Fig. 1. (N. A. Smirnova et al.) Displacement of active site water (left, PHD2 active center, PDB 2G19) upon binding of HIF peptide (right, modeling using FIH-HIF peptide structure, PDB 1H2K).
Fig. 4. (N. A. Smirnova et al.) Qualitative electrostatic potentials of PHD1 computer model (a), PHD2 crystal structure (b), and PHD3 computer model (c): red and blue shades represent negative and positive potentials, respectively. d) Location of β2β3 loop (green) and C-terminal domain (pink) with respect to bound HIF peptide in the PHD2-HIF crystal structure (PDB 3HQR).