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Architecture of TFIIIC and its role in RNA polymerase III pre-initiation complex assembly

Gary Male¹, Alexander von Appen¹, Sebastian Glatt¹, Nicholas M.I. Taylor^{1,†}, Michele Cristovao¹, Helga Groetsch¹, Martin Beck¹ & Christoph W. Müller¹

In eukaryotes, RNA Polymerase III (Pol III) is specifically responsible for transcribing genes encoding tRNAs and other short non-coding RNAs. The recruitment of Pol III to tRNA-encoding genes requires the transcription factors (TF) IIIB and IIIC. TFIIIC has been described as a conserved, multi-subunit protein complex composed of two subcomplexes, called τ A and τ B. How these two subcomplexes are linked and how their interaction affects the formation of the Pol III pre-initiation complex (PIC) is poorly understood. Here we use chemical cross-linking mass spectrometry and determine the molecular architecture of TFIIIC. We further report the crystal structure of the essential TPR array from τ A subunit τ 131 and characterize its interaction with a central region of τ B subunit τ 138. The identified τ 131- τ 138 interacting region is essential *in vivo* and overlaps with TFIIIB-binding sites, revealing a crucial interaction platform for the regulation of tRNA transcription initiation.

¹European Molecular Biology Laboratory (EMBL), Structural and Computational Biology Unit, Meyerhofstrasse 1, Heidelberg 69117, Germany.

[†]Present address: Ecole Polytechnique Federale de Lausanne, BSP 416 (Cubotron UNIL), Route de la Sorge, CH-1015 Lausanne, Switzerland. Correspondence and requests for materials should be addressed to C.W.M. (email: cmueller@embl.de).

Eukaryotes require the multi-subunit Pol III to transcribe genes encoding small, non-coding RNAs including tRNAs¹. Recruitment of Pol III to these genes requires the essential transcription factors TFIIB and TFIIC². TFIIB is assembled from three subunits, namely Brf1, Bdp1 and TBP³. TFIIC harbours six proteins in yeast, and has a molecular weight of approximately 500 kDa (ref. 4). The six subunits of yeast TFIIC are partitioned into two DNA-binding subcomplexes (τ A and τ B). Each subcomplex binds to its respective, highly conserved promoter sequence, named 'A box' and 'B box'^{5,6}. The binding of these intragenic promoters by TFIIC permits the assembly of TFIIB, upstream of the transcription start site, which subsequently leads to the recruitment of Pol III, the formation of a PIC and finally to transcription.

Both *in vitro* and *in vivo* studies have demonstrated that TFIIC is a highly flexible protein complex that can accommodate the varying lengths of DNA sequence between the A and B boxes of different tRNA genes^{7,8}. It is hypothesized that a flexible linker between the τ A and τ B subcomplexes allows TFIIC to fulfil these requirements^{9,10}. In yeast, τ A is composed of τ 131 (Tfc4), τ 95 (Tfc1) and τ 55 (Tfc7) and τ B of τ 138 (Tfc3), τ 91 (Tfc6) and τ 60 (Tfc8)⁵. All six subunits are essential *in vivo*³. In human, orthologues of all six yeast subunits have been identified, with sequence similarity highest amongst the τ A subunits¹¹.

While a significant amount of high-resolution structural and functional information exists for some individual TFIIC subunits^{12–14}, a detailed understanding of how the τ A and τ B subcomplexes are connected and which subunits could act as a flexible linker remains elusive (Fig. 1a). τ 95 of τ A has been proposed as a linker, based on co-immunoprecipitation experiments that show binding of this subunit to the τ B subunits τ 138 and τ 91 (ref. 15). A genetic study suggests that the two largest TFIIC subunits, τ 138 and τ 131, are responsible for connecting τ A and τ B¹⁶. The τ 138 subunit is currently the least well-characterized subunit of TFIIC. Photochemical crosslinking studies support the view that τ 138 recognizes the B box promoter of tRNA genes¹⁷, as does the mutation of a highly conserved glycine residue (G349E) within τ 138 that dramatically reduces the affinity of TFIIC for tDNA¹⁸. Interestingly, this mutation can be suppressed by point mutations within the τ 131 subunit, suggesting a direct physical interplay between these two subunits¹⁶. τ 131 shows the highest sequence conservation of the TFIIC subunits and is predicted to contain several tetra-trico peptide repeats (TPRs)¹⁹. TPRs typically contain 34 amino acids arranged into two antiparallel alpha-helices, with proteins often containing several of these motifs in an array²⁰. This arrangement can lead to an extended, right-handed super-helical structure, which can provide extended binding surfaces for other subunits within a protein assembly²¹. τ 131 fulfills this role within TFIIC, binding to subunits Brf1 and Bdp1 in a stepwise mechanism to help assemble TFIIB at tRNA genes, utilizing overlapping sites on an amino-terminal (N-terminal) 'TPR array'^{19,22–28}. It has been further hypothesized that the relative positioning of the TPRs and the extended τ 131 N terminus mask binding sites within the TPR array, leading to an auto-inhibited τ 131 state that must be relieved to allow Brf1 and Bdp1 binding^{27,28}. These rate-limiting steps in Pol III PIC formation may be overcome, at least in part, by flexibility within τ 131. Indeed, previous studies suggest conformational changes take place within τ 131 on the binding of Brf1 and Bdp1 (refs 25,29). Finally, τ 131 has also been shown to bind Pol III subunits Rpc53 and ABC10 α ^{30,31}. Molecular details of the interactions of τ 131 with τ A or τ B subunits have not been reported, although in humans it has been shown that the τ 131 orthologue (TFIIC102) interacts with the τ 95 orthologue (TFIIC63), again requiring the conserved TPR array³².

We set out to characterize the molecular architecture of TFIIC and identify the τ A– τ B linker region within TFIIC using a combination of structural and biochemical approaches. Our findings implicate a central role for the TPR array of τ 131 in linking τ A, τ B and TFIIB to regulate the formation of the Pol III PIC.

Results

The τ 131 TPR array crosslinks to a central region of τ 138. As a first step in identifying the link between τ A and τ B subcomplexes, we performed a chemical crosslinking mass spectrometry (XL-MS) approach on purified, endogenous TFIIC from *S. cerevisiae*. The protein complex was purified from a yeast strain, carrying a tandem affinity purification (TAP) tag on the τ 60 subunit. Pure and stoichiometric TFIIC could be obtained as assessed by size-exclusion chromatography and SDS–polyacrylamide gel electrophoresis (SDS–PAGE; Fig. 1b). The complex was shown to be functional by its ability to bind a double-stranded oligonucleotide containing A and B box sequences by electrophoretic mobility shift assay (EMSA; Fig. 1c). Using XL-MS, we identified 33 unique intersubunit and 89 unique intrasubunit crosslinks with high confidence at a linear discriminant (ld) score of > 25 (Fig. 1d and Supplementary Tables 1 and 2). Twelve of the intersubunit crosslinks bridge τ 131 with τ 138. The majority of these links connect the N-terminal TPR array of τ 131 to an unstructured, central region of τ 138. With the exception of three additional crosslinks identified between the τ 95 subunit and τ 138, these links represent the major τ A– τ B connection revealed by our approach. Our XL-MS analyses also provide additional insights into the overall architecture of TFIIC. Within the τ A subcomplex, six crosslinks connect the dimerization domains of τ 95 and τ 55, consistent with our previously reported crystal structure¹⁴. In addition, we identified four crosslinks between the τ 95 subunit and predicted TPRs at the C terminus of τ 131. Within the τ B subcomplex, there are surprisingly few crosslinks observed between the τ 60 and τ 91 subunits, despite the large interface between them¹². Xlink Analyzer³³ shows that some lysine residues are entirely buried in the τ 60– τ 91 interface and are therefore not accessible to the crosslinker. We also observe lysine residues surrounding this interface that are not detected by our XL-MS analysis, probably because they are buried in interfaces with other TFIIC subunits. Four crosslinks connect τ 91 with a disordered region between two predicted winged helix domains of τ 138, which is consistent with the proposal of a co-operative role between τ 91 and τ 138 for B box binding³⁴.

