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REVIEW

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# The large family of PC4-like domains – similar folds and functions throughout all kingdoms of life

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## ABSTRACT

RNA- and DNA-binding domains are essential building blocks for specific regulation of gene expression. While a number of canonical nucleic acid binding domains share sequence and structural conservation, others are less obviously linked by evolutionary traits. In this review, we describe a protein fold of about 150 aa in length, bearing a conserved  $\beta$ - $\beta$ - $\beta$ - $\alpha$ -linker- $\beta$ - $\beta$ - $\beta$ - $\alpha$  topology and similar nucleic acid binding properties but no apparent sequence conservation. The same overall fold can also be achieved by dimerization of two proteins, each bearing a  $\beta$ - $\beta$ - $\beta$ - $\alpha$  topology. These proteins include but are not limited to the transcription factors PC4 and P24 from humans and plants, respectively, the human RNA-transport factor Pur- $\alpha$  (also termed PURA), as well as the ssDNA-binding SP\_0782 protein from *Streptococcus pneumoniae* and the bacteriophage coat proteins PP7 and MS2. Besides their common overall topology, these proteins share common nucleic acids binding surfaces and thus functional similarity. We conclude that these PC4-like domains include proteins from all kingdoms of life and are much more abundant than previously known.

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## KEYWORDS

RNA/DNA binding; PC4-like; protein domain; protein fold; structural biology; topology; PURA; RRM; KH-domain

## Introduction

To date a considerable number of globular RNA- and DNA-binding domains have been described. The RNA binders include domains such as the RNA Recognition Motif (RRM), the double-stranded RNA-Binding Domain (dsRBD), the K-Homology (KH) Domain, the Pumilio- and FBP-homology domain (PUF domain) and the zinc finger [1]. Well-described DNA-binding domains include the helix-turn-helix motif, homeodomain, leucine zipper, zinc finger, winged helix, and the HMG-box [2,3].

Amongst them, a number of domains are known to bind to both, DNA and RNA [4]. Nucleic acid binding domains that are found in these non-discriminating proteins include RRMs, KH domains, dsRBDs, zinc-finger domains, and so-called PUR domains [4–6]. Even classical DNA-binding domains such as the homeodomain have been shown to specifically recognize RNA targets [7,8]. Thus, it appears that for several of the known nucleic-acid binding domains their fold allows for the recognition of both targets. Steric limitations such as a narrower major groove in RNAs might be overcome by specific sequence features that create for instance bulges.

For many proteins, sequence homology and similarities in domain folds go hand in hand, suggesting a common evolutionary origin. However, similar three-dimensional structures can also originate from completely unrelated protein sequences [9]. Well-known examples for related domain folds without sequence homologies are the  $\alpha$ - $\beta$  barrel and  $\beta$ -barrel proteins.

The Purine-rich binding protein  $\alpha$  (Pur- $\alpha$ , also termed PURA) is a DNA- and RNA-binding protein that has reported functions in DNA replication, transcriptional regulation, as

well as the temporal and spatial regulation of mRNAs [5]. Mutation in the *PURA* gene that encodes Pur- $\alpha$  results in a neuro-developmental disorder, termed PURA syndrome [10–12]. While studying the structural properties of Pur- $\alpha$  [13–15] and its similarities (using DALI server) [16], we noted that a number of sequence-unrelated nucleic-acid binding proteins adopt the same domain fold with identical connectivity of their secondary structures. Here we describe this family of proteins and highlight similarities as well as differences.

## Material and methods

The structure of *D. melanogaster* Pur- $\alpha$  (fragment 41–185, chain A, PDB ID: 3k44) [14] has been used as a model for the similarities search using *Dali* server (<http://ekhidna2.bio-center.helsinki.fi/dali/>) [16]. Sequence comparison as well as a phylogenetic tree have been calculated using *Clustal Omega* software (<https://www.ebi.ac.uk/Tools/msa/clustalo/>).

## Results

### *Members of the PC4-like superfamily are structurally and functionally related*

According to the Structural Classification of Proteins SCOP [17] proteins adopting a similar fold as Pur- $\alpha$  have been classified as members of the ssDNA-binding transcriptional regulator domain superfamily (SCOPIID: 3000513) with four families including the transcriptional coactivator

PC4 C-terminal domain family (SCOP identifier: 4001029). The name is derived from the human replication and transcription cofactor PC4 (PDB ID: 1pcf, which represents the first published high-resolution structure of this fold [18]. The protein structure classification database CATH [19] describes the transcriptional co-activator PC4 as 2.30.31 family.

Besides human PC4 [18] and Pur- $\alpha$  from pro- and eukaryotes [13–15], representative proteins of this domain family include the Whirly-family of single-stranded DNA-binding proteins from mitochondria and chloroplasts, like the P24 subunit of the plant transcription factor PBF-2 [20] and the mitochondrial transcriptional regulators MRP1/2 from *Trypanosoma brucei* [21]. Furthermore, the coat proteins of the bacteriophages PP7 and MS2 [22,23] show structural similarities and similar nucleic acids binding properties to the PC4 family. Below we describe in more detail these and other structural entities that adopt closely related three-dimensional arrangements with identical connectivity of their secondary-structure elements and provide a structure-guided suggestion for their sub-classification. In addition, a number of functionally uncharacterized protein domains also adopt this fold, albeit it is unclear whether they

also bind nucleic acids (for details, see Supplementary text and Supplementary Fig. S1).

### The overall domain arrangement of PC4-like domains

Despite high structural homology, most PC4-like domains lack sequence similarity and show a wide occurrence in all three kingdoms of life (Supplementary Table S1 and S2, Supplementary Fig. S2). This may suggest that the common overall domain fold and nucleic-acid binding function appeared through convergent evolution. Such domains can either be built from a single peptide chain with a  $\beta$ - $\beta$ - $\beta$ - $\alpha$ -linker- $\beta$ - $\beta$ - $\beta$ - $\alpha$  topology (type I; Fig. 1A) or from two identical peptides with  $\beta$ - $\beta$ - $\beta$ - $\alpha$  fold, forming an inter-molecular homodimer (type II; Fig. 1B). In both cases the  $\alpha$ -helices swap between both  $\beta$ - $\beta$ - $\beta$ - $\alpha$  repeats, so that the helix from one repeat interacts with the  $\beta$ -sheet of a second repeat and *vice versa*. This swapping of secondary structure elements gives extra stability to this fold. By observing this effect, we assume that the existence of just one repeat as folded entity is

