

Shulan Tian

List of Publications by Year in descending order

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Version: 2024-02-01

49
papers

15,772
citations

279487

23
h-index

233125

45
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49
all docs

49
docs citations

49
times ranked

19755
citing authors

| # | ARTICLE | IF | CITATIONS |
|----|--|-----|-----------|
| 1 | Differential transcriptomic profiling in ibrutinib-sensitive versus ibrutinib-resistant Richter syndrome. <i>Hematological Oncology</i> , 2022, 40, 302-306. | 0.8 | 2 |
| 2 | RBBP4-p300 axis modulates expression of genes essential for cell survival and is a potential target for therapy in glioblastoma. <i>Neuro-Oncology</i> , 2022, 24, 1261-1272. | 0.6 | 6 |
| 3 | Editorial: Clinical Genome Sequencing: Bioinformatics Challenges and Key Considerations. <i>Frontiers in Genetics</i> , 2022, 13, 896032. | 1.1 | 0 |
| 4 | Shared brain transcriptomic signature in TDP-43 type A FTLD patients with or without <i>GRN</i> mutations. <i>Brain</i> , 2022, 145, 2472-2485. | 3.7 | 6 |
| 5 | Epigenetic alteration contributes to the transcriptional reprogramming in T-cell prolymphocytic leukemia. <i>Scientific Reports</i> , 2021, 11, 8318. | 1.6 | 3 |
| 6 | Genetic variants related to successful migraine prophylaxis with verapamil. <i>Molecular Genetics & Genomic Medicine</i> , 2021, 9, e1680. | 0.6 | 8 |
| 7 | Heterogeneous delivery across the blood-brain barrier limits the efficacy of an EGFR-targeting antibody drug conjugate in glioblastoma. <i>Neuro-Oncology</i> , 2021, 23, 2042-2053. | 0.6 | 37 |
| 8 | Automated applicator digitization for high-dose-rate cervix brachytherapy using image thresholding and density-based clustering. <i>Brachytherapy</i> , 2020, 19, 111-118. | 0.2 | 11 |
| 9 | Chronic lymphocytic leukemia (CLL) risk is mediated by multiple enhancer variants within CLL risk loci. <i>Human Molecular Genetics</i> , 2020, 29, 2761-2774. | 1.4 | 6 |
| 10 | Direct to Drug screening as a precision medicine tool in multiple myeloma. <i>Blood Cancer Journal</i> , 2020, 10, 54. | 2.8 | 20 |
| 11 | Tumor mutational load predicts time to first treatment in chronic lymphocytic leukemia (CLL) and monoclonal B-cell lymphocytosis beyond the CLL international prognostic index. <i>American Journal of Hematology</i> , 2020, 95, 906-917. | 2.0 | 17 |
| 12 | HLA class-I and class-II restricted neoantigen loads predict overall survival in breast cancer. <i>Oncolmmunology</i> , 2020, 9, 1744947. | 2.1 | 26 |
| 13 | Identification of a Novel Role for PD-1 Signaling in Promotion Tumor Proliferation in B-Cell Lymphoma. <i>Blood</i> , 2020, 136, 10-12. | 0.6 | 0 |
| 14 | Distinct Gene Expression Signatures in Patients with Richter's Syndrome and Chronic Lymphocytic Leukemia with Prior Exposure to Ibrutinib. <i>Blood</i> , 2020, 136, 30-31. | 0.6 | 1 |
| 15 | Genomic Profiling Reveals Molecular Heterogeneity in Patients with Richter's Syndrome (RS) and Progressive Chronic Lymphocytic Leukemia (CLL). <i>Blood</i> , 2020, 136, 16-17. | 0.6 | 1 |
| 16 | Extensive transcriptomic study emphasizes importance of vesicular transport in C9orf72 expansion carriers. <i>Acta Neuropathologica Communications</i> , 2019, 7, 150. | 2.4 | 40 |
| 17 | Recurrent MSCE116K mutations in ALK-negative anaplastic large cell lymphoma. <i>Blood</i> , 2019, 133, 2776-2789. | 0.6 | 55 |
| 18 | Pathogenic Germ Line Variants in a Patient With Severe Toxicity From Breast Radiotherapy. <i>Clinical Breast Cancer</i> , 2019, 19, e400-e405. | 1.1 | 1 |

