

Marat D Kazanov

List of Publications by Year in Descending Order

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Version: 2024-04-23

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

46
papers

4,118
citations

27
h-index

51
g-index

51
ext. papers

6,665
ext. citations

12.9
avg, IF

7.13
L-index

#	Paper	IF	Citations
46	Analysis of gene expression and mutation data points on contribution of transcription to the mutagenesis by APOBEC enzymes. <i>NAR Cancer</i> , 2021 , 3, zcab025	5.2	2
45	Genomic footprints of activated telomere maintenance mechanisms in cancer. <i>Nature Communications</i> , 2020 , 11, 733	17.4	40
44	High-coverage whole-genome analysis of 1220 cancers reveals hundreds of genes deregulated by rearrangement-mediated cis-regulatory alterations. <i>Nature Communications</i> , 2020 , 11, 736	17.4	32
43	Patterns of somatic structural variation in human cancer genomes. <i>Nature</i> , 2020 , 578, 112-121	50.4	232
42	The repertoire of mutational signatures in human cancer. <i>Nature</i> , 2020 , 578, 94-101	50.4	849
41	Analyses of non-coding somatic drivers in 2,658 cancer whole genomes. <i>Nature</i> , 2020 , 578, 102-111	50.4	220
40	Pan-cancer analysis of whole genomes. <i>Nature</i> , 2020 , 578, 82-93	50.4	840
39	Pan-cancer analysis of whole genomes identifies driver rearrangements promoted by LINE-1 retrotransposition. <i>Nature Genetics</i> , 2020 , 52, 306-319	36.3	122
38	Disruption of chromatin folding domains by somatic genomic rearrangements in human cancer. <i>Nature Genetics</i> , 2020 , 52, 294-305	36.3	81
37	Comprehensive analysis of chromothripsis in 2,658 human cancers using whole-genome sequencing. <i>Nature Genetics</i> , 2020 , 52, 331-341	36.3	168
36	Retrospective evaluation of whole exome and genome mutation calls in 746 cancer samples. <i>Nature Communications</i> , 2020 , 11, 4748	17.4	10
35	Sex differences in oncogenic mutational processes. <i>Nature Communications</i> , 2020 , 11, 4330	17.4	23
34	Community assessment to advance computational prediction of cancer drug combinations in a pharmacogenomic screen. <i>Nature Communications</i> , 2019 , 10, 2674	17.4	119
33	Predictive models of protease specificity based on quantitative protease-activity profiling data. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2019 , 1867, 140253	4	0
32	Predicting human olfactory perception from chemical features of odor molecules. <i>Science</i> , 2017 , 355, 820-826	33.3	117
31	A DREAM Challenge to Build Prediction Models for Short-Term Discontinuation of Docetaxel in Metastatic Castration-Resistant Prostate Cancer. <i>JCO Clinical Cancer Informatics</i> , 2017 , 1, 1-15	5.2	7
30	Prediction of overall survival for patients with metastatic castration-resistant prostate cancer: development of a prognostic model through a crowdsourced challenge with open clinical trial data. <i>Lancet Oncology, The</i> , 2017 , 18, 132-142	21.7	90

