



FIGURE 3. Depiction of the X-ray structure of the complex between MDM2 and Nutlin-2. (a) Close-up of the p53-binding site on MDM2 (inhibitor omitted for clarity). The protein is represented by a surface on which hydrophobic areas are green, hydrophilic areas are blue, and exposed areas are red. (b) Nutlin-2 (depicted as a CPK model) bound to MDM2. Carbon atoms are shown in gray, nitrogen atoms in blue, oxygen atoms in red, and bromine atoms in brown. These images were drawn with the program MOE (Molecular Operating Environment). (c) Using an overlay of two MDM2 structures with the p53 peptide (Kussie et al. 1996) and Nutlin-2 (Vassilev et al. 2004) that is based solely on the MDM2 segments of the structures, this figure depicts how the various functional groups of the inhibitor mimic the three crucial side chains of the p53 peptide (i.e., Phe¹⁹, Trp²³, and Leu²⁶). The p53 peptide backbone is depicted as the yellow–gray ribbon, and the three side chains are shown with green spheres for the carbon atoms. Nutlin-2 is shown with carbon atoms colored cyan. This figure was drawn with MolScript.

Protein–Protein Interactions: A Molecular Cloning Manual, 2nd Ed., © 2005 by Cold Spring Harbor Laboratory Press, Chapter 46, Figure 3.