

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	SINGLE: Atomic-resolution structure identification of nanocrystals by graphene liquid cell EM. <i>Science Advances</i> , 2021, 7, .	4.7	13
2	SAGA and SAGA-like SLIK transcriptional coactivators are structurally and biochemically equivalent. <i>Journal of Biological Chemistry</i> , 2021, 296, 100671.	1.6	2
3	Correlating 3D Surface Atomic Structure and Catalytic Activities of Pt Nanocrystals. <i>Nano Letters</i> , 2021, 21, 1175-1183.	4.5	20
4	Point-group symmetry detection in three-dimensional charge density of biomolecules. <i>Bioinformatics</i> , 2020, 36, 2237-2243.	1.8	5
5	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
6	Critical differences in 3D atomic structure of individual ligand-protected nanocrystals in solution. <i>Science</i> , 2020, 368, 60-67.	6.0	103
7	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
8	Substrate Locking Promotes Dimer-Dimer Docking of an Enzyme Antibiotic Target. <i>Structure</i> , 2018, 26, 948-959.e5.	1.6	5
9	Rapid near-atomic resolution single-particle 3D reconstruction with SIMPLE. <i>Journal of Structural Biology</i> , 2018, 204, 172-181.	1.3	11
10	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
11	Structure of the poly-C9 component of the complement membrane attack complex. <i>Nature Communications</i> , 2016, 7, 10588.	5.8	112
12	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
13	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
14	Conformational Changes during Pore Formation by the Perforin-Related Protein Pleurotolysin. <i>PLoS Biology</i> , 2015, 13, e1002049.	2.6	114
15	Dynamic Motion and Communication in the Streptococcal C1 Phage Lysin, PlyC. <i>PLoS ONE</i> , 2015, 10, e0140219.	1.1	3
16	A New Model for Pore Formation by Cholesterol-Dependent Cytolysins. <i>PLoS Computational Biology</i> , 2014, 10, e1003791.	1.5	33
17	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
18	Stepwise visualization of membrane pore formation by suilysin, a bacterial cholesterol-dependent cytolysin. <i>ELife</i> , 2014, 3, e04247.	2.8	145

#	ARTICLE	IF	CITATIONS
19	Epitope Flexibility and Dynamic Footprint Revealed by Molecular Dynamics of a pMHC-TCR Complex. PLoS Computational Biology, 2012, 8, e1002404.	1.5	54
20	Structural and Dynamic Requirements for Optimal Activity of the Essential Bacterial Enzyme Dihydrodipicolinate Synthase. PLoS Computational Biology, 2012, 8, e1002537.	1.5	16
21	Predicting giant transmembrane β^2 -barrel architecture. Bioinformatics, 2012, 28, 1299-1302.	1.8	25
22	X-ray crystal structure of the streptococcal specific phage lysin PlyC. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 12752-12757.	3.3	80
23	Crystal, Solution and In silico Structural Studies of Dihydrodipicolinate Synthase from the Common Grapevine. PLoS ONE, 2012, 7, e38318.	1.1	32
24	Predicting Serpin/Protease Interactions. Methods in Enzymology, 2011, 501, 237-273.	0.4	7
25	S1 Pocket of a Bacterially Derived Subtilisin-like Protease Underpins Effective Tissue Destruction. Journal of Biological Chemistry, 2011, 286, 42180-42187.	1.6	17
26	Computational Methods for Studying Serpin Conformational Change and Structural Plasticity. Methods in Enzymology, 2011, 501, 295-323.	0.4	5
27	Crystallographic and Molecular Dynamics Analysis of Loop Motions Unmasking the Peptidoglycan-Binding Site in Stator Protein MotB of Flagellar Motor. PLoS ONE, 2011, 6, e18981.	1.1	28
28	Mastering the Canonical Loop of Serine Protease Inhibitors: Enhancing Potency by Optimising the Internal Hydrogen Bond Network. PLoS ONE, 2011, 6, e19302.	1.1	61
29	MUSTANG-MR Structural Sieving Server: Applications in Protein Structural Analysis and Crystallography. PLoS ONE, 2010, 5, e10048.	1.1	47
30	MrGrid: A Portable Grid Based Molecular Replacement Pipeline. PLoS ONE, 2010, 5, e10049.	1.1	2
31	High-throughput protein structure determination using grid computing. , 2009, , .		1