Dimitri Y Chirgadze

List of Publications by Year
in descending order

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67 papers	4,042 citations	126907 33 h-index	123424 61 g-index
72 all docs	72 docs citations	72 times ranked	5823 citing authors

#	Article	IF	Citations
1	Structural basis for the interaction of <scp>SARSâ€CoV</scp>â€2 virulence factor nsp1 with <scp>DNA</scp> polymerase Î±â€“primase. Protein Science, 2022, 31, 333-344.	7.6	23
2	Structural insights into inhibitor regulation of the DNA repair protein DNA-PKcs. Nature, 2022, 601, 643-648.	27.8	36
3	Mechanisms of inhibition and activation of extrasynaptic Î±Î² GABAA receptors. Nature, 2022, 602, 529-533.	27.8	31
4	Cryo-EM structures of staphylococcal IsdB bound to human hemoglobin reveal the process of heme extraction. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, e2116708119.	7.1	6
5	Differential assembly diversifies GABAA receptor structures and signalling. Nature, 2022, 604, 190-194.	27.8	36
6	The structure of EXTL3 helps to explain the different roles of bi-domain exostosins in heparan sulfate synthesis. Nature Communications, 2022, 13, .	12.8	14
7	Dimers of DNA-PK create a stage for DNA double-strand break repair. Nature Structural and Molecular Biology, 2021, 28, 13-19.	8.2	67
8	Cryo-EM of NHEJ supercomplexes provides insights into DNA repair. Molecular Cell, 2021, 81, 3400-3409.e3.	9.7	62
9	Using cryo-EM to understand antimycobacterial resistance in the catalase-peroxidase (KatG) from Mycobacterium tuberculosis. Structure, 2021, 29, 899-912.e4.	3.3	13
10	Single-particle cryo-EM at atomic resolution. Nature, 2020, 587, 152-156.	27.8	572
11	CryoEM structures of human CMGâ€“ATPÎ³Sâ€“DNA and CMGâ€“AND-1 complexes. Nucleic Acids Research, 2020, 48, 6980-6995.	14.5	56
12	The Influence of Pathogenic Mutations in Î±-Synuclein on Biophysical and Structural Characteristics of Amyloid Fibrils. ACS Nano, 2020, 14, 5213-5222.	14.6	58
13	Understanding the structure and role of DNA-PK in NHEJ: How X-ray diffraction and cryo-EM contribute in complementary ways. Progress in Biophysics and Molecular Biology, 2019, 147, 26-32.	2.9	15
14	Gluconeogenic precursor availability regulates flux through the glyoxylate shunt in Pseudomonas aeruginosa. Journal of Biological Chemistry, 2018, 293, 14260-14269.	3.4	43
15	DNA-PKcs structure suggests an allosteric mechanism modulating DNA double-strand break repair. Science, 2017, 355, 520-524.	12.6	155
16	Amyloid-like Fibrils from an Î±-Helical Transmembrane Protein. Biochemistry, 2017, 56, 3225-3233.	2.5	19
17	Characterization and structural determination of a new anti-MET function-blocking antibody with binding epitope distinct from the ligand binding domain. Scientific Reports, 2017, 7, 9000.	3.3	7
18	Zn(II) mediates vancomycin polymerization and potentiates its antibiotic activity against resistant bacteria. Scientific Reports, 2017, 7, 4893.	3.3	11

