

THE CRYSTAL STRUCTURE OF THE DNA-BINDING DOMAIN OF G1P FROM BACTERIOPHAGE SF6

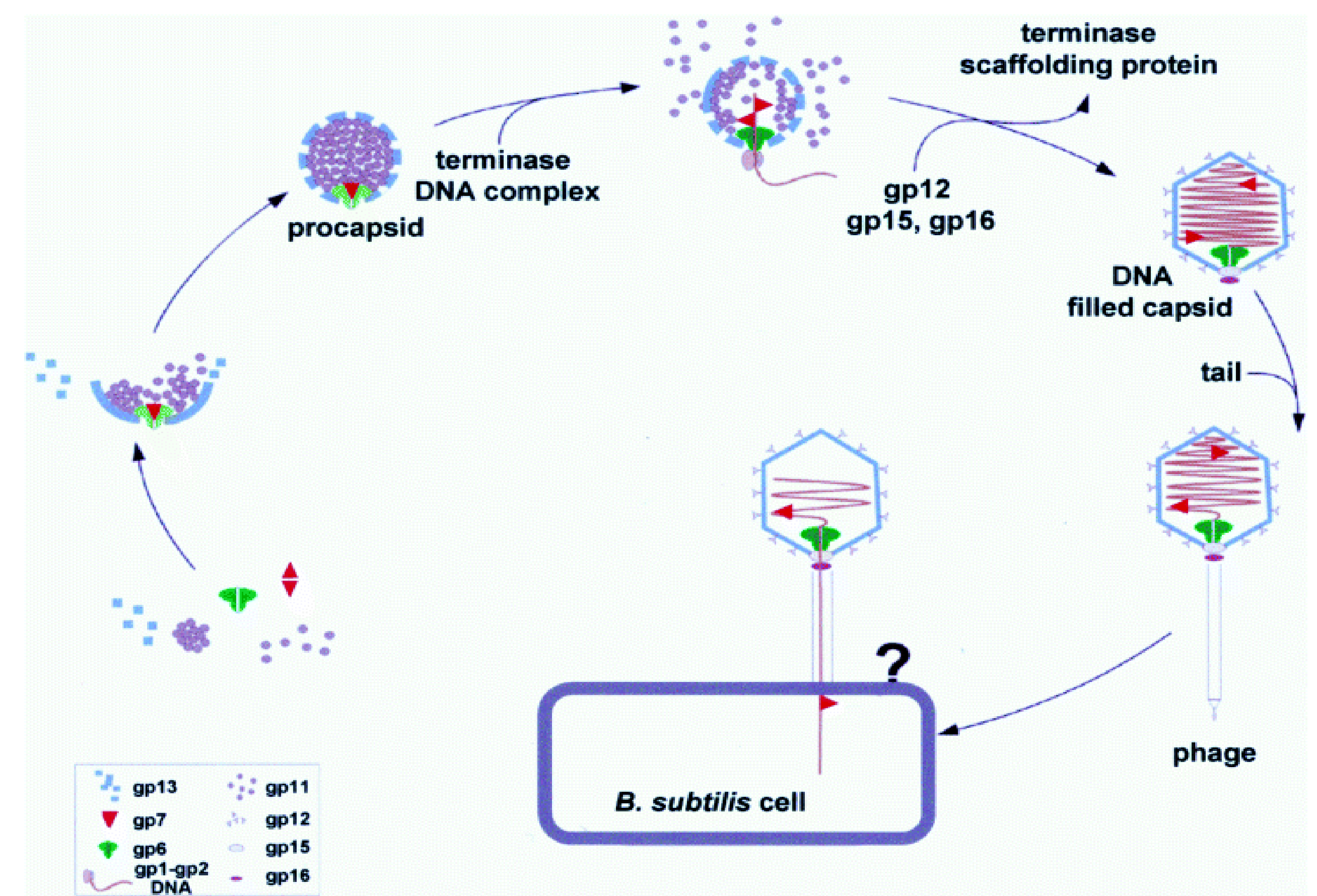
