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Erratum

In the article "Molecular Design and Functional Organization of the RecA Protein" by Dharia A. McGrew and Kendall L. Knight, which appeared in Volume 38, Issue 5 (2003) of *Critical Reviews in Biochemistry and Molecular Biology*, some of the figure legends were printed incorrectly. Following are the figures from that article, with the correct captions. The publisher apologizes for this error.

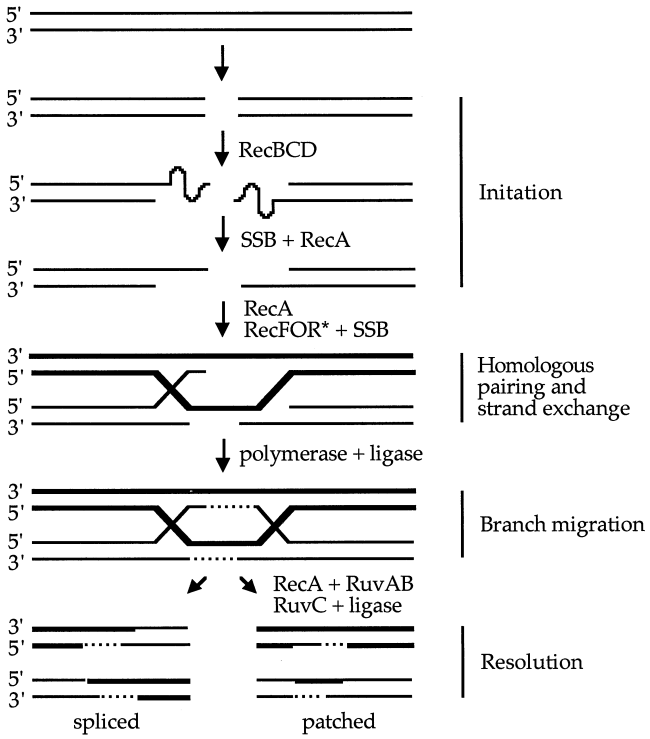

FIG. 1. Model of recombinational repair of DNA double-strand breaks. This model shows only a basic image of DSB repair via homologous recombination and includes proteins important to each step. The pathway is divided into 4 general steps, and those proteins involved in the "initiation" and "homologous pairing" steps are discussed in this review. The RecFOR* complex plays a role in regulating the assembly and disassembly of the RecA nucleoprotein filament (see text), but is widely considered to have its major role in gap repair rather than DSB repair.

