

# Azat G Gabdulkhakov

## List of Publications by Year in descending order

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Version: 2024-02-01

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  | 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         |
| 2  | 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         |
| 3  | 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         |
| 4  | Is RsfS a Hibernation Factor or a Ribosome Biogenesis Factor?. <i>Biochemistry (Moscow)</i> , 2022, 87, 500-510.   | 0.7 | 1         |
| 5  | 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         |
| 6  | 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        |
| 7  | 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         |
| 8  | The key role of E418 carboxyl group in the formation of Nt.BspD6I nickase active site: Structural and functional properties of Nt.BspD6I E418A mutant. <i>Journal of Structural Biology</i> , 2020, 210, 107508.       | 1.3 | 1         |
| 9  | 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         |
| 10 | 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         |
| 11 | 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        |
| 12 | Novel approaches for the lipid sponge phase crystallization of the <i>Rhodobacter sphaeroides</i> photosynthetic reaction center. <i>IUCr</i> , 2020, 7, 1084-1091.  | 1.0 | 6         |
| 13 | 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        |
| 14 | 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         |
| 15 | 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         |
| 16 | Controlling Photosynthetic Excitons by Selective Pigment Photooxidation. <i>Journal of Physical Chemistry B</i> , 2019, 123, 29-38.  | 1.2 | 18        |
| 17 | Investigations of Photosensitive Proteins by Serial Crystallography. <i>Biochemistry (Moscow)</i> , 2018, 83, S163-S175.   | 0.7 | 3         |
| 18 | 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         |

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|----|--|-----|-----------|
| 19 | Structural investigation of endoglucanase 2 from the filamentous fungus <i>Penicillium verruculosum</i> . <i>Crystallography Reports</i> , 2017, 62, 254-259.  | 0.1 | 1         |
| 20 | 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         |
| 21 | Investigation of structure of the ribosomal L12/P stalk. <i>Biochemistry (Moscow)</i> , 2016, 81, 1589-1601.   | 0.7 | 4         |
| 22 | 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         |
| 23 | 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         |
| 24 | 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        |
| 25 | 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         |
| 26 | 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         |
| 27 | Crystallographic analysis of archaeal ribosomal protein L11. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2015, 71, 1083-1087.   | 0.4 | 2         |
| 28 | 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         |
| 29 | 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        |
| 30 | 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        |
| 31 | 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         |
| 32 | Molecular dynamics studies of pathways of water movement in cyanobacterial photosystem II. <i>Crystallography Reports</i> , 2015, 60, 83-89.   | 0.1 | 9         |
| 33 | 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         |
| 34 | Structural and functional characterization of two-domain laccase from <i>Streptomyces viridochromogenes</i> . <i>Biochimie</i> , 2015, 112, 151-159.   | 1.3 | 42        |
| 35 | 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        |
| 36 | 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         |

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|----|---|-----|-----------|
| 37 | Analysis of molecular oxygen exit pathways in cyanobacterial photosystem II: Molecular dynamics studies. <i>Crystallography Reports</i> , 2015, 60, 884-888.  | 0.1 | 7         |
| 38 | 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         |
| 39 | Crystallization of mutant forms of the $\beta^3$ subunit of archaeal translation initiation factor 2. <i>Crystallography Reports</i> , 2014, 59, 71-74.   | 0.1 | 0         |
| 40 | Preliminary X-ray diffraction study of crystals of photosystem II from <i>Thermosynechococcus elongatus</i> . <i>Crystallography Reports</i> , 2014, 59, 75-77.   | 0.1 | 0         |
| 41 | Double Suppression of the $G\beta$ Protein Activity by RGS Proteins. <i>Molecular Cell</i> , 2014, 53, 663-671.   | 4.5 | 40        |
| 42 | 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         |
| 43 | 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         |
| 44 | Structural studies on photosystem II of cyanobacteria. <i>Biochemistry (Moscow)</i> , 2013, 78, 1524-1538.  | 0.7 | 6         |
| 45 | Crystallization and preliminary X-ray diffraction studies of <i>Drosophila melanogaster</i> $G\beta$ -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         |
| 46 | 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        |
| 47 | 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         |
| 48 | 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         |
| 49 | Revisiting the <i>Haloarcula marismortui</i> 50S ribosomal subunit model. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2013, 69, 997-1004.   | 2.5 | 40        |
| 50 | 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        |
| 51 | 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        |
| 52 | 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         |
| 53 | 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         |
| 54 | 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        |

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|----|---|-----|-----------|
| 55 | 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         |
| 56 | Uridine phosphorylase in biomedical, structural, and functional aspects: A review. <i>Crystallography Reports</i> , 2011, 56, 560-589.  | 0.1 | 9         |
| 57 | Crystal structure of ribosomal protein L1 from the bacterium <i>Aquifex aeolicus</i> . <i>Crystallography Reports</i> , 2011, 56, 603-607.  | 0.1 | 6         |
| 58 | 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         |
| 59 | Structural analysis of interdomain mobility in ribosomal L1 proteins. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2011, 67, 1023-1027.  | 2.5 | 6         |
| 60 | 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         |
| 61 | Structural Basis of Cyanobacterial Photosystem II Inhibition by the Herbicide Terbutryn. <i>Journal of Biological Chemistry</i> , 2011, 286, 15964-15972.   | 1.6 | 73        |
| 62 | 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         |
| 63 | Recent Progress in the Crystallographic Studies of Photosystem II. <i>ChemPhysChem</i> , 2010, 11, 1160-1171.   | 1.0 | 102       |
| 64 | 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        |
| 65 | 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        |
| 66 | 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        |
| 67 | 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        |
| 68 | 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       |
| 69 | 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         |
| 70 | Structural and thermodynamic studies of Bergerac-SH3 chimeras. <i>Biophysical Chemistry</i> , 2009, 139, 106-115.   | 1.5 | 7         |
| 71 | 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         |
| 72 | 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     |

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|----|--|-----|-----------|
| 73 | 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         |
| 74 | 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         |
| 75 | 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        |
| 76 | 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        |
| 77 | 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        |
| 78 | 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         |
| 79 | 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        |
| 80 | 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        |
| 81 | 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        |
| 82 | 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        |
| 83 | 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        |
| 84 | 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        |
| 85 | Asp49 phospholipase A2 "elaidoylamide complex: a new mode of inhibition. <i>Biochemical and Biophysical Research Communications</i> , 2004, 319, 1314-1321.  | 1.0 | 21        |
| 86 | 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         |