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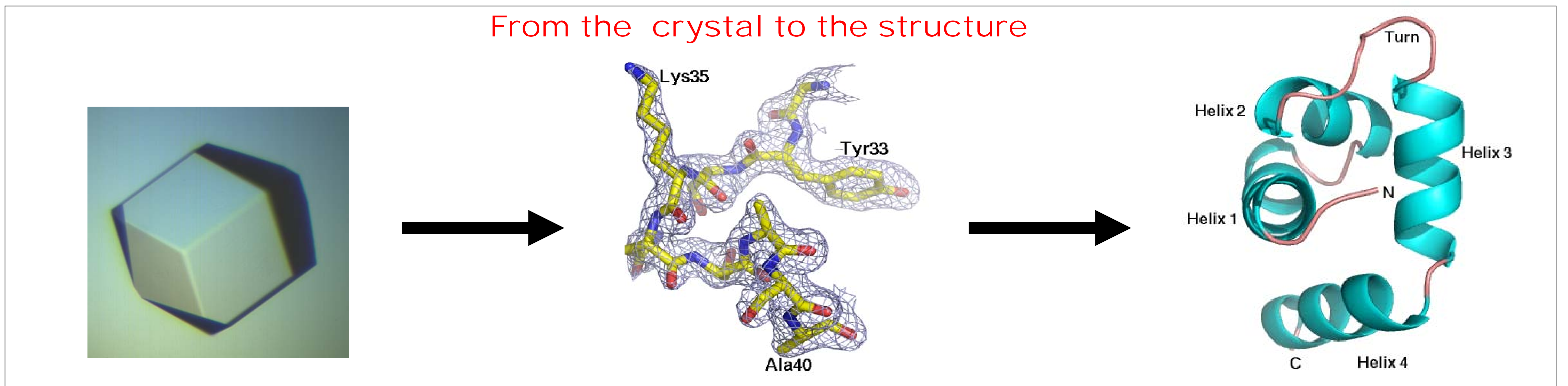
Background

