Manfred Kayser

List of Publications by Year
in descending order

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251 papers	25,648 citations	5891 81 h-index	7944 149 g-index
270 all docs	270 docs citations	270 times ranked	23482 citing authors

#	Article	IF	Citations
1	Defining the role of common variation in the genomic and biological architecture of adult human height. Nature Genetics, 2014, 46, 1173-1186.	9.4	1,818
2	Hundreds of variants clustered in genomic loci and biological pathways affect human height. Nature, 2010, 467, 832-838.	13.7	1,789
3	Updated comprehensive phylogenetic tree of global human mitochondrial DNA variation. Human Mutation, 2009, 30, E386-E394.	1.1	1,528
4	Evaluation of Y-chromosomal STRs: a multicenter study. International Journal of Legal Medicine, 1997, 110, 125-133.	1.2	648
5	Denisova Admixture and the First Modern Human Dispersals into Southeast Asia and Oceania. American Journal of Human Genetics, 2011, 89, 516-528.	2.6	525
6	Y-Chromosomal Diversity in Europe Is Clinal and Influenced Primarily by Geography, Rather than by Language. American Journal of Human Genetics, 2000, 67, 1526-1543.	2.6	519
7	Correlation between Genetic and Geographic Structure in Europe. Current Biology, 2008, 18, 1241-1248.	1.8	449
8	Improving human forensics through advances in genetics, genomics and molecular biology. Nature Reviews Genetics, 2011, 12, 179-192.	7.7	407
9	Effect of sleep deprivation on the human metabolome. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 10761-10766.	3.3	394
10	DNA Commission of the International Society of Forensic Genetics (ISFG): An update of the recommendations on the use of Y-STRs in forensic analysis. Forensic Science International, 2006, 157, 187-197.	1.3	366
11	The HIrisPlex system for simultaneous prediction of hair and eye colour from DNA. Forensic Science International: Genetics, 2013, 7, 98-115.	1.6	365
12	The Effective Mutation Rate at Y Chromosome Short Tandem Repeats, with Application to Human Population-Divergence Time. American Journal of Human Genetics, 2004, 74, 50-61.	2.6	353
13	Characteristics and Frequency of Germline Mutations at Microsatellite Loci from the Human Y Chromosome, as Revealed by Direct Observation in Father/Son Pairs. American Journal of Human Genetics, 2000, 66, 1580-1588.	2.6	334
14	Mutability of Y-Chromosomal Microsatellites: Rates, Characteristics, Molecular Bases, and Forensic Implications. American Journal of Human Genetics, 2010, 87, 341-353.	2.6	324
15	MicroRNA markers for forensic body fluid identification obtained from microarray screening and quantitative RT-PCR confirmation. International Journal of Legal Medicine, 2010, 124, 217-226.	1.2	289
16	Forensic DNA Phenotyping: Predicting human appearance from crime scene material for investigative purposes. Forensic Science International: Genetics, 2015, 18, 33-48.	1.6	289
17	Chromosome Y microsatellites: population genetic and evolutionary aspects. International Journal of Legal Medicine, 1997, 110, 134-140.	1.2	286
18	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

