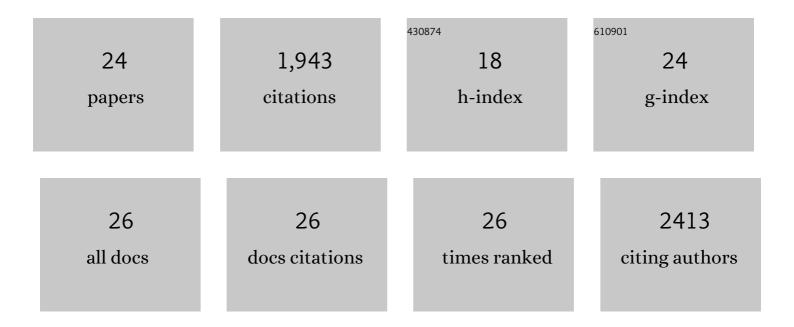
## Andrew R Thomson

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/2905589/publications.pdf Version: 2024-02-01



#	Article	IF	CITATIONS
1	Computational design of water-soluble α-helical barrels. Science, 2014, 346, 485-488.	12.6	306
2	A Basis Set of <i>de Novo</i> Coiled-Coil Peptide Oligomers for Rational Protein Design and Synthetic Biology. ACS Synthetic Biology, 2012, 1, 240-250.	3.8	226
3	A de novo peptide hexamer with a mutable channel. Nature Chemical Biology, 2011, 7, 935-941.	8.0	172
4	Installing hydrolytic activity into a completely de novo protein framework. Nature Chemistry, 2016, 8, 837-844.	13.6	172
5	De novo protein design: how do we expand into the universe of possible protein structures?. Current Opinion in Structural Biology, 2015, 33, 16-26.	5.7	150
6	Modular Design of Self-Assembling Peptide-Based Nanotubes. Journal of the American Chemical Society, 2015, 137, 10554-10562.	13.7	137
7	New currency for old rope: from coiled-coil assemblies to α-helical barrels. Current Opinion in Structural Biology, 2012, 22, 432-441.	5.7	130
8	CCBuilder: an interactive web-based tool for building, designing and assessing coiled-coil protein assemblies. Bioinformatics, 2014, 30, 3029-3035.	4.1	103
9	A monodisperse transmembrane Î $\pm$ -helical peptide barrel. Nature Chemistry, 2017, 9, 411-419.	13.6	97
10	Functionalized α-Helical Peptide Hydrogels for Neural Tissue Engineering. ACS Biomaterials Science and Engineering, 2015, 1, 431-439.	5.2	59
11	Constructing ion channels from water-soluble α-helical barrels. Nature Chemistry, 2021, 13, 643-650.	13.6	59
12	Controlling the Assembly of Coiled–Coil Peptide Nanotubes. Angewandte Chemie - International Edition, 2016, 55, 987-991.	13.8	53
13	ISAMBARD: an open-source computational environment for biomolecular analysis, modelling and design. Bioinformatics, 2017, 33, 3043-3050.	4.1	48
14	Maintaining and breaking symmetry in homomeric coiled-coil assemblies. Nature Communications, 2018, 9, 4132.	12.8	45
15	Navigating the Structural Landscape of De Novo α-Helical Bundles. Journal of the American Chemical Society, 2019, 141, 8787-8797.	13.7	42
16	The Ubiquitin C-Terminal Hydrolase L1 (UCH-L1) C Terminus Plays a Key Role in Protein Stability, but Its Farnesylation Is Not Required for Membrane Association in Primary Neurons. Journal of Biological Chemistry, 2014, 289, 36140-36149.	3.4	33
17	Hydra Mesoglea Proteome Identifies Thrombospondin as a Conserved Component Active in Head Organizer Restriction. Scientific Reports, 2018, 8, 11753.	3.3	30
18	Membrane-spanning α-helical barrels as tractable protein-design targets. Philosophical Transactions of the Royal Society B: Biological Sciences, 2017, 372, 20160213.	4.0	26

#	Article	IF	CITATIONS
19	Applying graph theory to protein structures: an Atlas of coiled coils. Bioinformatics, 2018, 34, 3316-3323.	4.1	17
20	Controlling the Assembly of Coiled–Coil Peptide Nanotubes. Angewandte Chemie, 2016, 128, 999-1003.	2.0	13
21	Construction of a Chassis for a Tripartite Protein-Based Molecular Motor. ACS Synthetic Biology, 2017, 6, 1096-1102.	3.8	11
22	β-Turn Mimics by Chemical Ligation. Organic Letters, 2020, 22, 4424-4428.	4.6	7
23	How Coiled-Coil Assemblies Accommodate Multiple Aromatic Residues. Biomacromolecules, 2021, 22, 2010-2019.	5.4	5
24	Structured cyclic peptide mimics by chemical ligation. Peptide Science, 2022, 114, .	1.8	1