

Supporting Information

Hanson *et al.* 10.1073/pnas.0810318105

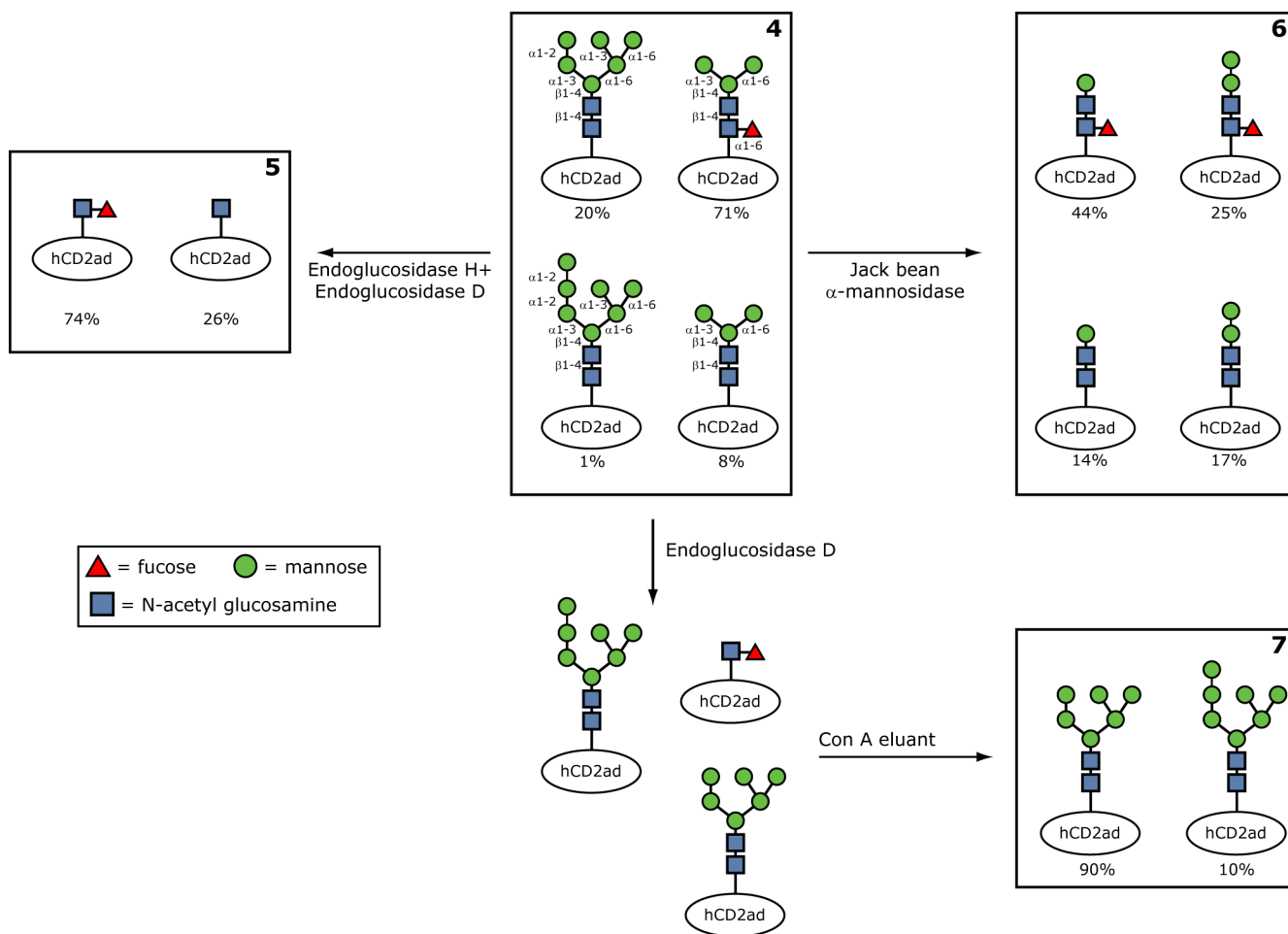
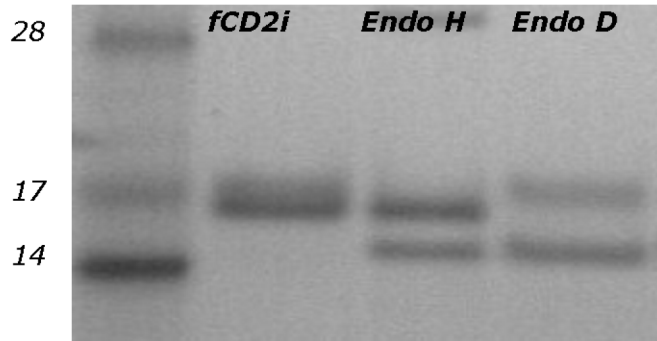


