Fan Liu

List of Publications by Year
in descending order

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86	5,153	108046	107981
papers	citations	37 h-index	68 g-index

99	99	99	7260
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	A Genome-Wide Scan on Individual Typology AngleÂFound Variants at SLC24A2 Associated withÂSkin Color Variation in Chinese Populations. Journal of Investigative Dermatology, 2022, 142, 1223-1227.e14.	0.3	6
2	Identification of novel loci influencing refractive error in East Asian populations using an extreme phenotype design. Journal of Genetics and Genomics, 2022, 49, 54-62.	1.7	1
3	Genetic evidence for facial variation being a composite phenotype of cranial variation and facial soft tissue thickness. Journal of Genetics and Genomics, 2022, , .	1.7	2
4	The impact of correlations between pigmentation phenotypes and underlying genotypes on genetic prediction of pigmentation traits. Forensic Science International: Genetics, 2021, 50, 102395.	1.6	7
5	A GWAS in Latin Americans identifies novel face shape loci, implicating VPS13B and a Denisovan introgressed region in facial variation. Science Advances, 2021, 7, .	4.7	32
6	Genome-wide association study in almost 195,000 individuals identifies 50 previously unidentified genetic loci for eye color. Science Advances, 2021, 7, .	4.7	36
7	Evidence for CAT gene being functionally involved in the susceptibility of COVIDâ€19. FASEB Journal, 2021, 35, e21384.	0.2	6
8	hReg-CNCC reconstructs a regulatory network in human cranial neural crest cells and annotates variants in a developmental context. Communications Biology, 2021, 4, 442.	2.0	10
9	DNA-based eyelid trait prediction in Chinese Han population. International Journal of Legal Medicine, 2021, 135, 1743-1752.	1.2	2
10	The effects of Tbx15 and Pax1 on facial and other physical morphology in mice. FASEB BioAdvances, 2021, 3, 1011-1019.	1.3	4
11	Exome-Wide Association Study Identifies East Asian-Specific Missense Variant MTHFR C136T Influencing Homocysteine Levels in Chinese Populations RH: ExWAS of tHCY in a Chinese Population. Frontiers in Genetics, 2021, 12, 717621.	1.1	1
12	Explaining sudden infant death with cardiac arrhythmias: Complete exon sequencing of nine cardiac arrhythmia genes in Dutch SIDS cases highlights new and known DNA variants. Forensic Science International: Genetics, 2020, 46, 102266.	1.6	9
13	A genomeâ€wide association study identifies <scp>FSHR</scp> rs2300441 associated with follicleâ€stimulating hormone levels. Clinical Genetics, 2020, 97, 869-877.	1.0	8
14	Validated inference of smoking habits from blood with a finite DNA methylation marker set. European Journal of Epidemiology, 2019, 34, 1055-1074.	2.5	31
15	Whole Genome Analyses of Chinese Population and De Novo Assembly of A Northern Han Genome. Genomics, Proteomics and Bioinformatics, 2019, 17, 229-247.	3.0	42
16	Update on the predictability of tall stature from DNA markers in Europeans. Forensic Science International: Genetics, 2019, 42, 8-13.	1.6	18
17	Validation of methylation-based forensic age estimation in time-series bloodstains on FTA cards and gauze at room temperature conditions. Forensic Science International: Genetics, 2019, 40, 168-174.	1.6	11
18	Genome-Wide Association Studies Identify MultipleÂGenetic Loci Influencing Eyebrow ColorÂVariation in Europeans. Journal of Investigative Dermatology, 2019, 139, 1601-1605.	0.3	17

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19	MC1R variants in childhood and adolescent melanoma: a retrospective pooled analysis of a multicentre cohort. The Lancet Child and Adolescent Health, 2019, 3, 332-342.	2.7	16
20	Predicting adult height from DNA variants in a European-Asian admixed population. International Journal of Legal Medicine, 2019, 133, 1667-1679.	1.2	6
21	Novel genetic loci affecting facial shape variation in humans. ELife, 2019, 8, .	2.8	58
22	Genome-wide association meta-analysis of individuals of European ancestry identifies new loci explaining a substantial fraction of hair color variation and heritability. Nature Genetics, 2018, 50, 652-656.	9.4	86
23	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.	1.4	51
24	The HIrisPlex-S system for eye, hair and skin colour prediction from DNA: Introduction and forensic developmental validation. Forensic Science International: Genetics, 2018, 35, 123-135.	1.6	199
25	Systematic feature selection improves accuracy of methylation-based forensic age estimation in Han Chinese males. Forensic Science International: Genetics, 2018, 35, 38-45.	1.6	46
26	Facial Wrinkles in Europeans: AÂGenome-Wide Association Study. Journal of Investigative Dermatology, 2018, 138, 1877-1880.	0.3	8
27	Investigation of metabolites for estimating blood deposition time. International Journal of Legal Medicine, 2018, 132, 25-32.	1.2	10
28	Novel pleiotropic risk loci for melanoma and nevus density implicate multiple biological pathways. Nature Communications, 2018, 9, 4774.	5.8	87
29	Genome-wide association studies and CRISPR/Cas9-mediated gene editing identify regulatory variants influencing eyebrow thickness in humans. PLoS Genetics, 2018, 14, e1007640.	1.5	20
30	Towards broadening Forensic DNA Phenotyping beyond pigmentation: Improving the prediction of head hair shape from DNA. Forensic Science International: Genetics, 2018, 37, 241-251.	1.6	38
31	Genome-wide association study in 176,678 Europeans reveals genetic loci for tanning response to sun exposure. Nature Communications, 2018, 9, 1684.	5.8	80
32	Likelihood ratio and posterior odds in forensic genetics: Two sides of the same coin. Forensic Science International: Genetics, 2017, 28, 203-210.	1.6	12
33	Novel quantitative pigmentation phenotyping enhances genetic association, epistasis, and prediction of human eye colour. Scientific Reports, 2017, 7, 43359.	1.6	27
34	Global skin colour prediction from DNA. Human Genetics, 2017, 136, 847-863.	1.8	99
35	Genome-wide compound heterozygote analysis highlights alleles associated with adult height in Europeans. Human Genetics, 2017, 136, 1407-1417.	1.8	19
36	Predicting hair cortisol levels with hair pigmentation genes: a possible hair pigmentation bias. Scientific Reports, 2017, 7, 8529.	1.6	16