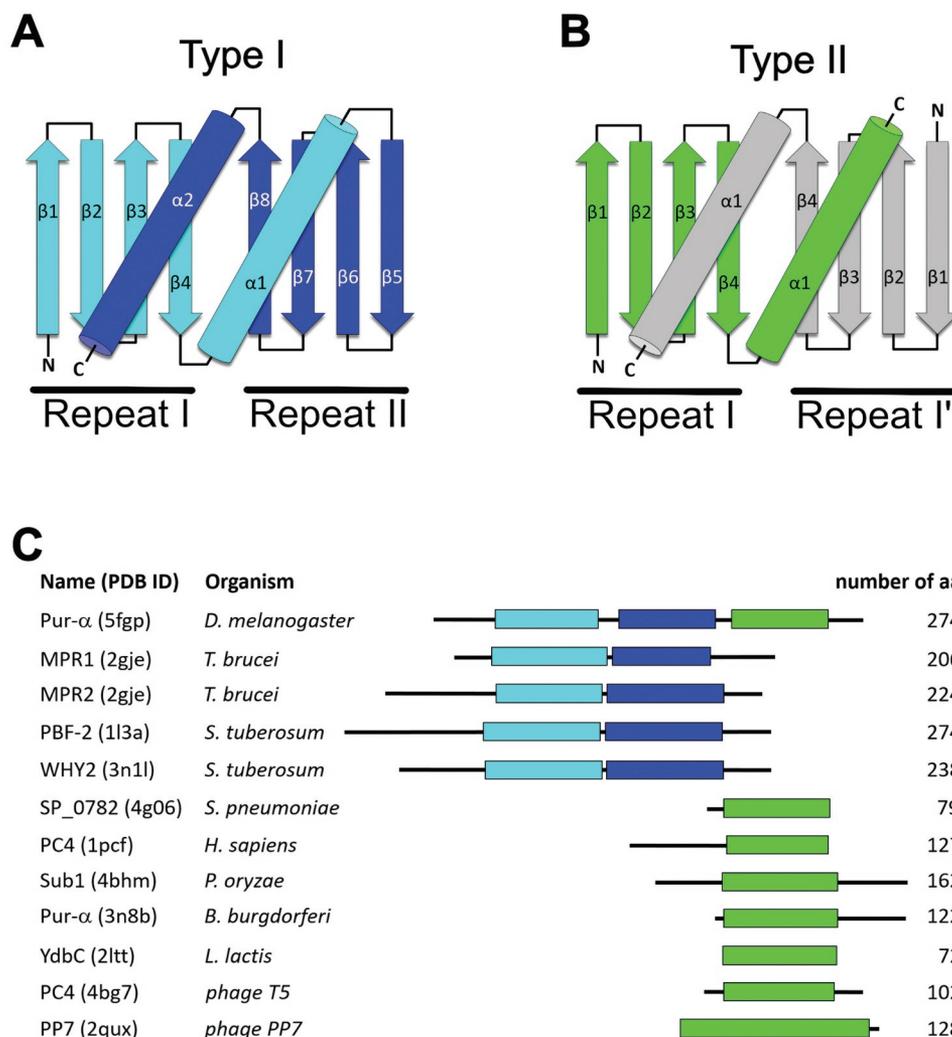


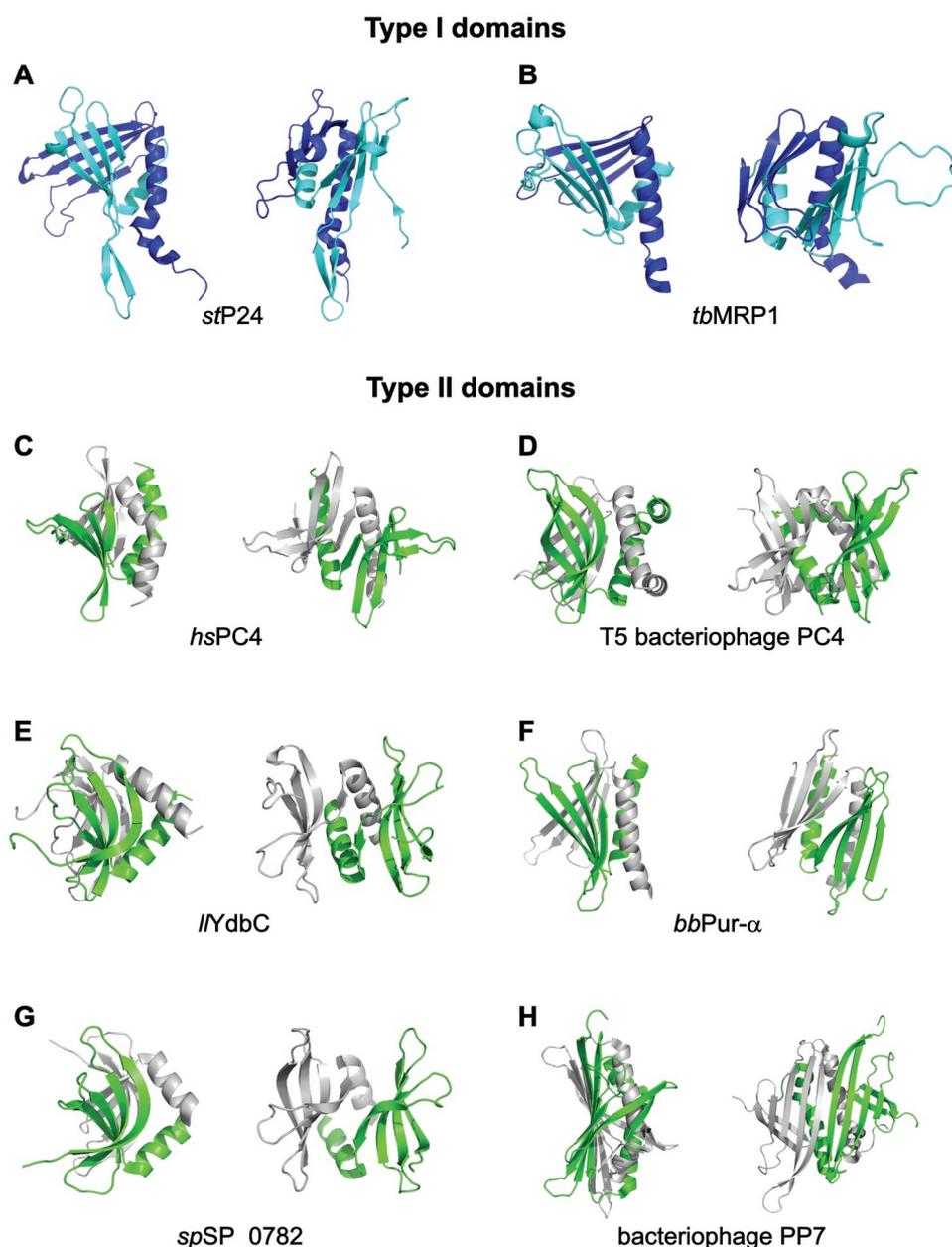
Figure 1. Topology diagram of type I (A) and type II (B) PC4-like fold. Domain organization for the selected proteins containing PC4-like domains (C).

