Sijia Wang

List of Publications by Year
in descending order

38 papers	1,131 citations	471509 17 h-index	434195 31 g-index
38 all docs	38 docs citations	38 times ranked	1932 citing authors

#	Article	IF	Citations
1	A Genome-Wide Scan on Individual Typology Angle Found Variants at SLC24A2 Associated with Skin Color Variation in Chinese Populations. Journal of Investigative Dermatology, 2022, 142, 1223-1227.e14.	0.7	6
2	Limb development genes underlie variation in human fingerprint patterns. Cell, 2022, 185, 95-112.e18.	28.9	30
3	NAFLD-related gene polymorphisms and all-cause and cause-specific mortality in an Asian population: the Shanghai Changfeng Study. Alimentary Pharmacology and Therapeutics, 2022, 55, 705-721.	3.7	17
4	From musk to body odor: Decoding olfaction through genetic variation. PLoS Genetics, 2022, 18, e1009564.	3.5	5
5	Genetic evidence for facial variation being a composite phenotype of cranial variation and facial soft tissue thickness. Journal of Genetics and Genomics, 2022, , .	3.9	2
6	BMP4 Exerts Anti-Neurogenic Effect via Inducing Id3 during Aging. Biomedicines, 2022, 10, 1147.	3.2	1
7	Single-cell transcriptomics reveals lineage trajectory of human scalp hair follicle and informs mechanisms of hair graying. Cell Discovery, 2022, 8, .	6.7	11
8	A genome-wide association study of facial morphology identifies novel genetic loci in Han Chinese. Journal of Genetics and Genomics, 2021, 48, 198-207.	3.9	8
9	Dissecting dynamics and differences of selective pressures in the evolution of human pigmentation. Biology Open, 2021, 10, .	1.2	4
10	A custom-designed panel sequencing study in 201 Chinese patients with craniosynostosis revealed novel variants and distinct mutation spectra. Journal of Genetics and Genomics, 2021, 48, 167-171.	3.9	3
11	hReg-CNCC reconstructs a regulatory network in human cranial neural crest cells and annotates variants in a developmental context. Communications Biology, 2021, 4, 442.	4.4	10
12	Insights into contribution of genetic variants towards the susceptibility of MAFLD revealed by the NMR-based lipoprotein profiling. Journal of Hepatology, 2021, 74, 974-977.	3.7	26
13	A Genome-Wide Association Study Finds Variants at 2p21 Associated with Self-Reported Sensitive Skin in the Han Chinese population. Journal of Investigative Dermatology, 2021, , .	0.7	1
14	Genetically predicted body composition in relation to cardiometabolic traits: a Mendelian randomization study. European Journal of Epidemiology, 2021, 36, 1157-1168.	5.7	12
15	Analysis of factors influencing patch test reactions: Results from a large-population-based study in Chinese. Journal of Cosmetic Dermatology, 2021, , .	1.6	2
16	Analysis of factors influencing skin reactions to sunscreens, skin whitening products, and deodorants: Results from a large-scale patch test dataset in China. Journal of Cosmetic Dermatology, 2021, , .	1.6	0
17	A cell-type deconvolution meta-analysis of whole blood EWAS reveals lineage-specific smoking-associated DNA methylation changes. Nature Communications, 2020, 11, 4779.	12.8	32
18	Type 2 Diabetes Is Causally Associated With Reduced Serum Osteocalcin: A Genomewide Association and Mendelian Randomization Study. Journal of Bone and Mineral Research, 2020, 36, 1694-1707.	2.8	23

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19	Genome-wide scan identified genetic variants associated with skin aging in a Chinese female population. Journal of Dermatological Science, 2019, 96, 42-49.	1.9	21
20	Novel genetic loci affecting facial shape variation in humans. ELife, 2019, 8, .	6.0	58
21	Meta-analysis of genome-wide association studies identifies 8 novel loci involved in shape variation of human head hair. Human Molecular Genetics, 2018, 27, 559-575.	2.9	51
22	A metagenomic approach to dissect the genetic composition of enterotypes in Han Chinese and two Muslim groups. Systematic and Applied Microbiology, 2018, 41, 1-12.	2.8	24
23	Understudied Skin Characteristics Awaiting Genetic Breakthroughs. Journal of Investigative Dermatology Symposium Proceedings, 2018, 19, S101-S102.	0.8	1
24	Genome-wide association studies and CRISPR/Cas9-mediated gene editing identify regulatory variants influencing eyebrow thickness in humans. PLoS Genetics, 2018, 14, e1007640.	3.5	20
25	Towards broadening Forensic DNA Phenotyping beyond pigmentation: Improving the prediction of head hair shape from DNA. Forensic Science International: Genetics, 2018, 37, 241-251.	3.1	38
26	Genome-wide variants of Eurasian facial shape differentiation and a prospective model of DNA based face prediction. Journal of Genetics and Genomics, 2018, 45, 419-432.	3.9	38
27	Genetic History of Xinjiang's Uyghurs Suggests Bronze Age Multiple-Way Contacts in Eurasia. Molecular Biology and Evolution, 2017, 34, 2572-2582.	8.9	63
28	Genetic variants associated with skin aging in the Chinese Han population. Journal of Dermatological Science, 2017, 86, 21-29.	1.9	25
29	A Genome-Wide Association Study of Basal Transepidermal Water Loss Finds that Variants at 9q34.3 Are Associated with Skin Barrier Function. Journal of Investigative Dermatology, 2017, 137, 979-982.	0.7	8
30	Multiethnic GWAS Reveals Polygenic Architecture of Earlobe Attachment. American Journal of Human Genetics, 2017, 101, 913-924.	6.2	29
31	Ancestry variation and footprints of natural selection along the genome in Latin American populations. Scientific Reports, 2016, 6, 21766.	3.3	29
32	Large-scale genome-wide scans do not support petaloid toenail as a Mendelian trait. Journal of Genetics and Genomics, 2016, 43, 702-704.	3.9	2
33	EDARV370A associated facial characteristics in Uyghur population revealing further pleiotropic effects. Human Genetics, 2016, 135, 99-108.	3.8	23
34	Genome-wide scans reveal variants at EDAR predominantly affecting hair straightness in Han Chinese and Uyghur populations. Human Genetics, 2016, 135, 1279-1286.	3.8	27
35	Traffic-Related Air Pollution Contributes to Development of Facial Lentigines: Further Epidemiological Evidence from Caucasians and Asians. Journal of Investigative Dermatology, 2016, 136, 1053-1056.	0.7	94
36	A 3.4-kb Copy-Number Deletion near EPAS1 Is Significantly Enriched in High-Altitude Tibetans but Absent from the Denisovan Sequence. American Journal of Human Genetics, 2015, 97, 54-66.	6.2	69

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37	The adaptive variant EDARV370A is associated with straight hair in East Asians. Human Genetics, 2013, 132, 1187-1191.	3.8	68
38	Modeling Recent Human Evolution in Mice by Expression of a Selected EDAR Variant. Cell, 2013, 152, 691-702.	28.9	250