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37	MHC Class II Risk Alleles and Amino Acid Residues in Idiopathic Membranous Nephropathy. Journal of the American Society of Nephrology: JASN, 2017, 28, 1651-1664.	3.0	82
38	Pigmentation-Independent Susceptibility Loci for Actinic Keratosis Highlighted by Compound Heterozygosity Analysis. Journal of Investigative Dermatology, 2017, 137, 77-84.	0.3	10
39	Human age estimation from blood using mRNA, DNA methylation, DNA rearrangement, and telomere length. Forensic Science International: Genetics, 2016, 24, 33-43.	1.6	102
40	The MC1R Gene and Youthful Looks. Current Biology, 2016, 26, 1213-1220.	1.8	64
41	Association of Melanocortin-1 Receptor Variants with Pigmentary Traits in Humans: AÂPooled Analysis from the M-Skip Project. Journal of Investigative Dermatology, 2016, 136, 1914-1917.	0.3	16
42	CollapsABEL: an R library for detecting compound heterozygote alleles in genome-wide association studies. BMC Bioinformatics, 2016, 17, 156.	1.2	10
43	Evaluation of mRNA markers for estimating blood deposition time: Towards alibi testing from human forensic stains with rhythmic biomarkers. Forensic Science International: Genetics, 2016, 21, 119-125.	1.6	37
44	An Automatic 3D Facial Landmarking Algorithm Using 2D Gabor Wavelets. IEEE Transactions on Image Processing, 2016, 25, 580-588.	6.0	31
45	Prediction of male-pattern baldness from genotypes. European Journal of Human Genetics, 2016, 24, 895-902.	1.4	44
46	MC1R variants increased the risk of sporadic cutaneous melanoma in darkerâ€pigmented <scp>C</scp>aucasians: A pooledâ€analysis from the Mâ€SKIP project. International Journal of Cancer, 2015, 136, 618-631.	2.3	92
47	Validation of image analysis techniques to measure skin aging features from facial photographs. Skin Research and Technology, 2015, 21, 392-402.	0.8	23
48	Genetics of skin color variation in Europeans: genome-wide association studies with functional follow-up. Human Genetics, 2015, 134, 823-835.	1.8	133
49	IRF4, MC1R and TYR genes are risk factors for actinic keratosis independent of skin color. Human Molecular Genetics, 2015, 24, 3296-3303.	1.4	36
50	A Genome-Wide Association Study Identifies the Skin Color Genes IRF4, MC1R, ASIP, and BNC2 Influencing Facial Pigmented Spots. Journal of Investigative Dermatology, 2015, 135, 1735-1742.	0.3	117
51	GAGA: A New Algorithm for Genomic Inference of Geographic Ancestry Reveals Fine Level Population Substructure in Europeans. PLoS Computational Biology, 2014, 10, e1003480.	1.5	7
52	Intrinsic and Extrinsic Risk Factors for Sagging Eyelids. JAMA Dermatology, 2014, 150, 836.	2.0	64
53	Of sex and IrisPlex eye colour prediction: A reply to Martinez-Cadenas et al.. Forensic Science International: Genetics, 2014, 9, e5-e6.	1.6	9
54	PHOX2B polyalanine repeat length is associated with sudden infant death syndrome and unclassified sudden infant death in the Dutch population. International Journal of Legal Medicine, 2014, 128, 621-9.	1.2	20

