

Vishwanath R Iyer

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/8800337/publications.pdf>

Version: 2024-02-01

33
papers

1,858
citations

394421

19
h-index

414414

32
g-index

40
all docs

40
docs citations

40
times ranked

3743
citing authors

#	ARTICLE	IF	CITATIONS
1	Emerging Epigenetic Therapies for Brain Tumors. <i>NeuroMolecular Medicine</i> , 2022, 24, 41-49.	3.4	7
2	Emerging Frontiers of Therapeutic Strategies for Brain Tumors: A <i>NeuroMolecular Medicine</i> Special Issue. <i>NeuroMolecular Medicine</i> , 2022, 24, 1-2.	3.4	0
3	The histone variant H2A.Z in yeast is almost exclusively incorporated into the +1 nucleosome in the direction of transcription. <i>Nucleic Acids Research</i> , 2020, 48, 157-170.	14.5	28
4	<i>ELF4</i> Is a Target of miR-124 and Promotes Neuroblastoma Proliferation and Undifferentiated State. <i>Molecular Cancer Research</i> , 2020, 18, 68-78.	3.4	14
5	The specificity of H2A.Z occupancy in the yeast genome and its relationship to transcription. <i>Current Genetics</i> , 2020, 66, 939-944.	1.7	5
6	PRC2 activates interferon-stimulated genes indirectly by repressing miRNAs in glioblastoma. <i>PLoS ONE</i> , 2019, 14, e0222435.	2.5	5
7	MicroRNAs reinforce repression of PRC2 transcriptional targets independently and through a feed-forward regulatory network. <i>Genome Research</i> , 2019, 29, 184-192.	5.5	14
8	Bivalent Chromatin Domains in Glioblastoma Reveal a Subtype-Specific Signature of Glioma Stem Cells. <i>Cancer Research</i> , 2018, 78, 2463-2474.	0.9	40
9	Detection and benchmarking of somatic mutations in cancer genomes using RNA-seq data. <i>PeerJ</i> , 2018, 6, e5362.	2.0	42
10	Identification and removal of sequencing artifacts produced by mispriming during reverse transcription in multiple RNA-seq technologies. <i>Rna</i> , 2018, 24, 1266-1274.	3.5	19
11	The ATP-dependent chromatin remodeler Chd1 is recruited by transcription elongation factors and maintains H3K4me3/H3K36me3 domains at actively transcribed and spliced genes. <i>Nucleic Acids Research</i> , 2017, 45, 7180-7190.	14.5	35
12	Ethylene induces combinatorial effects of histone H3 acetylation in gene expression in <i>Arabidopsis</i> . <i>BMC Genomics</i> , 2017, 18, 538.	2.8	51
13	The Determinants of Directionality in Transcriptional Initiation. <i>Trends in Genetics</i> , 2016, 32, 322-333.	6.7	31
14	Stem cell and neurogenic gene-expression profiles link prostate basal cells to aggressive prostate cancer. <i>Nature Communications</i> , 2016, 7, 10798.	12.8	166
15	Synthetic evolutionary origin of a proofreading reverse transcriptase. <i>Science</i> , 2016, 352, 1590-1593.	12.6	119
16	Subtype-specific addiction of the activated B-cell subset of diffuse large B-cell lymphoma to FOXP1. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, E577-E586.	7.1	36
17	MiR-191 Regulates Primary Human Fibroblast Proliferation and Directly Targets Multiple Oncogenes. <i>PLoS ONE</i> , 2015, 10, e0126535.	2.5	20
18	miR-503 represses human cell proliferation and directly targets the oncogene DDHD2 by non-canonical target pairing. <i>BMC Genomics</i> , 2015, 16, 40.	2.8	21

#	ARTICLE	IF	CITATIONS
19	Abstract 16047: Novel Association of Polymorphic Genetic Variants With Baseline PR Interval in Patients With Atrial Fibrillation: New Directions From a Prospective Study (DECAF). <i>Circulation</i> , 2015, 132, .	1.6	0
20	Chd1 co-localizes with early transcription elongation factors independently of H3K36 methylation and releases stalled RNA polymerase II at introns. <i>Epigenetics and Chromatin</i> , 2014, 7, 32.	3.9	25
21	Quantitative Genetics of CTCF Binding Reveal Local Sequence Effects and Different Modes of X-Chromosome Association. <i>PLoS Genetics</i> , 2014, 10, e1004798.	3.5	55
22	Simultaneous mapping of transcript ends at single-nucleotide resolution and identification of widespread promoter-associated non-coding RNA governed by TATA elements. <i>Nucleic Acids Research</i> , 2014, 42, 3736-3749.	14.5	93
23	Bright/Arid3A Acts as a Barrier to Somatic Cell Reprogramming through Direct Regulation of Oct4, Sox2, and Nanog. <i>Stem Cell Reports</i> , 2014, 2, 26-35.	4.8	47
24	Global Transcriptional Profiling Reveals Distinct Functions of Thymic Stromal Subsets and Age-Related Changes during Thymic Involution. <i>Cell Reports</i> , 2014, 9, 402-415.	6.4	87
25	An eQTL analysis of the human glioblastoma multiforme genome. <i>Genomics</i> , 2014, 103, 252-263.	2.9	14
26	A Mycâ€“microRNA network promotes exit from quiescence by suppressing the interferon response and cell-cycle arrest genes. <i>Nucleic Acids Research</i> , 2013, 41, 2239-2254.	14.5	49
27	Widespread Misinterpretable ChIP-seq Bias in Yeast. <i>PLoS ONE</i> , 2013, 8, e83506.	2.5	126
28	Nucleosome positioning: bringing order to the eukaryotic genome. <i>Trends in Cell Biology</i> , 2012, 22, 250-256.	7.9	50
29	High-resolution genome-wide in vivo footprinting of diverse transcription factors in human cells. <i>Genome Research</i> , 2011, 21, 456-464.	5.5	286
30	Dynamic Remodeling of Individual Nucleosomes Across a Eukaryotic Genome in Response to Transcriptional Perturbation. <i>PLoS Biology</i> , 2008, 6, e65.	5.6	353
31	Systematic profiling of cellular phenotypes and gene function using spotted cellular microarrays. <i>FASEB Journal</i> , 2006, 20, LB61.	0.5	0
32	Systematic profiling of cellular phenotypes with spotted cell microarrays reveals new mating pheromone response genes. <i>FASEB Journal</i> , 2006, 20, A928.	0.5	1
33	Exploring the post-transcriptional RNA world with DNA microarrays. <i>Trends in Biotechnology</i> , 2004, 22, 498-500.	9.3	2