

# Vladimir I Timofeev

## List of Publications by Year in descending order

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96  
papers

680  
citations

687220

13  
h-index

713332

21  
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96  
all docs

96  
docs citations

96  
times ranked

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citing authors

#	ARTICLE	IF	CITATIONS
1	X-ray investigation of gene-engineered human insulin crystallized from a solution containing polysialic acid. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2010, 66, 259-263.	0.7	48
2	Investigation of the Initial Crystallization Stage in Lysozyme Solutions by Small-Angle X-ray Scattering. <i>Crystal Growth and Design</i> , 2016, 16, 1792-1797.	1.4	48
3	Crystal growth of phosphopantetheine adenylyltransferase, carboxypeptidase t, and thymidine phosphorylase on the international space station by the capillary counter-diffusion method. <i>Crystallography Reports</i> , 2011, 56, 884-891.	0.1	39
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	In situ study of the state of lysozyme molecules at the very early stage of the crystallization process by small-angle X-ray scattering. <i>Crystallography Reports</i> , 2016, 61, 5-10.	0.1	29
6	X-ray study of the conformational changes in the molecule of phosphopantetheine adenylyltransferase from <i>Mycobacterium tuberculosis</i> during the catalyzed reaction. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2012, 68, 1660-1670.	2.5	28
7	Three-dimensional structure of thymidine phosphorylase from <i>E. coli</i> in complex with 3-azido-2-fluoro-3-dideoxyuridine. <i>Crystallography Reports</i> , 2013, 58, 842-853.	0.1	20
8	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
9	3-Azidothymidine in the active site of <i>Escherichia coli</i> thymidine phosphorylase: the peculiarity of the binding on the basis of X-ray study. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2014, 70, 1155-1165.	2.5	17
10	Activity modulation of the oligopeptidase B from <i>Serratia proteamaculans</i> by site-directed mutagenesis of amino acid residues surrounding catalytic triad histidine. <i>Biochimie</i> , 2017, 139, 125-136.	1.3	17
11	Structural insights into the broad substrate specificity of carboxypeptidase T from <i>Thermoactinomyces Vulgaris</i> . <i>FEBS Journal</i> , 2015, 282, 1214-1224.	2.2	15
12	Study of the Behavior of Lysozyme Oligomers in Solutions by the Molecular Dynamics Method. <i>Crystallography Reports</i> , 2018, 63, 947-950.	0.1	14
13	Protein crystal growth on the Russian segment of the International Space Station. <i>Crystallography Reports</i> , 2009, 54, 901-911.	0.1	13
14	Recombinant formate dehydrogenase from <i>Arabidopsis thaliana</i> : Preparation, crystal growth in microgravity, and preliminary X-ray diffraction study. <i>Crystallography Reports</i> , 2010, 55, 806-810.	0.1	13
15	Preparation of the Crystal Complex of Phosphopantetheine Adenylyltransferase from <i>Mycobacterium tuberculosis</i> with Coenzyme A and Investigation of Its Three-Dimensional Structure at 2.1-Å... Resolution. <i>Crystallography Reports</i> , 2010, 55, 1050-1059.	0.1	13
16	Study of the Influence of a Precipitant Cation on the Formation of Oligomers in Crystallization Solutions of Lysozyme Protein. <i>Crystallography Reports</i> , 2019, 64, 11-15.	0.1	13
17	Three-dimensional structure of phosphopantetheine adenylyltransferase from <i>Mycobacterium tuberculosis</i> in the apo form and in complexes with coenzyme A and dephosphocoenzyme A. <i>Crystallography Reports</i> , 2012, 57, 96-104.	0.1	12
18	Pre-crystallization phase formation of thermolysin hexamers in solution close to crystallization conditions. <i>Journal of Biomolecular Structure and Dynamics</i> , 2019, 37, 3058-3064.	2.0	12