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55	Developmental validation of the HIrisPlex system: DNA-based eye and hair colour prediction for forensic and anthropological usage. Forensic Science International: Genetics, 2014, 9, 150-161.	1.6	164
56	Common DNA variants predict tall stature in Europeans. Human Genetics, 2014, 133, 587-597.	1.8	48
57	The common occurrence of epistasis in the determination of human pigmentation and its impact on DNA-based pigmentation phenotype prediction. Forensic Science International: Genetics, 2014, 11, 64-72.	1.6	53
58	First all-in-one diagnostic tool for DNA intelligence: genome-wide inference of biogeographic ancestry, appearance, relatedness, and sex with the Identitas v1 Forensic Chip. International Journal of Legal Medicine, 2013, 127, 559-572.	1.2	51
59	The HIrisPlex system for simultaneous prediction of hair and eye colour from DNA. Forensic Science International: Genetics, 2013, 7, 98-115.	1.6	365
60	Comprehensive candidate gene study highlights UGT1A and BNC2 as new genes determining continuous skin color variation in Europeans. Human Genetics, 2013, 132, 147-158.	1.8	86
61	Colorful DNA polymorphisms in humans. Seminars in Cell and Developmental Biology, 2013, 24, 562-575.	2.3	55
62	A Genome-Wide Association Study Identifies Five Loci Influencing Facial Morphology in Europeans. PLoS Genetics, 2012, 8, e1002932.	1.5	274
63	DNA-based eye colour prediction across Europe with the IrisPlex system. Forensic Science International: Genetics, 2012, 6, 330-340.	1.6	105
64	Melanocortin-1 receptor, skin cancer and phenotypic characteristics (M-SKIP) project: study design and methods for pooling results of genetic epidemiological studies. BMC Medical Research Methodology, 2012, 12, 116.	1.4	12
65	Genetic determination of human facial morphology: links between cleft-lips and normal variation. European Journal of Human Genetics, 2011, 19, 1192-1197.	1.4	89
66	IrisPlex: A sensitive DNA tool for accurate prediction of blue and brown eye colour in the absence of ancestry information. Forensic Science International: Genetics, 2011, 5, 170-180.	1.6	275
67	Association of HSP70 and its Co-Chaperones with Alzheimer's Disease. Journal of Alzheimer's Disease, 2011, 25, 93-102.	1.2	21
68	Postnatal parental smoking: an important risk factor for SIDS. European Journal of Pediatrics, 2011, 170, 1281-1291.	1.3	59
69	Model-based prediction of human hair color using DNA variants. Human Genetics, 2011, 129, 443-454.	1.8	151
70	Detecting Low Frequent Loss-of-Function Alleles in Genome Wide Association Studies with Red Hair Color as Example. PLoS ONE, 2011, 6, e28145.	1.1	19
71	Estimating human age from T-cell DNA rearrangements. Current Biology, 2010, 20, R970-R971.	1.8	156
72	Digital Quantification of Human Eye Color Highlights Genetic Association of Three New Loci. PLoS Genetics, 2010, 6, e1000934.	1.5	161

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73	A Genome-Wide Screen for Depression in Two Independent Dutch Populations. Biological Psychiatry, 2010, 68, 187-196.	0.7	27
74	The apolipoprotein E gene and its age-specific effects on cognitive function. Neurobiology of Aging, 2010, 31, 1831-1833.	1.5	60
75	Eye color and the prediction of complex phenotypes from genotypes. Current Biology, 2009, 19, R192-R193.	1.8	226
76	A genome-wide association study of northwestern Europeans involves the C-type natriuretic peptide signaling pathway in the etiology of human height variation. Human Molecular Genetics, 2009, 18, 3516-3524.	1.4	76
77	A Study of the SORL1 Gene in Alzheimer's Disease and Cognitive Function. Journal of Alzheimer's Disease, 2009, 18, 51-64.	1.2	36
78	The MSX1 allele 4 homozygous child exposed to smoking at periconception is most sensitive in developing nonsyndromic orofacial clefts. Human Genetics, 2008, 124, 525-534.	1.8	30
79	Three Genome-wide Association Studies and a Linkage Analysis Identify HERC2 as a Human Iris Color Gene. American Journal of Human Genetics, 2008, 82, 411-423.	2.6	220
80	Three Genome-wide Association Studies and a Linkage Analysis Identify HERC2 as a Human Iris Color Gene. American Journal of Human Genetics, 2008, 82, 801.	2.6	4
81	Familial aggregation of preeclampsia and intrauterine growth restriction in a genetically isolated population in The Netherlands. European Journal of Human Genetics, 2008, 16, 1437-1442.	1.4	8
82	An approach for cutting large and complex pedigrees for linkage analysis. European Journal of Human Genetics, 2008, 16, 854-860.	1.4	55
83	Maternal Transmission of Multiple Sclerosis in a Dutch Population. Archives of Neurology, 2008, 65, 345-8.	4.9	58
84	Relationship of the Ubiquilin 1 gene with Alzheimer's and Parkinson's disease and cognitive function. Neuroscience Letters, 2007, 424, 1-5.	1.0	16
85	A Genomewide Screen for Late-Onset Alzheimer Disease in a Genetically Isolated Dutch Population. American Journal of Human Genetics, 2007, 81, 17-31.	2.6	145
86	Novel Genetic Loci Affecting Facial Shape Variation in Humans. SSRN Electronic Journal, 0, , .	0.4	0