

Gleb Bourenkov

List of Publications by Year in descending order

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97
papers

8,792
citations

57631

44
h-index

43802

91
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104
all docs

104
docs citations

104
times ranked

11154
citing authors

#	ARTICLE	IF	CITATIONS
1	Molecular Coevolution of Nuclear and Nucleolar Localization Signals inside the Basic Domain of HIV-1 Tat. <i>Journal of Virology</i> , 2022, 96, JVI0150521.	1.5	5
2	Variability in the Spatial Structure of the Central Loop in Cobra Cytotoxins Revealed by X-ray Analysis and Molecular Modeling. <i>Toxins</i> , 2022, 14, 149.	1.5	6
3	High-pressure crystallography shows noble gas intervention into protein-lipid interaction and suggests a model for anaesthetic action. <i>Communications Biology</i> , 2022, 5, 360.	2.0	4
4	Ground-state destabilization by electrostatic repulsion is not a driving force in orotidine-5- β -monophosphate decarboxylase catalysis. <i>Nature Catalysis</i> , 2022, 5, 332-341.	16.1	12
5	True-atomic-resolution insights into the structure and functional role of linear chains and low-barrier hydrogen bonds in proteins. <i>Nature Structural and Molecular Biology</i> , 2022, 29, 440-450.	3.6	21
6	Serial femtosecond and serial synchrotron crystallography can yield data of equivalent quality: A systematic comparison. <i>Science Advances</i> , 2021, 7, .	4.7	25
7	Structural insights into the inhibition of glycine reuptake. <i>Nature</i> , 2021, 591, 677-681.	13.7	69
8	X-ray screening identifies active site and allosteric inhibitors of SARS-CoV-2 main protease. <i>Science</i> , 2021, 372, 642-646.	6.0	240
9	Study of the applicability of nano-polycrystalline diamond as a material for refractive x-ray lenses. , 2021, , .		1
10	Profiling cellular diversity in sponges informs animal cell type and nervous system evolution. <i>Science</i> , 2021, 374, 717-723.	6.0	111
11	Binding specificities of human RNA-binding proteins toward structured and linear RNA sequences. <i>Genome Research</i> , 2020, 30, 962-973.	2.4	55
12	Multiscale computation delivers organophosphorus reactivity and stereoselectivity to immunoglobulin scavengers. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 22841-22848.	3.3	13
13	Molecular mechanism of light-driven sodium pumping. <i>Nature Communications</i> , 2020, 11, 2137.	5.8	67
14	A kinase bioscavenger provides antibiotic resistance by extremely tight substrate binding. <i>Science Advances</i> , 2020, 6, eaaz9861.	4.7	17
15	High-resolution structural insights into the heliorhodopsin family. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 4131-4141.	3.3	58
16	<i>MXCuBE2</i>: the dawn of <i>MXCuBE</i> Collaboration. <i>Journal of Synchrotron Radiation</i> , 2019, 26, 393-405.	1.0	30
17	Unique structure and function of viral rhodopsins. <i>Nature Communications</i> , 2019, 10, 4939.	5.8	59
18	Liquid application method for time-resolved analyses by serial synchrotron crystallography. <i>Nature Methods</i> , 2019, 16, 979-982.	9.0	74

