

Kristina Djinovic-Carugo

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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	Alpha-actinin structure and regulation. <i>Cellular and Molecular Life Sciences</i> , 2008 , 65, 2688-701	10.3	300
107	Functional plasticity of CH domains. <i>FEBS Letters</i> , 2002 , 513, 98-106	3.8	259
106	Structure of the alpha-actinin rod: molecular basis for cross-linking of actin filaments. <i>Cell</i> , 1999 , 98, 537-462	4.6	218
105	The spectrin repeat: a structural platform for cytoskeletal protein assemblies. <i>FEBS Letters</i> , 2002 , 513, 119-23	3.8	214
104	Conserved patterns in the Cu,Zn superoxide dismutase family. <i>Journal of Molecular Biology</i> , 1994 , 238, 366-86	6.5	202
103	Evolutionarily conserved human targets of adenosine to inosine RNA editing. <i>Nucleic Acids Research</i> , 2005 , 33, 1162-8	20.1	148
102	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
101	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
100	The sarcomeric cytoskeleton: from molecules to motion. <i>Journal of Experimental Biology</i> , 2016 , 219, 135-45	3.5	124
99	The structure and regulation of human muscle β -actinin. <i>Cell</i> , 2014 , 159, 1447-60	56.2	118
98	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
97	Novel bilobe components in <i>Trypanosoma brucei</i> identified using proximity-dependent biotinylation. <i>Eukaryotic Cell</i> , 2013 , 12, 356-67		98
96	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
95	Structural and functional characterisation of the chlorite dismutase from the nitrite-oxidizing bacterium "Candidatus Nitrospira defluvii": identification of a catalytically important amino acid residue. <i>Journal of Structural Biology</i> , 2010 , 172, 331-42	3.4	68
94	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
93	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
92	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

91	Structural insights into the dynamics and function of the C-terminus of the E. coli RNA chaperone Hfq. <i>Nucleic Acids Research</i> , 2011 , 39, 4900-15	20.1	65
90	Pathophysiology of protein aggregation and extended phenotyping in filaminopathy. <i>Brain</i> , 2012 , 135, 2642-60	11.2	60
89	Evolutionary constraints for dimer formation in prokaryotic Cu,Zn superoxide dismutase. <i>Journal of Molecular Biology</i> , 1999 , 285, 283-96	6.5	59
88	Crystal structure and its bearing towards an understanding of key biological functions of EpCAM. <i>Nature Communications</i> , 2014 , 5, 4764	17.4	58
87	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
86	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
85	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
84	Half a century of Ramachandran plots. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2013 , 69, 1333-41		50
83	Direct interaction of actin filaments with F-BAR protein pacsin2. <i>EMBO Reports</i> , 2014 , 15, 1154-62	6.5	47
82	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
81	Deciphering the BAR code of membrane modulators. <i>Cellular and Molecular Life Sciences</i> , 2017 , 74, 2413-2438	12.3	42
80	Structural basis for the interaction of protein S1 with the Escherichia coli ribosome. <i>Nucleic Acids Research</i> , 2015 , 43, 661-73	20.1	42
79	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
78	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
77	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
76	HspB1 phosphorylation regulates its intramolecular dynamics and mechanosensitive molecular chaperone interaction with filamin C. <i>Science Advances</i> , 2019 , 5, eaav8421	14.3	31
75	β -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
74	On the routine use of soft X-rays in macromolecular crystallography. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2001 , 57, 689-95		28

73	Structure of human promyelo-peroxidase (proMPO) and the role of the propeptide in processing and maturation. <i>Journal of Biological Chemistry</i> , 2017 , 292, 8244-8261	5.4	27
72	A novel non-canonical PIP-box mediates PARG interaction with PCNA. <i>Nucleic Acids Research</i> , 2017 , 45, 9741-9759	20.1	27
71	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
70	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
69	Structural flexibility of RNA as molecular basis for Hfq chaperone function. <i>Nucleic Acids Research</i> , 2012 , 40, 8072-84	20.1	27
68	Crystallographic study of azide-inhibited bovine Cu,Zn superoxide dismutase. <i>Journal of Molecular Biology</i> , 1994 , 240, 179-83	6.5	27
67	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
66	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
65	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
64	Structural analysis of full-length Hfq from Escherichia coli. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2011 , 67, 536-40		23
63	Fc α b-HER2 Interaction: a M β age \square Trois. Lessons from X-Ray and Solution Studies. <i>Structure</i> , 2017 , 25, 878-889.e5	5.2	22
62	Molecular Mechanism of Enzymatic Chlorite Detoxification: Insights from Structural and Kinetic Studies. <i>ACS Catalysis</i> , 2017 , 7, 7962-7976	13.1	22
61	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
60	Missing strings of residues in protein crystal structures. <i>Intrinsically Disordered Proteins</i> , 2015 , 3, e1095697		22
59	How many packing contacts are observed in protein crystals?. <i>Journal of Structural Biology</i> , 2012 , 180, 96-100	3.4	21
58	Chemistry and Molecular Dynamics Simulations of Heme b-HemQ and Coproheme-HemQ. <i>Biochemistry</i> , 2016 , 55, 5398-412	3.2	19
57	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
56	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

