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Reconstitution of mammalian Cleavage Factor II involved in 3' processing of mRNA precursors

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Abstract

Cleavage factor II (CF II) is a poorly characterized component of the multi-protein complex catalyzing 3' cleavage and polyadenylation of mammalian mRNA precursors. We have reconstituted CF II as a heterodimer of hPcf11 and hClp1. The heterodimer is active in partially reconstituted cleavage reactions, whereas hClp1 by itself is not. Pcf11 moderately stimulates the RNA 5' kinase activity of hClp1; the kinase activity is dispensable for RNA cleavage. CF II binds RNA with nanomolar affinity. Binding is mediated mostly by the two zinc fingers in the C-terminal region of hPcf11. RNA is bound without pronounced sequence-specificity, but extended G-rich sequences appear to be preferred. We discuss the possibility that CF II contributes to the recognition of cleavage/polyadenylation substrates through interaction with G-rich far-downstream sequence elements.

Introduction

Polyadenylated 3' ends of mRNAs are generated in a two-step processing reaction in which the primary transcript is first cleaved by an endonuclease and the upstream cleavage fragment is then polyadenylated, whereas the downstream fragment is degraded. The reactions are catalyzed, in a tightly coupled manner, by a multi-protein assembly. In mammals, four heterooligomeric complexes are part of this assembly, and many of the subunits contribute to the recognition of the substrate RNA (Xiang et al. 2014; Shi and Manley 2015): Cleavage and polyadenylation specificity factor (CPSF) consists of seven subunits (Shi et al. 2009), among which CPSF30 (= CPSF4) and WDR33 recognize the polyadenylation signal AAUAAA (Chan et al. 2014; Schönemann et al. 2014; Clerici et al. 2017; Sun et al. 2018), and Fip1 binds U-rich sequences (Kaufmann et al. 2004; Lackford et al. 2014). CPSF73 (= CPSF3) cleaves the RNA substrate (Mandel et al. 2006; Eaton et al. 2018). Cleavage stimulation factor (CstF) consists of two copies each of three subunits and binds GU-rich sequence elements downstream of the cleavage site (MacDonald et al. 1994; Beyer et al. 1997; Takagaki and Manley 1997; Martin et al. 2012; Hwang et al. 2016).

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Cleavage factor I (CF I) contains two copies each of two subunits and associates with UGUA sequences facilitating 3' processing from a position upstream of AAUAAA (Venkataraman et al. 2005; Yang et al. 2011; Martin et al. 2012; Zhu et al. 2018). Composition and function of cleavage factor II (CF II) will be discussed below. In addition to these complexes, poly(A) polymerase catalyzes poly(A) tail synthesis, and Rbbp6 plays an unknown role in the processing reaction (Di Giammartino et al. 2014). Poly(A) polymerase and a subcomplex of CPSF, mPSF, are sufficient for AAUAAA-dependent polyadenylation of an RNA resembling the cleaved reaction intermediate (Schönemann et al. 2014). In addition, the nuclear poly(A) binding protein (PABPN1) increases the processivity of polyadenylation and contributes to the synthesis of poly(A) tails of a defined length (Kühn et al. 2009; Kühn et al. 2017). This list of 3' processing factors may well be incomplete.

In addition to the sequence elements listed above, several other blocks of conserved sequences surrounding poly(A) sites have been identified by transcriptome-wide sequence comparisons; these include G-rich motifs located downstream of the CstF binding site (Hu et al. 2005). G-rich downstream elements have also been identified by mutational analyses of the SV40 late poly(A) site (Sadofsky et al. 1985; Qian and Wilusz 1991; Bagga et al. 1995) and other individual poly(A) sites (Yonaha and Proudfoot 1999; Arhin et al. 2002; Oberg et al. 2005; Dalziel et al. 2007).

CF II is the least characterized among the protein complexes constituting the 3' processing complex. A partial purification suggested that CF II contains hClp1 and hPcf11, orthologues of known 3' processing factors from *S. cerevisiae* (de Vries et al. 2000). It has remained uncertain whether CF II consists of just these two polypeptides. The MS analysis of a purified mammalian processing complex detected hPcf11 but not hClp1 (Shi et al. 2009). In yeast, a heterodimer of Pcf11 and Clp1 associates with a heterotetramer of Rna14 and Rna15 to form cleavage factor IA (CF IA) (Amrani et al. 1997; Minvielle-Sebastia et al. 1997; Gross and Moore 2001; Gordon et al. 2011; Stojko et al. 2017). The mammalian orthologues of Rna14 and Rna15, CstF77 (= CSTF3) and CstF64 (= CSTF2), are not stably associated

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with hClp1 and hPcf11 but instead constitute CstF together with a third subunit, CstF50 (= CSTF1), which has no counterpart in yeast (Xiang et al. 2014).

Yeast *clp1* mutants have defects in both steps of the 3' processing reaction (Haddad et al. 2012). While human and *C. elegans* Clp1 have an RNA 5' kinase activity (Weitzer and Martinez 2007; Dikfidan et al. 2014), yClp1 is catalytically inactive, suggesting that the activity is not essential for pre-mRNA 3' processing (Ramirez et al. 2008). This is supported by genetic analysis in mice: Homozygous Clp1 knock-out mice die at an early embryonic stage, but mice homozygous for a kinase-dead Clp1 variant survive for different periods after birth, depending on the genetic background, and have no apparent defect in pre-mRNA 3' processing (Hanada et al. 2013). Mammalian Clp1 is also part of the tRNA splicing endonuclease, but Pcf11 apparently is not (Paushkin et al. 2004; Weitzer and Martinez 2007). Genetic analyses in mice (Hanada et al. 2013) and humans (Karaca et al. 2014; Schaffer et al. 2014) support a role of Clp1 in tRNA splicing, but how the kinase activity is involved is unclear at the moment (Schaffer et al. 2014; Weitzer et al. 2015).

Mutations in yeast Pcf11 also affect both pre-mRNA cleavage and polyadenylation (Amrani et al. 1997). Yeast Pcf11 is the central subunit of CF IA, interacting with both yClp1 and with the Rna14-Rna15 complex (Gross and Moore 2001; Noble et al. 2007; Gordon et al. 2011). The crystal structure of a complex between yClp1 and a yPcf11 peptide shows interaction surfaces that appear conserved in higher eukaryotes (Noble et al. 2007). Pcf11 is one of the factors responsible for the connection between 3' end processing and transcription; the protein is specifically required for transcription termination (Birse et al. 1998; Sadowski et al. 2003; Luo et al. 2006; Zhang and Gilmour 2006; West and Proudfoot 2008; Porrua and Libri 2015), and its phosphorylation has been proposed to facilitate transcript release and export (Volanakis et al. 2017). Interestingly, Pcf11, together with Clp1, also participates in the termination of non-coding transcripts that use polyadenylation-independent pathways for 3' end formation (Kim et al. 2006; Hallais et al. 2013; O'Reilly et al. 2014; Grzechnik et al. 2015; Porrua and Libri 2015). The role of Pcf11 in coupling 3' end processing to transcription depends on its binding to the serine 2-phosphorylated C-terminal

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domain (CTD) of RNA polymerase II via a conserved N-terminal CTD interaction domain (CID) (Barilla et al. 2001; Licatalosi et al. 2002; Sadowski et al. 2003; Meinhart and Cramer 2004; Noble et al. 2005; Lunde et al. 2010). A second surface on the 'body' of RNA polymerase II may also be involved in the Pcf11 interaction (Pearson and Moore 2014).

Here we present a biochemical reconstitution of human CF II from recombinant hClp1 and hPcf11 and report that CF II contributes to the recognition of 3' processing substrates, possibly through binding to a G-rich far-downstream element.

Results

Human Clp1 and Pcf11 constitute CF II

In order to obtain more definitive information on the subunit composition of CF II, we used a cell line expressing His-FLAG-tagged hClp1 (Paushkin et al. 2004) and isolated the protein by two consecutive affinity purification steps. MS analysis of the main components identified, in addition to hClp1, the tRNA splicing endonuclease complex, as anticipated (Paushkin et al. 2004), and hPcf11 (Fig. 1A). Since the tRNA splicing endonuclease has so far not been directly implicated in 3' processing, this result suggests that CF II may consist of just hPcf11 and hClp1. These two polypeptides, with an N-terminal his-tag on hClp1, were therefore co-expressed in insect cells by means of the MultiBac system (Berger et al. 2004; Fitzgerald et al. 2006). Chromatography on Ni^{2+} beads resulted in the co-purification of both proteins, which remained associated during subsequent anion exchange chromatography and gel filtration (Fig. 1B, C, E, F). Identity and completeness of both polypeptides were confirmed by LC/MS/MS. In gel filtration, CF II eluted ahead of the largest standard protein with an extrapolated Stoke's radius of 7.1 nm (Fig. 1E). Glycerol gradient centrifugation indicated a sedimentation coefficient of 7S (data not shown). A native molecular weight of 207 kDa calculated from these data (Siegel and Monty 1966; Erickson 2009) is in good agreement with the theoretical molecular weight of a heterodimeric hPcf11•hClp1 complex (220.8 kDa), consistent with the stoichiometry of the orthologues in yeast CF IA (Gordon et al. 2011; Stojko et al. 2017).

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His-tagged hClp1 was also expressed by itself and purified by metal affinity chromatography. Subsequent gel filtration showed an apparent native molecular weight near 40 kDa, consistent with the calculated molecular weight of 48.7 kDa and, thus, a monomeric structure (Fig. 1G, H). Human Pcf11 expressed in the absence of hClp1 was insoluble.

The hClp1•hPcf11 complex supported AAUAAA-dependent 3' cleavage in partially reconstituted assays (Fig. 2C). The cleavage activity co-purified with the hClp1•hPcf11 complex on the MonoQ column (Fig. 1D). In contrast, hClp1 did not support cleavage (Fig. 2C). We conclude that hClp1 and hPcf11 constitute functional CF II.

CF II has RNA 5' kinase activity, which is not essential for 3' processing

The anticipated RNA 5' kinase activity of hClp1 was also manifest in CF II (Fig. 1B, E). Steady-state kinetics revealed that CF II had a moderately reduced K_M for ATP as compared to hClp1 (Fig. 2A; Table 1). The K_M for oligocytidine (C_{14}) was not noticeably affected (Fig. 2B; Table 1). Measured k_{cat} values for CF II were higher than those for hClp1, but this may have been due to technical reasons (see legend to Table 1). Also, hClp1 activity declined during storage whereas CF II was stable.