We went further in our analysis of the entire TFIIC complex by performing XL-MS on DNA-bound TFIIC, to determine whether the complex undergoes large conformational changes (Supplementary Tables 3 and 4). In general, we observed no fundamental changes in the intersubunit interaction network on tDNA binding (compare Fig. 1d and Supplementary Fig. 1). In particular, the bridge between the τ 131 and τ 138 subunits is maintained, indicating the importance of this link for the integrity and stability of TFIIC when bound to DNA. Interestingly, the four crosslinks connecting the τ 91 and τ 138 subunits are not detected when TFIIC is bound to DNA, suggesting a local change in conformation that prevents these previously crosslinked residues from accessing the crosslinker. It is tempting to speculate that this region is therefore involved in direct binding of TFIIC to DNA.

Structure of the τ 131 TPR array. τ 131 and τ 138 are the largest subunits of the τ A and τ B subcomplexes, respectively⁵. τ 131 was predicted to contain a highly conserved TPR array architecture at the N terminus with additional conserved TPRs predicted at the

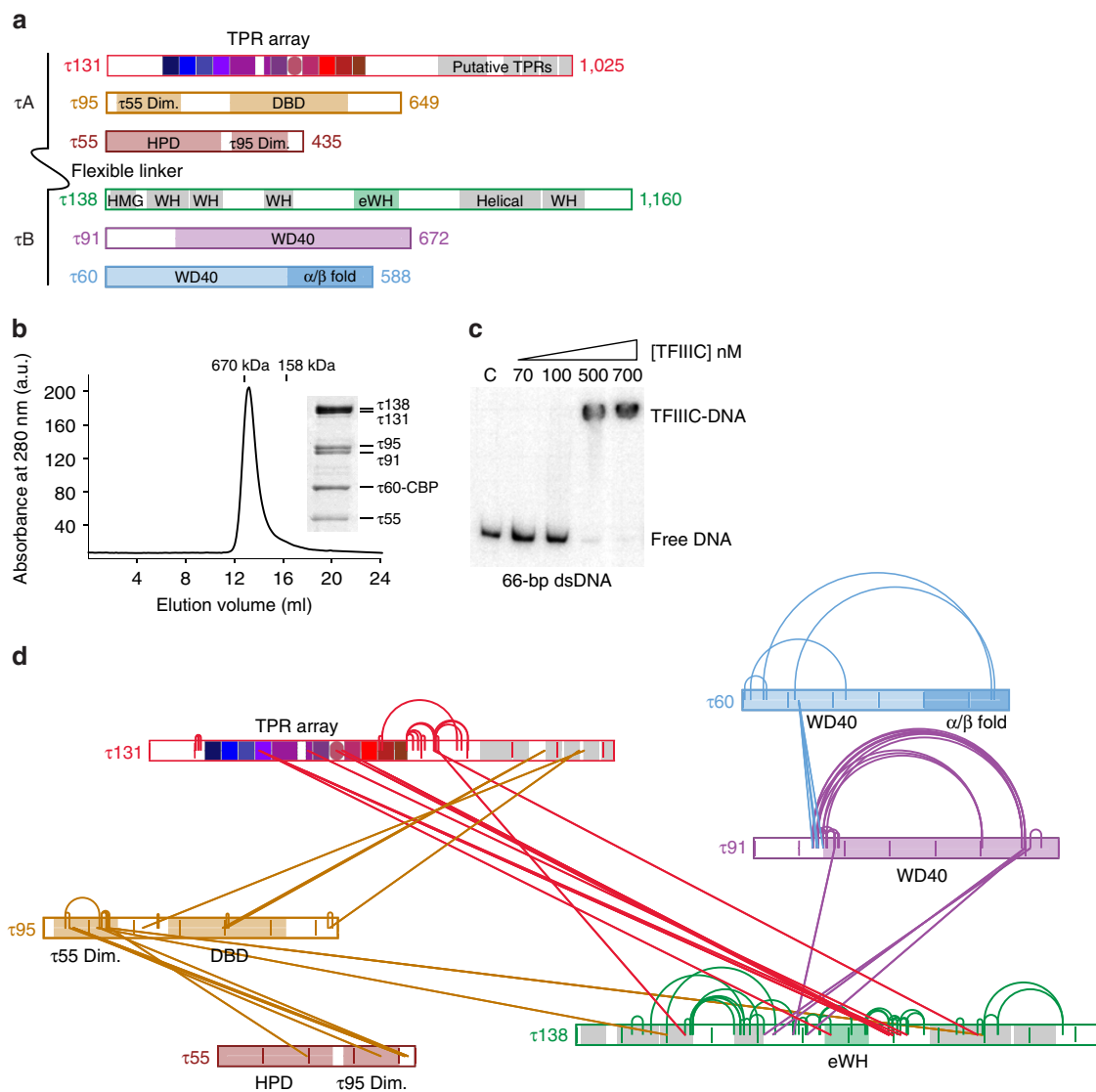


Figure 1 | XL-MS of purified, endogenous TFIIIC reveals a link between τ A and τ B. (a) Schematic representation of the six subunits of *S. cerevisiae* TFIIIC. The amino-acid lengths of the subunits are labelled at the C terminus. Domains of which crystal structures are available are highlighted. τ 55 and τ 95 Dim. = τ 55 and τ 95 dimerization domains; DBD, DNA-binding domain; HPD, histidine phosphatase domain. The tetra-trico peptide (TPR) array of τ 131 and the eWH domain of τ 138 are included, see text for details. Additional predicted structural regions of τ 131 and τ 138 are highlighted in grey. HMG, high mobility group box domain; WH = winged helix. (b) Analytical size-exclusion chromatography profile of TFIIIC using a Superose 6 10/300 column (GE Healthcare). Known molecular weight standards at 670 and 158 kDa are indicated. Inset, Coomassie-stained SDS-PAGE gel of an elution peak fraction. (c) EMSA experiment of TFIIIC bound to a double-stranded (ds) 66 base-pair (bp) tDNA^{Glu} oligonucleotide. C, control (no TFIIIC added). (d) Crosslinking map of TFIIIC. TFIIIC subunits are represented as in a with internal vertical lines representing 100 amino-acid markers. Intra crosslinks are depicted by arcs that connect residues within the same subunit. Inter crosslinks are depicted by lines which connect residues within different subunits. Image produced using xiNET⁵⁰.

C terminus¹⁹ (Fig. 2a). Given that our crosslinking data implicated the TPR array of τ 131 in connecting τ A and τ B, and the reported importance of this region for TFIIIB assembly, we determined the crystal structure of the TPR array (residues 123–566) in two different space groups (P₆₂ and P₄₃). Starting from a construct expressing residues 1–580 of τ 131, we identified a stable fragment by limited proteolysis and mass spectrometry corresponding to residues 123–566. We expressed this truncated *S. cerevisiae* τ 131 (123–566) protein in *E. coli*, purified it using affinity and size-exclusion chromatography and subsequently carried out crystallization trials. We were able to collect diffraction data up to 3.15 Å (P₆₂) and 3.4 Å (P₄₃) resolution. The lower-resolution structure was solved by multiple isomorphous replacement with anomalous signal (MIRAS),

using anomalous signal from crystals prepared with selenomethionine substituted proteins or native crystals soaked with p-chloromercuribenzenesulfonic acid to final R_{work}/R_{free} values of 20.9%/24.5%. The higher-resolution structure was solved using selenomethionine substituted protein in single anomalous dispersion (SAD) experiments and subsequently refined to R_{work}/R_{free} values of 25.0%/28.7%. The combination of selenomethionine and mercury (Hg) markers aided the building of the structures. (Table 1, Supplementary Figs 2 and 3a and Supplementary Table 5).

