Alexander Favorov

List of Publications by Year
in descending order

51	1,741	361413	330143
papers	citations	20 h-index	37 g-index

64	64	64	3213
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Supervised mutational signatures for obesity and other tissue-specific etiological factors in cancer. ELife, 2021, 10, .	6.0	12
2	Landscape of allele-specific transcription factor binding in the human genome. Nature Communications, 2021, 12, 2751.	12.8	55
3	Spatial correlation statistics enable transcriptome-wide characterization of RNA structure binding. Cell Reports Methods, 2021, 1, 100088.	2.9	2
4	Newly Identified Members of FGFR1 Splice Variants Engage in Cross-talk with AXL/AKT Axis in Salivary Adenoid Cystic Carcinoma. Cancer Research, 2021, 81, 1001-1013.	0.9	10
5	Rational genomic optimization of DNA detection for human papillomavirus type 16 in head and neck squamous cell carcinoma. Head and Neck, 2020, 42, 688-697.	2.0	2
6	Functional annotation of human long noncoding RNAs via molecular phenotyping. Genome Research, 2020, 30, 1060-1072.	5.5	109
7	Senescence and entrenchment in evolution of amino acid sites. Nature Communications, 2020, 11, 4603.	12.8	4
8	Extracellular Vesicles Released by Tumor Endothelial Cells Spread Immunosuppressive and Transforming Signals Through Various Recipient Cells. Frontiers in Cell and Developmental Biology, 2020, 8, 698.	3.7	18
9	HPV E2, E4, E5 drive alternative carcinogenic pathways in HPV positive cancers. Oncogene, 2020, 39, 6327-6339.	5.9	48
10	Chromatin structure regulates cancer-specific alternative splicing events in primary HPV-related oropharyngeal squamous cell carcinoma. Epigenetics, 2020, 15, 959-971.	2.7	17
11	Recounting the FANTOM CAGE-Associated Transcriptome. Genome Research, 2020, 30, 1073-1081.	5.5	35
12	Differential Variation Analysis Enables Detection of Tumor Heterogeneity Using Single-Cell RNA-Sequencing Data. Cancer Research, 2019, 79, 5102-5112.	0.9	23
13	What Do Neighbors Tell About You: The Local Context of Cis-Regulatory Modules Complicates Prediction of Regulatory Variants. Frontiers in Genetics, 2019, 10, 1078.	2.3	3
14	Differentially Methylated Super-Enhancers Regulate Target Gene Expression in Human Cancer. Scientific Reports, 2019, 9, 15034.	3.3	9
15	Allele-specific nonstationarity in evolution of influenza A virus surface proteins. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 21104-21112.	7.1	10
16	Chromatin dysregulation and DNA methylation at transcription start sites associated with transcriptional repression in cancers. Nature Communications, 2019, 10, 2188.	12.8	61
17	Splice Expression Variation Analysis (SEVA) for inter-tumor heterogeneity of gene isoform usage in cancer. Bioinformatics, 2018, 34, 1859-1867.	4.1	11
18	Integrated time course omics analysis distinguishes immediate therapeutic response from acquired resistance. Genome Medicine, 2018, 10, 37.	8.2	25

