Fan Liu

List of Publications by Citations

86 papers	3,729 citations	34 h-index	60 g-index
99 ext. papers	4,548 ext. citations	5.7 avg, IF	4.69 L-index

#	Paper	IF	Citations
86	The HIrisPlex system for simultaneous prediction of hair and eye colour from DNA. *Forensic Science International: Genetics*, **2013**, 7, 98-115	4.3	289
85	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, 170-80	4.3	221
84	A genome-wide association study identifies five loci influencing facial morphology in Europeans. *PLoS Genetics*, **2012**, 8, e1002932	6	194
83	Eye color and the prediction of complex phenotypes from genotypes. *Current Biology*, **2009**, 19, R192-3	6.3	190
82	Three genome-wide association studies and a linkage analysis identify HERC2 as a human iris color gene. *American Journal of Human Genetics*, **2008**, 82, 411-23	11	183
81	Digital quantification of human eye color highlights genetic association of three new loci. *PLoS Genetics*, **2010**, 6, e1000934	6	135
80	Estimating human age from T-cell DNA rearrangements. *Current Biology*, **2010**, 20, R970-1	6.3	130
79	A genomewide screen for late-onset Alzheimer disease in a genetically isolated Dutch population. *American Journal of Human Genetics*, **2007**, 81, 17-31	11	124
78	Model-based prediction of human hair color using DNA variants. *Human Genetics*, **2011**, 129, 443-54	6.3	123
77	Developmental validation of the HIrisPlex system: DNA-based eye and hair colour prediction for forensic and anthropological usage. *Forensic Science International: Genetics*, **2014**, 9, 150-61	4.3	110
76	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	4.3	106
75	Genetics of skin color variation in Europeans: genome-wide association studies with functional follow-up. *Human Genetics*, **2015**, 134, 823-35	6.3	97
74	DNA-based eye colour prediction across Europe with the IrisPlex system. *Forensic Science International: Genetics*, **2012**, 6, 330-40	4.3	82
73	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	4.3	80
72	Comprehensive candidate gene study highlights UGT1A and BNC2 as new genes determining continuous skin color variation in Europeans. *Human Genetics*, **2013**, 132, 147-58	6.3	70
71	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, 3516-24	5.6	70
70	MC1R variants increased the risk of sporadic cutaneous melanoma in darker-pigmented Caucasians: a pooled-analysis from the M-SKIP project. *International Journal of Cancer*, **2015**, 136, 618-31	7.5	67

69	Genetic determination of human facial morphology: links between cleft-lips and normal variation. *European Journal of Human Genetics*, **2011**, 19, 1192-7	5.3	67
68	Human age estimation from blood using mRNA, DNA methylation, DNA rearrangement, and telomere length. *Forensic Science International: Genetics*, **2016**, 24, 33-43	4.3	65
67	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	12.7	64
66	Global skin colour prediction from DNA. *Human Genetics*, **2017**, 136, 847-863	6.3	63
65	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	36.3	59
64	Genome-wide association study in 176,678 Europeans reveals genetic loci for tanning response to sun exposure. *Nature Communications*, **2018**, 9, 1684	17.4	51
63	The apolipoprotein E gene and its age-specific effects on cognitive function. *Neurobiology of Aging*, **2010**, 31, 1831-3	5.6	51
62	An approach for cutting large and complex pedigrees for linkage analysis. *European Journal of Human Genetics*, **2008**, 16, 854-60	5.3	48
61	Maternal transmission of multiple sclerosis in a dutch population. *Archives of Neurology*, **2008**, 65, 345-8		48
60	Colorful DNA polymorphisms in humans. *Seminars in Cell and Developmental Biology*, **2013**, 24, 562-75	7.5	47
59	Novel pleiotropic risk loci for melanoma and nevus density implicate multiple biological pathways. *Nature Communications*, **2018**, 9, 4774	17.4	47
58	Postnatal parental smoking: an important risk factor for SIDS. *European Journal of Pediatrics*, **2011**, 170, 1281-91	4.1	46
57	The MC1R Gene and Youthful Looks. *Current Biology*, **2016**, 26, 1213-20	6.3	42
56	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	4.3	39
55	Common DNA variants predict tall stature in Europeans. *Human Genetics*, **2014**, 133, 587-97	6.3	38
54	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, 559-72	3.1	38
53	Intrinsic and extrinsic risk factors for sagging eyelids. *JAMA Dermatology*, **2014**, 150, 836-43	5.1	38
52	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	5.6	33

