Structural insights into ACBD3 hijacking by picornaviruses

Dominika Chalupska[1], Bartosz Różycki[2], Martin Klima[1], and Evzen Boura[1,]*

[1]Institute of Organic Chemistry and Biochemistry of the Czech Academy of Sciences, Flemingovo nam. 2., 166 10 Prague 6, Czech Republic

[2]Institute of Physics of the Polish Academy of Sciences, Al. Lotnikow 32/46, 02-668 Warsaw, Poland

*correspondence to boura@uochb.cas.cz

Running title: Hijacking of full length ACBD3 by Aichi virus

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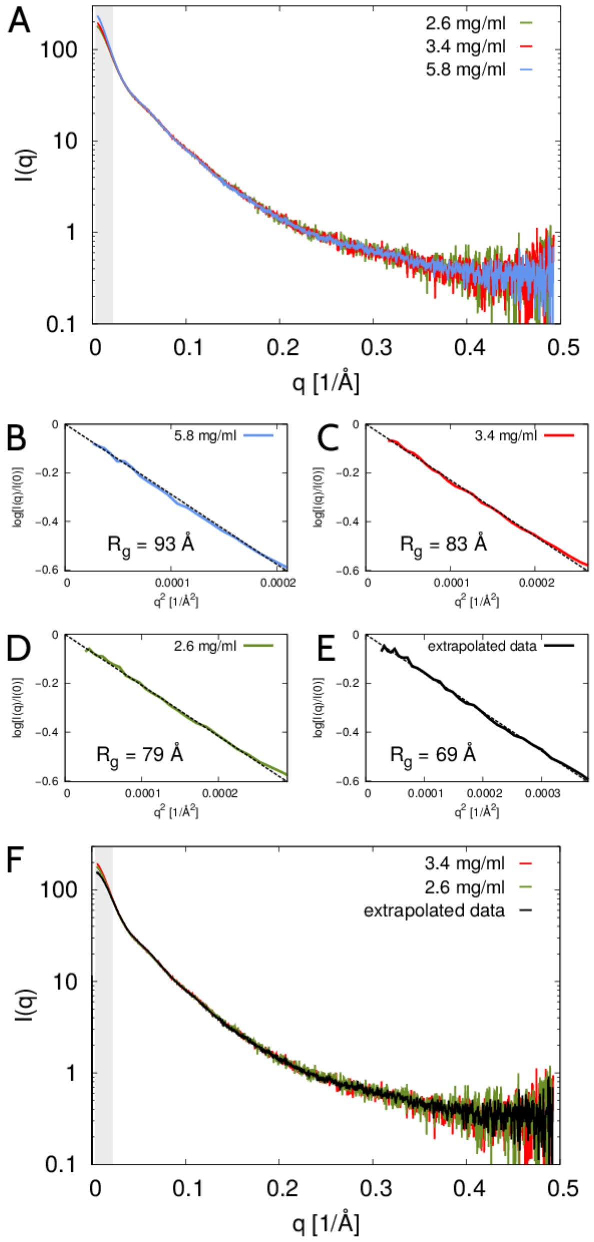
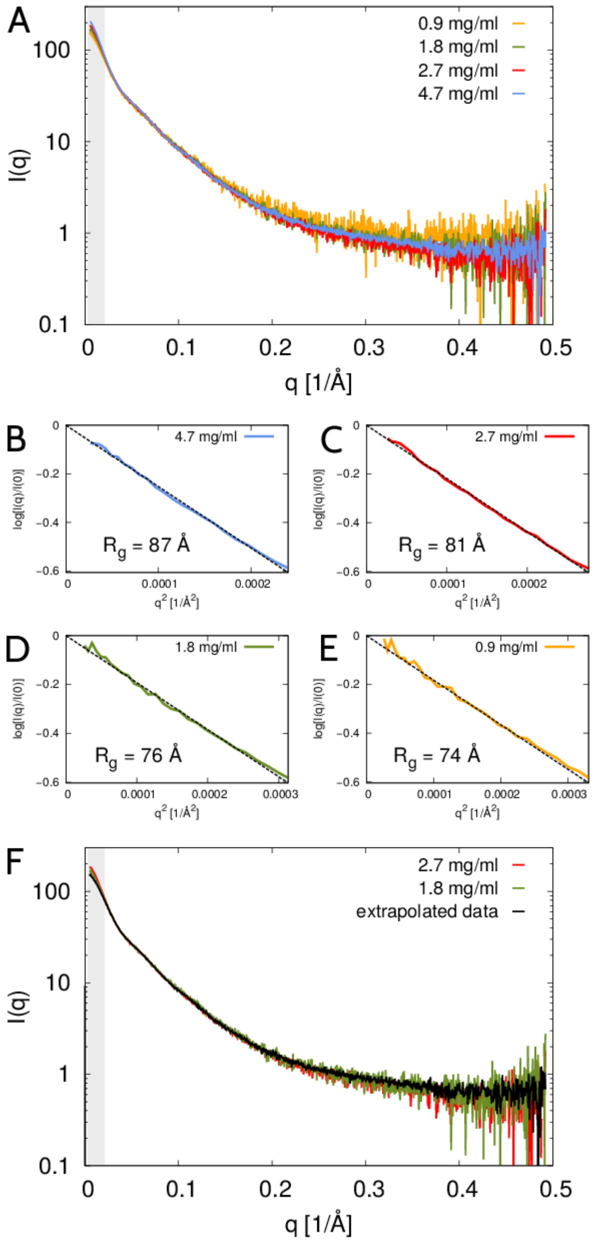
Supplementary Figures



SI Figure 1: SAXS data referring to the full-length ACBD3 protein. (A) SAXS intensity profiles at protein concentrations of 5.8, 3.4 and 2.6 mg/ml. The three SAXS intensity profiles overlay almost entirely. However, the gray bar indicates the region of scattering angles where systematic differences between the three SAXS intensity profiles are observed. (B-D) Gunier plots of the SAXS data collected at protein concentrations of 5.8, 3.4 and 2.6 mg/ml, respectively. These plots quantify the systematic differences between the three SAXS datasets in the Gunier regimes. The values of the apparent radius of gyration (Rg) are indicated. (E) Gunier plot of the extrapolated SAXS data. (F) Comparison of the extrapolated SAXS intensity profile with the SAXS intensity profiles at protein concentrations of 3.4 and 2.6 mg/ml.



SI Figure 2: Analogous to SM Figure 1 but for the full-length ACBD3:3A protein complex.