

Tsun-Po Yang

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/6739173/publications.pdf>

Version: 2024-02-01

24
papers

8,423
citations

361413

20
h-index

610901

24
g-index

25
all docs

25
docs citations

25
times ranked

19485
citing authors

#	ARTICLE	IF	CITATIONS
1	Genetic variation influencing DNA methylation provides insights into molecular mechanisms regulating genomic function. <i>Nature Genetics</i> , 2022, 54, 18-29.	21.4	60
2	Characterizing genetic intra-tumor heterogeneity across 2,658 human cancer genomes. <i>Cell</i> , 2021, 184, 2239-2254.e39.	28.9	260
3	CaMuS: simultaneous fitting and de novo imputation of cancer mutational signature. <i>Scientific Reports</i> , 2020, 10, 19316.	3.3	6
4	yyIncT Defines a Class of Divergently Transcribed lncRNAs and Safeguards the T-mediated Mesodermal Commitment of Human PSCs. <i>Cell Stem Cell</i> , 2019, 24, 318-327.e8.	11.1	44
5	Copy-number analysis and inference of subclonal populations in cancer genomes using ScIust. <i>Nature Protocols</i> , 2018, 13, 1488-1501.	12.0	51
6	<i>ATM</i> Deficiency Is Associated with Sensitivity to PARP1- and ATR Inhibitors in Lung Adenocarcinoma. <i>Cancer Research</i> , 2017, 77, 3040-3056.	0.9	81
7	Epigenome-wide association study of body mass index, and the adverse outcomes of adiposity. <i>Nature</i> , 2017, 541, 81-86.	27.8	743
8	Mutational signatures in esophageal adenocarcinoma define etiologically distinct subgroups with therapeutic relevance. <i>Nature Genetics</i> , 2016, 48, 1131-1141.	21.4	332
9	The genetics of blood pressure regulation and its target organs from association studies in 342,415 individuals. <i>Nature Genetics</i> , 2016, 48, 1171-1184.	21.4	362
10	Cigarette smoking reduces DNA methylation levels at multiple genomic loci but the effect is partially reversible upon cessation. <i>Epigenetics</i> , 2014, 9, 1382-1396.	2.7	285
11	An atlas of genetic influences on human blood metabolites. <i>Nature Genetics</i> , 2014, 46, 543-550.	21.4	1,084
12	Large-scale association analysis identifies new risk loci for coronary artery disease. <i>Nature Genetics</i> , 2013, 45, 25-33.	21.4	1,439
13	Mosaic PPM1D mutations are associated with predisposition to breast and ovarian cancer. <i>Nature</i> , 2013, 493, 406-410.	27.8	218
14	Global Analysis of DNA Methylation Variation in Adipose Tissue from Twins Reveals Links to Disease-Associated Variants in Distal Regulatory Elements. <i>American Journal of Human Genetics</i> , 2013, 93, 876-890.	6.2	330
15	Epigenome-Wide Scans Identify Differentially Methylated Regions for Age and Age-Related Phenotypes in a Healthy Ageing Population. <i>PLoS Genetics</i> , 2012, 8, e1002629.	3.5	620
16	Mapping cis- and trans-regulatory effects across multiple tissues in twins. <i>Nature Genetics</i> , 2012, 44, 1084-1089.	21.4	701
17	New gene functions in megakaryopoiesis and platelet formation. <i>Nature</i> , 2011, 480, 201-208.	27.8	401
18	The Architecture of Gene Regulatory Variation across Multiple Human Tissues: The MuTHER Study. <i>PLoS Genetics</i> , 2011, 7, e1002003.	3.5	392

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19	Maps of Open Chromatin Guide the Functional Follow-Up of Genome-Wide Association Signals: Application to Hematological Traits. <i>PLoS Genetics</i> , 2011, 7, e1002139.	3.5	38
20	Genevar: a database and Java application for the analysis and visualization of SNP-gene associations in eQTL studies. <i>Bioinformatics</i> , 2010, 26, 2474-2476.	4.1	282
21	Human aging-associated DNA hypermethylation occurs preferentially at bivalent chromatin domains. <i>Genome Research</i> , 2010, 20, 434-439.	5.5	646
22	easyExon – A Java-based GUI tool for processing and visualization of Affymetrix exon array data. <i>BMC Bioinformatics</i> , 2008, 9, 432.	2.6	17
23	Signature Evaluation Tool (SET): a Java-based tool to evaluate and visualize the sample discrimination abilities of gene expression signatures. <i>BMC Bioinformatics</i> , 2008, 9, 58.	2.6	10
24	ArrayFusion: a web application for multi-dimensional analysis of CGH, SNP and microarray data. <i>Bioinformatics</i> , 2006, 22, 2697-2698.	4.1	20