

John-Marc Chandonia

List of Publications by Year in descending order

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43
papers

15,999
citations

304602

22
h-index

276775

41
g-index

48
all docs

48
docs citations

48
times ranked

26473
citing authors

#	ARTICLE	IF	CITATIONS
1	WebLogo: A Sequence Logo Generator. <i>Genome Research</i> , 2004, 14, 1188-1190.	2.4	10,751
2	KBase: The United States Department of Energy Systems Biology Knowledgebase. <i>Nature Biotechnology</i> , 2018, 36, 566-569.	9.4	955
3	Data growth and its impact on the SCOP database: new developments. <i>Nucleic Acids Research</i> , 2007, 36, D419-D425.	6.5	854
4	The Sorcerer II Global Ocean Sampling Expedition: Expanding the Universe of Protein Families. <i>PLoS Biology</i> , 2007, 5, e16.	2.6	736
5	SCOPe: Structural Classification of Proteinsâ€™ extended, integrating SCOP and ASTRAL data and classification of new structures. <i>Nucleic Acids Research</i> , 2014, 42, D304-D309.	6.5	627
6	The ASTRAL Compendium in 2004. <i>Nucleic Acids Research</i> , 2004, 32, 189D-192.	6.5	480
7	The Impact of Structural Genomics: Expectations and Outcomes. <i>Science</i> , 2006, 311, 347-351.	6.0	366
8	SCOPe: classification of large macromolecular structures in the structural classification of proteinsâ€™ extended database. <i>Nucleic Acids Research</i> , 2019, 47, D475-D481.	6.5	122
9	ASTRAL compendium enhancements. <i>Nucleic Acids Research</i> , 2002, 30, 260-263.	6.5	117
10	New methods for accurate prediction of protein secondary structure. <i>Proteins: Structure, Function and Bioinformatics</i> , 1999, 35, 293-306.	1.5	114
11	High-resolution autoreactive epitope mapping and structural modeling of the 65 kDa form of human glutamic acid decarboxylase. <i>Journal of Molecular Biology</i> , 1999, 287, 983-999.	2.0	100
12	Neural networks for secondary structure and structural class predictions. <i>Protein Science</i> , 1995, 4, 275-285.	3.1	99
13	SCOPe: Manual Curation and Artifact Removal in the Structural Classification of Proteins â€™ extended Database. <i>Journal of Molecular Biology</i> , 2017, 429, 348-355.	2.0	85
14	Implications of structural genomics target selection strategies: Pfam5000, whole genome, and random approaches. <i>Proteins: Structure, Function and Bioinformatics</i> , 2004, 58, 166-179.	1.5	61
15	SCOPe: improvements to the structural classification of proteins â€™ extended database to facilitate variant interpretation and machine learning. <i>Nucleic Acids Research</i> , 2022, 50, D553-D559.	6.5	59
16	Large Circular Plasmids from Groundwater Plasmidomes Span Multiple Incompatibility Groups and Are Enriched in Multimetal Resistance Genes. <i>MBio</i> , 2019, 10, .	1.8	42
17	The importance of larger data sets for protein secondary structure prediction with neural networks. <i>Protein Science</i> , 1996, 5, 768-774.	3.1	39
18	The value of protein structure classification informationâ€™ Surveying the scientific literature. <i>Proteins: Structure, Function and Bioinformatics</i> , 2015, 83, 2025-2038.	1.5	37

