

Jean-Paul Armache

List of Publications by Year in descending order

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Version: 2024-02-01

32
papers

9,935
citations

279798

23
h-index

395702

33
g-index

38
all docs

38
docs citations

38
times ranked

14770
citing authors

#	ARTICLE	IF	CITATIONS
1	MotionCor2: anisotropic correction of beam-induced motion for improved cryo-electron microscopy. <i>Nature Methods</i> , 2017, 14, 331-332.	19.0	6,166
2	Structure of the TRPA1 ion channel suggests regulatory mechanisms. <i>Nature</i> , 2015, 520, 511-517.	27.8	522
3	Structures of the human and <i>Drosophila</i> 80S ribosome. <i>Nature</i> , 2013, 497, 80-85.	27.8	474
4	Structural Insight into Nascent Polypeptide Chain-Mediated Translational Stalling. <i>Science</i> , 2009, 326, 1412-1415.	12.6	263
5	Structure of Monomeric Yeast and Mammalian Sec61 Complexes Interacting with the Translating Ribosome. <i>Science</i> , 2009, 326, 1369-1373.	12.6	263
6	Structural basis of highly conserved ribosome recycling in eukaryotes and archaea. <i>Nature</i> , 2012, 482, 501-506.	27.8	210
7	A saposin-lipoprotein nanoparticle system for membrane proteins. <i>Nature Methods</i> , 2016, 13, 345-351.	19.0	209
8	Cryo-EM structure and rRNA model of a translating eukaryotic 80S ribosome at 5.5-Å resolution. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 19748-19753.	7.1	196
9	Î±-Helical nascent polypeptide chains visualized within distinct regions of the ribosomal exit tunnel. <i>Nature Structural and Molecular Biology</i> , 2010, 17, 313-317.	8.2	187
10	Structures of the Sec61 complex engaged in nascent peptide translocation or membrane insertion. <i>Nature</i> , 2014, 506, 107-110.	27.8	186
11	Structure of the no-go mRNA decay complex Dom34-Hbs1 bound to a stalled 80S ribosome. <i>Nature Structural and Molecular Biology</i> , 2011, 18, 715-720.	8.2	150
12	Cryo-EM structure of a fungal mitochondrial calcium uniporter. <i>Nature</i> , 2018, 559, 570-574.	27.8	125
13	Localization of eukaryote-specific ribosomal proteins in a 5.5-Å cryo-EM map of the 80S eukaryotic ribosome. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 19754-19759.	7.1	122
14	Structural Basis of Dot1L Stimulation by Histone H2B Lysine 120 Ubiquitination. <i>Molecular Cell</i> , 2019, 74, 1010-1019.e6.	9.7	115
15	Mechanism of eIF6-mediated Inhibition of Ribosomal Subunit Joining. <i>Journal of Biological Chemistry</i> , 2010, 285, 14848-14851.	3.4	107
16	Regulation of the Dot1 histone H3K79 methyltransferase by histone H4K16 acetylation. <i>Science</i> , 2021, 371, .	12.6	70
17	Cryo-EM structures of remodeler-nucleosome intermediates suggest allosteric control through the nucleosome. <i>ELife</i> , 2019, 8, .	6.0	70
18	Promiscuous behaviour of archaeal ribosomal proteins: Implications for eukaryotic ribosome evolution. <i>Nucleic Acids Research</i> , 2013, 41, 1284-1293.	14.5	59

#	ARTICLE	IF	CITATIONS
19	Cryo-EM of multiple cage architectures reveals a universal mode of clathrin self-assembly. <i>Nature Structural and Molecular Biology</i> , 2019, 26, 890-898.	8.2	56
20	Single-particle cryo-EM data acquisition by using direct electron detection camera. <i>Microscopy</i> (Oxford, England), 2016, 65, 35-41.	1.5	46
21	Structural basis for activation of voltage sensor domains in an ion channel TPC1. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E9095-E9104.	7.1	40
22	Proteomic Characterization of Archaeal Ribosomes Reveals the Presence of Novel Archaeal-Specific Ribosomal Proteins. <i>Journal of Molecular Biology</i> , 2011, 405, 1215-1232.	4.2	28
23	Sharing biological data: why, when, and how. <i>FEBS Letters</i> , 2021, 595, 847-863.	2.8	26
24	Nucleosome recognition and DNA distortion by the Chd1 remodeler in a nucleotide-free state. <i>Nature Structural and Molecular Biology</i> , 2022, 29, 121-129.	8.2	21
25	The first single particle analysis Map Challenge: A summary of the assessments. <i>Journal of Structural Biology</i> , 2018, 204, 291-300.	2.8	17
26	Differential ligand-selective control of opposing enzymatic activities within a bifunctional c-di-GMP enzyme. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	7.1	11
27	Solution structure of the natively assembled yeast ribosomal stalk determined by small-angle X-ray scattering. <i>Biochemical Journal</i> , 2012, 444, 205-209.	3.7	10
28	Single-particle cryo-EM: beyond the resolution. <i>National Science Review</i> , 2019, 6, 864-866.	9.5	9
29	The DARC site: a database of aligned ribosomal complexes. <i>Nucleic Acids Research</i> , 2012, 40, D495-D500.	14.5	7
30	Heme-Edge Residues Modulate Signal Transduction within a Bifunctional Homo-Dimeric Sensor Protein. <i>Biochemistry</i> , 2021, 60, 3801-3812.	2.5	4
31	Lake microbiome and trophic fluctuations of the ancient hemp rettery. <i>Scientific Reports</i> , 2022, 12, .	3.3	3
32	The Mechanism of Nucleosome Spacing by a Dimeric Chromatin Remodeling Enzyme. <i>Biophysical Journal</i> , 2014, 106, 69a-70a.	0.5	0