



Mutation that compromise the D14 – D3 interaction

Residues whose side chain conformations differ between apo KAI2 and karrikin-bound KAI2

Supplementary information, Figure S9 D14 residues that are important for D3 interaction are conserved. Sequence alignment of the conserved hydrolase folds (residues 51-318 in OsD14). Residues that we have mutationally identified as important for D3 interaction are highlighted by black boxes and those that changed conformation on the KAI2 surface upon karrikin binding are highlighted by red boxes.