

# Azat G Gabdulkhakov

## List of Publications by Year in descending order

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86  
papers

2,468  
citations

331538

21  
h-index

206029

48  
g-index

86  
all docs

86  
docs citations

86  
times ranked

2838  
citing authors

#	ARTICLE	IF	CITATIONS
1	Cyanobacterial photosystem II at 2.9-Å... resolution and the role of quinones, lipids, channels and chloride. <i>Nature Structural and Molecular Biology</i> , 2009, 16, 334-342.	3.6	1,105
2	Probing the Accessibility of the Mn4Ca Cluster in Photosystem II: Channels Calculation, Noble Gas Derivatization, and Cocrystallization with DMSO. <i>Structure</i> , 2009, 17, 1223-1234.	1.6	120
3	Recent Progress in the Crystallographic Studies of Photosystem II. <i>ChemPhysChem</i> , 2010, 11, 1160-1171.	1.0	102
4	Crystal structure of a mirror-image L-RNA aptamer (Spiegelmer) in complex with the natural L-protein target CCL2. <i>Nature Communications</i> , 2015, 6, 6923.	5.8	77
5	Structural Basis of Cyanobacterial Photosystem II Inhibition by the Herbicide Terbutryn. <i>Journal of Biological Chemistry</i> , 2011, 286, 15964-15972.	1.6	73
6	Structural insights into the catalytic mechanism of sphingomyelinases D and evolutionary relationship to glycerophosphodiester phosphodiesterases. <i>Biochemical and Biophysical Research Communications</i> , 2006, 342, 323-329.	1.0	63
7	Crystal Structure of Monomeric Photosystem II from <i>Thermosynechococcus elongatus</i> at 3.6-Å... Resolution. <i>Journal of Biological Chemistry</i> , 2010, 285, 26255-26262.	1.6	62
8	Ribosomal protein L1 recognizes the same specific structural motif in its target sites on the autoregulatory mRNA and 23S rRNA. <i>Nucleic Acids Research</i> , 2005, 33, 478-485.	6.5	56
9	X-ray structural studies of the fungal laccase from <i>Cerrena maxima</i> . <i>Journal of Biological Inorganic Chemistry</i> , 2006, 11, 963-973.	1.1	47
10	Structural and functional characterization of two-domain laccase from <i>Streptomyces viridochromogenes</i> . <i>Biochimie</i> , 2015, 112, 151-159.	1.3	42
11	Double Suppression of the G1± Protein Activity by RGS Proteins. <i>Molecular Cell</i> , 2014, 53, 663-671.	4.5	40
12	Revisiting the Haloarcula marismortui 50S ribosomal subunit model. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2013, 69, 997-1004.	2.5	40
13	Structure of the polypeptide crotamine from the Brazilian rattlesnake <i>Crotalus durissus terrificus</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2013, 69, 1958-1964.	2.5	37
14	Three-Dimensional Structure of N-Terminal Domain of DnaB Helicase and Helicase-Primase Interactions in <i>Helicobacter pylori</i> . <i>PLoS ONE</i> , 2009, 4, e7515.	1.1	34
15	Mechanism of ribosome shutdown by RsfS in <i>Staphylococcus aureus</i> revealed by integrative structural biology approach. <i>Nature Communications</i> , 2020, 11, 1656.	5.8	30
16	Purification, crystallization and preliminary X-ray study of the fungal laccase from <i>Cerrena maxima</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2006, 62, 954-957.	0.7	27
17	High-resolution crystal structure of the isolated ribosomal L1 stalk. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2012, 68, 1051-1057.	2.5	26
18	The structures of mutant forms of Hfq from <i>Pseudomonas aeruginosa</i> reveal the importance of the conserved His57 for the protein hexamer organization. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2010, 66, 760-764.	0.7	25

