

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	Lineage Conversion in Pediatric B-Cell Precursor Acute Leukemia under Blinatumomab Therapy. International Journal of Molecular Sciences, 2022, 23, 4019.	4.1	18
2	APOBEC mutagenesis is low in most types of non-B DNA structures. IScience, 2022, 25, 104535.	4.1	3
3	Analysis of gene expression and mutation data points on contribution of transcription to the mutagenesis by APOBEC enzymes. NAR Cancer, 2021, 3, zcab025.	3.1	11
4	Retrospective evaluation of whole exome and genome mutation calls in 746 cancer samples. Nature Communications, 2020, 11, 4748.	12.8	27
5	Sex differences in oncogenic mutational processes. Nature Communications, 2020, 11, 4330.	12.8	60
6	Genomic footprints of activated telomere maintenance mechanisms in cancer. Nature Communications, 2020, 11, 733.	12.8	87
7	High-coverage whole-genome analysis of 1220 cancers reveals hundreds of genes deregulated by rearrangement-mediated cis-regulatory alterations. Nature Communications, 2020, 11, 736.	12.8	50
8	Patterns of somatic structural variation in human cancer genomes. Nature, 2020, 578, 112-121.	27.8	560
9	The repertoire of mutational signatures in human cancer. Nature, 2020, 578, 94-101.	27.8	2,104
10	Analyses of non-coding somatic drivers in 2,658 cancer whole genomes. Nature, 2020, 578, 102-111.	27.8	424
11	Pan-cancer analysis of whole genomes. Nature, 2020, 578, 82-93.	27.8	1,966
12	Pan-cancer analysis of whole genomes identifies driver rearrangements promoted by LINE-1 retrotransposition. Nature Genetics, 2020, 52, 306-319.	21.4	275
13	Disruption of chromatin folding domains by somatic genomic rearrangements in human cancer. Nature Genetics, 2020, 52, 294-305.	21.4	180
14	Comprehensive analysis of chromothripsis in 2,658 human cancers using whole-genome sequencing. Nature Genetics, 2020, 52, 331-341.	21.4	431
15	Predictive models of protease specificity based on quantitative protease-activity profiling data. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2019, 1867, 140253.	2.3	1
16	Community assessment to advance computational prediction of cancer drug combinations in a pharmacogenomic screen. Nature Communications, 2019, 10, 2674.	12.8	240
17	Predicting human olfactory perception from chemical features of odor molecules. Science, 2017, 355, 820-826.	12.6	194
18	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. Lancet Oncology, The, 2017, 18, 132-142.	10.7	124

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19	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
20	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
21	Comparative immunogenicity and structural analysis of epitopes of different bacterial L-asparaginases. <i>BMC Cancer</i> , 2016, 16, 89.	2.6	33
22	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
23	CleavPredict: A Platform for Reasoning about Matrix Metalloproteinases Proteolytic Events. <i>PLoS ONE</i> , 2015, 10, e0127877.	2.5	32
24	Horizontal gene transfer and genome evolution in <i>Methanosarcina</i> . <i>BMC Evolutionary Biology</i> , 2015, 15, 102.	3.2	15
25	Mycobacterial Nicotinate Mononucleotide Adenylyltransferase. <i>Journal of Biological Chemistry</i> , 2015, 290, 7693-7706.	3.4	25
26	Sequence and Conformational Specificity in Substrate Recognition. <i>Journal of Biological Chemistry</i> , 2014, 289, 32783-32797.	3.4	30
27	Sequence-derived structural features driving proteolytic processing. <i>Proteomics</i> , 2014, 14, 42-50.	2.2	20
28	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
29	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
30	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
31	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
32	Genomic reconstruction of transcriptional regulatory networks in lactic acid bacteria. <i>BMC Genomics</i> , 2013, 14, 94.	2.8	38
33	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
34	Functional diversification of ROK-family transcriptional regulators of sugar catabolism in the Thermotogae phylum. <i>Nucleic Acids Research</i> , 2013, 41, 790-803.	14.5	44
35	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
36	Genomic Reconstruction of the Transcriptional Regulatory Network in <i>Bacillus subtilis</i> . <i>Journal of Bacteriology</i> , 2013, 195, 2463-2473.	2.2	54

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37	RegPrecise 3.0 – A resource for genome-scale exploration of transcriptional regulation in bacteria. BMC Genomics, 2013, 14, 745.	2.8	408
38	Genomics-Guided Analysis of NAD Recycling Yields Functional Elucidation of COG1058 as a New Family of Pyrophosphatases. PLoS ONE, 2013, 8, e65595.	2.5	14
39	Evolution of transcriptional regulation in closely related bacteria. BMC Evolutionary Biology, 2012, 12, 200.	3.2	10
40	Functional Specialization in Proline Biosynthesis of Melanoma. PLoS ONE, 2012, 7, e45190.	2.5	116
41	Glutamine versus Ammonia Utilization in the NAD Synthetase Family. PLoS ONE, 2012, 7, e39115.	2.5	36
42	Complete Genome and Proteome of <i>Acholeplasma laidlawii</i> . Journal of Bacteriology, 2011, 193, 4943-4953.	2.2	60
43	Structural Determinants of Limited Proteolysis. Journal of Proteome Research, 2011, 10, 3642-3651.	3.7	68
44	Comparative genomic reconstruction of transcriptional networks controlling central metabolism in the <i>Shewanella</i> genus. BMC Genomics, 2011, 12, S3.	2.8	59
45	Evolution of Prokaryotic Genes by Shift of Stop Codons. Journal of Molecular Evolution, 2011, 72, 138-146.	1.8	29
46	Segmentation of small objects in color images. Programming and Computer Software, 2008, 34, 173-182.	0.9	2
47	Abundance and functional diversity of riboswitches in microbial communities. BMC Genomics, 2007, 8, 347.	2.8	54
48	A new color image segmentation algorithm based on watershed transformation. , 2004, , .		4