

Conc. (mg/mL)	Exposure (s)	Porod $I_0$	Rg	Porod range	P(r) $I_0$	Rg	P(r) $d_{\max}$
2.73	0.5	31.674	22.9	23-506	31.93	22.53	65
2.73	5	31.983	22.6	25-504	30.8	22.2	63
2.73	0.5	31.965	22.6	23-503	30.1	22.22	64
1.36	0.5	17.342	22	24-501	16.14	21.63	61
1.36	5	16.188	21.7	27-499	16.27	21.73	61
1.36	0.5	15.55	21.2	29-498	16.28	22.17	65
0.68	0.5	8.9719	22.2	30-496	9.26	23.16	75
0.68	5	7.5183	21.1	36-490	9.37	23.61	75
0.68	0.5	NA	NA	NA	NA	NA	NA

Table 1:  $I_0$  and Rg statistics from the Porod and P(r) graph calculations. For each protein concentration a 0.5s, 5.0s, and second 0.5s exposure were generated. Due to the downward inflection at the low Q angles seen in the buffer subtracted data, each scattering profile was trimmed and that range used to calculate the Porod graph. The same range for each individual scattering profile was used along with the input  $d_{\max}$  to generate the P(r) graph. No values were reported for the second 0.5s exposure at concentration 0.68mg/mL presumably due to sufficient radiation damage at that low of a protein concentration. All graphs and reported  $I_0$  and Rg numbers generated using PRIMUS (Konarev *et al.*, 2003).