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19	Structural Genomics of Minimal Organisms and Protein Fold Space. <i>Journal of Structural and Functional Genomics</i> , 2005, 6, 63-70.	1.2	29
20	Survey of large protein complexes in <i>D. vulgaris</i> reveals great structural diversity. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 16580-16585.	3.3	29
21	Microbiome Metadata Standards: Report of the National Microbiome Data Collaborative's Workshop and Follow-On Activities. <i>MSystems</i> , 2021, 6, .	1.7	28
22	Target selection and deselection at the Berkeley Structural Genomics Center. <i>Proteins: Structure, Function and Bioinformatics</i> , 2005, 62, 356-370.	1.5	27
23	Structure-based inference of molecular functions of proteins of unknown function from Berkeley Structural Genomics Center. <i>Journal of Structural and Functional Genomics</i> , 2007, 8, 99-105.	1.2	26
24	High-throughput Isolation and Characterization of Untagged Membrane Protein Complexes: Outer Membrane Complexes of <i>Desulfovibrio vulgaris</i> . <i>Journal of Proteome Research</i> , 2012, 11, 5720-5735.	1.8	22
25	Comparative mapping of sequence-based and structure-based protein domains. <i>BMC Bioinformatics</i> , 2005, 6, 77.	1.2	16
26	Bacterial Interactomes: Interacting Protein Partners Share Similar Function and Are Validated in Independent Assays More Frequently Than Previously Reported. <i>Molecular and Cellular Proteomics</i> , 2016, 15, 1539-1555.	2.5	16
27	Temporal Dynamics of In-Field Bioreactor Populations Reflect the Groundwater System and Respond Predictably to Perturbation. <i>Environmental Science & Technology</i> , 2017, 51, 2879-2889.	4.6	15
28	StrBioLib: a Java library for development of custom computational structural biology applications. <i>Bioinformatics</i> , 2007, 23, 2018-2020.	1.8	14
29	Quantitative Tagless Copurification: A Method to Validate and Identify Protein-Protein Interactions. <i>Molecular and Cellular Proteomics</i> , 2016, 15, 2186-2202.	2.5	12
30	Towards a Rigorous Network of Protein-Protein Interactions of the Model Sulfate Reducer <i>Desulfovibrio vulgaris</i> Hildenborough. <i>PLoS ONE</i> , 2011, 6, e21470.	1.1	12
31	Characterization of a Metal-Resistant <i>Bacillus</i> Strain With a High Molybdate Affinity ModA From Contaminated Sediments at the Oak Ridge Reservation. <i>Frontiers in Microbiology</i> , 2020, 11, 587127.	1.5	11
32	Structural proteomics of minimal organisms: conservation of protein fold usage and evolutionary implications. , 2006, 6, 7.		10
33	NMR structure of the N-terminal domain of the replication initiator protein DnaA. <i>Journal of Structural and Functional Genomics</i> , 2007, 8, 11-17.	1.2	9
34	WIST: toolkit for rapid, customized LIMS development. <i>Bioinformatics</i> , 2011, 27, 437-438.	1.8	9
35	Structural genomics and structural biology: compare and contrast. <i>Genome Biology</i> , 2004, 5, 343.	13.9	8
36	Ecogenomics of Groundwater Phages Suggests Niche Differentiation Linked to Specific Environmental Tolerance. <i>MSystems</i> , 2021, 6, e0053721.	1.7	8

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37	Lessons from the CAGI Hopkins clinical panel challenge. <i>Human Mutation</i> , 2017, 38, 1155-1168.	1.1	6
38	New Local Potential Useful for Genome Annotation and 3D Modeling. <i>Journal of Molecular Biology</i> , 2003, 332, 835-850.	2.0	3
39	ANDY: a general, fault-tolerant tool for database searching on computer clusters. <i>Bioinformatics</i> , 2006, 22, 618-620.	1.8	3
40	Structural Genomics of Minimal Organisms: Pipeline and Results. <i>Methods in Molecular Biology</i> , 2008, 426, 475-496.	0.4	3
41	Complete Genome Sequence of <i>Bacillus cereus</i> Strain CPT56D-587-MTF, Isolated from a Nitrate- and Metal-Contaminated Subsurface Environment. <i>Microbiology Resource Announcements</i> , 2022, 11, e0014522.	0.3	1
42	Overview of Structural Genomics. , 2005, , 1-18.		0
43	Draft Genome Sequence of <i>Bacillus</i> sp. Strain EB106-08-02-XG196, Isolated from High-Nitrate-Contaminated Sediment. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.3	0