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19	Isolation, purification, crystallization, and preliminary X-ray diffraction study of the crystals of HU protein from <i>M. gallisepticum</i> . <i>Crystallography Reports</i> , 2015, 60, 880-883.	0.1	11
20	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
21	Structure-based inhibitors targeting the alpha-helical domain of the <i>Spiroplasma melliferum</i> histone-like HU protein. <i>Scientific Reports</i> , 2020, 10, 15128.	1.6	11
22	Structure of the complex of carboxypeptidase B and N-sulfamoyl-L-arginine. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2015, 71, 1335-1340.	0.4	10
23	Enhanced conformational flexibility of the histone-like (HU) protein from <i>Mycoplasma gallisepticum</i> . <i>Journal of Biomolecular Structure and Dynamics</i> , 2018, 36, 45-53.	2.0	10
24	Precipitant ions influence on lysozyme oligomers stability investigated by molecular dynamics simulation at different temperatures. <i>Journal of Biomolecular Structure and Dynamics</i> , 2021, 39, 7223-7230.	2.0	10
25	Dodecamers derived from the crystal structure were found in the pre-crystallization solution of the transaminase from the thermophilic bacterium <i>Thermobaculum terrenum</i> by small-angle X-ray scattering. <i>Journal of Biomolecular Structure and Dynamics</i> , 2020, 38, 2939-2944.	2.0	9
26	Immunoinformatics analysis to design novel epitope based vaccine candidate targeting the glycoprotein and nucleoprotein of Lassa mammarenavirus (LASMV) using strains from Nigeria. <i>Journal of Biomolecular Structure and Dynamics</i> , 2022, 40, 7283-7302.	2.0	9
27	Molecular dynamics complemented by site-directed mutagenesis reveals significant difference between the interdomain salt bridge networks stabilizing oligopeptidases B from bacteria and protozoa in their active conformations. <i>Journal of Biomolecular Structure and Dynamics</i> , 2020, 38, 4868-4882.	2.0	8
28	The binding of precipitant ions in the tetragonal crystals of hen egg white lysozyme. <i>Journal of Biomolecular Structure and Dynamics</i> , 2020, 38, 5159-5172.	2.0	8
29	Three-dimensional structure of recombinant carboxypeptidase T from <i>Thermoactinomyces vulgaris</i> without calcium ions. <i>Crystallography Reports</i> , 2011, 56, 596-602.	0.1	7
30	Three-dimensional structure of <i>E. Coli</i> purine nucleoside phosphorylase at 0.99 Å... resolution. <i>Crystallography Reports</i> , 2016, 61, 249-257.	0.1	7
31	Three-dimensional structure of phosphoribosyl pyrophosphate synthetase from <i>E. coli</i> at 2.71 Å... resolution. <i>Crystallography Reports</i> , 2016, 61, 44-54.	0.1	7
32	Structural plasticity and thermal stability of the histone-like protein from <i>Spiroplasma melliferum</i> are due to phenylalanine insertions into the conservative scaffold. <i>Journal of Biomolecular Structure and Dynamics</i> , 2018, 36, 4392-4404.	2.0	7
33	Structure of the carboxypeptidase B complex with N-sulfamoyl-L-phenylalanine – a transition state analog of non-specific substrate. <i>Journal of Biomolecular Structure and Dynamics</i> , 2018, 36, 956-965.	2.0	7
34	First Crystal Structure of Bacterial Oligopeptidase B in an Intermediate State: The Roles of the Hinge Region Modification and Spermine. <i>Biology</i> , 2021, 10, 1021.	1.3	7
35	Preparation, crystallization, and preliminary X-ray diffraction study of mutant carboxypeptidase T containing the primary specificity pocket of carboxypeptidase B. <i>Crystallography Reports</i> , 2010, 55, 802-805.	0.1	6
36	Computational designing of a novel subunit vaccine for human cytomegalovirus by employing the immunoinformatics framework. <i>Journal of Biomolecular Structure and Dynamics</i> , 0, , 1-23.	2.0	6