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19	DNA-PKcs, Allostery, and DNA Double-Strand Break Repair. Methods in Enzymology, 2017, 592, 145-157.	1.0	5
20	Structural basis for collagen recognition by the immune receptor OSCAR. Blood, 2016, 127, 529-537.	1.4	45
21	The crystal structure of <i>Clostridium perfringens</i> SleM, a muramidase involved in cortical hydrolysis during spore germination. Proteins: Structure, Function and Bioinformatics, 2016, 84, 1681-1689.	2.6	7
22	Structural and functional analysis of SleL, a peptidoglycan lysin involved in germination of B acillus spores. Proteins: Structure, Function and Bioinformatics, 2015, 83, 1787-1799.	2.6	12
23	Structure of a Single-Chain Fv Bound to the 17 N-Terminal Residues of Huntingtin Provides Insights into Pathogenic Amyloid Formation and Suppression. Journal of Molecular Biology, 2015, 427, 2166-2178.	4.2	21
24	Achieving high signal-to-noise in cell regulatory systems: Spatial organization of multiprotein transmembrane assemblies of FGFR and MET receptors. Progress in Biophysics and Molecular Biology, 2015, 118, 103-111.	2.9	21
25	A new look at sodium channel Î² subunits. Open Biology, 2015, 5, 140192.	3.6	111
26	Crystal structure of the PepSY-containing domain of the YpeB protein involved in germination of <i>bacillus</i> spores. Proteins: Structure, Function and Bioinformatics, 2015, 83, 1914-1921.	2.6	7
27	5-Formylcytosine alters the structure of the DNA double helix. Nature Structural and Molecular Biology, 2015, 22, 44-49.	8.2	140
28	Asymmetry in the Multiprotein Systems of Molecular Biology. , 2015, , 231-237.		2
29	Expanding the Solvent Chemical Space for Self-Assembly of Dipeptide Nanostructures. ACS Nano, 2014, 8, 1243-1253.	14.6	146
30	Crystal Structure and Molecular Imaging of the Nav Channel Î²3 Subunit Indicates a Trimeric Assembly. Journal of Biological Chemistry, 2014, 289, 10797-10811.	3.4	67
31	A Nanobody Binding to Non-Amyloidogenic Regions of the Protein Human Lysozyme Enhances Partial Unfolding but Inhibits Amyloid Fibril Formation. Journal of Physical Chemistry B, 2013, 117, 13245-13258.	2.6	42
32	Structural and functional insights into the role of the N-terminal Mps1 TPR domain in the SAC (spindle assembly checkpoint). Biochemical Journal, 2012, 448, 321-328.	3.7	19
33	Crystal structure of folliculin reveals a hidDENN function in genetically inherited renal cancer. Open Biology, 2012, 2, 120071.	3.6	97
34	Spatial and temporal organization of multi-protein assemblies: achieving sensitive control in information-rich cell-regulatory systems. Philosophical Transactions Series A, Mathematical, Physical, and Engineering Sciences, 2012, 370, 3023-3039.	3.4	28
35	Structural Insights into the Role of Domain Flexibility in Human DNA Ligase IV. Structure, 2012, 20, 1212-1222.	3.3	44
36	Spatial and Temporal Organisation of Multiprotein Systems of Cell Regulation and Signalling: What Can We Learn from NHEJ System of Double-Strand Break Repair?. NATO Science for Peace and Security Series A: Chemistry and Biology, 2012, , 1-31.	0.5	1