DNA packaging in tailed bacteriophages and in evolutionarily related herpes viruses is controlled by a viral-encoded terminase. In *Bacillus subtilis* SPP1 and SF6 bacteriophages the terminase complex consists of two proteins, G1P and G2P that binds to the viral DNA concatemer. G1P is involved in DNA binding and recruitment of G2P. G2P is composed of two domains with different activities. G2P N-terminal domain has ATPase activity while its C-terminal domain is an endonuclease. The G1P-G2P-DNA hetero-complex interacts with the portal protein G6P located at the unique vertex of the procapsid. The SPP1 DNA packaging motor has been characterised *in vitro* and a model for DNA packaging has been proposed. This model involves a headful mechanism in which G1P specifically recognises a region on the phage DNA called the *pac* site followed by cleavage of DNA by G2P and encapsidation. Here we present the structure of the N-terminal DNA binding domain of G1P (G1PNT) and propose a model for its binding to DNA.

The Terminase complex in viral DNA cycle



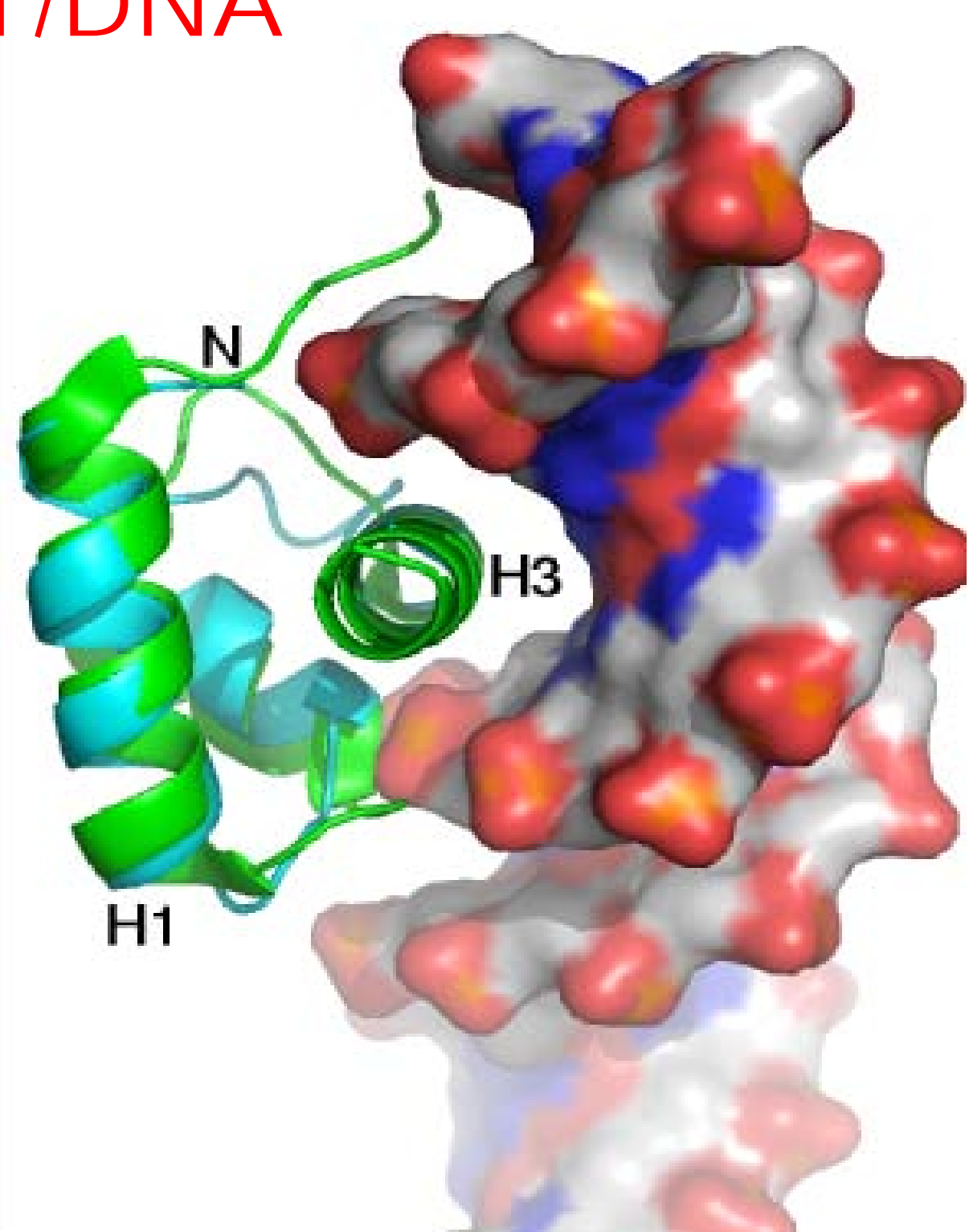
From the crystal to the structure



Structure solution The X-ray data were collected on crystals grown from 2.4 M Na-Malonate pH 7.0 at the BM14 beamline, ESRF and processed using DENZO and SCALEPACK. The structure was solved by Se-Met MAD using SHELX. The initial phases were extended to 1.58 Å with DM. Arp/wArp was used to automatically build a ~93% complete model and finished manually using COOT. The model was refined with REFMAC to the final R of 22.5% and R_{free} of 27.5%. Data analysis by SFCHECK showed that the crystal had a twinning fraction of 10% explaining the relatively high R factors. The electron density map shows the turn between helix2 and helix3.