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19	Mistletoe lectin I in complex with galactose and lactose reveals distinct sugar-binding properties. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2005, 61, 17-25.	0.7	22
20	Insights into metal ion binding in phospholipases A2: ultra high-resolution crystal structures of acidic phospholipase A2 in Ca <sup>2+</sup> free and bound states. <i>Biochimie</i> , 2006, 88, 543-549.	1.3	22
21	Asp49 phospholipase A2-elaidoylamide complex: a new mode of inhibition. <i>Biochemical and Biophysical Research Communications</i> , 2004, 319, 1314-1321.	1.0	21
22	Preliminary investigation of the three-dimensional structure of <i>Salmonella typhimurium</i> uridine phosphorylase in the crystalline state. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2005, 61, 337-340.	0.7	18
23	The X-ray structure of <i>Salmonella typhimurium</i> uridine nucleoside phosphorylase complexed with 2,2'-anhydrouridine, phosphate and potassium ions at 1.86 Å resolution. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2010, 66, 51-60.	2.5	18
24	Investigations of Accessibility of T2/T3 Copper Center of Two-Domain Laccase from <i>Streptomyces griseoflavus</i> Ac-993. <i>International Journal of Molecular Sciences</i> , 2019, 20, 3184.	1.8	18
25	Controlling Photosynthetic Excitons by Selective Pigment Photooxidation. <i>Journal of Physical Chemistry B</i> , 2019, 123, 29-38.	1.2	18
26	Three-dimensional structure of laccase from <i>Coriolus zonatus</i> at 2.6 Å resolution. <i>Crystallography Reports</i> , 2006, 51, 817-823.	0.1	15
27	Binding of the 5'-Triphosphate End of mRNA to the 3'-Subunit of Translation Initiation Factor 2 of the Crenarchaeon <i>Sulfolobus solfataricus</i> . <i>Journal of Molecular Biology</i> , 2015, 427, 3086-3095.	2.0	15
28	Purification, crystallization and preliminary X-ray diffraction analysis of crotamine, a myotoxic polypeptide from the Brazilian snake <i>Crotalus durissus terrificus</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2012, 68, 1052-1054.	0.7	14
29	Cryo-EM structure of the ribosome functional complex of the human pathogen <i>Staphylococcus aureus</i> at 3.2 Å resolution. <i>FEBS Letters</i> , 2020, 594, 3551-3567.	1.3	14
30	High-Resolution Crystal Structure of Spectrin SH3 Domain Fused with a Proline-Rich Peptide. <i>Journal of Biomolecular Structure and Dynamics</i> , 2011, 29, 485-495.	2.0	13
31	Protein-RNA affinity of ribosomal protein L1 mutants does not correlate with the number of intermolecular interactions. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2015, 71, 376-386.	2.5	12
32	Purification, crystallization and preliminary X-ray analysis of uridine phosphorylase from <i>Salmonella typhimurium</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2004, 60, 709-711.	2.5	11
33	Structural Studies of Component of Lysoamidase Bacteriolytic Complex from <i>Lysobacter</i> sp. XL1. <i>Protein Journal</i> , 2016, 35, 44-50.	0.7	10
34	Uridine phosphorylase in biomedical, structural, and functional aspects: A review. <i>Crystallography Reports</i> , 2011, 56, 560-589.	0.1	9
35	Molecular dynamics studies of pathways of water movement in cyanobacterial photosystem II. <i>Crystallography Reports</i> , 2015, 60, 83-89.	0.1	9
36	Crystal Structure of the 23S rRNA Fragment Specific to r-Protein L1 and Designed Model of the Ribosomal L1 Stalk from <i>Haloarcula marismortui</i> . <i>Crystals</i> , 2017, 7, 37.	1.0	9

