

Kristina Djinovic-Carugo

List of Publications by Year in Descending Order

Source: <https://exaly.com/author-pdf/7301401/kristina-djinovic-carugo-publications-by-year.pdf>

Version: 2024-04-20

This document has been generated based on the publications and citations recorded by exaly.com. For the latest version of this publication list, visit the link given above.

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

108
papers

4,072
citations

32
h-index

61
g-index

113
ext. papers

4,703
ext. citations

7.8
avg, IF

5.31
L-index

#	Paper	IF	Citations
108	Impact of the dynamics of the catalytic arginine on nitrite and chlorite binding by dimeric chlorite dismutase.. <i>Journal of Inorganic Biochemistry</i> , 2021 , 227, 111689	4.2	1
107	PHF3 regulates neuronal gene expression through the Pol II CTD reader domain SPOC. <i>Nature Communications</i> , 2021 , 12, 6078	17.4	1
106	Molecular basis of F-actin regulation and sarcomere assembly via myotilin. <i>PLoS Biology</i> , 2021 , 19, e3001448	14.8	3
105	Order from disorder in the sarcomere: FATZ forms a fuzzy but tight complex and phase-separated condensates with β -actinin. <i>Science Advances</i> , 2021 , 7,	14.3	1
104	FLNC-Associated Myofibrillar Myopathy: New Clinical, Functional, and Proteomic Data. <i>Neurology: Genetics</i> , 2021 , 7, e590	3.8	0
103	In-depth interrogation of protein thermal unfolding data with MoltenProt. <i>Protein Science</i> , 2021 , 30, 201-217	6.3	6
102	Arresting the Catalytic Arginine in Chlorite Dismutases: Impact on Heme Coordination, Thermal Stability, and Catalysis. <i>Biochemistry</i> , 2021 , 60, 621-634	3.2	3
101	Phosphoproteomics identifies dual-site phosphorylation in an extended basophilic motif regulating FILIP1-mediated degradation of filamin-C. <i>Communications Biology</i> , 2020 , 3, 253	6.7	9
100	A conformation-specific ON-switch for controlling CAR T cells with an orally available drug. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020 , 117, 14926-14935	11.5	22
99	Structures of three MORN repeat proteins and a re-evaluation of the proposed lipid-binding properties of MORN repeats. <i>PLoS ONE</i> , 2020 , 15, e0242677	3.7	10
98	Crystal structures and calorimetry reveal catalytically relevant binding mode of coproporphyrin and coproheme in coproporphyrin ferrochelatase. <i>FEBS Journal</i> , 2020 , 287, 2779-2796	5.7	11
97	Tailored Suits Fit Better: Customized Protein Crystallization Screens. <i>Crystal Growth and Design</i> , 2020 , 20, 984-994	3.5	1
96	Molecular mechanism of leukocidin GH-integrin CD11b/CD18 recognition and species specificity. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020 , 117, 317-327	11.5	8
95	PKAN neurodegeneration and residual PANK2 activities in patient erythrocytes. <i>Annals of Clinical and Translational Neurology</i> , 2020 , 7, 1340-1351	5.3	4
94	X-ray-induced photoreduction of heme metal centers rapidly induces active-site perturbations in a protein-independent manner. <i>Journal of Biological Chemistry</i> , 2020 , 295, 13488-13501	5.4	15
93	Calcium modulates the domain flexibility and function of an β -actinin similar to the ancestral β -actinin. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020 , 117, 22101-22112	11.5	5
92	Actinobacterial Coproheme Decarboxylases Use Histidine as a Distal Base to Promote Compound I Formation. <i>ACS Catalysis</i> , 2020 , 10, 5405-5418	13.1	10

