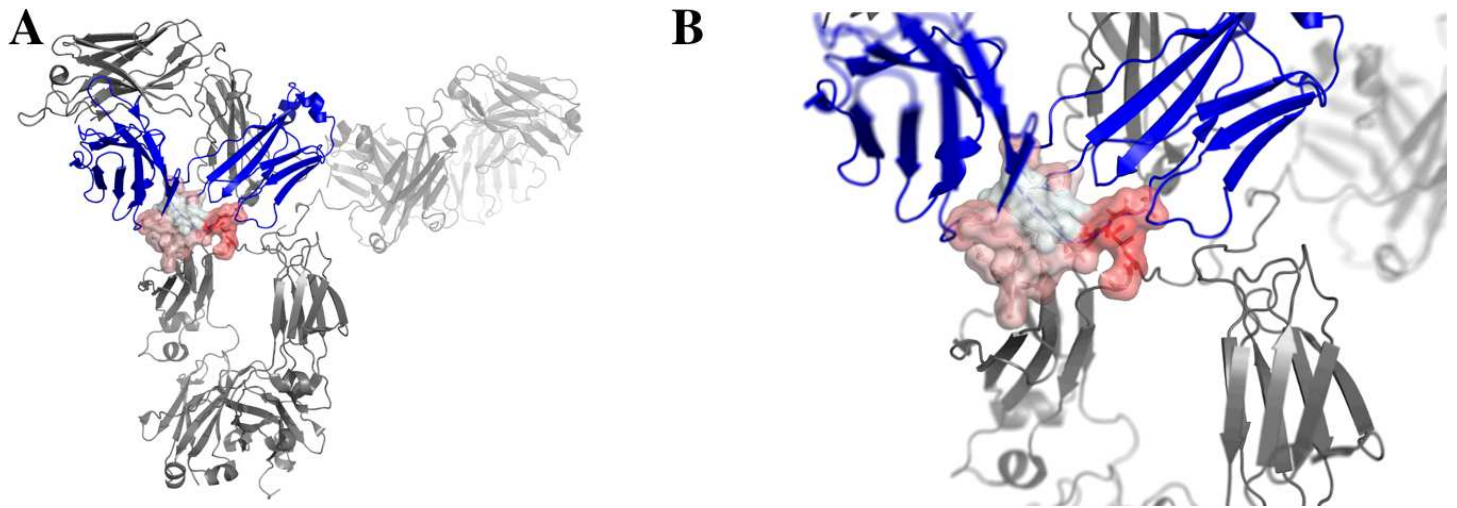


Supplementary Figure 1. The Structures within the Minimal Selected Ensemble of mAb1 in 20mM HisCl pH6.0 (A) Superposition of the crystal structure of human IgG1 (grey envelope) with one structural component of the MSE solution (Red ribbons). The RMSD between the two structures is $\sim 4.0\text{\AA}$ and supports the notion that the conformation present in the crystal occupies $\sim 20\text{-}30\%$ of solution conformations. (B) The four remaining structures within this MSE solution. The structures in silver and blue were determined to be qualitatively similar to the single molecule structures presented in *Sandin et al. 2004*. In total these structures illustrate the conformational diversity of mAb1 under these conditions



Supplementary Figure 2. The IgG Fab-FC interface(A)Overall view of the Fab-FC interface of IgG1B12. In the IgG crystal structure, one Fab is extended, while the proximal Fab is compact and makes contacts with the FC region of the IgG. This panel illustrates the overall structure of the IgG molecule and highlights the residues that make contacts between the proximal Fab and FC region. In this region, the residues that make contacts are shown in a surface rendering and are colored from silver to red in increasing terms of hydrophobicity. (B) A zoomed image centered on the residues that interface between the Fab and FC regions. The majority of these residues are hydrophobic and thus may represent a region where ArgCl can interact.