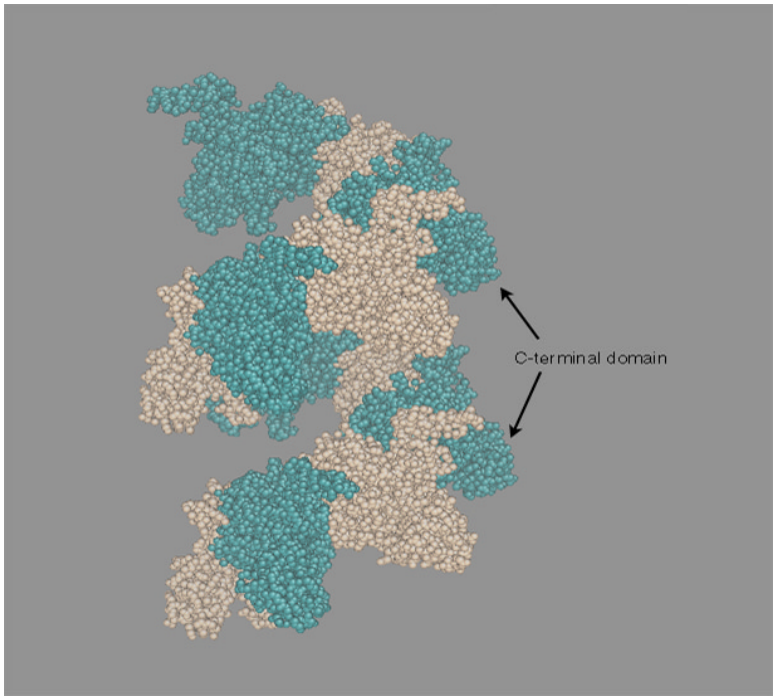

FIG. 2. Two turns of helical RecA protein filament. Twelve subunits in this image are colored in alternating teal and beige. This filament is oriented such that the 5′ end of bound DNA is at the top and the 3′ end at the bottom (Story *et al.*, 1992). The C-terminal domain is defined as residues 270–352, and the part visible in the structure (residues 270–328) is indicated. This image was created using main chain and side chain atoms in 2REB (Story *et al.*, 1992).

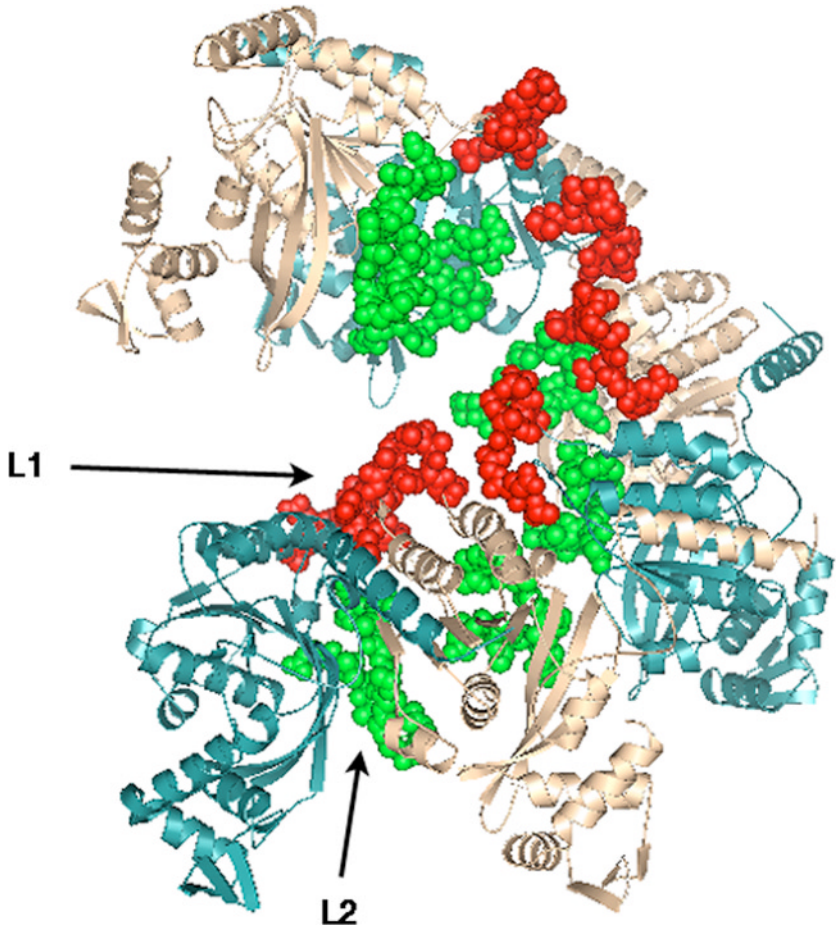

FIG. 4. *M. tuberculosis* RecA protein filament showing L1 and L2 regions. This image shows one turn of a RecA filament with the six subunits colored in alternating teal and beige. L1 residues are shown in red and L2 in green. This image was created using a composite of 1MO4 and 1MO5 from Datta *et al.* (2003a).