The structure reveals the presence of 10 TPR repeats, while only nine TPR repeats had been predicted. Rather than forming an extended super-helix, the TPR array is instead separated into two ‘arms’ by a central region that contains an extended helix and

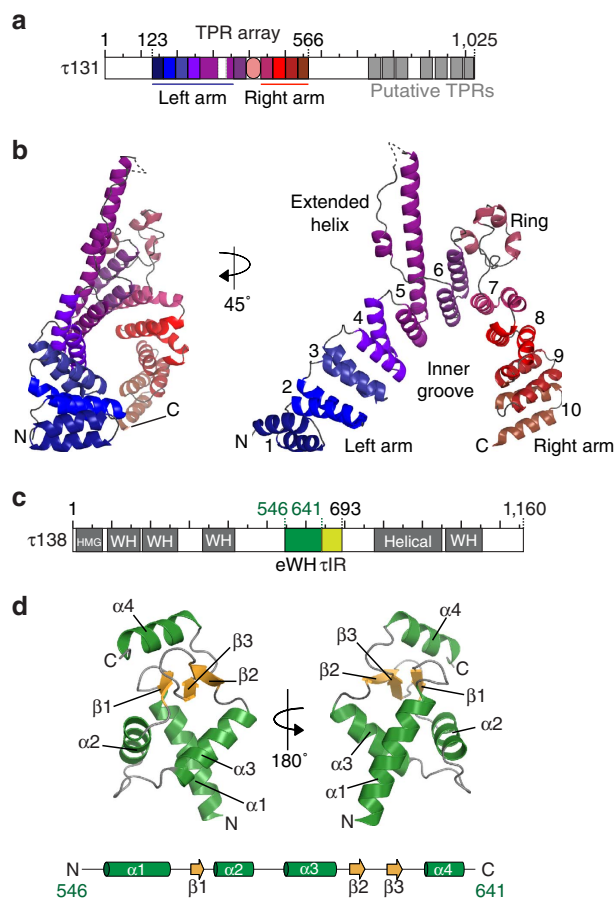


Figure 2 | Crystal structures of the TPR array of τ 131 and the central extended winged helix (eWH) domain of τ 138. (a) Schematic domain architecture of τ 131. The TPR array is highlighted and coloured according to the solved crystal structure in **b**. Putative TPRs are indicated in grey. (b) Crystal structure of the τ 131 (123–566) TPR array in ribbon representation. Two views are displayed, related by a 45° rotation. A dashed line indicates a region of the electron density where no residues could be built with confidence (residues 317–336). TPRs are numbered 1–10. (c) Schematic domain architecture of τ 138. Predicted winged helix (WH) domains, the high mobility group (HMG)-box domain and the helical region are shaded in grey. The central eWH domain is shaded in dark green. The τ IR is shaded in light green (see text for details). (d) Crystal structure of the τ 138 (546–641) eWH domain in ribbon representation. Two views are displayed, related by a 180° rotation. A schematic of the arrangement of α -helices and β -strands is displayed underneath the structure.

a disordered coil we call ‘ring’ domain (Fig. 2b). This insertion causes a bend in the TPR array, positioning the TPRs of the right arm closer to the TPRs of the left arm. This feature generates a potential binding pocket we call the ‘inner groove’. τ 131 is postulated as being highly flexible, consistent with its role in binding to multiple ligands at different stages in Pol III PIC assembly. A superimposition of the two crystal forms and an analysis of temperature factors reveal flexibility at TPRs 1–3, 8–10 and residues at the extremes of the extended helix (Supplementary Fig. 3b). Despite crystal contacts in these regions, the accommodation of the TPR array in these arrangements in two different crystal forms suggests that the conformational changes are indeed permitted within the TPR array.

Characterization of the τ 131– τ 138 interaction region. We next wanted to characterize further the central region of τ 138

(546–693) and understand which regions were crucial for interaction with the TPR array. We hypothesized that the inner groove of the TPR array may accommodate the predicted central winged helix domain of τ 138 (Fig. 2c). Surface analysis of the TPR array shows that the inner groove is lined with patches of conserved, often acidic surface residues that may bind to the predicted basic surface residues of τ 138 (Supplementary Figs 3c,d,e and 4). We first solved the structure of the central domain of τ 138 (546–641) using the sulphur-SAD technique (Table 1, Supplementary Table 5, Supplementary Fig. 5a). The 1.4 Å crystal structure ($R_{\text{work}}/R_{\text{free}}$ of 17.5%/19.8%) of this domain reveals a canonical winged helix domain that contains an additional C-terminal helix (Fig. 2d). This first structurally characterized part of τ 138 thus represents an ‘extended’ winged helix (eWH) domain³⁵. The eWH domain is moderately well conserved from yeast to human (Supplementary Fig. 5b,c,d), and contains basic patches that could also suggest a role in binding nucleic acids (Supplementary Fig. 5e). However, we only detect very weak unspecific binding of the eWH domain to single and double-stranded DNA (Supplementary Fig. 5f). Isothermal titration calorimetry (ITC) did not detect an interaction between the eWH and the TPR array (Supplementary Fig. 6a). However, when we tested a construct that contained the eWH domain with additional residues at the C terminus (546–693), we observed a K_d for the interaction with the TPR array of ~ 100 nM (Fig. 3a). A similar high-affinity interaction (~ 80 nM) could be measured with only the unstructured region of τ 138 (641–693) (Fig. 3b). Removal of residues 682–693 lowered the K_d of the interaction to ~ 2.6 μ M (Supplementary Fig. 6b), yet the region 641–681 was still essential to ensure the high-affinity interaction as tested peptides of 681–693 did not interact with the TPR array by ITC (data not shown). We thus concluded that the region 641–693 of τ 138, hereafter referred to as ‘ τ 131-Interaction Region (τ IR)’, is necessary and sufficient to bind the TPR array of τ 131.

To assess the *in vivo* importance of our *in vitro* results, we disrupted the chromosomal copy of τ 138 in yeast and introduced a plasmid carrying wild-type τ 138 and the URA3 gene under the control of the endogenous promoter, to maintain cell viability. This plasmid was then shuffled with a second plasmid carrying either the wild-type τ 138 or a deletion mutant of τ 138. We observed growth for cells transformed with the τ 138 wild-type plasmid on FOA medium, but cells carrying the τ 138 Δ eWH- τ IR or the Δ τ IR plasmid did not survive (Fig. 3c). This is a clear indication that these deletion mutants cannot complement the loss of wild-type τ 138. Removal of residues 681–693 leads to an intermediate phenotype of reduced yeast growth (Supplementary Fig. 6c). Interestingly, the removal of just the eWH domain is also lethal to yeast (Fig. 3c), indicating that despite it being dispensable for the interaction with τ 131 *in vitro*, it is still essential for proper TFIIC function *in vivo*.

τ 138 and Bdp1 binding is affected by mutations in TPR 8. Our structure of the τ 131 TPR array allows us, for the first time, to map and analyse mutations that have been previously described (Fig. 4a). In detail, mutations that increase Pol III transcription cluster mostly on TPR 2 (ref. 26), those that decrease Pol III transcription spread over TPRs 8–10 (ref. 22) and those that rescue a τ 138 temperature-sensitive mutation, map mostly to TPRs 7–8 (ref. 16). Having mapped the critical τ 131 interaction region of τ 138 to ~ 50 amino acids, we next questioned where the τ IR binds on the TPR array. Despite extensive efforts, we were unable to obtain structural information of the τ 131– τ IR complex although both polypeptides form a stable complex during size-exclusion chromatography. Instead, we analysed previously described mutations together with the surface conservation of the

Table 1 | Data collection and refinement statistics.

	τ 131 Native P6 ₂	τ 131 Native P4 ₃	τ 138 Native
Data collection			
Beamline	PETRAIII (P14)	ESRF (ID23-2)	ESRF (ID23-1)
Space group	P6 ₂	P4 ₃	H32
Cell dimensions			
<i>a</i> = <i>b</i> , <i>c</i> (Å)	116.36 95.98	105.13 98.74	129.09 68.04
Wavelength (Å)	0.97626	0.87260	0.9763
Resolution (Å)*, †	50–3.15 (3.23–3.15)	73.34–3.4 (3.58–3.4)	50–1.4 (1.44–1.4)
CC ½ (%)	0.99 (0.49)	0.99 (0.68)	0.99 (0.65)
R _{merge} (%)	7.4 (275.3)	8.2 (58.7)	5.1 (137.9)
<i>I</i> / σ <i>I</i>	34.41 (1.7)	8.6 (2.0)	21.3 (1.7)
Completeness (%)	99.9 (99.9)	99.9 (99.3)	99.9 (99.3)
Redundancy sites	39.3 (38.3)	4.0 (3.5)	10.1 (9.4)
Refinement			
Resolution (Å)	50–3.15	74.36–3.4	50–1.4
No. of reflections‡	12,884	14,867	42,553
R _{work} /R _{free} (%)	25.00/28.66	20.92/24.45	17.52/19.75
No. of non-H atoms			
Protein	3,442	3,379	1,581
Ligand/ion	0	0	12
Water	0	0	197
B-factors (Å ²)			
Protein	151.1	145.6	32.3
Ligand/ion	0	0	67.8
Water	0	0	38.0
r.m.s deviations			
Bond lengths (Å)	0.004	0.006	0.006
Bond angles (°)	0.713	1.1	0.947

r.m.s., root mean squared.