A single point mutation, K127A, introduced into the conserved active site of hClp1 (Dikfidan et al. 2014), reduced the kinase activity of CFII by only a factor of 30. However, triple mutations K127A, R288A, R293L (abbreviated KR) or D151A, R288A, R293L (abbreviated DR) reduced the activity to undetectable levels, less than 0.2% of the wild-type (data not shown). All mutant proteins could be co-purified in a complex with hPcf11 (data not shown). CF II containing the kinase-dead Clp1 variants was active in 3' cleavage (Fig. 2C). Thus, the kinase activity is not essential for 3' processing.

Domain organization of CF II

In contrast to Clp1 (Noble et al. 2007; Dikfidan et al. 2014), Pcf11 is structurally not very well characterized. A scheme of the protein is shown in Fig. 3A: The N-terminal CID (Meinhart and Cramer 2004) is followed by a helical domain of unknown function (Xu et al. 2015).

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Amino acids 295 - 565 comprise a highly charged region with 28.4 % basic and 14.8% acidic residues and a serine content of 14.8%. Amino acids 770 - 1123 contain 30 repeats of a motif of about thirteen amino acids (FEGP repeats for short) with a high content of proline and glycine (Fig. 3B). Between 22 and 36 repeats of the FEGP motif are conserved in Pcf11 orthologues in vertebrates, but not in *Drosophila*, *C. elegans* or yeast. Data base searches did not reveal similar repeats in other proteins. Most arginine residues in the FEGP repeats are asymmetrically dimethylated (Guo et al. 2014). Numerous dimethylarginine residues in the repeats were also detected in the MS analysis of our baculovirus-produced hPcf11 (data not shown). The C-terminus of Pcf11 contains two zinc fingers (Barilla et al. 2001; Sadowski et al. 2003; Guegueniat et al. 2017; Yang et al. 2017), which straddle the Clp1 interaction site (Noble et al. 2007). The region of yPcf11 responsible for the Rna14/Rna15 interaction is on the N-terminal side of the first zinc finger (Amrani et al. 1997) and has been narrowed down to aa 331-417 (Lionel Minvielle-Sebastia, personal communication). This region has no obvious counterpart in hPcf11.

The interaction between hPcf11 and hClp1 was analyzed by treatment of the complex with the MS-cleavable DSBU cross-linker that covalently links amino groups and, with a lower efficiency, hydroxy groups at a maximum Cα-Cα distance of ~ 30 Å (Müller et al. 2010). Cross-linked proteins were digested with trypsin and peptides analyzed by LC/MS/MS (Suppl. Table 1). The analysis revealed four intramolecular cross-links of hClp1. All were consistent, within the 30 Å distance, with a three-dimensional homology model of the protein based on the structures of the *S. cerevisiae* and *C. elegans* orthologues (Fig. 3C, D). The analysis also revealed eighteen intermolecular cross-links between hClp1 and hPCF11 (Fig. 3C). Five cross-links from Clp1 residues 54, 109 and 425 to the region 1371 - 1405 of hPcf11 were consistent with the interaction surfaces of the yeast orthologues (Noble et al. 2007) (Fig. 3D). Thus, the interaction between Clp1 and Pcf11 is conserved. Lysine residues 109, 202, 267 and 290 of hClp1 formed numerous cross-links to a region of hPcf11 between residues 520 and 731 (Fig. 3C, D). This region also contained multiple intramolecular cross-links between amino acids widely separated in the primary structure, suggesting the

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possibility of a globular fold. The two separate regions of hPcf11 that were cross-linked to hClp1 were also cross-linked with each other, indicating their neighborhood in the quaternary structure of CF II.

Limited trypsin digestion of CF II under native conditions resulted in rapid degradation of hPcf11, with accumulation of a stable fragment that migrated at a little over 50 KDa in SDS gels (Fig. 4A). Analysis by MS/MS and N-terminal Edman degradation suggested Ala1185 as the N-terminus of the trypsin-resistant fragment. The fragment remained associated with his-tagged hClp1 at the end of trypsin digestion. The corresponding engineered fragment hPcf11 ΔN1184 was also associated with hClp1 upon co-expression (data not shown). Even a short C-terminal hPcf11 fragment starting with the first zinc finger (ΔN1339) co-purified with hClp1 when the two were co-expressed in insect cells (Fig. 4B). Thus, the conserved interaction surface between the zinc fingers is sufficient for a stable interaction; the more N-terminal region of hPcf11 that is cross-linked to hClp1 is not required.

Several additional deletion variants of hPcf11 were co-expressed with hClp1 and purified for use in cleavage assays. ΔN769, starting with the FEGP repeats, was the shortest variant providing CF II function. In contrast, a complex of hClp1 and the fragment ΔN1123, starting just C-terminal of the FEGP repeats, was inactive (Fig. 4C). Both hPcf11 variants were co-purified with hClp1, and the complexes had similar activities in RNA binding assays (see below); thus, the inactive variant is not misfolded. CF II complexes containing even shorter hPCF11 fragments were also inactive in cleavage (data not shown). We conclude that the FEGP repeats are essential for pre-mRNA cleavage, but everything N-terminal of the repeats is dispensable. This includes the CID, in agreement with data obtained in yeast (Sadowski et al. 2003) and the highly charged region.

The stable association of yPcf11 and yClp1 with Rna14 and RNA15 suggests that CF II might interact with CstF (see Introduction). However, when CF II and CstF were mixed at a final concentration of 0.4 μM each and analyzed by gel filtration, no association was detected. Likewise, gel filtration did not detect an interaction between CF II and the C-terminal alpha-helical bundle of CstF-64 (purified as a His-Sumo fusion) (Qu et al. 2007). Gel

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filtration of a mixture of CF I and CF II at 0.7 µM each did not reveal an association either, and no interaction was found when CstF was added as a third component. Pull-down experiments in which FLAG-tagged CF II containing hPcf11 ΔN769 was incubated with CF I or CstF were likewise negative. CF II is an RNA binding protein (see below), and even weak interactions with other RNA binding proteins, not detectable by gel filtration or pull-down experiments, should be visible as cooperative RNA binding. However, when CF I, CF II and CstF were used in filter-binding experiments at concentrations below the K_D, mixing of the proteins in all possible combinations resulted in additive binding, i. e. no cooperativity was visible.

CF II binds RNA via the zinc fingers of hPcf11

Nitrocellulose filter-binding experiments revealed that CF II avidly bound to RNA: An RNA of 230 nt containing the SV40 late 3' processing site was bound with a K_{50} of ~ 0.5 nM. The adenovirus L3 3' processing site was bound with comparable affinity (Fig. 5A). The RNA binding activity co-migrated with CF II in anion exchange chromatography (Fig. 1B) and gel filtration (data not shown).

RNA binding by hClp1 was at least 300fold weaker compared to CF II and could not unequivocally be attributed to hClp1 as opposed to a potential contaminant of the protein preparation (data not shown). Thus, hPcf11 dominates the RNA binding activity of CF II. UV cross-linking followed by immunoprecipitation confirmed RNA binding to hPcf11 (Fig. 5B). So far, two RNA binding domains have been described in yPcf11: The CID weakly binds RNA (Zhang et al. 2005; Hollingworth et al. 2006), and the zinc finger domain has also been shown, by UV cross-linking, to interact with RNA. No sequence specificity was detected (Guegueniat et al. 2017). In gel shift assays with several RNAs, CF II containing full-length hPcf11 bound much more tightly than CF II containing N-terminally truncated hPcf11 variants (Fig. 5C and data not shown). These data are consistent with a contribution of the CID to RNA binding. The hPcf11 ΔN1184 fragment by itself bound with a similar affinity as the

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heterodimer with hClp1 (Fig. 5C), confirming that hClp1 does not significantly contribute to RNA binding.

In order to assess the role of the zinc fingers in RNA binding, we expressed and purified an hPcf11 fragment containing just the zinc fingers and the intervening Clp1 interaction sequence (zcz fragment; amino acids 1340 - 1505), fused to either His-Sumo or GST. Both fusion proteins, purified by different procedures, bound RNA in filter-binding and gel shift assays. The RNA binding activity co-migrated with the fusion proteins in anion exchange chromatography (data not shown). The RNA 191-230 was bound with an apparent K_D of 100 - 200 nM (Fig. 5D), approximately 200fold higher than the K_D of CF II (Table 2; see below). Thus, approximately 75% of the free energy of binding is provided by the two zinc fingers. The GST-zcz fusion protein bound G_{14} in gel shift assays but not the other homopolymeric 14mers. Thus, the RNA binding specificity of the zinc fingers matches the specificity of CF II (see below).

CF II prefers G-rich sequences

In gel shift assays, CF II bound G_{14} with high affinity (~ 2 nM), whereas the other three homopolymeric 14mers were bound weakly or very weakly. G_{17} was bound as tightly as G_{14}, but shorter G homopolymers were bound less well (Table 2). Thus, CF II appears to have an extended binding site of ~14 nucleotides.

PAR-CLIP experiments have mapped a peak of yPcf11 binding to pre-mRNAs 130 nt downstream of the cleavage site (Baejen et al. 2017); no specific sequence motif was identified. ChIP experiments also showed binding of *S. cerevisiae* and *S. pombe* Pcf11 downstream of the cleavage site (Mayer et al. 2012; Baejen et al. 2017; Wittmann et al. 2017). Based on this position of binding and the preference of CF II for G-rich sequences, we tested whether CF II might be responsible for the recognition of the G-rich downstream element mapped in the SV40 late polyadenylation signal (see Introduction). Indeed, a series of oligonucleotides gradually shortened to the G-rich motif (208-221) revealed tight binding (Table 2). However, two variant sequences with reduced G content (from 13/17 in 208-224 to

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10/17 in Δ2x and ΔΔ2x; Table 2) had similar affinities. Even a 16mer isolated as a good ligand for CstF (CstF selex; Table 2) was bound well, although it was not G-rich.

