

Sijia Wang

List of Publications by Year in descending order

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Version: 2024-02-01

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 | Modeling Recent Human Evolution in Mice by Expression of a Selected EDAR Variant. <i>Cell</i> , 2013, 152, 691-702. | 28.9 | 250 |
| 2 | Traffic-Related Air Pollution Contributes to Development of Facial Lentiginosities: Further Epidemiological Evidence from Caucasians and Asians. <i>Journal of Investigative Dermatology</i> , 2016, 136, 1053-1056. | 0.7 | 94 |
| 3 | A 3.4-kb Copy-Number Deletion near EPAS1 Is Significantly Enriched in High-Altitude Tibetans but Absent from the Denisovan Sequence. <i>American Journal of Human Genetics</i> , 2015, 97, 54-66. | 6.2 | 69 |
| 4 | The adaptive variant EDARV370A is associated with straight hair in East Asians. <i>Human Genetics</i> , 2013, 132, 1187-1191. | 3.8 | 68 |
| 5 | Genetic History of Xinjiang's Uyghurs Suggests Bronze Age Multiple-Way Contacts in Eurasia. <i>Molecular Biology and Evolution</i> , 2017, 34, 2572-2582. | 8.9 | 63 |
| 6 | Novel genetic loci affecting facial shape variation in humans. <i>ELife</i> , 2019, 8, . | 6.0 | 58 |
| 7 | Meta-analysis of genome-wide association studies identifies 8 novel loci involved in shape variation of human head hair. <i>Human Molecular Genetics</i> , 2018, 27, 559-575. | 2.9 | 51 |
| 8 | Towards broadening Forensic DNA Phenotyping beyond pigmentation: Improving the prediction of head hair shape from DNA. <i>Forensic Science International: Genetics</i> , 2018, 37, 241-251. | 3.1 | 38 |
| 9 | Genome-wide variants of Eurasian facial shape differentiation and a prospective model of DNA based face prediction. <i>Journal of Genetics and Genomics</i> , 2018, 45, 419-432. | 3.9 | 38 |
| 10 | A cell-type deconvolution meta-analysis of whole blood EWAS reveals lineage-specific smoking-associated DNA methylation changes. <i>Nature Communications</i> , 2020, 11, 4779. | 12.8 | 32 |
| 11 | Limb development genes underlie variation in human fingerprint patterns. <i>Cell</i> , 2022, 185, 95-112.e18. | 28.9 | 30 |
| 12 | Ancestry variation and footprints of natural selection along the genome in Latin American populations. <i>Scientific Reports</i> , 2016, 6, 21766. | 3.3 | 29 |
| 13 | Multiethnic GWAS Reveals Polygenic Architecture of Earlobe Attachment. <i>American Journal of Human Genetics</i> , 2017, 101, 913-924. | 6.2 | 29 |
| 14 | Genome-wide scans reveal variants at EDAR predominantly affecting hair straightness in Han Chinese and Uyghur populations. <i>Human Genetics</i> , 2016, 135, 1279-1286. | 3.8 | 27 |
| 15 | Insights into contribution of genetic variants towards the susceptibility of MAFLD revealed by the NMR-based lipoprotein profiling. <i>Journal of Hepatology</i> , 2021, 74, 974-977. | 3.7 | 26 |
| 16 | Genetic variants associated with skin aging in the Chinese Han population. <i>Journal of Dermatological Science</i> , 2017, 86, 21-29. | 1.9 | 25 |
| 17 | A metagenomic approach to dissect the genetic composition of enterotypes in Han Chinese and two Muslim groups. <i>Systematic and Applied Microbiology</i> , 2018, 41, 1-12. | 2.8 | 24 |
| 18 | EDARV370A associated facial characteristics in Uyghur population revealing further pleiotropic effects. <i>Human Genetics</i> , 2016, 135, 99-108. | 3.8 | 23 |