*Values in parentheses correspond to the highest-resolution shell.

†Resolution cutoff criteria according to ref. 51. Resolution limits according to *I*/ σ *I* of 2 are 3.2 Å for τ 131 in P6₂, 3.4 Å for τ 131 in P4₃, 1.45 Å for τ 138, respectively.‡Non-anomalous, anomalous: 28,928; number of reflections in R_{free} set is 1,468.

TPR array (Supplementary Fig. 3e), to predict where the τ IR may bind. We expressed and purified five τ 131 point mutants that all cluster on TPR 8 (Fig. 4b). With the exception of residue L469, all of these residues are acidic and surface exposed (Fig. 4c). The purified mutants all eluted at the same volume from a size-exclusion column when compared with the wild type, indicating that the mutations did not cause a destabilization of the proteins (Supplementary Fig. 7a). Using ITC, we determined binding affinities of the mutant τ 131 TPR arrays to the τ IR and the eWH- τ IR (Fig. 4d and Supplementary Fig. 7b). No binding of the mutants D468K and L469K to the τ 138 proteins could be detected by ITC. Mutants E472K and E498K showed much weaker binding, while the E497K mutant showed no significant decrease in binding affinity to the τ 138 proteins. These findings are consistent with results from GST pull-down assays (Fig. 4e and Supplementary Fig. 7c). We note that the L469K mutation likely causes a steric clash in the packing of TPR 8 with TPR 7 rather than abolishing a site-specific contact (Fig. 4c). Strikingly, the mutation of residues D468 and L469 has been previously implicated in a loss of binding to TFIIIB subunit Bdp1 (refs 16,22). We purified full-length, recombinant Bdp1 and performed GST pull-down assays. Bdp1 binding to the TPR array of τ 131 is strongly reduced in the D468K or L469K mutants (Fig. 4f). To our knowledge, this is the first time that a loss of interaction by both of these mutations has been probed directly using purified proteins. These results suggest that the binding hotspot for τ 138 thus overlaps with that of a binding site for Bdp1.

Brf1-TBP binds a distinct site from that of τ 138 and Bdp1.

Previous studies have proposed that τ 131 exists in an auto-inhibited form before assembly of TFIIIB²⁷. This auto-inhibition,

possibly by the masking of the τ 131 TPR array by the extended N terminus, may be relieved before or on recruitment of the Brf1 subunit of TFIIIB, paving the way for TBP and Bdp1 recruitment²⁸. To further our understanding of the overlap between TFIIIB and τ 138 binding, we purified a form of τ 131 that contained the extended N terminus (1–580)²⁵ as a GST fusion for interaction studies. As recombinant Brf1 is highly unstable, we were unable to produce sufficient quantities of pure, recombinant Brf1 protein for our studies. We therefore turned to a Brf1-TBP fusion protein that has been previously described and shown to functionally replace Brf1 both *in vitro* and *in vivo*³⁶.

We tested the binding of τ 138 (eWH- τ IR) and Bdp1 to τ 131 (1–580) (Fig. 5a). Both proteins bind stoichiometrically to this longer τ 131 protein, showing that the extended N terminus of τ 131 does not inhibit binding. We did not observe binding of Brf1-TBP to τ 131 (123–566) under our experimental conditions (data not shown); however, we did detect an interaction using τ 131 (1–580; Fig. 5a). The interaction was also observed with the D468K and the L469K mutants of τ 131 (1–580) (Fig. 5a). These results indicate that the extended N terminus of τ 131 is required for high-affinity binding to Brf1-TBP, and that the principal binding site on τ 131 is separate from the hotspot of τ 138 and Bdp1. The purified Brf1-TBP contained degradation products of the fusion protein corresponding to truncations lacking the N terminus of Brf1, as confirmed by MS (Supplementary Fig. 8). We observed that these degradation products were not pulled down by τ 131 (1–580; Fig. 5a), suggesting that the N terminus of Brf1, which includes the TFIIIB-like cyclin repeats, is required for the interaction.

To conclusively determine if the τ 138 binding site overlaps with Bdp1 and/or Brf1-TBP, we next used the GST- τ 131 (1–580)

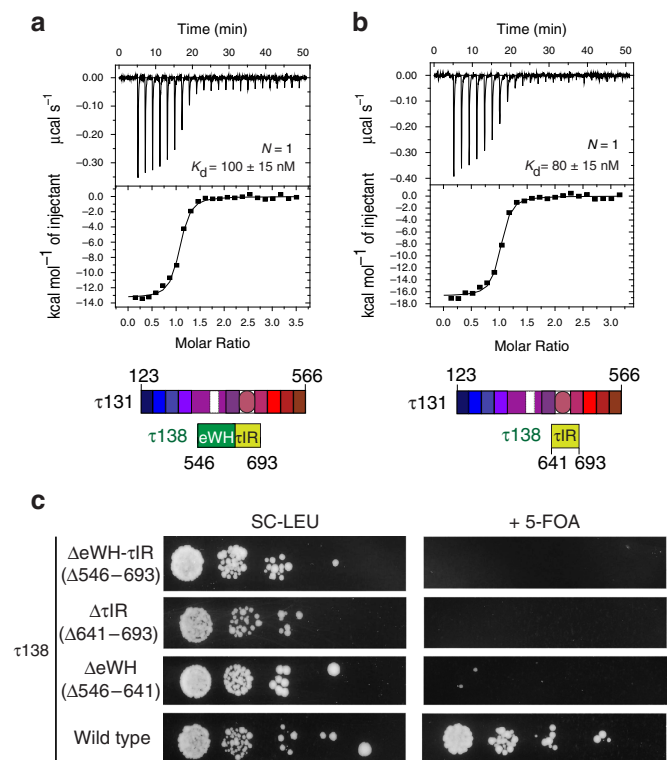


Figure 3 | The τ 131 TPR array interacts with high affinity to a central region of τ 138. ITC measurement using purified (a) τ 138 (546–693) and τ 131 (123–566); (b) τ 138 (641–693) and τ 131 (123–566); Calculated K_d values and stoichiometry (N) are indicated. 15 μ M of τ 138 was used in the cell and 150 μ M τ 131 was used in the syringe in each case. (c) Viability of τ 138 deletion mutants *in vivo* determined by the spot assay. A yeast strain carrying the plasmid pOL49 was transformed with the plasmids pRS415 Δ CEN τ 138 and pRS415 Δ CEN Δ 546–693 or Δ 641–693 or Δ 546–641 and plated on SC-URA-LEU medium. Serial 10-fold dilutions of all strains were spotted on SC-LEU and 5-fluoroorotic acid medium and were incubated for 72 h at 30 °C ($n = 3$).

and incubated it with τ 138 (eWH- τ IR), before titrating in increasing amounts of Bdp1 or Brf1-TBP. We observed a direct competition between τ 138 and Bdp1 for binding to τ 131 (Fig. 5b). These results were also replicated when using the shorter, TPR array of τ 131 (data not shown). In contrast, even a \sim 17-fold molar excess of Brf1-TBP could not compete out the τ 138- τ 131 interaction (Fig. 5c). Instead, both Brf1-TBP and τ 138 can bind simultaneously to τ 131, indicating that their binding sites are distinct.

