# Conformational protein structure shifts in aggregation prone conditions for MAb and Fab

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Antibody solution structures are critical for understanding the impact of formulation conditions upon structure and aggregation propensity. The aggregation kinetics of a Fab have been extensively mapped for pH3.5-9, ionic strength 0-250mM, and at 4-65C. Synchrotron X-ray scattering (SAXS) at 23C reveals a pH- and salt-dependent conformational structure shift in one region of the protein, that correlates with aggregation propensity. Meanwhile, SAXS and constrained modelling determined that IgG4 has an asymmetric solution structure. At pH 7.4 the relative Fab-Fc-Fab domain conformations were concentration dependent but the overall IgG4 size remained unaffected. At pH 3, conditions significant structural changes occurred over time that preceded an increased propensity to aggregate.

References:

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