

Kristina Djinovic-Carugo

List of Publications by Year in descending order

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Version: 2024-02-01

108
papers

5,218
citations

101384

36
h-index

98622

67
g-index

113
all docs

113
docs citations

113
times ranked

7341
citing authors

| # | ARTICLE | IF | CITATIONS |
|----|--|-----|-----------|
| 1 | Impact of the dynamics of the catalytic arginine on nitrite and chlorite binding by dimeric chlorite dismutase. <i>Journal of Inorganic Biochemistry</i> , 2022, 227, 111689. | 1.5 | 3 |
| 2 | A Potential Citrate Shunt in Erythrocytes of PKAN Patients Caused by Mutations in Pantothenate Kinase 2. <i>Biomolecules</i> , 2022, 12, 325. | 1.8 | 2 |
| 3 | In-depth interrogation of protein thermal unfolding data with MoltenProt. <i>Protein Science</i> , 2021, 30, 201-217. | 3.1 | 36 |
| 4 | Arresting the Catalytic Arginine in Chlorite Dismutases: Impact on Heme Coordination, Thermal Stability, and Catalysis. <i>Biochemistry</i> , 2021, 60, 621-634. | 1.2 | 4 |
| 5 | Molecular basis of F-actin regulation and sarcomere assembly via myotilin. <i>PLoS Biology</i> , 2021, 19, e3001148. | 2.6 | 9 |
| 6 | 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, . | 4.7 | 15 |
| 7 | FLNC-Associated Myofibrillar Myopathy. <i>Neurology: Genetics</i> , 2021, 7, e590. | 0.9 | 15 |
| 8 | PHF3 regulates neuronal gene expression through the Pol II CTD reader domain SPOC. <i>Nature Communications</i> , 2021, 12, 6078. | 5.8 | 21 |
| 9 | Crystal structures and calorimetry reveal catalytically relevant binding mode of coproporphyrin and coproheme in coproporphyrin ferrochelatase. <i>FEBS Journal</i> , 2020, 287, 2779-2796. | 2.2 | 22 |
| 10 | Tailored Suits Fit Better: Customized Protein Crystallization Screens. <i>Crystal Growth and Design</i> , 2020, 20, 984-994. | 1.4 | 2 |
| 11 | 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. | 3.3 | 17 |
| 12 | PKAN neurodegeneration and residual PANK2 activities in patient erythrocytes. <i>Annals of Clinical and Translational Neurology</i> , 2020, 7, 1340-1351. | 1.7 | 11 |
| 13 | 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. | 1.6 | 33 |
| 14 | 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. | 3.3 | 10 |
| 15 | Phosphoproteomics identifies dual-site phosphorylation in an extended basophilic motif regulating FILIP1-mediated degradation of filamin-C. <i>Communications Biology</i> , 2020, 3, 253. | 2.0 | 25 |
| 16 | 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. | 3.3 | 59 |
| 17 | Actinobacterial Coproheme Decarboxylases Use Histidine as a Distal Base to Promote Compound I Formation. <i>ACS Catalysis</i> , 2020, 10, 5405-5418. | 5.5 | 19 |
| 18 | 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. | 1.1 | 18 |

| # | ARTICLE | IF | CITATIONS |
|----|---|-----|-----------|
| 19 | Title is missing!. , 2020, 15, e0242677. | | 0 |
| 20 | Title is missing!. , 2020, 15, e0242677. | | 0 |
| 21 | Title is missing!. , 2020, 15, e0242677. | | 0 |
| 22 | Title is missing!. , 2020, 15, e0242677. | | 0 |
| 23 | Title is missing!. , 2020, 15, e0242677. | | 0 |
| 24 | Redox Cofactor Rotates during Its Stepwise Decarboxylation: Molecular Mechanism of Conversion of Coproheme to Heme <i>in vivo</i> . ACS Catalysis, 2019, 9, 6766-6782. | 5.5 | 28 |
| 25 | HspB1 phosphorylation regulates its intramolecular dynamics and mechanosensitive molecular chaperone interaction with filamin C. Science Advances, 2019, 5, eaav8421. | 4.7 | 52 |
| 26 | Protective properties of the cultured stem cell proteome studied in an animal model of acetaminophen-induced acute liver failure. Molecular Biology Reports, 2019, 46, 3101-3112. | 1.0 | 9 |
| 27 | Naked Metal Cations Swimming in Protein Crystals. Crystals, 2019, 9, 581. | 1.0 | 1 |
| 28 | Secreted heme peroxidase from Dictyostelium discoideum: Insights into catalysis, structure, and biological role. Journal of Biological Chemistry, 2018, 293, 1330-1345. | 1.6 | 10 |
| 29 | Roles of distal aspartate and arginine of B-class dye-decolorizing peroxidase in heterolytic hydrogen peroxide cleavage. Journal of Biological Chemistry, 2018, 293, 14823-14838. | 1.6 | 41 |
| 30 | Î±-Actinin/titin interaction: A dynamic and mechanically stable cluster of bonds in the muscle Z-disk. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, 1015-1020. | 3.3 | 41 |
| 31 | Deciphering the BAR code of membrane modulators. Cellular and Molecular Life Sciences, 2017, 74, 2413-2438. | 2.4 | 57 |
| 32 | Bacterial protease uses distinct thermodynamic signatures for substrate recognition. Scientific Reports, 2017, 7, 2848. | 1.6 | 14 |
| 33 | Fcab-HER2 Interaction: a MÃ©nage Ã Trois. Lessons from X-Ray and Solution Studies. Structure, 2017, 25, 878-889.e5. | 1.6 | 29 |
| 34 | Structure of human promyeloperoxidase (proMPO) and the role of the propeptide in processing and maturation. Journal of Biological Chemistry, 2017, 292, 8244-8261. | 1.6 | 38 |
| 35 | Molecular Mechanism of Enzymatic Chlorite Detoxification: Insights from Structural and Kinetic Studies. ACS Catalysis, 2017, 7, 7962-7976. | 5.5 | 26 |
| 36 | A novel non-canonical PIP-box mediates PARC interaction with PCNA. Nucleic Acids Research, 2017, 45, 9741-9759. | 6.5 | 30 |