The binding specificity of CF II was further investigated by selection of binders from a random pool ('bind-n-seq; Lambert et al. 2015). A pool containing synthetic RNA 14mers followed by an invariant GUUU sequence was used in a first selection round. The selected RNA was cloned, and the presence of a T7 promoter in the cloning adaptor allowed for subsequent transcription for a second round of selection. T7 transcription resulted in the addition of a GGG sequence at the 5' end. Sequences resulting from a first selection experiment were synthesized and tested in gel shift assays (BS2 sequences; Table 2). Only moderate affinities were observed, but variation of the selected sequence showed that the 5'GGG sequence improved CF II binding by five- to tenfold, supporting the importance of G residues for CF II binding. In contrast, the three invariant U residues at the 3' end were irrelevant. Therefore, winner sequences from subsequent selection experiments were synthesized with the 5' GGG extension but without the 3' UUU sequence (BS3 sequences; Table 2). In one type of experiment, RNA was selected with CF II and binding to Ni^{2+} beads. In both replicates of this experiment, multiple reads of the sequence BS3 CF II (Table 2), with some variation in position 6, were found; these sequences were not present in the no-protein control. In the second type of experiment, selection with hPcf11 ΔN1184 and nitrocellulose filter binding, sequences related to BS3 Pcf11 were enriched in both replicates. In this case, statistical analysis (Zambelli et al. 2014) identified the sequence BS3 Weeder (Fig. 5E). All three winner sequences tested were G-rich and bound CF II with high affinity (Table 2). Thus, the results support a preference of CF II for G residues.

Many of the G-rich oligonucleotides bound by CF II are predicted to form intramolecular G-quadruplex (G4) structures (Bedrat et al. 2016). Indeed, CD spectroscopy of selected oligonucleotides confirmed G4 formation (Fig. 5F). However, two results suggest that CF II binds its G-rich ligands in a non-G4 form: First, whereas G4 formation leads to an accelerated migration of RNA during native gel electrophoresis (Wang et al. 2017), the oligonucleotides listed in Table 2 migrated as expected from their lengths. Thus, we assume

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that the G4 structures detected by CD spectroscopy were intermolecular structures favored by high RNA concentrations (2 μM), whereas no structures were formed at the low concentrations (0.1 nM) used in gel shift assays. Second, both the oligonucleotide wt2x, derived from the SV40 late sequence 208-224 by a single mutation that generates a direct repeat of 8 nucleotides, and a mutant derivative, Δ2x, contain four blocks of $G_{\geq 2}$ and are thus predicted to form G4 structures. In contrast, oligonucleotide ΔΔ2x has the same nucleotide composition as Δ2x but only two G_2 blocks; thus, it should not form G4 structures. CD spectroscopy confirmed (presumably intermolecular) G4 formation by the wt2x and Δ2x oligonucleotides but not by ΔΔ2x (Fig. 5F). Still, CF II bound all three oligonucleotides with similarly high affinities (Table 2). Thus, all three RNAs are presumably bound in non-G4 conformations.

The association of the high-affinity RNA binder hPcf11 with the RNA kinase hClp1 would suggest that ligands preferred by hPcf11 should also be better substrates for hClp1. However, in a comparison of two oligonucleotides, C_{14} (poor binder) and 190-225 (good binder) (Table 2) no such difference was observed. The reason for this result is currently unknown.

Discussion

Among the protein complexes contributing to 3' processing of mammalian mRNA precursors, CstF and CF I have previously been reconstituted from recombinant proteins (Takagaki and Manley 1994; Rüegsegger et al. 1998; Yang et al. 2011; Yang et al. 2018). Of the central factor, CPSF, only the mPSF subcomplex, active in polyadenylation, has been reconstituted (Schönemann et al. 2014; Clerici et al. 2017; Clerici et al. 2018; Sun et al. 2018), but the subunit composition of CPSF is reasonably clear from biochemical experiments (Bienroth et al. 1991; Shi et al. 2009; Schönemann et al. 2014). In contrast, CF II had never been purified to the point that its subunit composition could be judged. Here we show by affinity purification of a tagged subunit and by overexpression in a heterologous system that CF II consists of

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just two polypeptides, hPcf11 and hClp1. These two proteins form a heterodimer, which is active in a partially reconstituted 3' processing reaction.

Human Clp1 and hPcf11 interact via conserved surfaces; this was predicted by X-ray crystallography of the yeast complex and sequence conservation in the human proteins (Noble et al. 2007) and was confirmed here by cross-linking and MS analysis. The hPcf11 subunit is essential for 3' processing; hClp1 by itself is inactive. Within hPcf11, the N-terminal CID is dispensable, in agreement with data in yeast (Sadowski et al. 2003). In contrast, a unique repeat structure, the FEGP repeats, is necessary for CF II activity. The exact function of the repeats remains to be determined. Whether or not hClp1 is essential for the reconstitution of pre-mRNA cleavage could not be tested, as hPcf11 was insoluble in the absence of its partner protein.

The biological role of the RNA 5' kinase activity of hClp1 remains unclear. We find that hClp1 maintains this activity when it forms a complex with hPcf11 and thus, presumably, in the 3' processing complex. However, mice homozygous for the K127A point mutation in the kinase active site of Clp1 have no obvious defect in pre-mRNA processing; their severe neurological phenotype appears to be related to a tRNA processing defect (Hanada et al. 2013). The interpretation of phenotypes is complicated by the weak residual kinase activity of the K127A mutant (this work) and by its disruptive effect on the tRNA splicing endonuclease complex (Hanada et al. 2013; Karaca et al. 2014; Schaffer et al. 2014). Similarly, mutations in the yClp1 ATP binding site disturb the association with yPcf11 and even affect binding of yPcf11 to the Rna14-Rna15 complex (Holbein et al. 2011; Ghazy et al. 2012; Haddad et al. 2012). Nevertheless, we were able to isolate mutant hClp1 with no detectable kinase activity as a complex with hPcf11; the complex proved active in pre-mRNA cleavage. Thus, at least under the conditions of the *in vitro* reaction, hClp1 kinase activity is not required for RNA cleavage, in agreement with the situation in yeast (Ramirez et al. 2008). Not only is hClp1 found as a component of the tRNA splicing endonuclease (Paushkin et al. 2004; Weitzer and Martinez 2007), but knock-down of the endonuclease subunit SEN2 has been reported to inhibit 3' processing of pre-mRNA (Paushkin et al. 2004). However, to our knowledge a tRNA

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endonuclease association has never been reported for hPcf11, and the endonuclease was not found in the CF II preparation of de Vries et al. (2000). Cleavage activity of CF II reconstituted in the absence of the tRNA endonuclease suggests that the enzyme is not directly involved in pre-mRNA 3' processing. The caveat is that a crude fraction was used for the reconstitution assays.

Yeast Pcf11 and yClp1 are stably associated with Rna14 and Rna15, forming the CF IA complex (Amrani et al. 1997; Gross and Moore 2001; Gordon et al. 2011). Yeast Pcf11 is thought to interact mostly with Rna14 (Gordon et al. 2011), but also with a conserved C-terminal domain of Rna15 (Qu et al. 2007). As the human orthologs of Rna14 and Rna15 are CstF-77K and CstF-64K, an interaction between CF II and CstF might be expected. However, the interaction surface in yPcf11, amino acids 331-417 (Lionel Minvielle-Sebastia, personal communication), does not appear to be conserved in the mammalian orthologue, and we found no evidence for an interaction. On the basis of co-purification and pull-down from nuclear extract, an association of CF II with CF I was suggested (de Vries et al. 2000). Our experiments with highly purified recombinant preparations revealed no such association. In agreement with the data of Rüegsegger et al. (1996), the negative results of our interaction assays suggest that protein-protein interactions within the 3' processing complex may be established mostly via CPSF. Indeed, isolated hClp1 bound CPSF in pull-down assays in nuclear extract (de Vries et al. 2000). Recombinant CPSF is not yet available in a form suitable for interaction assays with reconstituted CF II.

Our experiments revealed a high affinity of CF II for RNA. Binding is mediated predominantly by hPcf11. The length-dependence of CF II binding to a series of G homopolymers revealed that the protein requires ~ fourteen nucleotides for high affinity binding. A requirement for such an extended sequence is probably explained by the domain structure of hPcf11: The two zinc fingers provide the largest fraction of the total binding energy. Two zinc fingers can recognize nine nucleotides (Hudson et al. 2004). Binding of the remaining nucleotides must be mediated by more N-terminal regions of hPcf11, including the CID (Zhang et al. 2005; Hollingworth et al. 2006) and perhaps the highly charged region. An

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important role for RNA binding by Pcf11 is supported by the observation that mutations in the zinc fingers of yPcf11, in particular the second finger, strongly affect yeast growth and CF IA function in pre-mRNA processing (Guegueniat et al. 2017). CF II does not appear to have a very pronounced sequence-specificity of binding, but G-rich sequences were preferred. An enrichment of such motifs far downstream of the cleavage site (see Introduction) and the mapping of yPcf11 binding downstream of the cleavage site (Baejen et al. 2017) suggests that CF II might function in pre-mRNA processing via binding to these G-rich downstream elements. A role of CF II in the recognition of the pre-mRNA is consistent with the observation that knock-down of hPcf11 affects alternative polyadenylation (Li et al. 2015). Although the effects of hPcf11 knock-down were not strongly correlated with specific sequence motifs, several G-rich hexamers were overrepresented in the downstream region of proximal poly(A) sites that were downregulated by the knock-down, consistent with such hexamers being involved in hPcf11 binding. Members of the hnRNP H family of proteins have also been suggested to affect 3' end processing via binding to downstream G-rich sequence elements (Bagga et al. 1998; Veraldi et al. 2001; Arhin et al. 2002). The relative contributions of these proteins and CF II to the recognition of the G-rich elements remain to be established.

Materials and Methods

Purification of His-Flag-tagged CF II

A stable HEK293 cell line expressing His-FLAG-tagged hClp1 (Paushkin et al. 2004) was obtained from Christopher Trotta. Affinity purification via FLAG beads followed by Ni^{2+} beads was carried out as described (Paushkin et al. 2004). After SDS-polyacrylamide gel electrophoresis, the main bands were identified by MS analysis (Paul Jenö, Biozentrum, University of Basel).

