

# Cyril F Reboul

## List of Publications by Year in descending order

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Version: 2024-02-01

31  
papers

1,221  
citations

471061

17  
h-index

433756

31  
g-index

33  
all docs

33  
docs citations

33  
times ranked

2051  
citing authors

#	ARTICLE	IF	CITATIONS
1	Stepwise visualization of membrane pore formation by suliyisin, a bacterial cholesterol-dependent cytolysin. <i>ELife</i> , 2014, 3, e04247.	2.8	145
2	Conformational Changes during Pore Formation by the Perforin-Related Protein Pleurotolysin. <i>PLoS Biology</i> , 2015, 13, e1002049.	2.6	114
3	Structure of the poly-C9 component of the complement membrane attack complex. <i>Nature Communications</i> , 2016, 7, 10588.	5.8	112
4	Critical differences in 3D atomic structure of individual ligand-protected nanocrystals in solution. <i>Science</i> , 2020, 368, 60-67.	6.0	103
5	X-ray crystal structure of the streptococcal specific phage lysin PlyC. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 12752-12757.	3.3	80
6	Stonefish toxin defines an ancient branch of the perforin-like superfamily. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 15360-15365.	3.3	69
7	Giant MACPF/CDC pore forming toxins: A class of their own. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2016, 1858, 475-486.	1.4	61
8	Mastering the Canonical Loop of Serine Protease Inhibitors: Enhancing Potency by Optimising the Internal Hydrogen Bond Network. <i>PLoS ONE</i> , 2011, 6, e19302.	1.1	61
9	Epitope Flexibility and Dynamic Footprint Revealed by Molecular Dynamics of a pMHC-TCR Complex. <i>PLoS Computational Biology</i> , 2012, 8, e1002404.	1.5	54
10	Single-particle cryo-EM: Improved <i>ab initio</i> 3D reconstruction with SIMPLE/PRIME. <i>Protein Science</i> , 2018, 27, 51-61.	3.1	53
11	MUSTANG-MR Structural Sieving Server: Applications in Protein Structural Analysis and Crystallography. <i>PLoS ONE</i> , 2010, 5, e10048.	1.1	47
12	Cofactor-dependent conformational heterogeneity of GAD65 and its role in autoimmunity and neurotransmitter homeostasis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, E2524-E2529.	3.3	34
13	A New Model for Pore Formation by Cholesterol-Dependent Cytolysins. <i>PLoS Computational Biology</i> , 2014, 10, e1003791.	1.5	33
14	Crystal, Solution and In silico Structural Studies of Dihydrodipicolinate Synthase from the Common Grapevine. <i>PLoS ONE</i> , 2012, 7, e38318.	1.1	32
15	Crystallographic and Molecular Dynamics Analysis of Loop Motions Unmasking the Peptidoglycan-Binding Site in Stator Protein MotB of Flagellar Motor. <i>PLoS ONE</i> , 2011, 6, e18981.	1.1	28
16	Predicting giant transmembrane $\beta$ -barrel architecture. <i>Bioinformatics</i> , 2012, 28, 1299-1302.	1.8	25
17	SIMPLE 3.0. Stream single-particle cryo-EM analysis in real time. <i>Journal of Structural Biology: X</i> , 2020, 4, 100040.	0.7	23
18	A Stochastic Hill Climbing Approach for Simultaneous 2D Alignment and Clustering of Cryogenic Electron Microscopy Images. <i>Structure</i> , 2016, 24, 988-996.	1.6	22

#	ARTICLE	IF	CITATIONS
19	Correlating 3D Surface Atomic Structure and Catalytic Activities of Pt Nanocrystals. Nano Letters, 2021, 21, 1175-1183.	4.5	20
20	S1 Pocket of a Bacterially Derived Subtilisin-like Protease Underpins Effective Tissue Destruction. Journal of Biological Chemistry, 2011, 286, 42180-42187.	1.6	17
21	Structural and Dynamic Requirements for Optimal Activity of the Essential Bacterial Enzyme Dihydrodipicolinate Synthase. PLoS Computational Biology, 2012, 8, e1002537.	1.5	16
22	SINGLE: Atomic-resolution structure identification of nanocrystals by graphene liquid cell EM. Science Advances, 2021, 7, .	4.7	13
23	Rapid near-atomic resolution single-particle 3D reconstruction with SIMPLE. Journal of Structural Biology, 2018, 204, 172-181.	1.3	11
24	Predicting Serpin/Protease Interactions. Methods in Enzymology, 2011, 501, 237-273.	0.4	7
25	Computational Methods for Studying Serpin Conformational Change and Structural Plasticity. Methods in Enzymology, 2011, 501, 295-323.	0.4	5
26	Substrate Locking Promotes Dimer-Dimer Docking of an Enzyme Antibiotic Target. Structure, 2018, 26, 948-959.e5.	1.6	5
27	Point-group symmetry detection in three-dimensional charge density of biomolecules. Bioinformatics, 2020, 36, 2237-2243.	1.8	5
28	Dynamic Motion and Communication in the Streptococcal C1 Phage Lysin, PlyC. PLoS ONE, 2015, 10, e0140219.	1.1	3
29	MrGrid: A Portable Grid Based Molecular Replacement Pipeline. PLoS ONE, 2010, 5, e10049.	1.1	2
30	SAGA and SAGA-like SLIK transcriptional coactivators are structurally and biochemically equivalent. Journal of Biological Chemistry, 2021, 296, 100671.	1.6	2
31	High-throughput protein structure determination using grid computing. , 2009, , .		1