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37	Isolation, crystallization and preliminary crystallographic analysis of Salmonella typhimuriumuridine phosphorylase crystallized with 2,2'-anhydrouridine. Acta Crystallographica Section F: Structural Biology Communications, 2007, 63, 852-854.	0.7	5
38	Crystal structure of recombinant phosphoribosylpyrophosphate synthetase 2 from Thermus thermophilus HB27 complexed with ADP and sulfate ions. Acta Crystallographica Section F, Structural Biology Communications, 2017, 73, 369-375.	0.4	5
39	Screening of Conditions that Facilitate Crystallization of Oligopeptidase B from Serratia Proteamaculans by Differential Scanning Fluorimetry. Crystallography Reports, 2020, 65, 264-268.	0.1	5
40	Free Energy Change during the Formation of Crystalline Contact between Lysozyme Monomers under Different Physical and Chemical Conditions. Crystals, 2021, 11, 1121.	1.0	5
41	Three-dimensional structure of carboxypeptidase T from Thermoactinomyces vulgaris in complex with N-BOC-L-leucine. Biochemistry (Moscow), 2013, 78, 252-259.	0.7	4
42	Structure of recombinant prolidase from Thermococcus sibiricus in space group P2 <sub>1</sub> 2 <sub>1</sub> 2 <sub>1</sub> . Acta Crystallographica Section F, Structural Biology Communications, 2015, 71, 951-957.	0.4	4
43	Crystal structure of mutant carboxypeptidase T from Thermoactinomyces vulgaris with an implanted S1' subsite from pancreatic carboxypeptidase B. Acta Crystallographica Section F, Structural Biology Communications, 2018, 74, 638-643.	0.4	4
44	Virtual Screening Targeting Dimerization Signals of Two Mycoplasma HU Proteins Revealed Different Types of Inhibitors Interacting with Common Binding Determinants. Crystallography Reports, 2019, 64, 602-607.	0.1	4
45	The nature of the ligand's side chain interacting with the S1'-subsite of metallo-carboxypeptidase T (from Thermoactinomyces vulgaris) determines the geometry of the tetrahedral transition complex. PLoS ONE, 2019, 14, e0226636.	1.1	4
46	The comparative analysis of the properties and structures of purine nucleoside phosphorylases from thermophilic bacterium Thermus thermophilus HB27. Journal of Biomolecular Structure and Dynamics, 2022, 40, 3626-3641.	2.0	4
47	Features of the Three Dimensional Structure of the Mutant Form of Wolinella succinogenes L-Asparaginase in Complexes with L-Aspartic and L-Glutamic Acids. Russian Journal of Bioorganic Chemistry, 2020, 46, 171-180.	0.3	4
48	The Crystal Structure of Ni <sup>2+</sup> -p-tosyl-lysyl Chloromethylketone-Bound Oligopeptidase B from Serratia Proteamaculans Revealed a New Type of Inhibitor Binding. Crystals, 2021, 11, 1438.	1.0	4
49	Identification of the Precursor Cluster in the Crystallization Solution of Proteinase K Protein by Molecular Dynamics Methods. Crystals, 2022, 12, 484.	1.0	4
50	Crystallization and preliminary X-ray diffraction study of recombinant ribokinase from Thermus Species 2.9. Crystallography Reports, 2016, 61, 974-978.	0.1	3
51	Application of virtual screening and molecular dynamics for the analysis of selectivity of inhibitors of HU proteins targeted to the DNA-recognition site. Crystallography Reports, 2017, 62, 903-908.	0.1	3
52	Discovery of Selective Inhibitors of Imidazoleglycerol-Phosphate Dehydratase from Mycobacterium tuberculosis by Virtual Screening. Crystallography Reports, 2018, 63, 74-78.	0.1	3
53	Crystal structures of carboxypeptidase T complexes with transition-state analogs. Journal of Biomolecular Structure and Dynamics, 2018, 36, 3958-3966.	2.0	3
54	Molecular Dynamics Study of Triazole Derivative Binding to the Active Site of Imidazole Glycerol Phosphate Dehydratase from Mycobacterium tuberculosis. Crystallography Reports, 2019, 64, 608-610.	0.1	3

