(A) The structures of deacetoxycephalosporin C synthase (DAOCS; PDB code: 1E5I), a representative of the 2-OG-Fe(II) dioxygenase family, and the Factor Inhibiting Hypoxia inducible factor (FIH) (PDB code: 1H2K), which represents the JmjC family, were superimposed. This was done initially using the Cα positions of the Fe2+ ligands, and was then improved using the graphics program O (Jones et al., 1991). The alignments of the 2-OG-Fe(II) dioxygenase family and FIH/Epe1 alignments were put into register through these two superposed structures. The Fe(II) ligands are denoted with stars beneath the alignment. The positive charges that ligate the 2-OG are shown as green squares, and are in different positions in the 2-OG-Fe(II) family and the JmjC family. The secondary structure above the alignments shows the double-stranded beta-helix (DSBH) numbering system for the FIH structure.

DAOCS (P18548, Deacetoxycephalosporin C synthetase, Streptomyces clavuligerus), ABH3 (NP_631917, AlkB homologue 3, Homo sapiens), FIH (Q9NVT6, Homo sapiens), EPE1 (Q94603, Schizosaccharomyces pombe).

(B) Structural alignment of DAOCS (black Cα positions) and FIH (light grey, Cα positions) are shown. The residues that ligate the Fe(II) are shown. The residues that ligate the Fe(II) are shown. The differing positions of the positively charged residues that ligate the distal carboxylate group of 2-OG are shown with Cα positions coloured like their parent structures. Although these residues come from different parts of the fold, they occupy roughly the same positions in these dimensions.