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37	Non-homologous end-joining partners in a helical dance: structural studies of XLFâ€“XRCC4 interactions. Biochemical Society Transactions, 2011, 39, 1387-1392.	3.4	65
38	Structure of a Blinkin-BUBR1 Complex Reveals an Interaction Crucial for Kinetochore-Mitotic Checkpoint Regulation via an Unanticipated Binding Site. Structure, 2011, 19, 1691-1700.	3.3	68
39	Crystal structure of DNA-PKcs reveals a large open-ring cradle comprised of HEAT repeats. Nature, 2010, 463, 118-121.	27.8	195
40	Nanostructured films from hierarchical self-assembly of amyloidogenic proteins. Nature Nanotechnology, 2010, 5, 204-207.	31.5	338
41	Structural Biology of DNA Repair: Spatial Organisation of the Multicomponent Complexes of Nonhomologous End Joining. Journal of Nucleic Acids, 2010, 2010, 1-19.	1.2	24
42	Structural Basis for the Activity and Substrate Specificity of Fluoroacetyl-CoA Thioesterase FlK. Journal of Biological Chemistry, 2010, 285, 22495-22504.	3.4	24
43	Thyroid stimulating autoantibody M22 mimics TSH binding to the TSH receptor leucine rich domain: a comparative structural study of proteinâ€“protein interactions. Journal of Molecular Endocrinology, 2009, 42, 381-395.	2.5	33
44	The Crystal Structure of the N-Terminal Region of BUB1 Provides Insight into the Mechanism of BUB1 Recruitment to Kinetochores. Structure, 2009, 17, 105-116.	3.3	45
45	The effect of proteinâ€“precipitant interfaces and applied shear on the nucleation and growth of lysozyme crystals. Acta Crystallographica Section D: Biological Crystallography, 2009, 65, 1127-1139.	2.5	7
46	Inhibition of <i>Mycobacterium tuberculosis</i> Pantothenate Synthetase by Analogues of the Reaction Intermediate. ChemBioChem, 2008, 9, 2606-2611.	2.6	56
47	Crystal structure of human XLF/Cernunnos reveals unexpected differences from XRCC4 with implications for NHEJ. EMBO Journal, 2008, 27, 290-300.	7.8	106
48	FSH and TSH binding to their respective receptors: similarities, differences and implication for glycoprotein hormone specificity. Journal of Molecular Endocrinology, 2008, 41, 145-164.	2.5	27
49	Crystal Structure of Escherichia coli Ketopantoate Reductase in a Ternary Complex with NADP+ and Pantoate Bound. Journal of Biological Chemistry, 2007, 282, 8487-8497.	3.4	39
50	Crystal Structure of the TSH Receptor in Complex with a Thyroid-Stimulating Autoantibody. Thyroid, 2007, 17, 395-410.	4.5	205
51	Nucleophile Selectivity of Chorismate-Utilizing Enzymes. ChemBioChem, 2007, 8, 622-624.	2.6	8
52	Structure of an Xrcc4â€“DNA ligase IV yeast ortholog complex reveals a novel BRCT interaction mode. DNA Repair, 2006, 5, 362-368.	2.8	60
53	Crystal Structures of Yersinia enterocolitica Salicylate Synthase and its Complex with the Reaction Products Salicylate and Pyruvate. Journal of Molecular Biology, 2006, 357, 524-534.	4.2	45
54	Crystal structures of the PLP- and PMP-bound forms of BtrR, a dual functional aminotransferase involved in butirosin biosynthesis. Proteins: Structure, Function and Bioinformatics, 2006, 65, 220-230.	2.6	19

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55	Knowledge-Based Real-Space Explorations for Low-Resolution Structure Determination. Structure, 2006, 14, 1313-1320.	3.3	27
56	High-resolution crystal structure of the human Notch 1 ankyrin domain. Biochemical Journal, 2005, 392, 13-20.	3.7	51
57	Crystal structure of the Î²-chain of human hepatocyte growth factor-like/macrophage stimulating protein. FEBS Journal, 2005, 272, 5799-5807.	4.7	23
58	Characteristics of a Monoclonal Antibody to the Thyrotropin Receptor that Acts as a Powerful Thyroid-Stimulating Autoantibody Antagonist. Thyroid, 2005, 15, 672-682.	4.5	44
59	Characteristics of a Human Monoclonal Autoantibody to the Thyrotropin Receptor: Sequence Structure and Function. Thyroid, 2004, 14, 560-570.	4.5	92
60	Snapshot of Protein Structure Evolution Reveals Conservation of Functional Dimerization through Intertwined Folding. Structure, 2004, 12, 1489-1494.	3.3	15
61	Structural constraints on protein self-processing in L-aspartate-Â-decarboxylase. EMBO Journal, 2003, 22, 6193-6204.	7.8	56
62	Molecular Dissection of the Interaction between the Small G Proteins Rac1 and RhoA and Protein Kinase C-related Kinase 1 (PRK1). Journal of Biological Chemistry, 2003, 278, 50578-50587.	3.4	49
63	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. Journal of Molecular Biology, 2002, 319, 283-288.	4.2	22
64	Asymmetry in the Multiprotein Systems of Molecular Biology. Structural Chemistry, 2002, 13, 405-412.	2.0	13
65	Crystal structures of NK1-heparin complexes reveal the basis for NK1 activity and enable engineering of potent agonists of the MET receptor. EMBO Journal, 2001, 20, 5543-5555.	7.8	107
66	Crystal structure of the NK1 fragment of HGF/SF suggests a novel mode for growth factor dimerization and receptor binding. Nature Structural Biology, 1999, 6, 72-79.	9.7	110
67	Insights into the structure of hepatocyte growth factor/scatter factor (HGF/SF) and implications for receptor activation. FEBS Letters, 1998, 430, 126-129.	2.8	29