highly unlikely, unless the  $\alpha$ -helix adopts a different orientation, much closer to the  $\beta$ -sheet of the same repeat. With just one exception known so far, there are no proteins containing both types of domains (Fig. 1C).

### Type I domains fold as intra-molecular dimers

*P24 subunit of the chloroplast transcription factor PBF-2.* The first described nucleic-acid binding protein of this type was the P24 subunit of the potato chloroplast transcription factor PBF-2 (WHY1, PDB ID: 1l3a) [20] (Fig. 2A and Supplementary Fig. S3A). The respective domain of this protein folds from a single

peptide chain. The four  $\beta$ -strands of each repeat form a concave  $\beta$ -sheet that is additionally stabilized by the  $\alpha$ -helix at the C-terminus of this repeat. The two  $\beta$ - $\beta$ - $\beta$ - $\beta$ - $\alpha$  repeats interact with each other by undergoing coiled-coil-like contacts between their two swapped  $\alpha$ -helices of the repeats. In addition, the domain is stabilized by hydrophobic interactions of residues from the helices and the sheets. The two  $\beta$ -sheets adopt a dome-like shape, each side binding to ssDNA in a sequence-specific manner [20]. Compared to the other representatives of type I domain proteins outlined here, the P24 nucleic acid binding domain is the least symmetric and structurally most divergent example



**Figure 2.** Comparison of different protein structures exhibiting type I and II PC4-like fold. Each structure is depicted in two different orientations. The coordinates are taken from: (A) *Solanum tuberosum* P24 subunit of PBF-2 (PDB ID: 1l3a) [20], (B) *Trypanosoma brucei* MRP1 (PDB ID: 2gje) [21], (C) The human replication and transcription cofactor PC4 (PDB ID: 1pcf) [18], (D) Bacteriophage T5 homologue of PC4 (PDB ID: 4bg7) [36], (E) *Lactococcus lactis* DUF2128 family member YdbC (PDB ID: 2l1t) [37], (F) Pur- $\alpha$  from *Borrelia burgdorferi* (PDB ID: 3n8b) [13], (G) *Streptococcus pneumoniae* SP\_0782 protein (PDB ID: 5zkl) [39], (H) The bacteriophage coat protein PP7 (PDB ID: 2qux) [22]. The structures of type I PC4-like fold have been represented as cyan (repeat I) and navy blue (repeat II), whereas in the structures of type II PC4-like fold individual chains have been shown in green and grey. The figure has been prepared in PyMol v 1.3 (pymol.org).

(Fig. 2A). PBF-2 forms a homotetramer, which adopts a whirligig appearance [20,24] (Supplementary Fig. S4A). Characteristic for this quaternary complex of P24 is its central pore, with  $\beta$ -strands radiating outwards. P24 shares high structural similarity to other Whirly proteins and to the mitochondrial MRP1/2 protein complex.

*The mitochondrial RNA-binding proteins MRP1 and MRP2.* In the parasite *Trypanosoma brucei* mitochondrial editing of kinetoplastid RNA (kRNA) is carried out by the Ligase-containing supramolecular complex [25–28]. This multiprotein complex consists of critical core enzymes [29–33] as well as substoichiometric amounts of RNA-associated proteins, including the so-called Mitochondrial RNA binding Protein (MRP) complex with its two subunits MRP1 and MRP2 [33–35]. MRP1/MRP2 serve as a matchmaker by binding to guide RNAs (gRNAs) and facilitating their hybridization with cognate pre-edited mRNAs [21]. These two RNA binding proteins adopt a hetero-tetrameric arrangement (PDB ID: 2gia, 2gje, and 2gid) [21] similar to P24 (r.m.s.d. of 3.17 Å for 447 superimposed residues). Like the other type I domains, MRP1 and MRP2 share an overall conserved  $\beta$ - $\beta$ - $\beta$ - $\beta$ -linker- $\beta$ - $\beta$ - $\beta$ - $\beta$ - $\alpha$  topology, where each of the four  $\beta$ -strands within a given  $\beta$ - $\beta$ - $\beta$ - $\beta$ - $\alpha$  repeat contributes to the formation of a curved antiparallel  $\beta$ -sheet that packs perpendicularly against the  $\beta$ -sheet from the other repeat (Fig. 2B and Supplementary Fig. S3B). The folds of MRP1 and MRP2 are remarkably similar, despite the fact that their protein sequences display only 18% identity. Both proteins interact with RNA via one of its two  $\beta$ -sheets, mostly by recognizing its phosphate backbone.

### Type II domains fold as inter-molecular dimers

The human replication and transcription cofactor PC4 dimerizes and binds ssDNA through its C-terminal domain (CTD). The crystal structure also revealed that each subunit is formed by a curved four-stranded antiparallel  $\beta$ -sheet followed by a 45° kinked  $\alpha$ -helix (PDB ID: 1pcf) [18] (Fig. 2C and Supplementary Fig. S3C). ssDNA binding cavities are oriented in opposite directions to each other on the surface of both four-stranded  $\beta$ -sheets. Although the two  $\alpha$ -helices of the PC4 CTD dimer can be superimposed onto those of the WHY proteins, the corresponding  $\beta$ -sheet surfaces, which harbour their DNA binding regions, vary considerably in length, curvature and orientation. In addition, the WHY proteins do not possess the high symmetry of their monomers observed in the PC4 dimer [18]. This high symmetry as well as the curvature of its  $\beta$ -sheets allows the PC4 homodimer to form an unusually steep  $\beta$ -ridge, which is rarely present in such a pronounced form in other PC4-like domains. As discussed below, such  $\beta$ -ridges may be functionally important by contributing to dsDNA unwinding [18].