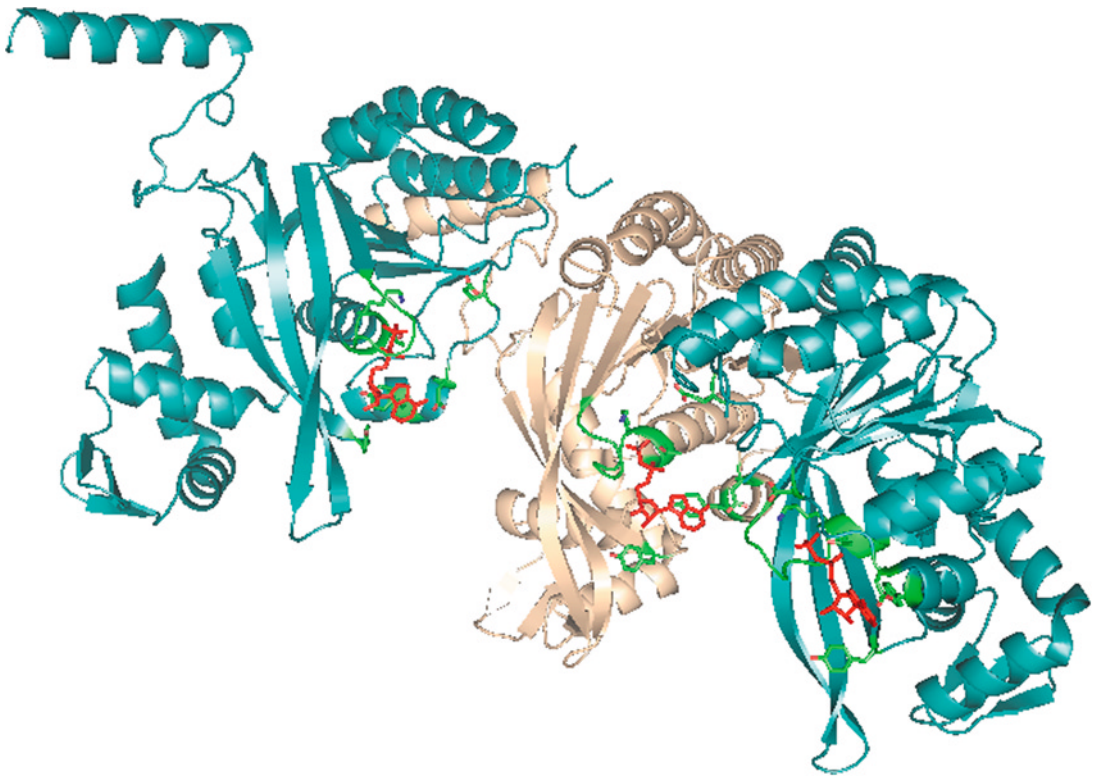

FIG. 5. RecA trimer showing ATP binding sites. This view of three subunits shows the inside surface of the RecA filament. Subunits are colored in alternating teal and beige. Main chain of the Walker A motif (P-loop; residues 66–72), is shown in green. Main chain and side chain of residues 72, 73, 96, 100, 103, and 264 are colored by atom (C, green; O, red; N, blue). ADP is in red. This image was created using 1REA from Story and Steitz (1992).

