

Figure 9.10 Measured overall dipole moment for mAb1 (solid circles) versus mAb2 (solid triangles) as a function of pH.

Adapted from [Singh et al. \(2014\)](#).

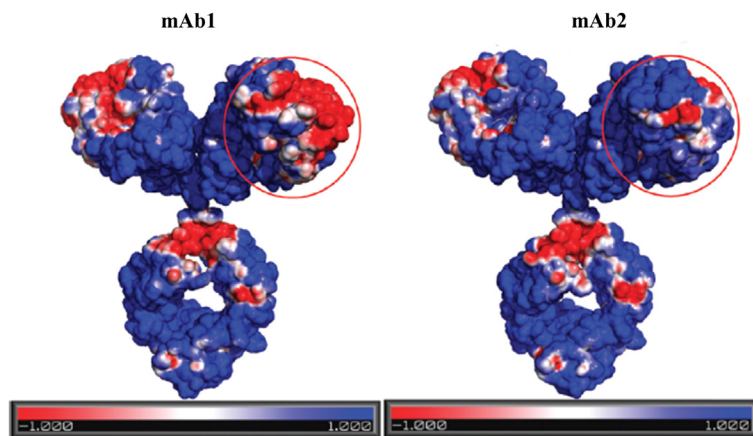


Figure 9.11 Computed electrostatic potential surfaces for mAb1 and mAb2.

Adapted from [Yadav et al. \(2012\)](#).

Linking amino acid sequence to self-association and viscoelastic behavior of mAb1 and mAb2

The viscosity and self-association of mAb1 and mAb2 have been thoroughly explored. These two mAbs bind to very different targets but were constructed using essentially the same human IgG₁ Fc construct. Thus, the main differences between these mAbs resides is their complementary determining region (CDR), and therefore provides an opportunity to make changes in the CDR to assess impact on self-association and