

Nathan R Zaccai

List of Publications by Year in descending order

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papers

2,053
citations

331670

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39
docs citations

39
times ranked

2710
citing authors

#	ARTICLE	IF	CITATIONS
1	Strikingly Different Roles of SARS-CoV-2 Fusion Peptides Uncovered by Neutron Scattering. <i>Journal of the American Chemical Society</i> , 2022, 144, 2968-2979.	13.7	30
2	FCHO controls AP2's initiating role in endocytosis through a PtdIns(4,5)P ₂ -dependent switch. <i>Science Advances</i> , 2022, 8, eabn2018.	10.3	14
3	Structures of a deAMPylation complex rationalise the switch between antagonistic catalytic activities of FICD. <i>Nature Communications</i> , 2021, 12, 5004.	12.8	13
4	Mechanism and evolution of the Zn-fingernail required for interaction of VARP with VPS29. <i>Nature Communications</i> , 2020, 11, 5031.	12.8	21
5	Navigating the Structural Landscape of De Novo α -Helical Bundles. <i>Journal of the American Chemical Society</i> , 2019, 141, 8787-8797.	13.7	42
6	Downsizing Proto-oncogene cFos to Short Helix-Constrained Peptides That Bind Jun. <i>ACS Chemical Biology</i> , 2017, 12, 2051-2061.	3.4	43
7	Contribution of the clathrin adaptor AP-1 subunit μ 1 to acidic cluster protein sorting. <i>Journal of Cell Biology</i> , 2017, 216, 2927-2943.	5.2	35
8	A central cavity within the holo-translocon suggests a mechanism for membrane protein insertion. <i>Scientific Reports</i> , 2016, 6, 38399.	3.3	54
9	Structural Basis of the Mispairing of an Artificially Expanded Genetic Information System. <i>CheM</i> , 2016, 1, 946-958.	11.7	17
10	Deuterium Labeling Together with Contrast Variation Small-Angle Neutron Scattering Suggests How Skp Captures and Releases Unfolded Outer Membrane Proteins. <i>Methods in Enzymology</i> , 2016, 566, 159-210.	1.0	46
11	Modular Design of Self-Assembling Peptide-Based Nanotubes. <i>Journal of the American Chemical Society</i> , 2015, 137, 10554-10562.	13.7	137
12	Skp Trimer Formation Is Insensitive to Salts in the Physiological Range. <i>Biochemistry</i> , 2015, 54, 7059-7062.	2.5	20
13	Outer membrane β -barrel protein folding is physically controlled by periplasmic lipid head groups and BamA. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 5878-5883.	7.1	164
14	Membrane protein thermodynamic stability may serve as the energy sink for sorting in the periplasm. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 4285-4290.	7.1	104
15	A Basis Set of <i>de Novo</i> Coiled-Coil Peptide Oligomers for Rational Protein Design and Synthetic Biology. <i>ACS Synthetic Biology</i> , 2012, 1, 240-250.	3.8	226
16	Cryo-transmission electron microscopy structure of a gigadalton peptide fiber of de novo design. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 13266-13271.	7.1	70
17	FKBP12 Activates the Cardiac Ryanodine Receptor Ca ²⁺ -Release Channel and Is Antagonised by FKBP12.6. <i>PLoS ONE</i> , 2012, 7, e31956.	2.5	56
18	A de novo peptide hexamer with a mutable channel. <i>Nature Chemical Biology</i> , 2011, 7, 935-941.	8.0	172

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19	Correlation of in situ mechanosensitive responses of the <i>Moraxella catarrhalis</i> adhesin UspA1 with fibronectin and receptor CEACAM1 binding. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 15174-15178.	7.1	28
20	Crystal structure of a 3-oxoacyl-(acylcarrier protein) reductase (BA3989) from <i>Bacillus anthracis</i> at 2.4 Å resolution. Proteins: Structure, Function and Bioinformatics, 2008, 70, 562-567.	2.6	22
21	Single-Channel Characterization of the Rabbit Recombinant RyR2 Reveals a Novel Inactivation Property of Physiological Concentrations of ATP. Journal of Membrane Biology, 2008, 222, 65-77.	2.1	11
22	Intrinsic fluorescence as an analytical probe of virus-like particle assembly and maturation. Biochemical and Biophysical Research Communications, 2008, 375, 351-355.	2.1	11
23	Crystallographic and in Silico Analysis of the Sialoside-binding Characteristics of the Siglec Sialoadhesin. Journal of Molecular Biology, 2007, 365, 1469-1479.	4.2	30
24	Refolding of a membrane protein in a microfluidics reactor. European Biophysics Journal, 2007, 36, 581-588.	2.2	7
25	Application of high-throughput technologies to a structural proteomics-type analysis of <i>Bacillus anthracis</i> . Acta Crystallographica Section D: Biological Crystallography, 2006, 62, 1267-1275.	2.5	24
26	Assembly of Human Papillomavirus Type-16 Virus-Like Particles: Multifactorial Study of Assembly and Competing Aggregation. Biotechnology Progress, 2006, 22, 554-560.	2.6	32
27	The Crystal Structure of Human CD1b with a Bound Bacterial Glycolipid. Journal of Immunology, 2004, 172, 2382-2388.	0.8	137
28	Structure-Guided Design of Sialic Acid-Based Siglec Inhibitors and Crystallographic Analysis in Complex with Sialoadhesin. Structure, 2003, 11, 557-567.	3.3	97
29	Generation of CD1 tetramers as a tool to monitor glycolipid-specific T cells. Philosophical Transactions of the Royal Society B: Biological Sciences, 2003, 358, 875-877.	4.0	12
30	CD4 T Cells Selected by Antigen Under Th2 Polarizing Conditions Favor an Elongated TCR β Chain Complementarity-Determining Region 3. Journal of Immunology, 2002, 168, 1018-1027.	0.8	17
31	Structure of human CD1b with bound ligands at 2.3 Å, a maze for alkyl chains. Nature Immunology, 2002, 3, 721-726.	14.5	234
32	Killer Cell Immunoglobulin Receptors and T Cell Receptors Bind Peptide-Major Histocompatibility Complex Class I with Distinct Thermodynamic and Kinetic Properties. Journal of Biological Chemistry, 1999, 274, 28329-28334.	3.4	110
33	HLA-B27 and disease pathogenesis: new structural and functional insights. Expert Reviews in Molecular Medicine, 1999, 1, 1-10.	3.9	10
34	Strikingly different roles of SARS-CoV-2 fusion peptides uncovered by SNR, SANS, QENS, and NSE experiments. Neutron News, 0, , 1-2.	0.2	0