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19	A Genome-Wide Association Study Identifies Five Loci Influencing Facial Morphology in Europeans. PLoS Genetics, 2012, 8, e1002932.	1.5	274
20	Direct evidence for positive selection of skin, hair, and eye pigmentation in Europeans during the last 5,000 y. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 4832-4837.	3.3	240
21	Forensic use of Y-chromosome DNA: a general overview. Human Genetics, 2017, 136, 621-635.	1.8	239
22	<i>HERC2</i> rs12913832 modulates human pigmentation by attenuating chromatin-loop formation between a long-range enhancer and the <i>OCA2</i> promoter. Genome Research, 2012, 22, 446-455.	2.4	232
23	Eye color and the prediction of complex phenotypes from genotypes. Current Biology, 2009, 19, R192-R193.	1.8	226
24	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
25	Melanesian and Asian Origins of Polynesians: mtDNA and Y Chromosome Gradients Across the Pacific. Molecular Biology and Evolution, 2006, 23, 2234-2244.	3.5	216
26	Signatures of Positive Selection in Genes Associated with Human Skin Pigmentation as Revealed from Analyses of Single Nucleotide Polymorphisms. Annals of Human Genetics, 2007, 71, 354-369.	0.3	212
27	A new future of forensic Y-chromosome analysis: Rapidly mutating Y-STRs for differentiating male relatives and paternal lineages. Forensic Science International: Genetics, 2012, 6, 208-218.	1.6	210
28	DNA-based prediction of human externally visible characteristics in forensics: Motivations, scientific challenges, and ethical considerations. Forensic Science International: Genetics, 2009, 3, 154-161.	1.6	205
29	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
30	Online reference database of European Y-chromosomal short tandem repeat (STR) haplotypes. Forensic Science International, 2001, 118, 106-113.	1.3	198
31	A Comprehensive Survey of Human Y-Chromosomal Microsatellites. American Journal of Human Genetics, 2004, 74, 1183-1197.	2.6	194
32	Genetic relationships of Asians and Northern Europeans, revealed by Y-chromosomal DNA analysis. American Journal of Human Genetics, 1997, 60, 1174-83.	2.6	190
33	An Extensive Analysis of Y-Chromosomal Microsatellite Haplotypes in Globally Dispersed Human Populations. American Journal of Human Genetics, 2001, 68, 990-1018.	2.6	186
34	A multiplex (m)RNA-profiling system for the forensic identification of body fluids and contact traces. Forensic Science International: Genetics, 2012, 6, 565-577.	1.6	185
35	DNA Commission of the International Society of Forensic Genetics: recommendations on forensic analysis using Y-chromosome STRs. Forensic Science International, 2001, 124, 5-10.	1.3	179
36	Melanesian origin of Polynesian Y chromosomes. Current Biology, 2000, 10, 1237-1246.	1.8	174

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37	Analysis of molecular variance (AMOVA) of Y-chromosome-specific microsatellites in two closely related human populations [published erratum appears in Hum Mol Genet 1997 May;6(5):828]. Human Molecular Genetics, 1996, 5, 1029-1033.	1.4	173
38	DNA Commission of the International Society of Forensic Genetics (ISFG): an update of the recommendations on the use of Y-STRs in forensic analysis. International Journal of Legal Medicine, 2006, 120, 191-200.	1.2	171
39	Signature of recent historical events in the European Y-chromosomal STR haplotype distribution. Human Genetics, 2005, 116, 279-291.	1.8	168
40	Evaluation of saliva as a source of human DNA for population and association studies. Analytical Biochemistry, 2006, 353, 272-277.	1.1	166
41	Proportioning Whole-Genome Single-Nucleotideâ€"Polymorphism Diversity for the Identification of Geographic Population Structure and Genetic Ancestry. American Journal of Human Genetics, 2006, 78, 680-690.	2.6	164
42	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
43	Identification of the remains of King Richard III. Nature Communications, 2014, 5, 5631.	5.8	163
44	Digital Quantification of Human Eye Color Highlights Genetic Association of Three New Loci. PLoS Genetics, 2010, 6, e1000934.	1.5	161
45	Reduced Y-Chromosome, but Not Mitochondrial DNA, Diversity in Human Populations from West New Guinea. American Journal of Human Genetics, 2003, 72, 281-302.	2.6	160
46	Demographic History of Oceania Inferred from Genome-wide Data. Current Biology, 2010, 20, 1983-1992.	1.8	158
47	Stable RNA markers for identification of blood and saliva stains revealed from whole genome expression analysis of time-wise degraded samples. International Journal of Legal Medicine, 2008, 122, 135-142.	1.2	157
48	Estimating human age from T-cell DNA rearrangements. Current Biology, 2010, 20, R970-R971.	1.8	156
49	Ancient genomes indicate population replacement in Early Neolithic Britain. Nature Ecology and Evolution, 2019, 3, 765-771.	3.4	156
50	Inferring Continental Ancestry of Argentineans from Autosomal, Yâ€Chromosomal and Mitochondrial DNA. Annals of Human Genetics, 2010, 74, 65-76.	0.3	155
51	Model-based prediction of human hair color using DNA variants. Human Genetics, 2011, 129, 443-454.	1.8	151
52	Toward Male Individualization with Rapidly Mutating Y-Chromosomal Short Tandem Repeats. Human Mutation, 2014, 35, 1021-1032.	1.1	151
53	Genomic and geographic distribution of SNP-defined runs of homozygosity in Europeans. Human Molecular Genetics, 2010, 19, 2927-2935.	1.4	146
54	A counter-clockwise northern route of the Y-chromosome haplogroup N from Southeast Asia towards Europe. European Journal of Human Genetics, 2007, 15, 204-211.	1.4	142