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19	Bioluminescence chemistry of fireworm <i>Odontosyllis</i> . Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 18911-18916.	3.3	33
20	Optical performance and radiation stability of polymer X-ray refractive nano-lenses. Journal of Synchrotron Radiation, 2019, 26, 714-719.	1.0	12
21	Clustering of atomic displacement parameters in bovine trypsin reveals a distributed lattice of atoms with shared chemical properties. Scientific Reports, 2019, 9, 19281.	1.6	7
22	CRL-based ultra-compact transfocator for X-ray focusing and microscopy. Journal of Synchrotron Radiation, 2019, 26, 1208-1212.	1.0	15
23	Visualization of protein crystals by high-energy phase-contrast X-ray imaging. Acta Crystallographica Section D: Structural Biology, 2019, 75, 947-958.	1.1	16
24	The complex analysis of X-ray mesh scans for macromolecular crystallography. Acta Crystallographica Section D: Structural Biology, 2018, 74, 355-365.	1.1	15
25	The structure of the N-terminal module of the cell wall hydrolase RipA and its role in regulating catalytic activity. Proteins: Structure, Function and Bioinformatics, 2018, 86, 912-923.	1.5	26
26	Microfluidic Chips for <i>In Situ</i> Crystal X-ray Diffraction and <i>In Situ</i> Dynamic Light Scattering for Serial Crystallography. Journal of Visualized Experiments, 2018, .	0.2	16
27	Structural and Functional Characterization of the BcsG Subunit of the Cellulose Synthase in <i>Salmonella typhimurium</i> . Journal of Molecular Biology, 2018, 430, 3170-3189.	2.0	29
28	Structural Study of the Complex Formed by Ceruloplasmin and Macrophage Migration Inhibitory Factor. Biochemistry (Moscow), 2018, 83, 701-707.	0.7	5
29	Identification of the point of diminishing returns in high-multiplicity data collection for sulfur SAD phasing. Journal of Synchrotron Radiation, 2017, 24, 19-28.	1.0	4
30	Mechanism of transmembrane signaling by sensor histidine kinases. Science, 2017, 356, .	6.0	132
31	Rat ceruloplasmin: a new labile copper binding site and zinc/copper mosaic. Metallomics, 2017, 9, 1828-1838.	1.0	14
32	P13, the EMBL macromolecular crystallography beamline at the low-emittance PETRA III ring for high- and low-energy phasing with variable beam focusing. Journal of Synchrotron Radiation, 2017, 24, 323-332.	1.0	155
33	Bayesian analysis of non-thermal structural changes induced by terahertz radiation in protein crystals. , 2016, .		0
34	A multichannel diffraction data-collection approach for studying structural dynamics with millisecond temporal resolution. IUCr, 2016, 3, 393-401.	1.0	19
35	The inhibition mechanism of human 20S proteasomes enables next-generation inhibitor design. Science, 2016, 353, 594-598.	6.0	170
36	The structure of a furin-antibody complex explains non-competitive inhibition by steric exclusion of substrate conformers. Scientific Reports, 2016, 6, 34303.	1.6	18

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37	Terahertz radiation induces non-thermal structural changes associated with FrÅ¼hlich condensation in a protein crystal. <i>Structural Dynamics</i> , 2015, 2, 054702.	0.9	56
38	<i>MeshAndCollect</i>: an automated multi-crystal data-collection workflow for synchrotron macromolecular crystallography beamlines. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2015, 71, 2328-2343.	2.5	108
39	Detailed Structureâ€™Function Correlations of <i>Bacillus subtilis</i> Acetolactate Synthase. <i>ChemBioChem</i> , 2015, 16, 110-118.	1.3	20
40	The oxygenating constituent of 3,6-diketocamphane monooxygenase from the CAM plasmid of <i>Pseudomonas putida</i>: the first crystal structure of a type II Baeyerâ€™Villiger monooxygenase. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2015, 71, 2344-2353.	2.5	20
41	Mapping the continuous reciprocal space intensity distribution of X-ray serial crystallography. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2014, 369, 20130333.	1.8	29
42	Serial crystallography on<i>in vivo</i>grown microcrystals using synchrotron radiation. <i>IUCr</i> , 2014, 1, 87-94.	1.0	204
43	A survey of global radiation damage to 15 different protein crystal types at room temperature: a new decay model. <i>Journal of Synchrotron Radiation</i> , 2013, 20, 14-22.	1.0	24
44	Ceruloplasmin: Macromolecular Assemblies with Iron-Containing Acute Phase Proteins. <i>PLoS ONE</i> , 2013, 8, e67145.	1.1	82
45	High angular resolution slope measuring deflectometry for the characterization of ultra-precise reflective x-ray optics. <i>Measurement Science and Technology</i> , 2012, 23, 074015.	1.4	9
46	Structural comparison of the poplar plastocyanin isoforms PCa and PCb sheds new light on the role of the copper site geometry in interactions with redox partners in oxygenic photosynthesis. <i>Journal of Inorganic Biochemistry</i> , 2012, 115, 174-181.	1.5	25
47	The application of hierarchical cluster analysis to the selection of isomorphous crystals. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2012, 68, 649-658.	2.5	80
48	Experimental procedure for the characterization ofÂˆradiation damage in macromolecular crystals. <i>Journal of Synchrotron Radiation</i> , 2011, 18, 381-386.	1.0	22
49	Optimization of data collection taking radiation damage into account. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2010, 66, 409-419.	2.5	106
50	Crystal Structure Analysis of Free and Substrate-Bound 6-Hydroxy-l-Nicotine Oxidase from <i>Arthrobacter nicotinovorans</i> . <i>Journal of Molecular Biology</i> , 2010, 396, 785-799.	2.0	33
51	<i>EDNA</i>: a framework for plugin-based applications applied to X-ray experiment online data analysis. <i>Journal of Synchrotron Radiation</i> , 2009, 16, 872-879.	1.0	200
52	High-Resolution Structural Analysis of a Novel Octaheme Cytochrome c Nitrite Reductase from the Haloalkaliphilic Bacterium <i>Thioalkalivibrio nitratireducens</i> . <i>Journal of Molecular Biology</i> , 2009, 389, 846-862.	2.0	78
53	Crystal structure of YagE, a putative DHDPSâ€™like protein from <i>Escherichia coli K12</i>. <i>Proteins: Structure, Function and Bioinformatics</i> , 2008, 71, 2102-2108.	1.5	5
54	CASK Functions as a Mg ²⁺ -Independent Neurexin Kinase. <i>Cell</i> , 2008, 133, 328-339.	13.5	246