55	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
54	Dimeric chlorite dismutase from the nitrogen-fixing cyanobacterium <i>Cyanothece</i> sp. PCC7425. <i>Molecular Microbiology</i> , 2015 , 96, 1053-68	4.1	17
53	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
52	Structural and biochemical studies on ATP binding and hydrolysis by the <i>Escherichia coli</i> RNA chaperone Hfq. <i>PLoS ONE</i> , 2012 , 7, e50892	3.7	16
51	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
50	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
49	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
48	Structural portrait of filamin interaction mechanisms. <i>Current Protein and Peptide Science</i> , 2010 , 11, 639-508	5.8	14
47	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
46	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
45	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
44	Packing bridges in protein crystal structures. <i>Journal of Applied Crystallography</i> , 2014 , 47, 458-461	3.8	13
43	Terminal assembly of sarcomeric filaments by intermolecular beta-sheet formation. <i>Trends in Biochemical Sciences</i> , 2009 , 34, 33-9	10.3	13
42	A proteomic Ramachandran plot (PRplot). <i>Amino Acids</i> , 2013 , 44, 781-90	3.5	12
41	The G-M-N motif determines ion selectivity in the yeast magnesium channel Mrs2p. <i>Metallomics</i> , 2013 , 5, 745-52	4.5	12
40	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
39	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
38	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

37	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
36	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
35	Bacterial protease uses distinct thermodynamic signatures for substrate recognition. <i>Scientific Reports</i> , 2017 , 7, 2848	4.9	10
34	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
33	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
32	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
31	Two-faced Fcab prevents polymerization with VEGF and reveals thermodynamics and the 2.15 Å crystal structure of the complex. <i>MAbs</i> , 2017 , 9, 1088-1104	6.6	9
30	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
29	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
28	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
27	Conformational plasticity and evolutionary analysis of the myotilin tandem Ig domains. <i>Scientific Reports</i> , 2017 , 7, 3993	4.9	7
26	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
25	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
24	Secreted heme peroxidase from : Insights into catalysis, structure, and biological role. <i>Journal of Biological Chemistry</i> , 2018 , 293, 1330-1345	5.4	6
23	A cell for producing xenon-derivative crystals for cryocrystallographic analysis. <i>Journal of Applied Crystallography</i> , 1998 , 31, 812-814	3.8	6
22	Human cytomegalovirus phosphoproteins are hypophosphorylated and intrinsically disordered. <i>Journal of General Virology</i> , 2017 , 98, 471-485	4.9	6
21	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
20	In-depth interrogation of protein thermal unfolding data with MoltenProt. <i>Protein Science</i> , 2021 , 30, 201-217	6.3	6

19	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
18	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
17	PKAN neurodegeneration and residual PANK2 activities in patient erythrocytes. <i>Annals of Clinical and Translational Neurology</i> , 2020 , 7, 1340-1351	5.3	4
16	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
15	Structures of three MORN repeat proteins and a re-evaluation of the proposed lipid-binding properties of MORN repeats		3
14	Molecular basis of F-actin regulation and sarcomere assembly via myotilin. <i>PLoS Biology</i> , 2021 , 19, e3001448	14.8	3
13	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
12	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
11	PHF3 regulates neuronal gene expression through the Pol II CTD reader domain SPOC. <i>Nature Communications</i> , 2021 , 12, 6078	17.4	1
10	Tailored Suits Fit Better: Customized Protein Crystallization Screens. <i>Crystal Growth and Design</i> , 2020 , 20, 984-994	3.5	1
9	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
8	Naked Metal Cations Swimming in Protein Crystals. <i>Crystals</i> , 2019 , 9, 581	2.3	1
7	FLNC-Associated Myofibrillar Myopathy: New Clinical, Functional, and Proteomic Data. <i>Neurology: Genetics</i> , 2021 , 7, e590	3.8	0
6	Structural Studies on Cytoskeletal Proteins. <i>Cellular and Molecular Biology Letters</i> , 2001 , 6, 199	8.1	
5	Structures of three MORN repeat proteins and a re-evaluation of the proposed lipid-binding properties of MORN repeats 2020 , 15, e0242677		
4	Structures of three MORN repeat proteins and a re-evaluation of the proposed lipid-binding properties of MORN repeats 2020 , 15, e0242677		
3	Structures of three MORN repeat proteins and a re-evaluation of the proposed lipid-binding properties of MORN repeats 2020 , 15, e0242677		
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