Tim J Stevens

List of Publications by Year
in descending order

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51 papers	6,929 citations	346980 22 h-index	445137 33 g-index
73 all docs	73 docs citations	73 times ranked	11886 citing authors

#	Article	IF	Citations
1	GOLPH3 and GOLPH3L are broad-spectrum COPI adaptors for sorting into intra-Golgi transport vesicles. Journal of Cell Biology, 2021, 220, .	2.3	26
2	Rho-Kinase Planar Polarization at Tissue Boundaries Depends on Phospho-regulation of Membrane Residence Time. Developmental Cell, 2020, 52, 364-378.e7.	3.1	38
3	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.	5.1	201
4	Separating Golgi Proteins from <i>Cis</i> to <i>Trans</i> Reveals Underlying Properties of Cisternal Localization. Plant Cell, 2019, 31, 2010-2034.	3.1	40
5	Proteome Mapping of a Cyanobacterium Reveals Distinct Compartment Organization and Cell-Dispersed Metabolism. Plant Physiology, 2019, 181, 1721-1738.	2.3	58
6	Triparental inheritance in <i>Dictyostelium</i>. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 2187-2192.	3.3	14
7	Prionâ€like protein aggregates exploit the RHO GTPase to cofilinâ€1 signaling pathway to enter cells. EMBO Journal, 2018, 37, .	3.5	24
8	Combining fluorescence imaging with Hi-C to study 3D genome architecture of the same single cell. Nature Protocols, 2018, 13, 1034-1061.	5.5	14
9	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.	0.6	26
10	Canonical and single-cell Hi-C reveal distinct chromatin interaction sub-networks of mammalian transcription factors. Genome Biology, 2018, 19, 174.	3.8	33
11	3D structures of individual mammalian genomes studied by single-cell Hi-C. Nature, 2017, 544, 59-64.	13.7	691
12	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.	2.8	42
13	Are There Knots in Chromosomes?. Polymers, 2017, 9, 317.	2.0	35
14	Hydrocarbons Are Essential for Optimal Cell Size, Division, and Growth of Cyanobacteria. Plant Physiology, 2016, 172, 1928-1940.	2.3	53
15	Structure calculation, refinement and validation using<i>CcpNmr Analysis</i>. Acta Crystallographica Section D: Biological Crystallography, 2015, 71, 154-161.	2.5	67
16	Single-cell Hi-C reveals cell-to-cell variability in chromosome structure. Nature, 2013, 502, 59-64.	13.7	1,347
17	Putative Glycosyltransferases and Other Plant Golgi Apparatus Proteins Are Revealed by LOPIT Proteomics Â. Plant Physiology, 2012, 160, 1037-1051.	2.3	149
18	CING: an integrated residue-based structure validation program suite. Journal of Biomolecular NMR, 2012, 54, 267-283.	1.6	106

#	ARTICLE	IF	CITATIONS
19	A software framework for analysing solid-state MAS NMR data. Journal of Biomolecular NMR, 2011, 51, 437-447.	1.6	138
20	The CCPN Metabolomics Project: a fast protocol for metabolite identification by 2D-NMR. Bioinformatics, 2011, 27, 885-886.	1.8	23
21	MEMOPS: Data modelling and automatic code generation. Journal of Integrative Bioinformatics, 2010, 7, .	1.0	2
22	DANGLE: A Bayesian inferential method for predicting protein backbone dihedral angles and secondary structure. Journal of Magnetic Resonance, 2010, 202, 223-233.	1.2	221
23	Straightforward and complete deposition of NMR data to the PDBe. Journal of Biomolecular NMR, 2010, 48, 85-92.	1.6	7
24	A structural dissection of amino acid substitutions in helical transmembrane proteins. Proteins: Structure, Function and Bioinformatics, 2010, 78, 2895-2907.	1.5	9
25	A Comprehensive Comparison of Transmembrane Domains Reveals Organelle-Specific Properties. Cell, 2010, 142, 158-169.	13.5	477
26	MEMOPS: data modelling and automatic code generation. Journal of Integrative Bioinformatics, 2010, 7, .	1.0	2
27	Lipophobicity and the residue environments of the transmembrane Î±â€helical bundle. Proteins: Structure, Function and Bioinformatics, 2009, 74, 32-49.	1.5	12
28	RCC1â€like repeat proteins: A pangenomic, structurally diverse new superfamily of Î²â€propeller domains. Proteins: Structure, Function and Bioinformatics, 2008, 70, 378-387.	1.5	18
29	A nomenclature and data model to describe NMR experiments. Journal of Biomolecular NMR, 2006, 36, 147-155.	1.6	17
30	The CCPN data model for NMR spectroscopy: Development of a software pipeline. Proteins: Structure, Function and Bioinformatics, 2005, 59, 687-696.	1.5	2,805
31	A framework for scientific data modeling and automated software development. Bioinformatics, 2005, 21, 1678-1684.	1.8	42
32	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.	1.5	27
33	Membrane proteins: the â€˜Wild Westâ€™ of structural biology. Trends in Biochemical Sciences, 2003, 28, 137-144.	3.7	129
34	A beginnersâ€™ guide. , 0, , 5-16.		2
35	Python basics. , 0, , 17-42.		0
36	Program control and logic. , 0, , 43-62.		0

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37	Files. , 0, , 78-99.		0
38	Object orientation. , 0, , 100-116.		0
39	Object data modelling. , 0, , 117-136.		0
40	Coding tips. , 0, , 160-180.		0
41	Biological sequences. , 0, , 181-207.		2
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