Expression clones

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Primers for the construction of *E. coli* expression plasmids are listed in Supplemental Table 2. All ORFs amplified by PCR were checked by sequencing.

Plasmids for *E. coli* expression of HisSumo-Pcf11zcz and HisSumo-Pcf11ΔN1184 were generated by amplification of the hPcf11 fragments and cloning into pETSumoAdapt (Bosse-Doenecke et al. 2008) with BsaI and NotI. For expression of HisSumo-CstF64 ΔN530 (aa 531-577), a PCR product was cloned into pET-SumoAdapt with BsaI and XhoI. A plasmid for GST-Pcf11zcz was made by cloning of a PCR fragment into pGEX6p1 (GE Healthcare) with BamHI and NotI.

ORFs coding for the following protein complexes were cloned into the Multibac system (Berger et al. 2004; Fitzgerald et al. 2006): CF II, composed of hClp1 and hPcf11, including mutant variants of both subunits; CstF, composed of CstF-77, CstF-64 and CstF-50; CF I, composed of CF I-68 and CF I-25. All cDNAs are listed in Suppl. Table 3, transfer plasmids and resulting baculoviruses in Suppl. Table 4, and tags in Suppl. Table 5. Additional details, including primers used for cloning, will be provided upon request.

Protein expression and purification

Protein purification was carried out under refrigeration. The pH of all buffers was adjusted at 5°C.

For CF II expression, Sf21 cells cultured in ExCell 420 serum-free medium (Sigma-Aldrich) at 27.5 °C and 125 rpm were infected with a baculovirus encoding hPcf11 and his-tagged hClp1 at an MOI ≥ 1. Cells were harvested ~72h after infection, washed with cold PBS, frozen in liquid N_2 and stored at -80°C. Cells were thawed on ice, resuspended in lysis buffer (50 mM Tris-HCl, pH 8.5, 200 mM KCl, 0.2 mM EDTA, 0.02% NP-40, 10% sucrose, 1 mM DTT, 1 mM PMSF, 1 µg/ml each pepstatin and leupeptin) to ~$1x10^7$ cells/ml and lysed by sonification. The lysate was clarified by centrifugation and applied to Ni-NTA agarose (Qiagen) (1 ml for 4 x 10^8 cells starting material). The mixture was rotated for 2 h under, packed into a column, washed with lysis buffer plus 10 mM imidazole, and protein was eluted with lysis buffer plus 500 mM imidazole. Fractions containing CF II were combined and

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slowly diluted with lysis buffer lacking KCl to a conductivity corresponding to 150 mM KCl. The solution (~ 5 mg protein) was applied to a 1 ml MonoQ column (GE Healthcare), which had been equilibrated in lysis buffer plus 150 mM KCl and was eluted with a gradient up to 1 M KCl in lysis buffer. Material from the MonoQ peak fractions (1.2 ml) was applied to a 100 ml Superose 6 column (GE Healthcare) equilibrated in 20 mM Tris-HCl, pH 8.5, 200 mM KCl, 0.1 mM EDTA, 10% sucrose, 1 mM DTT, 5 μM $ZnCl_2$. Calibration proteins were ferritin (440 kDa, Stoke's radius = 6.1 nm), catalase (232 kDa, 5.2 nm), BSA (66.4 kDa, 3.55 nm), ovalbumin (43 kDa, 3.0 nm) and RNase A (13.7 kDa, 1.64 nm). Fractions were analysed by SDS-polyacrylamide gel electrophoresis and Coomassie staining. CF II was quantified by comparison of hClp1 to a BSA standard curve. Peak fractions were combined and concentrated to ~1 μM. Gel filtration was omitted for most CFII variants containing hClp1 mutants. For CF II preparations destined to be used in cross-linking experiments, Tris was replaced by triethanolamine in all buffers. This had no effect on RNA binding or kinase activity.

His-tagged Clp1 was expressed and purified on Ni-NTA agarose as above. Material from the peak fraction (1.5 ml) was applied to a 120 ml Superdex 200 prep grade column (GE Healthcare) equilibrated in 20 mM Tris-HCl, pH 8.5, 200 mM KCl, 0.2 mM EDTA, 10% sucrose, 1 mM DTT, 0.1 mM ATP. The column was run and calibrated as above.

For expression of CstF, Sf21 cells were infected with a virus encoding all three subunits, including his-tagged CstF-77, and harvested as above. Cells were resuspended in 50 mM Tris-HCl, pH 8.0, 200 mM KCl, 0.5 mM EDTA, 0.02% NP-40, 10% glycerol, 1 mM DTT, 1 mM PMSF, 1 μg/ml pepstatin and leupeptin, and Ni-NTA purification was carried out as above. CstF-containing fractions (9 mg) were combined, dialysed against 50 mM Tris-HCl, pH 8.0, 75 mM KCl, 0.5 mM EDTA, 0.02% NP-40, 10 % glycerol, 0.5 mM DTT and applied to a 1 ml ResourceQ column (GE Healthcare) equilibrated with the same buffer. The column was eluted with a gradient to 1 M KCl in the same buffer. CstF-containing fractions were analyzed by SDS-PAGE, and protein content was quantified by Bradford assay.

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CF I (including his-tagged CFI-25) was expressed in Sf21 cells as above. Cells were resuspended in 50 mM Tris-HCl, pH 8.0, 300 mM KCl, 0.5 mM EDTA, 10% sucrose, 1 mM DTT, 1 mM PMSF, 1 µg/ml pepstatin and leupeptin, and Ni-NTA purification was carried out as before. Eluted protein (~6 mg) was diluted to a conductivity equivalent to 20 mM Tris-HCl, pH 8.0, 170 mM KCl, 10% sucrose, 1 mM DTT and applied to a 1 ml ResourceQ column equilibrated in this buffer. The column was eluted and analyzed as above.

HisSumo-Pcf11ΔN1184, HisSumo-Pcf11zcz and GST-Pcf11zcz were expressed in *E. coli* Rosetta cells in TB medium plus 20 µM $ZnCl_2$ with antibiotic selection. Expression was induced with 1 mM IPTG, and the culture was shaken overnight at 16-18°C. Cells were harvested and resuspended in lysis buffer (50 mM Tris-HCl, pH 8.0, 200 mM KCl, 10% sucrose). 20 µM $ZnCl_2$ was included for Pcf11zcz purifications, and 10 mM imidazole was included for his-tagged proteins. A spatula tip of DNase I and lysozyme, 1 mM DTT and protease inhibitors (as above) were added, cells were broken in a French Press, and the lysate was cleared by centrifugation. All buffers used in the subsequent purification contained 1 mM DTT. HisSumo-Pcf11ΔN1184 from a 1500 ml culture was absorbed to 3 ml NiNTA agarose, which was then washed with 20 mM imidazole, 1 M KCl and again 20 mM imidazole, all in lysis buffer. Protein was eluted with lysis buffer plus 250 mM imidazole. Fractions containing the desired protein were pooled, mixed with Ulp1 Sumo protease (a kind gift of Bodo Moritz) and dialyzed against lysis buffer plus 20 mM imidazole overnight. The protein was then passed over a Ni-NTA column, and the flow-through and wash fractions were applied to a MonoQ column, which was eluted with a gradient to 1 M KCl in 50 mM Tris-HCl, pH 8.0, 10% sucrose. HisSumo-Pcf11zcz was purified in a similar manner except that fractions eluted from Ni-NTA were directly applied to the MonoQ column without cleavage of the HisSumo tag and the MonoQ buffer contained 20 µM $ZnCl_2$. Lysate from a 1 l expression culture of GST-Pcf11zcz was applied to 1 ml of GSH-Sepharose (GE Healthcare), which was washed with 50 mM Tris-HCl, pH 8.0, 200 mM KCl, 10 % Sucrose, 2 mM DTT, 20 µM ZnCl2 and eluted with the same buffer plus 20 mM gluthathione. The protein was further purified by MonoQ chromatography as above.

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Expression of HisSumo-CstFΔN530 in *E. coli* BL21 codon plus was induced by 1 mM IPTG in 800 ml SB-Medium containing kanamycin at 18°C overnight. Cells were broken in a French press and proteins bound to Ni-NTA beads in buffer A (50 mM Tris-HCl, pH 8.0, 300 mM KCl, 10% glycerol, 10 mM imidazole, 0.02% NP-40, 1 mM DTT) containing PMSF, leupeptin and lepstatin at 1 µg/ml each. The protein was eluted by buffer A plus 500 mM imidazole. Fractions containing His-Sumo-CstF64ΔN530 were pooled and dialysed against buffer A with 50 mM KCl and no imidazole.

Full-length bovine poly(A) polymerase has been described (Kühn et al. 2009).

RNA

Cleavage substrate L3 and its 'delta' derivative with a point mutation in the AAUAAA sequence have been described (Humphrey et al. 1987). The SV40 late RNA was the -140/+70 fragment (Conway and Wickens 1987) cloned into pSP64. The corresponding 'delta' derivative had a U to G mutation in the polyadenylation signal. RNAs were made by in vitro transcription from DraI-linearized plasmids with SP6 RNA polymerase (Roche) under standard conditions in the presence of [α-^{32}P]-UTP and cap analog (NEB). Uncapped SV40 late 40-mer fragments were made by *in vitro* transcription from DNA oligonucleotide templates (Supplemental Table 2) with T7 RNA polymerase (NEB) in the presence of [α-^{32}P]-UTP and 20% DMSO. Synthetic RNAs were obtained from biomers.net GmbH (Ulm, Germany) and radiolabeled with polynucleotide kinase or with hClp1, which proved more efficient for some very G-rich oligonucleotides.

CD spectra were recorded in a J-815 Spectrometer (JASCO) between 340 nm and 220 nm at 1 cm path length. RNA concentration was 2 µM in 50 mM Tris-HCl, pH 8, 10% glycerol, 0.01% NP-40, 60 mM KCl, 40 mM NaCl at 20°C. Prior to measurement, the RNA was heated to 95°C for 5 min in 10 mM HEPES-NaOH, pH 7.0, and cooled on ice.