Discussion

On the basis of limited proteolysis and low-resolution scanning transmission light microscopy, TFIIC has long been described as a ‘dumb-bell’ shaped molecule consisting of two DNA-binding subcomplexes called τ A and τ B connected by a flexible linker^{9,10}. More detailed information about the overall architecture of TFIIC has been lacking. By combining structural information of individual subunits with our crosslinking data sets, we are able to provide a first model of the overall TFIIC architecture (Fig. 6a). Our XL-MS data, combined with *in vitro* and *in vivo* mapping, indicate that the τ IR establishes the main link between τ A and τ B, while the adjacent disordered regions on both sides of the eWH domain in τ 138 presumably provide the necessary flexibility for binding variously spaced A box and B box promoters (Figs 2c and 6a). The N-terminal TPR array of τ 131 provides a docking

platform for the τ IR, while C-terminal TPRs interact with the τ 95 subunit of τ A. Thus, τ 131 is crucial for linking the τ A and τ B subunits. Subunits τ 55 and τ 95, the two other subunits of the τ A subcomplex, share an unexpected structural similarity with the general transcription factor TFIIF¹⁴. Subunits τ 55 and τ 95 dimerize through a triple β -barrel domain consistent with several crosslinks that we observe between their dimerization domains, while the C-terminal DNA-binding domain of τ 95 contains a winged helix domain similar to TFIIF Rap30 (ref. 14). In addition to the τ IR, our XL-MS data reveal only one other possible link between τ A and τ B involving the dimerization domain of subunit τ 95 and subunit τ 138. The importance of this link will have to be substantiated in future studies. In τ B, the WD40 propeller subunits τ 60 and τ 91 have been previously proposed to form a platform for τ 138 interaction, thus cooperatively regulating B box binding of τ 138 (refs 12,34). We have observed crosslinks between the τ 91 subunit and a disordered region between the third predicted winged helix domain and the eWH domain of τ 138, which are not detected when TFIIC is bound to DNA (Supplementary Fig. 1). In addition, it has been shown that a mutation in the third winged helix domain of τ 138 (G349E) strongly reduces the affinity of TFIIC for DNA¹⁸. Considering these different bodies of evidence it is tempting to speculate that this region in τ 138 directly recognizes B box sequences.

In addition to advancing our understanding of TFIIC architecture, our study also provides surprising insights into the overlap between τ A, τ B and TFIIB interaction sites. Previous models have proposed that, due to its intrinsic flexibility, binding sites on the τ 131 TPR array that are crucial for the binding of Brf1 and Bdp1 are masked in the context of the full TPR array and the extended N terminus^{27,28}. This could be an important mode of regulation, preventing the assembly of TFIIB until conditions are optimal for transcription to proceed. Our results provide new insights into the co-ordination and regulation of this assembly. We find that the extended N terminus of τ 131 is absolutely required for high-affinity binding to Brf1-TBP. Under our experimental conditions, we were not able to detect an interaction between Brf1-TBP and the TPR array alone, although it seems certain that Brf1 can also bind here, as mutations that enhance Brf1 binding and stimulate Pol III transcription have been mapped to TPR 2 on the left arm of the array²⁶ (Fig. 4a). Bdp1 can bind to τ 131 without the presence of Brf1-TBP, and the extended N terminus of τ 131 plays no role in inhibition of binding. Finally, our competition experiments have demonstrated that τ 131 cannot accommodate τ 138 and Bdp1 at the same time, whereas Brf1-TBP and τ 138 can assemble simultaneously on τ 131. We thus propose that τ 138 prevents complete assembly of TFIIB, with the crucial Bdp1 binding site masked by a disordered region of τ 138, the τ IR (Fig. 6b).

On the basis of previous studies and the results presented here, we propose the following sequential model for TFIIB assembly—the assembly is initiated by the recruitment of Brf1 to τ 131, most likely by the completed assembly of TFIIC on a tRNA gene. The second TFIIB component, namely TBP, is then recruited via binding sites on Brf1 and via the τ B subunit τ 60 (refs 12,37). In the final step of TFIIB assembly, Bdp1 is recruited to the TFIIC/Brf1/TBP complex, competing with τ 138 for a binding hotspot on TPR 8 of τ 131. On binding, Bdp1 causes a conformational change or a break between τ A and τ B, displacing the critical τ IR from the TPR array of τ 131 and inducing the displacement of the τ B module. TFIIC (with the τ B module providing most of the DNA-binding affinity) is only required for assembling TFIIB but is dispensable for Pol III transcription² and is displaced from its DNA-binding site during Pol III transcription as shown by EMSAs in an *in vitro* reconstituted system³⁸. The mechanism by

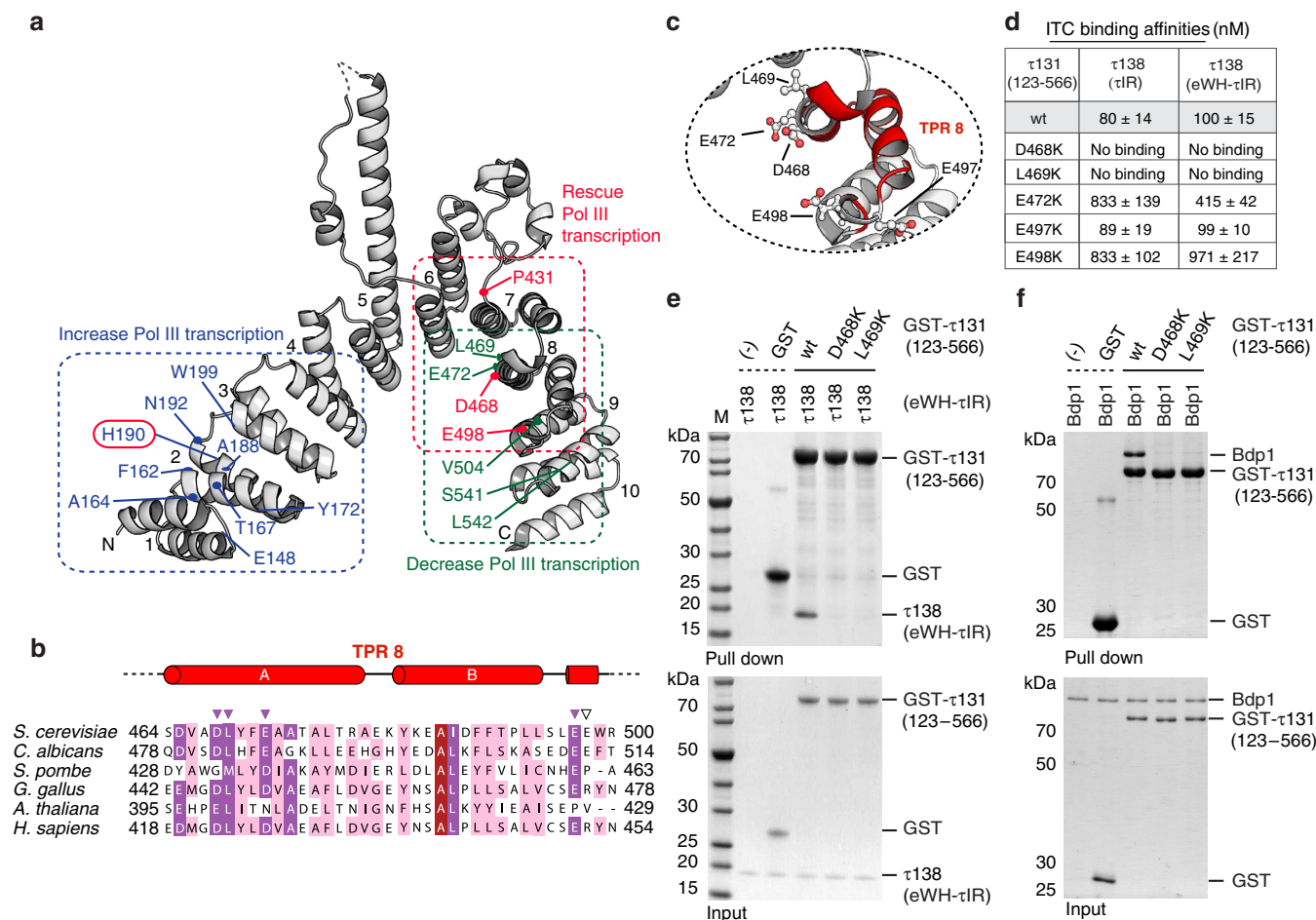


Figure 4 | A binding hotspot on the τ 131 TPR array for τ 138 and Bdp1. (a) Mapped mutants of the τ 131 TPR array (see text for details). **(b)** Sequence alignment of TPR 8. Identical residues are boxed in brick red, highly conserved in purple, medium conserved in pink and low conserved in white. Coloured arrowheads indicate the five mutated residues. **(c)** Close-up from the structure of TPR 8. The five residues selected for mutation are displayed as sticks; carbon atoms (grey); oxygen atoms (red). **(d)** Summary of ITC measurements using indicated τ 131 (123–566) point mutants with τ 138 (τ 1R) or τ 138 (eWH- τ 1R). Wild-type (wt) measurements are included for reference. **(e)** GST pull-down assays of purified wild-type (wt) and mutant GST-tagged τ 131 (123–566) variants with untagged τ 138 (eWH- τ 1R). (–) indicates a background control for nonspecific binding of τ 138 to the GST-affinity resin. A mixture of purified GST and untagged τ 138 was also used as a negative control. Lower gel shows 5% of the input and upper gel shows bound fractions. **(f)** GST pull-down assays of purified wild-type (wt) and mutant GST-tagged τ 131 (123–566) variants with untagged Bdp1. Negative controls and gel format as in **e**.