51	A study of the SORL1 gene in Alzheimer's disease and cognitive function. *Journal of Alzheimer's Disease*, **2009**, 18, 51-64	4.3	32
50	IRF4, MC1R and TYR genes are risk factors for actinic keratosis independent of skin color. *Human Molecular Genetics*, **2015**, 24, 3296-303	5.6	27
49	Prediction of male-pattern baldness from genotypes. *European Journal of Human Genetics*, **2016**, 24, 895-902	5.3	26
48	The MSX1 allele 4 homozygous child exposed to smoking at periconception is most sensitive in developing nonsyndromic orofacial clefts. *Human Genetics*, **2008**, 124, 525-34	6.3	25
47	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, 119-25	4.3	24
46	Towards broadening Forensic DNA Phenotyping beyond pigmentation: Improving the prediction of head hair shape from DNA. *Forensic Science International: Genetics*, **2018**, 37, 241-251	4.3	24
45	Novel genetic loci affecting facial shape variation in humans. *ELife*, **2019**, 8,	8.9	22
44	Whole Genome Analyses of Chinese Population and De Novo Assembly of A Northern Han Genome. *Genomics, Proteomics and Bioinformatics*, **2019**, 17, 229-247	6.5	21
43	Systematic feature selection improves accuracy of methylation-based forensic age estimation in Han Chinese males. *Forensic Science International: Genetics*, **2018**, 35, 38-45	4.3	21
42	A genome-wide screen for depression in two independent Dutch populations. *Biological Psychiatry*, **2010**, 68, 187-96	7.9	20
41	Validation of image analysis techniques to measure skin aging features from facial photographs. *Skin Research and Technology*, **2015**, 21, 392-402	1.9	19
40	Detecting low frequent loss-of-function alleles in genome wide association studies with red hair color as example. *PLoS ONE*, **2011**, 6, e28145	3.7	19
39	Novel quantitative pigmentation phenotyping enhances genetic association, epistasis, and prediction of human eye colour. *Scientific Reports*, **2017**, 7, 43359	4.9	18
38	Association of HSP70 and its co-chaperones with Alzheimer's disease. *Journal of Alzheimer's Disease* , **2011**, 25, 93-102	4.3	18
37	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	3.1	17
36	Relationship of the Ubiquilin 1 gene with Alzheimer's and Parkinson's disease and cognitive function. *Neuroscience Letters*, **2007**, 424, 1-5	3.3	14
35	Genome-wide association studies and CRISPR/Cas9-mediated gene editing identify regulatory variants influencing eyebrow thickness in humans. *PLoS Genetics*, **2018**, 14, e1007640	6	14
34	Association of Melanocortin-1 Receptor Variants with Pigmentary Traits in Humans: A Pooled Analysis from the M-Skip Project. *Journal of Investigative Dermatology*, **2016**, 136, 1914-1917	4.3	12

