

Acta Crystallographica Section F

Volume 70 (2014)

Supporting information for article:

Crystal and solution structure of the human RIG-I SF2 domain

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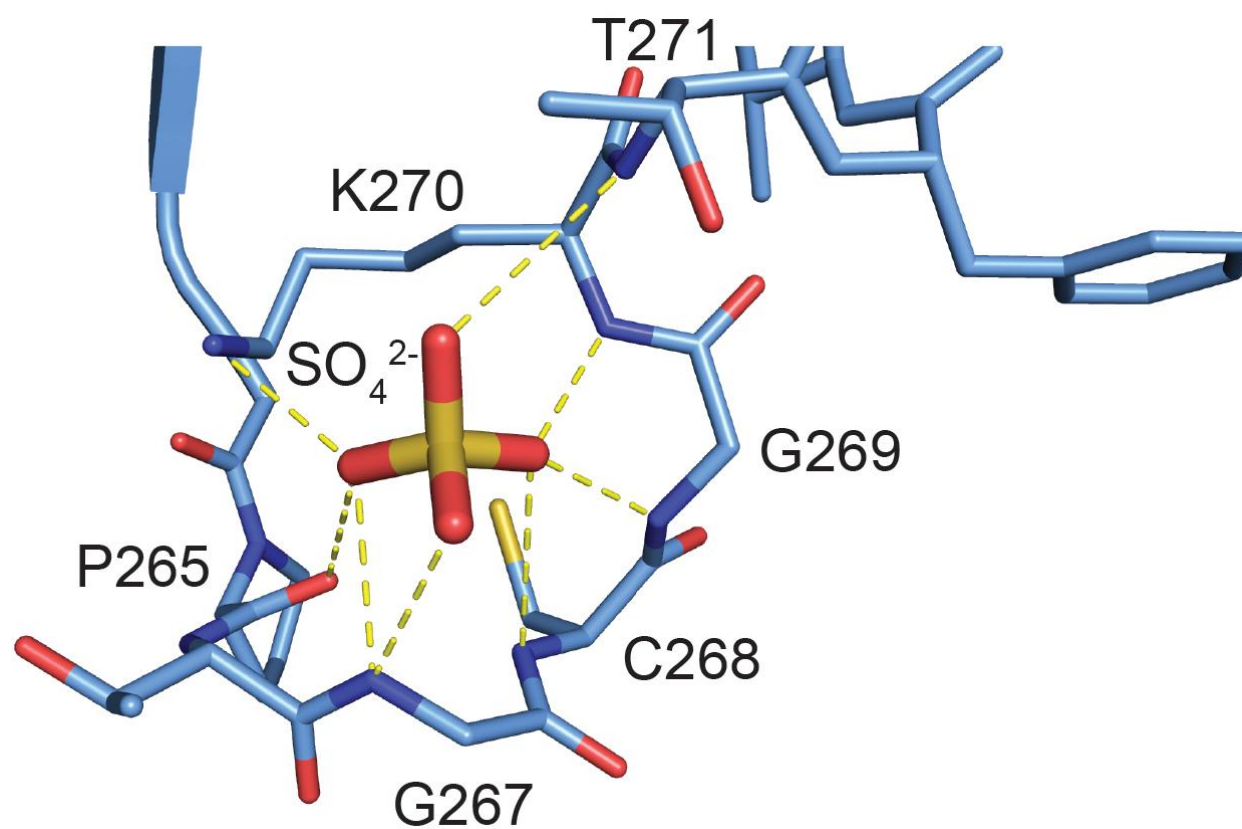


Figure S1 Coordination of the sulfate ion in the ATP-binding loop of RIG-I SF2.