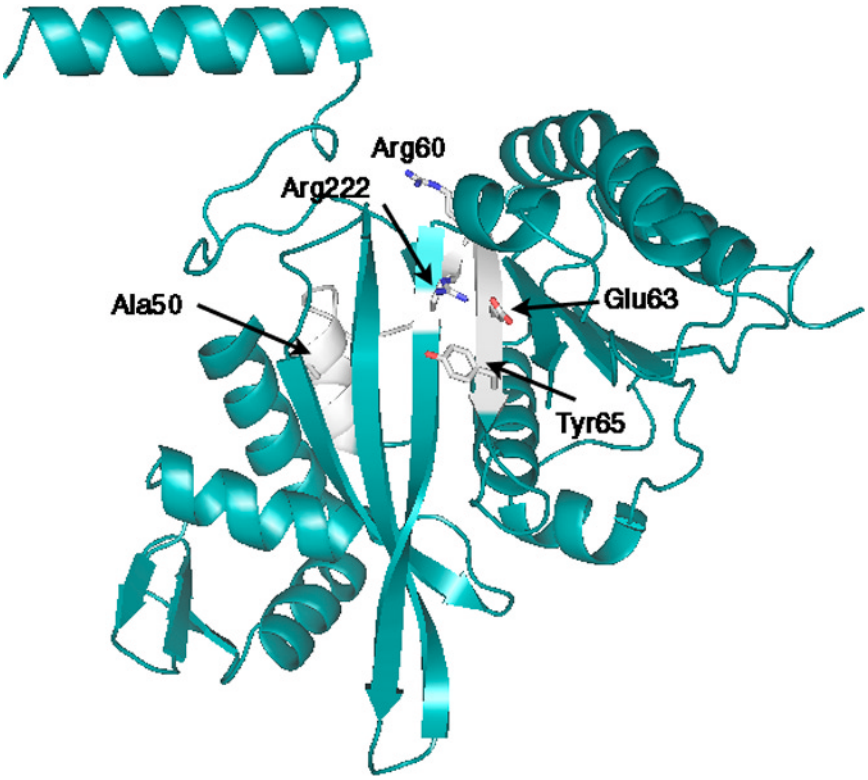

FIG. 7. Proposed MAW motif of RecA. The MAW motif (*M*ake *A*TP *W*ork) is defined by the αB/β1 regions (residues 45–65). Side chains are colored by atom (C, yellow; O, red; N, blue) as shown in 1REA (Story and Steitz, 1992).