In this context it is also worth mentioning the bacteriophage recombination-dependent DNA replication factor T5 [36]. Besides its function that is similar to the eukaryotic transcription coactivator PC4, both proteins share a sequence identity of 25% (Supplementary Table S2 and Supplementary Fig. S2). Its dimeric structure is extended by two helices in addition to the two conserved helices of the PC4-like fold, yielding the topology of the single repeat to be  $\beta$ - $\beta$ - $\beta$ - $\beta$ - $\alpha$ . The additional helix gives extra

stability to the already swapped dimer (PDB ID: 4bg7; Fig. 2D and Supplementary Fig. S3D).

YdbC is an ssDNA- and RNA-binding protein from the bacterium *Lactococcus lactis* and a member of the DUF2128 family, which also folds into a type II domain structure (PDB ID: 2ltd and 2ltd) [37] (Fig. 2E and Supplementary Fig. S3E). Its ability to bind single-stranded nucleic acids indicates that this class of proteins is not only structurally but also functionally related to the other proteins described here.

The same conclusion can be made after analysing the structure of Pur- $\alpha$  from gram-negative bacteria *Borrelia burgdorferi* (PDB ID: 3n8b) [13] (Fig. 2F and Supplementary Fig. S3F). Apart of its high structural similarity to our search model Pur- $\alpha$  from *D. melanogaster* [14], the ability to bind DNA oligomers with (GGN)<sub>n</sub> sequences has been shown for *B. burgdorferi* Pur- $\alpha$  indicating that this protein is likely also involved in cell cycle control and transcription.

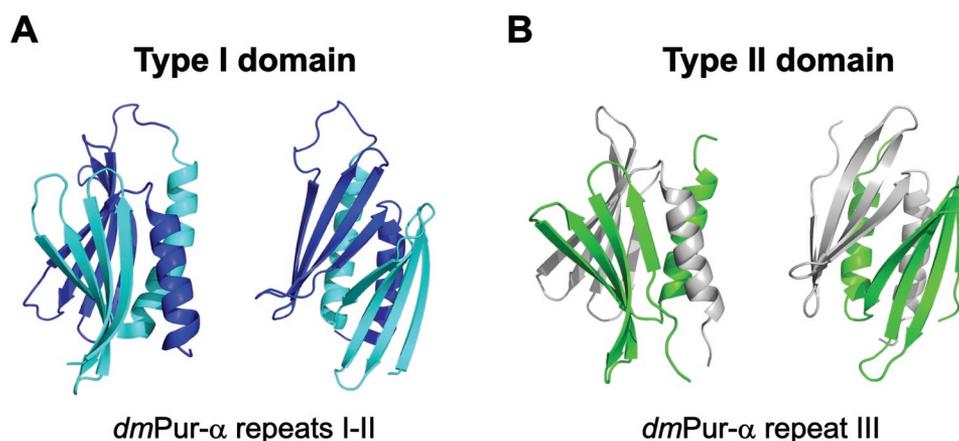
SP\_0782 protein (fragment 7–79) from *Streptococcus pneumoniae* yielded a high score in our structural similarity search ( $Z = 5.1$ ). It is potentially involved in maintenance of genome stability and natural transformation [38]. Its structure has been determined in complex with ssDNA (Northeast Structural Genomics Consortium; PDB ID: 5zkl [39]; Fig. 2G and Supplementary Fig. S3G). Binding of ssDNA to SP\_0782 suggests its potential involvement in gene transcription, recombination, DNA repair or replication.

*Bacteriophage coat protein PP7.* This protein serves as the structurally most dissimilar example for the type II domain fold. The structure of a truncated version of PP7 that is deficient in capsid assembly (PP7 $\Delta$ FG) in complex with a 25-nt RNA hairpin has been solved to 2.4 Å resolution (PDB ID: 2qux) [22]. While the canonical arrangement of secondary structure elements is maintained in this domain, in contrast to all other mentioned examples its two  $\beta$ -sheets form a continuous, flat surface to which dsRNA can bind. Another unique feature of the PP7 $\Delta$ FG protein is that the  $\beta$ -sheet of each repeat is composed of five  $\beta$ -strands and it contains an additional  $\beta$ -loop (Fig. 2H and Supplementary Fig. S3H). The topology of each PP7 $\Delta$ FG monomer is characteristic also for other ssRNA bacteriophage proteins such as the MS2 coat protein [40], the GA coat protein [41], the Q-beta capsid protein [42], and the bacteriophage FR capsid [43].

### Proteins containing both, type I and type II domains

An interesting addition to this theme is offered by the eukaryotic Pur- $\alpha$  protein. This protein is on one hand a transcription factor that binds to ssDNA [5,44–46]. On the other hand, Pur- $\alpha$  has been described as core factor of cytoplasmic mRNA-transport complexes, for which it binds to ssRNA [47–50]. To our knowledge, this DNA- and RNA-binding protein is the only reported factor containing type I as well as type II domains (Fig. 1C).

Pur- $\alpha$  contains three repeating sequence elements in its peptide chain [14,15]. Its N-terminal type I domain is formed by the so-called PUR repeats I and II, whereas its C-terminal type II domain folds via the interaction of two PUR repeats III from two distinct Pur- $\alpha$  molecules [14]. The PUR repeats I–II interact with each other to form a stable domain, in which about 1/3 of the surfaces of each  $\beta$ - $\beta$ - $\beta$ - $\beta$ - $\alpha$  repeat is buried



**Figure 3.** Structure of *Drosophila melanogaster* Pur- $\alpha$  protein exhibiting type I (A) (PUR repeat I-II; PDB ID: 5fgp) [15] and type II (B) (PUR repeat III; PDB ID: 5fgo) [15] PC4-like fold. Each structure is shown in two different orientations. The structure of type I is represented in cyan (repeat I) and navy blue (repeat II), whereas in the structure of type II PC4-like fold individual chains are shown in green and grey. The figure has been prepared in PyMol v 1.3 (pymol.org).

