

Dimitri Y Chirgadze

List of Publications by Year in descending order

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67
papers

4,042
citations

126907

33
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123424

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72
all docs

72
docs citations

72
times ranked

5823
citing authors

#	ARTICLE	IF	CITATIONS
1	Single-particle cryo-EM at atomic resolution. <i>Nature</i> , 2020, 587, 152-156.	27.8	572
2	Nanostructured films from hierarchical self-assembly of amyloidogenic proteins. <i>Nature Nanotechnology</i> , 2010, 5, 204-207.	31.5	338
3	Crystal Structure of the TSH Receptor in Complex with a Thyroid-Stimulating Autoantibody. <i>Thyroid</i> , 2007, 17, 395-410.	4.5	205
4	Crystal structure of DNA-PKcs reveals a large open-ring cradle comprised of HEAT repeats. <i>Nature</i> , 2010, 463, 118-121.	27.8	195
5	DNA-PKcs structure suggests an allosteric mechanism modulating DNA double-strand break repair. <i>Science</i> , 2017, 355, 520-524.	12.6	155
6	Expanding the Solvent Chemical Space for Self-Assembly of Dipeptide Nanostructures. <i>ACS Nano</i> , 2014, 8, 1243-1253.	14.6	146
7	5-Formylcytosine alters the structure of the DNA double helix. <i>Nature Structural and Molecular Biology</i> , 2015, 22, 44-49.	8.2	140
8	A new look at sodium channel β^2 subunits. <i>Open Biology</i> , 2015, 5, 140192.	3.6	111
9	Crystal structure of the NK1 fragment of HGF/SF suggests a novel mode for growth factor dimerization and receptor binding. <i>Nature Structural Biology</i> , 1999, 6, 72-79.	9.7	110
10	Crystal structures of NK1-heparin complexes reveal the basis for NK1 activity and enable engineering of potent agonists of the MET receptor. <i>EMBO Journal</i> , 2001, 20, 5543-5555.	7.8	107
11	Crystal structure of human XLF/Cernunnos reveals unexpected differences from XRCC4 with implications for NHEJ. <i>EMBO Journal</i> , 2008, 27, 290-300.	7.8	106
12	Crystal structure of folliculin reveals a hidDENN function in genetically inherited renal cancer. <i>Open Biology</i> , 2012, 2, 120071.	3.6	97
13	Characteristics of a Human Monoclonal Autoantibody to the Thyrotropin Receptor: Sequence Structure and Function. <i>Thyroid</i> , 2004, 14, 560-570.	4.5	92
14	Structure of a Blinkin-BUBR1 Complex Reveals an Interaction Crucial for Kinetochores-Mitotic Checkpoint Regulation via an Unanticipated Binding Site. <i>Structure</i> , 2011, 19, 1691-1700.	3.3	68
15	Crystal Structure and Molecular Imaging of the Nav Channel β^3 Subunit Indicates a Trimeric Assembly. <i>Journal of Biological Chemistry</i> , 2014, 289, 10797-10811.	3.4	67
16	Dimers of DNA-PK create a stage for DNA double-strand break repair. <i>Nature Structural and Molecular Biology</i> , 2021, 28, 13-19.	8.2	67
17	Non-homologous end-joining partners in a helical dance: structural studies of XLF-XRCC4 interactions. <i>Biochemical Society Transactions</i> , 2011, 39, 1387-1392.	3.4	65
18	Cryo-EM of NHEJ supercomplexes provides insights into DNA repair. <i>Molecular Cell</i> , 2021, 81, 3400-3409.e3.	9.7	62

