

Yuval Tabach

List of Publications by Year in descending order

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Version: 2024-02-01

33
papers

1,866
citations

430874

18
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414414

32
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all docs

38
docs citations

38
times ranked

3554
citing authors

#	ARTICLE	IF	CITATIONS
1	Machine-learning of complex evolutionary signals improves classification of SNVs. <i>NAR Genomics and Bioinformatics</i> , 2022, 4, lqac025.	3.2	4
2	Multi-omics data integration analysis identifies the spliceosome as a key regulator of DNA double-strand break repair. <i>NAR Cancer</i> , 2022, 4, zcac013.	3.1	5
3	Asymmetric inheritance of RNA toxicity in <i>C.Âelegans</i> expressing CTG repeats. <i>IScience</i> , 2022, 25, 104246.	4.1	2
4	DEPCOD: a tool to detect and visualize co-evolution of protein domains. <i>Nucleic Acids Research</i> , 2022, , .	14.5	0
5	CladeOScope: functional interactions through the prism of clade-wise co-evolution. <i>NAR Genomics and Bioinformatics</i> , 2021, 3, lqab024.	3.2	19
6	Current gene panels account for nearly all homologous recombination repair-associated multiple-case breast cancer families. <i>Npj Breast Cancer</i> , 2021, 7, 109.	5.2	3
7	Expanding the MECP2 network using comparative genomics reveals potential therapeutic targets for Rett syndrome. <i>ELife</i> , 2021, 10, .	6.0	9
8	Co-evolution based machine-learning for predicting functional interactions between human genes. <i>Nature Communications</i> , 2021, 12, 6454.	12.8	12
9	Aurintricarboxylic Acid Decreases RNA Toxicity in a <i>C. elegans</i> Model of Repeat Expansions. <i>Toxins</i> , 2021, 13, 910.	3.4	2
10	Reversal of diet-induced hepatic steatosis by peripheral CB1 receptor blockade in mice is p53/miRNA-22/SIRT1/PPAR α dependent. <i>Molecular Metabolism</i> , 2020, 42, 101087.	6.5	23
11	ACE2 Co-evolutionary Pattern Suggests Targets for Pharmaceutical Intervention in the COVID-19 Pandemic. <i>IScience</i> , 2020, 23, 101384.	4.1	15
12	Optimization of co-evolution analysis through phylogenetic profiling reveals pathway-specific signals. <i>Bioinformatics</i> , 2020, 36, 4116-4125.	4.1	10
13	MYORG Mutations: a Major Cause of Recessive Primary Familial Brain Calcification. <i>Current Neurology and Neuroscience Reports</i> , 2019, 19, 70.	4.2	14
14	Mapping global and local coevolution across 600 species to identify novel homologous recombination repair genes. <i>Genome Research</i> , 2019, 29, 439-448.	5.5	37
15	Expanded CUG Repeats Trigger Disease Phenotype and Expression Changes through the RNAi Machinery in <i>C. elegans</i> . <i>Journal of Molecular Biology</i> , 2019, 431, 1711-1728.	4.2	12
16	<i><sc>MYORG</sc></i> is associated with recessive primary familial brain calcification. <i>Annals of Clinical and Translational Neurology</i> , 2019, 6, 106-113.	3.7	25
17	Schlafen2 mutation in mice causes an osteopetrotic phenotype due to a decrease in the number of osteoclast progenitors. <i>Scientific Reports</i> , 2018, 8, 13005.	3.3	10
18	UV-Protection Timer Controls Linkage between Stress and Pigmentation Skin Protection Systems. <i>Molecular Cell</i> , 2018, 72, 444-456.e7.	9.7	34

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19	<scp>SHLD</scp> 2/ <scp>FAM</scp> 35A co-operates with <scp>REV</scp> 7 to coordinate <scp>DNA</scp> double-strand break repair pathway choice. EMBO Journal, 2018, 37, .	7.8	111
20	Mutated MITF-E87R in Melanoma Enhances Tumor Progression via S100A4. Journal of Investigative Dermatology, 2018, 138, 2216-2223.	0.7	7
21	A continuum of mRNP complexes in embryonic microRNA-mediated silencing. Nucleic Acids Research, 2017, 45, gkw872.	14.5	20
22	PhyloGene server for identification and visualization of co-evolving proteins using normalized phylogenetic profiles. Nucleic Acids Research, 2015, 43, W154-W159.	14.5	43
23	Interactions of Melanoma Cells with Distal Keratinocytes Trigger Metastasis via Notch Signaling Inhibition of MITF. Molecular Cell, 2015, 59, 664-676.	9.7	85
24	Identification of genes in toxicity pathways of trinucleotide-repeat RNA in C. elegans. Nature Structural and Molecular Biology, 2014, 21, 712-720.	8.2	23
25	High-Resolution Mapping Reveals a Conserved, Widespread, Dynamic mRNA Methylation Program in Yeast Meiosis. Cell, 2013, 155, 1409-1421.	28.9	554
26	Identification of small RNA pathway genes using patterns of phylogenetic conservation and divergence. Nature, 2013, 493, 694-698.	27.8	138
27	Human disease locus discovery and mapping to molecular pathways through phylogenetic profiling. Molecular Systems Biology, 2013, 9, 692.	7.2	54
28	Amplification of the 20q Chromosomal Arm Occurs Early in Tumorigenic Transformation and May Initiate Cancer. PLoS ONE, 2011, 6, e14632.	2.5	69
29	Modulation of the Vitamin D3 Response by Cancer-Associated Mutant p53. Cancer Cell, 2010, 17, 273-285.	16.8	228
30	Wide-Scale Analysis of Human Functional Transcription Factor Binding Reveals a Strong Bias towards the Transcription Start Site. PLoS ONE, 2007, 2, e807.	2.5	55
31	Transcriptional Programs following Genetic Alterations in p53, INK4A, and H-Ras Genes along Defined Stages of Malignant Transformation. Cancer Research, 2005, 65, 4530-4543.	0.9	52
32	The promoters of human cell cycle genes integrate signals from two tumor suppressive pathways during cellular transformation. Molecular Systems Biology, 2005, 1, 2005.0022.	7.2	64
33	Prolonged culture of telomerase-immortalized human fibroblasts leads to a premalignant phenotype. Cancer Research, 2003, 63, 7147-57.	0.9	121