

## CALCULATION OF SMALL ANGLE SCATTERING INTENSITIES FROM MOLECULAR DYNAMICS SIMULATION

FRANCI MERZEL<sup>1</sup> and JEREMY C. SMITH<sup>2</sup>

<sup>1</sup>National Institute of Chemistry, Hajdrihova 19, 1000 Ljubljana, Slovenia,

<sup>2</sup>IWR-Biocomputing, INF268, University Heidelberg, 69120 Heidelberg,  
Germany

**Abstract:** A method is presented to efficiently calculate small-angle neutron and X-ray solution scattering intensities from explicit - atom model of macromolecules and the surrounding solvent.

**Key Words:** X-Ray And Neutron Scattering, Multipole Expansion, Proteins

### INTRODUCTION

As small-angle solution X-ray and neutron scattering (SAS) techniques improve, there is increasing interest in developing methods to rapidly evaluate SAS profiles from explicit-atom coordinates [1, 2, 3], which are available from X-ray crystallography and NMR spectroscopy. In addition, simulation of molecular dynamics (MD) is frequently used with an explicit solvent to examine detailed macromolecular and solvent properties at the atomic level.

### METHOD

We define a model system to be one protein molecule (lysozyme) surrounded by the explicit water molecules forming a sphere. A 0.5 ns long trajectory of the system dynamics is obtained via MD simulation. The scattering intensity is given by the orientational average  $\langle \rangle_{\Omega}$  and the time average  $\langle \rangle_t$  over the square of the scattering amplitudes corresponding to different configurations which the scattering system adopts during the simulation. The small angle excess solution scattering intensity can be expressed as:

$$I(\mathbf{q}) = \left\langle \left\langle |A_0(\mathbf{q}, t) - B_0(\mathbf{q}, t)|^2 \right\rangle_{\Omega} \right\rangle_t$$

where  $A_0$  is the scattering amplitude of the atomic-detail system., and  $B_0$  describes the scattering amplitude of the system volume that is excluded from the background uniform bulk solvent. For computational efficiency, the scattering amplitudes are expressed in terms of multipole expansions:

$$A_0(\mathbf{q}, t) = \sum_j^N b_j \exp(-i\mathbf{q}\mathbf{r}_j(t)) = \sum_{lm} A_{lm}^0(\mathbf{q}, t) Y_{lm}(\Omega_{\mathbf{q}})$$

$$B_0(\mathbf{q}, t) = \bar{b}_0 \sum_j^N V_j f_j(\mathbf{q}) \exp(-i\mathbf{q}\mathbf{r}_j(t)) = \sum_{lm} B_{lm}^0(\mathbf{q}, t) Y_{lm}(\Omega_{\mathbf{q}})$$

where  $b_j$  denotes the scattering length of the  $j$ -th atom,  $\mathbf{r}_j(\mathbf{t})$  is the  $j$ -th atom time-dependent radius vector,  $V_j$  is its excluded volume, and  $f_j(\mathbf{q})$  is the corresponding form factor.  $N$  denotes the number of scattering particles, *i.e.* atoms, and  $\bar{b}_0$  is the bulk scattering density. The expression for the scattering intensity now reduces to the sum of the squares of the difference between the multipole coefficients  $A_{lm}^0 - B_{lm}^0$ .

## RESULTS AND DISCUSSION

An excellent agreement was found to exist between the simulation-derived and experimental profiles for solvated lysozyme. The differences between the profiles for the three types of experiment (X-ray scattering, neutron scattering in H<sub>2</sub>O solution, and neutron scattering in D<sub>2</sub>O solution) were also well reproduced. At the limit  $\mathbf{q} \rightarrow \mathbf{0}$ , the Guinier approximation allows the radius of gyration  $R_g$  of the scattering object to be derived. The radii of gyration from different types of scattering extracted from the experimental and calculated scattering profiles of lysozyme are listed in Table 1.

Tab. 1. Radii of gyration from different types of scattering.

	Exp. $R_g$ [nm]	calc. $R_g$ [nm]
X-ray	$1.54 \pm 0.02$	$1.53 \pm 0.02$
neut. in H <sub>2</sub> O	$1.38 \pm 0.02$	$1.36 \pm 0.02$
neut. in D <sub>2</sub> O	$1.24 \pm 0.02$	$1.25 \pm 0.02$

The currently-used method efficiently calculates SAS profiles from explicit-atom model of proteins and their surrounding solvent. The use of a multipole expansion permits the rapid calculation of SAS profiles from multiple configurations of systems consisting of large number of atoms.

## REFERENCES

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