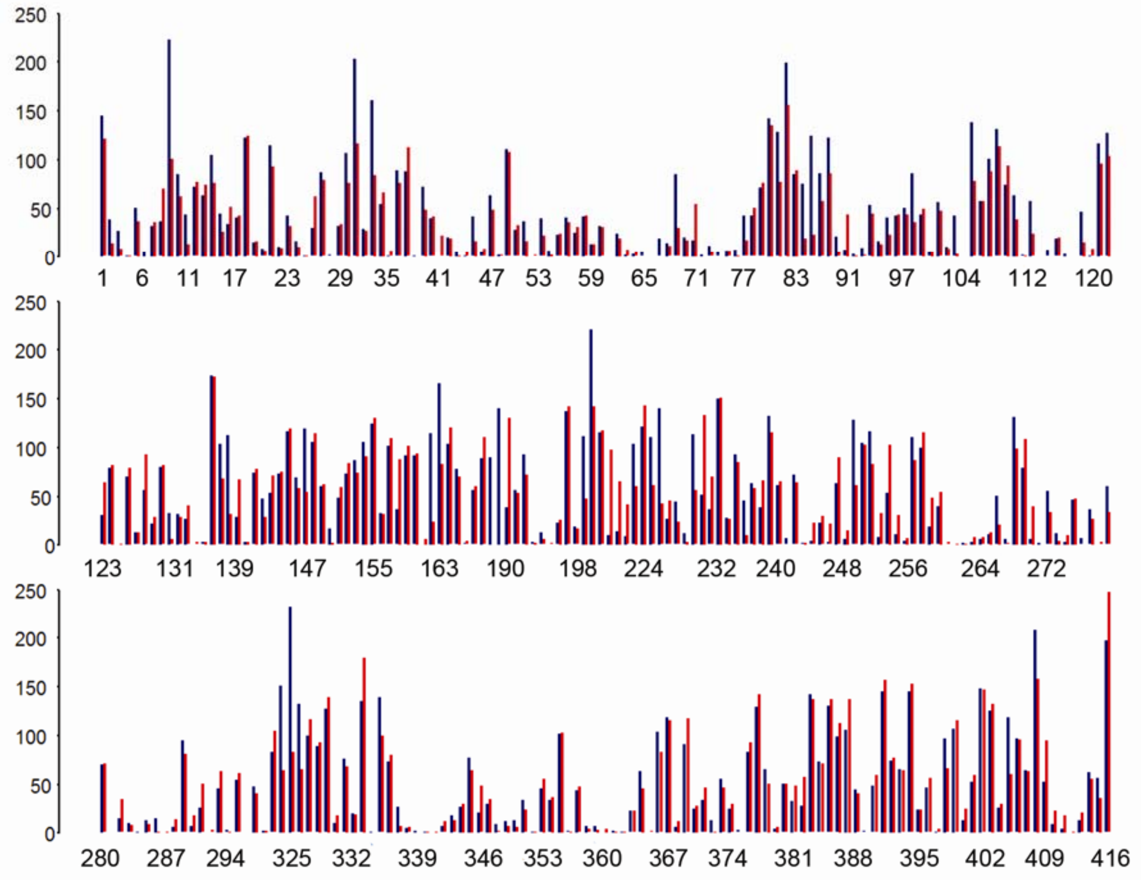
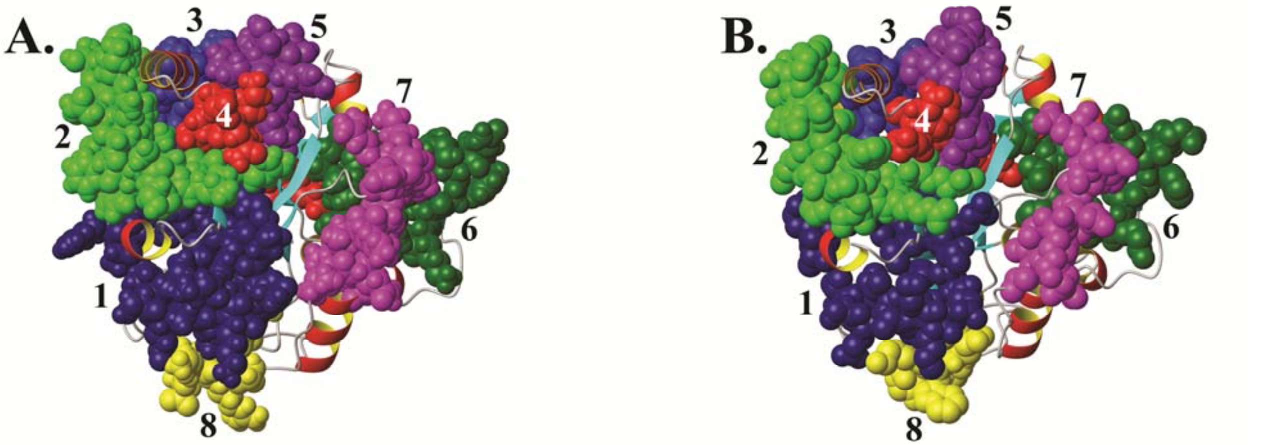
Figure S1:



