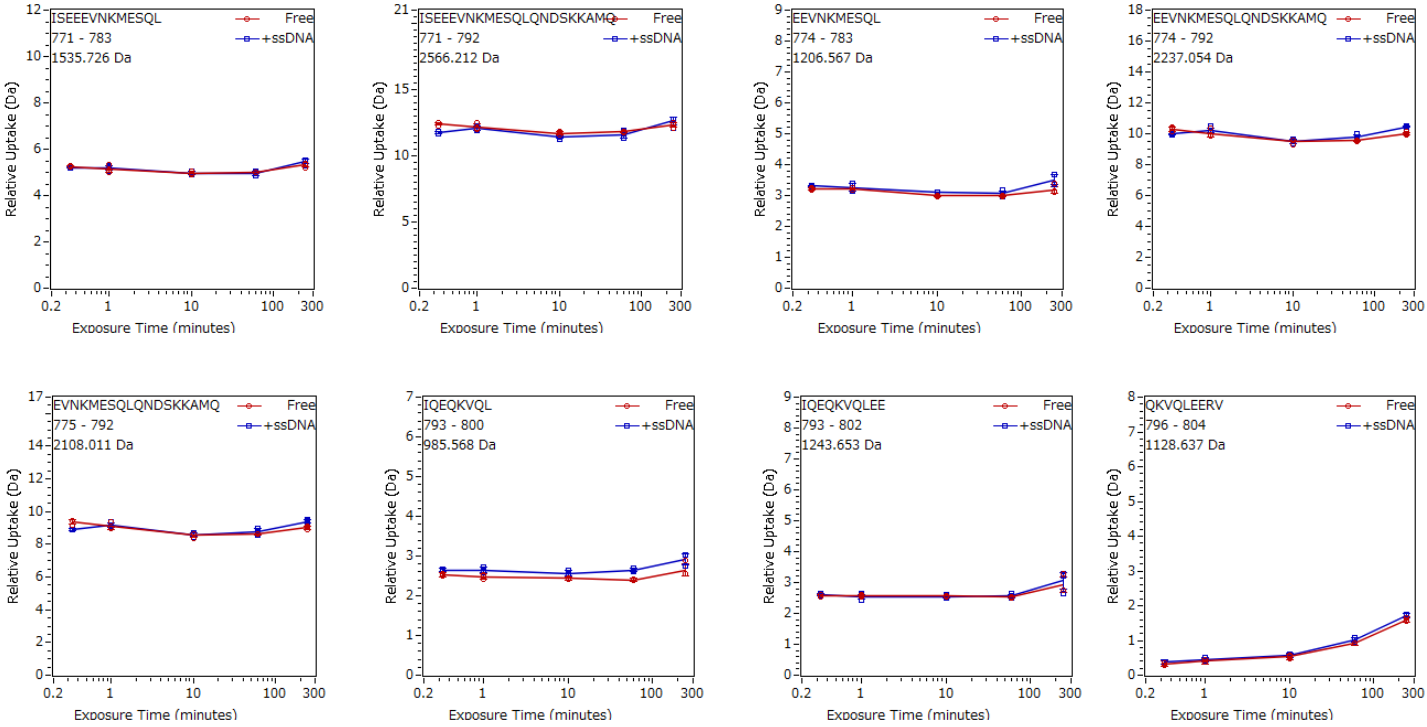

Table S1. The error analysis of the fitting parameters for each binding model

Model [a]	Fitting Parameter	Best-fit value	68.3 % error interval		RMSD / cal mol^{-1}
			Minimum	Maximum	
ABB	log (Ka$_1$)	7.652	7.232	8.162	200
	ΔH_1 / kcal mol $^{-1}$	-1.263	-1.543	-0.903	
	log (Ka$_2$/ Ka$_1$)	-2.050	-2.450	-1.700	
	ΔH_2 - ΔH_1 / kcal mol $^{-1}$	-3.514	-4.354	-2.844	
ABBB	log (Ka$_1$)	7.121	5.701	9.231	195
	ΔH_1 / kcal mol $^{-1}$	-1.841	-17.34	-0.8412	
	log (Ka$_2$/ Ka$_1$)	-1.409	-3.239	-0.4391	
	ΔH_2 - ΔH_1 / kcal mol $^{-1}$	2.364	-0.164	-	
	log (Ka$_3$/ Ka$_1$)	-1.971	-4.176	-	
	ΔH_3 - ΔH_2 / kcal mol $^{-1}$	-4.253	-	-3.453	
ABB [b]	log (Ka$_1$)	5.823	5.603	6.073	260
	ΔH_1 / kcal mol $^{-1}$	5.317	3.607	7.297	
	ΔH_2 - ΔH_1 / kcal mol $^{-1}$	-15.09	-19.09	-11.76	
AB	log (Ka)	7.252	6.252	-	793
	ΔH / kcal mol $^{-1}$	-5.795	-7.595	-4.495	

[a] A was defined as ssDNA and B was defined as hSmc2H-CC30/hSMC4H-CC30 heterodimer

[b] ABB model, assuming that the value of Ka$_1$ is equal to that of Ka$_2$

- : not found