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|----|---|-----|-----------|
| 37 | Conformational plasticity and evolutionary analysis of the myotilin tandem Ig domains. <i>Scientific Reports</i> , 2017, 7, 3993. | 1.6 | 11 |
| 38 | 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. | 2.6 | 11 |
| 39 | Human cytomegalovirus phosphoproteins are hypophosphorylated and intrinsically disordered. <i>Journal of General Virology</i> , 2017, 98, 471-485. | 1.3 | 9 |
| 40 | Vaccinia Virus Immunomodulator A46: A Lipid and Protein-Binding Scaffold for Sequestering Host TIR-Domain Proteins. <i>PLoS Pathogens</i> , 2016, 12, e1006079. | 2.1 | 19 |
| 41 | Congenital macrothrombocytopeniaâ€linked mutations in the actinâ€binding domain of Î±-actininâ€1 enhance Fâ€actin association. <i>FEBS Letters</i> , 2016, 590, 685-695. | 1.3 | 18 |
| 42 | Structure and calcium-binding studies of calmodulin-like domain of human non-muscle Î±-actinin-1. <i>Scientific Reports</i> , 2016, 6, 27383. | 1.6 | 22 |
| 43 | Criteria to Extract High-Quality Protein Data Bank Subsets for Structure Users. <i>Methods in Molecular Biology</i> , 2016, 1415, 139-152. | 0.4 | 7 |
| 44 | Chemistry and Molecular Dynamics Simulations of Heme b-HemQ and Coproheme-HemQ. <i>Biochemistry</i> , 2016, 55, 5398-5412. | 1.2 | 24 |
| 45 | From chlorite dismutase towards HemQâ€the role of the proximal H-bonding network in haeme binding. <i>Bioscience Reports</i> , 2016, 36, . | 1.1 | 22 |
| 46 | Hydrogen peroxideâ€mediated conversion of coproheme to heme <i>b</i> by HemQâ€lessons from the first crystal structure and kinetic studies. <i>FEBS Journal</i> , 2016, 283, 4386-4401. | 2.2 | 36 |
| 47 | The sarcomeric cytoskeleton: from molecules to motion. <i>Journal of Experimental Biology</i> , 2016, 219, 135-145. | 0.8 | 188 |
| 48 | 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. | 1.2 | 12 |
| 49 | Dimeric chlorite dismutase from the nitrogenâ€fixing cyanobacterium <i>Cyanothece</i> sp. PCC 7425. <i>Molecular Microbiology</i> , 2015, 96, 1053-1068. | 1.2 | 22 |
| 50 | Missing strings of residues in protein crystal structures. <i>Intrinsically Disordered Proteins</i> , 2015, 3, e1095697. | 1.9 | 39 |
| 51 | 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, 1264-1281. | 1.1 | 19 |
| 52 | Structural basis for the interaction of protein S1 with the <i>Escherichia coli</i> ribosome. <i>Nucleic Acids Research</i> , 2015, 43, 661-673. | 6.5 | 56 |
| 53 | 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. | 1.4 | 44 |
| 54 | Structural Insights into Ca ²⁺ -Calmodulin Regulation of Plectin 1a-Integrin Î²4 Interaction in Hemidesmosomes. <i>Structure</i> , 2015, 23, 558-570. | 1.6 | 28 |