(PDB ID: 3k44 and 5fgp; Fig. 3A and Supplementary Fig. S5A) [14,15]. The overall fold of the type I domain is very similar to its type II domain (PDB ID: 5fgo; Fig. 3B and Supplementary Fig. S5B), with a root mean square deviation (r.m.s.d.) of only 1.5 Å [15]. DNA- and RNA-binding studies combined with biophysical assessment of the oligomeric states of this protein suggest a division of functions between these domains. Although nucleic acid binding of the C-terminal PC4-like domain (type II; consisting of two PUR repeats III) has been demonstrated, the major interaction with nucleic acids seems to be mediated by its N-terminal PC4-like domain (type I; consisting of PUR repeats I–II) [13–15].

In humans, two paralogs of Pur- $\alpha$  have been reported, termed Pur- $\beta$  and Pur- $\gamma$  [51,52]. Based on co-immunoprecipitation experiments with cellular extracts it has been suggested that Pur- $\alpha$  forms heterodimers with Pur- $\beta$  [53] to modulate their respective functions. Based on our knowledge on the homodimerization of Pur- $\alpha$ , such heterodimerization could be formally possible via repeat III.

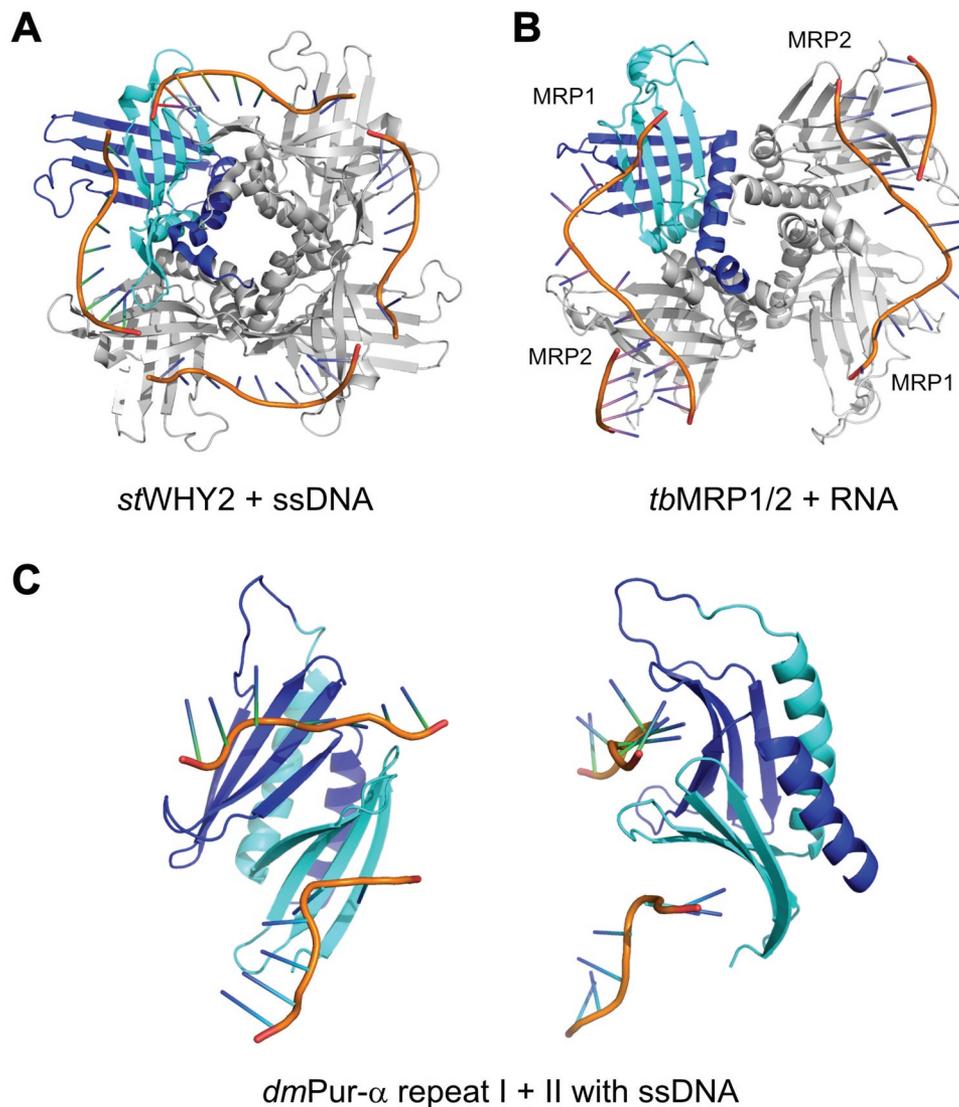
Mutations have been reported in humans that result in a deletion of the C-terminal PC4-like dimerization domain of Pur- $\alpha$  while leaving the more N-terminal DNA/RNA-binding domain intact. Patients with such mutations develop the neurodevelopmental disorder PURA syndrome [12], indicating that in addition to the N-terminal domain oligomerization by its type II domain is important for the function of Pur- $\alpha$ .

### Nucleic-acid binding by type I domains

Dedicated DNA-repair mechanisms are crucial to maintain the integrity of the genetic information. Plant chloroplasts and mitochondria express proteins belonging to the Whirly family, which contribute to DNA repair by binding single-stranded DNA. P24 and other Whirly proteins show high sequence conservation and are present in *Arabidopsis*, tomato and more distantly related species, such as wheat, rice, maize and loblolly pine [24]. The structural studies on the Whirly protein WHY2 from *Solanum tuberosum* in complex with ssDNA (PDB ID: 3n1l, 3n1 k, 3n1 j, 3n1i, and 3ra0) [54,55]

revealed details of its sequence-unspecific ssDNA binding mechanism. In WHY2 proteins, binding of ssDNA is observed primarily in a circular arrangement on the outer edges and in between the  $\beta$ -sheets of adjacent protomers of the Whirly-like tetramer (Fig. 4A and Supplementary Fig. S6A). While most single-stranded nucleic acid binding proteins use the core of their  $\beta$ -sheets as a primary binding platform [28], the WHY2-ssDNA interaction relies mainly on binding of the DNA between properly positioned domains. Binding to ssDNA exploits and is stabilized by the four-fold symmetry of the Whirly tetramer. The mode of ssDNA binding is dominated by stacking and hydrophobic interactions between adjacent nucleobases and between nucleobases and aromatic/hydrophobic protein residues (Supplementary Fig. S6B). Most of the nucleobases have their sequence-specific binding moieties exposed to the solvent, whereas the faces of the nucleobases make intimate contacts with residues of the protein surface [54]. Cappadocia and colleagues proved that the Whirly protein WHY2 can not only bind to melted DNA but actively melts dsDNA [54]. Thus, WHY2 and most likely other plant Whirly family members can destabilize DNA duplexes, probably by binding with a higher affinity to the single-stranded form of DNA and hence shifting the equilibrium in favour of ssDNA.

