Supplementary Figure S1.

Multiple sequence alignment of the VH-CH1 domains of different human immunoglobulin classes and subclasses.

Conserved residues are marked with shades of violet. Red boxes highlight positions 11, 122, 133, 196 , 209 and 220 (according to the IgA1 numbering scheme), which are discussed in detail throughout the structural analyses in the main text.

The sequences included correspond to the crystallographic structures aligned in Fig. 3B (main text). Human IgA2 corresponds to the one for which a structural model was proposed on the basis of solution scattering data and homology modelling (PDB ID 1R70). IgG4 corresponds to PDB ID 1AD9. The other sequences correspond to NCBI sequence records gi244188 (IgD), gi6110574 (IgG2), and gi6537296 (IgG3).

The alignment was done with the clustalOWS option implemented within the Jalview program (Waterhouse, A.M., Procter, J.B., Martin, D.M.A, Clamp, M.. and Barton, G.J. (2009) "Jalview Version 2 - a multiple sequence alignment editor and analysis workbench" *Bioinformatics* **25**(9): 1189-1191. doi: 10.1093/bioinformatics/btp033)