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| 55 | Structural biology of the lanthanidesâ€” mining rare earths in the Protein Data Bank. Journal of Inorganic Biochemistry, 2015, 143, 69-76. | 1.5 | 19 |
| 56 | Packing bridges in protein crystal structures. Journal of Applied Crystallography, 2014, 47, 458-461. | 1.9 | 14 |
| 57 | The Structure and Regulation of Human Muscle Î±-Actinin. Cell, 2014, 159, 1447-1460. | 13.5 | 178 |
| 58 | Manipulating Conserved Heme Cavity Residues of Chlorite Dismutase: Effect on Structure, Redox Chemistry, and Reactivity. Biochemistry, 2014, 53, 77-89. | 1.2 | 32 |
| 59 | Direct interaction of actin filaments with <sc>F</sc>â€”<sc>BAR</sc> protein pacsin2. EMBO Reports, 2014, 15, 1154-1162. | 2.0 | 56 |
| 60 | The Center for Optimized Structural Studies (COSS) platform for automation in cloning, expression, and purification of single proteins and proteinâ€”protein complexes. Amino Acids, 2014, 46, 1565-1582. | 1.2 | 15 |
| 61 | Crystal structure and its bearing towards an understanding of key biological functions of EpCAM. Nature Communications, 2014, 5, 4764. | 5.8 | 86 |
| 62 | A proteomic Ramachandran plot (PRplot). Amino Acids, 2013, 44, 781-790. | 1.2 | 17 |
| 63 | The G-M-N motif determines ion selectivity in the yeast magnesium channel Mrs2p. Metallomics, 2013, 5, 745. | 1.0 | 13 |
| 64 | Myopodin is an F-actin bundling protein with multiple independent actin-binding regions. Journal of Muscle Research and Cell Motility, 2013, 34, 61-69. | 0.9 | 15 |
| 65 | False positive RNA binding activities after Ni-affinity purification from <i>Escherichia coli</i>. RNA Biology, 2013, 10, 1066-1069. | 1.5 | 19 |
| 66 | Novel Bilobe Components in Trypanosoma brucei Identified Using Proximity-Dependent Biotinylation. Eukaryotic Cell, 2013, 12, 356-367. | 3.4 | 120 |
| 67 | Structural and functional characterization of the N-terminal domain of the yeast Mg²⁺ channel Mrs2. Acta Crystallographica Section D: Biological Crystallography, 2013, 69, 1653-1664. | 2.5 | 16 |
| 68 | Half a century of Ramachandran plots. Acta Crystallographica Section D: Biological Crystallography, 2013, 69, 1333-1341. | 2.5 | 71 |
| 69 | The Pseudomonas aeruginosa Catabolite Repression Control Protein Crc Is Devoid of RNA Binding Activity. PLoS ONE, 2013, 8, e64609. | 1.1 | 60 |
| 70 | Human Cardiac Ryanodine Receptor: Preparation, Crystallization and Preliminary X-ray Analysis of the N-terminal Region. Protein and Peptide Letters, 2013, 20, 1211-1216. | 0.4 | 3 |
| 71 | Structural flexibility of RNA as molecular basis for Hfq chaperone function. Nucleic Acids Research, 2012, 40, 8072-8084. | 6.5 | 29 |
| 72 | Pathophysiology of protein aggregation and extended phenotyping in filaminopathy. Brain, 2012, 135, 2642-2660. | 3.7 | 70 |