To assess the versatility of nucleic acid binding by the Whirly domain containing proteins, we also analysed the structure of the MRP1/MRP2 complex involved in kinetoplast RNA editing (PDB ID: 2gje) [21]. This complex also exhibits a tetrameric whirly appearance, but in contrast to the previously described structures, it forms a heterotetramer with affinity to RNA (Fig. 4B and Supplementary Fig. S6C). Despite the lack of sequence homology between MRP1/MRP2 and plant WHY proteins, their similarity in tertiary structure is obvious (Fig. 4A,B). However, there are differences between these two complexes with respect to their binding to nucleic acids. The MRP1/MRP2 complex interacts with the phosphate backbone of the RNA via its  $\beta$ -sheet, while the RNA bases are exposed to the solvent (Supplementary Fig. S6D). As a consequence, there are no base stacking or base-specific interactions observed between MRP1, MRP2 and RNA. Surprisingly, the MRP domains bind RNAs with nanomolar affinity despite their



**Figure 4.** DNA/RNA binding by type I PC4-like domains. The coordinates taken from: (A) *Solanum tuberosum* WHY2 in complex with ssDNA (PDB ID: 3n1l) [54], (B) *Trypanosoma brucei* MRP1/MRP2 complex with RNA (PDB ID: 2gje) [21], (C) *Drosophila melanogaster* Pur- $\alpha$  repeat I–II in complex with ssDNA (PDB ID: 5fgp) [15]. The figure has been prepared in PyMol v 1.3 (pymol.org).

lack of sequence specificity [21,56–58]. These binding features are different from the WHY2-DNA complex, where ssDNA is observed primarily on the edges and in between the  $\beta$ -sheets of adjacent protomers (compare Fig. 4A,B) [54,55].

Whereas MRP1/MRP2 binds ssRNA, WHY2 has been shown to bind ssDNA as well as to unwind dsDNA. Eukaryotic Pur- $\alpha$  combines the functions of both protein classes. Pur- $\alpha$  repeats I and II fold into the N-terminal, PC4-like nucleic acid binding domain that mediates sequence-specific binding to ssDNA, dsDNA, and ssRNA, with a reported preference for GGN repeats [48,51,59]. NMR titration experiments of *Drosophila* Pur- $\alpha$  repeat I–II with CGG repeats revealed almost indistinguishable chemical shift perturbations for DNA and RNA. This finding and very similar  $K_D$  values for CGG DNA and RNA indicate the same mode of binding for both types of nucleic acids [15]. Furthermore, the crystal structure of *Drosophila* Pur- $\alpha$  repeat I–II in complex with the GCGGCGG ssDNA (Fig. 4C and Supplementary Fig. S6E) reveals that one molecule of Pur- $\alpha$  repeat I–II can bind two molecules of ssDNA via base-specific

contacts to guanines [15] (Supplementary Fig. S6F). Both binding events appear at overlapping but non-identical surface regions and therefore might prefer different nucleic-acid motifs as has been previously suggested [48].

Besides its ability to bind RNA and DNA, eukaryotic Pur- $\alpha$  possesses dsDNA-destabilizing activity in an ATP-independent fashion [60]. It was suggested that this feature enables Pur- $\alpha$  to open up dsDNA at the replication fork, thus explaining its requirement in cell division. The crystal structure of *Drosophila* Pur- $\alpha$  in complex with DNA offered an explanation for its unwindase activity [15]. Most likely spontaneous breathing of odd dsDNA helices allows Pur- $\alpha$  to intercalate between both strands and to stabilize ssDNA. Since Pur- $\alpha$  forms a dimer, two domains with unwindase activity (i.e. repeats I–II) would be able to act in close vicinity on the DNA, allowing for unwinding of a larger DNA region (Supplementary Fig. S4B). Such locally melted DNA regions could then be further unwound by ATP-dependent DNA helicases. Since in NMR and binding experiments no difference in binding to DNA and RNA was observed for Pur- $\alpha$ , this

mechanism could in principle also apply to dsRNA unwinding. Consistent with such a function is the report that *Drosophila* Pur- $\alpha$  interacts with the RNA helicase Rm62 [61].

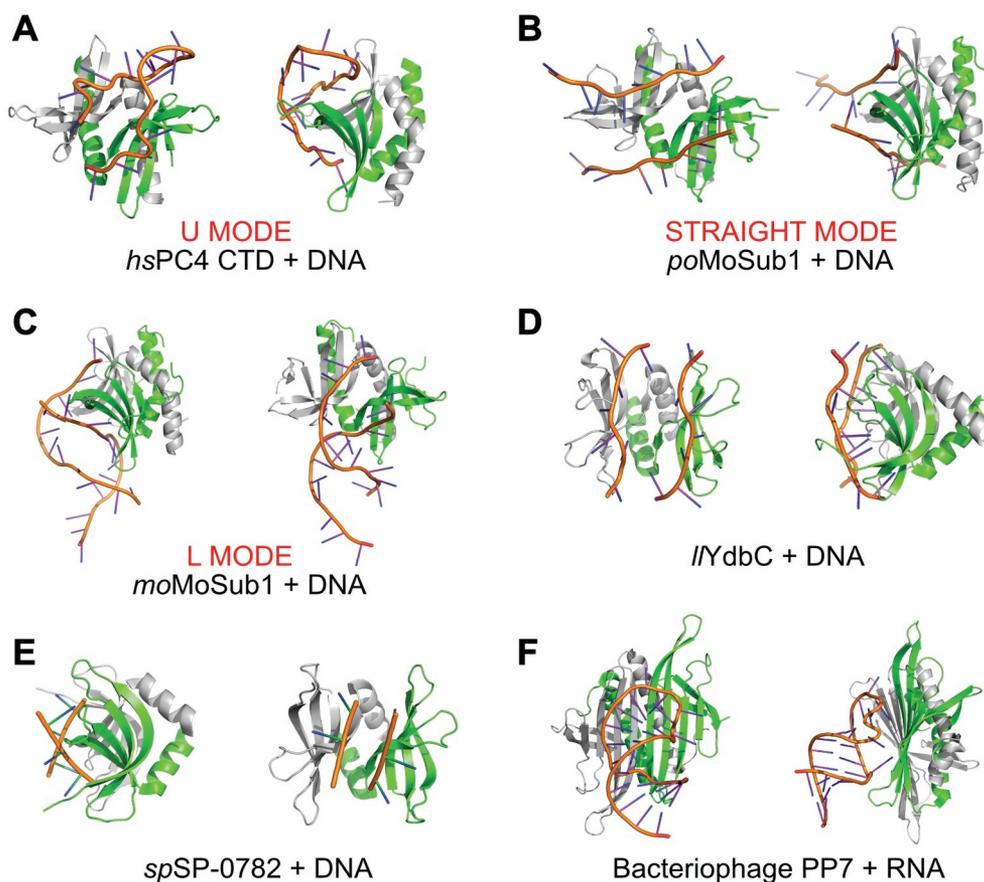
### Nucleic-acid binding by type II domains

