

Sean O'Donoghue

List of Publications by Year in descending order

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76
papers

5,335
citations

136950

32
h-index

114465

63
g-index

85
all docs

85
docs citations

85
times ranked

8578
citing authors

#	ARTICLE	IF	CITATIONS
1	Collaborative Sense-Making in Genomic Research: The Role of Visualisation. IEEE Transactions on Visualization and Computer Graphics, 2022, 28, 4477-4489.	4.4	2
2	PredictProtein - Predicting Protein Structure and Function for 29 Years. Nucleic Acids Research, 2021, 49, W535-W540.	14.5	135
3	Grand Challenges in Bioinformatics Data Visualization. Frontiers in Bioinformatics, 2021, 1, .	2.1	18
4	SARS-CoV-2 structural coverage map reveals viral protein assembly, mimicry, and hijacking mechanisms. Molecular Systems Biology, 2021, 17, e10079.	7.2	22
5	Temporal ordering of omics and multiomic events inferred from time-series data. Npj Systems Biology and Applications, 2020, 6, 22.	3.0	10
6	A benchmark dataset for analyzing and visualizing the dynamic epiproteome. Data in Brief, 2019, 25, 104000.	1.0	2
7	SnapShot: S-Phase Entry and Exit. Cell, 2019, 179, 802-802.e1.	28.9	2
8	Molecular Graphics: Bridging Structural Biologists and Computer Scientists. Structure, 2019, 27, 1617-1623.	3.3	42
9	Visualization and Analysis of Epiproteome Dynamics. Journal of Molecular Biology, 2019, 431, 1519-1539.	4.2	10
10	Versus - A tool for evaluating visualizations and image quality using a 2AFC methodology. Visual Informatics, 2018, 2, 225-234.	4.4	9
11	Dark Proteins Important for Cellular Function. Proteomics, 2018, 18, e1800227.	2.2	7
12	Visualization of Biomedical Data. Annual Review of Biomedical Data Science, 2018, 1, 275-304.	6.5	63
13	SnapShot: Phosphoregulation of Mitosis. Cell, 2017, 169, 1358-1358.e1.	28.9	12
14	Comparative eye-tracking evaluation of scatterplots and parallel coordinates. Visual Informatics, 2017, 1, 118-131.	4.4	18
15	The Dark Proteome Database. BioData Mining, 2017, 10, 24.	4.0	16
16	Developing a Visual Analytics Tool for Large-Scale Proteomics Time-Series Data. , 2016, , .		0
17	Using videogames to improve molecular graphics tools. , 2016, , .		1
18	Three-dimensional disorganization of the cancer genome occurs coincident with long-range genetic and epigenetic alterations. Genome Research, 2016, 26, 719-731.	5.5	312

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19	Evaluating Viewpoint Entropy for Ribbon Representation of Protein Structure. Computer Graphics Forum, 2016, 35, 181-190.	3.0	4
20	Monogenic and polygenic determinants of sarcoma risk: an international genetic study. Lancet Oncology, The, 2016, 17, 1261-1271.	10.7	161
21	Can Videogame Players Inform Better Scientific Visualization'. , 2016, , .		1
22	Integrated visual analysis of protein structures, sequences, and feature data. BMC Bioinformatics, 2015, 16, S7.	2.6	7
23	Visual Analytics of Gene Sets Comparison. , 2015, , .		1
24	Unexpected features of the dark proteome. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 15898-15903.	7.1	170
25	Evaluating the Effectiveness of Color to Convey Alignment Quality in Macromolecular Structures. , 2015, , .		2
26	Aquaria: simplifying discovery and insight from protein structures. Nature Methods, 2015, 12, 98-99.	19.0	58
27	Visual Analytics of Signalling Pathways Using Time Profiles. Advances in Experimental Medicine and Biology, 2015, 823, 3-22.	1.6	0
28	SnapShot: Insulin/IGF1 Signaling. Cell, 2015, 161, 948-948.e1.	28.9	19
29	How to learn about gene function: text-mining or ontologies?. Methods, 2015, 74, 3-15.	3.8	24
30	Comprehensive comparison of large-scale tissue expression datasets. PeerJ, 2015, 3, e1054.	2.0	102
31	COMPARTMENTS: unification and visualization of protein subcellular localization evidence. Database: the Journal of Biological Databases and Curation, 2014, 2014, bau012-bau012.	3.0	483
32	On the use of 1D, 2D, and 3D visualisation for molecular graphics. , 2014, , .		5
33	Visualising intrinsic disorder and conformational variation in protein ensembles. Faraday Discussions, 2014, 169, 179-193.	3.2	8
34	The Molecular Control Toolkit: Controlling 3D molecular graphics via gesture and voice. , 2013, , .		26
35	Visualising biological data: Current perspectives. , 2013, , .		0
36	Visual analytics of phosphorylation time-series data on insulin response. , 2013, , .		3