Pre-mRNA cleavage assays

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Cleavage assays contained 12.5 µl 2x cleavage buffer (40 mM HEPES-KOH, pH 8.0, 150 mM KCl, 4 mM DTT, 2 mM $MgCl_2$, 40 mM creatine phosphate, 1 mM 3'-dATP, 7 % (w/v) polyethylene glycol 6000, 0.1 mg/ml tRNA), 60 fmol substrate RNA, and up to 8 µl protein fractions. The volume was made up to 25 µl with filter binding buffer (see below). Reactions were incubated at 30°C for up to 2 h and stopped by the addition of SDS-containing buffer. After proteinase K digestion, RNA was ethanol precipitated and analyzed by polyacrylamide - urea gel electrophoresis and phosphoimaging.

For a partial purification of cleavage factors, HeLa cell nuclear extract (Ipracell, Mons, Belgium) was mixed with ammonium sulfate (30 % saturation) and stirred on ice for at least one hour. After centrifugation, the pellet was dissolved in purification buffer (20 mM HEPES-KOH, pH 8.0, 3 mM $MgCl_2$, 10 mM NaF, 0.2 mM EDTA, 0.5 mM DTT, 25% glycerol, 1x protease inhibitor cocktail [Biotools]) plus 300 mM KCl. An aliquot of 2.5 ml (13 mg protein) was fractionated over a 100 ml Superose 6 gel filtration column (GE Healthcare). This resulted in fractions that reconstituted pre-mRNA cleavage when 3 µl was supplemented with 100 fmol poly(A) polymerase and CF II. Active fractions were diluted to 80 mM KCl in purification buffer and passed over a Resource Q column (GE Healthcare), which was eluted with a gradient to 1 M KCl. Fractions were obtained that reconstituted cleavage when 1 µl was complemented with poly(A) polymerase, CF II and CstF at 50 - 100 fmol each. 50 - 100 fmol of CF I was also added, although the reaction did not depend on it.

Kinase assays

Reactions were performed at 30°C in 50 mM HEPES-KOH, pH 8.0, 100 mM KCl, 5 mM MgAc, 5 µM $ZnCl_2$, 10% sucrose, 0.02% NP-40, 1 mM DTT, 400 U/ml RNasin (Promega), C_{14} and ATP trace-labeled with ɣ-[^{32}P]-ATP. For titrations of C_{14}, ATP was used at 1 mM. The reaction mixture lacking ATP was pre-incubated for 5 min at 30°C and the reaction started by nucleotide addition. At different times, 5 µl aliquots were taken from the reaction, stopped with 5 µl 60 mM EDTA, 7 M urea and put on ice. Samples were heated for 3 min at 95°C and loaded on a denaturing 20% polyacrylamide gel. Phosphorylated C_{14} was

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quantified by phosphoimaging. For titrations of ATP, C_{14} was used at 20 µM. ATP contributed by the hClp1 column buffer was negligible. The reaction product was detected by adsorption to DEAE paper (Stayton and Kornberg 1983). Initial velocities were fitted to the Michaelis-Menten equation (SigmaPlot version 12.5). Kinase assays for the analysis of column fractions were done at 20 µM C_{14} and 0.625 or 1 mM ATP for 10 min.

RNA binding assays

Nitrocellulose filter binding was essentially done as described before (Kühn et al. 2003). RNA was heated at 95°C for 3 min in 10 mM HEPES-NaOH, pH 7.0, and cooled on ice before addition to the binding reaction. For the determination of apparent equilibrium dissociation constants, a fixed amount of RNA was titrated with increasing amounts of protein. Data were fitted to a 1:1 association equilibrium with a single rectangular hyperbolic function (SigmaPlot version 12.5).

For electrophoretic mobility shift assays, binding reactions were set up and preincubated as for NC filter binding and analyzed on 5% (60:1) polyacrylamide gels run in 0.5x TBE at 8°C. Gels were dried on Whatman 3MM paper, and RNA was detected and quantified with phosphoimaging. Free and bound RNA were quantified as fractions of the total radioactivity in each lane; no-protein reactions were subtracted as background from the bound fraction. Apparent equilibrium dissociation constants were calculated as above.

UV cross-linking was carried out with 2 µM of 5'-labeled U_{14} RNA and 0.5 µM CF II in 50 µl 25 mM Tris-HCl, pH 8.5, 100 mM KCl, 10% sucrose, 0.02% NP-40, 0.2 mM EDTA, 0.5 mM ATP, 5 mM MgCl, 0.5 mM DTT. The mix was preincubated for 5 min at RT and UV-irradiated at 250 nm for 1 min (Kühn et al. 2003). Cross-linked products were analyzed without RNase digestion via SDS–polyacrylamide gel electrophoresis and phosphoimaging or used for immunoprecipitation: 5 mg of protein A Sepharose CL-4B (GE Healthcare) per sample was washed in 25 mM Tris-HCl, pH 8.5, 10% sucrose, 0.02% NP-40, 0.2 mM EDTA, 0.5 mM DTT, 200 mM KCl, mixed with 10 µl polyclonal α-Pcf11 antibody serum (made by Isabelle Kaufmann) or pre-immune serum and incubated for 1 h with end-over-end rotation at

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8°C. Beads were washed three times with binding buffer and eluted with 4× SDS sample buffer for 5 min at 95°C. Cross-linked proteins were analyzed as above.

RNA selection

100 nM hPcf11ΔN1184 in 400 µl filter binding buffer (25 mM Tris-HCl, pH 8.0, 50 mM KCl, 2 mM $MgCl_2$, 0.01% NP-40, 1 mM DTT, 10% (v/v) glycerol, 0.1U/µl Ribolock [ThermoFischer]) was mixed with 15 µg phosphorylated 14-mer RNA of the sequence N_{14}GUUU and incubated for 30 min at room temperature with rotation. The mixture was filtered over a nitrocellulose membrane (GE Healthcare) equilibrated with filter binding buffer containing 15 µg/ml heparin, which was then washed with 20 ml ice-cold filter binding buffer. The spot where the binding reaction had been applied was cut out, and the RNA was eluted by addition of 250 µl 50% formamide, 1.8 M sodium acetate, 2 mM EDTA, 0.2% (w/v) SDS and shaking at 70°C for 30 min.

For full length CFII, 100 nM protein in 400 µl binding buffer (25 mM Tris-HCl, pH 7.5, 150 mM KCl, 3 mM MgCl2, 0.01% (v/v) NP-40, 1 mg/ml BSA, 5% (v/v) glycerol, 0.1U/µl Ribolock) was mixed with 20µl IMAC sepharose beads (GE Healthcare) preloaded with Ni^{2+} ions and 15 µg of the N14GUUU RNA pool and incubated for 30 min at room temperature with agitation. Beads were collected by centrifugation (1000 g, 2 min, 4°C) and washed three times with ice-cold binding buffer. Bound RNA was eluted in 200 µl 10 mM Tris-HCl, pH 7.0, 400 mM NaCl, 1 mM EDTA, 1% (w/v) SDS.

For both types of experiments, no-protein controls were also performed. Selected RNA molecules were purified by phenol-chloroform extraction and ethanol precipitation and ligated with a 3´-DNA adaptor (AAACTGGAATTCTCGGGTGCCAAGG-Amino-C7) and a 5´-RNA adaptor containing a T7 promoter sequence (GUUCAGUAAUACGACUCACUAUAGGG). The products were reverse-transcribed with the First Strand cDNA Synthesis Kit (Thermo) and the primer GCCTTGGCACCCGAGAATTCCAGTTT. PCR was used to amplify the cDNA sequence and introduce barcodes for next generation sequencing (NGS). PCR products were run on a 6%

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polyacrylamide urea gel, and the band at 150bp corresponding to the desired product was excised. The DNA was eluted overnight in 0.4 M NaCl and precipitated with ethanol, dissolved and stored for NGS analysis.

For the generation of RNA for a second round of selection, 50 ng of the PCR-pool was amplified with the primers AATGATACGGCGACCACCGAGATCTACACGTTCAGTAATACGACTCACTATAGG and GCCTTGGCACCCGAGAATTCCAGTTT. The PCR-product was purified with a PCR Clean-up Kit (Macherey-Nagel) and cleaved by addition of 1.5 µl FastDigest MssI (ThermoFisher), which recognizes the restriction site GTTTAAAC generated by ligation with the 3´adaptor. The cleaved DNA was transcribed with T7 polymerase, which yields a new pool of RNAs with the sequence GGG$(N)_{14}$GUUU. The RNA was purified on an 18% polyacrylamide urea gel, dephosphorylated with FastAP (ThermoFisher) and phosphorylated with polynucleotide kinase. 15 µg of the prepared RNA were used in a second selection cycle, ligated and amplified as described above.

Libraries were sequenced on a MiSeq instrument (Illumina) with a 150 cycle MiSeq Reagent Kit to which we added a custom Read1 sequencing primer (5´-GATCTACACGTTCAGTAATACGACTCACTATAGGG-3´). Analysis was restricted to sequences from the second round of selection. Reads were barcode sorted and filtered for sequences containing the 3´ adaptor and the full Mss1-cleavage site, indicative of ligation of an intact RNA from the selection pool. After clipping of the adaptor and invariant sequence, only reads of the correct length (17 nt) were used for further analysis. The first three nucleotides were trimmed, and the resulting 14-mer sequences were analyzed for enriched sequence motifs using Weeder2 (Zambelli et al. 2014). Between 14,000 and 44,000 useful reads were obtained per experiment.

Limited digestion of CF II

Per time point, 0.5 µg CF II was digested with 0.5 ng of sequencing-grade trypsin (Promega) in 15 µl 50 mM triethanolamine-HCl, pH 8.0, 200 mM KCl, 10% sucrose, 1 mM DTT at 16 °C.

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The reaction was stopped with 15 µl SDS loading buffer. For sequence analysis, 12.5 µg CF II was digested under comparable conditions. The reaction was stopped with 2 mM AEBSF, and the complex of his-tagged hClp1 and the trypsin-resistant hPcf11 fragment isolated on Ni-NTA agarose. The hPcf11 fragment was excised from an SDS-polyacrylamide gel, and fragments generated by trypsin or Asp-N digestion were analyzed by MS (Shevchenko et al. 2006). For Edman degradation, NiNTA-purified complex was separated by SDS-polyacrylamide gel electrophoresis and blotted to a PVDF membrane. After Ponceau S staining, the trypsin-resistant hPcf11 fragment was cut out and sequenced by the Proteome Factory AG (Berlin).