which *in vivo* TFIIC is displaced (and presumably disassembled) during transcription is currently unknown. However, we suggest that Bdp1 could induce the displacement of the τ B module as a regulatory mechanism essential for the initial round of Pol III transcription. Consistent with this model, a recent mass spectrometry study of TAP-purified Pol III from actively transcribing yeast cells detected co-eluting peptides from all three subunits of TFIIB and peptides from the τ 131 subunit, but not from any τ B subunit³⁹.

Methods

Purification of endogenous TFIIC. TFIIC was purified from *S. cerevisiae* strain SC2342 (provided by Cellzome AG), which expresses endogenous TFC8 (τ 60) fused with a C-terminal TAP-tag. Yeast cells were grown overnight in YPD medium at 30 °C and 200 r.p.m. in a BIOSTAT C30 fermenter (Sartorius) under controlled conditions and collected at an $OD_{600\text{nm}}$ of 5–6. The cell paste was resuspended in lysis buffer (250 mM Tris-HCl, pH 8, 40% glycerol, 250 mM $(\text{NH}_4)_2\text{SO}_4$, 1 mM EDTA, 12 mM β -mercaptoethanol) supplemented with protease inhibitors (Roche) before being lysed with glass beads in a BeadBeater (BioSpec). The lysate was centrifuged at 14,000 r.p.m. for 1 h at 4 °C, with the resulting supernatant then loaded onto a Heparin-Sepharose resin (GE Healthcare). The complex was eluted from the resin using high-salt buffer with 1 M $(\text{NH}_4)_2\text{SO}_4$ and then diluted back to low salt for incubation with IgG Sepharose (GE Healthcare) for 6 h. After washing, IgG beads were incubated with TEV protease overnight at

4 °C. IgG-cleaved TFIIC was recovered and subsequently purified by ionic exchange on a MonoQ column (GE Healthcare). TFIIC was then applied to a Superose 6 10/300 column which had been pre-equilibrated in the final buffer (25 mM HEPES pH 7.5, 150 mM NaCl, 1 mM DTT). The eluted protein was subsequently concentrated to 1 $\mu\text{g}\mu\text{l}^{-1}$.

Chemical crosslinking of TFIIC. Thirty μg (1 $\mu\text{g}\mu\text{l}^{-1}$) of purified TFIIC complex was crosslinked by addition of an iso-stoichiometric mixture of H12/D12 isotope-coded, di-succinimidyl-suberate (DSS, Creative Molecules). Equal amounts of crosslinker were added 10 times every 4 min to a final concentration of 2 mM. The crosslinking reactions were allowed to proceed for 40 min at 37 °C and quenched by the addition of ammonium bicarbonate to a final concentration of 50 mM for 10 min at 37 °C. Crosslinked proteins were denatured using urea and Rapigest (Waters) at a final concentration of 4 M and 0.05% (w/v), respectively. Samples were reduced using 10 mM DTT (30 min at 37 °C) and cysteines were carbamidomethylated with 15 mM iodoacetamide (30 min in the dark). Protein digestion was performed first using 1:100 (w/w) LysC (Wako Chemicals, Neuss, Germany) for 3.5 h at 37 °C then finalized with 1:50 (w/w) trypsin (Promega, Mannheim, Germany) overnight at 37 °C, after the urea concentration was diluted to 1.5 M. Samples were then acidified with 10% (v/v) TFA and desalted using MicroSpin columns (Harvard Apparatus). Crosslinked peptides were enriched using size-exclusion chromatography (SEC)⁴⁰. In brief, desalted peptides were reconstituted with SEC buffer (30% (v/v) ACN in 0.1% (v/v) TFA) and fractionated using a Superdex Peptide PC 3.2/30 column (GE) on a Ettan LC system (GE Healthcare) at a flow rate of 50 mlmin^{-1} . Fractions eluting between 1 and

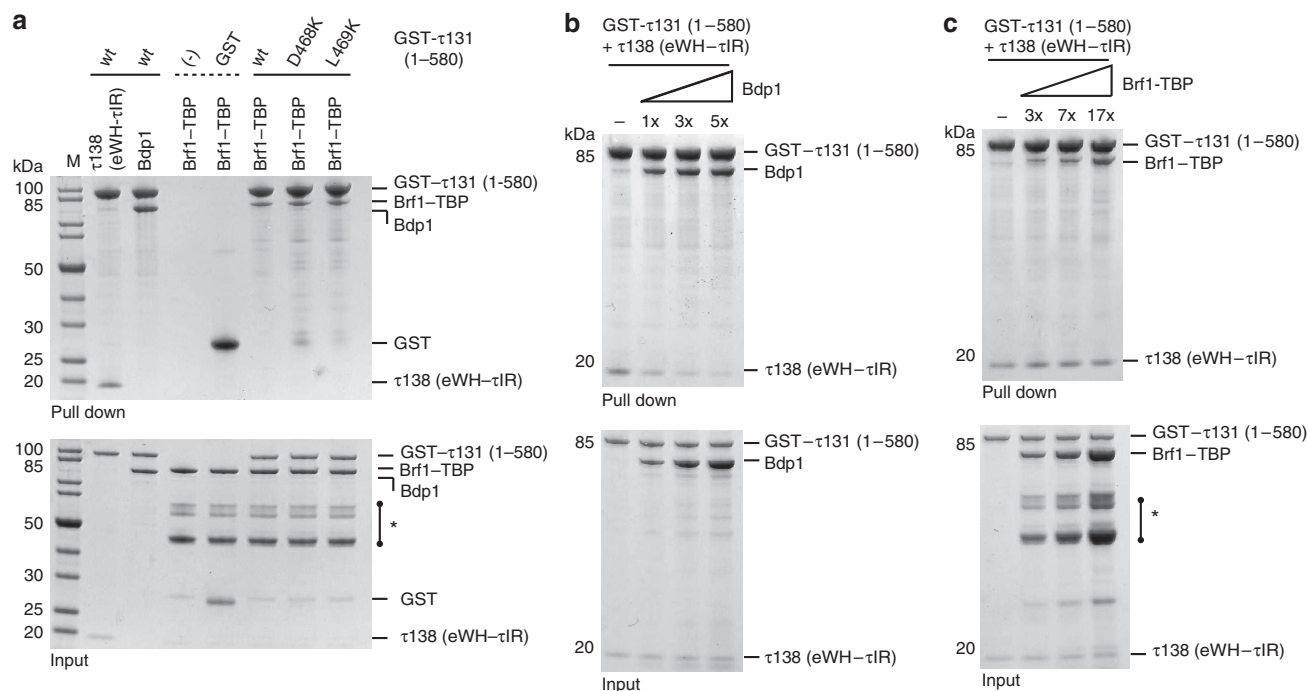


Figure 5 | Defining the overlap between TFIIB and τ 138 binding to τ 131. (a) GST pull-down assays of purified wild-type (wt) GST-tagged τ 131 (1-580) with untagged τ 138 (eWH- τ IR) and Bdp1, and purified wild-type (wt) and mutant GST-tagged τ 131 (1-580) variants with Brf1-TBP. (–) indicates a background control for nonspecific binding of Brf1-TBP to the GST-affinity resin. A mixture of purified GST and untagged Brf1-TBP was also used as a negative control. Lower gel shows 5% of the input and upper gel shows bound fractions. An * in the input gel indicates degradation products of Brf1-TBP. (b) GST pull-down competition assays of purified wild-type (wt) GST-tagged τ 131 (1-580) with untagged τ 138 (eWH- τ IR) and Bdp1. GST- τ 131 was preincubated with τ 138 before addition of the indicated molar excess of Bdp1. (–) indicates a control experiment where no Bdp1 was added. Gel format as in a. (c) GST pull-down competition assays of purified wild-type (wt) GST-tagged τ 131 (1-580) with untagged τ 138 (eWH- τ IR) and Brf1-TBP. GST- τ 131 was preincubated with τ 138 before addition of the indicated molar excess of Brf1-TBP. (–) indicates a control experiment where no Brf1-TBP was added. Gel format as in a. An * in the input gel indicates degradation products of Brf1-TBP.

