The structural basis of Mos1 transposase inhibition by the anti-retroviral drug Raltegravir.

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**Supplementary Figures**

**Supplementary Figure 1.** Structure based sequence alignments of the catalytic core domains of Mos1, Setmar, Sleeping Beauty (SB), HIV-1 integrase and PFV integrase.

Secondary structure elements of Mos1 (from PDBID: 3HOT) and PFV catalytic domains (from 3S3M) are shown above and below the alignments, respectively. Conserved residues are shown in white on a red background and similar residues are highlighted in red. TT represents a $\beta$-turn. The residues of the DD-34-D/N and DD-35-E motifs are highlighted by light and dark blue pentagons respectively. The conserved Tyr and Pro residues preceding the third active site residue are marked by red asterisks.
Supplementary Figure 1
**Supplementary Figure 2.** Stereo view of the Mos1-Raltegravir co-crystal structure with Mg$^{2+}$ in the active site (PDBID: 4MDB) showing the final 2f$_o$-f$_c$ electron density map contoured at 1.5σ.
Supplementary Figure 3. Stereo view of the Mos1-Raltegravir co-crystal structure with Mn$^{2+}$ in the active site (PDBID: 4MDA) showing the final 2f$_o$-f$_c$ electron density map contoured at 1.5σ.