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55	Molecular Dynamics Study of Binding of Substrates Bearing Two Positively Charged Residues to Oligopeptidase B from <i>Serratia proteamaculans</i> . <i>Crystallography Reports</i> , 2019, 64, 758-764.	0.1	3
56	Features of Optical Activity in Inorganic and Organic Materials. <i>Crystallography Reports</i> , 2020, 65, 653-677.	0.1	3
57	Crystallographic Study of Mutants and Complexes of Oligopeptidase B from <i>Serratia proteamaculans</i> . <i>Crystallography Reports</i> , 2020, 65, 909-914.	0.1	3
58	The Role of Cations of the Precipitant in the Interaction of Protein Molecules in the Lysozyme Oligomers in Crystallization Solutions. <i>Crystals</i> , 2021, 11, 1534.	1.0	3
59	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
60	Crystallization and preliminary X-ray diffraction study of porcine carboxypeptidase B. <i>Crystallography Reports</i> , 2015, 60, 367-369.	0.1	2
61	Crystallization and preliminary X-ray diffraction study of recombinant adenine phosphoribosyltransferase from the thermophilic bacterium <i>Thermus thermophilus</i> strain HB27. <i>Crystallography Reports</i> , 2017, 62, 580-583.	0.1	2
62	Three-dimensional structure of porcine pancreatic carboxypeptidase B with an acetate ion and two zinc atoms in the active site. <i>Crystallography Reports</i> , 2017, 62, 249-253.	0.1	2
63	Three-Dimensional Structure of Recombinant Adenine Phosphoribosyltransferase from Thermophilic Bacterial Strain <i>Thermus thermophilus</i> HB27. <i>Russian Journal of Bioorganic Chemistry</i> , 2018, 44, 504-510.	0.3	2
64	Crystal structure of <i>Escherichia coli</i> purine nucleoside phosphorylase in complex with 7-deazahypoxanthine. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2018, 74, 355-362.	0.4	2
65	Molecular Dynamics Study of Thymidine Phosphorylase from <i>E. coli</i> in the Apo Form and in Complexes with Substrates. <i>Crystallography Reports</i> , 2019, 64, 98-104.	0.1	2
66	Crystallization and Preliminary X-ray Diffraction Study of a Mutant of L-Asparaginase from <i>Wolinella succinogenes</i> . <i>Crystallography Reports</i> , 2019, 64, 910-913.	0.1	2
67	Three-Dimensional Structure of Branched-Chain Amino Acid Transaminase from <i>Thermoproteus uzoniensis</i> in Complex with L-Norvaline. <i>Crystallography Reports</i> , 2020, 65, 740-743.	0.1	2
68	Molecular Packing of a Mutant of L-Asparaginase from <i>Wolinella succinigenes</i> in Two Crystal Modifications. <i>Crystallography Reports</i> , 2020, 65, 586-592.	0.1	2
69	Inhibitor Targeting the Interface between Monomers of HU Protein from <i>Spiroplasma melliferum</i> Disrupts Conformational Dynamics and DNA-Binding Properties of the Protein. <i>Crystallography Reports</i> , 2020, 65, 903-908.	0.1	2
70	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. <i>Crystals</i> , 2022, 12, 712.	1.0	2
71	Crystallization and preliminary X-ray diffraction study of phosphoribosyl pyrophosphate synthetase from <i>E. Coli</i> . <i>Crystallography Reports</i> , 2015, 60, 685-688.	0.1	1
72	Crystallization and preliminary X-ray diffraction study of phosphopantetheine adenylyltransferase from <i>M. tuberculosis</i> crystallizing in space group P32. <i>Crystallography Reports</i> , 2015, 60, 682-684.	0.1	1