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37	Engineering the Catalytic Properties of Two-Domain Laccase from <i>Streptomyces griseoflavus</i> Ac-993. <i>International Journal of Molecular Sciences</i> , 2022, 23, 65.	1.8	9
38	Structural and thermodynamic studies of Bergerac-SH3 chimeras. <i>Biophysical Chemistry</i> , 2009, 139, 106-115.	1.5	7
39	Comparative analysis of three-dimensional structures of homodimers of uridine phosphorylase from <i>Salmonella typhimurium</i> in the unligated state and in a complex with potassium ion. <i>Crystallography Reports</i> , 2009, 54, 267-278.	0.1	7
40	Purification, crystallization and preliminary X-ray structure analysis of the laccase from <i>Ganoderma lucidum</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2011, 67, 926-929.	0.7	7
41	X-ray structure of <i>Salmonella typhimurium</i> uridine phosphorylase complexed with 5-fluorouracil and molecular modelling of the complex of 5-fluorouracil with uridine phosphorylase from <i>Vibrio cholerae</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2012, 68, 968-974.	2.5	7
42	Crystallization and X-ray diffraction studies of a two-domain laccase from <i>Streptomyces griseoflavus</i> . <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2015, 71, 1200-1204.	0.4	7
43	Analysis of molecular oxygen exit pathways in cyanobacterial photosystem II: Molecular dynamics studies. <i>Crystallography Reports</i> , 2015, 60, 884-888.	0.1	7
44	Topology of the polypeptide chain in the complex of agglutinin from castor bean seeds with $\beta$ -D-galactose in the crystalline state. <i>Crystallography Reports</i> , 2001, 46, 792-800.	0.1	6
45	Crystal structure of ribosomal protein L1 from the bacterium <i>Aquifex aeolicus</i> . <i>Crystallography Reports</i> , 2011, 56, 603-607.	0.1	6
46	Structural analysis of interdomain mobility in ribosomal L1 proteins. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2011, 67, 1023-1027.	2.5	6
47	Expression, purification, crystallization and preliminary X-ray structure analysis of <i>Vibrio cholerae</i> uridine phosphorylase in complex with thymidine. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2012, 68, 1394-1397.	0.7	6
48	Structural studies on photosystem II of cyanobacteria. <i>Biochemistry (Moscow)</i> , 2013, 78, 1524-1538.	0.7	6
49	Crystallization and preliminary X-ray study of <i>Vibrio cholerae</i> uridine phosphorylase in complex with 6-methyluracil. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2014, 70, 60-63.	0.4	6
50	Fab Fragment of VHH-Based Antibody Netakimab: Crystal Structure and Modeling Interaction with Cytokine IL-17A. <i>Crystals</i> , 2019, 9, 177.	1.0	6
51	Novel approaches for the lipid sponge phase crystallization of the <i>Rhodobacter sphaeroides</i> photosynthetic reaction center. <i>IUCrJ</i> , 2020, 7, 1084-1091.	1.0	6
52	Isolation, crystallization and preliminary crystallographic analysis of <i>Salmonella typhimurium</i> uridine phosphorylase crystallized with 2,2'-anhydrouridine. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2007, 63, 852-854.	0.7	5
53	Structural basis for the mechanism of inhibition of uridine phosphorylase from <i>Salmonella typhimurium</i> . <i>Crystallography Reports</i> , 2010, 55, 41-57.	0.1	5
54	Expression, purification, crystallization and preliminary X-ray structure analysis of wild-type and L(M196)H-mutant <i>Rhodobacter sphaeroides</i> reaction centres. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2013, 69, 506-509.	0.7	5

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55	Structural investigation of the thymidine phosphorylase from <i>Salmonella typhimurium</i> in the unliganded state and its complexes with thymidine and uridine. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2016, 72, 224-233.	0.4	5
56	Structural and functional properties of antimicrobial protein L5 of <i>Lysobacter</i> sp. XL1. <i>Applied Microbiology and Biotechnology</i> , 2018, 102, 10043-10053.	1.7	5
57	X-ray structure of the <i>Rhodobacter sphaeroides</i> reaction center with an M197 Phe→His substitution clarifies the properties of the mutant complex. <i>IUCr</i> , 2022, 9, 261-271.	1.0	5
58	Crystallization and preliminary X-ray diffraction analysis of <i>Salmonella typhimurium</i> uridine phosphorylase complexed with 5-fluorouracil. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2009, 65, 601-603.	0.7	4
59	Different effects of identical symmetry-related mutations near the bacteriochlorophyll dimer in the photosynthetic reaction center of <i>Rhodobacter sphaeroides</i> . <i>Biochemistry (Moscow)</i> , 2015, 80, 647-653.	0.7	4
60	Investigation of structure of the ribosomal L12/P stalk. <i>Biochemistry (Moscow)</i> , 2016, 81, 1589-1601.	0.7	4
61	X-ray structures of uridine phosphorylase from <i>Vibrio cholerae</i> in complexes with uridine, thymidine, uracil, thymine, and phosphate anion: Substrate specificity of bacterial uridine phosphorylases. <i>Crystallography Reports</i> , 2016, 61, 954-973.	0.1	4
62	Dimerization of long hibernation promoting factor from <i>Staphylococcus aureus</i> : Structural analysis and biochemical characterization. <i>Journal of Structural Biology</i> , 2020, 209, 107408.	1.3	4
63	Structure of the ribosomal P stalk base in archaean <i>Methanococcus jannaschii</i> . <i>Journal of Structural Biology</i> , 2020, 211, 107559.	1.3	4
64	Crystallization and preliminary X-ray diffraction studies of <i>Drosophila melanogaster</i> G $\alpha$ -subunit of heterotrimeric G protein in complex with the RGS domain of CG5036. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2013, 69, 61-64.	0.7	3
65	Structural and preliminary molecular dynamics studies of the <i>Rhodobacter sphaeroides</i> reaction center and its mutant form L(M196)H + H(M202)L. <i>Crystallography Reports</i> , 2014, 59, 536-541.	0.1	3
66	The L(M196)H mutation in <i>Rhodobacter sphaeroides</i> reaction center results in new electrostatic interactions. <i>Photosynthesis Research</i> , 2015, 125, 23-29.	1.6	3
67	Substrate specificity of pyrimidine nucleoside phosphorylases of NP-II family probed by X-ray crystallography and molecular modeling. <i>Crystallography Reports</i> , 2016, 61, 830-841.	0.1	3
68	Investigations of Photosensitive Proteins by Serial Crystallography. <i>Biochemistry (Moscow)</i> , 2018, 83, S163-S175.	0.7	3
69	Serine bacteriolytic protease L1 of <i>Lysobacter</i> sp. XL1 complexed with protease inhibitor AEBSF: features of interaction. <i>Process Biochemistry</i> , 2019, 80, 89-94.	1.8	3
70	X-Ray Structure and Molecular Dynamics Study of Uridine Phosphorylase from <i>Vibrio cholerae</i> in Complex with 2,2'-Anhydrouridine. <i>Crystallography Reports</i> , 2020, 65, 269-277.	0.1	3
71	A preliminary X-ray diffraction study of the laccase from <i>Coriolus zonatus</i> in the native state. <i>Crystallography Reports</i> , 2006, 51, 278-285.	0.1	2
72	Structure of the homodimer of uridine phosphorylase from <i>Salmonella typhimurium</i> in the native state at 1.9 Å... resolution. <i>Crystallography Reports</i> , 2007, 52, 1072-1078.	0.1	2