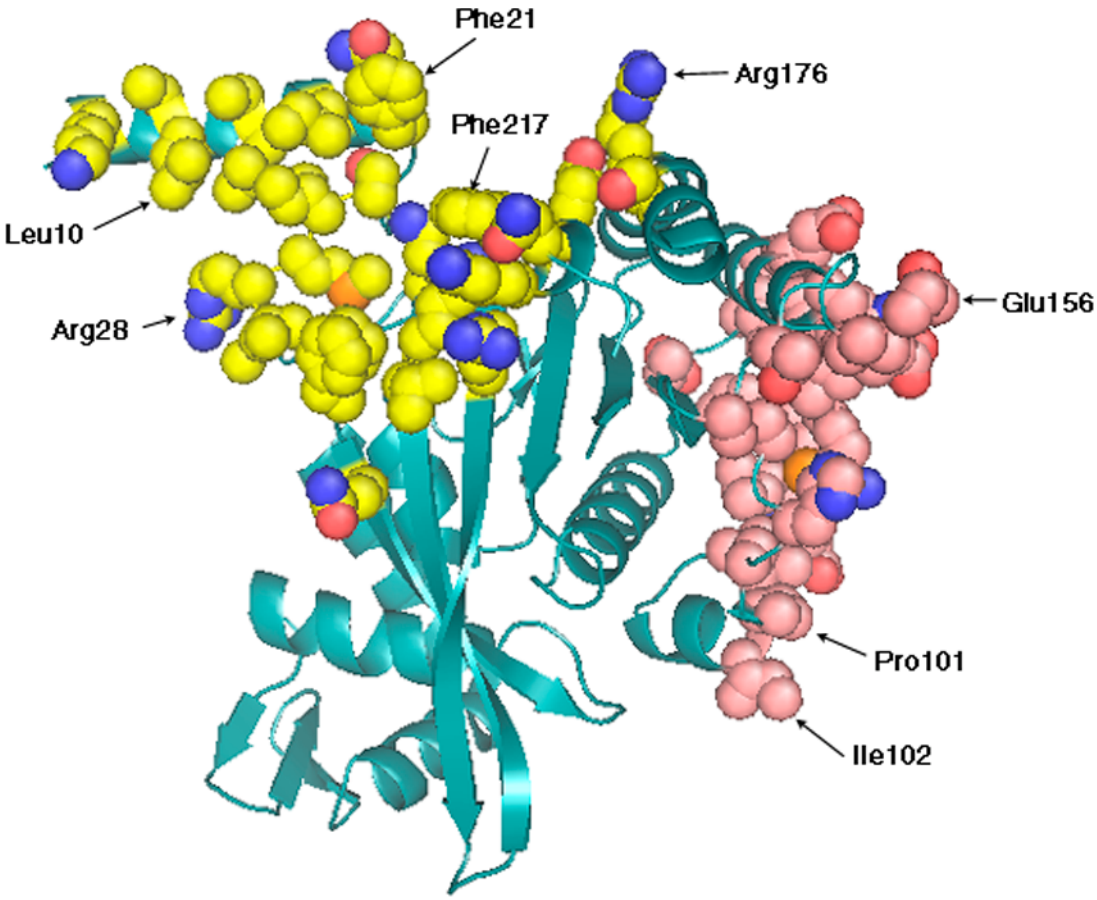

FIG. 8. RecA monomer showing both surfaces of the subunit-subunit interface. Formation of RecA filaments involves two distinct surfaces of the protein. On one surface side chain atoms are colored by atom (C, yellow; O, red; N, blue); on the other surface carbons have been shown in pink. Labeled residues are for orientation purposes only and are not meant to indicate any functional or structural importance. This image was created using 2REB in Story *et al*. (1992).