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55	Developmental validation of the IrisPlex system: Determination of blue and brown iris colour for forensic intelligence. Forensic Science International: Genetics, 2011, 5, 464-471.	1.6	141
56	Seeing the Wood for the Trees: A Minimal Reference Phylogeny for the Human Y Chromosome. Human Mutation, 2014, 35, 187-191.	1.1	141
57	Genetics of skin color variation in Europeans: genome-wide association studies with functional follow-up. Human Genetics, 2015, 134, 823-835.	1.8	133
58	Significant genetic differentiation between Poland and Germany follows present-day political borders, as revealed by Y-chromosome analysis. Human Genetics, 2005, 117, 428-443.	1.8	123
59	Comprehensive mutation analysis of 17 Y-chromosomal short tandem repeat polymorphisms included in the AmpFlSTRÂ® YfilerÂ® PCR amplification kit. International Journal of Legal Medicine, 2009, 123, 471-482.	1.2	121
60	A new method for the evaluation of matches in non-recombining genomes: application to Y-chromosomal short tandem repeat (STR) haplotypes in European males. Forensic Science International, 2000, 114, 31-43.	1.3	119
61	The Human Genetic History of Oceania: Near and Remote Views of Dispersal. Current Biology, 2010, 20, R194-R201.	1.8	117
62	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
63	Genome-wide Analysis Indicates More Asian than Melanesian Ancestry of Polynesians. American Journal of Human Genetics, 2008, 82, 194-198.	2.6	114
64	New markers for old stains: stable mRNA markers for blood and saliva identification from up to 16-year-old stains. International Journal of Legal Medicine, 2009, 123, 71-74.	1.2	114
65	A Genome Scan to Detect Candidate Regions Influenced by Local Natural Selection in Human Populations. Molecular Biology and Evolution, 2003, 20, 893-900.	3.5	113
66	Independent Histories of Human Y Chromosomes from Melanesia and Australia. American Journal of Human Genetics, 2001, 68, 173-190.	2.6	112
67	Mutations at Y-STR loci: implications for paternity testing and forensic analysis. Forensic Science International, 2001, 118, 116-121.	1.3	110
68	Predicting human height by Victorian and genomic methods. European Journal of Human Genetics, 2009, 17, 1070-1075.	1.4	108
69	The Impact of the Austronesian Expansion: Evidence from mtDNA and Y Chromosome Diversity in the Admiralty Islands of Melanesia. Molecular Biology and Evolution, 2008, 25, 1362-1374.	3.5	105
70	DNA-based eye colour prediction across Europe with the IrisPlex system. Forensic Science International: Genetics, 2012, 6, 330-340.	1.6	105
71	Yâ€chromosome analysis confirms highly sexâ€biased dispersal and suggests a low male effective population size in bonobos (<i>Pan paniscus</i>). Molecular Ecology, 2006, 15, 939-949.	2.0	104
72	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

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73	A Worldwide Survey of Human Male Demographic History Based on Y-SNP and Y-STR Data from the HGDP-CEPH Populations. Molecular Biology and Evolution, 2010, 27, 385-393.	3.5	101
74	Global skin colour prediction from DNA. Human Genetics, 2017, 136, 847-863.	1.8	99
75	Genome-wide data substantiate Holocene gene flow from India to Australia. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 1803-1808.	3.3	97
76	Diurnal Rhythms in Blood Cell Populations and the Effect of Acute Sleep Deprivation in Healthy Young Men. Sleep, 2012, 35, 933-940.	0.6	96
77	Recent progress, methods and perspectives in forensic epigenetics. Forensic Science International: Genetics, 2018, 37, 180-195.	1.6	94
78	Comparing six commercial autosomal STR kits in a large Dutch population sample. Forensic Science International: Genetics, 2014, 10, 55-63.	1.6	92
79	Homogeneity and distinctiveness of Polish paternal lineages revealed by Y chromosome microsatellite haplotype analysis. Human Genetics, 2002, 110, 592-600.	1.8	91
80	Effect of sleep deprivation on rhythms of clock gene expression and melatonin in humans. Chronobiology International, 2013, 30, 901-909.	0.9	90
81	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
82	Improving global and regional resolution of male lineage differentiation by simple single-copy Y-chromosomal short tandem repeat polymorphisms. Forensic Science International: Genetics, 2009, 3, 205-213.	1.6	87
83	Novel pleiotropic risk loci for melanoma and nevus density implicate multiple biological pathways. Nature Communications, 2018, 9, 4774.	5.8	87
84	Evaluating self-declared ancestry of U.S. Americans with autosomal, Y-chromosomal and mitochondrial DNA. Human Mutation, 2010, 31, E1875-E1893.	1.1	86
85	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
86	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
87	Y Chromosome STR Haplotypes and the Genetic Structure of U.S. Populations of African, European, and Hispanic Ancestry. Genome Research, 2003, 13, 624-634.	2.4	81
88	mRNA-based skin identification for forensic applications. International Journal of Legal Medicine, 2011, 125, 253-263.	1.2	80
89	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
90	Dating the age of admixture via wavelet transform analysis of genome-wide data. Genome Biology, 2011, 12, R19.	13.9	79

