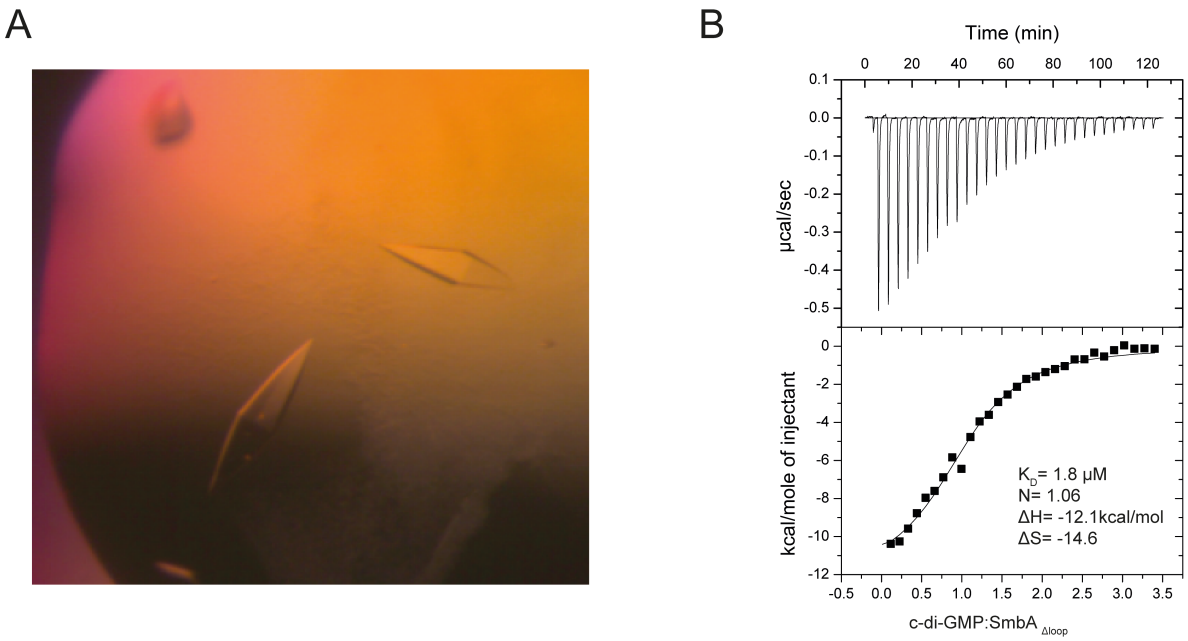