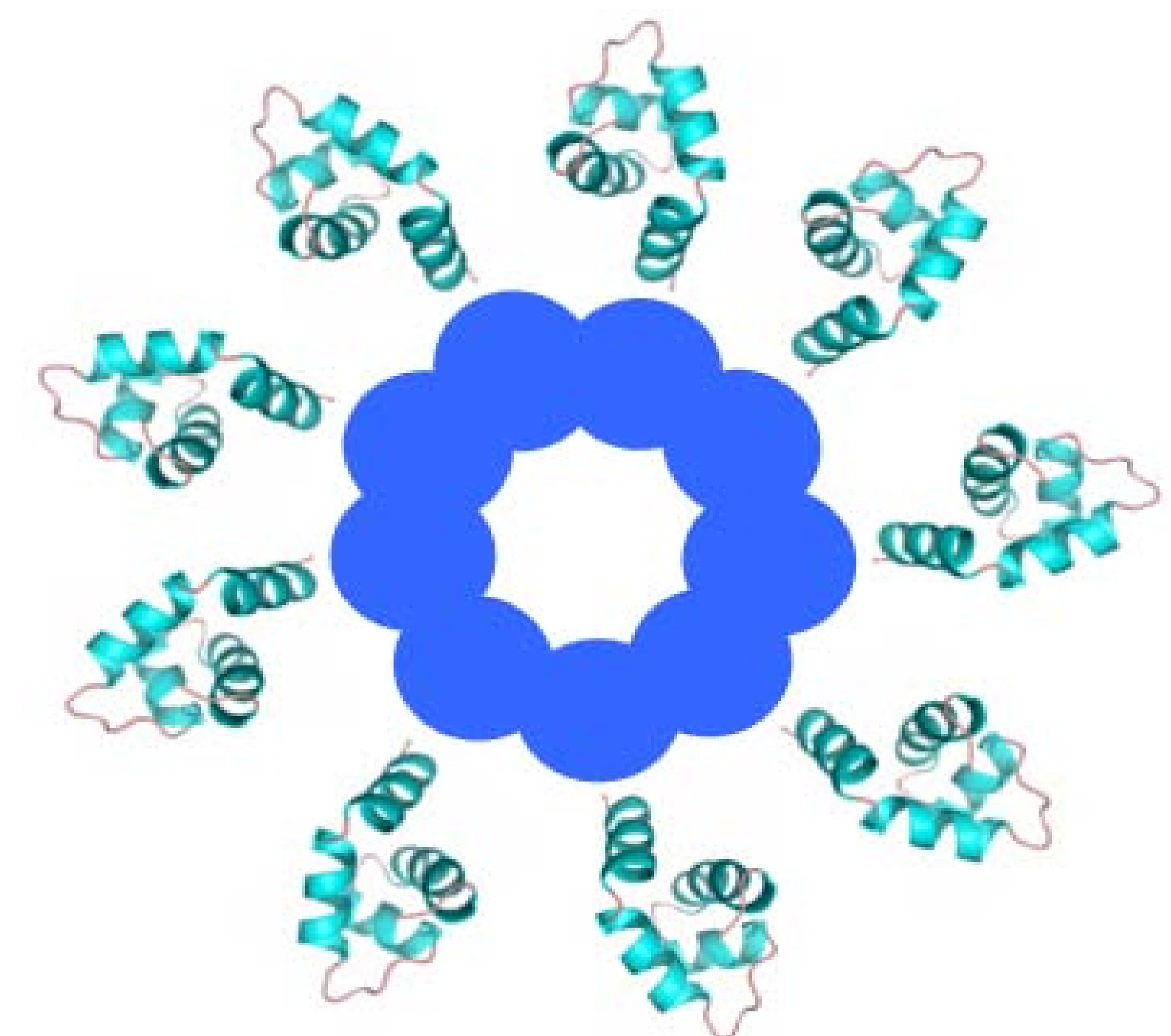
G1PNT crystal structure analysis The G1PNT model consists of 56 residues, folded into four α -helices connected by short loops. The first three helices of G1P form a Helix-Turn-Helix DNA binding motif, which is followed by a fourth helix. The fourth helix possibly acts as a linker between the DNA binding domain and the oligomerisation domain.

Model of G1PNT/DNA interaction



In the crystal structure of hTRF1 (PDB code 1w0t), the closest available structural homologue of G1P, helix 3 is inserted into the major groove of telomeric DNA. The interactions of helix 3 with the DNA are mediated by contacts from residues located in helix 2. The N-terminal arm inserted into the minor groove further enhances DNA binding specificity and affinity. Using this structure as a template it is possible to propose a model for the G1PNT complex with *pac* DNA, as the overall similarity of the DNA binding domain suggests a similar mode of interaction. The Figure shows the SSM superposition of G1PNT on hTRF1 in complex with telomeric DNA.

Model of G1P oligomer



G1P could oligomerise to form a "doughnut like" toroidal structure with the DBDs situated on the outer surface. This arrangement would allow the DNA to wrap around the protein in a circular manner. It is possible that flexibility between the DBDs and the oligomerisation domain (for example in the area of the linker helix 4) facilitates positional adjustment of individual DBDs during their interaction with the DNA.