The human replication and transcription cofactor PC4 dimerizes, adopting a type II domain fold, and binds ssDNA through its C-terminal domain (CTD). A crystal structure of the human PC4 CTD in complex with a single-stranded 20-mer DNA was solved by Werten and Moras [62]. It revealed how symmetry-related  $\beta$ -sheets of the PC4 CTD homodimer interact with juxtaposed five nucleotide-long DNA strands running in opposite directions (Fig. 5A and Supplementary Fig. S7A). Such melted DNA is bound with higher affinity than regular ssDNA in a sequence-independent manner [62,63]. Similar to the observed DNA binding by Pur- $\alpha$ , several DNA bases are involved in stacking interactions with the aromatic side chains of PC4 CTD (Supplementary Fig. S7B). For binding by two PC4 monomers of the same dimer ssDNA adopts a U-like shape (U mode) (Fig. 5A and Supplementary Fig. S7A) [64,65].

Another interesting example of versatile ssDNA binding is MoSub1, whose co-structure with ssDNA (PDB ID: 4bhm) exhibits an extended, straight conformation of two individual DNA strands (Fig. 5B and Supplementary Fig. S7C and S7D) [66]. In

the crystal packing two neighbouring MoSub1 dimers are linked to another by their bound ssDNA. This observation suggests that complementary strands of longer unwound regions interact with multimers of MoSub1 by forming a continuous left-handed double helix around a central protein filament. Such a filament could grow as the DNA unwinds further and additional MoSub1 homodimers join in (Supplementary Fig. S4C). DNA-dependent multimerization of MoSub1 homodimers is likely to be the driving force for the experimentally observed ATP-independent unwinding of duplex DNA by PC4 domains *in vitro* [62]. Similar modes of multimerization-driven unwinding have also been proposed for other ssDNA-binding proteins [67]. The MoSub1 ortholog from rice blast fungus shows another mode of nucleic acid binding (PDB ID: 5zg9) [65]. Here, the dT<sub>19</sub> G ssDNA is bound between two MoSub1 dimers, thereby connecting them (Fig. 5C, Supplementary Figs. S7E, S7F and S4D). The bound ssDNA adopts an L-like conformation, termed here L mode.

Also YdbC from *Lactococcus lactis*, which is a multifunctional nucleic acid-binding protein of the DUF2128 family, binds ssDNA in a straight mode (PDB ID: 2ltt) [37] (Fig. 5D and Supplementary Fig. S8A and S8B). With its type II fold, YdbC has remarkable structural similarity to the PC4 CTD and the Pur- $\alpha$  domains (Supplementary Table S1). The ability of YdbC dimers to bind to ssDNA with nanomolar affinities and thus the potential



**Figure 5.** DNA/RNA binding by type II PC4-like fold proteins. The coordinates are taken from: (A) *hsPC4* CTD in complex with ssDNA (U mode; PDB ID: 2c62) [64], (B) *Pyricularia oryzae* MoSub1 in complex with ssDNA (Straight mode; PDB ID: 4bhm) [66], (C) *Magnaporthe oryzae* MoSub1 in complex with ssDNA (L mode; PDB ID: 5zg9) [65], (D) *Lactococcus lactis* Ydbc in complex with ssDNA (PDB ID: 2ltt) [37], (E) *Streptococcus pneumoniae* SP\_0782 protein in complex with ssDNA dT12 (PDB ID: 5zkl) [39], (F) *Pseudomonas* phage protein PP7 in complex with RNA (PDB ID: 2qux) [22]. The figure has been prepared in PyMol v 1.3 (pymol.org).

to disrupt DNA duplexes indicates that these proteins also share strong functional similarities to the other proteins described here.

Very recently, DNA binding has been shown also for SP\_0782 protein (fragment 7–79) from *S. pneumoniae*. The complex of this protein with single stranded DNA dT12 (Northeast Structural Genomics Consortium; PDB ID: 5zkl [39]) shows a straight mode of DNA binding (Fig. 5E and Supplementary Fig. S8C and S8D).

The bacteriophage PP7ΔFG homodimer forms a type II domain, whose co-structure with a 25-nt translational operator RNA hairpin has been solved at 2.4 Å resolution (PDB ID: 2qux) [22] (Fig. 5F and Supplementary Fig. S8E and S8F). The anti-parallel association of two PP7ΔFG protomers form a ten-stranded, flat β-sheet that is not suited to separate two ssRNA strands. Instead, this protein interacts with a double-stranded RNA stem-loop. Although also other bacteriophage coat proteins such as MS2 share similar protein scaffolds, their RNA-binding surfaces have evolved to recognize distinct asymmetric RNA hairpins in a sequence-specific mode [22,23,68,69].

PP7 and MS2 were not classified in SCOP and CATH as members of the PC4-like family, however their folds as well as functional features suggest that these proteins belong to the PC4-like family. In addition, a critical argument for including them in the PC4-like family is their helix swapping feature. It is present in all members of the PC4-like family and stabilizes their domain fold.

In addition to the cases discussed above, we found other examples that did not pass our criteria to be classified as a member of the PC4-like family, but constitute interesting cases with considerable similarities to this family of proteins. For an example, see Supplementary Text and Supplementary Fig. S4E.