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19	Functional characterization of alternatively spliced GSN in head and neck squamous cell carcinoma. Translational Research, 2018, 202, 109-119.	5.0	15
20	Discovery and development of differentially methylated regions in human papillomavirusâ€related oropharyngeal squamous cell carcinoma. International Journal of Cancer, 2018, 143, 2425-2436.	5.1	35
21	Enter the Matrix: Factorization Uncovers Knowledge from Omics. Trends in Genetics, 2018, 34, 790-805.	6.7	181
22	Coloc-stats: a unified web interface to perform colocalization analysis of genomic features. Nucleic Acids Research, 2018, 46, W186-W193.	14.5	23
23	PatternMarkers & GWCoGAPS for novel data-driven biomarkers via whole transcriptome NMF. Bioinformatics, 2017, 33, 1892-1894.	4.1	39
24	Association of combinations of polymorphisms in fibroblast growth factor receptor 2 gene with breast cancer among various ethnic groups. Russian Journal of Genetics, 2017, 53, 1042-1047.	0.6	0
25	Integrated Analysis of Whole-Genome ChIP-Seq and RNA-Seq Data of Primary Head and Neck Tumor Samples Associates HPV Integration Sites with Open Chromatin Marks. Cancer Research, 2017, 77, 6538-6550.	0.9	50
26	A Novel Functional Splice Variant of AKT3 Defined by Analysis of Alternative Splice Expression in HPV-Positive Oropharyngeal Cancers. Cancer Research, 2017, 77, 5248-5258.	0.9	41
27	DNA methylation regulates TMEM16A/ANO1 expression through multiple CpG islands in head and neck squamous cell carcinoma. Scientific Reports, 2017, 7, 15173.	3.3	20
28	StereoGene: rapid estimation of genome-wide correlation of continuous or interval feature data. Bioinformatics, 2017, 33, 3158-3165.	4.1	22
29	Genetic risk factors for myocardial infarction more clearly manifest for early age of first onset. Molecular Biology Reports, 2017, 44, 315-321.	2.3	10
30	The combined effects of myocardial infarction risk factors: Simulation of the combined effects of gene variants, age, and smoking and an analysis of their interaction. Biophysics (Russian Federation), 2017, 62, 123-128.	0.7	0
31	Multilocus Analysis of Genetic Susceptibility to Myocardial Infarction in Russians: Replication Study. Acta Naturae, 2017, 9, 74-83.	1.7	6
32	CoGAPS matrix factorization algorithm identifies transcriptional changes in AP-2alpha target genes in feedback from therapeutic inhibition of the EGFR network. Oncotarget, 2016, 7, 73845-73864.	1.8	16
33	Inferring causal molecular networks: empirical assessment through a community-based effort. Nature Methods, 2016, 13, 310-318.	19.0	209
34	Whole-Genome DNA Methylation Analysis of Peripheral Blood Mononuclear Cells in Multiple Sclerosis Patients with Different Disease Courses. Acta Naturae, 2016, 8, 103-110.	1.7	24
35	Correlated Evolution of Nucleotide Positions within Splice Sites in Mammals. PLoS ONE, 2015, 10, e0144388.	2.5	8
36	Activation of Type I Interferon Signal Pathway in Patients with Multiple Sclerosis by the Russian Analog of Î²-Interferon-1b (transcriptional profiling data). Neuroscience and Behavioral Physiology, 2015, 45, 847-853.	0.4	0

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37	GWAS-identified multiple sclerosis risk loci involved in immune response: Validation in Russians. Journal of Neuroimmunology, 2015, 282, 85-91.	2.3	30
38	Natural variation of gene models in Drosophila melanogaster. BMC Genomics, 2015, 16, 198.	2.8	6
39	Variants of the Coagulation and Inflammation Genes Are Replicably Associated with Myocardial Infarction and Epistatically Interact in Russians. PLoS ONE, 2015, 10, e0144190.	2.5	24
40	Weak Negative and Positive Selection and the Drift Load at Splice Sites. Genome Biology and Evolution, 2014, 6, 1437-1447.	2.5	14
41	Heavyâ€“light chain interrelations of MS-associated immunoglobulins probed by deep sequencing and rational variation. Molecular Immunology, 2014, 62, 305-314.	2.2	23
42	Genome-wide association study as a method to analyze the genome architecture in polygenic diseases, with the example of multiple sclerosis. Molecular Biology, 2014, 48, 496-507.	1.3	8
43	Preserving biological heterogeneity with a permuted surrogate variable analysis for genomics batch correction. Bioinformatics, 2014, 30, 2757-2763.	4.1	102
44	Identifying Context-Specific Transcription Factor Targets From Prior Knowledge and Gene Expression Data. IEEE Transactions on Nanobioscience, 2013, 12, 142-149.	3.3	11
45	Polyreactive monoclonal autoantibodies in multiple sclerosis: functional selection from phage display library and characterization by deep sequencing analysis. Acta Naturae, 2013, 5, 94-104.	1.7	3
46	Exploring Massive, Genome Scale Datasets with the GenometriCorr Package. PLoS Computational Biology, 2012, 8, e1002529.	3.2	167
47	Identifying context-specific transcription factor targets from prior knowledge and gene expression data. , 2012, , .		2
48	Correlations between clusters of protein-DNA binding sites and the binding experimental data allow predicting a structure of regulatory modules. Biophysics (Russian Federation), 2012, 57, 138-139.	0.7	0
49	OnionTree XML: A Format to Exchange Gene-Related Probabilities. Journal of Biomolecular Structure and Dynamics, 2011, 29, 417-423.	3.5	0
50	CoGAPS: an R/C++ package to identify patterns and biological process activity in transcriptomic data. Bioinformatics, 2010, 26, 2792-2793.	4.1	84
51	A Markov Chain Monte Carlo Technique for Identification of Combinations of Allelic Variants Underlying Complex Diseases in Humans. Genetics, 2005, 171, 2113-2121.	2.9	81