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91	The Y-chromosome landscape of the Philippines: extensive heterogeneity and varying genetic affinities of Negrito and non-Negrito groups. European Journal of Human Genetics, 2011, 19, 224-230.	1.4	78
92	Ensemble landmarking of 3D facial surface scans. Scientific Reports, 2018, 8, 12.	1.6	78
93	Genetic Admixture History of Eastern Indonesia as Revealed by Y-Chromosome and Mitochondrial DNA Analysis. Molecular Biology and Evolution, 2009, 26, 1865-1877.	3.5	76
94	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
95	Human skin color is influenced by an intergenic DNA polymorphism regulating transcription of the nearby BNC2 pigmentation gene. Human Molecular Genetics, 2014, 23, 5750-5762.	1.4	73
96	Yleaf: Software for Human Y-Chromosomal Haplogroup Inference from Next-Generation Sequencing Data. Molecular Biology and Evolution, 2018, 35, 1291-1294.	3.5	73
97	Intrinsic and Extrinsic Risk Factors for Sagging Eyelids. JAMA Dermatology, 2014, 150, 836.	2.0	64
98	Maternal History of Oceania from Complete mtDNA Genomes: Contrasting Ancient Diversity with Recent Homogenization Due to the Austronesian Expansion. American Journal of Human Genetics, 2014, 94, 721-733.	2.6	64
99	The MC1R Gene and Youthful Looks. Current Biology, 2016, 26, 1213-1220.	1.8	64
100	From forensic epigenetics to forensic epigenomics: broadening DNA investigative intelligence. Genome Biology, 2017, 18, 238.	3.8	64
101	Body fluid identification using a targeted mRNA massively parallel sequencing approach â€“ results of a EUROFORGEN/EDNAP collaborative exercise. Forensic Science International: Genetics, 2018, 34, 105-115.	1.6	64
102	Improving empirical evidence on differentiating closely related men with RM Y-STRs: A comprehensive pedigree study from Pakistan. Forensic Science International: Genetics, 2016, 25, 45-51.	1.6	62
103	Postnatal parental smoking: an important risk factor for SIDS. European Journal of Pediatrics, 2011, 170, 1281-1291.	1.3	59
104	Bridging Near and Remote Oceania: mtDNA and NRY Variation in the Solomon Islands. Molecular Biology and Evolution, 2012, 29, 545-564.	3.5	58
105	Bona fide colour: DNA prediction of human eye and hair colour from ancient and contemporary skeletal remains. Investigative Genetics, 2013, 4, 3.	3.3	58
106	Novel genetic loci affecting facial shape variation in humans. ELife, 2019, 8, .	2.8	58
107	Colorful DNA polymorphisms in humans. Seminars in Cell and Developmental Biology, 2013, 24, 562-575.	2.3	55
108	A novel multiplex assay for simultaneously analysing 13 rapidly mutating Y-STRs. Forensic Science International: Genetics, 2015, 17, 91-98.	1.6	55

