Shulan Tian

List of Publications by Year
in descending order

Source: https://exaly.com/author-pdf/10729730/publications.pdf

Version: 2024-02-01

49 papers	15,772 citations	279487 23 h-index	233125 45 g-index
49 all docs	49 docs citations	49 times ranked	19755 citing authors

#	Article	IF	Citations
1	Induced Pluripotent Stem Cell Lines Derived from Human Somatic Cells. Science, 2007, 318, 1917-1920.	6.0	9,459
2	Human Induced Pluripotent Stem Cells Free of Vector and Transgene Sequences. Science, 2009, 324, 797-801.	6.0	2,167
3	Epigenomic Analysis of Multilineage Differentiation of Human Embryonic Stem Cells. Cell, 2013, 153, 1134-1148.	13.5	689
4	Whole-Genome Analysis of Histone H3 Lysine 4 and Lysine 27 Methylation in Human Embryonic Stem Cells. Cell Stem Cell, 2007, 1, 299-312.	5.2	637
5	Optic Vesicle-like Structures Derived from Human Pluripotent Stem Cells Facilitate a Customized Approach to Retinal Disease Treatment. Stem Cells, 2011, 29, 1206-1218.	1.4	413
6	Pembrolizumab in patients with CLL and Richter transformation or with relapsed CLL. Blood, 2017, 129, 3419-3427.	0.6	335
7	A Mesoderm-Derived Precursor for Mesenchymal Stem and Endothelial Cells. Cell Stem Cell, 2010, 7, 718-729.	5.2	269
8	Proteomic and phosphoproteomic comparison of human ES and iPS cells. Nature Methods, 2011, 8, 821-827.	9.0	254
9	Efficient generation of transgene-free induced pluripotent stem cells from normal and neoplastic bone marrow and cord blood mononuclear cells. Blood, 2011, 117, e109-e119.	0.6	231
10	Identification of the Hemogenic Endothelial Progenitor and Its Direct Precursor in Human Pluripotent Stem Cell Differentiation Cultures. Cell Reports, 2012, 2, 553-567.	2.9	174
11	Comparative RNA-seq Analysis in the Unsequenced Axolotl: The Oncogene Burst Highlights Early Gene Expression in the Blastema. PLoS Computational Biology, 2013, 9, e1002936.	1.5	125
12	Transcription and Histone Modifications in the Recombination-Free Region Spanning a Rice Centromere[W]. Plant Cell, 2005, 17, 3227-3238.	3.1	107
13	Genomic and Genetic Characterization of Rice Cen3 Reveals Extensive Transcription and Evolutionary Implications of a Complex Centromere. Plant Cell, 2006, 18, 2123-2133.	3.1	95
14	EBSeq-HMM: a Bayesian approach for identifying gene-expression changes in ordered RNA-seq experiments. Bioinformatics, 2015, 31, 2614-2622.	1.8	93
15	Genome-wide analyses as part of the international FTLD-TDP whole-genome sequencing consortium reveals novel disease risk factors and increases support for immune dysfunction in FTLD. Acta Neuropathologica, 2019, 137, 879-899.	3.9	90
16	PRC2 specifies ectoderm lineages and maintains pluripotency in primed but not naÃ¯ve ESCs. Nature Communications, 2017, 8, 672.	5.8	87
17	PARP Inhibitors for Sensitization of Alkylation Chemotherapy in Glioblastoma: Impact of Blood-Brain Barrier and Molecular Heterogeneity. Frontiers in Oncology, 2018, 8, 670.	1.3	60
18	Recurrent MSCE116K mutations in ALK-negative anaplastic large cell lymphoma. Blood, 2019, 133, 2776-2789.	0.6	55

