High resolution cryoEM structures oh human RAD51 on single-stranded and double-stranded DNA

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Around 10,000 DNA double-stranded breaks occur daily in *homo sapiens* and the successful repair of such breaks is crucial for the maintenance of cellular stability and integrity; failure to repair the breaks can lead to serious diseases such as cancer. Of the three mechanisms available for repair, the most robust is homologous recombination. Central to this process is the 37kDa recombinase protein RAD51 which begins by encasing the broken single strand as a single-start helix, forming the presynaptic filament. Following a search for a homologous DNA sequence, strand exchange is carried out, forming the postsynaptic filament of RAD51 on double-stranded DNA to complete the repair. There are 6.4 protomers per turn of the helix with a pitch of 103Å in the presynaptic filament, shortening to the lower pitch of 97Å in the postsynaptic filament. We have used electron cryo-microscopy followed by a combination of maximum likelihood methods with helical single particle techniques to calculate structures of filaments of human RAD51 on ssDNA and on dsDNA to a resolution of 3.5-5Å. These structural models have revealed details of the protomer-protomer interface of RAD51, its contacts with the DNA and some disease-causing mutations.