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73	Purification, crystallization, and preliminary X-ray diffraction study of purine nucleoside phosphorylase from <i>E. coli</i> . <i>Crystallography Reports</i> , 2015, 60, 521-524.	0.1	1
74	Crystallization and preliminary X-ray diffraction analysis of recombinant phosphoribosylpyrophosphate synthetase from the Thermophilic thermus thermophilus strain HB27. <i>Crystallography Reports</i> , 2017, 62, 78-81.	0.1	1
75	Virtual screening of selective inhibitors of phosphopantetheine adenylyltransferase from <i>Mycobacterium tuberculosis</i> . <i>Crystallography Reports</i> , 2017, 62, 405-410.	0.1	1
76	Mobile Loop in the Active Site of Metallocoarboxypeptidases as an Underestimated Determinant of Substrate Specificity. <i>Biochemistry (Moscow)</i> , 2018, 83, 1594-1602.	0.7	1
77	Crystallization and Preliminary X-ray Diffraction Study of Purine Nucleoside Phosphorylase from the Thermophilic Bacterium <i>Thermus thermophilus</i> Strain HB27. <i>Crystallography Reports</i> , 2018, 63, 761-764.	0.1	1
78	Crystal structure of <i>Escherichia coli</i> purine nucleoside phosphorylase complexed with acyclovir. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2018, 74, 402-409.	0.4	1
79	Structure of the microbial carboxypeptidase T complexed with the transition state analog N-sulfamoyl-L-lysine. <i>Biophysical Chemistry</i> , 2021, 270, 106535.	1.5	1
80	Simulation of A Bilayer Imitating the Inner Mitochondrial Membrane Using Coarse-Grained Molecular Dynamics. <i>Journal of Surface Investigation</i> , 2021, 15, 652-654.	0.1	1
81	Comparison of Spatial Structures and Packaging of Phosphorybosil Pyrophosphate Synthetase 2 from <i>Thermus thermophilus</i> HB27 in Rhombohedral and Tetragonal Crystals. <i>Crystals</i> , 2021, 11, 1128.	1.0	1
82	Effect of Disruption of the Interface between Monomers in a Dimer on the Structural and Dynamic Properties of the HU Protein from <i>Spiroplasma melliferum</i> . <i>Journal of Surface Investigation</i> , 2021, 15, 1020-1023.	0.1	1
83	Three-Dimensional Structure of Recombinant Thermophilic Ribokinase from <i>Thermus speñies</i> 2.9 in Complex with Adenosine Diphosphate. <i>Crystallography Reports</i> , 2021, 66, 769-776.	0.1	1
84	Preparation, Crystallization, and Preliminary X-Ray Diffraction Study of Mutant Carboxypeptidase T Bearing the Primary Specificity Pocket and the Active-Site Loop of Carboxypeptidase B. <i>Crystallography Reports</i> , 2020, 65, 900-902.	0.1	1
85	Molecular Dynamics Study of <i>Escherichia coli</i> Thymidine Phosphorylase in a Complex with 3'-Azidothymidine Inhibitor and Phosphate. <i>Russian Journal of Bioorganic Chemistry</i> , 2021, 47, 1231-1240.	0.3	1
86	The Role of Cations and Anions in the Formation of Crystallization Oligomers in Protein Solutions as Revealed by Combination of Small-Angle X-ray Scattering and Molecular Dynamics. <i>Crystals</i> , 2022, 12, 751.	1.0	1
87	Modeling of Phosphoribosylpyrophosphate Synthetase from <i>Thermus Thermophilus</i> in Complex with ATP and Ribose 5-Phosphate. <i>Crystallography Reports</i> , 2019, 64, 94-97.	0.1	0
88	Three-Dimensional Structure of a Mutant of Carboxypeptidase T from <i>Thermoactinomyces vulgaris</i> Bearing an Implanted S1' Subsite of Pancreatic Carboxypeptidase B Complexed with a Product Analog. <i>Crystallography Reports</i> , 2019, 64, 750-757.	0.1	0
89	An explanation for the narrow carbohydrate substrate specificity of adenine phosphoribosyltransferase from <i>Thermus thermophilus</i> from the model of the enzyme, substrate, and magnesium cation cofactor complex. <i>Journal of Biomolecular Structure and Dynamics</i> , 2019, 37, 4460-4464.	2.0	0
90	Crystal Packing of Phosphopantetheine Adenylyltransferase from <i>Mycobacterium tuberculosis</i> in Two Crystal Modifications. <i>Crystallography Reports</i> , 2020, 65, 84-90.	0.1	0

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91	Preparation, Crystallization, and Preliminary X-Ray Diffraction Study of Mutant Carboxypeptidase T Bearing the Hydrophilized Primary Specificity Pocket. <i>Crystallography Reports</i> , 2021, 66, 476-478.	0.1	0
92	Effect of the Simulation Box Size and Precipitant Concentration on the Behavior of Tetragonal Lysozyme Dimer. <i>Crystallography Reports</i> , 2021, 66, 525-528.	0.1	0
93	Study of the Interaction of Sorption and Catalytic Centers in Carboxypeptidase T by X-ray Analysis. <i>Crystals</i> , 2021, 11, 1088.	1.0	0
94	Molecular Dynamics of the Self-Organization of Dilinoleoyl Phosphatidylethanolamine Molecules. <i>Journal of Surface Investigation</i> , 2021, 15, 1012-1014.	0.1	0
95	Molecular Dynamics Calculations of the Interaction Energy of Imidazole Glycerol Phosphate Dehydratase from <i>Mycobacterium tuberculosis</i> with Triazole Derivatives. <i>Crystallography Reports</i> , 2020, 65, 755-756.	0.1	0
96	Modeling of the Lipid Bilayer Mimicking the Inner Mitochondrial Membrane. <i>Crystallography Reports</i> , 2021, 66, 1006-1009.	0.1	0