#	Article	IF	Citations
19	PD-1 Expression in Chronic Lymphocytic Leukemia/Small Lymphocytic Lymphoma (CLL/SLL) and Large B-cell Richter Transformation (DLBCL-RT). American Journal of Surgical Pathology, 2018, 42, 843-854.	2.1	54
20	Extensive transcriptomic study emphasizes importance of vesicular transport in C9orf72 expansion carriers. Acta Neuropathologica Communications, 2019, 7, 150.	2.4	40
21	A study of the relationships between oligonucleotide properties and hybridization signal intensities from NimbleGen microarray datasets. Nucleic Acids Research, 2008, 36, 2926-2938.	6.5	38
22	Heterogeneous delivery across the blood-brain barrier limits the efficacy of an EGFR-targeting antibody drug conjugate in glioblastoma. Neuro-Oncology, 2021, 23, 2042-2053.	0.6	37
23	Impact of post-alignment processing in variant discovery from whole exome data. BMC Bioinformatics, 2016, 17, 403.	1.2	28
24	HLA class-I and class-II restricted neoantigen loads predict overall survival in breast cancer. OncoImmunology, 2020, 9, 1744947.	2.1	26
25	Genome-Wide Epigenetic Studies in Human Disease: A Primer on -Omic Technologies. American Journal of Epidemiology, 2016, 183, kwv187.	1.6	23
26	An analytical workflow for accurate variant discovery in highly divergent regions. BMC Genomics, 2016, 17, 703.	1.2	22
27	ChIP-seq in studying epigenetic mechanisms of disease and promoting precision medicine: progresses and future directions. Epigenomics, 2016, 8, 1239-1258.	1.0	22
28	â€œDirect to Drugâ€•screening as a precision medicine tool in multiple myeloma. Blood Cancer Journal, 2020, 10, 54.	2.8	20
29	Tumor mutational load predicts time to first treatment in chronic lymphocytic leukemia (CLL) and monoclonal Bâ€cell lymphocytosis beyond the CLL international prognostic index. American Journal of Hematology, 2020, 95, 906-917.	2.0	17
30	Comprehensive Platelet Phenotypic Laboratory Testing and Bleeding History Scoring for Diagnosis of Suspected Hereditary Platelet Disorders. American Journal of Clinical Pathology, 2017, 148, 23-32.	0.4	16
31	Comparative analysis of de novo assemblers for variation discovery in personal genomes. Briefings in Bioinformatics, 2018, 19, 893-904.	3.2	14
32	Automated applicator digitization for high-dose-rate cervix brachytherapy using image thresholding and density-based clustering. Brachytherapy, 2020, 19, 111-118.	0.2	11
33	Identification of missing variants by combining multiple analytic pipelines. BMC Bioinformatics, 2018, 19, 139.	1.2	10
34	Genetic variants related to successful migraine prophylaxis with verapamil. Molecular Genetics & Genomic Medicine, 2021, 9, e1680.	0.6	8
35	Loss-of-function of DELLA protein SLN1 activates GA signaling in barley aleurone. Acta Physiologiae Plantarum, 2010, 32, 789-800.	1.0	7
36	Conserved Transcriptional Regulatory Programs Underlying Rice and Barley Germination. PLoS ONE, 2014, 9, e87261.	1.1	6

#	Article	IF	Citations
37	Identification of factors associated with duplicate rate in ChIP-seq data. PLoS ONE, 2019, 14, e0214723.	1.1	6
38	Chronic lymphocytic leukemia (CLL) risk is mediated by multiple enhancer variants within CLL risk loci. Human Molecular Genetics, 2020, 29, 2761-2774.	1.4	6
39	RBBP4-p300 axis modulates expression of genes essential for cell survival and is a potential target for therapy in glioblastoma. Neuro-Oncology, 2022, 24, 1261-1272.	0.6	6
40	Shared brain transcriptomic signature in TDP-43 type A FTLD patients with or without GRN mutations. Brain, 2022, 145, 2472-2485.	3.7	6
41	Epigenetic alteration contributes to the transcriptional reprogramming in T-cell prolymphocytic leukemia. Scientific Reports, 2021, 11, 8318.	1.6	3
42	Differential transcriptomic profiling in ibrutinibâ€naÃ¯ve versus ibrutinibâ€resistant Richter syndrome. Hematological Oncology, 2022, 40, 302-306.	0.8	2
43	Analyses of Genome-Wide Histone Modifications in the Mammalian Genome. , 2017, , 135-152.		1
44	Pathogenic Germ Line Variants in a Patient With Severe Toxicity From Breast Radiotherapy. Clinical Breast Cancer, 2019, 19, e400-e405.	1.1	1
45	Distinct Gene Expression Signatures in Patients with Richter's Syndrome and Chronic Lymphocytic Leukemia with Prior Exposure to Ibrutinib. Blood, 2020, 136, 30-31.	0.6	1
46	Genomic Profiling Reveals Molecular Heterogeneity in Patients with Richter's Syndrome (RS) and Progressive Chronic Lymphocytic Leukemia (CLL). Blood, 2020, 136, 16-17.	0.6	1
47	Identification of Hemogenic Endothelium and Its Direct Precursor in Human Embryonic Stem Cell Differentiation Cultures. Blood, 2011, 118, 1277-1277.	0.6	0
48	Identification of a Novel Role for PD-1 Signaling in Promotion Tumor Proliferation in B-Cell Lymphoma. Blood, 2020, 136, 10-12.	0.6	0
49	Editorial: Clinical Genome Sequencing: Bioinformatics Challenges and Key Considerations. Frontiers in Genetics, 2022, 13, 896032.	1.1	0