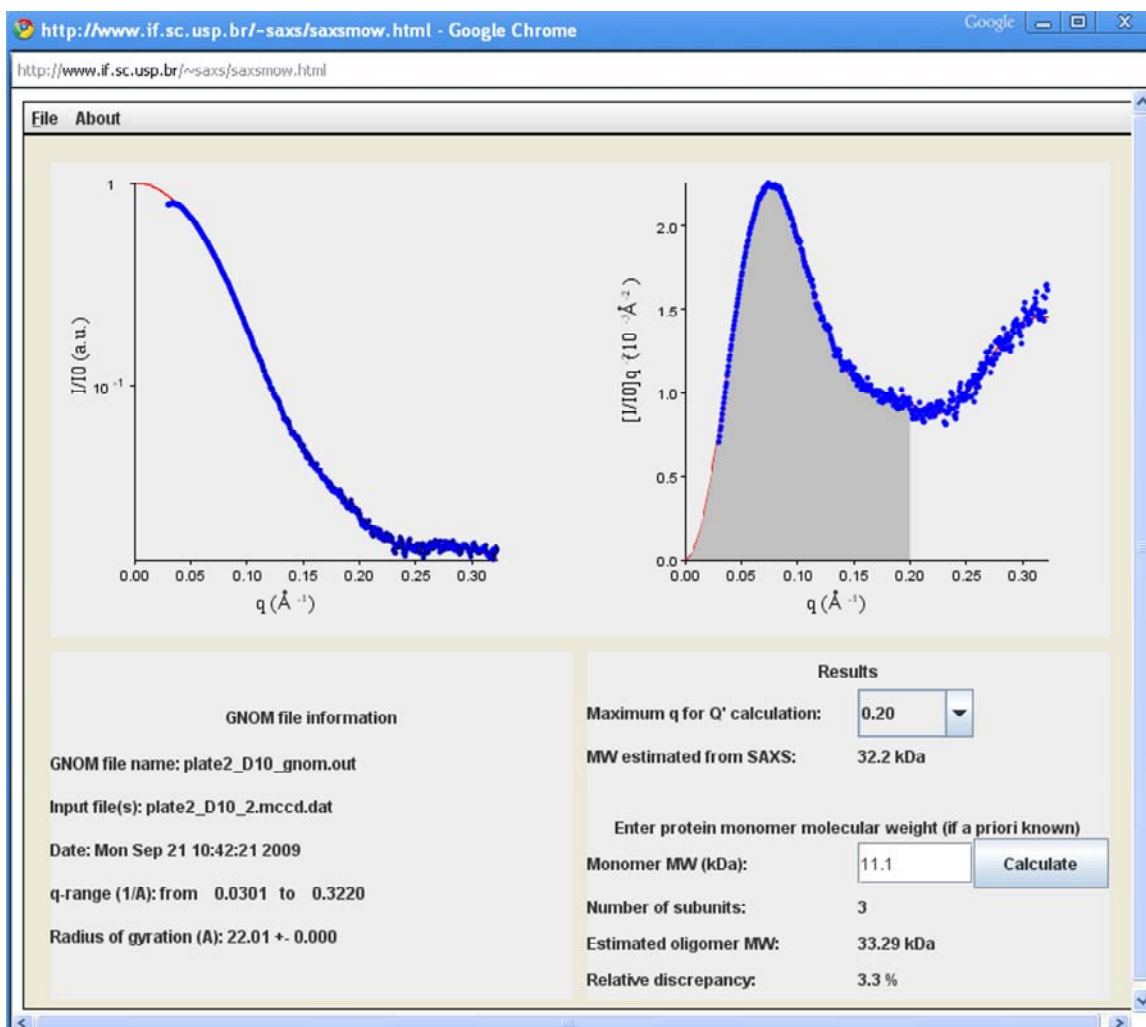


Figure 1: Molecular weight calculation from the 2.37mg/mL 5.0s scattering profile (SAXS MoW java applet (<http://www.if.sc.usp.br/~saxs/saxsmow.html>)) (Fischer *et al.*, 2010). At the  $q_{\max}=0.2$  the estimated molecular weight is 32.2kDa corresponding to a trimer based on a monomeric molecular weight of 11.1kDa calculated from the Rv1848 amino acid sequence.

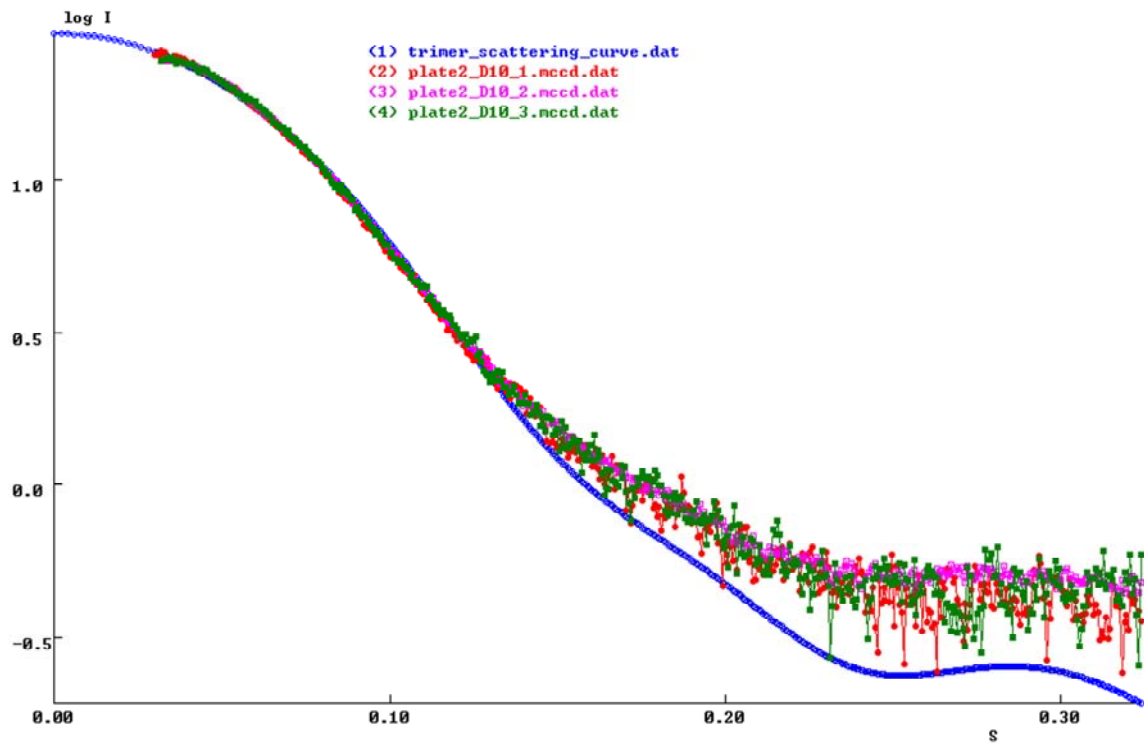


Figure 2: Trimmed scattering profiles (see supplementary figure1) of the 2.37mg/mL Rv1848 sample (first 0.5s exposure in red, 5.0s exposure in magenta, and second 0.5s exposure in green) and the crystallographic trimer ideal scattering profile (in blue) calculated using CRY SOL ( $\chi^2=2.843$ ) (Svergun *et al.*, 1995) overlaid using PRIMUS.