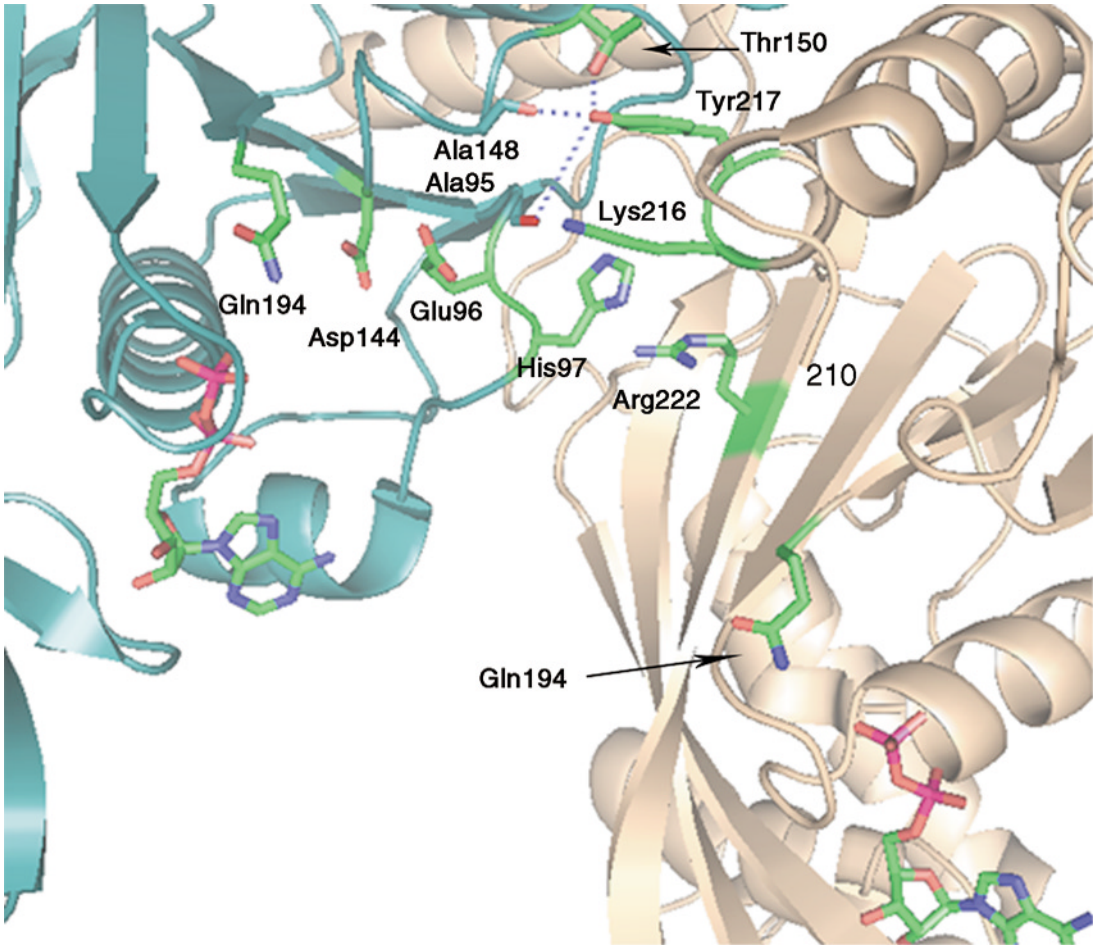

FIG. 11. Detail of region of the subunit interface involved in ATP-mediated transfer of allosteric information. Phe217 is replaced here with Tyr, which is within hydrogen bonding distance of the carbonyl oxygen of Ala95 and Ala148, and the –OH group of Thr150 in the neighboring subunit. The Tyr side chain was repositioned slightly relative to the position of Phe217 in the coordinate file to accommodate these three potential hydrogen bonds. No steric clashes resulted. This image shows other cross-subunit interactions that may be involved in oligomeric stabilization, *e.g.*, Lys216-Ala95 and Arg222-His97. The image was created using 1REA in Story and Steitz (1992). This model derives from work described in DeZutter *et al*. (2001). Coloring of side chains and overall orientation of the subunit interface is the same as in Figure 10.