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|----|--|-----|-----------|
| 19 | Type 2 Diabetes Is Causally Associated With Reduced Serum Osteocalcin: A Genomewide Association and Mendelian Randomization Study. <i>Journal of Bone and Mineral Research</i> , 2020, 36, 1694-1707. | 2.8 | 23 |
| 20 | Genome-wide scan identified genetic variants associated with skin aging in a Chinese female population. <i>Journal of Dermatological Science</i> , 2019, 96, 42-49. | 1.9 | 21 |
| 21 | Genome-wide association studies and CRISPR/Cas9-mediated gene editing identify regulatory variants influencing eyebrow thickness in humans. <i>PLoS Genetics</i> , 2018, 14, e1007640. | 3.5 | 20 |
| 22 | NAFLD-related gene polymorphisms and all-cause and cause-specific mortality in an Asian population: the Shanghai Changfeng Study. <i>Alimentary Pharmacology and Therapeutics</i> , 2022, 55, 705-721. | 3.7 | 17 |
| 23 | Genetically predicted body composition in relation to cardiometabolic traits: a Mendelian randomization study. <i>European Journal of Epidemiology</i> , 2021, 36, 1157-1168. | 5.7 | 12 |
| 24 | Single-cell transcriptomics reveals lineage trajectory of human scalp hair follicle and informs mechanisms of hair graying. <i>Cell Discovery</i> , 2022, 8, . | 6.7 | 11 |
| 25 | hReg-CNCC reconstructs a regulatory network in human cranial neural crest cells and annotates variants in a developmental context. <i>Communications Biology</i> , 2021, 4, 442. | 4.4 | 10 |
| 26 | A Genome-Wide Association Study of Basal Transepidermal Water Loss Finds that Variants at 9q34.3 Are Associated with Skin Barrier Function. <i>Journal of Investigative Dermatology</i> , 2017, 137, 979-982. | 0.7 | 8 |
| 27 | A genome-wide association study of facial morphology identifies novel genetic loci in Han Chinese. <i>Journal of Genetics and Genomics</i> , 2021, 48, 198-207. | 3.9 | 8 |
| 28 | A Genome-Wide Scan on Individual Typology Angle Found Variants at SLC24A2 Associated with Skin Color Variation in Chinese Populations. <i>Journal of Investigative Dermatology</i> , 2022, 142, 1223-1227.e14. | 0.7 | 6 |
| 29 | From musk to body odor: Decoding olfaction through genetic variation. <i>PLoS Genetics</i> , 2022, 18, e1009564. | 3.5 | 5 |
| 30 | Dissecting dynamics and differences of selective pressures in the evolution of human pigmentation. <i>Biology Open</i> , 2021, 10, . | 1.2 | 4 |
| 31 | A custom-designed panel sequencing study in 201 Chinese patients with craniosynostosis revealed novel variants and distinct mutation spectra. <i>Journal of Genetics and Genomics</i> , 2021, 48, 167-171. | 3.9 | 3 |
| 32 | Large-scale genome-wide scans do not support petaloid toenail as a Mendelian trait. <i>Journal of Genetics and Genomics</i> , 2016, 43, 702-704. | 3.9 | 2 |
| 33 | Analysis of factors influencing patch test reactions: Results from a large-population-based study in Chinese. <i>Journal of Cosmetic Dermatology</i> , 2021, , . | 1.6 | 2 |
| 34 | Genetic evidence for facial variation being a composite phenotype of cranial variation and facial soft tissue thickness. <i>Journal of Genetics and Genomics</i> , 2022, , . | 3.9 | 2 |
| 35 | Understudied Skin Characteristics Awaiting Genetic Breakthroughs. <i>Journal of Investigative Dermatology Symposium Proceedings</i> , 2018, 19, S101-S102. | 0.8 | 1 |
| 36 | A Genome-Wide Association Study Finds Variants at 2p21 Associated with Self-Reported Sensitive Skin in the Han Chinese population. <i>Journal of Investigative Dermatology</i> , 2021, , . | 0.7 | 1 |

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|----|---|-----|-----------|
| 37 | BMP4 Exerts Anti-Neurogenic Effect via Inducing Id3 during Aging. <i>Biomedicines</i> , 2022, 10, 1147. | 3.2 | 1 |
| 38 | Analysis of factors influencing skin reactions to sunscreens, skin whitening products, and deodorants: Results from a large-scale patch test dataset in China. <i>Journal of Cosmetic Dermatology</i> , 2021, , . | 1.6 | 0 |