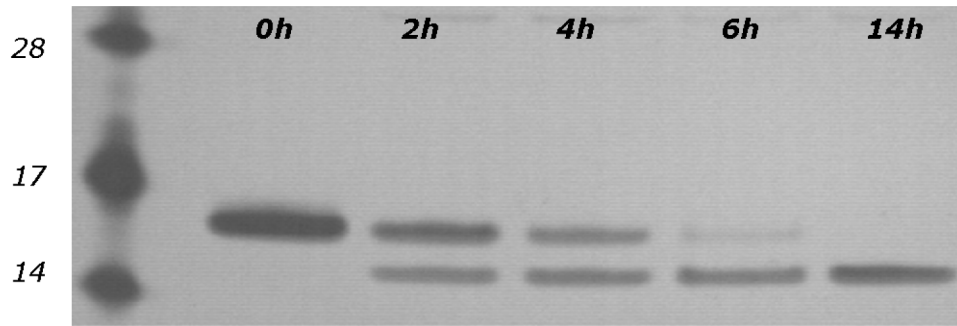
Fig. S1. Enzymatic remodeling of hCD2ad. Numbers under glycoforms indicate the percent of each glycoform in the mixture.

A. Individual digest (14h)



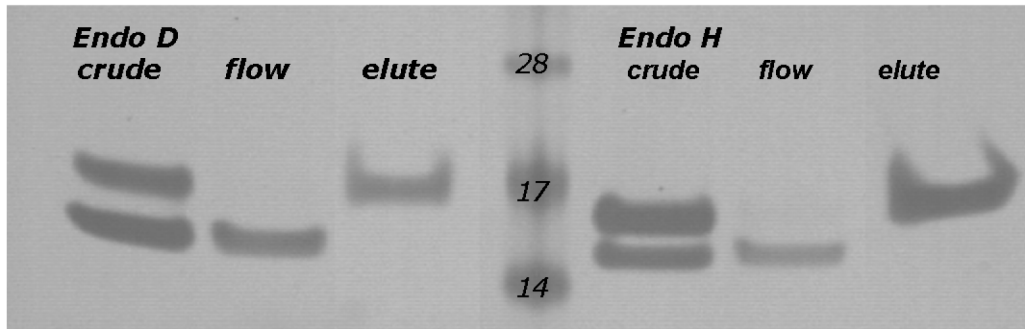
****Coomassie Blue Stain**

B. Double digest, Endo H & D, time course:



****SilverSnap Stain**

C. ConA purification of Endo digested fCD2i



****SilverSnap Stain**

Fig. S2. Analysis of enzymatic remodeling of hCD2ad variant 4 (labeled as fCD2i in the figure) with endoglycosidases by SDS/PAGE.

