

Ekaterina Morgunova

List of Publications by Year in descending order

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Version: 2024-02-01

40
papers

5,642
citations

236925

25
h-index

289244

40
g-index

44
all docs

44
docs citations

44
times ranked

9628
citing authors

#	ARTICLE	IF	CITATIONS
1	Structural insights into the interaction between transcription factors and the nucleosome. <i>Current Opinion in Structural Biology</i> , 2021, 71, 171-179.	5.7	11
2	Binding specificities of human RNA-binding proteins toward structured and linear RNA sequences. <i>Genome Research</i> , 2020, 30, 962-973.	5.5	55
3	Second career of a biosynthetic enzyme: Lumazine synthase as a virus-like nanoparticle in vaccine development. <i>Biotechnology Reports (Amsterdam, Netherlands)</i> , 2020, 27, e00494.	4.4	18
4	Impact of constitutional TET2 haploinsufficiency on molecular and clinical phenotype in humans. <i>Nature Communications</i> , 2019, 10, 1252.	12.8	67
5	The interaction landscape between transcription factors and the nucleosome. <i>Nature</i> , 2018, 562, 76-81.	27.8	259
6	Two distinct DNA sequences recognized by transcription factors represent enthalpy and entropy optima. <i>ELife</i> , 2018, 7, .	6.0	32
7	Damaging heterozygous mutations in NFKB1 lead to diverse immunologic phenotypes. <i>Journal of Allergy and Clinical Immunology</i> , 2017, 140, 782-796.	2.9	113
8	Impact of cytosine methylation on DNA binding specificities of human transcription factors. <i>Science</i> , 2017, 356, .	12.6	912
9	Structural perspective of cooperative transcription factor binding. <i>Current Opinion in Structural Biology</i> , 2017, 47, 1-8.	5.7	175
10	DNA-dependent formation of transcription factor pairs alters their binding specificity. <i>Nature</i> , 2016, 534, S15-S16.	27.8	280
11	Structural insights into the DNA-binding specificity of E2F family transcription factors. <i>Nature Communications</i> , 2015, 6, 10050.	12.8	43
12	DNA-dependent formation of transcription factor pairs alters their binding specificity. <i>Nature</i> , 2015, 527, 384-388.	27.8	462
13	Whole-Genome Sequencing Identifies <i>STAT4</i> as a Putative Susceptibility Gene in Classic Kaposi Sarcoma. <i>Journal of Infectious Diseases</i> , 2015, 211, 1842-1851.	4.0	25
14	Conservation of transcription factor binding specificities across 600 million years of bilateria evolution. <i>ELife</i> , 2015, 4, .	6.0	316
15	DNA-Binding Specificities of Human Transcription Factors. <i>Cell</i> , 2013, 152, 327-339.	28.9	1,085
16	Loss of SUFU Function in Familial Multiple Meningioma. <i>American Journal of Human Genetics</i> , 2012, 91, 520-526.	6.2	137
17	An intact eight-membered water chain in drosophilid alcohol dehydrogenases is essential for optimal enzyme activity. <i>FEBS Journal</i> , 2012, 279, 2940-2956.	4.7	8
18	Novel mutation in Wilms' tumour 1 gene associated with steroid-resistant nephrotic syndrome. <i>CKJ: Clinical Kidney Journal</i> , 2011, 4, 17-19.	2.9	1

