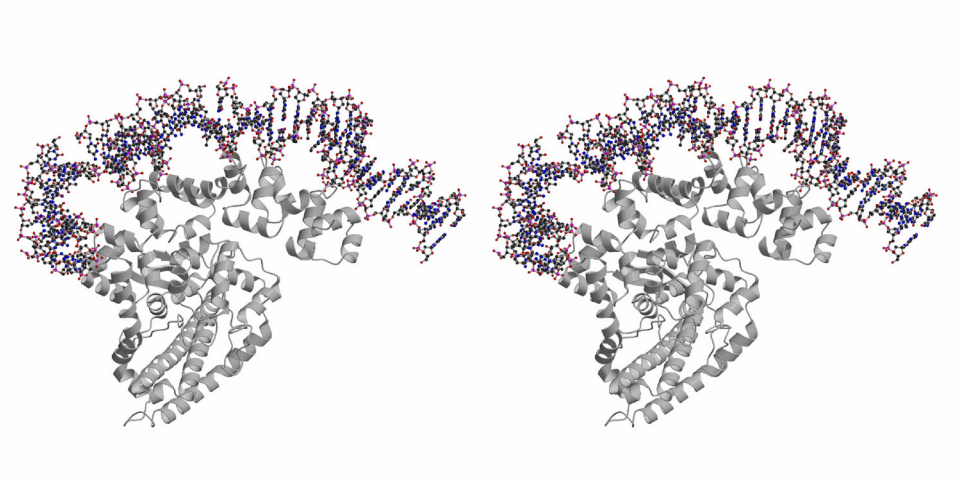

Supplementary Figure 3. Stereo diagram of the topoisomerase V structure with a model for DNA. The model was built by superposing the $(HhH)_2$ domain of the RuvA/DNA complex (Ariyoshi et al., 2000) on each of the four $(Hhh)_2$ domains in the topoisomerase V fragment structure. Four different superpositions were done. After superposing the proteins, the DNA in each of the four superposed RuvA/DNA models was collected into one file. As can be seen, the DNA fragments modeled into the first two $(HhH)_2$ domains do not form a continuous helix, although the DNA molecules appear to follow a similar path. The DNA in the last two $(HhH)_2$ domains forms a continuous helix. A large conformation in the DNA, the protein, or both would be required to form a complex with a continuous DNA molecule and the four $(HhH)_2$ domains. Note also that none of the DNA molecules come close to the active site region and that an additional conformational change would be required to allow the DNA to enter the active site.