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109	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
110	Phylogenetic resolution of complex mutational features at Y-STR DYS390 in aboriginal Australians and Papuans. Molecular Biology and Evolution, 1998, 15, 1108-1114.	3.5	51
111	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
112	Simultaneous Whole Mitochondrial Genome Sequencing with Short Overlapping Amplicons Suitable for Degraded DNA Using the Ion Torrent Personal Genome Machine. Human Mutation, 2015, 36, 1236-1247.	1.1	51
113	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
114	Identification of highly polymorphic microsatellites in the rhesus macaque Macaca mulatta by cross-species amplification. Molecular Ecology, 1996, 5, 157-159.	2.0	49
115	Development of the VISAGE enhanced tool and statistical models for epigenetic age estimation in blood, buccal cells and bones. Aging, 2021, 13, 6459-6484.	1.4	49
116	Common DNA variants predict tall stature in Europeans. Human Genetics, 2014, 133, 587-597.	1.8	48
117	Developing a set of ancestry-sensitive DNA markers reflecting continental origins of humans. BMC Genetics, 2009, 10, 69.	2.7	47
118	Allele-specific transcriptional regulation of IRF4 in melanocytes is mediated by chromatin looping of the intronic rs12203592 enhancer to the IRF4 promoter. Human Molecular Genetics, 2015, 24, 2649-2661.	1.4	47
119	The Use of Forensic DNA Phenotyping in Predicting Appearance and Biogeographic Ancestry. Deutsches A&#x0308;rzteblatt International, 2019, 51-52, 873-880.	0.6	47
120	Apparent intrachromosomal exchange on the human Y chromosome explained by population history. European Journal of Human Genetics, 2003, 11, 304-314.	1.4	46
121	HIrisPlex-S system for eye, hair, and skin color prediction from DNA: Massively parallel sequencing solutions for two common forensically used platforms. Forensic Science International: Genetics, 2019, 43, 102152.	1.6	45
122	Prediction of male-pattern baldness from genotypes. European Journal of Human Genetics, 2016, 24, 895-902.	1.4	44
123	Development and validation of the VISAGE AmpliSeq basic tool to predict appearance and ancestry from DNA. Forensic Science International: Genetics, 2020, 48, 102336.	1.6	43
124	Asian online Y-STR Haplotype Reference Database. Legal Medicine, 2003, 5, S160-S163.	0.6	42
125	Evaluation of haplotype discrimination capacity of 35 Y-chromosomal short tandem repeat loci. Forensic Science International, 2008, 174, 182-188.	1.3	42
126	Bringing colour back after 70 years: Predicting eye and hair colour from skeletal remains of World War II victims using the HIrisPlex system. Forensic Science International: Genetics, 2017, 26, 48-57.	1.6	42

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127	Forensic Y-SNP analysis beyond SNaPshot: High-resolution Y-chromosomal haplogrouping from low quality and quantity DNA using Ion AmpliSeq and targeted massively parallel sequencing. Forensic Science International: Genetics, 2019, 41, 93-106.	1.6	42
128	Development of Y-chromosomal microsatellite markers for nonhuman primates. Molecular Ecology, 2004, 13, 2921-2930.	2.0	41
129	Online Y-chromosomal Short Tandem Repeat Haplotype Reference Database (YHRD) for U.S. Populations. Journal of Forensic Sciences, 2002, 47, 513-519.	0.9	41
130	Estimating trace deposition time with circadian biomarkers: a prospective and versatile tool for crime scene reconstruction. International Journal of Legal Medicine, 2010, 124, 387-395.	1.2	40
131	Relating two deep-rooted pedigrees from Central Germany by high-resolution Y-STR haplotyping. Forensic Science International: Genetics, 2007, 1, 125-128.	1.6	39
132	Simultaneous Analysis of Hundreds of Y-Chromosomal SNPs for High-Resolution Paternal Lineage Classification using Targeted Semiconductor Sequencing. Human Mutation, 2015, 36, 151-159.	1.1	39
133	Aboriginal Australian mitochondrial genome variation â€“ an increased understanding of population antiquity and diversity. Scientific Reports, 2017, 7, 43041.	1.6	39
134	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
135	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
136	An efficient multiplex genotyping approach for detecting the major worldwide human Y-chromosome haplogroups. International Journal of Legal Medicine, 2011, 125, 879-885.	1.2	36
137	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
138	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
139	Development of an Italian RM Y-STR haplotype database: Results of the 2013 GEFI collaborative exercise. Forensic Science International: Genetics, 2015, 15, 56-63.	1.6	35
140	Epigenetic discrimination of identical twins from blood under the forensic scenario. Forensic Science International: Genetics, 2017, 31, 67-80.	1.6	35
141	Epigenome-wide association meta-analysis of DNA methylation with coffee and tea consumption. Nature Communications, 2021, 12, 2830.	5.8	35
142	Novel taxonomy-independent deep learning microbiome approach allows for accurate classification of different forensically relevant human epithelial materials. Forensic Science International: Genetics, 2019, 41, 72-82.	1.6	34
143	Identification of a candidate genetic variant for the high prevalence of type II diabetes in Polynesians. European Journal of Human Genetics, 2007, 15, 584-589.	1.4	33
144	Identification and characterization of novel rapidly mutating Yâ€chromosomal short tandem repeat markers. Human Mutation, 2020, 41, 1680-1696.	1.1	33