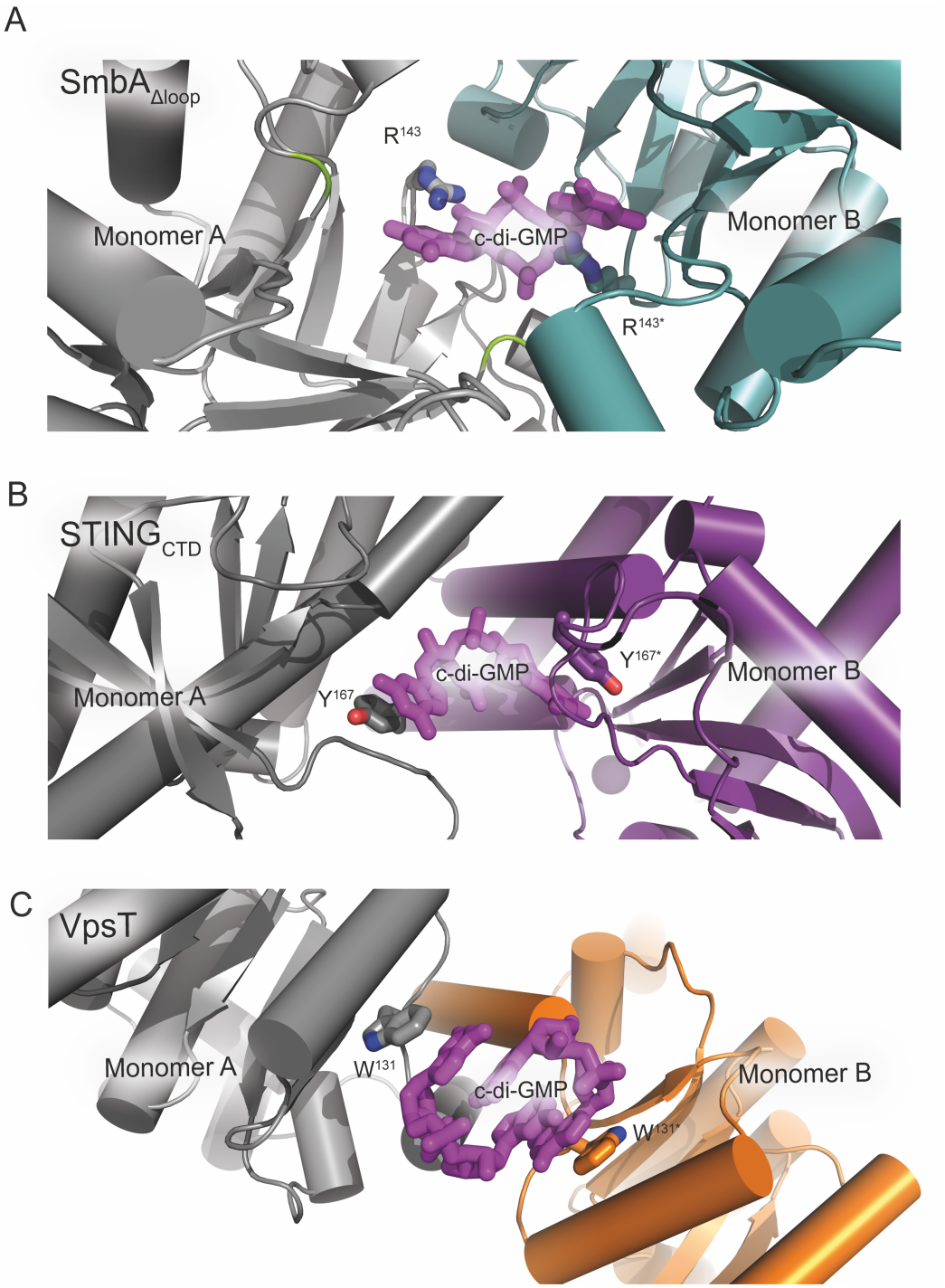
Supplementary figures



