

Gleb Bourenkov

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/3649091/publications.pdf>

Version: 2024-02-01

97
papers

8,792
citations

57631

44
h-index

43802

91
g-index

104
all docs

104
docs citations

104
times ranked

11154
citing authors

#	ARTICLE	IF	CITATIONS
1	Structure of TPR Domain–Peptide Complexes. <i>Cell</i> , 2000, 101, 199-210.	13.5	1,126
2	Mechanism of inhibition of the human matrix metalloproteinase stromelysin-1 by TIMP-1. <i>Nature</i> , 1997, 389, 77-81.	13.7	572
3	The structures of HslU and the ATP-dependent protease HslU–HslV. <i>Nature</i> , 2000, 403, 800-805.	13.7	406
4	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
5	Structure of cytochrome c nitrite reductase. <i>Nature</i> , 1999, 400, 476-480.	13.7	352
6	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
7	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
8	Crystal structures of the membrane-binding C2 domain of human coagulation factor V. <i>Nature</i> , 1999, 402, 434-439.	13.7	258
9	CASK Functions as a Mg ²⁺ -Independent Neurexin Kinase. <i>Cell</i> , 2008, 133, 328-339.	13.5	246
10	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
11	Serial crystallography on <i>in vivo</i> grown microcrystals using synchrotron radiation. <i>IUCr</i> , 2014, 1, 87-94.	1.0	204
12	<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
13	The inhibition mechanism of human 20 <i>S</i> proteasomes enables next-generation inhibitor design. <i>Science</i> , 2016, 353, 594-598.	6.0	170
14	P13, the EMBL macromolecular crystallography beamline at the low-emittance PETRA III ring for high- and low-energy phasing with variable beam focusing. <i>Journal of Synchrotron Radiation</i> , 2017, 24, 323-332.	1.0	155
15	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
16	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
17	Mechanism of transmembrane signaling by sensor histidine kinases. <i>Science</i> , 2017, 356, .	6.0	132
18	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

#	ARTICLE	IF	CITATIONS
19	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
20	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
21	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
22	Profiling cellular diversity in sponges informs animal cell type and nervous system evolution. <i>Science</i> , 2021, 374, 717-723.	6.0	111
23	X-ray Structure of Human proMMP-1. <i>Journal of Biological Chemistry</i> , 2005, 280, 9578-9585.	1.6	110
24	<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
25	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
26	Optimization of data collection taking radiation damage into account. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2010, 66, 409-419.	2.5	106
27	Choice of data-collection parameters based on statistic modelling. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2003, 59, 1145-1153.	2.5	105
28	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
29	<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
30	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
31	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
32	A quantitative approach to data-collection strategies. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2006, 62, 58-64.	2.5	85
33	Flexibility, conformational diversity and two dimerization modes in complexes of ribosomal protein L12. <i>EMBO Journal</i> , 2000, 19, 174-186.	3.5	84
34	Ceruloplasmin: Macromolecular Assemblies with Iron-Containing Acute Phase Proteins. <i>PLoS ONE</i> , 2013, 8, e67145.	1.1	82
35	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
36	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

#	ARTICLE	IF	CITATIONS
37	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
38	Liquid application method for time-resolved analyses by serial synchrotron crystallography. <i>Nature Methods</i> , 2019, 16, 979-982.	9.0	74
39	Structural insights into the inhibition of glycine reuptake. <i>Nature</i> , 2021, 591, 677-681.	13.7	69
40	Molecular mechanism of light-driven sodium pumping. <i>Nature Communications</i> , 2020, 11, 2137.	5.8	67
41	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
42	Unique structure and function of viral rhodopsins. <i>Nature Communications</i> , 2019, 10, 4939.	5.8	59
43	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
44	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
45	Binding specificities of human RNA-binding proteins toward structured and linear RNA sequences. <i>Genome Research</i> , 2020, 30, 962-973.	2.4	55
46	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
47	The Zinc Finger-Associated Domain of the <i>Drosophila</i> Transcription Factor <i>Grauzone</i> Is a Novel Zinc-Coordinating Protein-Protein Interaction Module. <i>Structure</i> , 2003, 11, 1393-1402.	1.6	47
48	X-ray structure of MalY from <i>Escherichia coli</i> : a pyridoxal 5â€²-phosphate-dependent enzyme acting as a modulator in mal gene expression. <i>EMBO Journal</i> , 2000, 19, 831-842.	3.5	44
49	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
50	The crystal structure of methenyltetrahydromethanopterin cyclohydrolase from the hyperthermophilic archaeon <i>Methanopyrus kandleri</i> . <i>Structure</i> , 1999, 7, 1257-1268.	1.6	43
51	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
52	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
53	Structure and Function of Threonine Synthase from Yeast. <i>Journal of Biological Chemistry</i> , 2002, 277, 12396-12405.	1.6	34
54	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

