

Bruno P Klaholz

List of Publications by Year in descending order

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Version: 2024-02-01

48
papers

3,083
citations

236925

25
h-index

189892

50
g-index

52
all docs

52
docs citations

52
times ranked

5387
citing authors

#	ARTICLE	IF	CITATIONS
1	New tools for the analysis and validation of cryo-EM maps and atomic models. <i>Acta Crystallographica Section D: Structural Biology</i> , 2018, 74, 814-840.	2.3	575
2	Structure of the human 80S ribosome. <i>Nature</i> , 2015, 520, 640-645.	27.8	406
3	Visualization of chemical modifications in the human 80S ribosome structure. <i>Nature</i> , 2017, 551, 472-477.	27.8	277
4	N6-Methyladenosine methyltransferase ZCCHC4 mediates ribosomal RNA methylation. <i>Nature Chemical Biology</i> , 2019, 15, 88-94.	8.0	258
5	Nuclear position dictates DNA repair pathway choice. <i>Genes and Development</i> , 2014, 28, 2450-2463.	5.9	167
6	Visualization of release factor 3 on the ribosome during termination of protein synthesis. <i>Nature</i> , 2004, 427, 862-865.	27.8	131
7	ClusterViSu, a method for clustering of protein complexes by Voronoi tessellation in super-resolution microscopy. <i>Scientific Reports</i> , 2016, 6, 24084.	3.3	125
8	Câ€“HÃ•Ã•O Hydrogen Bonds in the Nuclear Receptor RARÎ³” a Potential Tool for Drug Selectivity. <i>Structure</i> , 2002, 10, 1197-1204.	3.3	84
9	Structureâ€“function insights reveal the human ribosome as a cancer target for antibiotics. <i>Nature Communications</i> , 2016, 7, 12856.	12.8	75
10	The integrative role of cryo electron microscopy in molecular and cellular structural biology. <i>Biology of the Cell</i> , 2017, 109, 81-93.	2.0	58
11	Structural insight into the mechanism of stabilization of the 7SK small nuclear RNA by LARP7. <i>Nucleic Acids Research</i> , 2015, 43, 3373-3388.	14.5	54
12	Focused classification and refinement in high-resolution cryo-EM structural analysis of ribosome complexes. <i>Current Opinion in Structural Biology</i> , 2017, 46, 140-148.	5.7	53
13	Targeting the Human 80S Ribosome in Cancer: From Structure to Function and Drug Design for Innovative Adjuvant Therapeutic Strategies. <i>Cells</i> , 2020, 9, 629.	4.1	45
14	The molecular structure of the left-handed supra-molecular helix of eukaryotic polyribosomes. <i>Nature Communications</i> , 2014, 5, 5294.	12.8	43
15	Conformation transitions of eukaryotic polyribosomes during multi-round translation. <i>Nucleic Acids Research</i> , 2015, 43, 618-628.	14.5	43
16	SharpViSu: integrated analysis and segmentation of super-resolution microscopy data. <i>Bioinformatics</i> , 2016, 32, 2239-2241.	4.1	40
17	Ribosomal RNA 2â€“O-methylation as a novel layer of inter-tumour heterogeneity in breast cancer. <i>NAR Cancer</i> , 2020, 2, zcaa036.	3.1	40
18	3DClusterViSu: 3D clustering analysis of super-resolution microscopy data by 3D Voronoi tessellations. <i>Bioinformatics</i> , 2018, 34, 3004-3012.	4.1	37

