

George Minasov

List of Publications by Year in descending order

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76
papers

4,180
citations

117625

34
h-index

118850

62
g-index

84
all docs

84
docs citations

84
times ranked

5332
citing authors

#	ARTICLE	IF	CITATIONS
1	Evolution of an Antibiotic Resistance Enzyme Constrained by Stability and Activity Trade-offs. <i>Journal of Molecular Biology</i> , 2002, 320, 85-95.	4.2	421
2	Structural, Kinetic and Proteomic Characterization of Acetyl Phosphate-Dependent Bacterial Protein Acetylation. <i>PLoS ONE</i> , 2014, 9, e94816.	2.5	249
3	A "Hydrat-Ion" Spine in a B-DNA Minor Groove. <i>Journal of the American Chemical Society</i> , 1999, 121, 3590-3595.	13.7	209
4	An Ultrahigh Resolution Structure of TEM-1 β -Lactamase Suggests a Role for Glu166 as the General Base in Acylation. <i>Journal of the American Chemical Society</i> , 2002, 124, 5333-5340.	13.7	205
5	Atomic-resolution crystal structures of B-DNA reveal specific influences of divalent metal ions on conformation and packing. <i>Journal of Molecular Biology</i> , 1999, 291, 83-99.	4.2	183
6	The Dickerson-Drew B-DNA Dodecamer Revisited at Atomic Resolution. <i>Journal of the American Chemical Society</i> , 1999, 121, 470-471.	13.7	173
7	Crystal structure and improved antisense properties of 2'-O-(2-methoxyethyl)-RNA. <i>Nature Structural Biology</i> , 1999, 6, 535-539.	9.7	155
8	Detection of alkali metal ions in DNA crystals using state-of-the-art X-ray diffraction experiments. <i>Nucleic Acids Research</i> , 2001, 29, 1208-1215.	14.5	148
9	High-resolution structures of the SARS-CoV-2 $2\text{-O}^6\text{-methyltransferase}$ reveal strategies for structure-based inhibitor design. <i>Science Signaling</i> , 2020, 13, .	3.6	143
10	X-ray crystallographic analysis of the hydration of A- and B-form DNA at atomic resolution. <i>Biopolymers</i> , 1998, 48, 234.	2.4	120
11	Metal ions and flexibility in a viral RNA pseudoknot at atomic resolution. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002, 99, 4302-4307.	7.1	116
12	Identification of novel small molecule inhibitors against NS2B/NS3 serine protease from Zika virus. <i>Antiviral Research</i> , 2017, 139, 49-58.	4.1	113
13	Probing the Influence of Stereoelectronic Effects on the Biophysical Properties of Oligonucleotides: A Comprehensive Analysis of the RNA Affinity, Nuclease Resistance, and Crystal Structure of Ten 2'-O-Ribonucleic Acid Modifications. <i>Biochemistry</i> , 2005, 44, 9045-9057.	2.5	104
14	Independent Movement, Dimerization and Stability of Tandem Repeats of Chicken Brain β -Spectrin. <i>Journal of Molecular Biology</i> , 2004, 344, 495-511.	4.2	97
15	Structural Aspects for Evolution of β -Lactamases from Penicillin-Binding Proteins. <i>Journal of the American Chemical Society</i> , 2003, 125, 9612-9618.	13.7	96
16	Crystal Structures of YkuL and Its Complex with Second Messenger Cyclic Di-GMP Suggest Catalytic Mechanism of Phosphodiester Bond Cleavage by EAL Domains. <i>Journal of Biological Chemistry</i> , 2009, 284, 13174-13184.	3.4	96
17	Crystal Structure of Homo-DNA and Nature's Choice of Pentose over Hexose in the Genetic System. <i>Journal of the American Chemical Society</i> , 2006, 128, 10847-10856.	13.7	94
18	The Deacylation Mechanism of AmpC β -Lactamase at Ultrahigh Resolution. <i>Journal of the American Chemical Society</i> , 2006, 128, 2970-2976.	13.7	78

