

George Minasov

List of Publications by Year in descending order

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Version: 2024-02-01

76
papers

4,180
citations

126708

33
h-index

123241

61
g-index

84
all docs

84
docs citations

84
times ranked

5332
citing authors

#	ARTICLE	IF	CITATIONS
1	Structural studies reveal unique features of nsp16 from SARS-CoV-2, a protein essential for immune system evasion and a possible drug target. <i>FASEB Journal</i> , 2022, 36, .	0.2	0
2	Phage-assisted evolution of botulinum neurotoxin proteases with reprogrammed specificity. <i>Science</i> , 2021, 371, 803-810.	6.0	46
3	The ChiS-Family DNA-Binding Domain Contains a Cryptic Helix-Turn-Helix Variant. <i>MBio</i> , 2021, 12, .	1.8	3
4	2â€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, .	3.3	46
5	Mn ²⁺ coordinates Cap-0-RNA to align substrates for efficient 2â€²-O-methyl transfer by SARS-CoV-2 nsp16. <i>Science Signaling</i> , 2021, 14, .	1.6	17
6	1237. Characterization and crystallization of OXA-935, a novel class D OXA-10-like beta-lactamase, found in <i>Pseudomonas aeruginosa</i> . <i>Open Forum Infectious Diseases</i> , 2021, 8, S708-S708.	0.4	0
7	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.	3.1	4
8	High-resolution structures of the SARS-CoV-2 2â€²-O-methyltransferase reveal strategies for structure-based inhibitor design. <i>Science Signaling</i> , 2020, 13, .	1.6	143
9	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.	3.3	39
10	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.	3.1	3
11	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.	2.9	31
12	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, .	1.8	24
13	Structural comparison of <i>p</i> -hydroxybenzoate hydroxylase (PobA) from <i>Pseudomonas putida</i> with PobA from other <i>Pseudomonas</i> spp. and other monooxygenases. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2019, 75, 507-514.	0.4	3
14	Structure of the <i>Bacillus anthracis</i> dTDP-l-rhamnose biosynthetic pathway enzyme: dTDP-l-d-glucose 4,6-dehydratase, RfbB. <i>Journal of Structural Biology</i> , 2018, 202, 175-181.	1.3	8
15	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, .	1.6	39
16	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.	1.8	14
17	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, .	1.1	23
18	Metal ions and flexibility in a viral RNA pseudoknot at atomic resolution. <i>Journal of Hand Surgery Asian-Pacific volume</i> , The, 2018, , 316-321.	0.2	0

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19	Identification of novel small molecule inhibitors against NS2B/NS3 serine protease from Zika virus. <i>Antiviral Research</i> , 2017, 139, 49-58.	1.9	113
20	Structure of the <i>Bacillus anthracis</i> dTDP-L-rhamnose-biosynthetic enzyme dTDP-4-dehydrorhamnose reductase (RfbD). <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2017, 73, 644-650.	0.4	6
21	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.	0.4	2
22	Structure of the <i>Bacillus anthracis</i> dTDP-L-rhamnose-biosynthetic enzyme dTDP-4-dehydrorhamnose 3,5-epimerase (RfbC). <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2017, 73, 664-671.	0.4	6
23	Crystal Structures of the SpoIID Lytic Transglycosylases Essential for Bacterial Sporulation. <i>Journal of Biological Chemistry</i> , 2016, 291, 14915-14926.	1.6	15
24	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.	1.8	37
25	An Unusual Cation-Binding Site and Distinct Domain-Domain Interactions Distinguish Class II Enolpyruvylshikimate-3-phosphate Synthases. <i>Biochemistry</i> , 2016, 55, 1239-1245.	1.2	18
26	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.	1.7	75
27	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
28	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
29	Structural, Kinetic and Proteomic Characterization of Acetyl Phosphate-Dependent Bacterial Protein Acetylation. <i>PLoS ONE</i> , 2014, 9, e94816.	1.1	249
30	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.	1.6	12
31	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
32	Structure and protective efficacy of the <i>Staphylococcus aureus</i> autocleaving protease EpiP. <i>FASEB Journal</i> , 2014, 28, 1780-1793.	0.2	17
33	Structure of the LdcB LD-Carboxypeptidase Reveals the Molecular Basis of Peptidoglycan Recognition. <i>Structure</i> , 2014, 22, 949-960.	1.6	31
34	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
35	Structure Determination, Refinement, and Validation. <i>Methods in Molecular Biology</i> , 2014, 1140, 239-249.	0.4	0
36	Structural analysis of GNAT acetyltransferases and protein acetylation. <i>Acta Crystallographica Section A: Foundations and Advances</i> , 2014, 70, C299-C299.	0.0	0

