Table S2. Essential node pairs detected in four Fel d 1 simulated systems. Nodes that appear more than once are grouped by color. Interactions detected between pairs by PDBsum for the crystallographic structure are in parentheses.

	Interface (Chain A - Chain B)	**Chain A**	**Chain B**
Without Ca^{2+}	Lys29-Asp82 (1HB, NBC) Leu132-Leu94	Cys44-Cys118 (DS) Ile64-Val102	Leu41-Tyr119 (NBC) Phe85-Met134 (NBC)
With Ca^{2+}	Leu31-Leu94 Asn91-Leu129 (NBC) Leu132-Phe85 (NBC)	Cys3-Ala74 Val10-Phe84	Val6-Tyr81 Asn37-Arg127
Minimal Glycosylation	Phe85-Asp130 (NBC) Val128-Leu94 Ser139-Thr76 (NBC)	Val6-Phe80 Ile40-Asn122 (NBC)	Val6-Phe80 Asn37-Arg127
Full Glycosylation	Phe85-Leu132 (NBC) Asn89-Leu129 (NBC) Thr135-Phe85 (NBC)	Lys7-Phe80 Asn37-Arg127 (2HB)	Cys3-Tyr65 Asn37-Val128

HB: hydrogen bond(s), NBC: non-bonded contacts, DS: disulfide bridge.
Note: There is a pair in the simulation with Ca^{2+} (Leu129B-Arg127B) that connects the interface pair (Asn91-Leu129) to the 'hinge' pair (Arg127-Asn37).