91	Structures of three MORN repeat proteins and a re-evaluation of the proposed lipid-binding properties of MORN repeats 2020 , 15, e0242677		
90	Structures of three MORN repeat proteins and a re-evaluation of the proposed lipid-binding properties of MORN repeats 2020 , 15, e0242677		
89	Structures of three MORN repeat proteins and a re-evaluation of the proposed lipid-binding properties of MORN repeats 2020 , 15, e0242677		
88	Structures of three MORN repeat proteins and a re-evaluation of the proposed lipid-binding properties of MORN repeats 2020 , 15, e0242677		
87	Structures of three MORN repeat proteins and a re-evaluation of the proposed lipid-binding properties of MORN repeats 2020 , 15, e0242677		
86	Redox Cofactor Rotates during Its Stepwise Decarboxylation: Molecular Mechanism of Conversion of Coproheme to Heme. <i>ACS Catalysis</i> , 2019 , 9, 6766-6782	13.1	17
85	HspB1 phosphorylation regulates its intramolecular dynamics and mechanosensitive molecular chaperone interaction with filamin C. <i>Science Advances</i> , 2019 , 5, eaav8421	14.3	31
84	Protective properties of the cultured stem cell proteome studied in an animal model of acetaminophen-induced acute liver failure. <i>Molecular Biology Reports</i> , 2019 , 46, 3101-3112	2.8	6
83	Naked Metal Cations Swimming in Protein Crystals. <i>Crystals</i> , 2019 , 9, 581	2.3	1
82	Secreted heme peroxidase from : Insights into catalysis, structure, and biological role. <i>Journal of Biological Chemistry</i> , 2018 , 293, 1330-1345	5.4	6
81	Roles of distal aspartate and arginine of B-class dye-decolorizing peroxidase in heterolytic hydrogen peroxide cleavage. <i>Journal of Biological Chemistry</i> , 2018 , 293, 14823-14838	5.4	23
80	Actinin/titin interaction: A dynamic and mechanically stable cluster of bonds in the muscle Z-disk. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017 , 114, 1015-1020	11.5	28
79	Deciphering the BAR code of membrane modulators. <i>Cellular and Molecular Life Sciences</i> , 2017 , 74, 2413-2438	11.9	42
78	Bacterial protease uses distinct thermodynamic signatures for substrate recognition. <i>Scientific Reports</i> , 2017 , 7, 2848	4.9	10
77	Fcab-HER2 Interaction: a MÅage ¶Trois. Lessons from X-Ray and Solution Studies. <i>Structure</i> , 2017 , 25, 878-889.e5	5.2	22
76	Structure of human promyeloperoxidase (proMPO) and the role of the propeptide in processing and maturation. <i>Journal of Biological Chemistry</i> , 2017 , 292, 8244-8261	5.4	27
75	Molecular Mechanism of Enzymatic Chlorite Detoxification: Insights from Structural and Kinetic Studies. <i>ACS Catalysis</i> , 2017 , 7, 7962-7976	13.1	22
74	A novel non-canonical PIP-box mediates PARG interaction with PCNA. <i>Nucleic Acids Research</i> , 2017 , 45, 9741-9759	20.1	27