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55	Open and Closed Structures of the UDP-glucose Pyrophosphorylase from <i>Leishmania major</i> . <i>Journal of Biological Chemistry</i> , 2007, 282, 13003-13010.	1.6	48
56	Mechanism of Phosphoryl Transfer Catalyzed by Shikimate Kinase from <i>Mycobacterium tuberculosis</i> . <i>Journal of Molecular Biology</i> , 2006, 364, 411-423.	2.0	63
57	A quantitative approach to data-collection strategies. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2006, 62, 58-64.	2.5	85
58	Structure and function of Tim14 and Tim16, the J and J-like components of the mitochondrial protein import motor. <i>EMBO Journal</i> , 2006, 25, 4675-4685.	3.5	107
59	The endoproteinase furin contains two essential Ca ²⁺ ions stabilizing its N-terminus and the unique S1 specificity pocket. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2005, 61, 505-512.	2.5	36
60	X-ray Structure of Human proMMP-1. <i>Journal of Biological Chemistry</i> , 2005, 280, 9578-9585.	1.6	110
61	<i>Staphylococcus aureus</i> Aminopeptidase S Is a Founding Member of a New Peptidase Clan. <i>Journal of Biological Chemistry</i> , 2005, 280, 27792-27799.	1.6	21
62	The 1.3 Å... Crystal Structure of the Flavoprotein YqjM Reveals a Novel Class of Old Yellow Enzymes. <i>Journal of Biological Chemistry</i> , 2005, 280, 27904-27913.	1.6	116
63	The NC1 dimer of human placental basement membrane collagen IV: does a covalent crosslink exist?. <i>Biological Chemistry</i> , 2005, 386, 759-66.	1.2	11
64	Substrate Access to the Active Sites in Aminopeptidase T, a Representative of a New Metallopeptidase Clan. <i>Journal of Molecular Biology</i> , 2005, 354, 403-412.	2.0	12
65	Crystal structure of the p14/MP1 scaffolding complex: How a twin couple attaches mitogen-activated protein kinase signaling to late endosomes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 10984-10989.	3.3	89
66	Structural basis for the interaction of <i>Escherichia coli</i> NusA with protein N of phage \hat{A} . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 13762-13767.	3.3	28
67	Crystallization and preliminary X-ray diffraction analysis of the 16-haem cytochrome of <i>Desulfovibrio gigas</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2004, 60, 968-970.	2.5	3
68	Structure of the N-Terminal Domain of the Adenylyl Cyclase-Associated Protein (CAP) from <i>Dictyostelium discoideum</i> . <i>Structure</i> , 2003, 11, 1171-1178.	1.6	44
69	The Zinc Finger-Associated Domain of the <i>Drosophila</i> Transcription Factor Grauzone Is a Novel Zinc-Coordinating Protein-Protein Interaction Module. <i>Structure</i> , 2003, 11, 1393-1402.	1.6	47
70	Choice of data-collection parameters based on statistic modelling. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2003, 59, 1145-1153.	2.5	105
71	The crystal structure of the proprotein processing proteinase furin explains its stringent specificity. <i>Nature Structural and Molecular Biology</i> , 2003, 10, 520-526.	3.6	313
72	Coenzyme F420-dependent Methylenetetrahydromethanopterin Dehydrogenase (Mtd) from <i>Methanopyrus kandleri</i> : A Methanogenic Enzyme with an Unusual Quarternary Structure. <i>Journal of Molecular Biology</i> , 2003, 332, 1047-1057.	2.0	39