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19	Virtual screening, selection and development of a benzindolone structural scaffold for inhibition of lumazine synthase. <i>Bioorganic and Medicinal Chemistry</i> , 2010, 18, 3518-3534.	3.0	23
20	Structural study and thermodynamic characterization of inhibitor binding to lumazine synthase from <i>Bacillus anthracis</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2010, 66, 1001-1011.	2.5	19
21	Structural insights into the adaptation of proliferating cell nuclear antigen (PCNA) from <i>Haloferax volcanii</i> to a high-salt environment. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2009, 65, 1081-1088.	2.5	14
22	Of crystals, structure factors and diffraction images. <i>Journal of Applied Crystallography</i> , 2008, 41, 659-659.	4.5	6
23	A New Series of N-[2,4-Dioxo-6-d-ribitylamino-1,2,3,4-tetrahydropyrimidin-5-yl]oxalamic Acid Derivatives as Inhibitors of Lumazine Synthase and Riboflavin Synthase: Design, Synthesis, Biochemical Evaluation, Crystallography, and Mechanistic Implications. <i>Journal of Organic Chemistry</i> , 2008, 73, 2715-2724.	3.2	26
24	Lumazine Synthase from <i>Candida albicans</i> as an Anti-fungal Target Enzyme. <i>Journal of Biological Chemistry</i> , 2007, 282, 17231-17241.	3.4	55
25	Isolation, crystallization and preliminary crystallographic analysis of <i>Salmonella typhimurium</i> uridine phosphorylase crystallized with 2,2'-anhydrouridine. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2007, 63, 852-854.	0.7	5
26	Comparative analysis of spatial organization of laccases from <i>Cerrena maxima</i> and <i>Coriolus zonatus</i> . <i>Crystallography Reports</i> , 2007, 52, 826-837.	0.6	1
27	Structural and thermodynamic insights into the binding mode of five novel inhibitors of lumazine synthase from <i>Mycobacterium tuberculosis</i> . <i>FEBS Journal</i> , 2006, 273, 4790-4804.	4.7	34
28	Three-dimensional structure of laccase from <i>Coriolus zonatus</i> at 2.6 Å... resolution. <i>Crystallography Reports</i> , 2006, 51, 817-823.	0.6	15
29	X-ray structural studies of the fungal laccase from <i>Cerrena maxima</i> . <i>Journal of Biological Inorganic Chemistry</i> , 2006, 11, 963-973.	2.6	47
30	Characterization of the interactions of the nephrin intracellular domain. <i>FEBS Journal</i> , 2005, 272, 228-243.	4.7	48
31	Crystal Structure of Lumazine Synthase from <i>Mycobacterium tuberculosis</i> as a Target for Rational Drug Design: A Binding Mode of a New Class of Purinetrione Inhibitors. <i>Biochemistry</i> , 2005, 44, 2746-2758.	2.5	70
32	Purification, crystallization and preliminary X-ray analysis of uridine phosphorylase from <i>Salmonella typhimurium</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2004, 60, 709-711.	2.5	11
33	Structural insight into the complex formation of latent matrix metalloproteinase 2 with tissue inhibitor of metalloproteinase 2. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002, 99, 7414-7419.	7.1	201
34	Characterization of Recombinant Soluble Macrophage Scavenger Receptor MARCO. <i>Journal of Biological Chemistry</i> , 2002, 277, 33378-33385.	3.4	62
35	Structure of Human Pro-Matrix Metalloproteinase-2: Activation Mechanism Revealed. <i>Science</i> , 1999, 284, 1667-1670.	12.6	505
36	Three-dimensional structure of human tissue inhibitor of metalloproteinases-2 at 2.1 Å... resolution. <i>Journal of Molecular Biology</i> , 1998, 284, 1133-1140.	4.2	91

#	ARTICLE	IF	CITATIONS
37	New approaches to chromatographic purification of bovine dopamine- β -hydroxylase. Journal of Chromatography A, 1995, 711, 113-118.	3.7	5
38	Atomic structure at 2.5 Å... resolution of uridine phosphorylase from <i>E. coli</i> refined in the monoclinic crystal lattice. FEBS Letters, 1995, 367, 183-187.	2.8	44
39	Successive Deposition of Alternate Layers of Polyelectrolytes and a Charged Virus. Langmuir, 1994, 10, 4232-4236.	3.5	307
40	The atomic structure of Carnation Mottle Virus capsid protein. FEBS Letters, 1994, 338, 267-271.	2.8	46