Chemical cross-linking of CF II

For cross-linking, CF II was purified in buffers in which Tris was substituted by triethanolamine. 180 µl CF II (1 µM in column buffer) was mixed with 20 µl DSBU (12.8 mM in DMSO) (Müller et al. 2010) and incubated for 30 min at room temperature. The reaction was quenched with 200 µl of 2x SDS loading buffer containing Tris, and proteins were separated on a 4-12 % SDS-polyacrylamide gel. In-gel digestion of cross-linked protein complexes with trypsin, data acquisition and analysis were done as described (Götze et al. 2015; Arlt et al. 2016). Three gel bands of high molecular weight cross-linked complexes were analyzed separately by LC/MS/MS using three different collision energies (30% or 35% NCE or 29 +/- 5% stepped NCE). Cross-links identified at least twice at an FDR ≤ 1% were taken into account and manually validated. Data are available via ProteomeXchange with identifier PXD010177.

Acknowledgments

We are grateful to Mathias Lorbeer for generating the CF I and CstF viruses and developing the first purification protocols; to Michael Götze for advice on data analysis of protein-protein cross-linking; to Christopher Trotta for the stable cell line expressing His-Flag-hClp1; to Paul Jenö for the analysis of purified His-Flag-hClp1; to Tobias Gruber for help with CD

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spectroscopy; to Bodo Moritz for the Ulp1 sumo protease; to Gudrun Scholz, Sandra Grund and Moritz Schmidt for help with cloning and protein purification; and to Lionel Minvielle-Sebastia for communicating unpublished results. This work was supported by grants from the Deutsche Forschungsgemeinschaft to EW (WA 548 15/1 and GRK 1591) and to GM (PP 1935).

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Table 1: Steady-state parameters for the RNA 5' kinase activity of CFII and hClp1

Substrate	Protein	k_{cat} [s^{-1}]	K_M [μM]	k_{cat}/K_M [1/s·M]
ATP	CF II	2.8±0.8	700±200	4300±1400
	hClp1	1.3±0.5	2500±1100	500±100
C_{14}	CF II	4.5±1.4	2.5±0.4	$1.8x10^6$±$0.4x10^6$
	hClp1	(1.6/0.7)	2.4/1.6	($0.7x10^6$/$0.4x10^6$)

Kinase assays were carried out as described in Materials and Methods. K_M and V_{max} were obtained from standard Michaelis-Menten analysis, and V_{max} values were converted to k_{cat}. The C_{14} titration with hClp1 was carried out twice, and the parameters derived from the two experiments are both listed. All other numbers listed represent the average ± standard deviation (n = 3-4). The k_{cat} values for hClp1 and the resulting k_{cat}/K_M values are put in brackets because the activity of hClp1 declined upon storage; CF II, in contrast, was stable. This contributes to a lower apparent k_{cat} of hClp1 but should not affect K_M determinations. Note also that the ATP concentration used for C_{14} titrations was 1.2 x K_M for CF II but 0.75 x K_M for hClp1; saturating concentrations would have required prohibitively large amounts of radioactivity. Finally, different assays were used to measure kinase activity in ATP versus C_{14} titrations (see Materials and Methods).

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Table 2: Affinities of CF II for RNA oligonucleotides

Name	Sequence	apparent K_D [nM]
G_{10}		45
G_{11}		41
G_{12}		21±9
G_{13}		21±12
G_{14}		2.0±1.3
G_{17}		1.9±0.9
U_{14}		72
C_{14}		>1000
A_{14}		315
191-230	GGGUUUAUGUUUCAGGUUCAGGGGGAGGUGUGGGAGGUUUUUU	0.4±0.2
190-225	UUUUAUGUUUCAGGUUCAGGGGGAGGUGUGGGAGGU	0.2±0.1
202-224	GGUUCAGGGGGAGGUGUGGGAGG	0.8
208-225	GGGGGAGGUGUGGGAGGU	2.6
208-224	GGGGGAGGUGUGGGAGG	5.2
208-221	GGGGGAGGUGUGGG	3.4
wt2x	GGGGGAGGUGgGGGAGG	2.0
Δ2x	GGGaaAGGUGgGaaAGG	1.9
ΔΔ2x	GaGaGAGGUGaGaGAGG	2.3
CstF SELEX	UGUGUUUUAUUGUGU	4.4
BS2	GGGUUUAAGUGGGUCACGUUUAAAC	11
BS2-Δ1	GGGUUUAAGUGGGUCACG	13
BS2-Δ2	CCCUUUAAGUGGGUCACG	54
BS2-Δ3	UUUAAGUGGGUCACG	105
BS3 CFII	GGGUUACGCGUGAGGACG	1.7
BS3 Pcf11	GGGUUUAGUGCGCACGUG	5.9±0.9
BS3 Weeder	GGGUUUAGUGGGGGGGUG	2.4±0.6

RNA oligonucleotides were titrated with CF II in gel shift experiments. 191-230 is a T7 transcript starting with three G residues introduced for T7 transcription, followed by nucleotides 191-230 of the complete SV40 late transcript. In this numbering, U191 is at position +16 downstream of the cleavage site (Sheets et al. 1987). All other oligonucleotides were synthesized chemically. The G-rich downstream element identified by (Qian and Wilusz 1991) is underlined. The sequence wt2x converts the natural sequence into a perfect tandem repeat. Oligos Δ2x and ΔΔ2x are further mutant derivatives. Mutant positions are shown in lower-case letters. The CstF SELEX sequence is based on (Beyer et al. 1997). The BS2 sequence was obtained in a first selection experiment with CF II. BS3 CF II represents the most frequent sequence read with CF II selected on Ni^{2+} beads. BS3 Pcf11 is the sequence

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most often found in selections with Pcf11ΔN1184 and nitrocellulose filter binding. BS3 Weeder represents the enriched motif identified in this latter experiment by Weeder (Zambelli et al. 2014). Each titration was fitted to a binary interaction model. Average ± standard deviation is reported for experiments with n≥3. Simple numbers represent the average of n=2, except for G_{10} (n=1).

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Figure legends:

Fig. 1: CF II is a heterodimer of hClp1 and hPcf11 and co-purifies with RNA 5' kinase, RNA binding and 3' cleavage activity. (A) His-FLAG-tagged hClp1 was affinity purified from a stable cell line by two consecutive purification steps on FLAG beads and Ni^{2+} beads. The silver-stained SDS gel shows the eluates from the first (middle lane) and second purification step (right lane). The two bands marked in the FLAG eluate are PRTM5 and MEP50, known FLAG-binding proteins. Sen2, Sen54 and tRIE are subunits of the tRNA splicing endonuclease. (B) MonoQ column profile of his-tagged hClp1 and hPcf11 co-expressed in baculovirus-infected insect cells (see Material and Methods). RNA binding was measured by nitrocellulose filter binding assays with 0.5 µl of a 1:100 dilution of the fractions indicated and 100 fmol of SV40 late RNA (see Materials and Methods). Kinase activity was assayed as described in Materials and Methods. (C) Fractions of the column shown in (B) were analyzed by SDS-polyacrylamide gel electrophoresis. Arrowheads indicate hPcf11 and hClp1. (D) Fractions of the column shown in (B) were assayed for reconstitution of 3' cleavage as described in Materials and Methods. Assays contained poly(A) polymerase (PAP), a fraction (GF) generated by ammonium sulfate precipitation of HeLa cell nuclear extract and Superose 6 gel filtration, and 2 µl of the MonoQ column fractions. The reactions were carried out with wild-type L3 RNA or L3Δ RNA with a point mutation in the AAUAAA signal. With both RNAs, the first four lanes following the marker lane show negative controls, as indicated. (E) Gel filtration of CF II on a Superose 6 column. Arrows indicate the void volume (V) and the elution peaks of marker proteins with their Stoke's radii (see Materials and Methods). (F) SDS polyacrylamide gel electrophoresis of the column fractions of (E). (G) Superdex 200 gel filtration column profile of His-tagged hClp1 expressed in baculovirus-infected cells (see Materials and Methods). RNA kinase activity was measured as described in Materials and Methods. The void volume (V) and peak positions of marker proteins with their Stoke's radii are indicated. (H) SDS polyacrylamide gel electrophoresis of the column fractions of (G).

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Fig. 2: CF II has RNA 5' kinase activity, which is not required for RNA cleavage. (A) Initial velocities of the 5' kinase activities of CF II or hClp1 were measured at varying concentrations of [γ-^{32}P]-ATP and a constant concentration of C_{14} as described in Materials and Methods. (B) Initial velocities of the 5' kinase activities of CF II or hClp1 were measured at a constant concentration of [γ-^{32}P]-ATP and varying concentrations of C_{14}. In both (A) and (B), plots represent fits to the Michaelis-Menten equation. Data points with error bars representing the standard deviation were averaged from n ≥3. Titrations for hClp1 were done twice, and both experiments are shown (see legend to Table 1). (C) Cleavage assays contained 5, 25, 50 or 200 fmol of hClp1 or of wild-type CF II or of CF II with clustered point mutations in the active site of hCp1 (KR: K127A, R288A, R293L; DR: D151A, R288A, R293L). These proteins were tested in a complementation system containing the SV40 late RNA, poly(A) polymerase, CF I, CstF and a protein fraction generated from HeLa cell nuclear extract by ammonium sulfate precipitation, gel filtration and MonoQ chromatography as described in Materials and Methods. Omission of the MonoQ fraction or all proteins was used as negative controls and addition of nuclear extract (NXT) as a positive control, as indicated. Filled and hollow arrowheads indicate substrate RNA and 5' cleavage product, respectively. Controls with a mutant RNA showed that the cleavage activities were dependent on the AAUAAA sequence (data not shown).

