

# 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	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
2	Receptor binding and priming of the spike protein of SARS-CoV-2 for membrane fusion. <i>Nature</i> , 2020, 588, 327-330.	13.7	684
3	SARS-CoV-2 and bat RaTG13 spike glycoprotein structures inform on virus evolution and furin-cleavage effects. <i>Nature Structural and Molecular Biology</i> , 2020, 27, 763-767.	3.6	471
4	Structure of the haemagglutinin-esterase-fusion glycoprotein of influenza C virus. <i>Nature</i> , 1998, 396, 92-96.	13.7	218
5	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
6	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
7	The effect of the D614G substitution on the structure of the spike glycoprotein of SARS-CoV-2. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	131
8	Influenza hemagglutinin membrane anchor. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 10112-10117.	3.3	115
9	SARS-CoV-2 can recruit a heme metabolite to evade antibody immunity. <i>Science Advances</i> , 2021, 7, .	4.7	107
10	Structural transitions in influenza haemagglutinin at membrane fusion. <i>Nature</i> , 2020, 583, 150-153.	13.7	87
11	Cryomicroscopy provides structural snapshots of influenza virus membrane fusion. <i>Nature Structural and Molecular Biology</i> , 2016, 23, 853-858.	3.6	75
12	Cryo-EM model validation recommendations based on outcomes of the 2019 EMDataResource challenge. <i>Nature Methods</i> , 2021, 18, 156-164.	9.0	73
13	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
14	Structure and binding properties of Pangolin-CoV spike glycoprotein inform the evolution of SARS-CoV-2. <i>Nature Communications</i> , 2021, 12, 837.	5.8	55
15	Validating maps from single particle electron cryomicroscopy. <i>Current Opinion in Structural Biology</i> , 2015, 34, 135-144.	2.6	50
16	Evolution of the SARS-CoV-2 spike protein in the human host. <i>Nature Communications</i> , 2022, 13, 1178.	5.8	44
17	Antibody-mediated disruption of the SARS-CoV-2 spike glycoprotein. <i>Nature Communications</i> , 2020, 11, 5337.	5.8	43
18	Stimulated release of intraluminal vesicles from Weibel-Palade bodies. <i>Blood</i> , 2019, 133, 2707-2717.	0.6	29

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19	CryoEM structures of open dimers of gyrase A in complex with DNA illuminate mechanism of strand passage. <i>ELife</i> , 2018, 7, .	2.8	26
20	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
21	Three-Dimensional Architecture of the Human BRCA1-A Histone Deubiquitinase Core Complex. <i>Cell Reports</i> , 2016, 17, 3099-3106.	2.9	20
22	Structural basis for Fullerene geometry in a human endogenous retrovirus capsid. <i>Nature Communications</i> , 2019, 10, 5822.	5.8	20
23	CDK1 controls CHMP7-dependent nuclear envelope reformation. <i>ELife</i> , 2021, 10, .	2.8	19
24	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
25	In situ structure and organization of the influenza C virus surface glycoprotein. <i>Nature Communications</i> , 2021, 12, 1694.	5.8	12
26	High-resolution structures of malaria parasite actomyosin and actin filaments. <i>PLoS Pathogens</i> , 2022, 18, e1010408.	2.1	12
27	Structure of an Influenza Neuraminidaseâ€“Diabody Complex by Electron Cryomicroscopy and Image Analysis. <i>Journal of Molecular Biology</i> , 2003, 334, 721-731.	2.0	7
28	From high symmetry to high resolution in biological electron microscopy: a commentary on Crowther (1971) â€“Procedures for three-dimensional reconstruction of spherical viruses by Fourier synthesis from electron micrographsâ€™. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2015, 370, 20140345.	1.8	6
29	A resolution record for cryoEM. <i>Faculty Reviews</i> , 2021, 10, 64.	1.7	1