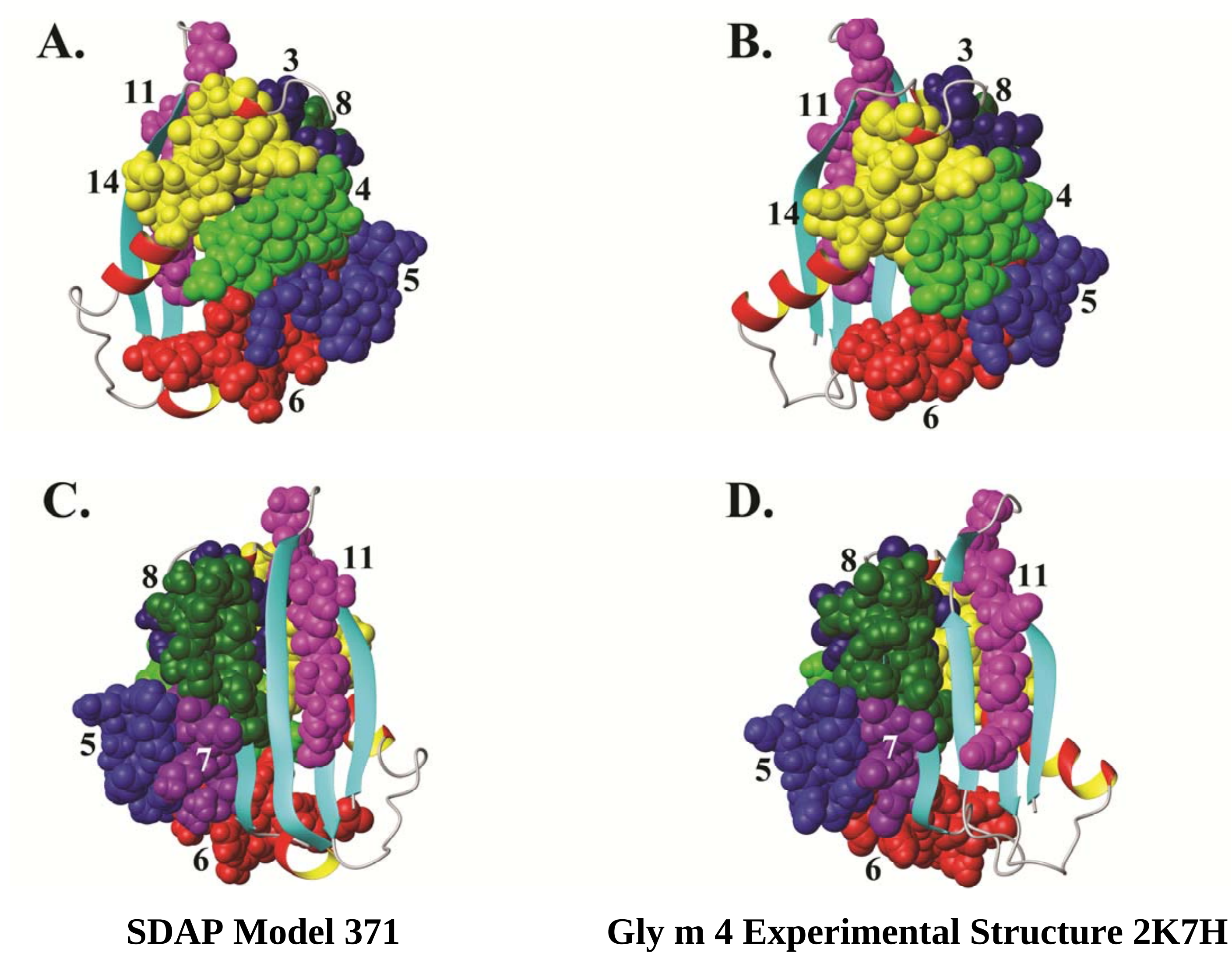
<u>Fig. S1:</u> Solvent accessible areas of individual residues in Å^2 for the 3D model (in blue) and the X-ray crystal structure (3S7E) (in red) of Ara h 1. Residue numbers follow the numbering of residues in the model co-ordinate set.