#	ARTICLE	IF	CITATIONS
55	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
56	<i>MXCuBE2</i> : the dawn of <i>MXCuBE</i> Collaboration. Journal of Synchrotron Radiation, 2019, 26, 393-405.	1.0	30
57	Mapping the continuous reciprocal space intensity distribution of X-ray serial crystallography. Philosophical Transactions of the Royal Society B: Biological Sciences, 2014, 369, 20130333.	1.8	29
58	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
59	Structural basis for the interaction of <i>Escherichia coli</i> NusA with protein N of phage λ . Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 13762-13767.	3.3	28
60	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
61	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. Journal of Inorganic Biochemistry, 2012, 115, 174-181.	1.5	25
62	Serial femtosecond and serial synchrotron crystallography can yield data of equivalent quality: A systematic comparison. Science Advances, 2021, 7, .	4.7	25
63	A survey of global radiation damage to 15 different protein crystal types at room temperature: a new decay model. Journal of Synchrotron Radiation, 2013, 20, 14-22.	1.0	24
64	Experimental procedure for the characterization of radiation damage in macromolecular crystals. Journal of Synchrotron Radiation, 2011, 18, 381-386.	1.0	22
65	<i>Staphylococcus aureus</i> Aminopeptidase S is a Founding Member of a New Peptidase Clan. Journal of Biological Chemistry, 2005, 280, 27792-27799.	1.6	21
66	True-atomic-resolution insights into the structure and functional role of linear chains and low-barrier hydrogen bonds in proteins. Nature Structural and Molecular Biology, 2022, 29, 440-450.	3.6	21
67	Detailed Structure-Function Correlations of <i>Bacillus subtilis</i> Acetolactate Synthase. ChemBioChem, 2015, 16, 110-118.	1.3	20
68	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 Baeyer-Villiger monooxygenase. Acta Crystallographica Section D: Biological Crystallography, 2015, 71, 2344-2353.	2.5	20
69	A multicrystal diffraction data-collection approach for studying structural dynamics with millisecond temporal resolution. IUCr, 2016, 3, 393-401.	1.0	19
70	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
71	A kinase bioscavenger provides antibiotic resistance by extremely tight substrate binding. Science Advances, 2020, 6, eaaz9861.	4.7	17
72	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

#	ARTICLE	IF	CITATIONS
73	Visualization of protein crystals by high-energy phase-contrast X-ray imaging. <i>Acta Crystallographica Section D: Structural Biology</i> , 2019, 75, 947-958.	1.1	16
74	The complex analysis of X-ray mesh scans for macromolecular crystallography. <i>Acta Crystallographica Section D: Structural Biology</i> , 2018, 74, 355-365.	1.1	15
75	CRL-based ultra-compact translocator for X-ray focusing and microscopy. <i>Journal of Synchrotron Radiation</i> , 2019, 26, 1208-1212.	1.0	15
76	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
77	Rat ceruloplasmin: a new labile copper binding site and zinc/copper mosaic. <i>Metallomics</i> , 2017, 9, 1828-1838.	1.0	14
78	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
79	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
80	Optical performance and radiation stability of polymer X-ray refractive nano-lenses. <i>Journal of Synchrotron Radiation</i> , 2019, 26, 714-719.	1.0	12
81	Ground-state destabilization by electrostatic repulsion is not a driving force in orotidine-5'-monophosphate decarboxylase catalysis. <i>Nature Catalysis</i> , 2022, 5, 332-341.	16.1	12
82	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
83	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
84	Clustering of atomic displacement parameters in bovine trypsin reveals a distributed lattice of atoms with shared chemical properties. <i>Scientific Reports</i> , 2019, 9, 19281.	1.6	7
85	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
86	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
87	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
88	Crystal structure of YagE, a putative DHDS-like protein from <i>Escherichia coli</i> K12. <i>Proteins: Structure, Function and Bioinformatics</i> , 2008, 71, 2102-2108.	1.5	5
89	Structural Study of the Complex Formed by Ceruloplasmin and Macrophage Migration Inhibitory Factor. <i>Biochemistry (Moscow)</i> , 2018, 83, 701-707.	0.7	5
90	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

#	ARTICLE	IF	CITATIONS
91	Identification of the point of diminishing returns in high-multiplicity data collection for sulfur SAD phasing. <i>Journal of Synchrotron Radiation</i> , 2017, 24, 19-28.	1.0	4
92	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
93	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
94	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
95	Study of the applicability of nano-polycrystalline diamond as a material for refractive x-ray lenses. , 2021, , .		1
96	High-Temperature Superionic Phase of Mixed Proton Conductor $[Rb_{0.57}(NH_4)_{0.43}]_3H(SeO_4)_2$: Dynamic Twinning and Anomalous Display of Dynamically Disordered Hydrogen Atoms. , 2000, 218, 365.		1
97	Bayesian analysis of non-thermal structural changes induced by terahertz radiation in protein crystals. , 2016, , .		0