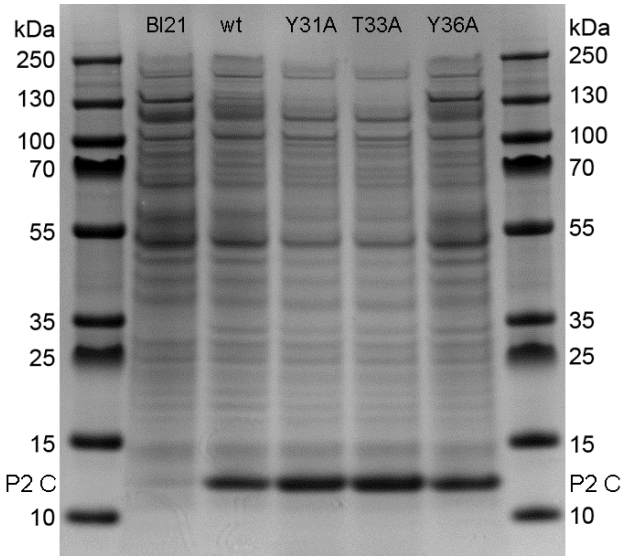
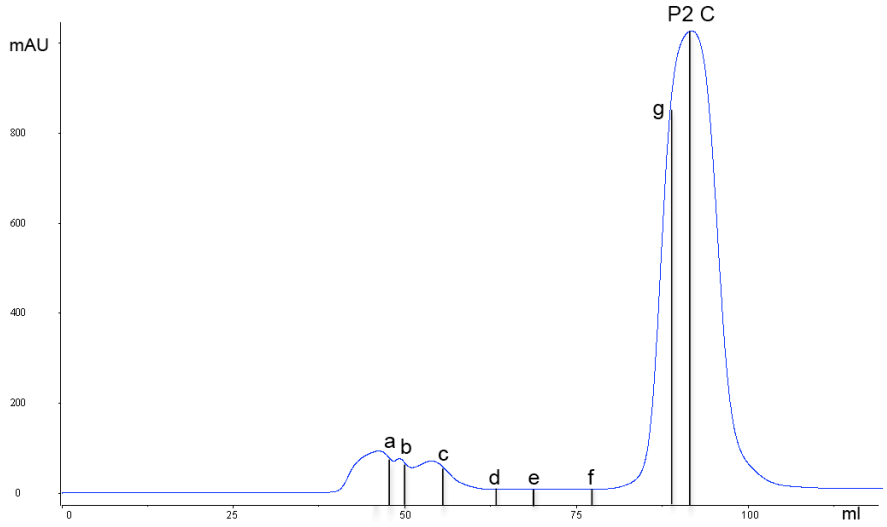
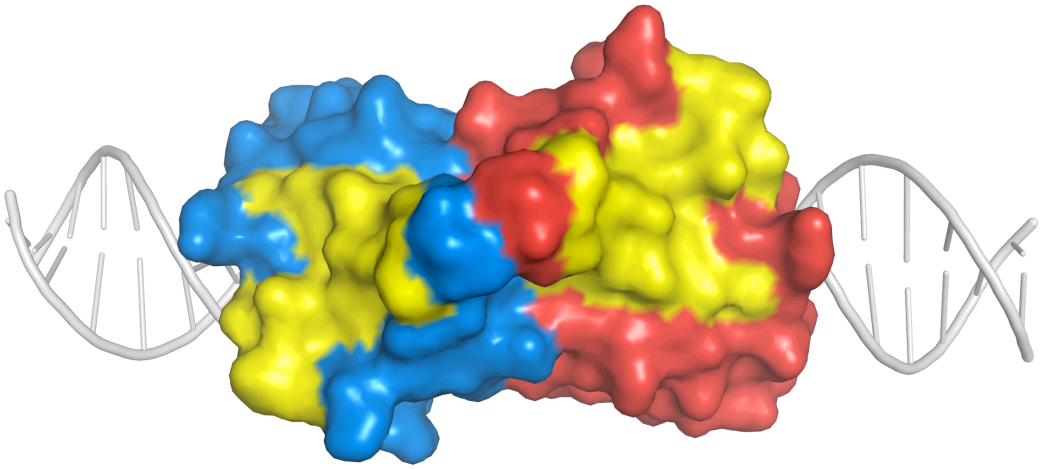


Supplementary figure S1:
Tyr31, Thr33, Tyr36 are exposed on the surface of P2 C and extends out in solution. Based on the structure, mutating these residues is not expected to influence the folding and stability of the protein. This can also be clearly seen from the coomassie stained SDS PAGE gel of clarified lysates from mutants. The expression levels are similar between wild type and mutant P2 C. Lane 1: ladder; Lane 2: Bl21 (DE3) cells; Lane 3: Wild type P2 C; Lane 4: Y31A; Lane 5: T33A; Lane 6: Y36A, Lane 7: ladder.



Supplementary figure S2:
Gel filtration profile of P2 C. A Superdex 200 gel filtration column (GE Healthcare) was used. The position of P2 C, and the position of the size standards used, is indicated as follows: *a* 886 kDa; *b* 669 kDa; *c* 443 kDa; *d* 200 kDa; *e* 150 kDa; *f* 66 kDa; *g* 29 kDa. P2 C elutes with a molecular weight corresponding to 20.5 kDa. This is in good agreement with the expected molecular weight of the P2 C dimer (22 kDa).



Supplementary figure S3:
Surface representation of the P2 C dimer as it would sit on top on the DNA. The DNA binding helix is located below the protein. All residues conserved in the alignment presented in figure 1 are colored yellow. The non-conserved residues in one monomer are colored blue and the non-conserved residues in the other monomer are colored red. The solvent exposed surface formed by conserved residues is facing away from the DNA.