

Konstantin Boyko

List of Publications by Year in descending order

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48
papers

731
citations

516215

16
h-index

580395

25
g-index

52
all docs

52
docs citations

52
times ranked

862
citing authors

#	ARTICLE	IF	CITATIONS
1	High-Resolution Structural Analysis of a Novel Octaheme Cytochrome c Nitrite Reductase from the Haloalkaliphilic Bacterium <i>Thioalkalivibrio nitratreducens</i> . <i>Journal of Molecular Biology</i> , 2009, 389, 846-862.	2.0	78
2	Molecular and catalytic properties of a novel cytochrome c nitrite reductase from nitrate-reducing haloalkaliphilic sulfur-oxidizing bacterium <i>Thioalkalivibrio nitratreducens</i> . <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2006, 1764, 715-723.	1.1	59
3	Properties of bacterial and archaeal branched-chain amino acid aminotransferases. <i>Biochemistry (Moscow)</i> , 2017, 82, 1572-1591.	0.7	37
4	Comparison of histone-like HU protein DNA-binding properties and HU/IHF protein sequence alignment. <i>PLoS ONE</i> , 2017, 12, e0188037.	1.1	37
5	Novel Genetically Encoded Bright Positive Calcium Indicator NCaMP7 Based on the mNeonGreen Fluorescent Protein. <i>International Journal of Molecular Sciences</i> , 2020, 21, 1644.	1.8	33
6	Structural insight into the substrate specificity of PLP fold type IV transaminases. <i>Applied Microbiology and Biotechnology</i> , 2020, 104, 2343-2357.	1.7	32
7	First structure of archaeal branched-chain amino acid aminotransferase from <i>Thermoproteus uzoniensis</i> specific for L-amino acids and R-amines. <i>Extremophiles</i> , 2016, 20, 215-225.	0.9	28
8	Thermostable Branched-Chain Amino Acid Transaminases From the Archaea <i>Geoglobus acetivorans</i> and <i>Archaeoglobus fulgidus</i> : Biochemical and Structural Characterization. <i>Frontiers in Bioengineering and Biotechnology</i> , 2019, 7, 7.	2.0	26
9	3D structure of the natural tetrameric form of human butyrylcholinesterase as revealed by cryoEM, SAXS and MD. <i>Biochimie</i> , 2019, 156, 196-205.	1.3	26
10	Comparative structural and functional analysis of two octaheme nitrite reductases from closely related <i>Thioalkalivibrio</i> species. <i>FEBS Journal</i> , 2012, 279, 4052-4061.	2.2	25
11	Structural insight into the molecular basis of polyextremophilicity of short-chain alcohol dehydrogenase from the hyperthermophilic archaeon <i>Thermococcus sibiricus</i> . <i>Biochimie</i> , 2012, 94, 2628-2638.	1.3	23
12	Expression, purification, crystallization and preliminary X-ray crystallographic analysis of the histone-like HU protein from <i>Spiroplasma melliferum</i> KC3. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2015, 71, 24-27.	0.4	23
13	Structural basis of the high thermal stability of the histone-like HU protein from the mollicute <i>Spiroplasma melliferum</i> KC3. <i>Scientific Reports</i> , 2016, 6, 36366.	1.6	23
14	Structure of an <i>Acinetobacter</i> Broad-Range Prophage Endolysin Reveals a C-Terminal α -Helix with the Proposed Role in Activity against Live Bacterial Cells. <i>Viruses</i> , 2018, 10, 309.	1.5	23
15	Biochemical and structural insights into PLP fold type IV transaminase from <i>Thermobaculum terrenum</i> . <i>Biochimie</i> , 2019, 158, 130-138.	1.3	19
16	Protein crystallization under microgravity conditions. Analysis of the results of Russian experiments performed on the International Space Station in 2005-2015. <i>Crystallography Reports</i> , 2016, 61, 718-729.	0.1	18
17	FGCaMP7, an Improved Version of Fungi-Based Ratiometric Calcium Indicator for In Vivo Visualization of Neuronal Activity. <i>International Journal of Molecular Sciences</i> , 2020, 21, 3012.	1.8	17
18	ATP-dependent DNA ligase from <i>Thermococcus</i> sp. 1519 displays a new arrangement of the OB-fold domain. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2012, 68, 1440-1447.	0.7	16