S1 Fig. SmbA$_{\Delta loop}$ crystals and binding parameters of SmbA$_{\Delta loop}$ with c-di-GMP.

(A) SmbA$_{\Delta loop}$ crystals in complex with c-di-GMP.

(B) ITC of SmbA$_{\Delta loop}$ (10 µM) binding to the c-di-GMP molecule (150 µM). The binding stoichiometry, ΔH, ΔS, and K_D are marked.

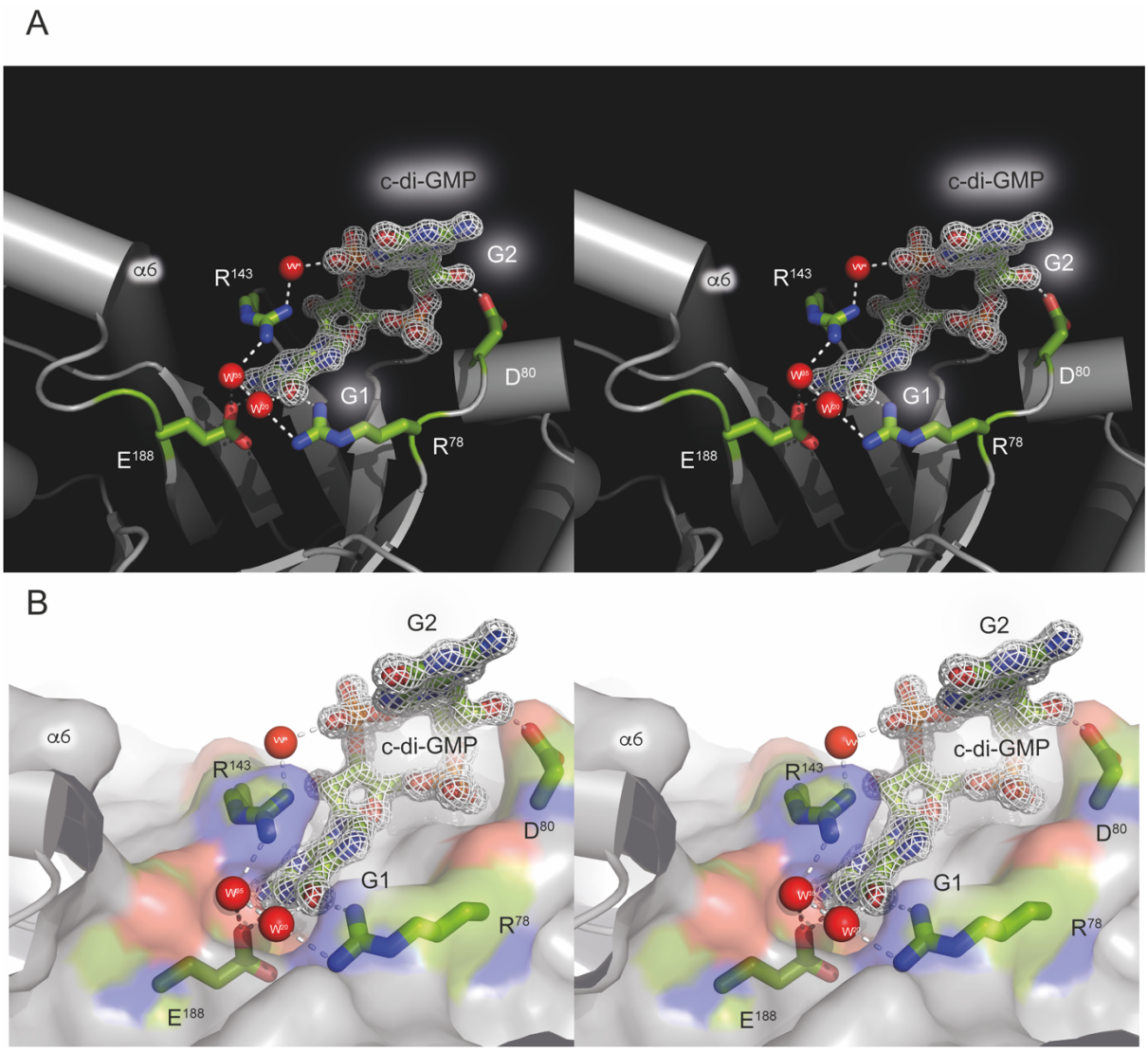


S2 Fig. c-di-GMP bound at dimer interface found in STING and VpsT. c-di-GMP bind at the crystallographic dimer interface shown in the stick model (magenta). Residues involved in base stacking are shown in a stick. Monomers are colored differently.

(A) $SmbA_{\Delta loop}$ c-di-GMP contact at the 2-fold crystallographic dimer interface,

(B) STING dimerization interface (PDB code-4F5Y).

(C) VpsT dimerization interface (PDB code-3KLO).



S3 Fig. An expanded stereo view of the SmbA$_{\Delta loop}$ residues interacting with c-di-GMP.

(A) Stereo view of the 2Fo-Fc omit maps contoured at 1.2 σ. The molecular structure of c-di-GMP is embedded in the map. The colour code is similar to that in Fig. 3A. The R143 guanidinium group stacks very well with the guanyl base of c-di-GMP., while R78 is engaged in lateral H-bonding.

(B) Stereo view of the c-di-GMP molecule drawn as surface representation (negatively charged atoms in red, positively charged atoms in blue and carbon atoms in green). Hydrogen bonds are marked by dotted lines in white.