Structural characterization of the intrinsically disordered saliva protein Histatin 5: A combined SAXS and Monte Carlo simulation study

Carolina Cragnelll[1], Marie Skepö[1]

[1]*Theoretical Chemistry, Lund University, Lund, Sweden*

**carolina.cragnell@teokem.lu.se*

For more than 30 years, a coarse-grained model based on the primitive model, in combination with Monte Carlo simulations, have been used to model polyelectrolytes and polyampholytes under various conditions. Sometimes this model is also refered to as the bead-necklace model.

Our aim is to apply this model for intrinsically disordered proteins, and verify the simulation results by experiments. As model proteins we are using the salivary protein Histatin 5, a 24 AA long peptide, which has a strong fungicidal property [1]. In vitro, it has been found that this fungicidal action is strongly dependent on ionic strength [2, 3]. Conformational properties of Histatin 5 are considered to be of importance.

We would like to present results showing good agreement between the scattering curves for Histatin 5 obtained from SAXS and the simulations. At high salt concentration, the protein behaves as a neutral polymer, and at low salt concentration, a repulsive peak is obtained at low q. In the latter regime, it is the net charge of the protein that is of importance for the intermolecular interaction, charge distribution plays a minor role. Preliminary results also indicate that the peptide conformations are dependent on pH (in the salivary pH range) and the prescence of divalent ions. This indicates that electrostatic interactions indeed are important for the Histatin 5 bulk structure.

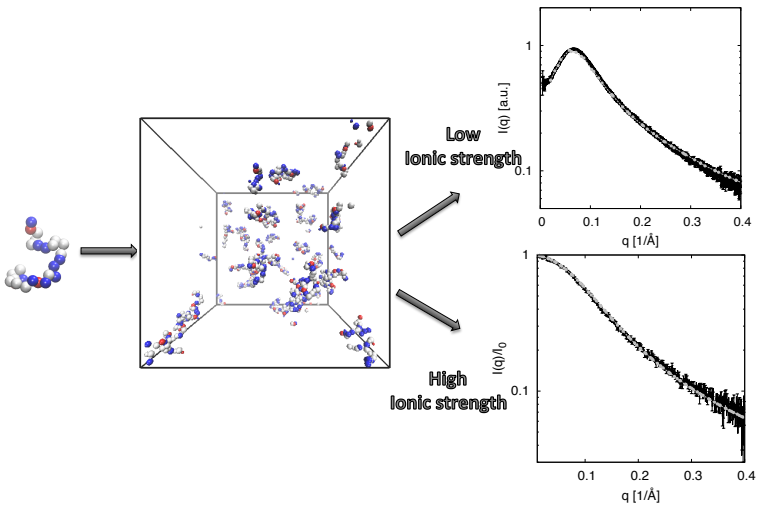

Figure Snapshots from simulations and the corresponding calculated structure factors at high and low ionic strength, respectively. The black curves are the measured SAXS intensities obtained at ESRF, Grenoble, France.

[1] Oppenheim, F.G et al. *J. Biol. Chem*., 1988, **263**, 7472–7477.
[2] Helmerhorst, E.J. et al. *Biol. Chem.* 1999, **274**, 7286-7291.
[3] Jang, W.S. et al M. *Molecular Microbiology*, 2010, **77**, 354-370.