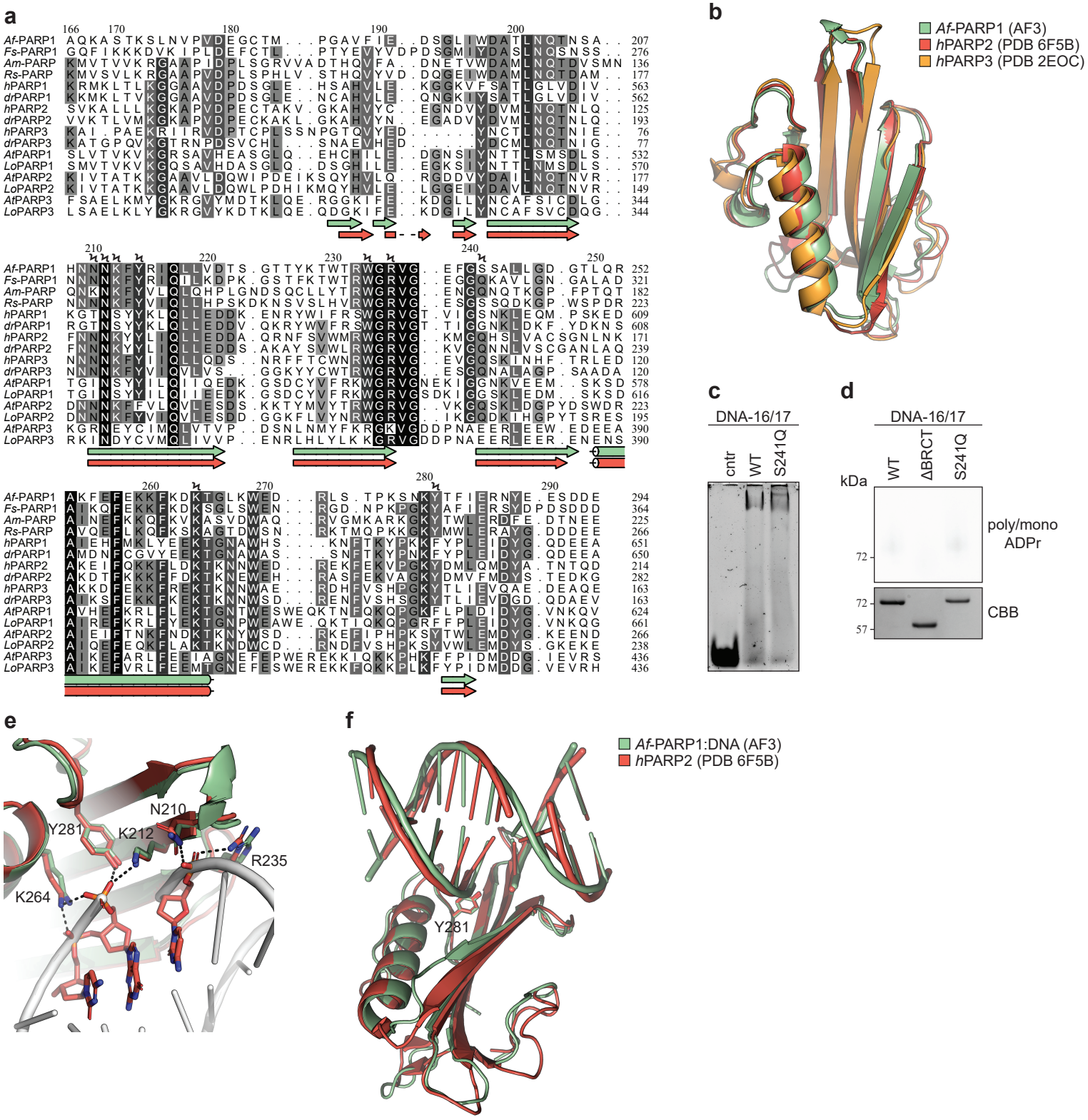

Extended Data Figure 2. DNA damage recognition by the *Af*-PARP1 WGR domain.

(a) Multiple sequence alignment of selected PARP-derived WGR domains from Fungi, Animalia, and Plantae. Residue numbers for Af-PARP1 and key DNA interaction residues (ϟ) are indicated above the alignment. Secondary structures for *Af*-PARP1 (AlphaFold 3 model; green) and *h*PARP2 (PDB 6F5B; red) are given below the alignment.

(b) Ribbon representation of the structural alignment of *Af*-PARP1 WGR domain (AlphaFold 3 model) with the experimentally determined WGR domains from *h*PARP2 and -3.

(c) EMSA assay assessing the influence of Ser241 on the ability of the WGR domain to bind double-strand breaks. *Af*-PARP1 WT or S241Q (5 μM) were incubated with DNA mimetic (1 μM) for 1 h, seprated via native PAGE and DNA visulised with SYBR safe staining.

(d) Assessment of the influence of Ser241 on the catalytic activity of *Af*-PARP1 in presence of 5'-phosphorylated DNA double-strand break mimetic. WT or S241Q *Af*-PARP1 (0.5 μM) were incubated with DNA (0.6 μM) and NAD^+ (500 μM) and formation of PAR detected using immunoblot.

(e) Ribbon-liquorice representation of the DNA coordination by *h*PARP2 (PDB 6F5B; red/white) overlaid with the *Af*-PARP1 WGR domain derived from the apo AlphaFold 3 model (green). Residues indicated represent *Af*-PARP1 numbering.

(f) Ribbon-liquorice representation of the structural alignment of *Af*-PARP1:DNA AlphaFold 3 model (only WGR domain shown) with the experimentally determined WGR:DNA complex from *h*PARP2. *Af*-PARP1 Tyr281 is indicated for orientation.