

## Proteopedia Entry: Coiled-coil Structure of Keratins

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Type I and type II keratins represent a large family of proteins that are encoded by 54 genes in the human genome. Matched pairs of these keratins form heterodimers that constitute the basic building blocks of cytoskeletal intermediate filaments and epidermal derivatives of hair, nail and horn. Keratins have an important place in the history of the elucidation of protein structure as in 1951, Pauling et al. suggested the first model for  $\alpha$ -helix structure for wool  $\alpha$ -keratins, in the absence of knowledge of the sequence of keratins [1]. The first sequence of a cytoskeletal keratin was determined in 1982 [2]. By analyzing the sequences of type I and type II keratins using secondary structure prediction methods Hanukoglu and Fuchs suggested a model for the structure of keratins and other intermediate filaments proteins [3]. This model depicted a conserved central  $\sim$ 310 residue long rod with four helical domains and highly variable N and C terminal domains that were suggested to participate in linking of subunits and interaction with other proteins. Keratins are very difficult to solubilize as they readily form clusters even in denaturing urea solutions. To partially overcome this problem in 2012, Lee et al. coexpressed the longest helical segment 2B from a pair of keratins (K14 and K5) and determined the first crystal structure of a keratin helical segment [4]. The coiled-coil helical structure of this 2B segment is shown in Fig. 1. This structure confirms the four helix model suggested by secondary structure predictions [3]. The Proteopedia entry presents interactive views of the keratin helical structure and the roles of hydrophobic residues as opposed to charged residues in the formation of coiled-coil structure of filaments.

Incorporation of keratins in biochemistry and molecular biology courses could contribute to the understanding of the principles of protein structure, families of homologous proteins and the evolution of the genes that encode for them, and formation of the cytoskeletal scaffold in cell biology.

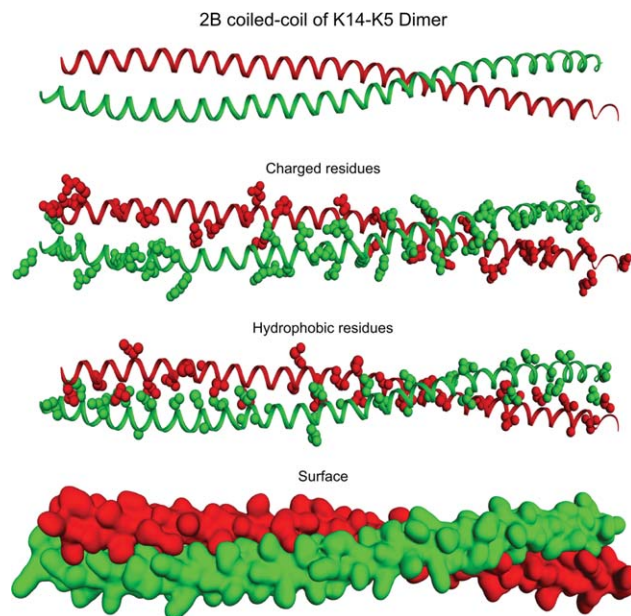


FIG 1

Coiled-coil structure of 2B helical segments of type I keratin K14 (red) and type II keratin K5 (green) from PDB 3TNU [4]. For charged and hydrophobic residues only the R groups are shown. Note that while the R groups of charged residues are rarely in close proximity, the R-groups of many hydrophobic residues are in contact along the interface of the two keratins. The surface model, based on the van der Waals (VDW) radius of atoms, shows the tight coupling between the two proteins.

ogy. Coiled-coil structures are widespread in the biological world [5], and keratins represent simple examples to illustrate the forces that bind these structures. Sequence based prediction of keratin structural domains can be taught as an illustrative example of the usefulness of protein structure prediction methods.

Link: <http://proteopedia.org/wiki/index.php/Keratins>

### References

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Received 12 September 2013; accepted 16 September 2013  
DOI 10.1002/bmb.20746

Published online 22 November 2013 in Wiley Online Library  
(wileyonlinelibrary.com)



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