73	Conformational plasticity and evolutionary analysis of the myotilin tandem Ig domains. <i>Scientific Reports</i> , 2017 , 7, 3993	4.9	7
72	Two-faced Fcab prevents polymerization with VEGF and reveals thermodynamics and the 2.15Å crystal structure of the complex. <i>MAbs</i> , 2017 , 9, 1088-1104	6.6	9
71	Human cytomegalovirus phosphoproteins are hypophosphorylated and intrinsically disordered. <i>Journal of General Virology</i> , 2017 , 98, 471-485	4.9	6
70	Hydrogen peroxide-mediated conversion of coproheme to heme b by HemQ-lessons from the first crystal structure and kinetic studies. <i>FEBS Journal</i> , 2016 , 283, 4386-4401	5.7	23
69	The sarcomeric cytoskeleton: from molecules to motion. <i>Journal of Experimental Biology</i> , 2016 , 219, 135-145	12.4	
68	Structural characterization of a <i>Vatairea macrocarpa</i> lectin in complex with a tumor-associated antigen: A new tool for cancer research. <i>International Journal of Biochemistry and Cell Biology</i> , 2016 , 72, 27-39	5.6	11
67	Vaccinia Virus Immunomodulator A46: A Lipid and Protein-Binding Scaffold for Sequestering Host TIR-Domain Proteins. <i>PLoS Pathogens</i> , 2016 , 12, e1006079	7.6	17
66	Congenital macrothrombocytopenia-linked mutations in the actin-binding domain of β -actinin-1 enhance F-actin association. <i>FEBS Letters</i> , 2016 , 590, 685-95	3.8	14
65	Structure and calcium-binding studies of calmodulin-like domain of human non-muscle β -actinin-1. <i>Scientific Reports</i> , 2016 , 6, 27383	4.9	15
64	Criteria to Extract High-Quality Protein Data Bank Subsets for Structure Users. <i>Methods in Molecular Biology</i> , 2016 , 1415, 139-52	1.4	6
63	Chemistry and Molecular Dynamics Simulations of Heme b-HemQ and Coproheme-HemQ. <i>Biochemistry</i> , 2016 , 55, 5398-412	3.2	19
62	From chlorite dismutase towards HemQ - the role of the proximal H-bonding network in haeme binding. <i>Bioscience Reports</i> , 2016 , 36,	4.1	14
61	Structural insights into Ca ²⁺ -calmodulin regulation of Plectin 1a-integrin β interaction in hemidesmosomes. <i>Structure</i> , 2015 , 23, 558-570	5.2	23
60	Structural biology of the lanthanides-mining rare earths in the Protein Data Bank. <i>Journal of Inorganic Biochemistry</i> , 2015 , 143, 69-76	4.2	18
59	Dimeric chlorite dismutase from the nitrogen-fixing cyanobacterium <i>Cyanothece</i> sp. PCC7425. <i>Molecular Microbiology</i> , 2015 , 96, 1053-68	4.1	17
58	Missing strings of residues in protein crystal structures. <i>Intrinsically Disordered Proteins</i> , 2015 , 3, e1095697		22
57	The Heptameric SmAP1 and SmAP2 Proteins of the Crenarchaeon <i>Sulfolobus Solfataricus</i> Bind to Common and Distinct RNA Targets. <i>Life</i> , 2015 , 5, 1264-81	3	12
56	Structural basis for the interaction of protein S1 with the <i>Escherichia coli</i> ribosome. <i>Nucleic Acids Research</i> , 2015 , 43, 661-73	20.1	42

55	Structure and heme-binding properties of HemQ (chlorite dismutase-like protein) from <i>Listeria monocytogenes</i> . <i>Archives of Biochemistry and Biophysics</i> , 2015 , 574, 36-48	4.1	32
54	Manipulating conserved heme cavity residues of chlorite dismutase: effect on structure, redox chemistry, and reactivity. <i>Biochemistry</i> , 2014 , 53, 77-89	3.2	27
53	Direct interaction of actin filaments with F-BAR protein pacsin2. <i>EMBO Reports</i> , 2014 , 15, 1154-62	6.5	47
52	The Center for Optimized Structural Studies (COSS) platform for automation in cloning, expression, and purification of single proteins and protein-protein complexes. <i>Amino Acids</i> , 2014 , 46, 1565-82	3.5	13
51	Crystal structure and its bearing towards an understanding of key biological functions of EpCAM. <i>Nature Communications</i> , 2014 , 5, 4764	17.4	58
50	Packing bridges in protein crystal structures. <i>Journal of Applied Crystallography</i> , 2014 , 47, 458-461	3.8	13
49	The structure and regulation of human muscle β -actinin. <i>Cell</i> , 2014 , 159, 1447-60	56.2	118
48	A proteomic Ramachandran plot (PRplot). <i>Amino Acids</i> , 2013 , 44, 781-90	3.5	12
47	The G-M-N motif determines ion selectivity in the yeast magnesium channel Mrs2p. <i>Metallomics</i> , 2013 , 5, 745-52	4.5	12
46	Myopodin is an F-actin bundling protein with multiple independent actin-binding regions. <i>Journal of Muscle Research and Cell Motility</i> , 2013 , 34, 61-9	3.5	11
45	False positive RNA binding activities after Ni-affinity purification from <i>Escherichia coli</i> . <i>RNA Biology</i> , 2013 , 10, 1066-9	4.8	15
44	Novel bilobe components in <i>Trypanosoma brucei</i> identified using proximity-dependent biotinylation. <i>Eukaryotic Cell</i> , 2013 , 12, 356-67		98
43	Structural and functional characterization of the N-terminal domain of the yeast Mg ²⁺ channel Mrs2. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2013 , 69, 1653-64		9
42	Half a century of Ramachandran plots. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2013 , 69, 1333-41		50
41	The <i>Pseudomonas aeruginosa</i> catabolite repression control protein Crc is devoid of RNA binding activity. <i>PLoS ONE</i> , 2013 , 8, e64609	3.7	38
40	Human cardiac ryanodine receptor: preparation, crystallization and preliminary X-ray ANALYSIS of the N-terminal region. <i>Protein and Peptide Letters</i> , 2013 , 20, 1211-6	1.9	3
39	How many packing contacts are observed in protein crystals?. <i>Journal of Structural Biology</i> , 2012 , 180, 96-100	3.4	21
38	Redox thermodynamics of high-spin and low-spin forms of chlorite dismutases with diverse subunit and oligomeric structures. <i>Biochemistry</i> , 2012 , 51, 9501-12	3.2	27