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37	Structures of the surface exposed proteins of Gram positive bacteria. Acta Crystallographica Section A: Foundations and Advances, 2014, 70, C432-C432.	0.0	0
38	Large Scale Structural Rearrangement of a Serine Hydrolase from Francisella tularensis Facilitates Catalysis. Journal of Biological Chemistry, 2013, 288, 10522-10535.	1.6	28
39	Development of Novel In Vivo Chemical Probes to Address CNS Protein Kinase Involvement in Synaptic Dysfunction. PLoS ONE, 2013, 8, e66226.	1.1	58
40	Structure of the Type III Secretion Effector Protein ExoU in Complex with Its Chaperone SpcU. PLoS ONE, 2012, 7, e49388.	1.1	36
41	Structural characterization and comparison of three acyl-carrier-protein synthases from pathogenic bacteria. Acta Crystallographica Section D: Biological Crystallography, 2012, 68, 1359-1370.	2.5	8
42	Structural analysis of a 3-deoxy-D-arabino-heptulosonate 7-phosphate synthase with an N-terminal chorismate mutase-like regulatory domain. Protein Science, 2012, 21, 887-895.	3.1	31
43	Abstract 4751: Structure and inhibition of mitogen-activated protein kinase kinase 4 (MEK4): A prostate cancer pro-invasion protein. , 2012, , .		0
44	A Conserved Surface Loop in Type I Dehydroquinase Dehydratases Positions an Active Site Arginine and Functions in Substrate Binding. Biochemistry, 2011, 50, 2357-2363.	1.2	12
45	Characterization of the Deoxynucleotide Triphosphate Triphosphohydrolase (dNTPase) Activity of the EF1143 Protein from Enterococcus faecalis and Crystal Structure of the Activator-Substrate Complex. Journal of Biological Chemistry, 2011, 286, 33158-33166.	1.6	31
46	Insights into the Mechanism of Type I Dehydroquinase Dehydratases from Structures of Reaction Intermediates. Journal of Biological Chemistry, 2011, 286, 3531-3539.	1.6	27
47	Structural and Molecular Mechanism for Autoprocessing of MARTX Toxin of Vibrio cholerae at Multiple Sites. Journal of Biological Chemistry, 2009, 284, 26557-26568.	1.6	75
48	Crystal Structures of YkuL and Its Complex with Second Messenger Cyclic Di-GMP Suggest Catalytic Mechanism of Phosphodiester Bond Cleavage by EAL Domains. Journal of Biological Chemistry, 2009, 284, 13174-13184.	1.6	96
49	The 2.2 Å... resolution crystal structure of Bacillus cereus Nif3-family protein YqfO reveals a conserved dimetal-binding motif and a regulatory domain. Protein Science, 2007, 16, 1285-1293.	3.1	19
50	Crystal structure of an apo form of Shigella flexneri ArsH protein with an NADPH-dependent FMN reductase activity. Protein Science, 2007, 16, 2483-2490.	3.1	37
51	Crystal Structure of Homo-DNA and Nature's Choice of Pentose over Hexose in the Genetic System. Journal of the American Chemical Society, 2006, 128, 10847-10856.	6.6	94
52	The Deacylation Mechanism of AmpC β -Lactamase at Ultrahigh Resolution. Journal of the American Chemical Society, 2006, 128, 2970-2976.	6.6	78
53	Probing the Influence of Stereoelectronic Effects on the Biophysical Properties of Oligonucleotides: Comprehensive Analysis of the RNA Affinity, Nuclease Resistance, and Crystal Structure of Ten 2'-O-Ribonucleic Acid Modifications. Biochemistry, 2005, 44, 9045-9057.	1.2	104
54	Independent Movement, Dimerization and Stability of Tandem Repeats of Chicken Brain β -Spectrin. Journal of Molecular Biology, 2004, 344, 495-511.	2.0	97

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55	Structure and Function of the Ribosomal Frameshifting Pseudoknot RNA from Beet Western Yellow Virus. <i>Helvetica Chimica Acta</i> , 2003, 86, 1709-1727.	1.0	6
56	Recognition and Resistance in TEM β -Lactamase. <i>Biochemistry</i> , 2003, 42, 8434-8444.	1.2	47
57	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.	2.4	37
58	Thermodynamic Cycle Analysis and Inhibitor Design against Beta-Lactamase. <i>Biochemistry</i> , 2003, 42, 14483-14491.	1.2	14
59	Structural Aspects for Evolution of β -Lactamases from Penicillin-Binding Proteins. <i>Journal of the American Chemical Society</i> , 2003, 125, 9612-9618.	6.6	96
60	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.	3.3	116
61	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.	1.6	72
62	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.	6.6	205
63	Evolution of an Antibiotic Resistance Enzyme Constrained by Stability and Activity Trade-offs. <i>Journal of Molecular Biology</i> , 2002, 320, 85-95.	2.0	421
64	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.	2.0	35
65	Noncovalent interaction energies in covalent complexes: TEM-1 β -lactamase and β -lactams. <i>Proteins: Structure, Function and Bioinformatics</i> , 2002, 47, 86-96.	1.5	48
66	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.	2.2	45
67	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.	0.4	25
68	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.	6.5	148
69	Crystal structure of an RNA duplex containing phenyl-ribonucleotides, hydrophobic isosteres of the natural pyrimidines. <i>Rna</i> , 2000, 6, 1516-1528.	1.6	8
70	Structural Basis of Cleavage by RNase H of Hybrids of Arabinonucleic Acids and RNA. <i>Biochemistry</i> , 2000, 39, 3525-3532.	1.2	48
71	Crystal structure and improved antisense properties of 2'-O-(2-methoxyethyl)-RNA. <i>Nature Structural Biology</i> , 1999, 6, 535-539.	9.7	155
72	The Dickerson-Drew B-DNA Dodecamer Revisited at Atomic Resolution. <i>Journal of the American Chemical Society</i> , 1999, 121, 470-471.	6.6	173

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73	A "Hydrat-Ion" Spine in a B-DNA Minor Groove. Journal of the American Chemical Society, 1999, 121, 3590-3595.	6.6	209
74	Atomic-resolution crystal structures of B-DNA reveal specific influences of divalent metal ions on conformation and packing. Journal of Molecular Biology, 1999, 291, 83-99.	2.0	183
75	X-ray crystallographic analysis of the hydration of A- and B-form DNA at atomic resolution. , 1998, 48, 234.		120
76	An efficient and possibly general packing mode for crystals of B-DNA oligonucleotides. Journal of Crystal Growth, 1992, 122, 136-143.	0.7	2