

Peter B Rosenthal

List of Publications by Year in descending order

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Version: 2024-02-01

29
papers

5,282
citations

361296

20
h-index

434063

31
g-index

42
all docs

42
docs citations

42
times ranked

8526
citing authors

#	ARTICLE	IF	CITATIONS
1	Evolution of the SARS-CoV-2 spike protein in the human host. Nature Communications, 2022, 13, 1178.	5.8	44
2	High-resolution structures of malaria parasite actomyosin and actin filaments. PLoS Pathogens, 2022, 18, e1010408.	2.1	12
3	Structure and binding properties of Pangolin-CoV spike glycoprotein inform the evolution of SARS-CoV-2. Nature Communications, 2021, 12, 837.	5.8	55
4	Cryo-EM model validation recommendations based on outcomes of the 2019 EMDataResource challenge. Nature Methods, 2021, 18, 156-164.	9.0	73
5	The effect of the D614G substitution on the structure of the spike glycoprotein of SARS-CoV-2. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	3.3	131
6	In situ structure and organization of the influenza C virus surface glycoprotein. Nature Communications, 2021, 12, 1694.	5.8	12
7	SARS-CoV-2 can recruit a heme metabolite to evade antibody immunity. Science Advances, 2021, 7, .	4.7	107
8	A resolution record for cryoEM. Faculty Reviews, 2021, 10, 64.	1.7	1
9	CDK1 controls CHMP7-dependent nuclear envelope reformation. ELife, 2021, 10, .	2.8	19
10	Receptor binding and priming of the spike protein of SARS-CoV-2 for membrane fusion. Nature, 2020, 588, 327-330.	13.7	684
11	Antibody-mediated disruption of the SARS-CoV-2 spike glycoprotein. Nature Communications, 2020, 11, 5337.	5.8	43
12	Structural transitions in influenza haemagglutinin at membrane fusion pH. Nature, 2020, 583, 150-153.	13.7	87
13	SARS-CoV-2 and bat RaTG13 spike glycoprotein structures inform on virus evolution and furin-cleavage effects. Nature Structural and Molecular Biology, 2020, 27, 763-767.	3.6	471
14	Stimulated release of intraluminal vesicles from Weibel-Palade bodies. Blood, 2019, 133, 2707-2717.	0.6	29
15	Structural basis for Fullerene geometry in a human endogenous retrovirus capsid. Nature Communications, 2019, 10, 5822.	5.8	20
16	Influenza hemagglutinin membrane anchor. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 10112-10117.	3.3	115
17	CryoEM structures of open dimers of gyrase A in complex with DNA illuminate mechanism of strand passage. ELife, 2018, 7, .	2.8	26
18	Three-Dimensional Architecture of the Human BRCA1-A Histone Deubiquitinase Core Complex. Cell Reports, 2016, 17, 3099-3106.	2.9	20

#	ARTICLE	IF	CITATIONS
19	Cryomicroscopy provides structural snapshots of influenza virus membrane fusion. <i>Nature Structural and Molecular Biology</i> , 2016, 23, 853-858.	3.6	75
20	Validating maps from single particle electron cryomicroscopy. <i>Current Opinion in Structural Biology</i> , 2015, 34, 135-144.	2.6	50
21	From high symmetry to high resolution in biological electron microscopy: a commentary on Crowther (1971) "Procedures for three-dimensional reconstruction of spherical viruses by Fourier synthesis from electron micrographs". <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2015, 370, 20140345.	1.8	6
22	Web server for tilt-pair validation of single particle maps from electron cryomicroscopy. <i>Journal of Structural Biology</i> , 2014, 186, 122-131.	1.3	18
23	Cryomicroscopy of radiation sensitive specimens on unmodified graphene sheets: Reduction of electron-optical effects of charging. <i>Journal of Structural Biology</i> , 2013, 183, 531-536.	1.3	21
24	Tilt-Pair Analysis of Images from a Range of Different Specimens in Single-Particle Electron Cryomicroscopy. <i>Journal of Molecular Biology</i> , 2011, 413, 1028-1046.	2.0	138
25	Structural organization of a filamentous influenza A virus. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 10685-10690.	3.3	201
26	Structural organization of Weibel-Palade bodies revealed by cryo-EM of vitrified endothelial cells. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 17407-17412.	3.3	72
27	Optimal Determination of Particle Orientation, Absolute Hand, and Contrast Loss in Single-particle Electron Cryomicroscopy. <i>Journal of Molecular Biology</i> , 2003, 333, 721-745.	2.0	2,024
28	Structure of an Influenza Neuraminidase "Diabody Complex by Electron Cryomicroscopy and Image Analysis. <i>Journal of Molecular Biology</i> , 2003, 334, 721-731.	2.0	7
29	Structure of the haemagglutinin-esterase-fusion glycoprotein of influenza C virus. <i>Nature</i> , 1998, 396, 92-96.	13.7	218