

Claudia Andreini

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

43
papers

3,577
citations

27
h-index

50
g-index

50
ext. papers

4,318
ext. citations

6.6
avg. IF

5.32
L-index

#	Paper	IF	Citations
43	The Intriguing Role of Iron-Sulfur Clusters in the CIAPIN1 Protein Family. <i>Inorganics</i> , 2022 , 10, 52	2.9	
42	PDBe-KB: collaboratively defining the biological context of structural data. <i>Nucleic Acids Research</i> , 2021 ,	20.1	7
41	Upgraded AMBER Force Field for Zinc-Binding Residues and Ligands for Predicting Structural Properties and Binding Affinities in Zinc-Proteins. <i>ACS Omega</i> , 2020 , 5, 15301-15310	3.9	8
40	Basic Iron-Sulfur Centers. <i>Metal Ions in Life Sciences</i> , 2020 , 20,	2.6	1
39	HIV-1 Tat Protein Enters Dysfunctional Endothelial Cells via Integrins and Renders Them Permissive to Virus Replication. <i>International Journal of Molecular Sciences</i> , 2020 , 22,	6.3	4
38	Multi-metal Restriction by Calprotectin Impacts De Novo Flavin Biosynthesis in <i>Acinetobacter baumannii</i> . <i>Cell Chemical Biology</i> , 2019 , 26, 745-755.e7	8.2	35
37	Upgrading and Validation of the AMBER Force Field for Histidine and Cysteine Zinc(II)-Binding Residues in Sites with Four Protein Ligands. <i>Journal of Chemical Information and Modeling</i> , 2019 , 59, 3803-3816 ¹⁸	6.1	18
36	MetalPDB in 2018: a database of metal sites in biological macromolecular structures. <i>Nucleic Acids Research</i> , 2018 , 46, D459-D464	20.1	81
35	The human iron-proteome. <i>Metallomics</i> , 2018 , 10, 1223-1231	4.5	48
34	To what extent do structural changes in catalytic metal sites affect enzyme function?. <i>Journal of Inorganic Biochemistry</i> , 2018 , 179, 40-53	4.2	33
33	The cellular economy of the <i>Saccharomyces cerevisiae</i> zinc proteome. <i>Metallomics</i> , 2018 , 10, 1755-1776	4.5	43
32	Identification of the zinc, copper and cadmium metalloproteome of the protozoan <i>Tetrahymena thermophila</i> by systematic bioinformatics. <i>Archives of Microbiology</i> , 2017 , 199, 1141-1149	3	16
31	Differential Effects of Iron, Zinc, and Copper on Cell Growth and Resistance to. <i>Frontiers in Cellular and Infection Microbiology</i> , 2017 , 7, 536	5.9	16
30	The Relationship between Environmental Dioxygen and Iron-Sulfur Proteins Explored at the Genome Level. <i>PLoS ONE</i> , 2017 , 12, e0171279	3.7	30
29	MetalPredator: a web server to predict iron-sulfur cluster binding proteomes. <i>Bioinformatics</i> , 2016 , 32, 2850-2	7.2	31
28	Exploiting Bacterial Operons To Illuminate Human Iron-Sulfur Proteins. <i>Journal of Proteome Research</i> , 2016 , 15, 1308-22	5.6	30
27	Minimal Functional Sites in Metalloproteins and Their Usage in Structural Bioinformatics. <i>International Journal of Molecular Sciences</i> , 2016 , 17,	6.3	7

