Sean O'Donoghue

List of Publications by Year
in descending order

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	Visualization of omics data for systems biology. Nature Methods, 2010, 7, S56-S68.	19.0	548
2	COMPARTMENTS: unification and visualization of protein subcellular localization evidence. Database: the Journal of Biological Databases and Curation, 2014, 2014, bau012-bau012.	3.0	483
3	Comparison of ARM and HEAT protein repeats. Journal of Molecular Biology, 2001, 309, 1-18.	4.2	464
4	Automated NOESY interpretation with ambiguous distance restraints: the refined NMR solution structure of the pleckstrin homology domain from Î²-spectrin 1 1Edited by P. E. Wright. Journal of Molecular Biology, 1997, 269, 408-422.	4.2	414
5	Automated Assignment of Ambiguous Nuclear Overhauser Effects with ARIA. Methods in Enzymology, 2001, 339, 71-90.	1.0	319
6	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
7	Ambiguous NOEs and automated NOE assignment. Progress in Nuclear Magnetic Resonance Spectroscopy, 1998, 32, 107-139.	7.5	198
8	The structure of a novel insecticidal neurotoxin, Ï‰-atracotoxin-HV1, from the venom of an Australian funnel web spider. Nature Structural Biology, 1997, 4, 559-566.	9.7	172
9	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
10	Monogenic and polygenic determinants of sarcoma risk: an international genetic study. Lancet Oncology, The, 2016, 17, 1261-1271.	10.7	161
11	Adaptation of protein surfaces to subcellular location 1 1Edited by F. E. Cohen. Journal of Molecular Biology, 1998, 276, 517-525.	4.2	158
12	Visualization of macromolecular structures. Nature Methods, 2010, 7, S42-S55.	19.0	137
13	PredictProtein - Predicting Protein Structure and Function for 29 Years. Nucleic Acids Research, 2021, 49, W535-W540.	14.5	135
14	Visualizing biological dataâ€”now and in the future. Nature Methods, 2010, 7, S2-S4.	19.0	115
15	Comprehensive comparison of large-scale tissue expression datasets. PeerJ, 2015, 3, e1054.	2.0	102
16	Arena3D: visualization of biological networks in 3D. BMC Systems Biology, 2008, 2, 104.	3.0	95
17	High Resolution NMR Solution Structure of the Leucine Zipper Domain of the c-Jun Homodimer. Journal of Biological Chemistry, 1996, 271, 13663-13667.	3.4	93
18	Reflect: augmented browsing for the life scientist. Nature Biotechnology, 2009, 27, 508-510.	17.5	91

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19	Text mining for biology - the way forward: opinions from leading scientists. Genome Biology, 2008, 9, S7.	9.6	74
20	Visualization of Biomedical Data. Annual Review of Biomedical Data Science, 2018, 1, 275-304.	6.5	63
21	Aquaria: simplifying discovery and insight from protein structures. Nature Methods, 2015, 12, 98-99.	19.0	58
22	Defective Lamin A-Rb Signaling in Hutchinson-Gilford Progeria Syndrome and Reversal by Farnesyltransferase Inhibition. PLoS ONE, 2010, 5, e11132.	2.5	58
23	Removing the two C-terminal residues of actin affects the filament structure. Archives of Biochemistry and Biophysics, 1992, 293, 110-116.	3.0	55
24	Martini: using literature keywords to compare gene sets. Nucleic Acids Research, 2010, 38, 26-38.	14.5	51
25	Caipirini: using gene sets to rank literature. BioData Mining, 2012, 5, 1.	4.0	47
26	Solution structure of endothelin-3 determined using NMR spectroscopy. Biochemistry, 1992, 31, 5640-5645.	2.5	45
27	NMR studies of the aggregation of glucagon-like peptide-1: formation of a symmetric helical dimer. FEBS Letters, 2002, 515, 165-170.	2.8	43
28	Molecular Graphics: Bridging Structural Biologists and Computer Scientists. Structure, 2019, 27, 1617-1623.	3.3	42
29	Structure of actin observed by fluorescence resonance energy transfer spectroscopy. Journal of Muscle Research and Cell Motility, 1992, 13, 132-145.	2.0	41
30	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. Journal of Biomolecular NMR, 1996, 8, 193-206.	2.8	38
31	Unraveling the symmetry ambiguity in a hexamer: calculation of the R6 human insulin structure. Journal of Biomolecular NMR, 2000, 16, 93-108.	2.8	37
32	Catalysis by Hamster Dihydroorotase: Zinc Binding, Site-Directed Mutagenesis, and Interaction with Inhibitors. Biochemistry, 1995, 34, 11344-11352.	2.5	35
33	The Transport and Metabolism of Urea inChara australis. Journal of Experimental Botany, 1988, 39, 763-774.	4.8	26
34	The Molecular Control Toolkit: Controlling 3D molecular graphics via gesture and voice. , 2013, , .		26
35	Determination of the structure of symmetric coiled-coil proteins from NMR data: application of the leucine zipper proteins Jun and GCN4. Protein Engineering, Design and Selection, 1993, 6, 557-564.	2.1	24
36	Sisyphus and prediction of protein structure. Bioinformatics, 1997, 13, 345-356.	4.1	24

