Tsun-Po Yang

List of Publications by Year
in descending order

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	Large-scale association analysis identifies new risk loci for coronary artery disease. Nature Genetics, 2013, 45, 25-33.	21.4	1,439
2	An atlas of genetic influences on human blood metabolites. Nature Genetics, 2014, 46, 543-550.	21.4	1,084
3	Epigenome-wide association study of body mass index, and the adverse outcomes of adiposity. Nature, 2017, 541, 81-86.	27.8	743
4	Mapping cis- and trans-regulatory effects across multiple tissues in twins. Nature Genetics, 2012, 44, 1084-1089.	21.4	701
5	Human aging-associated DNA hypermethylation occurs preferentially at bivalent chromatin domains. Genome Research, 2010, 20, 434-439.	5.5	646
6	Epigenome-Wide Scans Identify Differentially Methylated Regions for Age and Age-Related Phenotypes in a Healthy Ageing Population. PLoS Genetics, 2012, 8, e1002629.	3.5	620
7	New gene functions in megakaryopoiesis and platelet formation. Nature, 2011, 480, 201-208.	27.8	401
8	The Architecture of Gene Regulatory Variation across Multiple Human Tissues: The MuTHER Study. PLoS Genetics, 2011, 7, e1002003.	3.5	392
9	The genetics of blood pressure regulation and its target organs from association studies in 342,415 individuals. Nature Genetics, 2016, 48, 1171-1184.	21.4	362
10	Mutational signatures in esophageal adenocarcinoma define etiologically distinct subgroups with therapeutic relevance. Nature Genetics, 2016, 48, 1131-1141.	21.4	332
11	Global Analysis of DNA Methylation Variation in Adipose Tissue from Twins Reveals Links to Disease-Associated Variants in Distal Regulatory Elements. American Journal of Human Genetics, 2013, 93, 876-890.	6.2	330
12	Cigarette smoking reduces DNA methylation levels at multiple genomic loci but the effect is partially reversible upon cessation. Epigenetics, 2014, 9, 1382-1396.	2.7	285
13	Genevar: a database and Java application for the analysis and visualization of SNP-gene associations in eQTL studies. Bioinformatics, 2010, 26, 2474-2476.	4.1	282
14	Characterizing genetic intra-tumor heterogeneity across 2,658 human cancer genomes. Cell, 2021, 184, 2239-2254.e39.	28.9	260
15	Mosaic PPM1D mutations are associated with predisposition to breast and ovarian cancer. Nature, 2013, 493, 406-410.	27.8	218
16	ATM Deficiency Is Associated with Sensitivity to PARP1- and ATR Inhibitors in Lung Adenocarcinoma. Cancer Research, 2017, 77, 3040-3056.	0.9	81
17	Genetic variation influencing DNA methylation provides insights into molecular mechanisms regulating genomic function. Nature Genetics, 2022, 54, 18-29.	21.4	60
18	Copy-number analysis and inference of subclonal populations in cancer genomes using Sclust. Nature Protocols, 2018, 13, 1488-1501.	12.0	51

#	Article	IF	Citations
19	yylncT Defines a Class of Divergently Transcribed lncRNAs and Safeguards the T-mediated Mesodermal Commitment of Human PSCs. Cell Stem Cell, 2019, 24, 318-327.e8.	11.1	44
20	Maps of Open Chromatin Guide the Functional Follow-Up of Genome-Wide Association Signals: Application to Hematological Traits. PLoS Genetics, 2011, 7, e1002139.	3.5	38
21	ArrayFusion: a web application for multi-dimensional analysis of CGH, SNP and microarray data. Bioinformatics, 2006, 22, 2697-2698.	4.1	20
22	easyExon â€“ A Java-based GUI tool for processing and visualization of Affymetrix exon array data. BMC Bioinformatics, 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. BMC Bioinformatics, 2008, 9, 58.	2.6	10
24	CaMuS: simultaneous fitting and de novo imputation of cancer mutational signature. Scientific Reports, 2020, 10, 19316.	3.3	6