Figures/Preliminary Results:

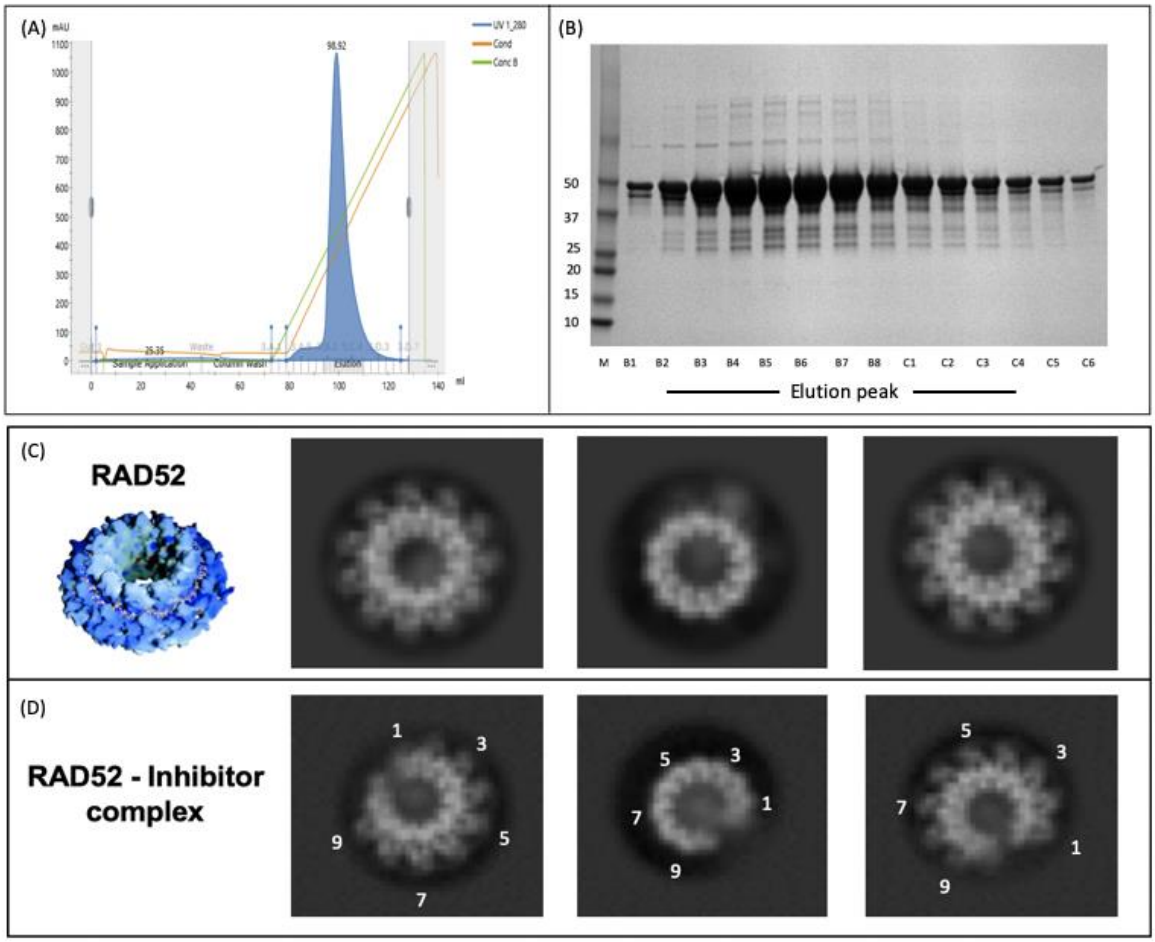

Figure 1 (A) Chromatographic profile of the purified RAD52 protein on a Superdex S200 column. (B) SDS-PAGE analysis of the elution peak fractions of the purified RAD52 protein. The elution peak corresponds to fractions B2 to C4. (C) FEI Titan Krios G3i 300 kV X-FEG TEM was used for data collection. Aliquots of 2.5 µL purified RAD52 protein sample was applied onto Quantifoil R2/1 Cu grids, manually blotted with filter paper and plunge-frozen in liquid ethane. Super-resolution movies of RAD52 were recorded on a Gatan K2 direct electron detection camera in counting mode with a pixel size of 1.03-Å/pixel at the specimen scale. The 26 frames in each movie were subjected to drift correction using motioncorr and averaged to produce one micrograph. Defocus for each micrograph was determined by CTFFind3, and a total of 44,328 particles were manually picked from cryo-EM graphs. Figure shows the RAD52 X-ray generated 3D model (left) and cryo-EM 2D classification of the RAD52 protein highlighting its undecameric ring structure. (D) Initial screening of the RAD52-inhibitor complex suggests RAD52 inhibitors disrupt the 11-mer ring structure of the RAD52 protein.