26	Hidden relationships between metalloproteins unveiled by structural comparison of their metal sites. <i>Scientific Reports</i> , 2015 , 5, 9486	4.9	8
25	Metals(3), a database-mining tool for the identification of structurally similar metal sites. <i>Journal of Biological Inorganic Chemistry</i> , 2014 , 19, 937-45	3.7	20
24	Metals2: a tool for the structural alignment of minimal functional sites in metal-binding proteins and nucleic acids. <i>Journal of Chemical Information and Modeling</i> , 2013 , 53, 3064-75	6.1	10
23	MetalPDB: a database of metal sites in biological macromolecular structures. <i>Nucleic Acids Research</i> , 2013 , 41, D312-9	20.1	86
22	A bioinformatics view of zinc enzymes. <i>Journal of Inorganic Biochemistry</i> , 2012 , 111, 150-6	4.2	131
21	MACiE: exploring the diversity of biochemical reactions. <i>Nucleic Acids Research</i> , 2012 , 40, D783-9	20.1	60
20	FindGeo: a tool for determining metal coordination geometry. <i>Bioinformatics</i> , 2012 , 28, 1658-60	7.2	29
19	HIV-1 tat promotes integrin-mediated HIV transmission to dendritic cells by binding Env spikes and competes neutralization by anti-HIV antibodies. <i>PLoS ONE</i> , 2012 , 7, e48781	3.7	40
18	Minimal functional sites allow a classification of zinc sites in proteins. <i>PLoS ONE</i> , 2011 , 6, e26325	3.7	98
17	A simple protocol for the comparative analysis of the structure and occurrence of biochemical pathways across superkingdoms. <i>Journal of Chemical Information and Modeling</i> , 2011 , 51, 730-8	6.1	21
16	Metal-MACiE: a database of metals involved in biological catalysis. <i>Bioinformatics</i> , 2009 , 25, 2088-9	7.2	53
15	Structural analysis of metal sites in proteins: non-heme iron sites as a case study. <i>Journal of Molecular Biology</i> , 2009 , 388, 356-80	6.5	44
14	Metalloproteomes: a bioinformatic approach. <i>Accounts of Chemical Research</i> , 2009 , 42, 1471-9	24.3	214
13	Occurrence of copper proteins through the three domains of life: a bioinformatic approach. <i>Journal of Proteome Research</i> , 2008 , 7, 209-16	5.6	151
12	Metal ions in biological catalysis: from enzyme databases to general principles. <i>Journal of Biological Inorganic Chemistry</i> , 2008 , 13, 1205-18	3.7	647
11	Non-heme iron through the three domains of life. <i>Proteins: Structure, Function and Bioinformatics</i> , 2007 , 67, 317-24	4.2	62
10	Predicting zinc binding at the proteome level. <i>BMC Bioinformatics</i> , 2007 , 8, 39	3.6	70
9	Mycobacterial cells have dual nickel-cobalt sensors: sequence relationships and metal sites of metal-responsive repressors are not congruent. <i>Journal of Biological Chemistry</i> , 2007 , 282, 32298-310	5.4	77

8	Counting the zinc-proteins encoded in the human genome. <i>Journal of Proteome Research</i> , 2006 , 5, 196-201	6.1	693
7	Zinc through the three domains of life. <i>Journal of Proteome Research</i> , 2006 , 5, 3173-8	5.6	434
6	SPINE bioinformatics and data-management aspects of high-throughput structural biology. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2006 , 62, 1184-95		15
5	Predicting metals sensed by ArsR-SmtB repressors: allosteric interference by a non-effector metal. <i>Molecular Microbiology</i> , 2006 , 59, 1341-56	4.1	35
4	Improving Prediction of Zinc Binding Sites by Modeling the Linkage Between Residues Close in Sequence. <i>Lecture Notes in Computer Science</i> , 2006 , 309-320	0.9	5
3	Comparative analysis of the ADAM and ADAMTS families. <i>Journal of Proteome Research</i> , 2005 , 4, 881-8	5.6	26
2	A hint to search for metalloproteins in gene banks. <i>Bioinformatics</i> , 2004 , 20, 1373-80	7.2	106
1	Bioinformatic comparison of structures and homology-models of matrix metalloproteinases. <i>Journal of Proteome Research</i> , 2004 , 3, 21-31	5.6	31