Correction to Insights from Fragment Hit Binding Assays by Molecular Simulations

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The structure used to generate the simulations is 2BOK, not 1FAX (as we mentioned in the paper). The build system also generated some small gaps not present in 2BOK where multiple coordinates were available. These are residues 61, 124, 131, 132, 185, 186, 223. The rest of the setup is as reported in the original paper.