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19	Structural and Molecular Mechanism for Autoprocessing of MARTX Toxin of <i>Vibrio cholerae</i> at Multiple Sites. <i>Journal of Biological Chemistry</i> , 2009, 284, 26557-26568.	3.4	75
20	Targeting Human Central Nervous System Protein Kinases: An Isoform Selective p38 β -MAPK Inhibitor That Attenuates Disease Progression in Alzheimer's Disease Mouse Models. <i>ACS Chemical Neuroscience</i> , 2015, 6, 666-680.	3.5	75
21	The Structural Bases of Antibiotic Resistance in the Clinically Derived Mutant β -Lactamases TEM-30, TEM-32, and TEM-34. <i>Journal of Biological Chemistry</i> , 2002, 277, 32149-32156.	3.4	72
22	Development of Novel In Vivo Chemical Probes to Address CNS Protein Kinase Involvement in Synaptic Dysfunction. <i>PLoS ONE</i> , 2013, 8, e66226.	2.5	58
23	Structural Basis of Cleavage by RNase H of Hybrids of Arabinonucleic Acids and RNA,. <i>Biochemistry</i> , 2000, 39, 3525-3532.	2.5	48
24	Noncovalent interaction energies in covalent complexes: TEM-1 β -lactamase and β -lactams. <i>Proteins: Structure, Function and Bioinformatics</i> , 2002, 47, 86-96.	2.6	48
25	Recognition and Resistance in TEM β -Lactamase. <i>Biochemistry</i> , 2003, 42, 8434-8444.	2.5	47
26	Phage-assisted evolution of botulinum neurotoxin proteases with reprogrammed specificity. <i>Science</i> , 2021, 371, 803-810.	12.6	46
27	2'-O methylation of RNA cap in SARS-CoV-2 captured by serial crystallography. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	7.1	46
28	X-ray crystal structure of a locked nucleic acid (LNA) duplex composed of a palindromic 10-mer DNA strand containing one LNA thymine monomer. <i>Chemical Communications</i> , 2001, , 651-652.	4.1	45
29	The bacterial Ras/Rap1 site-specific endopeptidase RRSP cleaves Ras through an atypical mechanism to disrupt Ras-ERK signaling. <i>Science Signaling</i> , 2018, 11, .	3.6	39
30	A comparative genomics approach identifies contact-dependent growth inhibition as a virulence determinant. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 6811-6821.	7.1	39
31	2'-O-[2-[2-(N,N-Dimethylamino)ethoxy]ethyl] Modified Oligonucleotides: Symbiosis of Charge Interaction Factors and Stereoelectronic Effects. <i>Organic Letters</i> , 2003, 5, 2017-2020.	4.6	37
32	Crystal structure of an apo form of <i>Shigella flexneri</i> ArsH protein with an NADPH-dependent FMN reductase activity. <i>Protein Science</i> , 2007, 16, 2483-2490.	7.6	37
33	Structure of the Essential <i>Mtb</i> FadD32 Enzyme: A Promising Drug Target for Treating Tuberculosis. <i>ACS Infectious Diseases</i> , 2016, 2, 579-591.	3.8	37
34	Structure of the Type III Secretion Effector Protein ExoU in Complex with Its Chaperone SpcU. <i>PLoS ONE</i> , 2012, 7, e49388.	2.5	36
35	Structural Basis for Mobility in the 1.1Å... Crystal Structure of the NG Domain of <i>Thermus aquaticus</i> Ffh. <i>Journal of Molecular Biology</i> , 2002, 320, 783-799.	4.2	35
36	Characterization of the Deoxynucleotide Triphosphate Triphosphohydrolase (dNTPase) Activity of the EF1143 Protein from <i>Enterococcus faecalis</i> and Crystal Structure of the Activator-Substrate Complex. <i>Journal of Biological Chemistry</i> , 2011, 286, 33158-33166.	3.4	31