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19	Structure of an Xrcc4â€“DNA ligase IV yeast ortholog complex reveals a novel BRCT interaction mode. <i>DNA Repair</i> , 2006, 5, 362-368.	2.8	60
20	The Influence of Pathogenic Mutations in Î±-Synuclein on Biophysical and Structural Characteristics of Amyloid Fibrils. <i>ACS Nano</i> , 2020, 14, 5213-5222.	14.6	58
21	Structural constraints on protein self-processing in L-aspartate-Â-decarboxylase. <i>EMBO Journal</i> , 2003, 22, 6193-6204.	7.8	56
22	Inhibition of <i>Mycobacterium tuberculosis</i> Pantothenate Synthetase by Analogues of the Reaction Intermediate. <i>ChemBioChem</i> , 2008, 9, 2606-2611.	2.6	56
23	CryoEM structures of human CMGâ€“ATPÎ³Sâ€“DNA and CMGâ€“AND-1 complexes. <i>Nucleic Acids Research</i> , 2020, 48, 6980-6995.	14.5	56
24	High-resolution crystal structure of the human Notch 1 ankyrin domain. <i>Biochemical Journal</i> , 2005, 392, 13-20.	3.7	51
25	Molecular Dissection of the Interaction between the Small G Proteins Rac1 and RhoA and Protein Kinase C-related Kinase 1 (PRK1). <i>Journal of Biological Chemistry</i> , 2003, 278, 50578-50587.	3.4	49
26	Crystal Structures of <i>Yersinia enterocolitica</i> Salicylate Synthase and its Complex with the Reaction Products Salicylate and Pyruvate. <i>Journal of Molecular Biology</i> , 2006, 357, 524-534.	4.2	45
27	The Crystal Structure of the N-Terminal Region of BUB1 Provides Insight into the Mechanism of BUB1 Recruitment to Kinetochores. <i>Structure</i> , 2009, 17, 105-116.	3.3	45
28	Structural basis for collagen recognition by the immune receptor OSCAR. <i>Blood</i> , 2016, 127, 529-537.	1.4	45
29	Characteristics of a Monoclonal Antibody to the Thyrotropin Receptor that Acts as a Powerful Thyroid-Stimulating Autoantibody Antagonist. <i>Thyroid</i> , 2005, 15, 672-682.	4.5	44
30	Structural Insights into the Role of Domain Flexibility in Human DNA Ligase IV. <i>Structure</i> , 2012, 20, 1212-1222.	3.3	44
31	Gluconeogenic precursor availability regulates flux through the glyoxylate shunt in <i>Pseudomonas aeruginosa</i> . <i>Journal of Biological Chemistry</i> , 2018, 293, 14260-14269.	3.4	43
32	A Nanobody Binding to Non-Amyloidogenic Regions of the Protein Human Lysozyme Enhances Partial Unfolding but Inhibits Amyloid Fibril Formation. <i>Journal of Physical Chemistry B</i> , 2013, 117, 13245-13258.	2.6	42
33	Crystal Structure of <i>Escherichia coli</i> Ketopantoate Reductase in a Ternary Complex with NADP+ and Pantoate Bound. <i>Journal of Biological Chemistry</i> , 2007, 282, 8487-8497.	3.4	39
34	Structural insights into inhibitor regulation of the DNA repair protein DNA-PKcs. <i>Nature</i> , 2022, 601, 643-648.	27.8	36
35	Differential assembly diversifies GABAA receptor structures and signalling. <i>Nature</i> , 2022, 604, 190-194.	27.8	36
36	Thyroid stimulating autoantibody M22 mimics TSH binding to the TSH receptor leucine rich domain: a comparative structural study of proteinâ€“protein interactions. <i>Journal of Molecular Endocrinology</i> , 2009, 42, 381-395.	2.5	33

