Supplementary Figure 1. Analytical ultracentrifugation measurements. Sedimentation velocity distribution of the hGINS complex at 42,000 rpm and 20°C. The concentration of the protein complex was adjusted to an OD280nm of 0.5Au in 10mM HEPES pH7.5; 150mM NaCl.
Supplementary Figure 2. (A) Euler angle distribution for the class averages in hGINS complex volume as provided by EMAN. The brightness of dots represent the number of images in each class on a logarithmic scale (more brightness imply larger number of images). (B) Plot of Fourier shell correlation curve between two independent hGINS models.
Supplementary Figure 3. Comparison of the hGINS and PCNA dimensions. A molecule of double strand DNA is depicted inside the PCNA channel.
Supplementary Figure 4

Supplementary Figure 4. Purification of hGINS:Fab complex. (A) SDS–PAGE analysis of purified antiPsf2 antibody. (B) SDS–PAGE analysis of the antibody digestion with papain and separation of Fab fragments from Fc fragments by Protein A affinity chromatography. Lane 1, antibody digestion with papain; lane 2, flowthrough from Protein A column; lane 3, elution from Protein A column. (C) SDS–PAGE analysis of antiPsf2Fab fragment further purified using a MonoQ column (see Supplementary information). (D) Size-exclusion chromatography of the hGINS:Fab complex. hGINS and antiPsf2-Fab fragment were mixed at a molar ratio of 1:4, incubated at room temperature for 1.5 hours and applied to a Superdex 200 10/300 GL column. (E) Peak fractions analyzed by SDS–PAGE. Lane 1, input; lanes 2-5, fractions collected corresponding the elution of the hGINS:Fab complex. HC: heavy chain; LC: light chain; Fc: fragment constant; Fab: fragment antigen binding.