Fig. 3: Domain organization and cross-linking of CF II. (A) Domains of hPcf11. Highlighted are the CID (CTD Interaction Domain; residues 14-142), an α-helical region (183-297), a highly charged, basic region (295 - 550) overlapping with the region cross-linked to hClp1 (XL; 500-770), the FEGP repeats (770-1124), the zinc fingers (ZF; 1343-1368 and 1443-1478) and the hClp1 interaction region (IR;1371-1439). The bars at the bottom indicate regions of hPcf11 present in the deletion variants. (B) Alignment of consecutive residues 770 - 1126 of hPcf11 reveals FEGP repeats. The alignment was produced with JalView (Waterhouse et al. 2009). (C) Overview of cross-links in CF II. The circle represents the primary structures of hClp1 and hPcf11 with amino acid numbering indicated. Blue lines

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indicate intermolecular and red lines intramolecular cross-links. The Clp1 interaction region of Pcf11 based on the crystal structure of the yeast proteins is in grey. (D) Cross-link sites in a model of hClp1 (green) with the superimposed peptide from yPcf11 (red) (PDB accession number: 4OI4). Lysine side-chains forming inter- or intramolecular cross-links are shown. Intramolecular cross-links are shown in orange with participating side-chains and C_α-C_α-distances (in Ångstrom) indicated. The structure of hClp1 was modeled with the Robetta Server (http://robetta.bakerlab.org) (Kim et al. 2004).

Fig. 4: Domains of hPcf11. (A) Trypsin digestion identifies a stable C-terminal hPcf11 fragment. Human Pcf11 was digested with trypsin for the times indicated (see Materials and Methods). Proteins were analyzed on an SDS-polyacrylamide gel and stained with Coomassie. Black and white arrowheads indicate full-length hPcf11 and hClp1, respectively, and the asterisk marks the stable hPcf11 fragment. (B) The C-terminal region of hPcf11 containing the hClp1 interaction sequence flanked by the zinc fingers suffices for stable hClp1 binding. Untagged hClp1 and his-tagged hPcf11ΔN1339 were co-expressed and purified via Ni-NTA and MonoQ chromatography. The figure shows an analysis of the MonoQ peak fractions by SDS-polyacrylamide gel electrophoresis and Coomassie staining. Black and white arrowheads indicate hClp1 and the hPcf11 fragment, respectively. Identity and completeness of the hPcf11 fragment were confirmed by LC/MS/MS. (C) A C-terminal hPcf11 fragment starting with the FEGP repeats supports pre-mRNA cleavage. Cleavage assays were performed with the L3 RNA and mutant control and proteins as described in the legend to Fig. 2B. Controls were as in Fig. 2B. CF II ΔN769 and ΔN1123 refers to the heterodimers reconstituted with the respective hPcf11 mutants. Black and white arrowheads indicate substrate RNA and 5' cleavage product, respectively.

Fig. 5: CF II binds RNA via the zinc fingers of Pcf11. (A) Nitrocellulose filter-binding experiments showing binding of CF II to SV40 late and L3 RNAs. Hyperbolic fitting indicated K_{50} values of 0.4 nM for the SV40 late and 0.9 nM for the L3 RNA. (B) CF II was incubated

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with 5'-labeled U_{14} and irradiated with UV light. An aliquot of the cross-linked material was then subjected to immunoprecipitation with antibodies against hPcf11 or pre-immune serum as a control. Input and precipitated material were analyzed by SDS-polyacrylamide gel electrophoresis and phosphoimaging. (C) Gel shift experiments with the RNA oligonucleotide 208-221 (Table 2) comparing wild-type CF II, CF II reconstituted with hPcf11ΔN1184, and hPcf11ΔN1184 by itself. Fits indicated K_{50} values of 3.3 nM for CF II and >100 nM for the two other proteins. (D) Binding of HisSumo-hPcf11zcz (single titration) and GST-hPcf11zcz (average of n = 2) to RNA oligonucleotide 191-230 (Table 2). Extrapolated K_{50} values were ~ 100 and 200 nM. For comparison, binding of the same RNA to CF II is shown (K_{50} = 0.5 nM). (E) Sequence logo derived from a selection carried out with hPcf11ΔN1184 and nitrocellulose filter binding. (F) CD spectra of RNA oligonucleotides wt2x and Δ2x show a maximum at 260 nm, indicating a G quadruplex structure, whereas ΔΔ2x has a spectrum similar to that of unstructured U_{14}. The 260 nm peak of Δ2x was sensitive to heating to 90°C.

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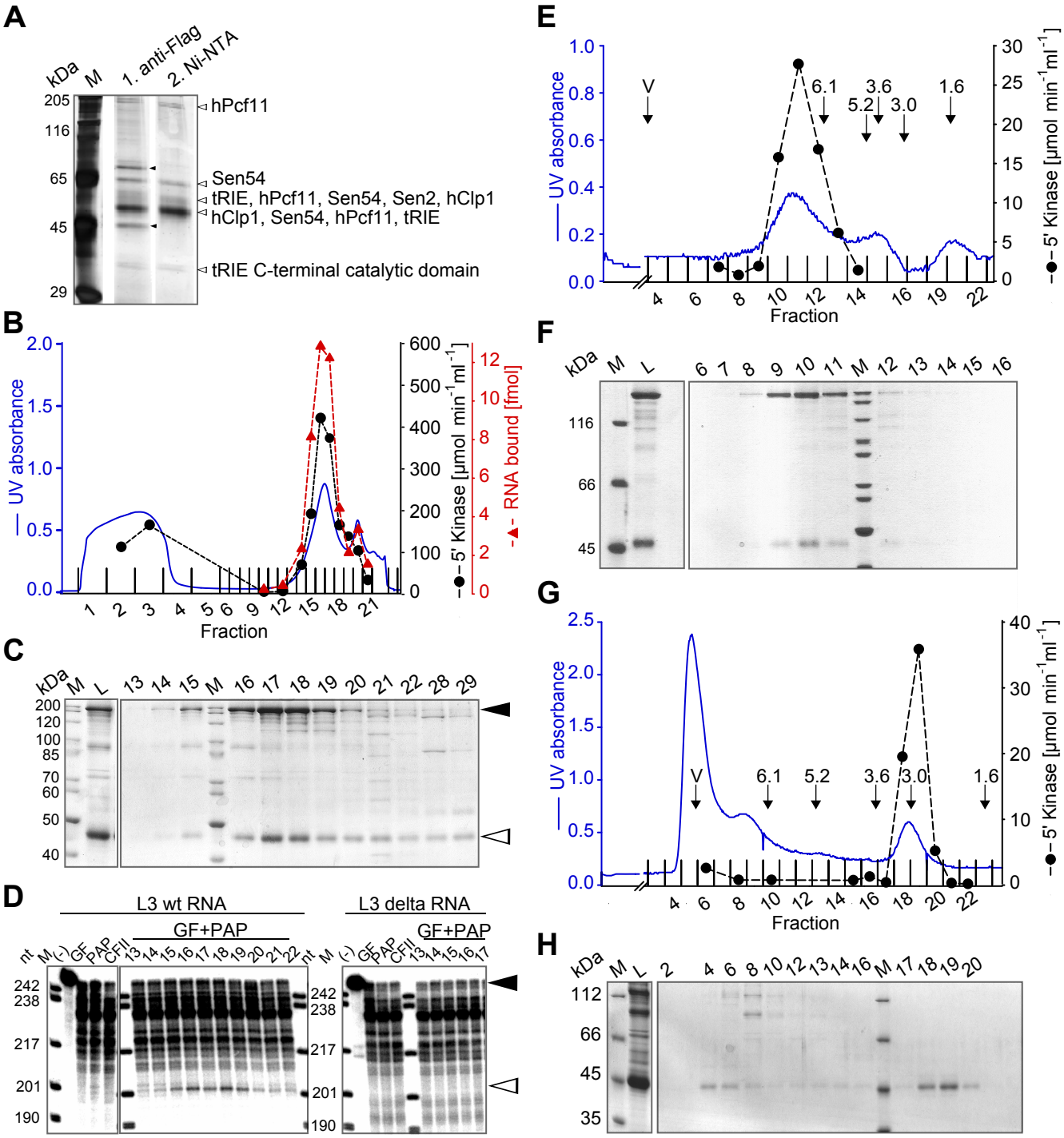

Figure 1, Schaefer et al.

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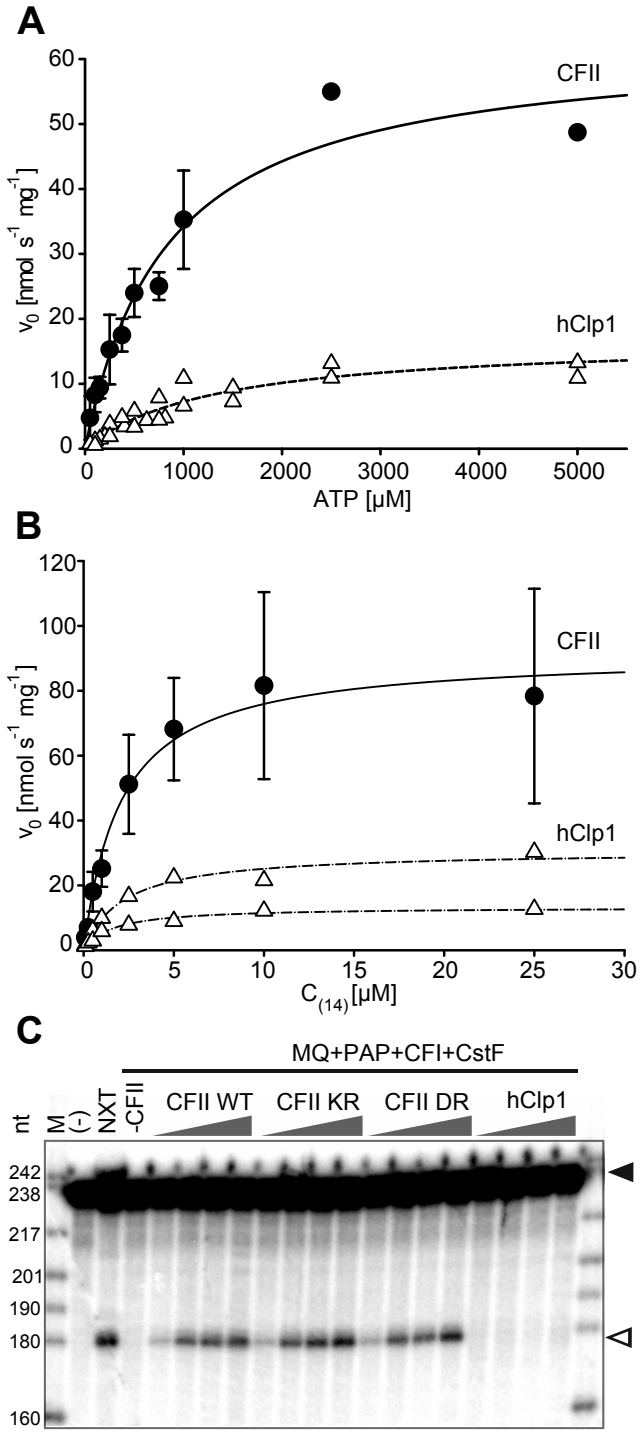

Figure 2, Schaefer et al.