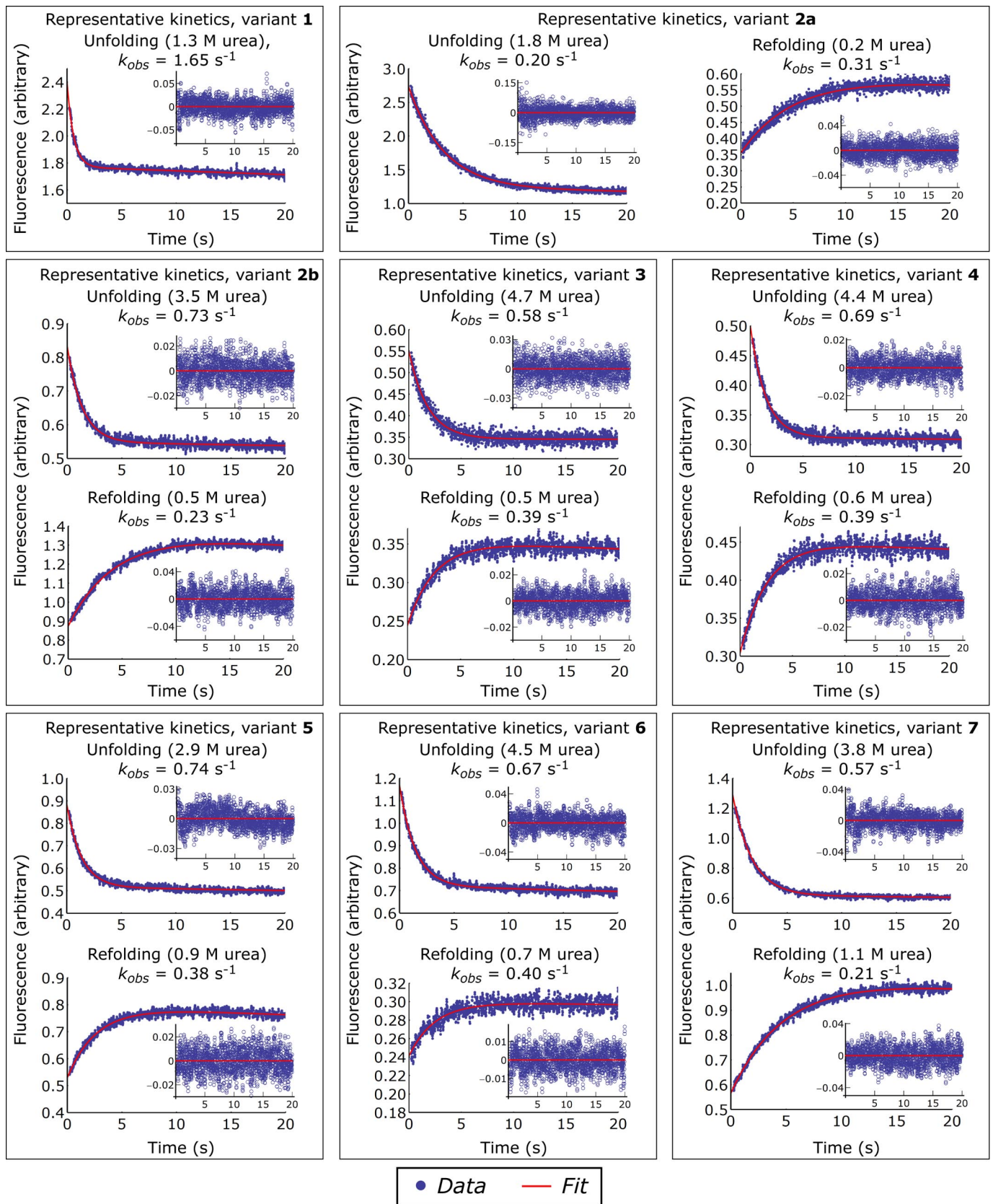
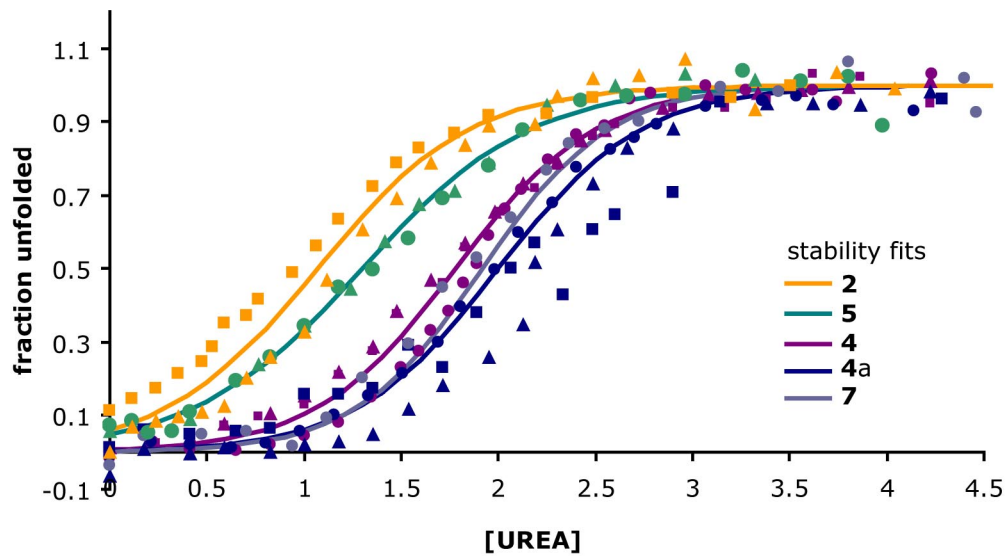