1.5 ml were evaporated to dryness and reconstituted in 50 μ l 5% (v/v) ACN in 0.1% (v/v) FA.

Mass spectrometry analysis of crosslinked peptides. Between 2% and 10% of the amount contained in the collected SEC fractions were analysed by liquid chromatography-coupled tandem mass spectrometry (MS/MS) using a nanoAcquity UPLC system (Waters) connected online to LTQ-Orbitrap Velos Pro instrument (Thermo). Peptides were separated on a BEH300 C18 (75 mm \times 250 μ m, 1.7 μ m) nanoAcquity UPLC column (Waters) using a stepwise 60 min gradient between 3% and 85% (v/v) ACN in 0.1% (v/v) FA. Data acquisition was performed using a TOP-20 strategy where survey-MS scans (m/z range 375–1,600) were acquired in the Orbitrap ($R = 30,000$) and up to 20 of the most abundant ions per full scan were fragmented by collision-induced dissociation (normalized collision energy = 40, activation $Q = 0.250$) and analysed in the LTQ. To focus the acquisition on larger crosslinked peptides, charge states 1, 2 and unknown were rejected. Dynamic exclusion was enabled with repeat count = 1, exclusion duration = 60 s, list size = 500 and mass window ± 15 p.p.m. Ion target values were 1,000,000 (or 500 ms maximum fill time) for full scans and 10,000 (or 50 ms maximum fill time) for MS/MS scans. All the samples were analysed in technical duplicates. To assign the fragment ion spectra, raw files were converted to centroid mzXML using the Mass Matrix file converter tool and then searched using xQuest⁴¹ against a fasta database containing the sequences of the crosslinked proteins. Posterior probabilities were calculated using xProphet⁴¹ and results were filtered using the following parameters: false discovery rate = 0.05, min delta score = 0.95, MS1 tolerance window of 4 to 7 p.p.m., ld-score > 25.

Yeast strains. Plasmid pOL49 (a kind gift from O. Lefebvre) carrying a wild-type copy of τ 138 (ref. 42) was transformed into a diploid yeast strain carrying a chromosomal deletion of τ 138 (Euroscarf, Acc. Number Y20406). Haploid segregants carrying the τ 138 deletion and the pOL49 plasmid were identified and isolated. τ 138 was cloned by PCR amplification of genomic DNA, with primers spanning 500 bp up- and downstream of the coding sequence, and inserted into a plasmid carrying LEU selection (pRS415) to obtain pRS415- τ 138. pRS415 is originally a CEN plasmid but since the genomic copy of τ 138 carries a CEN sequence, this was removed from the pRS415- τ 138 plasmid via restriction-free

cloning⁴³. The new plasmid was named pRS415 Δ CEN τ 138. Restriction-free cloning was performed on plasmid pRS415 Δ CEN τ 138 to create the deletion mutants.

Cell viability—spot assays. Yeast strain carrying the plasmid pOL49 was transformed with the pRS415 Δ CEN τ 138 plasmid set (including wild type, mutants and empty plasmid without τ 138 gene) and plated on selective media (to select for both plasmids). Single colonies from fresh plates grown for 2 days at 30 $^{\circ}$ C were suspended in PBS to a final OD_{600 nm} of 0.4. Serial 10-fold dilutions of the different transformants were spotted on SC-LEU medium and 5-fluoroorotic acid containing medium, and incubated for 72 h at 30 $^{\circ}$ C. $n = 3$.

Protein expression and purification. The sequences for τ 131 (123–566) and full-length Bdp1 were cloned into the pETM11 vector in frame with a TEV protease-cleavable N-terminal 6xHis tag and were transformed into BL21 Star (DE3) pRARE *E. coli* cells for expression. The codon-optimized sequence for τ 138 (546–641) was cloned into the pETM30 vector in frame with a TEV protease-cleavable N-terminal 6xHis-GST tag and was transformed into BL21 (DE3) Gold *E. coli* cells for expression.

Cells were grown in TB till an OD_{600 nm} of 0.8, and protein expression was induced for 16 h at 18 $^{\circ}$ C with 0.5 mM isopropyl- β -D-thiogalactoside. Cells were harvested by centrifugation and resuspended in buffer A (5% glycerol, 50 mM Tris pH 7.5, 500 mM NaCl, 20 mM imidazole, 4 mM MgCl₂, Complete EDTA-free Protease Inhibitor Cocktail (Roche), DNase1 (Roche), 2 mM β -mercaptoethanol) before being lysed by homogenization (Avestin Emulsiflex-C3). The lysate was centrifuged at 20,000 r.p.m. and the resulting supernatant was incubated with 2 ml Nickel-NTA agarose resin (Qiagen), preincubated in buffer B (50 mM Tris pH 7.5, 300 mM NaCl, 20 mM imidazole, 2 mM β -mercaptoethanol), for 1 h at 4 $^{\circ}$ C. The resin was applied to a disposable column and washed with 20 column volumes of buffer B, 20 column volumes of buffer B containing 1 M NaCl and again with 20 column volumes of buffer B. The protein was eluted off the column using buffer B containing 250 mM imidazole and incubated with TEV protease for 16 h at 4 $^{\circ}$ C in buffer B. Cleaved protein was reapplied to the resin and collected in the flow-through, before being applied to a pre-equilibrated (20 mM Tris pH 7.5, 150 mM NaCl, 2 mM DTT) preparative S200 26/60 column (GE Healthcare). Cloning of the

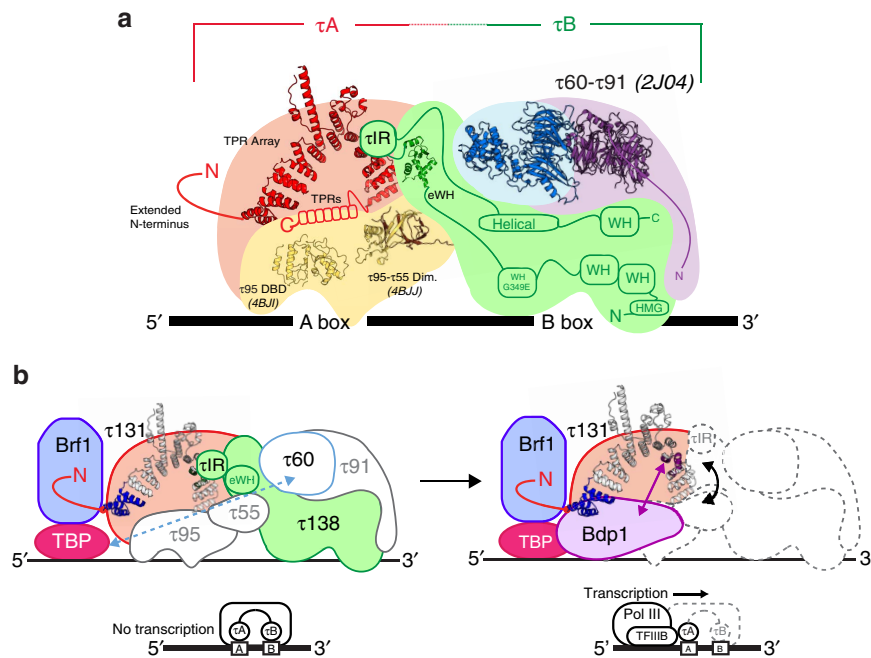


Figure 6 | The role of τ 131 in Pol III PIC formation. (a) Our current view of the arrangement of τ A and τ B subunits within TFIIC based on interaction studies, crystal structures and crosslinking. Structures from this study are included, as well as previous structures with PDB codes indicated: the WD40 dimer structure of τ 60– τ 91 (ref. 12), and the τ 95 DNA-binding domain (DBD)¹⁴ and τ 95– τ 55 dimerization homologues from *S. pombe*¹⁴. Note that the non-conserved τ 55 histidine phosphatase domain (HPD) is omitted¹³. The extended N terminus and C-terminal TPRs of τ 131 are indicated schematically. Predicted structural regions of τ 138 are also indicated, including the G349E mutation. The disordered N terminus of τ 91 is included schematically. (b) Model indicating two stages of PIC formation. In the first stage, recruitment of Brf1 to the PIC requires the extended N terminus of τ 131 (red curve) and the N-terminal TPRs of the TPR array (highlighted in blue). TBP makes interactions with Brf1 and the τ 60 subunit of τ B. The link between τ 131 and τ 138 is maintained. In the second stage, the recruitment of Bdp1 involves conformational changes in the arms of the TPR array. τ IR is displaced and the τ A– τ B link is altered, possibly leading to the disassembly of TFIIC. TFIIB is now assembled and recruits Pol III, together with τ 131, for transcription.