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145	Towards simultaneous individual and tissue identification: A proof-of-principle study on parallel sequencing of STRs, amelogenin, and mRNAs with the Ion Torrent PGM. Forensic Science International: Genetics, 2015, 17, 122-128.	1.6	32
146	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
147	Impact of SNP microarray analysis of compromised DNA on kinship classification success in the context of investigative genetic genealogy. Forensic Science International: Genetics, 2022, 56, 102625.	1.6	32
148	An Automatic 3D Facial Landmarking Algorithm Using 2D Gabor Wavelets. IEEE Transactions on Image Processing, 2016, 25, 580-588.	6.0	31
149	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
150	Patterns of Y-Chromosome Diversity Intersect with the Trans-New Guinea Hypothesis. Molecular Biology and Evolution, 2007, 24, 2546-2555.	3.5	30
151	Online Y-chromosomal short tandem repeat haplotype reference database (YHRD) for U.S. populations. Journal of Forensic Sciences, 2002, 47, 513-9.	0.9	30
152	Unexpected Island Effects at an Extreme: Reduced Y Chromosome and Mitochondrial DNA Diversity in Nias. Molecular Biology and Evolution, 2011, 28, 1349-1361.	3.5	29
153	Genetic variation in regulatory <scp>DNA</scp> elements: the case of <i><scp>OCA</scp>2</i> transcriptional regulation. Pigment Cell and Melanoma Research, 2014, 27, 169-177.	1.5	29
154	Developmental validation of mitochondrial DNA genotyping assays for adept matrilineal inference of biogeographic ancestry at a continental level. Forensic Science International: Genetics, 2014, 11, 39-51.	1.6	29
155	BMD Loci Contribute to Ethnic and Developmental Differences in Skeletal Fragility across Populations: Assessment of Evolutionary Selection Pressures. Molecular Biology and Evolution, 2015, 32, 2961-2972.	3.5	29
156	Analysis of 36 Y-STR marker units including a concordance study among 2085 Dutch males. Forensic Science International: Genetics, 2015, 14, 174-181.	1.6	29
157	Multiplex genotyping system for efficient inference of matrilineal genetic ancestry with continental resolution. Investigative Genetics, 2011, 2, 6.	3.3	27
158	MtDNA SNP multiplexes for efficient inference of matrilineal genetic ancestry within Oceania. Forensic Science International: Genetics, 2012, 6, 425-436.	1.6	27
159	Forensic ancestry analysis with two capillary electrophoresis ancestry informative marker (AIM) panels: Results of a collaborative EDNAP exercise. Forensic Science International: Genetics, 2015, 19, 56-67.	1.6	27
160	Dissecting Daily and Circadian Expression Rhythms of Clock-Controlled Genes in Human Blood. Journal of Biological Rhythms, 2016, 31, 68-81.	1.4	27
161	Novel quantitative pigmentation phenotyping enhances genetic association, epistasis, and prediction of human eye colour. Scientific Reports, 2017, 7, 43359.	1.6	27
162	Lifestyle and Physiological Factors Associated with Facial Wrinkling in MenÂand Women. Journal of Investigative Dermatology, 2017, 137, 1692-1699.	0.3	27

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163	Evaluation of the VISAGE Basic Tool for Appearance and Ancestry Prediction Using PowerSeq Chemistry on the MiSeq FGx System. Genes, 2020, 11, 708.	1.0	27
164	Antiquity and diversity of aboriginal Australian <scp>Y</scp>â€chromosomes. American Journal of Physical Anthropology, 2016, 159, 367-381.	2.1	26
165	Microbiome-based body site of origin classification of forensically relevant blood traces. Forensic Science International: Genetics, 2020, 47, 102280.	1.6	26
166	Increasing phylogenetic resolution still informative for Y chromosomal studies on West-European populations. Forensic Science International: Genetics, 2014, 9, 179-185.	1.6	25
167	Genetic Ancestry of Rapanui before and after European Contact. Current Biology, 2017, 27, 3209-3215.e6.	1.8	25
168	Investigating the impact of age-depended hair colour darkening during childhood on DNA-based hair colour prediction with the HIrisPlex system. Forensic Science International: Genetics, 2018, 36, 26-33.	1.6	25
169	Development and optimization of the VISAGE basic prototype tool for forensic age estimation. Forensic Science International: Genetics, 2020, 48, 102322.	1.6	25
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