Luciano A Abriata

List of Publications by Year
in descending order

Source: https://exaly.com/author-pdf/8659133/publications.pdf

Version: 2024-02-01

70 papers	2,352 citations	318942 23 h-index	286692 43 g-index
85 all docs	85 docs citations	85 times ranked	3813 citing authors

#	Article	IF	Citations
1	How Technologies Assisted Science Learning at Home During the COVID-19 Pandemic. DNA and Cell Biology, 2022, 41, 19-24.	0.9	9
2	Online tools to easily build virtual molecular models for display in augmented and virtual reality on the web. Journal of Molecular Graphics and Modelling, 2022, 114, 108164.	1.3	20
3	State-of-the-art web services forde novoprotein structure prediction. Briefings in Bioinformatics, 2021, 22, .	3.2	13
4	Siteâ€Specific Phosphorylation of Huntingtin Exonâ€...1 Recombinant Proteins Enabled by the Discovery of Novel Kinases. ChemBioChem, 2021, 22, 217-231.	1.3	18
5	Bottom-up de novo design of functional proteins with complex structural features. Nature Chemical Biology, 2021, 17, 492-500.	3.9	65
6	Assessment of transferable forcefields for protein simulations attests improved description of disordered states and secondary structure propensities, and hints at multi-protein systems as the next challenge for optimization. Computational and Structural Biotechnology Journal, 2021, 19, 2626-2636.	1.9	25
7	Inositol pyrophosphates promote the interaction of SPX domains with the coiled-coil motif of PHR transcription factors to regulate plant phosphate homeostasis. Nature Communications, 2021, 12, 384.	5.8	105
8	A minimalistic cyclic ice-binding peptide from phage display. Nature Communications, 2021, 12, 2675.	5.8	26
9	3D architecture and structural flexibility revealed in the subfamily of large glutamate dehydrogenases by a mycobacterial enzyme. Communications Biology, 2021, 4, 684.	2.0	3
10	MoleculARweb: A Web Site for Chemistry and Structural Biology Education through Interactive Augmented Reality out of the Box in Commodity Devices. Journal of Chemical Education, 2021, 98, 2243-2255.	1.1	26
11	Reviewing Challenges of Predicting Protein Melting Temperature Change Upon Mutation Through the Full Analysis of a Highly Detailed Dataset with High-Resolution Structures. Molecular Biotechnology, 2021, 63, 863-884.	1.3	13
12	Investigating Crosstalk Among PTMs Provides Novel Insight Into the Structural Basis Underlying the Differential Effects of Nt17 PTMs on Mutant Httex1 Aggregation. Frontiers in Molecular Biosciences, 2021, 8, 686086.	1.6	8
13	Democratizing interactive, immersive experiences for science education with WebXR. Nature Computational Science, 2021, 1, 631-632.	3.8	13
14	S-acylation controls SARS-CoV-2 membrane lipid organization and enhances infectivity. Developmental Cell, 2021, 56, 2790-2807.e8.	3.1	80
15	Control and Characterization of the Compactness of Single-Chain Nanoparticles. Macromolecules, 2021, 54, 11459-11467.	2.2	11
16	Structural and DNA binding properties of mycobacterial integration host factor mIHF. Journal of Structural Biology, 2020, 209, 107434.	1.3	3
17	Ligand Binding to the Collagen VI Receptor Triggers a Talin-to-RhoA Switch that Regulates Receptor Endocytosis. Developmental Cell, 2020, 53, 418-430.e4.	3.1	12
18	Building blocks for commodity augmented reality-based molecular visualization and modeling in web browsers. PeerJ Computer Science, 2020, 6, e260.	2.7	13

