LARGE T ANTIGEN ON THE SIMIAN VIRUS 40 ORIGIN OF REPLICATION: A 3D SNAPSHOT PRIOR TO DNA REPLICATION

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Figure S1

(A) The Fourier shell correlation (FSC) curve for the average volume (dark blue line) was calculated by splitting the complete dataset of 13,860 particles in two halves to calculate two independent reconstructions (Saxton and Baumeister, 1982), giving a 0.5 cut-off value of 27.5 Å. The calculation of the FSC curves for the four sub-volumes was also done as already described for the average volume. The colour-code used in the article applies here. The 0.5 cut-off values were 29.5 Å for the volume with the highest curvature (yellow), the one with the medium curvature (green), and the straight and shortest (red) and 30.5 Å for the straight and longest (cyan). The curve for the five times the signal to noise ratio (black) is also shown for comparative purposes. (B) One of the proofs to assess the quality of the fitting of the X-ray
helicase structure onto the average map was to also calculate its FSC curve (magenta) within one of the hexamers (hexamer 2). The 0.5 cut-off value was 31.9 Å. The curve for five times the signal to noise ratio is shown in black and the resolution curve for the average volume in dark blue.

**Figure S2**

Grids with the Tag-ori complexes were used to record tilt-pairs of images at 50° and 0°. The 0° images were analyzed using multi-reference alignment against two 2D averages, one straight (A) and another one bent (B). Two groups were thus segregated, one with 177 straight particles and one with 232 bent particles. The 0° images were only used for alignment purposes. The 50° tilt counterparts were then used to obtain the corresponding two random conical tilt volumes. (C and E) The volume obtained with the straight particles, Vol 1, is straight in all directions while (D and F) the one obtained with bent particles, Vol 2, is bent in certain directions. Views (C-D) are related, by a rotation of 90° along its main longitudinal axes, to the views (E-F). The volumes were very low-pass filtered. The isosurface renderings display 75% of the expected protein mass. The results of the random conical tilt test led us to conclude that the different degree of bending of the particles in the
projection images is not only due to different axial orientations, but reflects a genuine intrinsic structural heterogeneity of the Tag-ori complex.

**Figure S3**

(A) Angular distribution of the projection images in the average volume. Each projection image is represented by a point in the semi sphere. Pure top-views are at the pole of the semi sphere, whereas pure side-views are on the equator. (B-E) Diagram showing the phi angle (that is, the angle of rotation around the main longitudinal axes of the particles) for the 4 sub-volumes; (B) corresponds to the volume with higher curvature, (C) to the volume with medium curvature, (D) to the long and straight volume and (E) to the short and straight one.
Bibliography