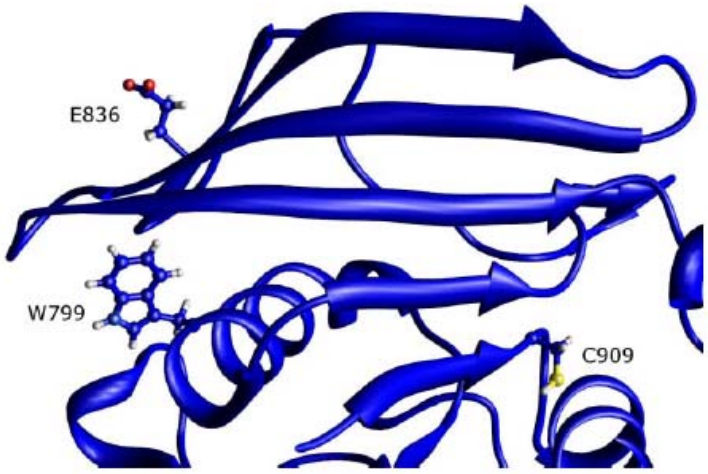
SUPPLEMENTARY DATA

Supplementary Table 1. Results for models produced by the HHPRED server from template structures with lower (31-36%) identity. Templates structures are indicated by their protein databank IDs. The percentage sequence identity between template structure and the IA2 structure 2I1Y.pdb is shown in the second column. The cysteine equivalents to C909 were not involved in disulphide bonds in any of the template structures and the crystallization conditions for the template structures are shown in the fourth column. The root mean square deviation (RMSD) of the positions of greater than 280 residues is between 1.2 and 1.7 Å and shows that overall fold is retained when HHPRED models the wild type protein sequence using these templates. The models produced with the C909A mutated sequence have RMSDs between 0.16 and 0.91 Å when compared to the model produced by HHPRED for the wild-type sequence using the same template. The overall fold for these models is therefore unperturbed by the C909A mutation.

	Sequence identity (%)	**Disulphide at C909 equivalent in template**	**Crystallization conditions**	**RMSD (Å) for > 280 residues**	
				2I1Y.pdb to WT_HHPRED	**WT_HHPRED to C909A_HHPRED**
2I1Y	100	No	25% PEG 3350, 10% glycerol, 0.1M bis-tris, 0.2M ammonium acetate, pH 6.0	N/A	0.161
3S3E	32	No	15% PEG 4000, 0.12 M citrate pH6.5, 10% isopropanol, 10% N-butanediol	1.482	0.747
2OC3	31	No	0.1M hepes, 25% PEG 3350, 6% jeffamine, pH 6.8	1.434	0.822
2PA5	33	No	25% PEG 3350, 0.2M K thiocyanate, 10% ethylene glycol, 0.15M bis-tris propane, pH 6.15	1.462	0.910
2OOQ	35	No	0.2M LiCl, 0.1M hepes, 20% PEG 6000, 10% ethylene glycol, pH7.0	1.252	0.683
3I36	36	No	20% PEG1K, 0.1M MES, pH 6.5	1.372	0.755
2HC1	34	No – but initial conditions reducing	20% PEG 8K, 0.22M MgCl2, 1% BME, 0.1% BOG, 5 mM DTT, 0.18 M ammonium acetate pH 8.2	1.698	0.717

SUPPLEMENTARY DATA

Supplementary Figure 1. Ribbon diagram showing the relationship between W799, C909 and E836. W799 is closely packed against the back of a beta sheet connecting C909 to E836. It is possible that modifications at W799 or C909 may tilt this sheet which may in turn affect the E836 epitope. We postulate that this may explain why the W799A mutation affects both C909 and E836 epitopes.



Supplementary Figure 2. *SDS-PAGE using a 10-20% Tris-Tricine gel of 20000 cpm in vitro ^{35}S labelled IA-2ic (42 kDa) and IA-2 PTP (33 kDa) visualized by autoradiography. Lane (1) IA-2ic wild type, lane (2) IA-2 C909S, lane (3) IA-2 C909A, lane (4) IA-2 E837K, lane (5) IA-2 C909S and E836K, lane (6) IA-2 PTP, lane (7) IA-2 PTP W799A, lane (8) IA-2β PTP and lane (9) IA-2β 945S. No difference in the quality of the mutated labels was seen compared with the wild type (lanes 1, 6 and 8).*