

Frank Alber

List of Publications by Year in descending order

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Version: 2024-02-01

46
papers

5,166
citations

201674

27
h-index

243625

44
g-index

54
all docs

54
docs citations

54
times ranked

6431
citing authors

#	ARTICLE	IF	CITATIONS
1	Uncovering the Principles of Genome Folding by 3D Chromatin Modeling. Cold Spring Harbor Perspectives in Biology, 2022, 14, a039693.	5.5	12
2	Integrative approaches in genome structure analysis. Structure, 2022, 30, 24-36.	3.3	8
3	Integrative genome modeling platform reveals essentiality of rare contact events in 3D genome organizations. Nature Methods, 2022, 19, 938-949.	19.0	20
4	Assessment of scoring functions to rank the quality of 3D subtomogram clusters from cryo-electron tomography. Journal of Structural Biology, 2021, 213, 107727.	2.8	2
5	Abstract 24: Multi-feature ensemble learning on cell-free dna for accurately detecting and locating cancer. Cancer Research, 2021, 81, 24-24.	0.9	3
6	Visualizing subcellular rearrangements in intact \hat{I}^2 cells using soft x-ray tomography. Science Advances, 2020, 6, .	10.3	36
7	Spatial Principles of Chromatin Architecture Associated With Organ-Specific Gene Regulation. Frontiers in Cardiovascular Medicine, 2019, 5, 186.	2.4	15
8	De Novo Structural Pattern Mining in Cellular Electron Cryotomograms. Structure, 2019, 27, 679-691.e14.	3.3	40
9	Producing genome structure populations with the dynamic and automated PGS software. Nature Protocols, 2018, 13, 915-926.	12.0	67
10	Opportunities and Challenges in Building a Spatiotemporal Multi-scale Model of the Human Pancreatic \hat{I}^2 Cell. Cell, 2018, 173, 11-19.	28.9	179
11	Quantitative imaging of chromatin decompaction in living cells. Molecular Biology of the Cell, 2018, 29, 1763-1777.	2.1	20
12	CancerDetector: ultrasensitive and non-invasive cancer detection at the resolution of individual reads using cell-free DNA methylation sequencing data. Nucleic Acids Research, 2018, 46, e89-e89.	14.5	131
13	Comprehensive characterization of neutrophil genome topology. Genes and Development, 2017, 31, 141-153.	5.9	67
14	TomoMiner and TomoMinerCloud: A Software Platform for Large-Scale Subtomogram Structural Analysis. Structure, 2017, 25, 951-961.e2.	3.3	12
15	CancerLocator: non-invasive cancer diagnosis and tissue-of-origin prediction using methylation profiles of cell-free DNA. Genome Biology, 2017, 18, 53.	8.8	204
16	Integrative modelling of cellular assemblies. Current Opinion in Structural Biology, 2017, 46, 102-109.	5.7	15
17	The three-dimensional genome organization of Drosophila melanogaster through data integration. Genome Biology, 2017, 18, 145.	8.8	86
18	Simulating cryo electron tomograms of crowded cell cytoplasm for assessment of automated particle picking. BMC Bioinformatics, 2016, 17, 405.	2.6	33

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19	Mining 3D genome structure populations identifies major factors governing the stability of regulatory communities. <i>Nature Communications</i> , 2016, 7, 11549.	12.8	36
20	Global reorganization of budding yeast chromosome conformation in different physiological conditions. <i>Journal of Cell Biology</i> , 2016, 212, 321-334.	5.2	36
21	Population-based 3D genome structure analysis reveals driving forces in spatial genome organization. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, E1663-72.	7.1	182
22	TopDom: an efficient and deterministic method for identifying topological domains in genomes. <i>Nucleic Acids Research</i> , 2016, 44, e70-e70.	14.5	246
23	$\hat{\Gamma}^3$ -TEMPy: Simultaneous Fitting of Components in 3D-EM Maps of Their Assembly Using a Genetic Algorithm. <i>Structure</i> , 2015, 23, 2365-2376.	3.3	34
24	Hi-Corrector: a fast, scalable and memory-efficient package for normalizing large-scale Hi-C data. <i>Bioinformatics</i> , 2015, 31, 960-962.	4.1	69
25	Comparative 3D Genome Structure Analysis of the Fission and the Budding Yeast. <i>PLoS ONE</i> , 2015, 10, e0119672.	2.5	20
26	Conformational States of Macromolecular Assemblies Explored by Integrative Structure Calculation. <i>Structure</i> , 2013, 21, 1500-1508.	3.3	29
27	Automated target segmentation and real space fast alignment methods for high-throughput classification and averaging of crowded cryo-electron subtomograms. <i>Bioinformatics</i> , 2013, 29, i274-i282.	4.1	13
28	Physical tethering and volume exclusion determine higher-order genome organization in budding yeast. <i>Genome Research</i> , 2012, 22, 1295-1305.	5.5	190
29	High-throughput subtomogram alignment and classification by Fourier space constrained fast volumetric matching. <i>Journal of Structural Biology</i> , 2012, 178, 152-164.	2.8	52
30	Genome architectures revealed by tethered chromosome conformation capture and population-based modeling. <i>Nature Biotechnology</i> , 2012, 30, 90-98.	17.5	524
31	High precision alignment of cryo-electron subtomograms through gradient-based parallel optimization. <i>BMC Systems Biology</i> , 2012, 6, S18.	3.0	17
32	Gradient-based high precision alignment of cryo-electron subtomograms. , 2011, , 279-284.		3
33	Exploring the spatial and temporal organization of a cell's proteome. <i>Journal of Structural Biology</i> , 2011, 173, 483-496.	2.8	36
34	Template-free detection of macromolecular complexes in cryo electron tomograms. <i>Bioinformatics</i> , 2011, 27, i69-i76.	4.1	37
35	A fast mathematical programming procedure for simultaneous fitting of assembly components into cryoEM density maps. <i>Bioinformatics</i> , 2010, 26, i261-i268.	4.1	21
36	3D Rotation Invariant Features for the Characterization of Molecular Density Maps. , 2009, , .		4

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37	Integrative Structure Determination of Protein Assemblies by Satisfaction of Spatial Restraints. <i>Computational Biology</i> , 2008, , 99-114.	0.2	6
38	Integrating Diverse Data for Structure Determination of Macromolecular Assemblies. <i>Annual Review of Biochemistry</i> , 2008, 77, 443-477.	11.1	204
39	Determining the architectures of macromolecular assemblies. <i>Nature</i> , 2007, 450, 683-694.	27.8	499
40	The molecular architecture of the nuclear pore complex. <i>Nature</i> , 2007, 450, 695-701.	27.8	947
41	Simple fold composition and modular architecture of the nuclear pore complex. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 2172-2177.	7.1	243
42	Structural Modeling of Protein Interactions by Analogy: Application to PSD-95. <i>PLoS Computational Biology</i> , 2006, 2, e153.	3.2	39
43	Structural Characterization of Assemblies from Overall Shape and Subcomplex Compositions. <i>Structure</i> , 2005, 13, 435-445.	3.3	27
44	Unraveling the interface of signal recognition particle and its receptor by using chemical cross-linking and tandem mass spectrometry. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 16454-16459.	7.1	72
45	Components of Coated Vesicles and Nuclear Pore Complexes Share a Common Molecular Architecture. <i>PLoS Biology</i> , 2004, 2, e380.	5.6	357
46	A structural perspective on protein-protein interactions. <i>Current Opinion in Structural Biology</i> , 2004, 14, 313-324.	5.7	260