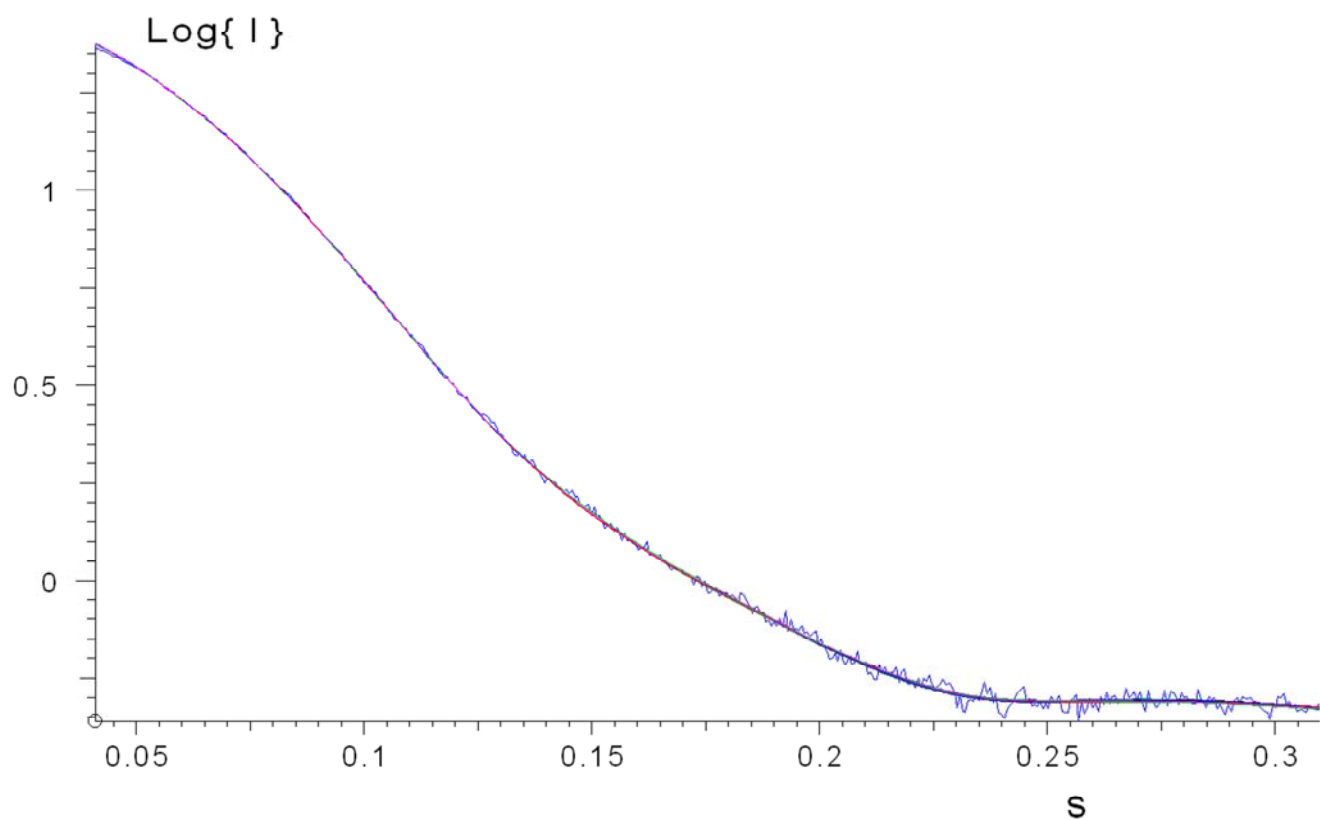


Figure 3: The ideal scattering profiles generated from the individual GASBOR envelope calculations overlaid on the 2.37mg/mL 5.0s exposure buffer subtracted data ( $S$  range 0.04 to 0.32) with an average  $\chi^2 = 1.48 \pm 0.48$ .

References:

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- Konarev, P. V., Volkov, V. V., Sokolova, A. V., Koch, M. H. J. & Svergun, D. I. (2003).  
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