#	ARTICLE	IF	CITATIONS
19	MeCP2 is a microsatellite binding protein that protects CA repeats from nucleosome invasion. <i>Science</i> , 2021, 372, .	12.6	36
20	Tetracyclines Modify Translation by Targeting Key Human rRNA Substructures. <i>Cell Chemical Biology</i> , 2018, 25, 1506-1518.e13.	5.2	35
21	The palindromic DNA-bound USP/EcR nuclear receptor adopts an asymmetric organization with allosteric domain positioning. <i>Nature Communications</i> , 2014, 5, 4139.	12.8	33
22	X-ray and Cryo-electron Microscopy Structures of Monalysin Pore-forming Toxin Reveal Multimerization of the Pro-form. <i>Journal of Biological Chemistry</i> , 2015, 290, 13191-13201.	3.4	33
23	Visualizing the Role of 2â€™-OH rRNA Methylations in the Human Ribosome Structure. <i>Biomolecules</i> , 2018, 8, 125.	4.0	32
24	Dynamics of uS19 C-Terminal Tail during the Translation Elongation Cycle in Human Ribosomes. <i>Cell Reports</i> , 2020, 31, 107473.	6.4	32
25	Structure-function analyses unravel distinct effects of allosteric inhibitors of HIV-1 integrase on viral maturation and integration. <i>Journal of Biological Chemistry</i> , 2018, 293, 6172-6186.	3.4	31
26	Molecular recognition and catalysis in translation termination complexes. <i>Trends in Biochemical Sciences</i> , 2011, 36, 282-292.	7.5	29
27	Deriving and refining atomic models in crystallography and cryo-EM: the latest <i>Phenix</i> tools to facilitate structure analysis. <i>Acta Crystallographica Section D: Structural Biology</i> , 2019, 75, 878-881.	2.3	28
28	Structure Sorting of Multiple Macromolecular States in Heterogeneous Cryo-EM Samples by 3D Multivariate Statistical Analysis. <i>Open Journal of Statistics</i> , 2015, 05, 820-836.	0.7	27
29	Structure of the protein core of translation initiation factor 2 in apo, GTP-bound and GDP-bound forms. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2013, 69, 925-933.	2.5	26
30	Cryo-EM study of start codon selection during archaeal translation initiation. <i>Nature Communications</i> , 2016, 7, 13366.	12.8	25
31	CENP-A nucleosome clusters form rosette-like structures around HJURP during G1. <i>Nature Communications</i> , 2019, 10, 4436.	12.8	25
32	Volta phase plate data collection facilitates image processing and cryo-EM structure determination. <i>Journal of Structural Biology</i> , 2018, 202, 191-199.	2.8	24
33	On effective and optical resolutions of diffraction data sets. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2013, 69, 1921-1934.	2.5	19
34	The HIV-1 integrase-LEDGF allosteric inhibitor MUT-A: resistance profile, impairment of virus maturation and infectivity but without influence on RNA packaging or virus immunoreactivity. <i>Retrovirology</i> , 2017, 14, 50.	2.0	18
35	Myod1 and GR coordinate myofiber-specific transcriptional enhancers. <i>Nucleic Acids Research</i> , 2021, 49, 4472-4492.	14.5	18
36	Live cell immunogold labelling of RNA polymerase II. <i>Scientific Reports</i> , 2015, 5, 8324.	3.3	17

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37	Structureâ€“function relationships in nuclear receptors: the facts. Trends in Biochemical Sciences, 2015, 40, 287-290.	7.5	12
38	Importance of the Sequence-Directed DNA Shape for Specific Binding Site Recognition by the Estrogen-Related Receptor. Frontiers in Endocrinology, 2017, 8, 140.	3.5	12
39	Structural basis of nanobody recognition of grapevine fanleaf virus and of virus resistance loss. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 10848-10855.	7.1	10
40	Structural basis for safe and efficient energy conversion in a respiratory supercomplex. Nature Communications, 2022, 13, 545.	12.8	10
41	Identification of Mg ²⁺ ions next to nucleotides in cryo-EM maps using electrostatic potential maps. Acta Crystallographica Section D: Structural Biology, 2021, 77, 534-539.	2.3	9
42	The Ribosome Holds the RNA Polymerase on Track in Bacteria. Trends in Biochemical Sciences, 2017, 42, 686-689.	7.5	5
43	Structural features of the salivary gland hypertrophy virus of the tsetse fly revealed by cryo-electron microscopy and tomography. Virology, 2018, 514, 165-169.	2.4	5
44	Practical Aspects of Super-Resolution Imaging and Segmentation of Macromolecular Complexes by dSTORM. Methods in Molecular Biology, 2021, 2247, 271-286.	0.9	5
45	IBISS, a versatile and interactive tool for integrated sequence and 3D structure analysis of large macromolecular complexes. Bioinformatics, 2015, 31, 3339-3344.	4.1	3
46	Setup and Troubleshooting of Volta Phase Plate Cryo-EM Data Collection. Methods in Molecular Biology, 2021, 2305, 291-299.	0.9	3
47	Let's see how tmRNA rescues a stuck ribosome. EMBO Journal, 2010, 29, 3747-3749.	7.8	1
48	Studying the Structural Organization of Polyribosomes with Alexander S. Spirin. Biochemistry (Moscow), 2021, 86, 1053-1059.	1.5	1