Nicholas Michael Ian Taylor

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Structural basis of torque generation in the bi-directional bacterial flagellar motor. Trends in Biochemical Sciences, 2022, 47, 160-172.	7.5	35
2	Cryo-EM structure of native human thyroglobulin. Nature Communications, 2022, 13, 61.	12.8	9
3	Bacterial Swimming. Inference, 2022, 7, .	0.0	0
4	Tail Structure and Dynamics. , 2021, , 186-193.		0
5	Structural basis for recognition of bacterial cell wall teichoic acid by pseudo-symmetric SH3b-like repeats of a viral peptidoglycan hydrolase. Chemical Science, 2021, 12, 576-589.	7.4	11
6	Structure and Function of Stator Units of the Bacterial Flagellar Motor. Cell, 2020, 183, 244-257.e16.	28.9	151
7	Membrane Protein Cryo-EM: Cryo-Grid Optimization and Data Collection with Protein in Detergent. Methods in Molecular Biology, 2020, 2127, 227-244.	0.9	4
8	FAM111 protease activity undermines cellular fitness and is amplified by gainâ€ofâ€function mutations in human disease. EMBO Reports, 2020, 21, e50662.	4.5	37
9	Structure and Function of the Branched Receptor-Binding Complex of Bacteriophage CBA120. Journal of Molecular Biology, 2019, 431, 3718-3739.	4.2	67
10	Structure and transformation of bacteriophage A511 baseplate and tail upon infection of <i>Listeria</i> Âcells. EMBO Journal, 2019, 38, .	7.8	34
11	Cryo-EM structure of the rhodopsin-Gαi-βγ complex reveals binding of the rhodopsin C-terminal tail to the gβ subunit. ELife, 2019, 8, .	6.0	52
12	Two new polymorphic structures of human full-length alpha-synuclein fibrils solved by cryo-electron microscopy. ELife, 2019, 8, .	6.0	220
13	Contractile injection systems of bacteriophages and related systems. Molecular Microbiology, 2018, 108, 6-15.	2.5	119
14	Structural basis of small-molecule inhibition of human multidrug transporter ABCG2. Nature Structural and Molecular Biology, 2018, 25, 333-340.	8.2	258
15	Cryo-EM structures of a human ABCG2 mutant trapped in ATP-bound and substrate-bound states. Nature, 2018, 563, 426-430.	27.8	188
16	Cryo-EM structure of alpha-synuclein fibrils. ELife, 2018, 7, .	6.0	444
17	Cryo-EM of the Bacteriophage Tail Tube at Better than 3.5 Ã Resolution. Biophysical Journal, 2017, 112, 573a-574a.	0.5	1
18	Structure of the human multidrug transporter ABCG2. Nature, 2017, 546, 504-509.	27.8	332

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19	Refined Cryo-EM Structure of the T4 Tail Tube: Exploring the Lowest Dose Limit. Structure, 2017, 25, 1436-1441.e2.	3.3	40
20	Structure of the T4 baseplate and its function in triggering sheath contraction. Nature, 2016, 533, 346-352.	27.8	231
21	Architecture of TFIIIC and its role in RNA polymerase III pre-initiation complex assembly. Nature Communications, 2015, 6, 7387.	12.8	57
22	Solving the RNA polymerase I structural puzzle. Acta Crystallographica Section D: Biological Crystallography, 2014, 70, 2570-2582.	2.5	23
23	Backstage the RNA Polymerase I Structure: The Art of Crystallography. Acta Crystallographica Section A: Foundations and Advances, 2014, 70, C330-C330.	0.1	0
24	Crystal structure of the 14-subunit RNA polymeraseÂl. Nature, 2013, 502, 644-649.	27.8	179
25	RNA polymerase III-specific general transcription factor IIIC contains a heterodimer resembling TFIIF Rap30/Rap74. Nucleic Acids Research, 2013, 41, 9183-9196.	14.5	23
26	Structural and Functional Characterization of a Phosphatase Domain within Yeast General Transcription Factor IIIC. Journal of Biological Chemistry, 2013, 288, 15110-15120.	3.4	13
27	The Elongator subcomplex Elp456 is a hexameric RecA-like ATPase. Nature Structural and Molecular Biology, 2012, 19, 314-320.	8.2	85
28	Structural studies of the RNA polymerase III transcription factor IIIC. Acta Crystallographica Section A: Foundations and Advances, 2011, 67, C821-C821.	0.3	0