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37	Structural analysis of a 3-deoxy-2-carabinoheptulosonate 7-phosphate synthase with an N-terminal chorismate mutase-like regulatory domain. <i>Protein Science</i> , 2012, 21, 887-895.	7.6	31
38	Structure of the LdcB LD-Carboxypeptidase Reveals the Molecular Basis of Peptidoglycan Recognition. <i>Structure</i> , 2014, 22, 949-960.	3.3	31
39	A Selective and Brain Penetrant p38 β -MAPK Inhibitor Candidate for Neurologic and Neuropsychiatric Disorders That Attenuates Neuroinflammation and Cognitive Dysfunction. <i>Journal of Medicinal Chemistry</i> , 2019, 62, 5298-5311.	6.4	31
40	Large Scale Structural Rearrangement of a Serine Hydrolase from <i>Francisella tularensis</i> Facilitates Catalysis. <i>Journal of Biological Chemistry</i> , 2013, 288, 10522-10535.	3.4	28
41	Insights into the Mechanism of Type I Dehydroquinase Dehydratases from Structures of Reaction Intermediates. <i>Journal of Biological Chemistry</i> , 2011, 286, 3531-3539.	3.4	27
42	STUDIES OF A CHEMICALLY MODIFIED OLIGODEOXYNUCLEOTIDE CONTAINING A 5-ATOM AMIDE BACKBONE WHICH EXHIBITS IMPROVED BINDING TO RNA. <i>Nucleosides, Nucleotides and Nucleic Acids</i> , 2001, 20, 991-994.	1.1	25
43	The Cyclic AMP Receptor Protein Regulates Quorum Sensing and Global Gene Expression in <i>Yersinia pestis</i> during Planktonic Growth and Growth in Biofilms. <i>MBio</i> , 2019, 10, .	4.1	24
44	Structural and immunological characterization of <i>E. coli</i> derived recombinant CRM197 protein used as carrier in conjugate vaccines. <i>Bioscience Reports</i> , 2018, 38, .	2.4	23
45	The 2.2 Å... resolution crystal structure of <i>Bacillus cereus</i> Nif3-family protein YqfO reveals a conserved dimetal-binding motif and a regulatory domain. <i>Protein Science</i> , 2007, 16, 1285-1293.	7.6	19
46	Adherence to Dunitz stereochemical principles requires significant structural rearrangements in Schiff-base formation: insights from transaldolase complexes. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2014, 70, 544-552.	2.5	19
47	An Unusual Cation-Binding Site and Distinct Domain-Domain Interactions Distinguish Class II Enolpyruvylshikimate-3-phosphate Synthases. <i>Biochemistry</i> , 2016, 55, 1239-1245.	2.5	18
48	Structure and protective efficacy of the <i>Staphylococcus aureus</i> autocleaving protease EpiP. <i>FASEB Journal</i> , 2014, 28, 1780-1793.	0.5	17
49	Mn ²⁺ coordinates Cap-0-RNA to align substrates for efficient 2'-O-methyl transfer by SARS-CoV-2 nsp16. <i>Science Signaling</i> , 2021, 14, .	3.6	17
50	The structure of bradyzoite-specific enolase from <i>Toxoplasma gondii</i> reveals insights into its dual cytoplasmic and nuclear functions. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2015, 71, 417-426.	2.5	16
51	Structural and functional analysis of betaine aldehyde dehydrogenase from <i>Staphylococcus aureus</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2015, 71, 1159-1175.	2.5	16
52	Crystal Structures of the SpoIID Lytic Transglycosylases Essential for Bacterial Sporulation. <i>Journal of Biological Chemistry</i> , 2016, 291, 14915-14926.	3.4	15
53	Thermodynamic Cycle Analysis and Inhibitor Design against Beta-Lactamase. <i>Biochemistry</i> , 2003, 42, 14483-14491.	2.5	14
54	CSGID Solves Structures and Identifies Phenotypes for Five Enzymes in <i>Toxoplasma gondii</i> . <i>Frontiers in Cellular and Infection Microbiology</i> , 2018, 8, 352.	3.9	14

