

Title:

Computationally Driven Deletion of Broadly Distributed T cell Epitopes in a Biotherapeutic Candidate

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Short Title

Optimized Epitope Deletion

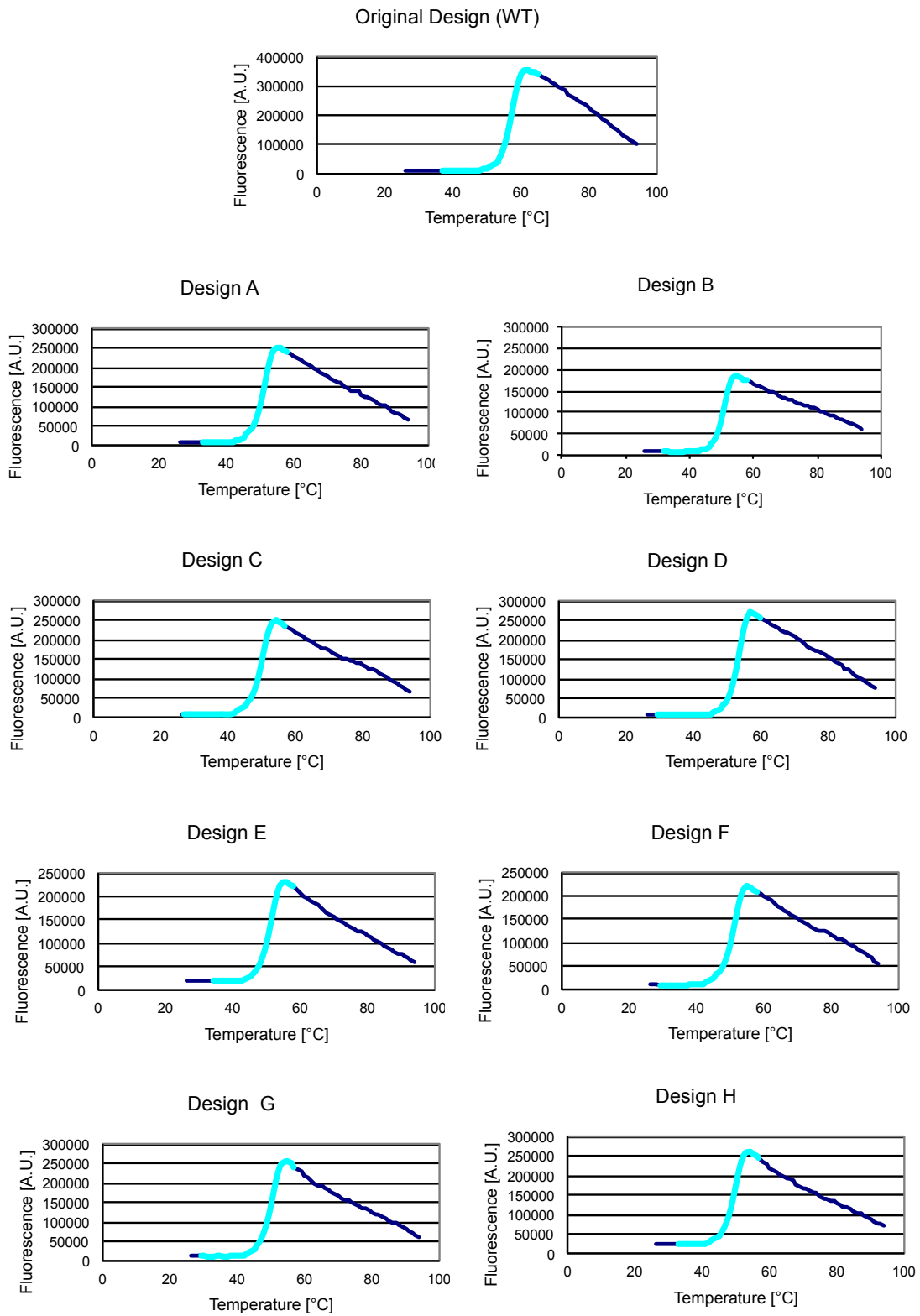


Figure S1 – Differential scanning fluorimetry melting curves for variant enzymes. Protein unfolding is characterized by an increase in fluorescence.

Table S1. ProPred Binding Predictions and Measured Peptide-MHC II IC₅₀ Values

Peptide	# Predicted Epitopes ^a				Experimental IC ₅₀ ^b			
	Allele DRB1*				Allele DRB1*			
	0101	0401	0701	1501	0101	0401	0701	1501
A13	1	2	2	1	>250	22.94	0.8185	12.1
A13D	0	0	0	0	>250	>250	56.13	61.25
A13E	0	1	0	0	>250	71.12	74.46	>250
K21	0	1	0	0	3.58	3.623	41.49	5.378
K21E	0	0	0	0	16.7	11.37	40.43	16.79
R105	2	2	1	2	>250	>250	20.64	12.27
R105S	1	1	1	1	26.73	>250	>250	69.45
R133	0	0	0	1	161.6	>250	72.85	0.133
R133H	0	0	0	1	27.09	>250	35.11	0.1752
R210	0	0	1	2	>250	>250	>250	21.18
R210H	0	0	0	0	>250	>250	>250	91.5
M235	2	1	0	0	12.41	23.64	16.95	>250
M235D	0	0	0	0	>250	>250	28.02	>250
M235Q	0	0	0	0	12.12	37.46	23.1	>250
I262	1	1	2	1	22.17	0.4567	1.675	0.3233
I262T	0	1	1	0	>250	2.185	4.147	5.725

^a For each allele, values indicate the number of predicted epitopes within a synthetic peptide. Positive correlations between predicted and measured peptide binding are shaded (experimental binding threshold set at 100 μ M).

^b IC₅₀ values less than 1 μ M are considered strong binders (black), 1 μ M \leq IC₅₀ < 10 μ M moderate binders (dark grey), 10 μ M \leq IC₅₀ < 100 μ M weak binders (light grey), and IC₅₀ \geq 100 μ M are classified as non-binders (no shading).