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37	Caipirini: using gene sets to rank literature. <i>BioData Mining</i> , 2012, 5, 1.	4.0	47
38	Reflect: A practical approach to web semantics. <i>Web Semantics</i> , 2010, 8, 182-189.	2.9	14
39	Visualization of macromolecular structures. <i>Nature Methods</i> , 2010, 7, S42-S55.	19.0	137
40	Visualization of omics data for systems biology. <i>Nature Methods</i> , 2010, 7, S56-S68.	19.0	548
41	Visualizing biological data—now and in the future. <i>Nature Methods</i> , 2010, 7, S2-S4.	19.0	115
42	Martini: using literature keywords to compare gene sets. <i>Nucleic Acids Research</i> , 2010, 38, 26-38.	14.5	51
43	Defective Lamin A-Rb Signaling in Hutchinson-Gilford Progeria Syndrome and Reversal by Farnesyltransferase Inhibition. <i>PLoS ONE</i> , 2010, 5, e11132.	2.5	58
44	Reflect: augmented browsing for the life scientist. <i>Nature Biotechnology</i> , 2009, 27, 508-510.	17.5	91
45	Arena3D: visualization of biological networks in 3D. <i>BMC Systems Biology</i> , 2008, 2, 104.	3.0	95
46	Text mining for biology - the way forward: opinions from leading scientists. <i>Genome Biology</i> , 2008, 9, S7.	9.6	74
47	Error distribution derived NOE distance restraints. <i>Proteins: Structure, Function and Bioinformatics</i> , 2006, 64, 652-664.	2.6	12
48	The SRS 3D module: integrating structures, sequences and features. <i>Bioinformatics</i> , 2004, 20, 2476-2478.	4.1	20
49	The PSSH database of alignments between protein sequences and tertiary structures. <i>Nucleic Acids Research</i> , 2003, 31, 494-498.	14.5	11
50	Calculation of Symmetric Oligomer Structures from NMR Data. , 2002, , 131-161.		7
51	NMR studies of the aggregation of glucagon-like peptide-1: formation of a symmetric helical dimer. <i>FEBS Letters</i> , 2002, 515, 165-170.	2.8	43
52	Solution structure of the coiled-coil trimerization domain from lung surfactant protein D. <i>Journal of Biomolecular NMR</i> , 2002, 24, 89-102.	2.8	11
53	Automated Assignment of Ambiguous Nuclear Overhauser Effects with ARIA. <i>Methods in Enzymology</i> , 2001, 339, 71-90.	1.0	319
54	Comparison of ARM and HEAT protein repeats. <i>Journal of Molecular Biology</i> , 2001, 309, 1-18.	4.2	464

