Yuval Tabach

List of Publications by Year
in descending order

33	1,866	430874 18	414414 32
papers	citations	h-index	g-index

38	38	38	3554
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	High-Resolution Mapping Reveals a Conserved, Widespread, Dynamic mRNA Methylation Program in Yeast Meiosis. Cell, 2013, 155, 1409-1421.	28.9	554
2	Modulation of the Vitamin D3 Response by Cancer-Associated Mutant p53. Cancer Cell, 2010, 17, 273-285.	16.8	228
3	Identification of small RNA pathway genes using patterns of phylogenetic conservation and divergence. Nature, 2013, 493, 694-698.	27.8	138
4	Prolonged culture of telomerase-immortalized human fibroblasts leads to a premalignant phenotype. Cancer Research, 2003, 63, 7147-57.	0.9	121
5	<scp>SHLD</scp> 2/ <scp>FAM</scp> 35A coâ€operates with <scp>REV</scp> 7 to coordinate <scp>DNA</scp> doubleâ€strand break repair pathway choice. EMBO Journal, 2018, 37, .	7.8	111
6	Interactions of Melanoma Cells with Distal Keratinocytes Trigger Metastasis via Notch Signaling Inhibition of MITF. Molecular Cell, 2015, 59, 664-676.	9.7	85
7	Amplification of the 20q Chromosomal Arm Occurs Early in Tumorigenic Transformation and May Initiate Cancer. PLoS ONE, 2011, 6, e14632.	2.5	69
8	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
9	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
10	Human disease locus discovery and mapping to molecular pathways through phylogenetic profiling. Molecular Systems Biology, 2013, 9, 692.	7.2	54
11	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
12	PhyloGene server for identification and visualization of co-evolving proteins using normalized phylogenetic profiles. Nucleic Acids Research, 2015, 43, W154-W159.	14.5	43
13	Mapping global and local coevolution across 600 species to identify novel homologous recombination repair genes. Genome Research, 2019, 29, 439-448.	5.5	37
14	UV-Protection Timer Controls Linkage between Stress and Pigmentation Skin Protection Systems. Molecular Cell, 2018, 72, 444-456.e7.	9.7	34
15	<scp>MYORG</scp> is associated with recessive primary familial brain calcification. Annals of Clinical and Translational Neurology, 2019, 6, 106-113.	3.7	25
16	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
17	Reversal of diet-induced hepatic steatosis by peripheral CB1 receptor blockade in mice is p53/miRNA-22/SIRT1/PPARÎ± dependent. Molecular Metabolism, 2020, 42, 101087.	6.5	23
18	A continuum of mRNP complexes in embryonic microRNA-mediated silencing. Nucleic Acids Research, 2017, 45, gkw872.	14.5	20

#	ARTICLE	IF	CITATIONS
19	CladeOScope: functional interactions through the prism of clade-wise co-evolution. NAR Genomics and Bioinformatics, 2021, 3, lqab024.	3.2	19
20	ACE2 Co-evolutionary Pattern Suggests Targets for Pharmaceutical Intervention in the COVID-19 Pandemic. IScience, 2020, 23, 101384.	4.1	15
21	MYORG Mutations: a Major Cause of Recessive Primary Familial Brain Calcification. Current Neurology and Neuroscience Reports, 2019, 19, 70.	4.2	14
22	Expanded CUG Repeats Trigger Disease Phenotype and Expression Changes through the RNAi Machinery in C. elegans. Journal of Molecular Biology, 2019, 431, 1711-1728.	4.2	12
23	Co-evolution based machine-learning for predicting functional interactions between human genes. Nature Communications, 2021, 12, 6454.	12.8	12
24	Schlafen2 mutation in mice causes an osteopetrotic phenotype due to a decrease in the number of osteoclast progenitors. Scientific Reports, 2018, 8, 13005.	3.3	10
25	Optimization of co-evolution analysis through phylogenetic profiling reveals pathway-specific signals. Bioinformatics, 2020, 36, 4116-4125.	4.1	10
26	Expanding the MECP2 network using comparative genomics reveals potential therapeutic targets for Rett syndrome. ELife, 2021, 10, .	6.0	9
27	Mutated MITF-E87R in Melanoma Enhances Tumor Progression via S100A4. Journal of Investigative Dermatology, 2018, 138, 2216-2223.	0.7	7
28	Multi-omics data integration analysis identifies the spliceosome as a key regulator of DNA double-strand break repair. NAR Cancer, 2022, 4, zcac013.	3.1	5
29	Machine-learning of complex evolutionary signals improves classification of SNVs. NAR Genomics and Bioinformatics, 2022, 4, lqac025.	3.2	4
30	Current gene panels account for nearly all homologous recombination repair-associated multiple-case breast cancer families. Npj Breast Cancer, 2021, 7, 109.	5.2	3
31	Aurintricarboxylic Acid Decreases RNA Toxicity in a C. elegans Model of Repeat Expansions. Toxins, 2021, 13, 910.	3.4	2
32	Asymmetric inheritance of RNA toxicity in C.Âelegans expressing CTG repeats. IScience, 2022, 25, 104246.	4.1	2
33	DEPCOD: a tool to detect and visualize co-evolution of protein domains. Nucleic Acids Research, 2022, , .	14.5	0