

Marat D Kazanov

List of Publications by Year in descending order

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Version: 2024-02-01

48
papers

8,441
citations

172457

29
h-index

206112

48
g-index

51
all docs

51
docs citations

51
times ranked

13952
citing authors

#	ARTICLE	IF	CITATIONS
1	The repertoire of mutational signatures in human cancer. <i>Nature</i> , 2020, 578, 94-101.	27.8	2,104
2	Pan-cancer analysis of whole genomes. <i>Nature</i> , 2020, 578, 82-93.	27.8	1,966
3	Patterns of somatic structural variation in human cancer genomes. <i>Nature</i> , 2020, 578, 112-121.	27.8	560
4	Comprehensive analysis of chromothripsis in 2,658 human cancers using whole-genome sequencing. <i>Nature Genetics</i> , 2020, 52, 331-341.	21.4	431
5	Analyses of non-coding somatic drivers in 2,658 cancer whole genomes. <i>Nature</i> , 2020, 578, 102-111.	27.8	424
6	RegPrecise 3.0 – A resource for genome-scale exploration of transcriptional regulation in bacteria. <i>BMC Genomics</i> , 2013, 14, 745.	2.8	408
7	Pan-cancer analysis of whole genomes identifies driver rearrangements promoted by LINE-1 retrotransposition. <i>Nature Genetics</i> , 2020, 52, 306-319.	21.4	275
8	Community assessment to advance computational prediction of cancer drug combinations in a pharmacogenomic screen. <i>Nature Communications</i> , 2019, 10, 2674.	12.8	240
9	Predicting human olfactory perception from chemical features of odor molecules. <i>Science</i> , 2017, 355, 820-826.	12.6	194
10	Disruption of chromatin folding domains by somatic genomic rearrangements in human cancer. <i>Nature Genetics</i> , 2020, 52, 294-305.	21.4	180
11	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.	8.9	137
12	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</i> , The, 2017, 18, 132-142.	10.7	124
13	Functional Specialization in Proline Biosynthesis of Melanoma. <i>PLoS ONE</i> , 2012, 7, e45190.	2.5	116
14	Evolution of Pan-Genomes of <i>Escherichia coli</i> , <i>Shigella</i> spp., and <i>Salmonella enterica</i> . <i>Journal of Bacteriology</i> , 2013, 195, 2786-2792.	2.2	115
15	Genomic footprints of activated telomere maintenance mechanisms in cancer. <i>Nature Communications</i> , 2020, 11, 733.	12.8	87
16	APOBEC-Induced Cancer Mutations Are Uniquely Enriched in Early-Replicating, Gene-Dense, and Active Chromatin Regions. <i>Cell Reports</i> , 2015, 13, 1103-1109.	6.4	80
17	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.	7.1	75
18	Structural Determinants of Limited Proteolysis. <i>Journal of Proteome Research</i> , 2011, 10, 3642-3651.	3.7	68

#	ARTICLE	IF	CITATIONS
19	Complete Genome and Proteome of <i>Acholeplasma laidlawii</i> . <i>Journal of Bacteriology</i> , 2011, 193, 4943-4953.	2.2	60
20	Sex differences in oncogenic mutational processes. <i>Nature Communications</i> , 2020, 11, 4330.	12.8	60
21	Comparative genomic reconstruction of transcriptional networks controlling central metabolism in the <i>Shewanella</i> genus. <i>BMC Genomics</i> , 2011, 12, S3.	2.8	59
22	Abundance and functional diversity of riboswitches in microbial communities. <i>BMC Genomics</i> , 2007, 8, 347.	2.8	54
23	Genomic Reconstruction of the Transcriptional Regulatory Network in <i>Bacillus subtilis</i> . <i>Journal of Bacteriology</i> , 2013, 195, 2463-2473.	2.2	54
24	ANA HEp-2 cells image classification using number, size, shape and localization of targeted cell regions. <i>Pattern Recognition</i> , 2014, 47, 2360-2366.	8.1	53
25	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.	12.8	50
26	Functional diversification of ROK-family transcriptional regulators of sugar catabolism in the <i>Thermotogae</i> phylum. <i>Nucleic Acids Research</i> , 2013, 41, 790-803.	14.5	44
27	Comparative genomics of metabolic capacities of regulons controlled by cis-regulatory RNA motifs in bacteria. <i>BMC Genomics</i> , 2013, 14, 597.	2.8	39
28	Genomic reconstruction of transcriptional regulatory networks in lactic acid bacteria. <i>BMC Genomics</i> , 2013, 14, 94.	2.8	38
29	Glutamine versus Ammonia Utilization in the NAD Synthetase Family. <i>PLoS ONE</i> , 2012, 7, e39115.	2.5	36
30	Comparative immunogenicity and structural analysis of epitopes of different bacterial L-asparaginases. <i>BMC Cancer</i> , 2016, 16, 89.	2.6	33
31	CleavPredict: A Platform for Reasoning about Matrix Metalloproteinases Proteolytic Events. <i>PLoS ONE</i> , 2015, 10, e0127877.	2.5	32
32	Sequence and Conformational Specificity in Substrate Recognition. <i>Journal of Biological Chemistry</i> , 2014, 289, 32783-32797.	3.4	30
33	Evolution of Prokaryotic Genes by Shift of Stop Codons. <i>Journal of Molecular Evolution</i> , 2011, 72, 138-146.	1.8	29
34	Retrospective evaluation of whole exome and genome mutation calls in 746 cancer samples. <i>Nature Communications</i> , 2020, 11, 4748.	12.8	27
35	Mycobacterial Nicotinate Mononucleotide Adenylyltransferase. <i>Journal of Biological Chemistry</i> , 2015, 290, 7693-7706.	3.4	25
36	Sequence-derived structural features driving proteolytic processing. <i>Proteomics</i> , 2014, 14, 42-50.	2.2	20

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37	Lineage Conversion in Pediatric B-Cell Precursor Acute Leukemia under Blinatumomab Therapy. <i>International Journal of Molecular Sciences</i> , 2022, 23, 4019.	4.1	18
38	Horizontal gene transfer and genome evolution in <i>Methanosarcina</i> . <i>BMC Evolutionary Biology</i> , 2015, 15, 102.	3.2	15
39	Genomics-Guided Analysis of NAD Recycling Yields Functional Elucidation of COG1058 as a New Family of Pyrophosphatases. <i>PLoS ONE</i> , 2013, 8, e65595.	2.5	14
40	Classification of ANA HEp-2 slide images using morphological features of stained patterns. <i>Pattern Recognition Letters</i> , 2016, 82, 79-84.	4.2	12
41	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.	2.1	12
42	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.	3.1	11
43	Evolution of transcriptional regulation in closely related bacteria. <i>BMC Evolutionary Biology</i> , 2012, 12, 200.	3.2	10
44	Characterization of bacterial NMN deamidase as a Ser/Lys hydrolase expands diversity of serine amidohydrolases. <i>FEBS Letters</i> , 2014, 588, 1016-1023.	2.8	6
45	A new color image segmentation algorithm based on watershed transformation. , 2004, , .		4
46	APOBEC mutagenesis is low in most types of non-B DNA structures. <i>IScience</i> , 2022, 25, 104535.	4.1	3
47	Segmentation of small objects in color images. <i>Programming and Computer Software</i> , 2008, 34, 173-182.	0.9	2
48	Predictive models of protease specificity based on quantitative protease-activity profiling data. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2019, 1867, 140253.	2.3	1