## Ekaterina Morgunova

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/6106503/publications.pdf

Version: 2024-02-01

40 papers 5,642 citations

236925 25 h-index 289244 40 g-index

44 all docs

44 docs citations

times ranked

44

9628 citing authors

#	Article	IF	CITATIONS
1	DNA-Binding Specificities of Human Transcription Factors. Cell, 2013, 152, 327-339.	28.9	1,085
2	Impact of cytosine methylation on DNA binding specificities of human transcription factors. Science, 2017, 356, .	12.6	912
3	Structure of Human Pro-Matrix Metalloproteinase-2: Activation Mechanism Revealed. Science, 1999, 284, 1667-1670.	12.6	505
4	DNA-dependent formation of transcription factor pairs alters their binding specificity. Nature, 2015, 527, 384-388.	27.8	462
5	Conservation of transcription factor binding specificities across 600 million years of bilateria evolution. ELife, 2015, 4, .	6.0	316
6	Successive Deposition of Alternate Layers of Polyelectrolytes and a Charged Virus. Langmuir, 1994, 10, 4232-4236.	3 <b>.</b> 5	307
7	DNA-dependent formation of transcription factor pairs alters their binding specificity. Nature, 2016, 534, S15-S16.	27.8	280
8	The interaction landscape between transcription factors and the nucleosome. Nature, 2018, 562, 76-81.	27.8	259
9	Structural insight into the complex formation of latent matrix metalloproteinase 2 with tissue inhibitor of metalloproteinase 2. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 7414-7419.	7.1	201
10	Structural perspective of cooperative transcription factor binding. Current Opinion in Structural Biology, 2017, 47, 1-8.	5.7	175
11	Loss of SUFU Function in Familial Multiple Meningioma. American Journal of Human Genetics, 2012, 91, 520-526.	6.2	137
12	Damaging heterozygous mutations in NFKB1 lead to diverse immunologic phenotypes. Journal of Allergy and Clinical Immunology, 2017, 140, 782-796.	2.9	113
13	Three-dimensional structure of human tissue inhibitor of metalloproteinases-2 at 2.1 Ã resolution. Journal of Molecular Biology, 1998, 284, 1133-1140.	4.2	91
14	Crystal Structure of Lumazine Synthase fromMycobacterium tuberculosisas a Target for Rational Drug Design: Binding Mode of a New Class of Purinetrione Inhibitorsâ€,‡. Biochemistry, 2005, 44, 2746-2758.	2.5	70
15	Impact of constitutional TET2 haploinsufficiency on molecular and clinical phenotype in humans. Nature Communications, 2019, 10, 1252.	12.8	67
16	Characterization of Recombinant Soluble Macrophage Scavenger Receptor MARCO. Journal of Biological Chemistry, 2002, 277, 33378-33385.	3.4	62
17	Lumazine Synthase from Candida albicans as an Anti-fungal Target Enzyme. Journal of Biological Chemistry, 2007, 282, 17231-17241.	3.4	55
18	Binding specificities of human RNA-binding proteins toward structured and linear RNA sequences. Genome Research, 2020, 30, 962-973.	5.5	55

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19	Characterization of the interactions of the nephrin intracellular domain. FEBS Journal, 2005, 272, 228-243.	4.7	48
20	X-ray structural studies of the fungal laccase from Cerrena maxima. Journal of Biological Inorganic Chemistry, 2006, 11, 963-973.	2.6	47
21	The atomic structure of Carnation Mottle Virus capsid protein. FEBS Letters, 1994, 338, 267-271.	2.8	46
22	Atomic structure at 2.5 $\tilde{A}$ resolution of uridine phosphorylase from E. colias refined in the monoclinic crystal lattice. FEBS Letters, 1995, 367, 183-187.	2.8	44
23	Structural insights into the DNA-binding specificity of E2F family transcription factors. Nature Communications, 2015, 6, 10050.	12.8	43
24	Structural and thermodynamic insights into the binding mode of five novel inhibitors of lumazine synthase from Mycobacterium tuberculosis. FEBS Journal, 2006, 273, 4790-4804.	4.7	34
25	Two distinct DNA sequences recognized by transcription factors represent enthalpy and entropy optima. ELife, 2018, 7, .	6.0	32
26	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. Journal of Organic Chemistry, 2008, 73, 2715-2724.	3.2	26
27	Whole-Genome Sequencing Identifies <i>STAT4</i> sas a Putative Susceptibility Gene in Classic Kaposi Sarcoma. Journal of Infectious Diseases, 2015, 211, 1842-1851.	4.0	25
28	Virtual screening, selection and development of a benzindolone structural scaffold for inhibition of lumazine synthase. Bioorganic and Medicinal Chemistry, 2010, 18, 3518-3534.	3.0	23
29	Structural study and thermodynamic characterization of inhibitor binding to lumazine synthase from i>Bacillus anthracis i>. Acta Crystallographica Section D: Biological Crystallography, 2010, 66, 1001-1011.	2.5	19
30	Second career of a biosynthetic enzyme: Lumazine synthase as a virus-like nanoparticle in vaccine development. Biotechnology Reports (Amsterdam, Netherlands), 2020, 27, e00494.	4.4	18
31	Three-dimensional structure of laccase from Coriolus zonatus at 2.6 Ã resolution. Crystallography Reports, 2006, 51, 817-823.	0.6	15
32	Structural insights into the adaptation of proliferating cell nuclear antigen (PCNA) fromHaloferax volcaniito a high-salt environment. Acta Crystallographica Section D: Biological Crystallography, 2009, 65, 1081-1088.	2.5	14
33	Purification, crystallization and preliminary X-ray analysis of uridine phosphorylase fromSalmonella typhimurium. Acta Crystallographica Section D: Biological Crystallography, 2004, 60, 709-711.	2.5	11
34	Structural insights into the interaction between transcription factors and the nucleosome. Current Opinion in Structural Biology, 2021, 71, 171-179.	5.7	11
35	An intact eightâ€membered water chain in drosophilid alcohol dehydrogenases is essential for optimal enzyme activity. FEBS Journal, 2012, 279, 2940-2956.	4.7	8
36	Of crystals, structure factors and diffraction images. Journal of Applied Crystallography, 2008, 41, 659-659.	4.5	6

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37	New approaches to chromatographic purification of bovine dopamine- $\hat{l}^2$ -hydroxylase. Journal of Chromatography A, 1995, 711, 113-118.	3.7	5
38	Isolation, crystallization and preliminary crystallographic analysis ofSalmonella typhimuriumuridine phosphorylase crystallized with 2,2′-anhydrouridine. Acta Crystallographica Section F: Structural Biology Communications, 2007, 63, 852-854.	0.7	5
39	Comparative analysis of spatial organization of laccases from Cerrena maxima and Coriolus zonatus. Crystallography Reports, 2007, 52, 826-837.	0.6	1
40	Novel mutation in Wilms' tumour 1 gene associated with steroid-resistant nephrotic syndrome. CKJ: Clinical Kidney Journal, 2011, 4, 17-19.	2.9	1