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37	Mechanisms of inhibition and activation of extrasynaptic $\hat{\Gamma}^2$ GABAA receptors. <i>Nature</i> , 2022, 602, 529-533.	27.8	31
38	Insights into the structure of hepatocyte growth factor/scatter factor (HGF/SF) and implications for receptor activation. <i>FEBS Letters</i> , 1998, 430, 126-129.	2.8	29
39	Spatial and temporal organization of multi-protein assemblies: achieving sensitive control in information-rich cell-regulatory systems. <i>Philosophical Transactions Series A, Mathematical, Physical, and Engineering Sciences</i> , 2012, 370, 3023-3039.	3.4	28
40	Knowledge-Based Real-Space Explorations for Low-Resolution Structure Determination. <i>Structure</i> , 2006, 14, 1313-1320.	3.3	27
41	FSH and TSH binding to their respective receptors: similarities, differences and implication for glycoprotein hormone specificity. <i>Journal of Molecular Endocrinology</i> , 2008, 41, 145-164.	2.5	27
42	Structural Biology of DNA Repair: Spatial Organisation of the Multicomponent Complexes of Nonhomologous End Joining. <i>Journal of Nucleic Acids</i> , 2010, 2010, 1-19.	1.2	24
43	Structural Basis for the Activity and Substrate Specificity of Fluoroacetyl-CoA Thioesterase Flk. <i>Journal of Biological Chemistry</i> , 2010, 285, 22495-22504.	3.4	24
44	Crystal structure of the $\hat{\Gamma}^2$ -chain of human hepatocyte growth factor-like/macrophage stimulating protein. <i>FEBS Journal</i> , 2005, 272, 5799-5807.	4.7	23
45	Structural basis for the interaction of $\langle \text{SARS-CoV} \rangle$ virulence factor nsp1 with $\langle \text{DNA} \rangle$ polymerase $\hat{\Gamma}^2$ primase. <i>Protein Science</i> , 2022, 31, 333-344.	7.6	23
46	A New Crystal Form of the NK1 Splice Variant of HGF/SF Demonstrates Extensive Hinge Movement and Suggests That the NK1 Dimer Originates by Domain Swapping. <i>Journal of Molecular Biology</i> , 2002, 319, 283-288.	4.2	22
47	Structure of a Single-Chain Fv Bound to the 17 N-Terminal Residues of Huntingtin Provides Insights into Pathogenic Amyloid Formation and Suppression. <i>Journal of Molecular Biology</i> , 2015, 427, 2166-2178.	4.2	21
48	Achieving high signal-to-noise in cell regulatory systems: Spatial organization of multiprotein transmembrane assemblies of FGFR and MET receptors. <i>Progress in Biophysics and Molecular Biology</i> , 2015, 118, 103-111.	2.9	21
49	Crystal structures of the PLP- and PMP-bound forms of BtrR, a dual functional aminotransferase involved in butirosin biosynthesis. <i>Proteins: Structure, Function and Bioinformatics</i> , 2006, 65, 220-230.	2.6	19
50	Structural and functional insights into the role of the N-terminal Mps1 TPR domain in the SAC (spindle assembly checkpoint). <i>Biochemical Journal</i> , 2012, 448, 321-328.	3.7	19
51	Amyloid-like Fibrils from an $\hat{\Gamma}^2$ -Helical Transmembrane Protein. <i>Biochemistry</i> , 2017, 56, 3225-3233.	2.5	19
52	Snapshot of Protein Structure Evolution Reveals Conservation of Functional Dimerization through Intertwined Folding. <i>Structure</i> , 2004, 12, 1489-1494.	3.3	15
53	Understanding the structure and role of DNA-PK in NHEJ: How X-ray diffraction and cryo-EM contribute in complementary ways. <i>Progress in Biophysics and Molecular Biology</i> , 2019, 147, 26-32.	2.9	15
54	The structure of EXTL3 helps to explain the different roles of bi-domain exostosins in heparan sulfate synthesis. <i>Nature Communications</i> , 2022, 13, .	12.8	14

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55	Asymmetry in the Multiprotein Systems of Molecular Biology. <i>Structural Chemistry</i> , 2002, 13, 405-412.	2.0	13
56	Using cryo-EM to understand antimycobacterial resistance in the catalase-peroxidase (KatG) from <i>Mycobacterium tuberculosis</i> . <i>Structure</i> , 2021, 29, 899-912.e4.	3.3	13
57	Structural and functional analysis of SleL, a peptidoglycan lysin involved in germination of <i>Bacillus</i> spores. <i>Proteins: Structure, Function and Bioinformatics</i> , 2015, 83, 1787-1799.	2.6	12
58	Zn(II) mediates vancomycin polymerization and potentiates its antibiotic activity against resistant bacteria. <i>Scientific Reports</i> , 2017, 7, 4893.	3.3	11
59	Nucleophile Selectivity of Chorismate-Utilizing Enzymes. <i>ChemBioChem</i> , 2007, 8, 622-624.	2.6	8
60	The effect of protein-precipitant interfaces and applied shear on the nucleation and growth of lysozyme crystals. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2009, 65, 1127-1139.	2.5	7
61	Crystal structure of the PepSY-containing domain of the YpeB protein involved in germination of <i>Bacillus</i> spores. <i>Proteins: Structure, Function and Bioinformatics</i> , 2015, 83, 1914-1921.	2.6	7
62	The crystal structure of <i>Clostridium perfringens</i> SleM, a muramidase involved in cortical hydrolysis during spore germination. <i>Proteins: Structure, Function and Bioinformatics</i> , 2016, 84, 1681-1689.	2.6	7
63	Characterization and structural determination of a new anti-MET function-blocking antibody with binding epitope distinct from the ligand binding domain. <i>Scientific Reports</i> , 2017, 7, 9000.	3.3	7
64	Cryo-EM structures of staphylococcal IsdB bound to human hemoglobin reveal the process of heme extraction. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, e2116708119.	7.1	6
65	DNA-PKcs, Allostery, and DNA Double-Strand Break Repair. <i>Methods in Enzymology</i> , 2017, 592, 145-157.	1.0	5
66	Asymmetry in the Multiprotein Systems of Molecular Biology. , 2015, , 231-237.		2
67	Spatial and Temporal Organisation of Multiprotein Systems of Cell Regulation and Signalling: What Can We Learn from NHEJ System of Double-Strand Break Repair?. <i>NATO Science for Peace and Security Series A: Chemistry and Biology</i> , 2012, , 1-31.	0.5	1