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19	The Uncommon Active Site of D-Amino Acid Transaminase from <i>Haliscomenobacter hydrossis</i> : Biochemical and Structural Insights into the New Enzyme. <i>Molecules</i> , 2021, 26, 5053.	1.7	14
20	Covalent modifications of the catalytic tyrosine in octahaem cytochrome <i>c</i> nitrite reductase and their effect on the enzyme activity. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2012, 68, 144-153.	2.5	13
21	From gene to structure: The protein factory of the NBICS Centre of Kurchatov Institute. <i>Crystallography Reports</i> , 2013, 58, 442-449.	0.1	12
22	Thermal Inactivation of a Cold-Active Esterase PMGL3 Isolated from the Permafrost Metagenomic Library. <i>Biomolecules</i> , 2019, 9, 880.	1.8	12
23	Promising approaches to crystallization of macromolecules suppressing the convective mass transport to the growing crystal. <i>Russian Chemical Reviews</i> , 2015, 84, 853-859.	2.5	11
24	Functional characterization of PLP fold type IV transaminase with a mixed type of activity from <i>Haliangium ochraceum</i> . <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2019, 1867, 575-585.	1.1	11
25	Structures of complexes of octahaem cytochrome <i>c</i> nitrite reductase from <i>Thioalkalivibrio nitratireducens</i> with sulfite and cyanide. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2010, 66, 1043-1047.	2.5	10
26	Crystal structure of PMGL2 esterase from the hormone-sensitive lipase family with GCSAG motif around the catalytic serine. <i>PLoS ONE</i> , 2020, 15, e0226838.	1.1	10
27	Structural characterization of the novel aminoglycoside phosphotransferase AphVIII from <i>Streptomyces rimosus</i> with enzymatic activity modulated by phosphorylation. <i>Biochemical and Biophysical Research Communications</i> , 2016, 477, 595-601.	1.0	9
28	LSSmScarlet, dCyRFP2s, dCyOFP2s and CRISPRed2s, Genetically Encoded Red Fluorescent Proteins with a Large Stokes Shift. <i>International Journal of Molecular Sciences</i> , 2021, 22, 12887.	1.8	9
29	Crystallization and preliminary X-ray analysis of cytochrome <i>c</i> nitrite reductase from <i>Thioalkalivibrio nitratireducens</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2006, 62, 215-217.	0.7	8
30	Isolation and oligomeric composition of cytochrome <i>c</i> nitrite reductase from the haloalkaliphilic bacterium <i>Thioalkalivibrio nitratireducens</i> . <i>Biochemistry (Moscow)</i> , 2008, 73, 164-170.	0.7	8
31	Structure of the dodecamer of the aminopeptidase APDkam598 from the archaeon <i>Desulfurococcus kamchatkensis</i> . <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2015, 71, 277-285.	0.4	8
32	Structural characterization of geranylgeranyl pyrophosphate synthase GACE1337 from the hyperthermophilic archaeon <i>Geoglobus acetivorans</i> . <i>Extremophiles</i> , 2018, 22, 877-888.	0.9	7
33	Identification, functional and structural characterization of novel aminoglycoside phosphotransferase APH(3â€³)-Id from <i>Streptomyces rimosus</i> subsp. <i>rimosus</i> ATCC 10970. <i>Archives of Biochemistry and Biophysics</i> , 2019, 671, 111-122.	1.4	7
34	Diaminopelargonic acid transaminase from <i>Psychrobacter cryohalolentis</i> is active towards (S)-(-)-1-phenylethylamine, aldehydes and α -diketones. <i>Applied Microbiology and Biotechnology</i> , 2018, 102, 9621-9633.	1.7	6
35	Structural and Biochemical Characterization of a Cold-Active PMGL3 Esterase with Unusual Oligomeric Structure. <i>Biomolecules</i> , 2021, 11, 57.	1.8	6
36	The mRubyFT Protein, Genetically Encoded Blue-to-Red Fluorescent Timer. <i>International Journal of Molecular Sciences</i> , 2022, 23, 3208.	1.8	5

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37	Structure of recombinant prolidase from <i>Thermococcus sibiricus</i> in space group $P2_12_12_1$. Acta Crystallographica Section F, Structural Biology Communications, 2015, 71, 951-957.	0.4	4
38	Structure of the DNMT3B ADD domain suggests the absence of a DNMT3A-like autoinhibitory mechanism. Biochemical and Biophysical Research Communications, 2022, 619, 124-129.	1.0	4
39	NADP-Dependent Aldehyde Dehydrogenase from Archaeon <i>Pyrobaculum</i> sp.1860: Structural and Functional Features. Archaea, 2016, 2016, 1-14.	2.3	3
40	Identification of the ligand in the structure of the protein with unknown function STM4435 from <i>Salmonella typhimurium</i> . Doklady Biochemistry and Biophysics, 2014, 457, 121-124.	0.3	2
41	New Gene of Aminoglycoside Phosphotransferase aph(3'')-Id from <i>Streptomyces rimosus</i> ATCC10970, Encoding Streptomycin Resistance. Russian Journal of Genetics, 2018, 54, 1254-1258.	0.2	2
42	Three-Dimensional Structure of Branched-Chain Amino Acid Transaminase from <i>Thermoproteus uzoniensis</i> in Complex with L-Norvaline. Crystallography Reports, 2020, 65, 740-743.	0.1	2
43	Elucidation of the Conformational Transition of Oligopeptidase B by an Integrative Approach Based on the Combination of X-ray, SAXS, and Essential Dynamics Sampling Simulation. Crystals, 2022, 12, 712.	1.0	2
44	Purification, isolation, crystallization, and preliminary X-ray diffraction study of the BTB domain of the centrosomal protein 190 from <i>Drosophila melanogaster</i> . Crystallography Reports, 2017, 62, 909-911.	0.1	0
45	Preliminary small-angle X-ray scattering and X-ray diffraction studies of the BTB domain of lola protein from <i>Drosophila melanogaster</i> . Crystallography Reports, 2017, 62, 912-915.	0.1	0
46	Crystallization and Preliminary X-Ray Diffraction Analysis of the ZAD Domain of the Serendipity-d Protein from <i>Drosophila melanogaster</i> . Crystallography Reports, 2020, 65, 593-595.	0.1	0
47	Prevalence of rectal prolapse in piglets in the presence of mycotoxins in mash. Naukovij VĀ-snik VeterinarnoĀ Medicini, 2021, , 168-175.	0.1	0
48	A Puzzling Protein from <i>Variovorax paradoxus</i> Has a PLP Fold Type IV Transaminase Structure and Binds PLP without Catalytic Lysine. Crystals, 2022, 12, 619.	1.0	0