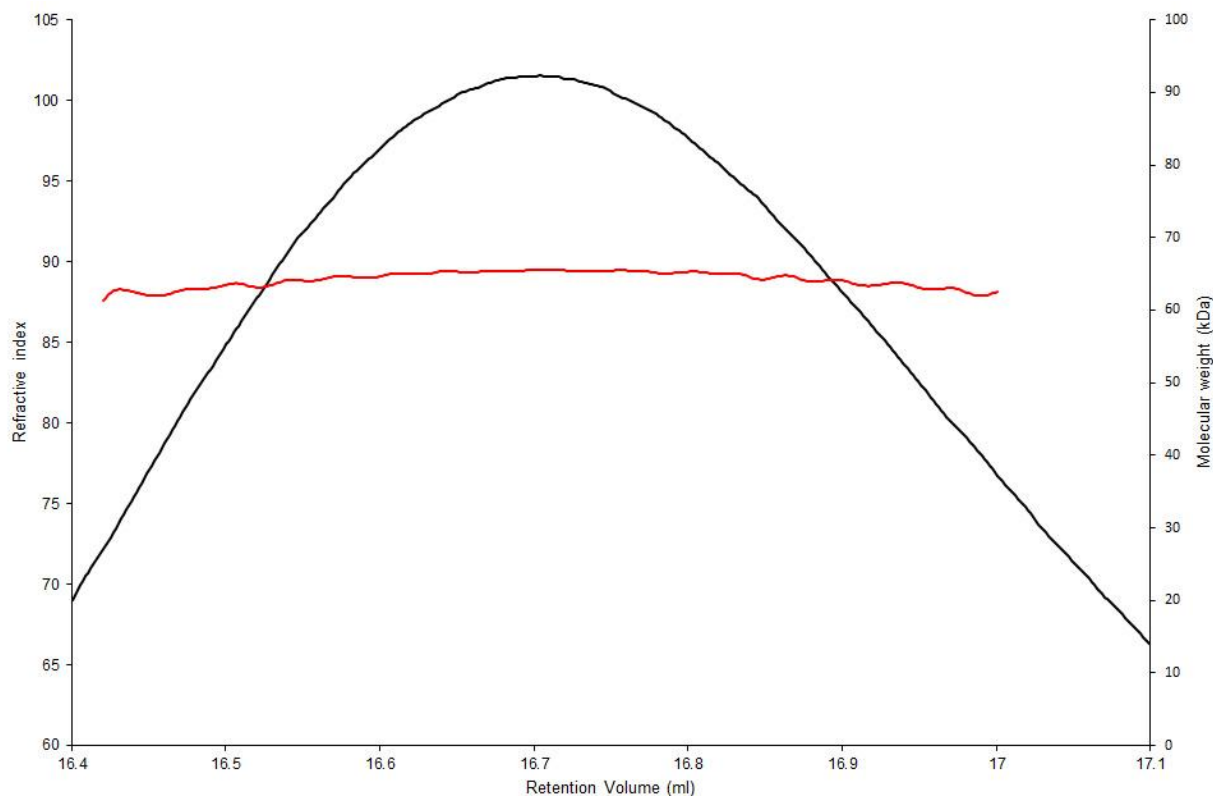


Figure S2 Size-exclusion coupled static light-scattering (SEC-RALS) data of RIG-I SF2. The black curve shows the refractive index (left axis) vs. retention volume of the RIG-I SF2 peak with the corresponding molecular weight (red curve, right axis) of a 3mg/ml sample loaded on the size exclusion column. The molecular weight is constant over the whole range of the peak indicating a very homogenous sample (polydispersity $M_w/M_z = 1.0$). The average molecular weight determined by SEC-RALS is $M_w^{\text{SEC-RALS}} = 64.2$ kDa and thus in very good agreement with monomeric RIG-I SF2 ($M_w^{\text{theoretical}} = 66.0$ kDa).