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73	Structure of adenylylsulfate reductase from the hyperthermophilic <i>Archaeoglobus fulgidus</i> at 1.6-Å resolution. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002, 99, 1836-1841.	3.3	78
74	The 1.9-Å crystal structure of the noncollagenous (NC1) domain of human placenta collagen IV shows stabilization via a novel type of covalent Met-Lys cross-link. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002, 99, 6607-6612.	3.3	130
75	Structure and Function of Threonine Synthase from Yeast. <i>Journal of Biological Chemistry</i> , 2002, 277, 12396-12405.	1.6	34
76	Purification, Crystallization, and Preliminary X-ray Diffraction Analysis of the Tricorn Protease Hexamer from <i>Thermoplasma acidophilum</i> . <i>Journal of Structural Biology</i> , 2001, 134, 83-87.	1.3	5
77	Adrenodoxin Reductase-Adrenodoxin Complex Structure Suggests Electron Transfer Path in Steroid Biosynthesis. <i>Journal of Biological Chemistry</i> , 2001, 276, 2786-2789.	1.6	152
78	An Extended RNA Binding Surface through Arrayed S1 and KH Domains in Transcription Factor NusA. <i>Molecular Cell</i> , 2001, 7, 1177-1189.	4.5	87
79	The protein crystallography beamline BW6 at DORIS – automatic operation and high-throughput data collection. <i>Nuclear Instruments and Methods in Physics Research, Section A: Accelerators, Spectrometers, Detectors and Associated Equipment</i> , 2001, 467-468, 1358-1362.	0.7	2
80	Crystallization and preliminary X-ray analysis of recombinant full-length human m-calpain. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2000, 56, 73-75.	2.5	6
81	The structures of HslU and the ATP-dependent protease HslU–HslV. <i>Nature</i> , 2000, 403, 800-805.	13.7	406
82	The coiled-coil trigger site of the rod domain of cortexillin I unveils a distinct network of interhelical and intrahelical salt bridges. <i>Structure</i> , 2000, 8, 223-230.	1.6	114
83	Flexibility, conformational diversity and two dimerization modes in complexes of ribosomal protein L12. <i>EMBO Journal</i> , 2000, 19, 174-186.	3.5	84
84	X-ray structure of MalY from <i>Escherichia coli</i> : a pyridoxal 5-phosphate-dependent enzyme acting as a modulator in mal gene expression. <i>EMBO Journal</i> , 2000, 19, 831-842.	3.5	44
85	Crystal structures of mutant monomeric hexokinase I reveal multiple ADP binding sites and conformational changes relevant to allosteric regulation 1 Edited by P. E. Wright. <i>Journal of Molecular Biology</i> , 2000, 296, 1001-1015.	2.0	95
86	Crystal structure of a NifS-like protein from <i>Thermotoga maritima</i> : implications for iron sulphur cluster assembly. <i>Journal of Molecular Biology</i> , 2000, 297, 451-464.	2.0	135
87	Structure of TPR Domain–Peptide Complexes. <i>Cell</i> , 2000, 101, 199-210.	13.5	1,126
88	High-Temperature Superionic Phase of Mixed Proton Conductor [Rb _{0.57} (NH ₄) _{0.43}] ₃ H(SeO ₄) ₂ : Dynamic Twinning and Anomalous Display of Dynamically Disordered Hydrogen Atoms. , 2000, 218, 365.		1
89	Structure of cytochrome c nitrite reductase. <i>Nature</i> , 1999, 400, 476-480.	13.7	352
90	Crystal structures of the membrane-binding C2 domain of human coagulation factor V. <i>Nature</i> , 1999, 402, 434-439.	13.7	258

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91	The crystal structure of methenyltetrahydromethanopterin cyclohydrolase from the hyperthermophilic archaeon <i>Methanopyrus kandleri</i> . <i>Structure</i> , 1999, 7, 1257-1268.	1.6	43
92	Crystal structure of the first dissimilatory nitrate reductase at 1.9 Å... solved by MAD methods. <i>Structure</i> , 1999, 7, 65-79.	1.6	288
93	The mechanism of regulation of hexokinase: new insights from the crystal structure of recombinant human brain hexokinase complexed with glucose and glucose-6-phosphate. <i>Structure</i> , 1998, 6, 39-50.	1.6	122
94	Crystal structure of the catalytic domain of human tumor necrosis factor- α -converting enzyme. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1998, 95, 3408-3412.	3.3	368
95	<i>Thermus thermophilus</i> cytochrome- c 552 : a new highly thermostable cytochrome- c structure obtained by MAD phasing 1 Edited by K. Nagai. <i>Journal of Molecular Biology</i> , 1997, 271, 629-644.	2.0	90
96	Mechanism of inhibition of the human matrix metalloproteinase stromelysin-1 by TIMP-1. <i>Nature</i> , 1997, 389, 77-81.	13.7	572
97	A Bayesian Approach to Laue Diffraction Analysis and its Potential for Time-Resolved Protein Crystallography. <i>Acta Crystallographica Section A: Foundations and Advances</i> , 1996, 52, 797-811.	0.3	14