Fig. S3. Representative hCD2ad variant kinetic plots and fits. Residuals are shown as insets.



Stability from Thermodynamics					Stability from Kinetics	
hCD2ad variant		$\Delta G_{f,0}$ (kcal/mol)	m_{eq} (kcal/mol M)	n	$\Delta G_{f,0}$ (kcal/mol)	m_{eq} (kcal/mol M)
2	●	-1.6 ± 0.4	1.5 ± 0.2	2	-1.5 ± 0.1	1.62 ± 0.09
5	●	-1.8 ± 0.3	1.4 ± 0.1	2	-1.6 ± 0.1	1.53 ± 0.14
4	●	-2.9 ± 0.2	1.6 ± 0.1	3	-2.9 ± 0.2	1.57 ± 0.14
4a	●	-3.2 ± 0.8	1.5 ± 0.2	3	—	—
7	●	-3.5 ± 0.8	1.8 ± 0.3	2	-2.5 ± 0.1	1.66 ± 0.08

Fig. S4. Representative hCD2ad variant urea denaturation curves. Stabilities obtained by equilibrium thermodynamics and kinetics are in agreement, which is a good indication of 2-state behavior.

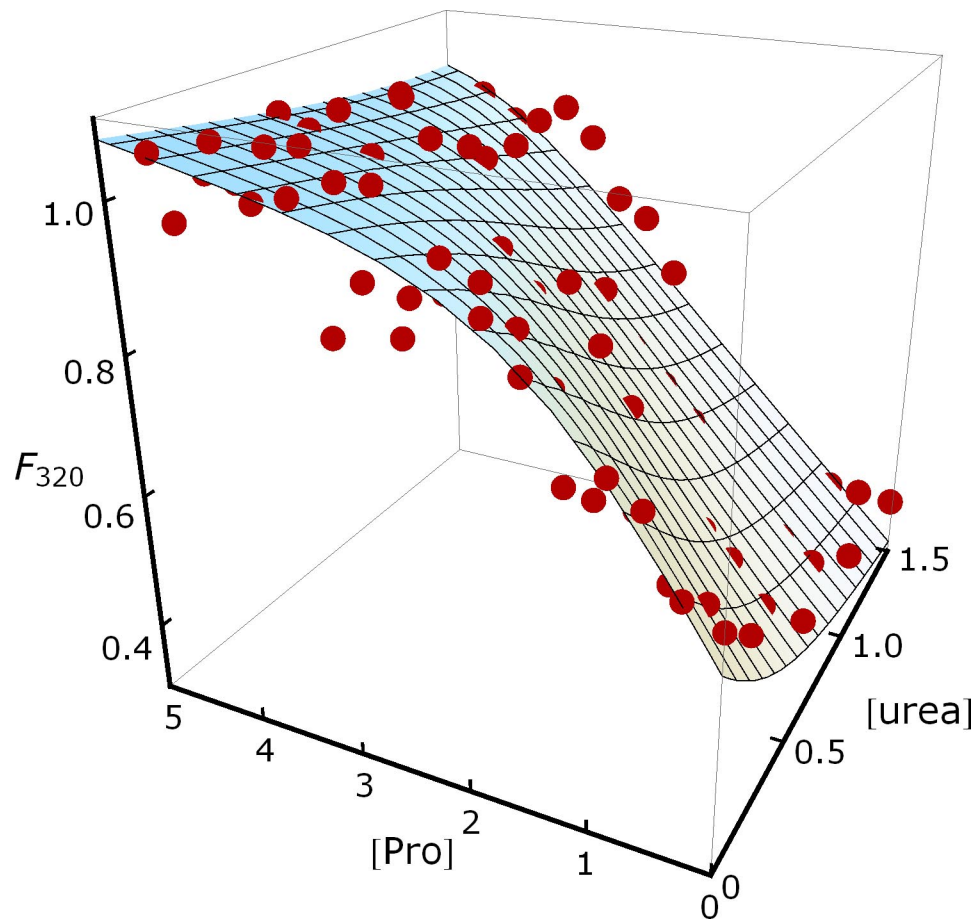


Fig. S5. hCD2ad variant 1 urea/proline denaturation/renaturation surface and fit. Points represent experimental F_{320} values and the surface represents the fit to these values. F_{320} is measured in arbitrary units.

Table S1. MS characterization of hCD2ad glycoforms from HEK cells (hCD2ad variant 3)

N-glycan type	MS _{found}	RA	Structure
Hybrid	15,441	100	GlcNAcMan ₅ GlcNAc ₂
Complex	15,646	79	LacNAc ₂ ManGlcNAc ₂
Oligomannose	15,372	67	Man ₆ GlcNAc ₂
Complex	15,793	60	LacNAc ₂ ManGlcNAc ₂ + Fuc
Hybrid	15,591	60	LacNAc ₂ Man ₅ GlcNAc ₂
