Tim J Stevens

List of Publications by Year
in descending order

51 papers	6,929 citations	304743 22 h-index	395702 33 g-index
73 all docs	73 docs citations	73 times ranked	10675 citing authors

#	Article	IF	Citations
1	The CCPN data model for NMR spectroscopy: Development of a software pipeline. Proteins: Structure, Function and Bioinformatics, 2005, 59, 687-696.	2.6	2,805
2	Single-cell Hi-C reveals cell-to-cell variability in chromosome structure. Nature, 2013, 502, 59-64.	27.8	1,347
3	3D structures of individual mammalian genomes studied by single-cell Hi-C. Nature, 2017, 544, 59-64.	27.8	691
4	A Comprehensive Comparison of Transmembrane Domains Reveals Organelle-Specific Properties. Cell, 2010, 142, 158-169.	28.9	477
5	DANGLE: A Bayesian inferential method for predicting protein backbone dihedral angles and secondary structure. Journal of Magnetic Resonance, 2010, 202, 223-233.	2.1	221
6	A Comprehensive Subcellular Atlas of the Toxoplasma Proteome via hyperLOPIT Provides Spatial Context for Protein Functions. Cell Host and Microbe, 2020, 28, 752-766.e9.	11.0	201
7	Putative Glycosyltransferases and Other Plant Golgi Apparatus Proteins Are Revealed by LOPIT Proteomics Â. Plant Physiology, 2012, 160, 1037-1051.	4.8	149
8	A software framework for analysing solid-state MAS NMR data. Journal of Biomolecular NMR, 2011, 51, 437-447.	2.8	138
9	Membrane proteins: the â€˜Wild Westâ€™ of structural biology. Trends in Biochemical Sciences, 2003, 28, 137-144.	7.5	129
10	CING: an integrated residue-based structure validation program suite. Journal of Biomolecular NMR, 2012, 54, 267-283.	2.8	106
11	Structure calculation, refinement and validation using<i>CcpNmr Analysis</i>. Acta Crystallographica Section D: Biological Crystallography, 2015, 71, 154-161.	2.5	67
12	Proteome Mapping of a Cyanobacterium Reveals Distinct Compartment Organization and Cell-Dispersed Metabolism. Plant Physiology, 2019, 181, 1721-1738.	4.8	58
13	Hydrocarbons Are Essential for Optimal Cell Size, Division, and Growth of Cyanobacteria. Plant Physiology, 2016, 172, 1928-1940.	4.8	53
14	A framework for scientific data modeling and automated software development. Bioinformatics, 2005, 21, 1678-1684.	4.1	42
15	Multiple marker abundance profiling: combining selected reaction monitoring and dataâ€dependent acquisition for rapid estimation of organelle abundance in subcellular samples. Plant Journal, 2017, 92, 1202-1217.	5.7	42
16	Separating Golgi Proteins from <i>Cis</i> to <i>Trans</i> Reveals Underlying Properties of Cisternal Localization. Plant Cell, 2019, 31, 2010-2034.	6.6	40
17	Rho-Kinase Planar Polarization at Tissue Boundaries Depends on Phospho-regulation of Membrane Residence Time. Developmental Cell, 2020, 52, 364-378.e7.	7.0	38
18	Are There Knots in Chromosomes?. Polymers, 2017, 9, 317.	4.5	35

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19	Canonical and single-cell Hi-C reveal distinct chromatin interaction sub-networks of mammalian transcription factors. Genome Biology, 2018, 19, 174.	8.8	33
20	Design of a data model for developing laboratory information management and analysis systems for protein production. Proteins: Structure, Function and Bioinformatics, 2004, 58, 278-284.	2.6	27
21	Calculation of 3D genome structures for comparison of chromosome conformation capture experiments with microscopy: An evaluation of single-cell Hi-C protocols. Nucleus, 2018, 9, 190-201.	2.2	26
22	GOLPH3 and GOLPH3L are broad-spectrum COPI adaptors for sorting into intra-Golgi transport vesicles. Journal of Cell Biology, 2021, 220, .	5.2	26
23	Prionâ€like protein aggregates exploit the RHO GTPase to cofilinâ€1 signaling pathway to enter cells. EMBO Journal, 2018, 37, .	7.8	24
24	The CCPN Metabolomics Project: a fast protocol for metabolite identification by 2D-NMR. Bioinformatics, 2011, 27, 885-886.	4.1	23
25	RCC1â€like repeat proteins: A pangenomic, structurally diverse new superfamily of Î²â€propeller domains. Proteins: Structure, Function and Bioinformatics, 2008, 70, 378-387.	2.6	18
26	A nomenclature and data model to describe NMR experiments. Journal of Biomolecular NMR, 2006, 36, 147-155.	2.8	17
27	Combining fluorescence imaging with Hi-C to study 3D genome architecture of the same single cell. Nature Protocols, 2018, 13, 1034-1061.	12.0	14
28	Triparental inheritance in *Dictyostelium*. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 2187-2192.	7.1	14
29	Lipophobicity and the residue environments of the transmembrane Î±â€helical bundle. Proteins: Structure, Function and Bioinformatics, 2009, 74, 32-49.	2.6	12
30	A structural dissection of amino acid substitutions in helical transmembrane proteins. Proteins: Structure, Function and Bioinformatics, 2010, 78, 2895-2907.	2.6	9
31	Straightforward and complete deposition of NMR data to the PDBe. Journal of Biomolecular NMR, 2010, 48, 85-92.	2.8	7
32	MEMOPS: Data modelling and automatic code generation. Journal of Integrative Bioinformatics, 2010, 7, .	1.5	2
33	A beginnersâ€™ guide. , 0, , 5-16.		2
34	Biological sequences. , 0, , 181-207.		2
35	MEMOPS: data modelling and automatic code generation. Journal of Integrative Bioinformatics, 2010, 7, .	1.5	2
36	Python basics. , 0, , 17-42.		0

#	Article	IF	Citations
37	Program control and logic. , 0, , 43-62.		0
38	Files. , 0, , 78-99.		0
39	Object orientation. , 0, , 100-116.		0
40	Object data modelling. , 0, , 117-136.		0
41	Coding tips. , 0, , 160-180.		0
42	Pairwise sequence alignments. , 0, , 208-231.		0
43	Multiple-sequence alignments. , 0, , 232-243.		0
44	Sequence variation and evolution. , 0, , 244-277.		0
45	Macromolecular structures. , 0, , 278-315.		0
46	Array data. , 0, , 316-340.		0
47	High-throughput sequence analyses. , 0, , 341-360.		0
48	Clustering and discrimination. , 0, , 486-510.		0
49	Hard problems. , 0, , 545-565.		0
50	Graphical interfaces. , 0, , 566-581.		0
51	Improving speed. , 0, , 582-605.		0