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37	How to learn about gene function: text-mining or ontologies?. Methods, 2015, 74, 3-15.	3.8	24
38	SARSâ€CoVâ€2 structural coverage map reveals viral protein assembly, mimicry, and hijacking mechanisms. Molecular Systems Biology, 2021, 17, e10079.	7.2	22
39	Stereospecificity of Substrate Usage by Glyoxalase 1: Nuclear Magnetic Resonance Studies of Kinetics and Hemithioacetal Substrate Conformation. Biochemistry, 1994, 33, 3548-3559.	2.5	21
40	Molecular dynamics and accuracy of NMR structures: Effects of error bounds and data removal. Proteins: Structure, Function and Bioinformatics, 1999, 34, 453-463.	2.6	20
41	The SRS 3D module: integrating structures, sequences and features. Bioinformatics, 2004, 20, 2476-2478.	4.1	20
42	SnapShot: Insulin/IGF1 Signaling. Cell, 2015, 161, 948-948.e1.	28.9	19
43	Tertiary structure prediction using mean-force potentials and internal energy functions: successful prediction for coiled-coil geometries. Folding & Design, 1997, 2, S47-S52.	4.5	18
44	Comparative eye-tracking evaluation of scatterplots and parallel coordinates. Visual Informatics, 2017, 1, 118-131.	4.4	18
45	Grand Challenges in Bioinformatics Data Visualization. Frontiers in Bioinformatics, 2021, 1, .	2.1	18
46	The Dark Proteome Database. BioData Mining, 2017, 10, 24.	4.0	16
47	Reflect: A practical approach to web semantics. Web Semantics, 2010, 8, 182-189.	2.9	14
48	Determination of the solution structure of a platelet-adhesion peptide of von Willebrand factor. Biochemistry, 1992, 31, 11152-11158.	2.5	13
49	Models of the actin monomer and filament from fluorescence resonance-energy transfer. FEBS Journal, 1992, 205, 591-601.	0.2	13
50	Error distribution derived NOE distance restraints. Proteins: Structure, Function and Bioinformatics, 2006, 64, 652-664.	2.6	12
51	SnapShot: Phosphoregulation of Mitosis. Cell, 2017, 169, 1358-1358.e1.	28.9	12
52	Solution structure of the coiled-coil trimerization domain from lung surfactant protein D. Journal of Biomolecular NMR, 2002, 24, 89-102.	2.8	11
53	The PSSH database of alignments between protein sequences and tertiary structures. Nucleic Acids Research, 2003, 31, 494-498.	14.5	11
54	Visualization and Analysis of Epiproteome Dynamics. Journal of Molecular Biology, 2019, 431, 1519-1539.	4.2	10

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55	Temporal ordering of omics and multiomic events inferred from time-series data. Npj Systems Biology and Applications, 2020, 6, 22.	3.0	10
56	Versusâ€"A tool for evaluating visualizations and image quality using a 2AFC methodology. Visual Informatics, 2018, 2, 225-234.	4.4	9
57	Visualising intrinsic disorder and conformational variation in protein ensembles. Faraday Discussions, 2014, 169, 179-193.	3.2	8
58	Calculation of Symmetric Oligomer Structures from NMR Data. , 2002, , 131-161.		7
59	Integrated visual analysis of protein structures, sequences, and feature data. BMC Bioinformatics, 2015, 16, S7.	2.6	7
60	Dark Proteins Important for Cellular Function. Proteomics, 2018, 18, e1800227.	2.2	7
61	On the use of 1D, 2D, and 3D visualisation for molecular graphics. , 2014, , .		5
62	Structural interpretation of fluorescence resonanceâ€"energy transfer measurements. Bioinformatics, 1991, 7, 471-477.	4.1	4
63	Evaluating Viewpoint Entropy for Ribbon Representation of Protein Structure. Computer Graphics Forum, 2016, 35, 181-190.	3.0	4
64	Visual analytics of phosphorylation time-series data on insulin response. , 2013, , .		3
65	Evaluating the Effectiveness of Color to Convey Alignment Quality in Macromolecular Structures. , 2015, , .		2
66	A benchmark dataset for analyzing and visualizing the dynamic epiproteome. Data in Brief, 2019, 25, 104000.	1.0	2
67	SnapShot: S-Phase Entry and Exit. Cell, 2019, 179, 802-802.e1.	28.9	2
68	Collaborative Sense-Making in Genomic Research: The Role of Visualisation. IEEE Transactions on Visualization and Computer Graphics, 2022, 28, 4477-4489.	4.4	2
69	Reflect: Augmented Browsing for the Life Scientist. Nature Precedings, 0, , .	0.1	1
70	Visual Analytics of Gene Sets Comparison. , 2015, , .		1
71	Using videogames to improve molecular graphics tools. , 2016, , .		1
72	Can Videogame Players Inform Better Scientific Visualization'. , 2016, , .		1

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73	Reflect: A Practical Approach to Web Semantics. SSRN Electronic Journal, 0, , .	0.4	1
74	Visualising biological data: Current perspectives. , 2013, , .		0
75	Visual Analytics of Signalling Pathways Using Time Profiles. Advances in Experimental Medicine and Biology, 2015, 823, 3-22.	1.6	0
76	Developing a Visual Analytics Tool for Large-Scale Proteomics Time-Series Data. , 2016, , .		0