#	Article	IF	Citations
19	De novo development of proteolytically resistant therapeutic peptides for oral administration. Nature Biomedical Engineering, 2020, 4, 560-571.	11.6	65
20	De novo protein design enables the precise induction of RSV-neutralizing antibodies. Science, 2020, 368, .	6.0	137
21	Will Cryo-Electron Microscopy Shift the Current Paradigm in Protein Structure Prediction?. Journal of Chemical Information and Modeling, 2020, 60, 2443-2447.	2.5	8
22	About the need to make computational models of biological macromolecules available and discoverable. Bioinformatics, 2020, 36, 2952-2954.	1.8	7
23	Computational Tools for Structural Analysis of Proteins. , 2019, , 539-549.		0
24	A further leap of improvement in tertiary structure prediction in CASP13 prompts new routes for future assessments. Proteins: Structure, Function and Bioinformatics, 2019, 87, 1100-1112.	1.5	73
25	Population Structure, Molecular Epidemiology, and Î²-Lactamase Diversity among Stenotrophomonas maltophilia Isolates in the United States. MBio, 2019, 10, .	1.8	52
26	pH-Induced Binding of the Axial Ligand in an Engineered Cu_A Site Favors the Ì€_u State. Inorganic Chemistry, 2019, 58, 15687-15691.	1.9	0
27	Active Site-Induced Evolutionary Constraints Follow Fold Polarity Principles in Soluble Globular Enzymes. Molecular Biology and Evolution, 2019, 36, 1728-1733.	3.5	7
28	An experiment-informed signal transduction model for the role of the Staphylococcus aureus MecR1 protein in Î²-lactam resistance. Scientific Reports, 2019, 9, 19558.	1.6	11
29	Transmembrane Prolines Mediate Signal Sensing and Decoding in Bacillus subtilis DesK Histidine Kinase. MBio, 2019, 10, .	1.8	21
30	Nucleo-cytosolic Shuttling of ARGONAUTE1 Prompts a Revised Model of the Plant MicroRNA Pathway. Molecular Cell, 2018, 69, 709-719.e5.	4.5	193
31	Augmenting Research, Education, and Outreach with Client-Side Web Programming. Trends in Biotechnology, 2018, 36, 473-476.	4.9	13
32	Assessment of dataâ€assisted prediction by inclusion of crosslinking/massâ€spectrometry and small angle Xâ€ray scattering data in the 12th Critical Assessment of protein Structure Prediction experiment. Proteins: Structure, Function and Bioinformatics, 2018, 86, 215-227.	1.5	4
33	Electron transfer in an acidophilic bacterium: interaction between a diheme cytochrome and a cupredoxin. Chemical Science, 2018, 9, 4879-4891.	3.7	17
34	Definition and classification of evaluation units for tertiary structure prediction in CASP12 facilitated through semiâ€automated metrics. Proteins: Structure, Function and Bioinformatics, 2018, 86, 16-26.	1.5	12
35	Mitochondrial cytochrome c oxidase biogenesis: Recent developments. Seminars in Cell and Developmental Biology, 2018, 76, 163-178.	2.3	225
36	Assessment of hard target modeling in CASP12 reveals an emerging role of alignmentâ€based contact prediction methods. Proteins: Structure, Function and Bioinformatics, 2018, 86, 97-112.	1.5	79

#	Article	IF	Citations
37	Structural database resources for biological macromolecules. Briefings in Bioinformatics, 2017, 18, bbw049.	3.2	13
38	Signal Sensing and Transduction by Histidine Kinases as Unveiled through Studies on a Temperature Sensor. Accounts of Chemical Research, 2017, 50, 1359-1366.	7.6	46
39	Structural, physicochemical and dynamic features conserved within the aerolysin pore-forming toxin family. Scientific Reports, 2017, 7, 13932.	1.6	38
40	Functional assays for the assessment of the pathogenicity of variants in GOSR2, an ER-to-Golgi SNARE involved in progressive myoclonus epilepsies. DMM Disease Models and Mechanisms, 2017, 10, 1391-1398.	1.2	11
41	Web Apps Come of Age for Molecular Sciences. Informatics, 2017, 4, 28.	2.4	20
42	Detection and sequence/structure mapping of biophysical constraints to protein variation in saturated mutational libraries and protein sequence alignments with a dedicated server. BMC Bioinformatics, 2016, 17, 242.	1.2	18
43	Immobilization of the N-terminal helix stabilizes prefusion paramyxovirus fusion proteins. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, E3844-51.	3.3	4
44	Molecular Effects of Concentrated Solutes on Protein Hydration, Dynamics, and Electrostatics. Biophysical Journal, 2016, 111, 743-755.	0.2	29
45	Optimization of Conformational Dynamics in an Epistatic Evolutionary Trajectory. Molecular Biology and Evolution, 2016, 33, 1768-1776.	3.5	51
46	A coiled coil switch mediates cold sensing by the thermosensory protein <scp>DesK</scp>. Molecular Microbiology, 2015, 98, 258-271.	1.2	50
47	Reversible Switching of Redoxâ€Active Molecular Orbitals and Electron Transfer Pathways in Cu_A Sites of Cytochromeâ€…c Oxidase. Angewandte Chemie - International Edition, 2015, 54, 9555-9559.	7.2	11
48	How Structural and Physicochemical Determinants Shape Sequence Constraints in a Functional Enzyme. PLoS ONE, 2015, 10, e0118684.	1.1	41
49	Assessing the potential of atomistic molecular dynamics simulations to probe reversible protein-protein recognition and binding. Scientific Reports, 2015, 5, 10549.	1.6	50
50	The importance of dynamics in integrative modeling of supramolecular assemblies. Current Opinion in Structural Biology, 2015, 31, 28-34.	2.6	20
51	GtrA Protein Rv3789 Is Required for Arabinosylation of Arabinogalactan in Mycobacterium tuberculosis. Journal of Bacteriology, 2015, 197, 3686-3697.	1.0	26
52	Redox-state sensing by hydrogen bonds in the CuA center of cytochrome c oxidase. Journal of Inorganic Biochemistry, 2014, 132, 18-20.	1.5	5
53	Molecular dynamics simulations of apocupredoxins: insights into the formation and stabilization of copper sites under entatic control. Journal of Biological Inorganic Chemistry, 2014, 19, 565-575.	1.1	19
54	Control of the Electronic Ground State on an Electronâ€Transfer Copper Site by Secondâ€Sphere Perturbations. Angewandte Chemie - International Edition, 2014, 53, 6188-6192.	7.2	18