τ 131 point mutants was carried out using protocols and reagents provided in the Quikchange Lightning kit (Agilent). Mutants were purified by the same method as the wild type.

Protein expression and purification of Brf1–TBP. The sequence of the Brf1–TBP fusion protein Brf1 (1–382)–TBP (61–240)–Brf1 (439–596) has been described previously³⁶. The sequence was cloned into the pETM13 vector in frame with a non-cleavable C-terminal 6xHis tag. The vector was transformed into BL21 Star (DE3) pRARE *E. coli* cells and grown in TB till an $OD_{600\text{nm}}$ of 0.8. Protein expression was induced for 16 h at 18 °C with 0.5 mM isopropyl- β -D-thiogalactoside. Lysis and histidine-affinity purification was as described above, but with 5% glycerol added to all ‘B’ buffers. Eluted protein was diluted in buffer C (5% glycerol, 50 mM Tris pH 7.5, 2 mM DTT) so that the final NaCl concentration was 150 mM. The sample was applied to a 5 ml HiTrap SP HP column (GE Healthcare) that had been pre-equilibrated in buffer D (5% glycerol, 50 mM Tris pH 7.5, 150 mM NaCl, 2 mM DTT). The column was washed with 20 column volumes of buffer D, before a gradient of 40 column volumes into buffer E (5% glycerol, 50 mM Tris pH 7.5, 1 M NaCl, 2 mM DTT) was applied.

Crystallization and X-ray structure determination. For τ 131 (123–566), crystals of the $P4_3$ and $P6_2$ space group were grown at 20 °C by the hanging-drop vapour diffusion method at a concentration of 49 mg ml^{−1} and 60 mg ml^{−1} respectively, with a 1:1 ratio of protein and crystallization solutions. For $P4_3$, the crystallization solution contained 0.1 M bicine pH 8.9 and 0.85 M MgCl₂. Crystals were cryo-protected by soaking in mother liquor containing 30% glycerol before being flash-frozen in liquid nitrogen. For $P6_2$, the crystallization solution contained 0.2 M MgCl₂, 0.1 M Tris pH 8.3 and 42.5% ethylene glycol. Crystals were flash-frozen in liquid nitrogen using the already present ethylene glycol as a cryo-protectant. X-ray data for native, selenomethionine-incorporated and Hg crystals were collected at the ESRF and PETRAIII beamlines. The data was processed with X-ray diffuse scattering (XDS)⁴⁴. The $P4_3$ crystals were also consistently indexed with pointless and each data set was further scaled with SCALA. Derivatives were scaled to the native data set with scaleit. The $P6_2$ structure was solved by SAD combined with density modification using the programme autoSHARP⁴⁵. The $P4_3$ structure was solved by MIRAS combined with density modification using autoSHARP. For both structures, iterative model building and refinement was carried out using Coot⁴⁶ and Phenix⁴⁷, respectively. The initial models were used as molecular replacements

models for native, higher-resolution data sets using PHASER⁴⁸. The final models were validated using MolProbity⁴⁹.

For τ 138 (546–641), crystals were grown at 20 °C by the hanging-drop vapour diffusion method at a concentration of 30 mg ml^{−1}. Protein solution and crystallization solution were mixed in a 1:1 ratio. The crystallization solution contained 1.15 M Na citrate pH 6.2 and 0.1 M Na cacodylate. Crystals were cryo-protected by soaking in mother liquor containing 15% glycerol before being flash-frozen in liquid nitrogen. Data were collected on an in-house rotating anode to record single-wavelength anomalous signal from sulphur atoms. The data were processed using XDS. The initial substructure, based on anomalous signal from sulphur atoms, was solved using autoSHARP. Six sulphur sites were identified, indicating two molecules in the asymmetric unit. Phasing equations were solved and density modification was performed using autoSharp. Automatic building of an initial model was carried out using AutoBuild in Phenix. A higher-resolution native data set on a second crystal was collected at the ID23-1 beamline at the ESRF, and was processed using XDS. The structure was solved by molecular replacement with Phaser using the initial model from the sulphur-SAD experiment above. Iterative model building and refinement was then carried out using Coot and Phenix respectively. The final model was validated using MolProbity.

GST pull-down experiments. GST-tagged τ 131 and τ 138 proteins were expressed in BL21 (DE3) Gold *E. coli* cells, and purified with a GST preparative FF 16/10 column (GE Healthcare) followed by size-exclusion chromatography using a pre-equilibrated (20 mM Tris pH 7.5, 150 mM NaCl, 2 mM DTT) S200 26/60 column (GE Healthcare). For pull-down experiments, 15 μ g of GST-tagged τ 131 or τ 138 protein and their tested binding partners were incubated with 25 μ l Glutathione Sepharose 4B beads in buffer F (50 mM Tris pH 7.5, 150 mM NaCl, 2 mM DTT, 0.1% Tween20) at 4 °C for 4 h. τ 138 (300 nm) and Bdp1, and 1 μ M of Brf1–TBP were used when testing binding to the GST– τ 131 constructs. Wild-type (900 nm) and mutant τ 131 was used when testing the binding to GST– τ 138 (641–693). After incubation, the beads were washed three times with buffer F, before being heated to 100 °C in Laemmli sample buffer for 5 min.

ITC experiments. ITC was performed using a MicroCal ITC200 System (GE Healthcare). All samples were dialyzed into ITC buffer (20 mM Tris pH 7.5,

150 mM NaCl, 2 mM β -mercaptoethanol). Protein concentration in the cell and syringe was 15 and 150 μ M, respectively. Experiments were performed at 25 °C.

EMSA of TFIIC and τ 138 (546–641). The sequence of the 66 base-pair oligonucleotide (5'-CGA TAT AGT GTA ACG GCT ATC ACA TCA CGC TTT CAC CGT GGA GAC CGG GGT TCG ACT CCC CGT ATC-3') contains A and B box elements from a tDNA^{Glu} sequence (underlined). HPLC-purified oligonucleotides were ³²P end-labelled by T4 Polynucleotide Kinase before subsequent gel purification by denaturing 15% urea-PAGE. To form double-stranded oligonucleotides, the ³²P-labelled oligonucleotides were heated to 95 °C for 2 min, cooled to 25 °C and incubated in EMSA buffer (20 mM Tris pH 7.5, 150 mM NaCl, 1 mM MgCl₂, 2 mM DTT). For the EMSA, single-stranded or double-stranded oligonucleotides were incubated with TFIIC or τ 138 (546–641) at 25 °C for 30 min, before being run at 120 V on a 4.5% acrylamide gel in Tris-glycine buffer. The gel was dried and autoradiographed with X-ray film (Biomax, MR-film, Kodak).

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Author contributions

G.M., N.M.I.T. and S.G. determined and analysed the different crystal structures; G.M., N.M.I.T. and H.G. carried out the biochemical analysis; M.C. and H.G. produced the yeast strains, A.v.A. and M.B. carried out and analysed the crosslinking

experiments; G.M., S.G., M.B. and C.W.M. wrote the manuscript with input from all authors.

Additional information

Accession codes: The coordinates and structure factors of the τ 131 TPR array in space group P43 and P62 (PDB 5AEM and 5AIO) and τ 138 eWH (PDB 5AIM) have been deposited with the European Protein Data Bank.

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