STRUCTURAL BIOLOGY

Volume 72 (2016)

Supporting information for article:

The structure of VgrG1 from *Pseudomonas aeruginosa*, the needle tip of the bacterial type VI secretion system

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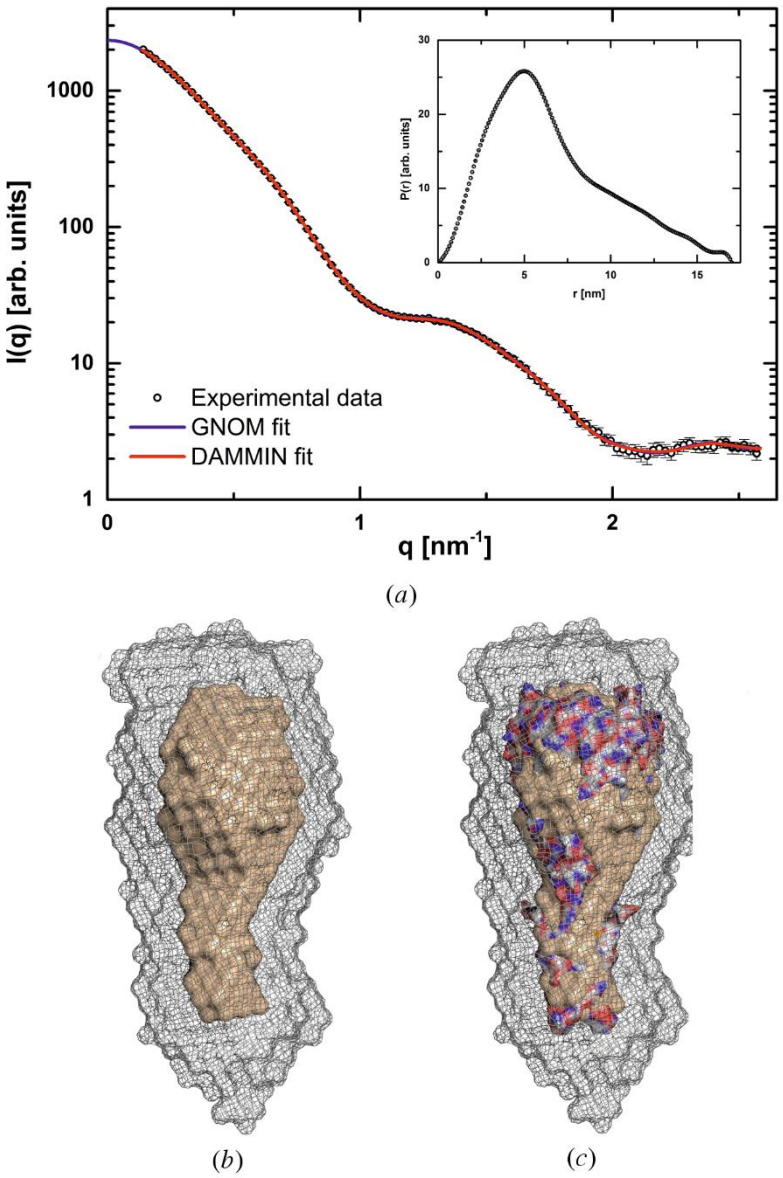

Figure S1 Small-angle X-ray scattering (SAXS) experiment supports a trimeric quaternary structure of VgrG1 in solution. (*a*) SAXS scattering profile of VgrG1 protein. Black circles represent the experimental data, the blue represent the fitting of the experimental data performed with GNOM, and the red line represent the fitting of the data to obtain the ab initio model performed with the program DAMMIN. Inset: pair distances distribution function. (*b*) *Ab initio* SAXS model generated with the program DAMMIN. The model is represented by the gray mesh, and the smaller brown surface inside represents the average minimal model. (*c*) Fitting of VgrG1 (represented as a surface with the electrostatic potential) inside the *ab initio* SAXS model (brown).

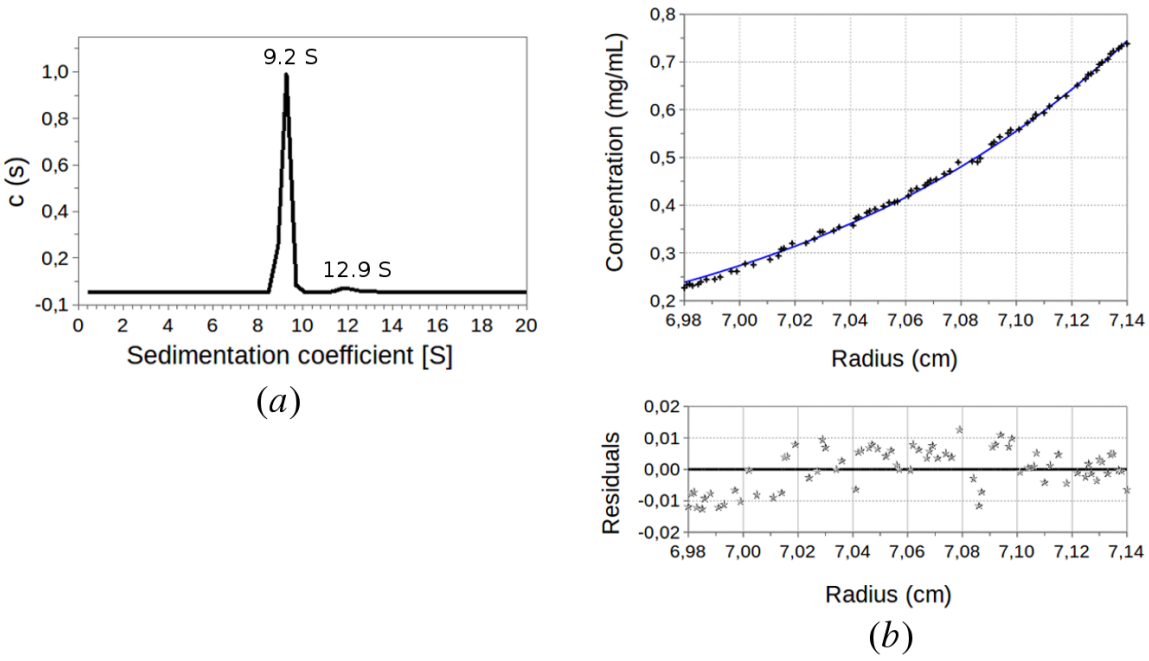

Figure S2 Analytical ultracentrifugation experiments of VgrG1 protein in solution. (*a*) Sedimentation velocity of VgrG1 at 7 μM (0.5 mg/mL), monitored by absorbance at 280 nm. The differential coefficient distribution (c(s)) curve suggests that VgrG1 presents a predominant species in a 93.9 % with a sedimentation coefficient of 9.2 ± 0.1 S and a second peak (5.8 %) with 12.9 ± 0.1 S. The apparent molecular weights (210.99 kDa and 349.3 kDa for predominant and minor peaks, respectively) were calculated from the c(s) distribution, with a frictional ratio of 1.38. (*b*) Equilibrium sedimentation of VgrG1, with scan data acquisition at 280 nm and at 6.5 krpm of velocity. The residuals (lower panel) show the fitting between the experimental data and an ideal single-species model (blue line). Experimental data resulted in an average molecular mass of around 197.2 ± 5.1 kDa, at a concentration of 7 μM.