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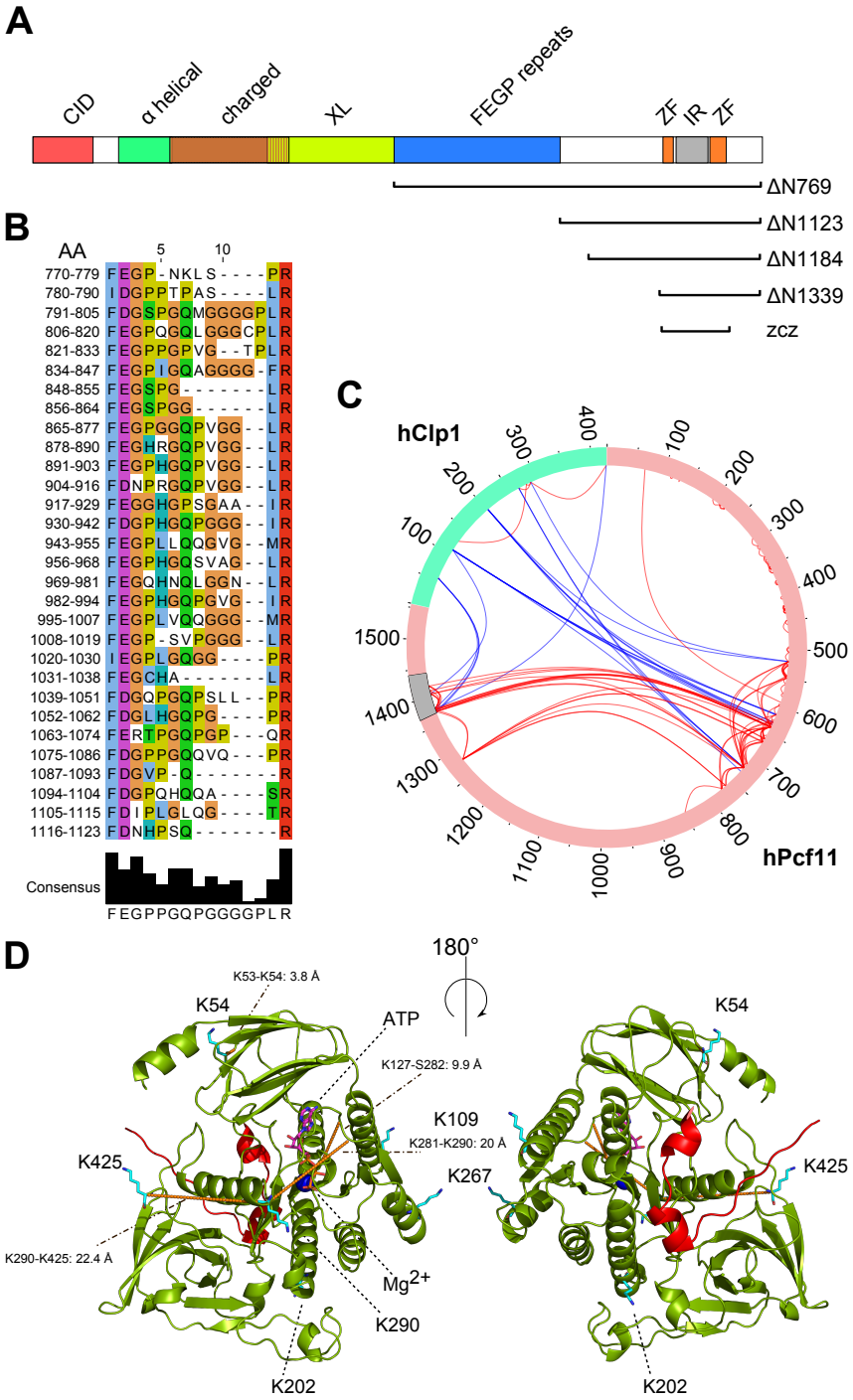

Figure 3, Schaefer et al.

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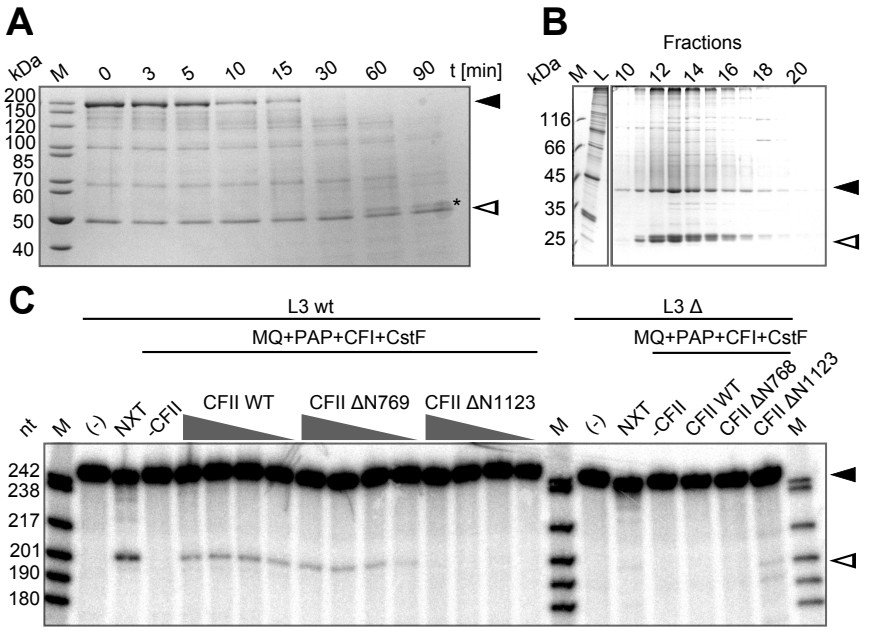

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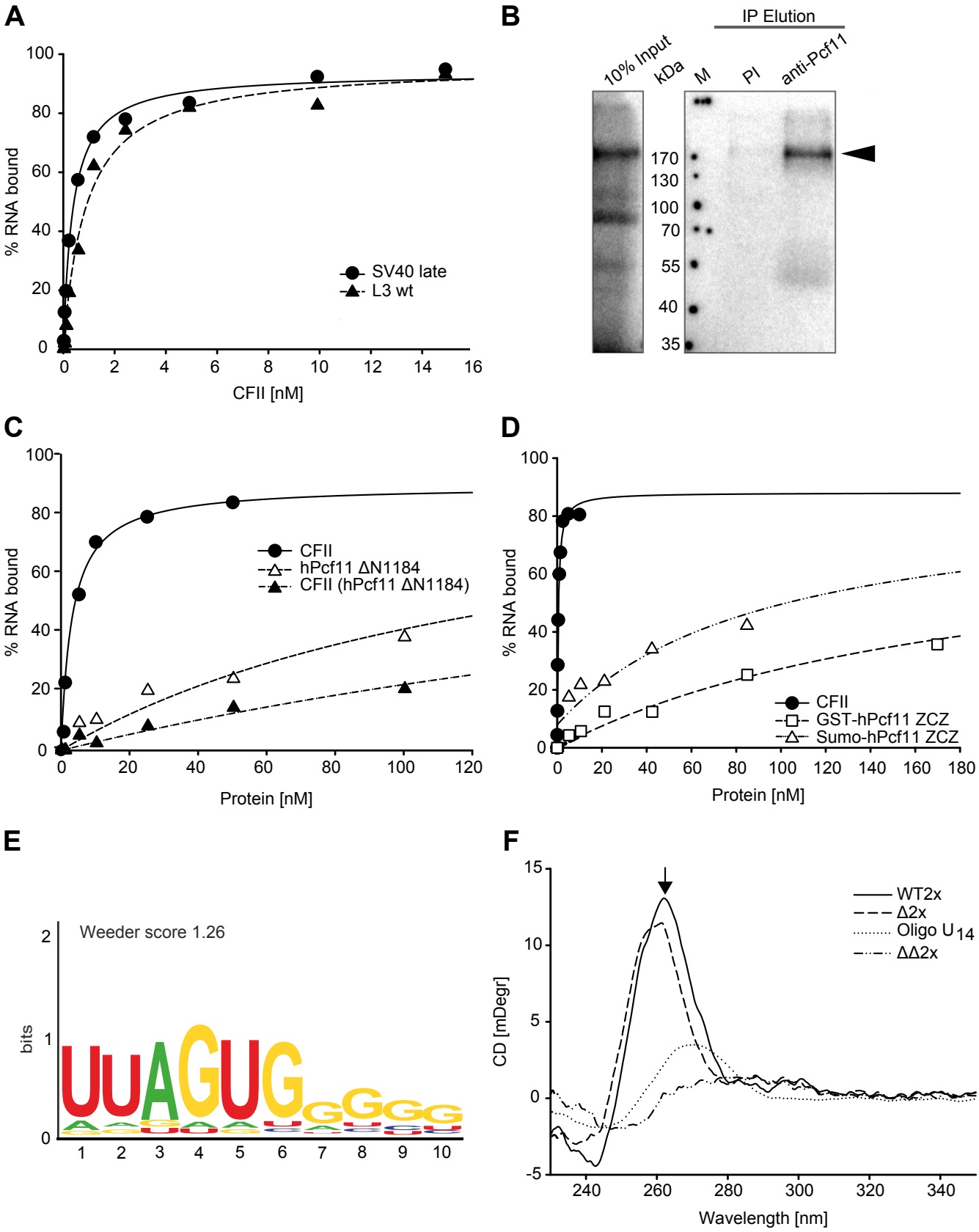

Figure 5, Schaefer et al.