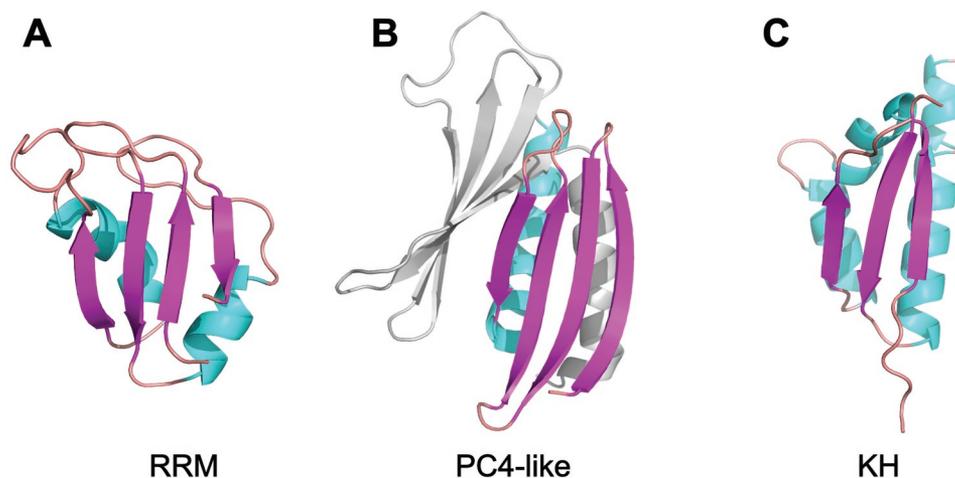
## Discussion

From the examples given above a picture emerges in which PC4-like domains show a conserved fold and a function in nucleic acids binding. The presence or absence of the β-ridge and the additional secondary structure elements, the length of the β-strands, curvature of the β-sheets and their relative

orientation affect the binding preferences, stoichiometry of the formed complexes with the nucleic acids as well as an oligomeric state of the PC4-like domains. Since no significant sequence similarity has been found between most members of this superfamily, it seems likely that the PC4-like fold with its RNA/DNA binding properties evolved independently in all kingdoms of life.

A common feature of many nucleic acid binding proteins, especially RNA binding proteins, is a curved β-sheet surface, which serves as binding site for extended RNAs [70]. For PC4-like domains with nucleic acids binding properties, we found a great variation in their shapes of β-sheets. Symmetric β-sheets with rather shallow curvatures are observed in the P24 subunit of PBF-2 (Fig. 2A). Both, the type I and II domains of Pur-α show β-sheets with a modest curvature, while keeping the overall two-fold symmetry of the molecule (Figs. 2F, 3A,B & 4C). In the human replication and transcription cofactor PC4 (Figs. 2C & 5A), DUF2128 family member YdbC (Figs. 2E & 5D) as well as in SP\_0782 protein (Figs. 2G & 5E) the domain still shows high symmetry but its β-sheets show a significantly stronger curvature. In other cases, the β-sheets differ in their orientation towards each other, resulting in asymmetric domains. For instance, in *st*WHY2 (Fig. 4A), as well as in *tb*MRP1/MRP2 (Fig. 4B) one β-sheet is rather planar while the second one tends to wrap around it. This lack of symmetry limits the domain to bind only one ssDNA/RNA chain. Based on the cases reported here, such asymmetric features appear to be constrained to type I domains, as to our knowledge only symmetric homodimers of type II domains have been reported yet. Since many of the examples described in the manuscript are proteins involved in DNA unwinding, we assume that high symmetry of the PC4-like fold would be favourable. As observed from all the examples, this high symmetry can be achieved by assembling homodimer from two identical repeats.

In cases of WHY2 and MRP1/MRP2 their symmetries are increased by forming higher order oligomers and thus allowing for unwinding of double-stranded nucleic acids. Even for Pur-α, whose N-terminal type I domain already has a symmetric fold (Fig. 3A), dimerization via its C-terminal PUR repeat III might



**Figure 6.** Structural comparison of the scaffold of the RNA binding domains: (A) RRM (PDB ID: 2up1) [79], (B) PC4-like domain (PDB ID: 3k44) [14], and (C) KH domain (PDB ID: 6gqe) [80]. The figure has been prepared in *PyMol* v 1.3 (pymol.org).

help to render unwinding more efficient [14,15]. Upon dimerization, two N-terminal domains are brought into close vicinity, potentially allowing for cooperativity of their unwinding activity (Supplementary Fig. S4B).

$\beta$ -sheets of nucleic acids binding proteins are common interaction surfaces for RNAs and to a much lesser extent also for DNAs [70]. Similar to PC4-like domains, several of these domains stabilize the folding of their  $\beta$ -sheets via interactions with  $\alpha$ -helices. For instance, the RNA recognition motif (RRM) is a protein domain consisting of a four-stranded  $\beta$ -sheet, which accommodates nucleic acids on its curved surface [71–77]. Despite different topology ( $\beta$ - $\alpha$ - $\beta$ - $\alpha$ - $\beta$ ), the three-dimensional arrangement of the four  $\beta$ -strands and one or more  $\alpha$ -helices in an RRM domain resembles a single repeat of the PC4-like scaffold (Fig. 6A,B). Similar to the PC4-like scaffold, RRM shows high versatility in RNA sequence and shape recognition [78]. Considering these structural and functional similarities, one may speculate that the RRM and PC4-like folds co-evolved. In contrast to these examples, KH-domains with  $\beta$ - $\alpha$ -( $\alpha$ )- $\beta$ - $\beta$ - $\alpha$  topology do not interact with the nucleic acids via their  $\beta$ -sheet surfaces. However, it is interesting to note that also this domain, with its three-stranded  $\beta$ -sheet and two or three associated helices, has a related three-dimensional orientation of secondary structure elements (Fig. 6C). It seems obvious that during evolution domains with a  $\beta$ -sheet and associated  $\alpha$ -helices have proven particularly useful for RNA interactions.

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## Availability

*Dali* server used for the analysis described in this manuscript is available under this link: [http://ekhidna2.biocenter.helsinki.fi/dali/\(16\)](http://ekhidna2.biocenter.helsinki.fi/dali/(16))

*Clustal Omega* software for sequence comparison as well as a phylogenetic tree calculation is available here: <https://www.ebi.ac.uk/Tools/msa/clustalo/>

## Disclosure statement

No potential conflict of interest was reported by the authors.

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