

Ivan Yu Gushchin

List of Publications by Year in descending order

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Version: 2024-02-01

55
papers

1,590
citations

331259

21
h-index

344852

36
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61
all docs

61
docs citations

61
times ranked

1841
citing authors

#	ARTICLE	IF	CITATIONS
1	Mechanisms of Formation, Structure, and Dynamics of Lipoprotein Discs Stabilized by Amphiphilic Copolymers: A Comprehensive Review. <i>Nanomaterials</i> , 2022, 12, 361.	1.9	12
2	Structure and dynamics of the SARS-CoV-2 envelope protein monomer. <i>Proteins: Structure, Function and Bioinformatics</i> , 2022, 90, 1102-1114.	1.5	18
3	True-atomic-resolution insights into the structure and functional role of linear chains and low-barrier hydrogen bonds in proteins. <i>Nature Structural and Molecular Biology</i> , 2022, 29, 440-450.	3.6	21
4	Rational Design of a Split Flavin-Based Fluorescent Reporter. <i>ACS Synthetic Biology</i> , 2021, 10, 72-83.	1.9	14
5	Insights into the mechanisms of light-oxygen-voltage domain color tuning from a set of high-resolution X-ray structures. <i>Proteins: Structure, Function and Bioinformatics</i> , 2021, 89, 1005-1016.	1.5	11
6	Small Angle X-ray Scattering Study of a Histidine Kinase Embedded in Styrene-Maleic Acid Copolymer Lipid Particles. <i>FASEB Journal</i> , 2021, 35, .	0.2	3
7	Nitrate- and Nitrite-Sensing Histidine Kinases: Function, Structure, and Natural Diversity. <i>International Journal of Molecular Sciences</i> , 2021, 22, 5933.	1.8	8
8	Molecular model of a sensor of two-component signaling system. <i>Scientific Reports</i> , 2021, 11, 10774.	1.6	14
9	Role of hydrogen bond alternation and charge transfer states in photoactivation of the Orange Carotenoid Protein. <i>Communications Biology</i> , 2021, 4, 539.	2.0	30
10	High-resolution structure of a naturally red-shifted LOV domain. <i>Biochemical and Biophysical Research Communications</i> , 2021, 567, 143-147.	1.0	9
11	Inverse Conformational Selection in Lipid-Protein Binding. <i>Journal of the American Chemical Society</i> , 2021, 143, 13701-13709.	6.6	16
12	The molecular basis of spectral tuning in blue- and red-shifted flavin-binding fluorescent proteins. <i>Journal of Biological Chemistry</i> , 2021, 296, 100662.	1.6	17
13	Similarities and Differences between Na ⁺ and K ⁺ Distributions around DNA Obtained with Three Popular Water Models. <i>Journal of Chemical Theory and Computation</i> , 2021, 17, 7246-7259.	2.3	16
14	Crystal structure of human 14-3-3 η complexed with the noncanonical phosphopeptide from proapoptotic BAD. <i>Biochemical and Biophysical Research Communications</i> , 2021, 583, 100-105.	1.0	3
15	Extreme dependence of <i>Chloroflexus aggregans</i> LOV domain thermo- and photostability on the bound flavin species. <i>Photochemical and Photobiological Sciences</i> , 2021, 20, 1645-1656.	1.6	6
16	Phylogeny and Structure of Fatty Acid Photodecarboxylases and Glucose-Methanol-Choline Oxidoreductases. <i>Catalysts</i> , 2020, 10, 1072.	1.6	16
17	Design, expression, purification and crystallization of human 14-3-3 η protein chimera with phosphopeptide from proapoptotic protein BAD. <i>Protein Expression and Purification</i> , 2020, 175, 105707.	0.6	6
18	Molecular mechanism of light-driven sodium pumping. <i>Nature Communications</i> , 2020, 11, 2137.	5.8	67