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|----|---|-----|-----------|
| 73 | How many packing contacts are observed in protein crystals?. <i>Journal of Structural Biology</i> , 2012, 180, 96-100. | 1.3 | 24 |
| 74 | Redox Thermodynamics of High-Spin and Low-Spin Forms of Chlorite Dismutases with Diverse Subunit and Oligomeric Structures. <i>Biochemistry</i> , 2012, 51, 9501-9512. | 1.2 | 30 |
| 75 | 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, 1031-1038. | 1.1 | 18 |
| 76 | Structural and Biochemical Studies on ATP Binding and Hydrolysis by the Escherichia coli RNA Chaperone Hfq. <i>PLoS ONE</i> , 2012, 7, e50892. | 1.1 | 17 |
| 77 | 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, 1713-1721. | 2.4 | 65 |
| 78 | Functional analysis of the conserved hydrophobic gate region of the magnesium transporter CorA. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2011, 1808, 1587-1591. | 1.4 | 7 |
| 79 | 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. | 2.6 | 124 |
| 80 | 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. | 1.9 | 45 |
| 81 | Structural analysis of full-length Hfq from <i>Escherichia coli</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2011, 67, 536-540. | 0.7 | 29 |
| 82 | 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, 4900-4915. | 6.5 | 74 |
| 83 | Unexpected Diversity of Chlorite Dismutases: a Catalytically Efficient Dimeric Enzyme from <i>Nitrospira winogradskyi</i> . <i>Journal of Bacteriology</i> , 2011, 193, 2408-2417. | 1.0 | 76 |
| 84 | Structural Portrait of Filamin Interaction Mechanisms. <i>Current Protein and Peptide Science</i> , 2010, 11, 639-650. | 0.7 | 15 |
| 85 | Purification of recombinant growth hormone by clear native gels for conformational analyses: preservation of conformation and receptor binding. <i>Amino Acids</i> , 2010, 39, 859-869. | 1.2 | 8 |
| 86 | 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, 658-661. | 0.7 | 4 |
| 87 | Opening of tandem calponin homology domains regulates their affinity for F-actin. <i>Nature Structural and Molecular Biology</i> , 2010, 17, 614-616. | 3.6 | 91 |
| 88 | Structural and functional characterisation of the chlorite dismutase from the nitrite-oxidizing bacterium <i>Candidatus Nitrospira defluviaria</i> : Identification of a catalytically important amino acid residue. <i>Journal of Structural Biology</i> , 2010, 172, 331-342. | 1.3 | 79 |
| 89 | 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, 10609-10613. | 3.3 | 77 |
| 90 | Terminal assembly of sarcomeric filaments by intermolecular β -sheet formation. <i>Trends in Biochemical Sciences</i> , 2009, 34, 33-39. | 3.7 | 14 |

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| 91 | Can soaked-in scavengers protect metalloprotein active sites from reduction during data collection?. <i>Journal of Synchrotron Radiation</i> , 2009, 16, 191-204. | 1.0 | 61 |
| 92 | Structural Basis of Heme Binding in the Cu,Zn Superoxide Dismutase from <i>Haemophilus ducreyi</i> . <i>Journal of Molecular Biology</i> , 2009, 386, 406-418. | 2.0 | 15 |
| 93 | Î±-Actinin structure and regulation. <i>Cellular and Molecular Life Sciences</i> , 2008, 65, 2688-2701. | 2.4 | 382 |
| 94 | Novel structural insights into F-actin-binding and novel functions of calponin homology domains. <i>Current Opinion in Structural Biology</i> , 2008, 18, 702-708. | 2.6 | 62 |
| 95 | Evolutionarily conserved human targets of adenosine to inosine RNA editing. <i>Nucleic Acids Research</i> , 2005, 33, 1162-1168. | 6.5 | 177 |
| 96 | 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, 33447-33455. | 1.6 | 81 |
| 97 | Crystal structure of nitrous oxide reductase from <i>Paracoccus denitrificans</i> at 1.6 Å resolution. <i>Biochemical Journal</i> , 2003, 369, 77-88. | 1.7 | 158 |
| 98 | Functional plasticity of CH domains. <i>FEBS Letters</i> , 2002, 513, 98-106. | 1.3 | 291 |
| 99 | The spectrin repeat: a structural platform for cytoskeletal protein assemblies. <i>FEBS Letters</i> , 2002, 513, 119-123. | 1.3 | 249 |
| 100 | On the routine use of soft X-rays in macromolecular crystallography. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2001, 57, 689-695. | 2.5 | 35 |
| 101 | Structural Studies on Cytoskeletal Proteins. <i>Cellular and Molecular Biology Letters</i> , 2001, 6, 199. | 2.7 | 0 |
| 102 | Revisiting the Catalytic CuZ Cluster of Nitrous Oxide (N ₂ O) Reductase. <i>Journal of Biological Chemistry</i> , 2000, 275, 41133-41136. | 1.6 | 166 |
| 103 | Molecular Basis for Cross-Linking of Actin Filaments: Structure of the Î±-Actinin Rod. <i>Cell</i> , 1999, 98, 537-546. | 13.5 | 237 |
| 104 | Evolutionary constraints for dimer formation in prokaryotic Cu,Zn superoxide dismutase 1 Edited by R. Huber. <i>Journal of Molecular Biology</i> , 1999, 285, 283-296. | 2.0 | 63 |
| 105 | A cell for producing xenon-derivative crystals for cryocrystallographic analysis. <i>Journal of Applied Crystallography</i> , 1998, 31, 812-814. | 1.9 | 20 |
| 106 | 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, 6043-6049. | 1.2 | 48 |
| 107 | Conserved Patterns in the Cu,Zn Superoxide Dismutase Family. <i>Journal of Molecular Biology</i> , 1994, 238, 366-386. | 2.0 | 222 |
| 108 | Crystallographic Study of Azide-inhibited Bovine Cu,Zn Superoxide Dismutase. <i>Journal of Molecular Biology</i> , 1994, 240, 179-183. | 2.0 | 32 |