Hybrid	15,282	56	LacNAc ₂ Man ₄ GlcNAc ₂

RA, relative abundance

Table S2. MS characterization of hCD2ad insect glycoforms

N-glycan type	MW _{expected}	RA			
		Sf9-1	Sf9-2	Sf9-3	Tn5
Man ₃ GlcNAc ₂ (Fuc)	15,031	74	70	70	55
Man ₆ GlcNAc ₂	15,373	15	24	20	28
Man ₃ GlcNAc ₂	14,887	10	6	20	10
Man ₇ GlcNAc ₂	15,535	1		2	7

Sf9-1 to Sf9-3 and Tn5 are four preparations of hCD2ad variant 4. % RA, percentage of total relative abundance. Sf9-1 to -3 represent different preparations of hCD2ad from Sf9 host. Tn5 is a different insect expression host; see [SI Appendix](#).

Table S3. MS characterization of remodeled hCD2ad variants (see Fig. 1C and Fig. S1)

hCD2ad variant	MW _{expected}	MW _{found}	%	Structure	Enzyme step
5, sample 1	14,344	14,342	72	FucGlcNAc	Endo D cut
		14,195	28	GlcNAc	
5, sample 2	14,344	14,342	75	FucGlcNAc	Endo D/H cut
		14,195	25	GlcNAc	
6	14,708	14,709	44	Man ₁ GlcNAc ₂ (Fuc)	α-Mannosidase
		14,870	25	Man ₂ GlcNAc ₂ (Fuc)	
		14,723	17	Man ₂ GlcNAc ₂	
		14,559	14	Man ₁ GlcNAc ₂	
7	15,373	15,371	90	Man ₆ GlcNAc ₂	Endo D uncut
		15,533	10	Man ₇ GlcNAc ₂	
G	14,197	14,196		GlcNAc	Endo H cut
Paucimannose	15,034	15,031	100	Man ₃ GlcNAc ₂ (Fuc)	Endo H uncut
PNGase A or F treated	13,994	13,994	100	Asn65Asp	PNGase

Other Supporting Information Files

[Dataset S1](#)

[SI Appendix](#)