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19	Sensor Histidine Kinase NarQ Activates via Helical Rotation, Diagonal Scissoring, and Eventually Piston-Like Shifts. <i>International Journal of Molecular Sciences</i> , 2020, 21, 3110.	1.8	9
20	Principal component analysis highlights the influence of temperature, curvature and cholesterol on conformational dynamics of lipids. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2020, 1862, 183253.	1.4	5
21	Effects of Proline Substitutions on the Thermostable LOV Domain from <i>Chloroflexus aggregans</i> . <i>Crystals</i> , 2020, 10, 256.	1.0	14
22	Crystal Structure of a Proteolytic Fragment of the Sensor Histidine Kinase NarQ. <i>Crystals</i> , 2020, 10, 149.	1.0	5
23	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
24	Unique structure and function of viral rhodopsins. <i>Nature Communications</i> , 2019, 10, 4939.	5.8	59
25	Headgroup Structure and Cation Binding in Phosphatidylserine Lipid Bilayers. <i>Journal of Physical Chemistry B</i> , 2019, 123, 9066-9079.	1.2	43
26	Structure and mechanisms of sodium-pumping KR2 rhodopsin. <i>Science Advances</i> , 2019, 5, eaav2671.	4.7	68
27	A thermostable flavin-based fluorescent protein from <i>Chloroflexus aggregans</i> : a framework for ultra-high resolution structural studies. <i>Photochemical and Photobiological Sciences</i> , 2019, 18, 1793-1805.	1.6	30
28	Assembly of Spinach Chloroplast ATP Synthase Rotor Ring Protein-Lipid Complex. <i>Frontiers in Molecular Biosciences</i> , 2019, 6, 135.	1.6	7
29	Microbial Rhodopsins. <i>Sub-Cellular Biochemistry</i> , 2018, 87, 19-56.	1.0	39
30	Efficient non-cytotoxic fluorescent staining of halophiles. <i>Scientific Reports</i> , 2018, 8, 2549.	1.6	19
31	Transmembrane Signal Transduction in Two-Component Systems: Piston, Scissoring, or Helical Rotation?. <i>BioEssays</i> , 2018, 40, 1700197.	1.2	43
32	Integral Membrane Proteins Can Be Crystallized Directly from Nanodiscs. <i>Crystal Growth and Design</i> , 2017, 17, 945-948.	1.4	29
33	New Insights on Signal Propagation by Sensory Rhodopsin II/Transducer Complex. <i>Scientific Reports</i> , 2017, 7, 41811.	1.6	24
34	Fast iodide-SAD phasing for high-throughput membrane protein structure determination. <i>Science Advances</i> , 2017, 3, e1602952.	4.7	38
35	Mechanism of transmembrane signaling by sensor histidine kinases. <i>Science</i> , 2017, 356, .	6.0	132
36	Sodium and Engineered Potassium Light-Driven Pumps. , 2017, , 79-92.		5

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37	Effects of Coarse Graining and Saturation of Hydrocarbon Chains on Structure and Dynamics of Simulated Lipid Molecules. <i>Scientific Reports</i> , 2017, 7, 11476.	1.6	14
38	Inward H ⁺ pump xenorhodopsin: Mechanism and alternative optogenetic approach. <i>Science Advances</i> , 2017, 3, e1603187.	4.7	93
39	Membrane proteins involved in bacterial phospholipid biosynthesis as drug targets?. <i>Acta Crystallographica Section A: Foundations and Advances</i> , 2017, 73, C397-C397.	0.0	0
40	Structure of the light-driven sodium pump <i>ScpK</i> and its implications for optogenetics. <i>FEBS Journal</i> , 2016, 283, 1232-1238.	2.2	41
41	Principal Component Analysis of Lipid Molecule Conformational Changes in Molecular Dynamics Simulations. <i>Journal of Chemical Theory and Computation</i> , 2016, 12, 1019-1028.	2.3	26
42	An Approach to Heterologous Expression of Membrane Proteins. The Case of Bacteriorhodopsin. <i>PLoS ONE</i> , 2015, 10, e0128390.	1.1	22
43	Structural and Functional Investigation of Flavin Binding Center of the NqrC Subunit of Sodium-Translocating NADH:Quinone Oxidoreductase from <i>Vibrio harveyi</i> . <i>PLoS ONE</i> , 2015, 10, e0118548.	1.1	21
44	ESR of a retinal protein with unusual properties from <i>Exiguobacterium sibiricum</i> . <i>Biochemistry (Moscow)</i> , 2015, 80, 688-700.	0.7	15
45	Crystal structure of a light-driven sodium pump. <i>Nature Structural and Molecular Biology</i> , 2015, 22, 390-395.	3.6	146
46	Crystal Structure of <i>Escherichia coli</i> -Expressed <i>Haloarcula marismortui</i> Bacteriorhodopsin I in the Trimeric Form. <i>PLoS ONE</i> , 2014, 9, e112873.	1.1	14
47	Low-dose X-ray radiation induces structural alterations in proteins. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2014, 70, 2675-2685.	2.5	39
48	High-Resolution Structure of a Membrane Protein Transferred from Amphipol to a Lipidic Mesophase. <i>Journal of Membrane Biology</i> , 2014, 247, 997-1004.	1.0	39
49	X-ray structure of a CDP-alcohol phosphatidyltransferase membrane enzyme and insights into its catalytic mechanism. <i>Nature Communications</i> , 2014, 5, 4169.	5.8	39
50	Ground state structure of D75N mutant of sensory rhodopsin II in complex with its cognate transducer. <i>Journal of Photochemistry and Photobiology B: Biology</i> , 2013, 123, 55-58.	1.7	10
51	Structural insights into the proton pumping by unusual proteorhodopsin from nonmarine bacteria. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 12631-12636.	3.3	83
52	Two Distinct States of the HAMP Domain from Sensory Rhodopsin Transducer Observed in Unbiased Molecular Dynamics Simulations. <i>PLoS ONE</i> , 2013, 8, e66917.	1.1	19
53	A novel dimerization interface of cyclic nucleotide binding domain, which is disrupted in presence of cAMP: implications for CNG channels gating. <i>Journal of Molecular Modeling</i> , 2012, 18, 4053-4060.	0.8	1
54	Role of the HAMP Domain Region of Sensory Rhodopsin Transducers in Signal Transduction. <i>Biochemistry</i> , 2011, 50, 574-580.	1.2	13

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55	Active State of Sensory Rhodopsin II: Structural Determinants for Signal Transfer and Proton Pumping. Journal of Molecular Biology, 2011, 412, 591-600.	2.0	31