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Erratum

Directed Evolution of High-Affinity Antibody Mimics Using mRNA Display

In our recent article (Chem. Biol. *9*, 933–942), the color of some amino-acid residues in the ribbon diagrams in the published Figure 1B did not match the color of the same residues in the sequence alignment or the color referred to in the figure legend. In the corrected figure below, the color code is the same in Figure 1A, Figure 1B, and in the legend to Figure 1.

1. Main, A.L., Harvey, T.S., Baron, M., Boyd, J., and Campbell, I.D. (1992). The three-dimensional structure of the tenth type III module of fibronectin: an insight into RGD-mediated interactions. Cell *71*, 671–678.
2. Spinelli, S., Frenken, L., Bourgeois, D., de Ron, L., Bos, W., Verrips, T., Anguille, C., Cambillau, C., and Tegoni, M. (1996). The crystal structure of a llama heavy chain variable domain. Nat. Struct. Biol. *3*, 752–757.

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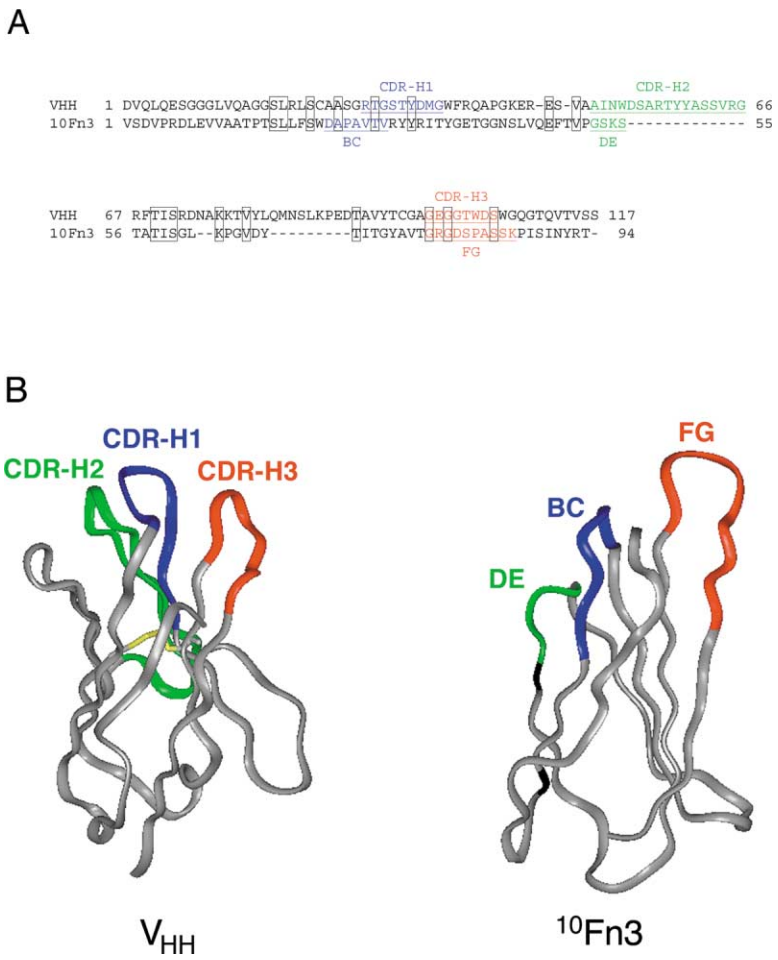

Figure 1. Comparison of the Primary Sequences and of the Tertiary Structures of a Llama V_{HH} Domain and the Wild-Type Human ^{10}Fn3 Domain

A comparison of the primary sequences and of the tertiary structures of a llama V_{HH} domain ([2], this was reference 70 in the original article), which is the smallest antibody fragment known to bind to an antigen, and the wild-type, human ^{10}Fn3 domain ([1], this was reference 56 in the original article), the scaffold for a new class of antibody mimics. Alignment of primary sequences (A) and structural comparison (B) between these two domains demonstrate that, despite the lack of significant sequence identity, the V_{HH} and the ^{10}Fn3 fold into similar β sheet sandwiches. The disulfide bond between Cys 22 and Cys 92 of the V_{HH} domain is shown in yellow; there are no disulfides in the ^{10}Fn3 domain. The complementarity-determining regions of the V_{HH} and the residues randomized in the ^{10}Fn3-based libraries are shown in color (underlined in the sequence). Blue: CDR-H1 of the llama V_{HH} and residues 23–29 of the ^{10}Fn3 BC loop; green: CDR-H2 of the llama V_{HH} and residues 52–55 of the ^{10}Fn3 DE loop; red: CDR-H3 of the llama V_{HH} and residues 77–86 of the ^{10}Fn3 FG loop. In the sequence alignment, the homologous residues are boxed. The ^{10}Fn3 residues outside the randomized loops that were found to have mutated in approximately 45% of the selected clones are marked in black in the ribbon representation of the ^{10}Fn3 structure.