37	Impact of subunit and oligomeric structure on the thermal and conformational stability of chlorite dismutases. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2012 , 1824, 1031-8	4	18
36	Structural and biochemical studies on ATP binding and hydrolysis by the Escherichia coli RNA chaperone Hfq. <i>PLoS ONE</i> , 2012 , 7, e50892	3.7	16
35	Homodimeric β -galactosidase from <i>Lactobacillus delbrueckii</i> subsp. <i>bulgaricus</i> DSM 20081: expression in <i>Lactobacillus plantarum</i> and biochemical characterization. <i>Journal of Agricultural and Food Chemistry</i> , 2012 , 60, 1713-21	5.7	57
34	Structural flexibility of RNA as molecular basis for Hfq chaperone function. <i>Nucleic Acids Research</i> , 2012 , 40, 8072-84	20.1	27
33	Pathophysiology of protein aggregation and extended phenotyping in filaminopathy. <i>Brain</i> , 2012 , 135, 2642-60	11.2	60
32	Functional analysis of the conserved hydrophobic gate region of the magnesium transporter CorA. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2011 , 1808, 1587-91	3.8	7
31	Mutations in the N-terminal actin-binding domain of filamin C cause a distal myopathy. <i>American Journal of Human Genetics</i> , 2011 , 88, 729-740	11	101
30	Heterologous overexpression of <i>Glomerella cingulata</i> FAD-dependent glucose dehydrogenase in <i>Escherichia coli</i> and <i>Pichia pastoris</i> . <i>Microbial Cell Factories</i> , 2011 , 10, 106	6.4	35
29	Structural analysis of full-length Hfq from <i>Escherichia coli</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2011 , 67, 536-40		23
28	Structural insights into the dynamics and function of the C-terminus of the <i>E. coli</i> RNA chaperone Hfq. <i>Nucleic Acids Research</i> , 2011 , 39, 4900-15	20.1	65
27	Unexpected diversity of chlorite dismutases: a catalytically efficient dimeric enzyme from <i>Nitrobacter winogradskyi</i> . <i>Journal of Bacteriology</i> , 2011 , 193, 2408-17	3.5	66
26	Opening of tandem calponin homology domains regulates their affinity for F-actin. <i>Nature Structural and Molecular Biology</i> , 2010 , 17, 614-6	17.6	71
25	Structural and functional characterisation of the chlorite dismutase from the nitrite-oxidizing bacterium " <i>Candidatus Nitrospira defluvii</i> ": identification of a catalytically important amino acid residue. <i>Journal of Structural Biology</i> , 2010 , 172, 331-42	3.4	68
24	Structural portrait of filamin interaction mechanisms. <i>Current Protein and Peptide Science</i> , 2010 , 11, 639-50		14
23	Purification of recombinant growth hormone by clear native gels for conformational analyses: preservation of conformation and receptor binding. <i>Amino Acids</i> , 2010 , 39, 859-69	3.5	8
22	Crystallization and preliminary X-ray diffraction analysis of the N-terminal domain of Mrs2, a magnesium ion transporter from yeast inner mitochondrial membrane. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2010 , 66, 658-61		4
21	Structural study of X-ray induced activation of carbonic anhydrase. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009 , 106, 10609-13	11.5	66
20	Terminal assembly of sarcomeric filaments by intermolecular beta-sheet formation. <i>Trends in Biochemical Sciences</i> , 2009 , 34, 33-9	10.3	13

