

# Tatiana Rokitina

## List of Publications by Year in descending order

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43  
papers

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citations

567247

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25  
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44  
docs citations

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times ranked

897  
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#	ARTICLE	IF	CITATIONS
1	Zinedin, SG2NA, and Striatin Are Calmodulin-binding, WD Repeat Proteins Principally Expressed in the Brain. <i>Journal of Biological Chemistry</i> , 2000, 275, 19970-19977.	3.4	106
2	Additive interaction of oxaliplatin and 17-allylamino-17-demethoxygeldanamycin in colon cancer cell lines results from inhibition of nuclear factor kappaB signaling. <i>Cancer Research</i> , 2003, 63, 8600-5.	0.9	49
3	Targeting of Proteins of the Striatin Family to Dendritic Spines: Role of the Coiled-Coil Domain. <i>Traffic</i> , 2006, 7, 74-84.	2.7	39
4	Geldanamycin and its 17-allylamino-17-demethoxy analogue antagonize the action of Cisplatin in human colon adenocarcinoma cells: differential caspase activation as a basis for interaction. <i>Cancer Research</i> , 2003, 63, 3241-6.	0.9	39
5	Quantitative Effects on c-Jun N-Terminal Protein Kinase Signaling Determine Synergistic Interaction of Cisplatin and 17-Allylamino-17-Demethoxygeldanamycin in Colon Cancer Cell Lines. <i>Molecular Pharmacology</i> , 2004, 65, 235-243.	2.3	38
6	Comparison of histone-like HU protein DNA-binding properties and HU/IHF protein sequence alignment. <i>PLoS ONE</i> , 2017, 12, e0188037.	2.5	37
7	Inhibition of G1/S transition potentiates oxaliplatin-induced cell death in colon cancer cell lines. <i>Biochemical Pharmacology</i> , 2007, 73, 1715-1726.	4.4	35
8	Novel Genetically Encoded Bright Positive Calcium Indicator NCaMP7 Based on the mNeonGreen Fluorescent Protein. <i>International Journal of Molecular Sciences</i> , 2020, 21, 1644.	4.1	33
9	Cloning of Human Striatin cDNA (STRN), Gene Mapping to 2p22â€“p21, and Preferential Expression in Brain. <i>Genomics</i> , 1998, 51, 136-139.	2.9	25
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.	4.7	25
11	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.	0.8	23
12	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.	3.3	23
13	Biochemical and structural insights into PLP fold type IV transaminase from <i>Thermobaculum terrenum</i> . <i>Biochimie</i> , 2019, 158, 130-138.	2.6	19
14	Trinuclear copper biocatalytic center forms an active site of thiocyanate dehydrogenase. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 5280-5290.	7.1	19
15	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.	2.6	17
16	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.	4.1	17
17	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.	3.8	14
18	Identification of branched-chain amino acid aminotransferases active towards (R)-(+)-1-phenylethylamine among PLP fold type IV transaminases. <i>Journal of Biotechnology</i> , 2018, 271, 26-28.	3.8	13

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19	Two independent routes of post-translational chemistry in fluorescent protein FusionRed. International Journal of Biological Macromolecules, 2020, 155, 551-559.	7.5	12
20	Functional characterization of PLP fold type IV transaminase with a mixed type of activity from <i>Haliangium ochraceum</i> . Biochimica Et Biophysica Acta - Proteins and Proteomics, 2019, 1867, 575-585.	2.3	11
21	Structure-based inhibitors targeting the alpha-helical domain of the <i>Spiroplasma melliferum</i> histone-like HU protein. Scientific Reports, 2020, 10, 15128.	3.3	11
22	Comprehensive Atlas of the Myelin Basic Protein Interaction Landscape. Biomolecules, 2021, 11, 1628.	4.0	11
23	Novel fragment-like inhibitors of EphA2 obtained by experimental screening and modelling. Mendeleev Communications, 2010, 20, 263-265.	1.6	10
24	Enhanced conformational flexibility of the histone-like (HU) protein from <i>Mycoplasma gallisepticum</i> . Journal of Biomolecular Structure and Dynamics, 2018, 36, 45-53.	3.5	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. Journal of Biomolecular Structure and Dynamics, 2020, 38, 2939-2944.	3.5	9
26	Rational design and synthesis of novel Syk-kinase inhibitors. Mendeleev Communications, 2012, 22, 73-74.	1.6	8
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. Journal of Biomolecular Structure and Dynamics, 2020, 38, 4868-4882.	3.5	8
28	Structural plasticity and thermal stability of the histone-like protein from <i>Spiroplasma melliferum</i> are due to phenylalanine insertions into the conservative scaffold. Journal of Biomolecular Structure and Dynamics, 2018, 36, 4392-4404.	3.5	7
29	First Crystal Structure of Bacterial Oligopeptidase B in an Intermediate State: The Roles of the Hinge Region Modification and Spermine. Biology, 2021, 10, 1021.	2.8	7
30	Diaminopelargonic acid transaminase from <i>Psychrobacter cryohalolentis</i> is active towards (S)-(-)-1-phenylethylamine, aldehydes and $\alpha$ -diketones. Applied Microbiology and Biotechnology, 2018, 102, 9621-9633.	3.6	6
31	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.	0.8	4
32	Abnormal pigment epithelium-derived factor processing in progressive myopia. Experimental Eye Research, 2016, 152, 1-9.	2.6	4
33	Crystal structure of mutant carboxypeptidase T from <i>Thermoactinomyces vulgaris</i> with an implanted S1 <sup>2</sup> subsite from pancreatic carboxypeptidase B. Acta Crystallographica Section F, Structural Biology Communications, 2018, 74, 638-643.	0.8	4
34	The nature of the ligand's side chain interacting with the S1'-subsite of metallo-carboxypeptidase T (from <i>Thermoactinomyces vulgaris</i> ) determines the geometry of the tetrahedral transition complex. PLoS ONE, 2019, 14, e0226636.	2.5	4
35	The Crystal Structure of N <sup>1</sup> -p-tosyl-lysyl Chloromethylketone-Bound Oligopeptidase B from <i>Serratia Proteamaculans</i> Revealed a New Type of Inhibitor Binding. Crystals, 2021, 11, 1438.	2.2	4
36	Deconvolution of the MBP-Bri2 Interaction by a Yeast Two Hybrid System and Synergy of the AlphaFold2 and High Ambiguity Driven Protein-Protein Docking. Crystals, 2022, 12, 197.	2.2	4

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37	Novel PARP1 inhibitors potentiate doxorubicin antitumor activity in vitro. Mendeleev Communications, 2015, 25, 364-366.	1.6	3
38	NADP-Dependent Aldehyde Dehydrogenase from Archaeon <i>Pyrobaculum</i> sp.1860: Structural and Functional Features. Archaea, 2016, 2016, 1-14.	2.3	3
39	Crystal structures of carboxypeptidase T complexes with transition-state analogs. Journal of Biomolecular Structure and Dynamics, 2018, 36, 3958-3966.	3.5	3
40	Efficacy of Novel Syk-Kinase Inhibitors MT-SYK-03 and MT-SYK-322 in Cellular Models of Autoimmunity and Cancer. Mendeleev Communications, 2012, 22, 287-289.	1.6	2
41	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.	2.2	2
42	Probing the role of the residues in the active site of the transaminase from <i>Thermobaculum terrenum</i> . PLoS ONE, 2021, 16, e0255098.	2.5	1
43	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.	2.2	0