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|----|---|------|-----------|
| 19 | Identification of factors associated with duplicate rate in ChIP-seq data. PLoS ONE, 2019, 14, e0214723. | 1.1 | 6 |
| 20 | 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 |
| 21 | Comparative analysis of de novo assemblers for variation discovery in personal genomes. Briefings in Bioinformatics, 2018, 19, 893-904. | 3.2 | 14 |
| 22 | 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 |
| 23 | Identification of missing variants by combining multiple analytic pipelines. BMC Bioinformatics, 2018, 19, 139. | 1.2 | 10 |
| 24 | PARP Inhibitors for Sensitization of Alkylating Chemotherapy in Glioblastoma: Impact of Blood-Brain Barrier and Molecular Heterogeneity. Frontiers in Oncology, 2018, 8, 670. | 1.3 | 60 |
| 25 | Pembrolizumab in patients with CLL and Richter transformation or with relapsed CLL. Blood, 2017, 129, 3419-3427. | 0.6 | 335 |
| 26 | 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 |
| 27 | PRC2 specifies ectoderm lineages and maintains pluripotency in primed but not naïve ESCs. Nature Communications, 2017, 8, 672. | 5.8 | 87 |
| 28 | Analyses of Genome-Wide Histone Modifications in the Mammalian Genome. , 2017, , 135-152. | | 1 |
| 29 | Genome-Wide Epigenetic Studies in Human Disease: A Primer on -Omic Technologies. American Journal of Epidemiology, 2016, 183, kww187. | 1.6 | 23 |
| 30 | An analytical workflow for accurate variant discovery in highly divergent regions. BMC Genomics, 2016, 17, 703. | 1.2 | 22 |
| 31 | Impact of post-alignment processing in variant discovery from whole exome data. BMC Bioinformatics, 2016, 17, 403. | 1.2 | 28 |
| 32 | ChIP-seq in studying epigenetic mechanisms of disease and promoting precision medicine: progresses and future directions. Epigenomics, 2016, 8, 1239-1258. | 1.0 | 22 |
| 33 | EBSeq-HMM: a Bayesian approach for identifying gene-expression changes in ordered RNA-seq experiments. Bioinformatics, 2015, 31, 2614-2622. | 1.8 | 93 |
| 34 | Conserved Transcriptional Regulatory Programs Underlying Rice and Barley Germination. PLoS ONE, 2014, 9, e87261. | 1.1 | 6 |
| 35 | Epigenomic Analysis of Multilineage Differentiation of Human Embryonic Stem Cells. Cell, 2013, 153, 1134-1148. | 13.5 | 689 |
| 36 | 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 |

| # | ARTICLE | IF | CITATIONS |
|----|---|-----|-----------|
| 37 | Identification of the Hemogenic Endothelial Progenitor and Its Direct Precursor in Human Pluripotent Stem Cell Differentiation Cultures. <i>Cell Reports</i> , 2012, 2, 553-567. | 2.9 | 174 |
| 38 | Proteomic and phosphoproteomic comparison of human ES and iPS cells. <i>Nature Methods</i> , 2011, 8, 821-827. | 9.0 | 254 |
| 39 | Optic Vesicle-like Structures Derived from Human Pluripotent Stem Cells Facilitate a Customized Approach to Retinal Disease Treatment. <i>Stem Cells</i> , 2011, 29, 1206-1218. | 1.4 | 413 |
| 40 | Efficient generation of transgene-free induced pluripotent stem cells from normal and neoplastic bone marrow and cord blood mononuclear cells. <i>Blood</i> , 2011, 117, e109-e119. | 0.6 | 231 |
| 41 | Identification of Hemogenic Endothelium and Its Direct Precursor in Human Embryonic Stem Cell Differentiation Cultures. <i>Blood</i> , 2011, 118, 1277-1277. | 0.6 | 0 |
| 42 | Loss-of-function of DELLA protein SLN1 activates GA signaling in barley aleurone. <i>Acta Physiologiae Plantarum</i> , 2010, 32, 789-800. | 1.0 | 7 |
| 43 | A Mesoderm-Derived Precursor for Mesenchymal Stem and Endothelial Cells. <i>Cell Stem Cell</i> , 2010, 7, 718-729. | 5.2 | 269 |
| 44 | Human Induced Pluripotent Stem Cells Free of Vector and Transgene Sequences. <i>Science</i> , 2009, 324, 797-801. | 6.0 | 2,167 |
| 45 | A study of the relationships between oligonucleotide properties and hybridization signal intensities from NimbleGen microarray datasets. <i>Nucleic Acids Research</i> , 2008, 36, 2926-2938. | 6.5 | 38 |
| 46 | Whole-Genome Analysis of Histone H3 Lysine 4 and Lysine 27 Methylation in Human Embryonic Stem Cells. <i>Cell Stem Cell</i> , 2007, 1, 299-312. | 5.2 | 637 |
| 47 | Induced Pluripotent Stem Cell Lines Derived from Human Somatic Cells. <i>Science</i> , 2007, 318, 1917-1920. | 6.0 | 9,459 |
| 48 | Genomic and Genetic Characterization of Rice Cen3 Reveals Extensive Transcription and Evolutionary Implications of a Complex Centromere. <i>Plant Cell</i> , 2006, 18, 2123-2133. | 3.1 | 95 |
| 49 | Transcription and Histone Modifications in the Recombination-Free Region Spanning a Rice Centromere[W]. <i>Plant Cell</i> , 2005, 17, 3227-3238. | 3.1 | 107 |