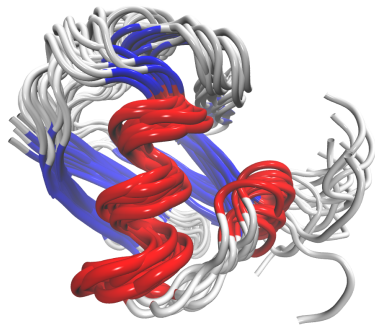
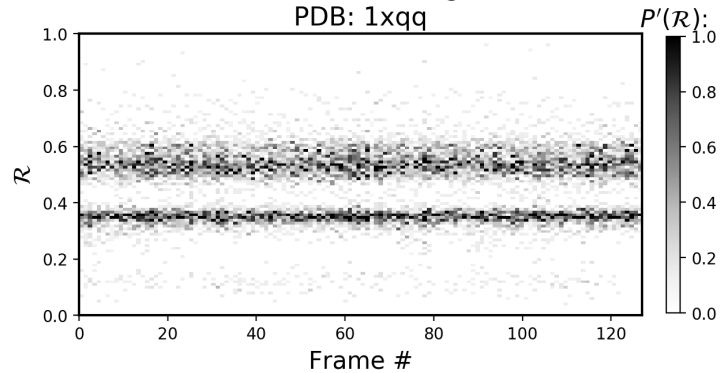


(a)



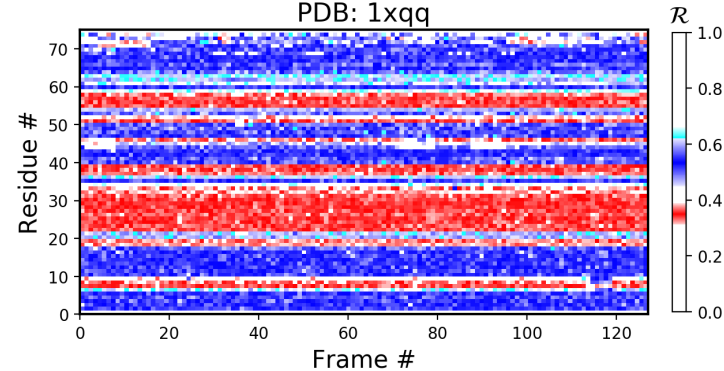
(b)

Per-model  $\mathcal{R}$ -histogram  
PDB: 1xqq



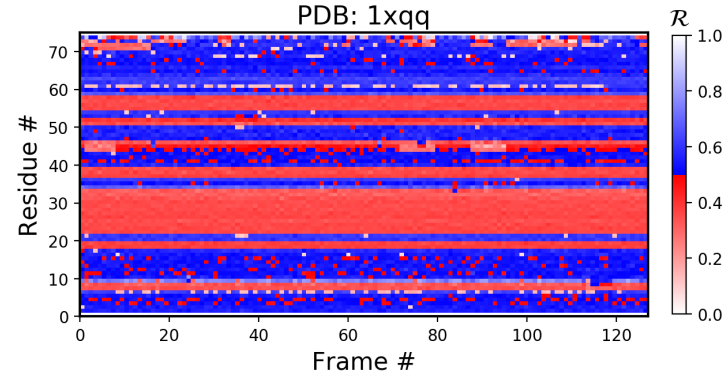
(c)

Per-residue  $\mathcal{R}$ ; CMAP: SecondaryStructure  
PDB: 1xqq



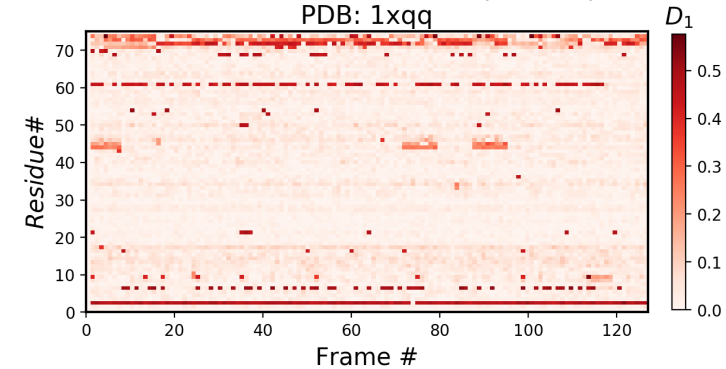
(d)

Per-residue  $\mathcal{R}$ ; CMAP: Chirality  
PDB: 1xqq



(e)

Per-residue deviation  $D_1 = |\mathcal{R}_t - \mathcal{R}_1|$   
PDB: 1xqq



(f)

Per-residue deviation  $D_{-1} = |\mathcal{R}_t - \mathcal{R}_{t-1}|$   
PDB: 1xqq