SDAP Model 802

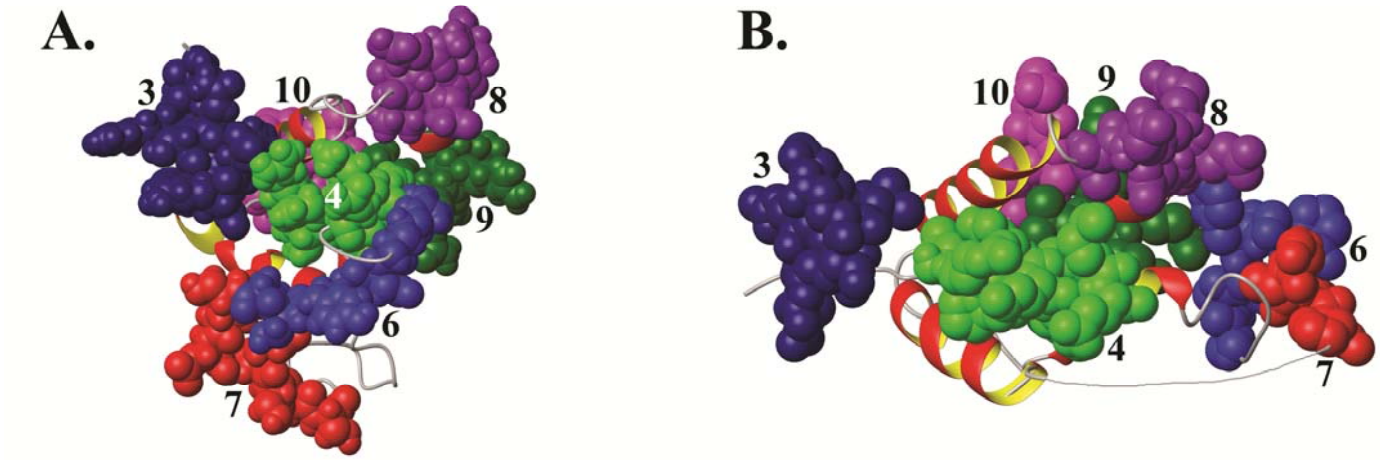
Hev b 2 Experimental Structure 3EM5

Figure S2. Comparison of the structural regions of Hev b 2 that correspond to the linear peptides that bind IgE antibodies. A) 3D model and B) X-ray crystal structure of Hev b 2.



SDAP Model 371 **Gly m 4 Experimental Structure 2K7H**

Figure S3. Comparison of the structural regions of Gly m 4 that correspond to the linear peptides that bind IgE antibodies. Two views are shown for the 3D model (A and C) and the X-ray crystal structure (B and D) of Gly m 4.



SDAP Model 283 **Ara h 2 Experimental Structure 3OB4**

Figure S4. Comparison of the structural regions of Ara h 2 that correspond to the linear peptides that bind IgE antibodies. Epitopes 3, 4, 6-10, listed in the Ara h 2 entry page of SDAP (http://fermi.utmb.edu/SDAP/), were mapped on the 3D model (A) and X-ray crystal structure (B) of Ara h 2.