#	Article	IF	Citations
55	Dissecting the Effects of Concentrated Carbohydrate Solutions on Protein Diffusion, Hydration, and Internal Dynamics. Journal of Physical Chemistry B, 2014, 118, 5310-5321.	1.2	24
56	A dimerization interface mediated by functionally critical residues creates interfacial disulfide bonds and copper sites in CueP. Journal of Inorganic Biochemistry, 2014, 140, 199-201.	1.5	5
57	All-atom simulations of crowding effects on ubiquitin dynamics. Physical Biology, 2013, 10, 045006.	0.8	13
58	Native CuA redox sites are largely resilient to pH variations within a physiological range. Chemical Communications, 2013, 49, 5381.	2.2	18
59	Investigation of non-corrin cobalt(II)-containing sites in protein structures of the Protein Data Bank. Acta Crystallographica Section B: Structural Science, Crystal Engineering and Materials, 2013, 69, 176-183.	0.5	6
60	Off-the-Vine Ripening of Tomato Fruit Causes Alteration in the Primary Metabolite Composition. Metabolites, 2013, 3, 967-978.	1.3	37
61	Investigation of non-corrin cobalt(II)-containing sites in protein structures of the Protein Data Bank. Acta Crystallographica Section B: Structural Science, 2013, 69, 176-183.	1.8	0
62	Flexibility of the metal-binding region in apo-cupredoxins. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 9254-9259.	3.3	67
63	Analysis of copperâ€“ligand bond lengths in X-ray structures of different types of copper sites in proteins. Acta Crystallographica Section D: Biological Crystallography, 2012, 68, 1223-1231.	2.5	21
64	Sequenceâ€“functionâ€“stability relationships in proteins from datasets of functionally annotated variants: The case of TEM Î²â€lactamases. FEBS Letters, 2012, 586, 3330-3335.	1.3	24
65	Alternative ground states enable pathway switching in biological electron transfer. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 17348-17353.	3.3	31
66	Utilization of NMR spectroscopy to study biological fluids and metabolic processes: Two introductory activities. Concepts in Magnetic Resonance Part A: Bridging Education and Research, 2012, 40A, 171-178.	0.2	18
67	A Simple Spreadsheet Program To Simulate and Analyze the Far-UV Circular Dichroism Spectra of Proteins. Journal of Chemical Education, 2011, 88, 1268-1273.	1.1	22
68	Electronic Structure of the Ground and Excited States of the CuA Site by NMR Spectroscopy. Journal of the American Chemical Society, 2009, 131, 1939-1946.	6.6	47
69	Mechanism of CuA assembly. Nature Chemical Biology, 2008, 4, 599-601.	3.9	113
70	Engineered Mononuclear Variants in Bacillus cereus Metallo-Î²-lactamase BcII Are Inactive. Biochemistry, 2008, 47, 8590-8599.	1.2	25