# Lifeng Tian

## List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/8081558/publications.pdf

Version: 2024-02-01

| | | 516710 | 265206 |
|---|---|---|---|
| 47 | 1,931 | 16 | 42 |
| papers | citations | h-index | g-index |

| | | | |
|---|---|---|---|
| 51 | 51 | 51 | 5034 |
| all docs | docs citations | times ranked | citing authors |

| # | Article | IF | Citations |
|---|---|---|---|
| 1 | Application of deep learning algorithm on whole genome sequencing data uncovers structural variants associated with multiple mental disorders in African American patients. Molecular Psychiatry, 2022, 27, 1469-1478. | 7.9 | 13 |
| 2 | Expansion of Schizophrenia Gene Network Knowledge Using Machine Learning Selected Signals From Dorsolateral Prefrontal Cortex and Amygdala RNA-seq Data. Frontiers in Psychiatry, 2022, 13, 797329. | 2.6 | 9 |
| 3 | Burden of rare coding variants reveals genetic heterogeneity between obese and non-obese asthma patients in the African American population. Respiratory Research, 2022, 23, 116. | 3.6 | 1 |
| 4 | Mutation burden analysis of six common mental disorders in African Americans by whole genome sequencing. Human Molecular Genetics, 2022, 31, 3769-3776. | 2.9 | 4 |
| 5 | Association of DLL1 with type 1 diabetes in patients characterized by low polygenic risk score. Metabolism: Clinical and Experimental, 2021, 114, 154418. | 3.4 | 6 |
| 6 | <i>FLNC</i> and <i>MYLK2</i> Gene Mutations in a Chinese Family with Different Phenotypes of Cardiomyopathy. International Heart Journal, 2021, 62, 127-134. | 1.0 | 6 |
| 7 | Rare Recurrent Variants in Noncoding Regions Impact Attention-Deficit Hyperactivity Disorder (ADHD) Gene Networks in Children of both African American and European American Ancestry. Genes, 2021, 12, 310. | 2.4 | 10 |
| 8 | Machine Learning Reduced Gene/Non-Coding RNA Features That Classify Schizophrenia Patients Accurately and Highlight Insightful Gene Clusters. International Journal of Molecular Sciences, 2021, 22, 3364. | 4.1 | 4 |
| 9 | Serum levels of the IgA isotype switch factor TGFâ€Î²1 are elevated in patients with COVIDâ€19. FEBS Letters, 2021, 595, 1819-1824. | 2.8 | 16 |
| 10 | Deep learning prediction of attention-deficit hyperactivity disorder in African Americans by copy number variation. Experimental Biology and Medicine, 2021, 246, 2317-2323. | 2.4 | 8 |
| 11 | Insights into non-autoimmune type 1 diabetes with 13 novel loci in low polygenic risk score patients. Scientific Reports, 2021, 11, 16013. | 3.3 | 7 |
| 12 | Expression Pattern of the SARS-CoV-2 Entry Genes ACE2 and TMPRSS2 in the Respiratory Tract. Viruses, 2020, 12, 1174. | 3.3 | 27 |
| 13 | High prevalence of elevated serum liver enzymes in Chinese children suggests metabolic syndrome as a common risk factor. Journal of Paediatrics and Child Health, 2020, 56, 1590-1596. | 0.8 | 1 |
| 14 | Non-coding structural variation differentially impacts attention-deficit hyperactivity disorder (ADHD) gene networks in African American vs Caucasian children. Scientific Reports, 2020, 10, 15252. | 3.3 | 5 |
| 15 | COVID-19: Look to the Future, Learn from the Past. Viruses, 2020, 12, 1226. | 3.3 | 8 |
| 16 | Role of the ADCY9 gene in cardiac abnormalities of the Rubinstein-Taybi syndrome. Orphanet Journal of Rare Diseases, 2020, 15, 101. | 2.7 | 2 |
| 17 | The Infection Rate of COVID-19 in Wuhan, China: Combined Analysis of Population Samples. Journal of Medical Internet Research, 2020, 22, e20914. | 4.3 | 2 |
| 18 | Interpretation of Maturity-Onset Diabetes of the Young Genetic Variants Based on American College of Medical Genetics and Genomics Criteria: Machine-Learning Model Development. JMIR Biomedical Engineering, 2020, 5, e20506. | 1.2 | 2 |