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55	A Conserved Surface Loop in Type I Dehydroquinase Dehydratases Positions an Active Site Arginine and Functions in Substrate Binding. <i>Biochemistry</i> , 2011, 50, 2357-2363.	2.5	12
56	Mechanisms of Allosteric Activation and Inhibition of the Deoxyribonucleoside Triphosphate Triphosphohydrolase from <i>Enterococcus faecalis</i> . <i>Journal of Biological Chemistry</i> , 2014, 289, 2815-2824.	3.4	12
57	Crystal structure of an RNA duplex containing phenyl-ribonucleotides, hydrophobic isosteres of the natural pyrimidines. <i>Rna</i> , 2000, 6, 1516-1528.	3.5	8
58	Structural characterization and comparison of three acyl-carrier-protein synthases from pathogenic bacteria. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2012, 68, 1359-1370.	2.5	8
59	Structure of the <i>Bacillus anthracis</i> dTDP-L-rhamnose biosynthetic pathway enzyme: dTDP-4-dehydro- α -D-glucose 4,6-dehydratase, RfbB. <i>Journal of Structural Biology</i> , 2018, 202, 175-181.	2.8	8
60	Structure and Function of the Ribosomal Frameshifting Pseudoknot RNA from Beet Western Yellow Virus. <i>Helvetica Chimica Acta</i> , 2003, 86, 1709-1727.	1.6	6
61	Structural characterization of a hypothetical protein: a potential agent involved in trimethylamine metabolism in <i>Catenulispora acidiphila</i> . <i>Journal of Structural and Functional Genomics</i> , 2014, 15, 33-40.	1.2	6
62	Structure of the <i>Bacillus anthracis</i> dTDP-L-rhamnose-biosynthetic enzyme dTDP-4-dehydro-rhamnose reductase (RfbD). <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2017, 73, 644-650.	0.8	6
63	Structure of the <i>Bacillus anthracis</i> dTDP-L-rhamnose-biosynthetic enzyme dTDP-4-dehydro-rhamnose 3,5-epimerase (RfbC). <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2017, 73, 664-671.	0.8	6
64	Structure of galactarate dehydratase, a new fold in an enolase involved in bacterial fitness after antibiotic treatment. <i>Protein Science</i> , 2020, 29, 711-722.	7.6	4
65	Comparison of metal-bound and unbound structures of aminopeptidase B proteins from <i>Escherichia coli</i> and <i>Yersinia pestis</i> . <i>Protein Science</i> , 2020, 29, 1618-1628.	7.6	3
66	The ChiS-Family DNA-Binding Domain Contains a Cryptic Helix-Turn-Helix Variant. <i>MBio</i> , 2021, 12, .	4.1	3
67	Structural comparison of <i>Pseudomonas putida</i> hydroxybenzoate hydroxylase (PobA) from <i>Pseudomonas</i> spp. and other monooxygenases. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2019, 75, 507-514.	0.8	3
68	An efficient and possibly general packing mode for crystals of B-DNA oligonucleotides. <i>Journal of Crystal Growth</i> , 1992, 122, 136-143.	1.5	2
69	Structure of the <i>Bacillus anthracis</i> dTDP-L-rhamnose-biosynthetic enzyme glucose-1-phosphate thymidyltransferase (RfbA). <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2017, 73, 621-628.	0.8	2
70	Abstract 4751: Structure and inhibition of mitogen-activated protein kinase kinase 4 (MEK4): A prostate cancer pro-invasion protein. , 2012, , .		0
71	Structure Determination, Refinement, and Validation. <i>Methods in Molecular Biology</i> , 2014, 1140, 239-249.	0.9	0
72	Structural analysis of GNAT acetyltransferases and protein acetylation. <i>Acta Crystallographica Section A: Foundations and Advances</i> , 2014, 70, C299-C299.	0.1	0

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73	Structures of the surface exposed proteins of Gram positive bacteria. Acta Crystallographica Section A: Foundations and Advances, 2014, 70, C432-C432.	0.1	0
74	Metal ions and flexibility in a viral RNA pseudoknot at atomic resolution. journal of hand surgery Asian-Pacific volume, The, 2018, , 316-321.	0.4	0
75	1237. Characterization and crystallization of OXA-935, a novel class D OXA-10-like beta-lactamase, found in <i>Pseudomonas aeruginosa</i> . Open Forum Infectious Diseases, 2021, 8, S708-S708.	0.9	0
76	Structural studies reveal unique features of nsp16 from SARS-CoV-2, a protein essential for immune system evasion and a possible drug target. FASEB Journal, 2022, 36, .	0.5	0