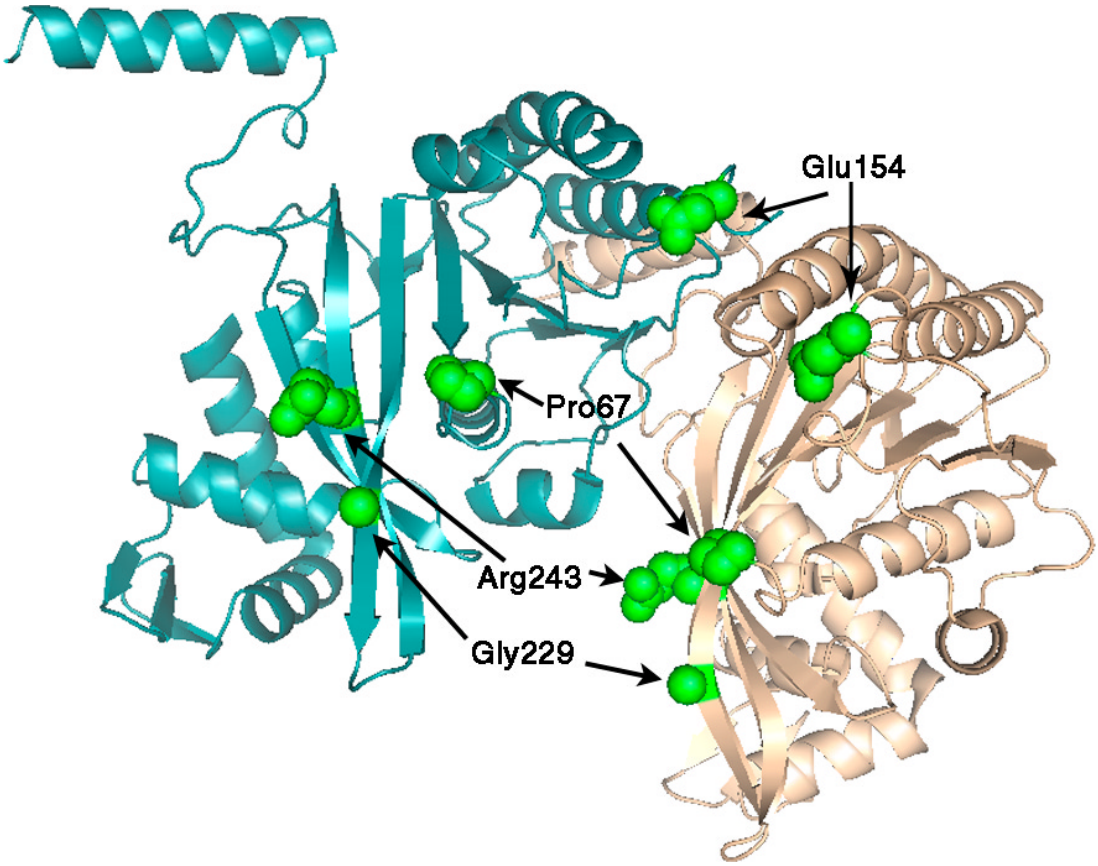

FIG. 13. Model of dimeric RecA showing residues of potential sites of contact with coprotease substrates. The side chains of these residues all lie on the inside of the RecA filament and can be accommodated within a continuous surface that runs the length of the filament. The main chain of subunit 1 is colored beige and subunit 2 is teal. Residues 67, 154, 229, and 243 in each subunit are shown in green. This image was created using 2REB in Story and Steitz (1992).

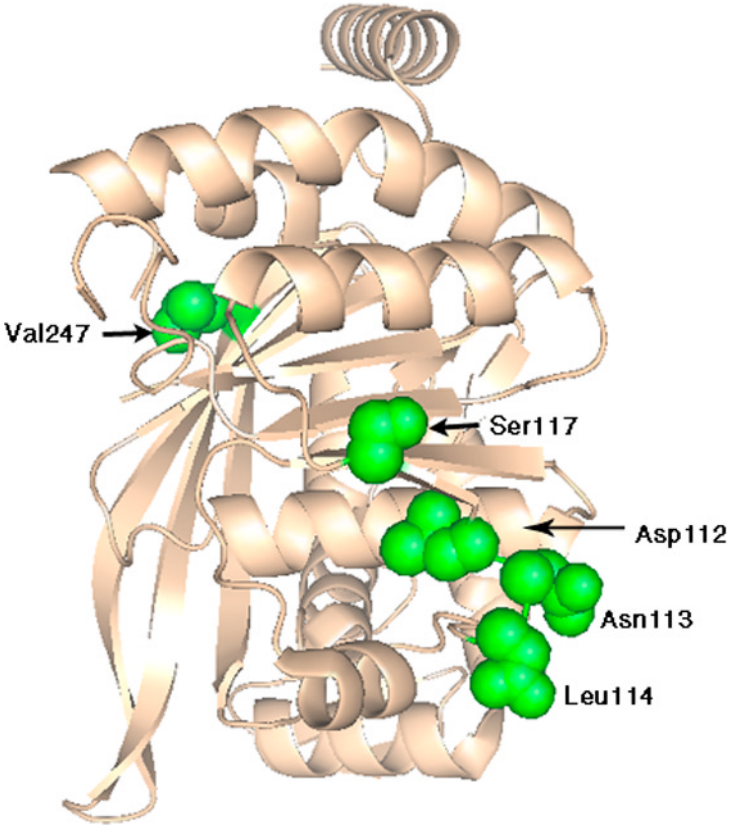

FIG. 14. Potential sites of interaction between RecA and UmuD$'_2$ C (pol V). Mutations at each of these positions were selected as UmuR mutants. Four of the five residues shown (Asp112, Asn113, Leu114, and Ser117) are on the surface of the subunit interface that would be at the 3′ end of bound DNA (Story *et al.*, 1992). This image was created using 2REB in Story *et al*. (1992).