19	Can soaked-in scavengers protect metalloprotein active sites from reduction during data collection?. <i>Journal of Synchrotron Radiation</i> , 2009 , 16, 191-204	2.4	55
18	Structural basis of heme binding in the Cu,Zn superoxide dismutase from <i>Haemophilus ducreyi</i> . <i>Journal of Molecular Biology</i> , 2009 , 386, 406-18	6.5	12
17	Novel structural insights into F-actin-binding and novel functions of calponin homology domains. <i>Current Opinion in Structural Biology</i> , 2008 , 18, 702-8	8.1	58
16	Alpha-actinin structure and regulation. <i>Cellular and Molecular Life Sciences</i> , 2008 , 65, 2688-701	10.3	300
15	Evolutionarily conserved human targets of adenosine to inosine RNA editing. <i>Nucleic Acids Research</i> , 2005 , 33, 1162-8	20.1	148
14	Unique features of the sodC-encoded superoxide dismutase from <i>Mycobacterium tuberculosis</i> , a fully functional copper-containing enzyme lacking zinc in the active site. <i>Journal of Biological Chemistry</i> , 2004 , 279, 33447-55	5.4	67
13	Crystal structure of nitrous oxide reductase from <i>Paracoccus denitrificans</i> at 1.6 Å resolution. <i>Biochemical Journal</i> , 2003 , 369, 77-88	3.8	139
12	Functional plasticity of CH domains. <i>FEBS Letters</i> , 2002 , 513, 98-106	3.8	259
11	The spectrin repeat: a structural platform for cytoskeletal protein assemblies. <i>FEBS Letters</i> , 2002 , 513, 119-23	3.8	214
10	On the routine use of soft X-rays in macromolecular crystallography. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2001 , 57, 689-95		28
9	Structural Studies on Cytoskeletal Proteins. <i>Cellular and Molecular Biology Letters</i> , 2001 , 6, 199	8.1	
8	Revisiting the catalytic CuZ cluster of nitrous oxide (N ₂ O) reductase. Evidence of a bridging inorganic sulfur. <i>Journal of Biological Chemistry</i> , 2000 , 275, 41133-6	5.4	138
7	Structure of the alpha-actinin rod: molecular basis for cross-linking of actin filaments. <i>Cell</i> , 1999 , 98, 537-46	3.6	218
6	Evolutionary constraints for dimer formation in prokaryotic Cu,Zn superoxide dismutase. <i>Journal of Molecular Biology</i> , 1999 , 285, 283-96	6.5	59
5	A cell for producing xenon-derivative crystals for cryocrystallographic analysis. <i>Journal of Applied Crystallography</i> , 1998 , 31, 812-814	3.8	6
4	Modulation of the catalytic rate of Cu,Zn superoxide dismutase in single and double mutants of conserved positively and negatively charged residues. <i>Biochemistry</i> , 1995 , 34, 6043-9	3.2	45
3	Conserved patterns in the Cu,Zn superoxide dismutase family. <i>Journal of Molecular Biology</i> , 1994 , 238, 366-86	6.5	202
2	Crystallographic study of azide-inhibited bovine Cu,Zn superoxide dismutase. <i>Journal of Molecular Biology</i> , 1994 , 240, 179-83	6.5	27

1	Structures of three MORN repeat proteins and a re-evaluation of the proposed lipid-binding properties of MORN repeats	3
---	---	---