

# Frank Alber

## List of Publications by Year in descending order

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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	The molecular architecture of the nuclear pore complex. <i>Nature</i> , 2007, 450, 695-701.	27.8	947
2	Genome architectures revealed by tethered chromosome conformation capture and population-based modeling. <i>Nature Biotechnology</i> , 2012, 30, 90-98.	17.5	524
3	Determining the architectures of macromolecular assemblies. <i>Nature</i> , 2007, 450, 683-694.	27.8	499
4	Components of Coated Vesicles and Nuclear Pore Complexes Share a Common Molecular Architecture. <i>PLoS Biology</i> , 2004, 2, e380.	5.6	357
5	A structural perspective on protein-protein interactions. <i>Current Opinion in Structural Biology</i> , 2004, 14, 313-324.	5.7	260
6	TopDom: an efficient and deterministic method for identifying topological domains in genomes. <i>Nucleic Acids Research</i> , 2016, 44, e70-e70.	14.5	246
7	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
8	Integrating Diverse Data for Structure Determination of Macromolecular Assemblies. <i>Annual Review of Biochemistry</i> , 2008, 77, 443-477.	11.1	204
9	CancerLocator: non-invasive cancer diagnosis and tissue-of-origin prediction using methylation profiles of cell-free DNA. <i>Genome Biology</i> , 2017, 18, 53.	8.8	204
10	Physical tethering and volume exclusion determine higher-order genome organization in budding yeast. <i>Genome Research</i> , 2012, 22, 1295-1305.	5.5	190
11	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
12	Opportunities and Challenges in Building a Spatiotemporal Multi-scale Model of the Human Pancreatic $\beta$ Cell. <i>Cell</i> , 2018, 173, 11-19.	28.9	179
13	CancerDetector: ultrasensitive and non-invasive cancer detection at the resolution of individual reads using cell-free DNA methylation sequencing data. <i>Nucleic Acids Research</i> , 2018, 46, e89-e89.	14.5	131
14	The three-dimensional genome organization of <i>Drosophila melanogaster</i> through data integration. <i>Genome Biology</i> , 2017, 18, 145.	8.8	86
15	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
16	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
17	Comprehensive characterization of neutrophil genome topology. <i>Genes and Development</i> , 2017, 31, 141-153.	5.9	67
18	Producing genome structure populations with the dynamic and automated PGS software. <i>Nature Protocols</i> , 2018, 13, 915-926.	12.0	67

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19	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
20	De Novo Structural Pattern Mining in Cellular Electron Cryotomograms. <i>Structure</i> , 2019, 27, 679-691.e14.	3.3	40
21	Structural Modeling of Protein Interactions by Analogy: Application to PSD-95. <i>PLoS Computational Biology</i> , 2006, 2, e153.	3.2	39
22	Template-free detection of macromolecular complexes in cryo electron tomograms. <i>Bioinformatics</i> , 2011, 27, i69-i76.	4.1	37
23	Exploring the spatial and temporal organization of a cell's proteome. <i>Journal of Structural Biology</i> , 2011, 173, 483-496.	2.8	36
24	Mining 3D genome structure populations identifies major factors governing the stability of regulatory communities. <i>Nature Communications</i> , 2016, 7, 11549.	12.8	36
25	Global reorganization of budding yeast chromosome conformation in different physiological conditions. <i>Journal of Cell Biology</i> , 2016, 212, 321-334.	5.2	36
26	Visualizing subcellular rearrangements in intact $\hat{1}^2$ cells using soft x-ray tomography. <i>Science Advances</i> , 2020, 6, .	10.3	36
27	$\hat{1}^3$ -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
28	Simulating cryo electron tomograms of crowded cell cytoplasm for assessment of automated particle picking. <i>BMC Bioinformatics</i> , 2016, 17, 405.	2.6	33
29	Conformational States of Macromolecular Assemblies Explored by Integrative Structure Calculation. <i>Structure</i> , 2013, 21, 1500-1508.	3.3	29
30	Structural Characterization of Assemblies from Overall Shape and Subcomplex Compositions. <i>Structure</i> , 2005, 13, 435-445.	3.3	27
31	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
32	Quantitative imaging of chromatin decompaction in living cells. <i>Molecular Biology of the Cell</i> , 2018, 29, 1763-1777.	2.1	20
33	Comparative 3D Genome Structure Analysis of the Fission and the Budding Yeast. <i>PLoS ONE</i> , 2015, 10, e0119672.	2.5	20
34	Integrative genome modeling platform reveals essentiality of rare contact events in 3D genome organizations. <i>Nature Methods</i> , 2022, 19, 938-949.	19.0	20
35	High precision alignment of cryo-electron subtomograms through gradient-based parallel optimization. <i>BMC Systems Biology</i> , 2012, 6, S18.	3.0	17
36	Integrative modelling of cellular assemblies. <i>Current Opinion in Structural Biology</i> , 2017, 46, 102-109.	5.7	15

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37	Spatial Principles of Chromatin Architecture Associated With Organ-Specific Gene Regulation. <i>Frontiers in Cardiovascular Medicine</i> , 2019, 5, 186.	2.4	15
38	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
39	TomoMiner and TomoMinerCloud: A Software Platform for Large-Scale Subtomogram Structural Analysis. <i>Structure</i> , 2017, 25, 951-961.e2.	3.3	12
40	Uncovering the Principles of Genome Folding by 3D Chromatin Modeling. <i>Cold Spring Harbor Perspectives in Biology</i> , 2022, 14, a039693.	5.5	12
41	Integrative approaches in genome structure analysis. <i>Structure</i> , 2022, 30, 24-36.	3.3	8
42	Integrative Structure Determination of Protein Assemblies by Satisfaction of Spatial Restraints. <i>Computational Biology</i> , 2008, , 99-114.	0.2	6
43	3D Rotation Invariant Features for the Characterization of Molecular Density Maps. , 2009, , .		4
44	Gradient-based high precision alignment of cryo-electron subtomograms. , 2011, , 279-284.		3
45	Abstract 24: Multi-feature ensemble learning on cell-free dna for accurately detecting and locating cancer. <i>Cancer Research</i> , 2021, 81, 24-24.	0.9	3
46	Assessment of scoring functions to rank the quality of 3D subtomogram clusters from cryo-electron tomography. <i>Journal of Structural Biology</i> , 2021, 213, 107727.	2.8	2