| # | Article | IF | Citations |
|---|---|---|---|
| 19 | ARAF recurrent mutation causes central conducting lymphatic anomaly treatable with a MEK inhibitor. Nature Medicine, 2019, 25, 1116-1122. | 30.7 | 136 |
| 20 | Application of ACMG criteria to classify variants in the human gene mutation database. Journal of Human Genetics, 2019, 64, 1091-1095. | 2.3 | 10 |
| 21 | Association of Rare Recurrent Copy Number Variants With Congenital Heart Defects Based on Next-Generation Sequencing Data From Family Trios. Frontiers in Genetics, 2019, 10, 819. | 2.3 | 15 |
| 22 | Expanding the Genetic Landscape of Usher-Like Phenotypes. , 2019, 60, 4701. | | 9 |
| 23 | Combining targeted panel-based resequencing and copy-number variation analysis for the diagnosis of inherited syndromic retinopathies and associated ciliopathies. Scientific Reports, 2018, 8, 5285. | 3.3 | 28 |
| 24 | Heterozygous Deletion Impacting SMARCAD1 in the Original Kindred with Absent Dermatoglyphs and Associated Features (Baird, 1964). Journal of Pediatrics, 2018, 194, 248-252.e2. | 1.8 | 6 |
| 25 | Bayesian analysis of genome-wide inflammatory bowel disease data sets reveals new risk loci. European Journal of Human Genetics, 2018, 26, 265-274. | 2.8 | 17 |
| 26 | Pathogenic variant in EPHB4 results in central conducting lymphatic anomaly. Human Molecular Genetics, 2018, 27, 3233-3245. | 2.9 | 73 |
| 27 | Increasing diagnostic yield by RNA-Sequencing in rare diseaseâ€"bypass hurdles of interpreting intronic or splice-altering variants. Annals of Translational Medicine, 2018, 6, 126-126. | 1.7 | 9 |
| 28 | Loss-of-Function Mutations in KIF15 Underlying a Braddock-Carey Genocopy. Human Mutation, 2017, 38, 507-510. | 2.5 | 8 |
| 29 | A genome-wide association study of anorexia nervosa suggests a risk locus implicated in dysregulated leptin signaling. Scientific Reports, 2017, 7, 3847. | 3.3 | 23 |
| 30 | Exome Sequencing Reveals Mutations in AIRE as a Cause of Isolated Hypoparathyroidism. Journal of Clinical Endocrinology and Metabolism, 2017, 102, 1726-1733. | 3.6 | 35 |
| 31 | Early Infantile Epileptic Encephalopathy in anSTXBP1Patient with Lactic Acidemia and Normal Mitochondrial Respiratory Chain Function. Case Reports in Genetics, 2016, 2016, 1-5. | 0.2 | 6 |
| 32 | Association of a rare NOTCH4 coding variant with systemic sclerosis: a family-based whole exome sequencing study. BMC Musculoskeletal Disorders, 2016, 17, 462. | 1.9 | 12 |
| 33 | Mutation in IRF2BP2 is responsible for a familial form of common variable immunodeficiency disorder. Journal of Allergy and Clinical Immunology, 2016, 138, 544-550.e4. | 2.9 | 54 |
| 34 | Analysis of 589,306 genomes identifies individuals resilient to severe Mendelian childhood diseases. Nature Biotechnology, 2016, 34, 531-538. | 17.5 | 273 |
| 35 | GRIN2D Recurrent De Novo Dominant Mutation Causes a Severe Epileptic Encephalopathy Treatable with NMDA Receptor Channel Blockers. American Journal of Human Genetics, 2016, 99, 802-816. | 6.2 | 138 |
| 36 | An integrative approach to investigate the respective roles of single-nucleotide variants and copy-number variants in Attention-Deficit/Hyperactivity Disorder. Scientific Reports, 2016, 6, 22851. | 3.3 | 18 |

| # | Article | IF | Citations |
|---|---|---|---|
| 37 | Expanding the SPECC1L mutation phenotypic spectrum to include Teebi hypertelorism syndrome. American Journal of Medical Genetics, Part A, 2015, 167, 2497-2502. | 1.2 | 26 |
| 38 | Delayed diagnosis of congenital myasthenia due to associated mitochondrial enzyme defect. Neuromuscular Disorders, 2015, 25, 257-261. | 0.6 | 16 |
| 39 | Transcriptome of the human retina, retinal pigmented epithelium and choroid. Genomics, 2015, 105, 253-264. | 2.9 | 71 |
| 40 | Advantage of Whole Exome Sequencing over Allele-Specific and Targeted Segment Sequencing in Detection of NovelTULP1Mutation in Leber Congenital Amaurosis. Ophthalmic Genetics, 2015, 36, 333-338. | 1.2 | 12 |
| 41 | An atypical form of AOA2 with myoclonus associated with mutations in SETX and AFG3L2. BMC Medical Genetics, 2015, 16, 16. | 2.1 | 12 |
| 42 | Genetic predisposition to neuroblastoma mediated by a LMO1 super-enhancer polymorphism. Nature, 2015, 528, 418-421. | 27.8 | 263 |
| 43 | Application of Whole Exome Sequencing in Six Families with an Initial Diagnosis of Autosomal Dominant Retinitis Pigmentosa: Lessons Learned. PLoS ONE, 2015, 10, e0133624. | 2.5 | 19 |
| 44 | Expanding the phenotype of PRPS1 syndromes in females: neuropathy, hearing loss and retinopathy. Orphanet Journal of Rare Diseases, 2014, 9, 190. | 2.7 | 31 |
| 45 | Inherited bone marrow failure associated with germline mutation of ACD, the gene encoding telomere protein TPP1. Blood, 2014, 124, 2767-2774. | 1.4 | 97 |
| 46 | An Acquired Mutation in Deubiquitinating Enzyme USP11 Associated with Clonal Hematopoiesis in Diamond Blackfan Anemia. Blood, 2014, 124, 1596-1596. | 1.4 | 0 |
| 47 | Low concordance of multiple variant-calling pipelines: practical implications for exome and genome sequencing. Genome Medicine, 2013, 5, 28. | 8.2 | 381 |