33	An Automatic 3D Facial Landmarking Algorithm Using 2D Gabor Wavelets. *IEEE Transactions on Image Processing*, **2016**, 25, 580-8	8.7	12
32	Genome-wide compound heterozygote analysis highlights alleles associated with adult height in Europeans. *Human Genetics*, **2017**, 136, 1407-1417	6.3	12
31	Predicting hair cortisol levels with hair pigmentation genes: a possible hair pigmentation bias. *Scientific Reports*, **2017**, 7, 8529	4.9	11
30	Genome-wide association study in almost 195,000 individuals identifies 50 previously unidentified genetic loci for eye color. *Science Advances*, **2021**, 7,	14.3	11
29	Validated inference of smoking habits from blood with a finite DNA methylation marker set. *European Journal of Epidemiology*, **2019**, 34, 1055-1074	12.1	10
28	Update on the predictability of tall stature from DNA markers in Europeans. *Forensic Science International: Genetics*, **2019**, 42, 8-13	4.3	10
27	EDAR, LYPLAL1, PRDM16, PAX3, DKK1, TNFSF12, CACNA2D3, and SUPT3H gene variants influence facial morphology in a Eurasian population. *Human Genetics*, **2019**, 138, 681-689	6.3	10
26	Genome-Wide Association Studies Identify Multiple Genetic Loci Influencing Eyebrow Color Variation in Europeans. *Journal of Investigative Dermatology*, **2019**, 139, 1601-1605	4.3	10
25	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	4.7	10
24	Likelihood ratio and posterior odds in forensic genetics: Two sides of the same coin. *Forensic Science International: Genetics*, **2017**, 28, 203-210	4.3	9
23	CollapsABEL: an R library for detecting compound heterozygote alleles in genome-wide association studies. *BMC Bioinformatics*, **2016**, 17, 156	3.6	9
22	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	14.5	8
21	Of sex and IrisPlex eye colour prediction: a reply to Martinez-Cadenas et al. *Forensic Science International: Genetics*, **2014**, 9, e5-6	4.3	8
20	GAGA: a new algorithm for genomic inference of geographic ancestry reveals fine level population substructure in Europeans. *PLoS Computational Biology*, **2014**, 10, e1003480	5	7
19	Familial aggregation of preeclampsia and intrauterine growth restriction in a genetically isolated population in The Netherlands. *European Journal of Human Genetics*, **2008**, 16, 1437-42	5.3	7
18	A GWAS in Latin Americans identifies novel face shape loci, implicating VPS13B and a Denisovan introgressed region in facial variation. *Science Advances*, **2021**, 7,	14.3	7
17	Pigmentation-Independent Susceptibility Loci for Actinic Keratosis Highlighted by Compound Heterozygosity Analysis. *Journal of Investigative Dermatology*, **2017**, 137, 77-84	4.3	6
16	Investigation of metabolites for estimating blood deposition time. *International Journal of Legal Medicine*, **2018**, 132, 25-32	3.1	6

15	Predicting adult height from DNA variants in a European-Asian admixed population. *International Journal of Legal Medicine*, **2019**, 133, 1667-1679	3.1	5
14	A genome-wide association study identifies FSHR rs2300441 associated with follicle-stimulating hormone levels. *Clinical Genetics*, **2020**, 97, 869-877	4	5
13	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	4.3	4
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	4.3	4
11	Facial Wrinkles in Europeans: A Genome-Wide Association Study. *Journal of Investigative Dermatology*, **2018**, 138, 1877-1880	4.3	4
10	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	11	4
9	Evidence for CAT gene being functionally involved in the susceptibility of COVID-19. *FASEB Journal*, **2021**, 35, e21384	0.9	2
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	6.7	2
7	DNA-based eyelid trait prediction in Chinese Han population. *International Journal of Legal Medicine* , **2021**, 135, 1743-1752	3.1	2
6	Exome-Wide Association Study Identifies East Asian-Specific Missense Variant C136T Influencing Homocysteine Levels in Chinese Populations RH: ExWAS of tHCY in a Chinese Population. *Frontiers in Genetics*, **2021**, 12, 717621	4.5	1
5	The impact of correlations between pigmentation phenotypes and underlying genotypes on genetic prediction of pigmentation traits. *Forensic Science International: Genetics*, **2021**, 50, 102395	4.3	1
4	Retraction Note: EDAR, LYPLAL1, PRDM16, PAX3, DKK1, TNFSF12, CACNA2D3, and SUPT3H gene variants influence facial morphology in a Eurasian population. *Human Genetics*, **2021**, 140, 1499	6.3	1
3	The effects of and on facial and other physical morphology in mice.. *FASEB BioAdvances*, **2021**, 3, 1011-1019	2.8	0
2	Retraction Note: Predicting adult height from DNA variants in a European-Asian admixed population. *International Journal of Legal Medicine*, **2021**, 135, 2151	3.1	
1	Identification of novel loci influencing refractive error in East Asian populations using an extreme phenotype design. *Journal of Genetics and Genomics*, **2021**, 49, 54-54	4	