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73	Crystallization of the two-domain N-terminal fragment of the archaeal ribosomal protein L10(P0) in complex with a specific fragment of 23S rRNA. <i>Crystallography Reports</i> , 2011, 56, 702-704.	0.1	2
74	Three-dimensional structure of photosystem II from <i>Thermosynechococcus elongates</i> in complex with terbutryn. <i>Crystallography Reports</i> , 2011, 56, 1054-1059.	0.1	2
75	The base of the ribosomal P stalk from <i>Methanococcus jannaschii</i> : crystallization and preliminary X-ray studies. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2013, 69, 1288-1290.	0.7	2
76	Crystallographic analysis of archaeal ribosomal protein L11. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2015, 71, 1083-1087.	0.4	2
77	NMR and crystallographic structural studies of the Elongation factor P from <i>Staphylococcus aureus</i> . <i>European Biophysics Journal</i> , 2020, 49, 223-230.	1.2	2
78	The role of positive charged residue in the proton-transfer mechanism of two-domain laccase from <i>Streptomyces griseoflavus</i> Ac-993. <i>Journal of Biomolecular Structure and Dynamics</i> , 2022, 40, 8324-8331.	2.0	2
79	Crystal structure of a mutant of archaeal ribosomal protein L1 from <i>Methanococcus jannaschii</i> . <i>Crystallography Reports</i> , 2014, 59, 394-398.	0.1	1
80	Structural investigation of endoglucanase 2 from the filamentous fungus <i>Penicillium verruculosum</i> . <i>Crystallography Reports</i> , 2017, 62, 254-259.	0.1	1
81	The key role of E418 carboxyl group in the formation of Nt.BspD61 nickase active site: Structural and functional properties of Nt.BspD61 E418A mutant. <i>Journal of Structural Biology</i> , 2020, 210, 107508.	1.3	1
82	Is RsfS a Hibernation Factor or a Ribosome Biogenesis Factor?. <i>Biochemistry (Moscow)</i> , 2022, 87, 500-510.	0.7	1
83	Crystallization of mutant forms of the $\hat{I}^3$ subunit of archaeal translation initiation factor 2. <i>Crystallography Reports</i> , 2014, 59, 71-74.	0.1	0
84	Preliminary X-ray diffraction study of crystals of photosystem II from <i>Thermosynechococcus elongates</i> . <i>Crystallography Reports</i> , 2014, 59, 75-77.	0.1	0
85	Three-dimensional structures of unligated uridine phosphorylase from <i>Yersinia pseudotuberculosis</i> at 1.4 Å... resolution and its complex with an antibacterial drug. <i>Crystallography Reports</i> , 2015, 60, 525-531.	0.1	0
86	Structure of a complex of uridine phosphorylase from <i>Yersinia pseudotuberculosis</i> with the modified bacteriostatic antibacterial drug determined by X-ray crystallography and computer analysis. <i>Crystallography Reports</i> , 2015, 60, 217-226.	0.1	0