## Li-Li Tang

## List of Publications by Year in descending order

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1307594 752698 23 424 7 20 citations g-index h-index papers 23 23 23 978 citing authors all docs docs citations times ranked

#	Article	IF	CITATIONS
1	Deep sequencing of the MHC region in the Chinese population contributes to studies of complex disease. Nature Genetics, 2016, 48, 740-746.	21.4	188
2	Universal Stem-Loop Primer Method for Screening and Quantification of MicroRNA. PLoS ONE, 2014, 9, e115293.	2.5	63
3	Inflammasomes in Common Immune-Related Skin Diseases. Frontiers in Immunology, 2020, 11, 882.	4.8	50
4	$\hat{l}\pm$ -Solanine inhibits vascular endothelial growth factor expression by down-regulating the ERK1/2-HIF-1 $\hat{l}\pm$ and STAT3 signaling pathways. European Journal of Pharmacology, 2016, 771, 93-98.	<b>3.</b> 5	26
5	Integrative methylome and transcriptome analysis to dissect key biological pathways for psoriasis in Chinese Han population. Journal of Dermatological Science, 2018, 91, 285-291.	1.9	20
6	Identification of a Novel Mutation in SASH1 Gene in a Chinese Family With Dyschromatosis Universalis Hereditaria and Genotype-Phenotype Correlation Analysis. Frontiers in Genetics, 2020, 11, 841.	2.3	9
7	Assay for Transposase-Accessible Chromatin Using Sequencing Analysis Reveals a Widespread Increase in Chromatin Accessibility in Psoriasis. Journal of Investigative Dermatology, 2021, 141, 1745-1753.	0.7	8
8	<i>CYP2S1</i> might regulate proliferation and immune response of keratinocyte in psoriasis. Epigenetics, 2021, 16, 618-628.	2.7	7
9	Novel Mutation of the <i>NCSTN</i> Gene Identified in a Chinese Acne Inversa Family. Annals of Dermatology, 2020, 32, 237.	0.9	7
10	Chromatin accessibility and transcriptome integrative analysis revealed AP-1-mediated genes potentially modulate histopathology features in psoriasis. Clinical Epigenetics, 2022, 14, 38.	4.1	6
11	Genotype combination contributes to psoriasis: An exhaustive algorithm perspective. PLoS ONE, 2017, 12, e0186067.	2.5	5
12	Novel mutations in Chinese Han patients with tuberous sclerosis complex: Case series and review of the published work. Journal of Dermatology, 2018, 45, 867-870.	1.2	5
13	Genetic Analysis of KRT9 Gene Revealed Previously Known Mutations and Genotype-Phenotype Correlations in Epidermolytic Palmoplantar Keratoderma. Frontiers in Genetics, 2018, 9, 645.	2.3	5
14	Rare mutations in NLRP3 and NLRP12 associated with familial cold autoinflammatory syndrome: two Chinese pedigrees. Clinical Rheumatology, $0$ , , .	2.2	5
15	Novel compound heterozygous variants in the <i>XPC</i> gene identified in a Chinese xeroderma pigmentosum group C patient with ovarian teratoma. Journal of Dermatology, 2018, 45, e300-e301.	1.2	4
16	A KRT16 mutation in the first Chinese pedigree with Pachyonychia congenita and review of the literatures. Journal of Cosmetic Dermatology, 2019, 18, 1930-1934.	1.6	4
17	DNA methylation profile of psoriatic skins from different body locations. Epigenomics, 2019, 11, 1613-1625.	2.1	3
18	A novel mutation of COL7A1 in a Chinese DEBâ€Pt family and review of the literature. Journal of Cosmetic Dermatology, 2020, 19, 1508-1512.	1.6	3

#	Article	IF	CITATIONS
19	The progression of the tubulointerstitial fibrosis driven by stress-induced "proliferation–death― vicious circle. Medical Hypotheses, 2014, 82, 643-647.	1.5	2
20	Case Report: Chanarin-Dorfman Syndrome: A Novel Homozygous Mutation in ABHD5 Gene in a Chinese Case and Genotype-Phenotype Correlation Analysis. Frontiers in Genetics, 2022, 13, 847321.	2.3	2
21	Annular epidermolytic ichthyosis with palmoplantar keratosis: a unique phenotype associated with interfamilial phenotypic heterogeneity. European Journal of Dermatology, 2020, 30, 294-299.	0.6	1
22	Genomic DNA methylation in HLA-Cw*0602 carriers and non-carriers of psoriasis. Journal of Dermatological Science, 2020, 99, 23-29.	1.9	1
23	Changes of Regulatory T Cells in the Early Stage of Obesity Mice and Their Modulation on Macrophage Subtypes in Visceral Adipose Tissue. Zhongguo Yi Xue Ke Xue Yuan Xue Bao Acta Academiae Medicinae Sinicae, 2016, 38, 399-403.	0.2	0