29	Comparative immunogenicity and structural analysis of epitopes of different bacterial L-asparaginases. <i>BMC Cancer</i> , 2016 , 16, 89	4.8	17
28	Classification of ANA HEP-2 slide images using morphological features of stained patterns. <i>Pattern Recognition Letters</i> , 2016 , 82, 79-84	4.7	8
27	Mycobacterial nicotinate mononucleotide adenylyltransferase: structure, mechanism, and implications for drug discovery. <i>Journal of Biological Chemistry</i> , 2015 , 290, 7693-706	5.4	17
26	APOBEC-Induced Cancer Mutations Are Uniquely Enriched in Early-Replicating, Gene-Dense, and Active Chromatin Regions. <i>Cell Reports</i> , 2015 , 13, 1103-1109	10.6	57
25	CleavPredict: A Platform for Reasoning about Matrix Metalloproteinases Proteolytic Events. <i>PLoS ONE</i> , 2015 , 10, e0127877	3.7	27
24	Horizontal gene transfer and genome evolution in Methanosarcina. <i>BMC Evolutionary Biology</i> , 2015 , 15, 102	3	13
23	ANA HEP-2 cells image classification using number, size, shape and localization of targeted cell regions. <i>Pattern Recognition</i> , 2014 , 47, 2360-2366	7.7	42
22	Basis for substrate recognition and distinction by matrix metalloproteinases. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014 , 111, E4148-55	11.5	49
21	Evaluation and comparison of current fetal ultrasound image segmentation methods for biometric measurements: a grand challenge. <i>IEEE Transactions on Medical Imaging</i> , 2014 , 33, 797-813	11.7	91
20	Characterization of bacterial NMN deamidase as a Ser/Lys hydrolase expands diversity of serine amidohydrolases. <i>FEBS Letters</i> , 2014 , 588, 1016-23	3.8	5
19	Sequence and conformational specificity in substrate recognition: several human Kunitz protease inhibitor domains are specific substrates of mesotrypsin. <i>Journal of Biological Chemistry</i> , 2014 , 289, 32783-97	5.4	23
18	Sequence-derived structural features driving proteolytic processing. <i>Proteomics</i> , 2014 , 14, 42-50	4.8	14
17	Genomic reconstruction of transcriptional regulatory networks in lactic acid bacteria. <i>BMC Genomics</i> , 2013 , 14, 94	4.5	27
16	Comparative genomics of metabolic capacities of regulons controlled by cis-regulatory RNA motifs in bacteria. <i>BMC Genomics</i> , 2013 , 14, 597	4.5	32
15	Functional diversification of ROK-family transcriptional regulators of sugar catabolism in the Thermotogae phylum. <i>Nucleic Acids Research</i> , 2013 , 41, 790-803	20.1	30
14	Evolution of pan-genomes of Escherichia coli, Shigella spp., and Salmonella enterica. <i>Journal of Bacteriology</i> , 2013 , 195, 2786-92	3.5	86
13	Genomic reconstruction of the transcriptional regulatory network in Bacillus subtilis. <i>Journal of Bacteriology</i> , 2013 , 195, 2463-73	3.5	39
12	RegPrecise 3.0--a resource for genome-scale exploration of transcriptional regulation in bacteria. <i>BMC Genomics</i> , 2013 , 14, 745	4.5	229

11	Genomics-guided analysis of NAD recycling yields functional elucidation of COG1058 as a new family of pyrophosphatases. <i>PLoS ONE</i> , 2013 , 8, e65595	3.7	13
10	Evolution of transcriptional regulation in closely related bacteria. <i>BMC Evolutionary Biology</i> , 2012 , 12, 200	3	7
9	Functional specialization in proline biosynthesis of melanoma. <i>PLoS ONE</i> , 2012 , 7, e45190	3.7	92
8	Glutamine versus ammonia utilization in the NAD synthetase family. <i>PLoS ONE</i> , 2012 , 7, e39115	3.7	30
7	Comparative genomic reconstruction of transcriptional networks controlling central metabolism in the <i>Shewanella</i> genus. <i>BMC Genomics</i> , 2011 , 12 Suppl 1, S3	4.5	44
6	Evolution of prokaryotic genes by shift of stop codons. <i>Journal of Molecular Evolution</i> , 2011 , 72, 138-46	3.1	23
5	Complete genome and proteome of <i>Acholeplasma laidlawii</i> . <i>Journal of Bacteriology</i> , 2011 , 193, 4943-53	3.5	49
4	Structural determinants of limited proteolysis. <i>Journal of Proteome Research</i> , 2011 , 10, 3642-51	5.6	44
3	Segmentation of small objects in color images. <i>Programming and Computer Software</i> , 2008 , 34, 173-182	0.8	2
2	Abundance and functional diversity of riboswitches in microbial communities. <i>BMC Genomics</i> , 2007 , 8, 347	4.5	47
1	A new color image segmentation algorithm based on watershed transformation 2004 ,		2