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55	Unraveling the symmetry ambiguity in a hexamer: calculation of the R6 human insulin structure. <i>Journal of Biomolecular NMR</i> , 2000, 16, 93-108.	2.8	37
56	Molecular dynamics and accuracy of NMR structures: Effects of error bounds and data removal. <i>Proteins: Structure, Function and Bioinformatics</i> , 1999, 34, 453-463.	2.6	20
57	Ambiguous NOEs and automated NOE assignment. <i>Progress in Nuclear Magnetic Resonance Spectroscopy</i> , 1998, 32, 107-139.	7.5	198
58	Adaptation of protein surfaces to subcellular location 1 Edited by F. E. Cohen. <i>Journal of Molecular Biology</i> , 1998, 276, 517-525.	4.2	158
59	Sisyphus and prediction of protein structure. <i>Bioinformatics</i> , 1997, 13, 345-356.	4.1	24
60	Automated NOESY interpretation with ambiguous distance restraints: the refined NMR solution structure of the pleckstrin homology domain from β -spectrin 1 Edited by P. E. Wright. <i>Journal of Molecular Biology</i> , 1997, 269, 408-422.	4.2	414
61	The structure of a novel insecticidal neurotoxin, δ -atractoxin-HV1, from the venom of an Australian funnel web spider. <i>Nature Structural Biology</i> , 1997, 4, 559-566.	9.7	172
62	Tertiary structure prediction using mean-force potentials and internal energy functions: successful prediction for coiled-coil geometries. <i>Folding & Design</i> , 1997, 2, S47-S52.	4.5	18
63	High Resolution NMR Solution Structure of the Leucine Zipper Domain of the c-Jun Homodimer. <i>Journal of Biological Chemistry</i> , 1996, 271, 13663-13667.	3.4	93
64	Calculation of symmetric multimer structures from NMR data using a priori knowledge of the monomer structure, co-monomer restraints, and interface mapping: The case of leucine zippers. <i>Journal of Biomolecular NMR</i> , 1996, 8, 193-206.	2.8	38
65	Catalysis by Hamster Dihydroorotase: Zinc Binding, Site-Directed Mutagenesis, and Interaction with Inhibitors. <i>Biochemistry</i> , 1995, 34, 11344-11352.	2.5	35
66	Stereospecificity of Substrate Usage by Glyoxalase 1: Nuclear Magnetic Resonance Studies of Kinetics and Hemithioacetal Substrate Conformation. <i>Biochemistry</i> , 1994, 33, 3548-3559.	2.5	21
67	Determination of the structure of symmetric coiled-coil proteins from NMR data: application of the leucine zipper proteins Jun and GCN4. <i>Protein Engineering, Design and Selection</i> , 1993, 6, 557-564.	2.1	24
68	Solution structure of endothelin-3 determined using NMR spectroscopy. <i>Biochemistry</i> , 1992, 31, 5640-5645.	2.5	45
69	Determination of the solution structure of a platelet-adhesion peptide of von Willebrand factor. <i>Biochemistry</i> , 1992, 31, 11152-11158.	2.5	13
70	Removing the two C-terminal residues of actin affects the filament structure. <i>Archives of Biochemistry and Biophysics</i> , 1992, 293, 110-116.	3.0	55
71	Structure of actin observed by fluorescence resonance energy transfer spectroscopy. <i>Journal of Muscle Research and Cell Motility</i> , 1992, 13, 132-145.	2.0	41
72	Models of the actin monomer and filament from fluorescence resonance-energy transfer. <i>FEBS Journal</i> , 1992, 205, 591-601.	0.2	13

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73	Structural interpretation of fluorescence resonance energy transfer measurements. <i>Bioinformatics</i> , 1991, 7, 471-477.	4.1	4
74	The Transport and Metabolism of Urea in <i>Chara australis</i> . <i>Journal of Experimental Botany</i> , 1988, 39, 763-774.	4.8	26
75	Reflect: Augmented Browsing for the Life Scientist. <i>Nature Precedings</i> , 0, , .	0.1	1
76	Reflect: A Practical Approach to Web Semantics. <i>SSRN Electronic Journal</i> , 0, , .	0.4	1