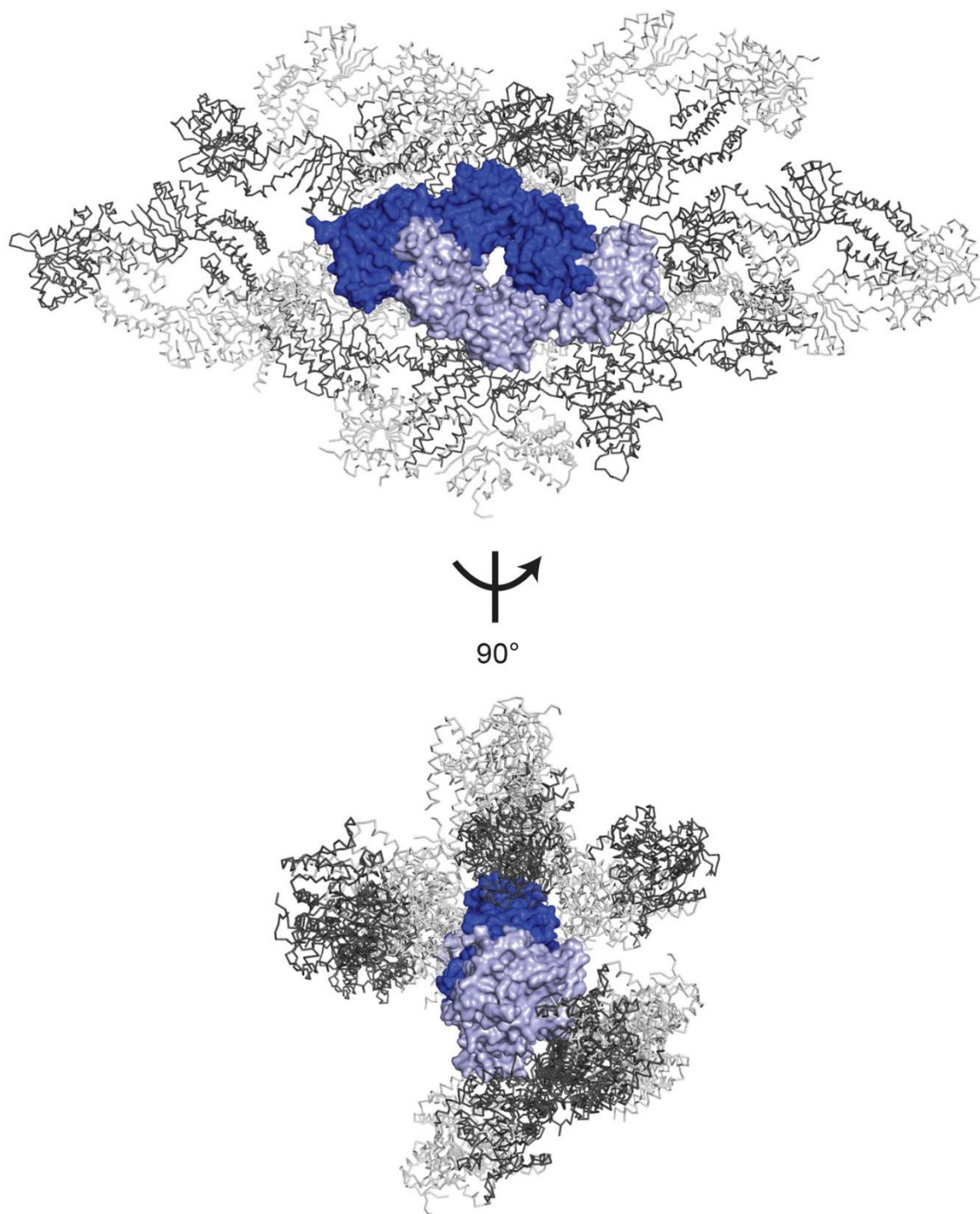


Figure S3 Illustration of the crystal packing of the RIG-I SF2 reported in this study. The crystallographic dimer (shown as surface representation in light and dark blue) and its surrounding symmetry mates shown as grey ribbons. In addition to the stabilizing interactions within the dimer, the symmetry mates influence the overall shape by extensive crystal contacts from top and bottom.