Christopher Phillips

List of Publications by Year
in descending order

186 papers	8,259 citations	38742 50 h-index	56724 83 g-index
189 all docs	189 docs citations	189 times ranked	4940 citing authors

#	Article	IF	Citations
1	Combining current knowledge on DNA methylation-based age estimation towards the development of a superior forensic DNA intelligence tool. Forensic Science International: Genetics, 2022, 57, 102637.	3.1	15
2	A collaborative exercise on DNA methylation-based age prediction and body fluid typing. Forensic Science International: Genetics, 2022, 57, 102656.	3.1	15
3	A common epigenetic clock from childhood to old age. Forensic Science International: Genetics, 2022, 60, 102743.	3.1	16
4	Development of the VISAGE enhanced tool and statistical models for epigenetic age estimation in blood, buccal cells and bones. Aging, 2021, 13, 6459-6484.	3.1	49
5	The analysis of ancestry with small-scale forensic panels of genetic markers. Emerging Topics in Life Sciences, 2021, 5, 443-453.	2.6	4
6	Investigative genetic genealogy: Current methods, knowledge and practice. Forensic Science International: Genetics, 2021, 52, 102474.	3.1	73
7	Development and Evaluation of the Ancestry Informative Marker Panel of the VISAGE Basic Tool. Genes, 2021, 12, 1284.	2.4	20
8	Epigenetic age prediction in semen â€“ marker selection and model development. Aging, 2021, 13, 19145-19164.	3.1	23
9	Impact of excessive alcohol abuse on age prediction using the VISAGE enhanced tool for epigenetic age estimation in blood. International Journal of Legal Medicine, 2021, 135, 2209-2219.	2.2	9
10	Evaluation of a custom QIAseq targeted DNA panel with 164 ancestry informative markers sequenced with the Illumina MiSeq. Scientific Reports, 2021, 11, 21040.	3.3	3
11	PIMA: A population informative multiplex for the Americas. Forensic Science International: Genetics, 2020, 44, 102200.	3.1	7
12	The MASTiFF panelâ€”a versatile multiple-allele SNP test for forensics. International Journal of Legal Medicine, 2020, 134, 441-450.	2.2	8
13	Characterization of ancestry informative markers in the Tigray population of Ethiopia: A contribution to the identification process of dead migrants in the Mediterranean Sea. Forensic Science International: Genetics, 2020, 45, 102207.	3.1	6
14	Building a custom large-scale panel of novel microhaplotypes for forensic identification using MiSeq and Ion S5 massively parallel sequencing systems. Forensic Science International: Genetics, 2020, 45, 102213.	3.1	70
15	The first GHEP-ISFG collaborative exercise on forensic applications of massively parallel sequencing. Forensic Science International: Genetics, 2020, 49, 102391.	3.1	6
16	Forensic evaluation of the Asia Pacific ancestry-informative MAPlex assay. Forensic Science International: Genetics, 2020, 48, 102344.	3.1	17
17	A Comparison of Forensic Age Prediction Models Using Data From Four DNA Methylation Technologies. Frontiers in Genetics, 2020, 11, 932.	2.3	26
18	Broadening the Applicability of a Custom Multi-Platform Panel of Microhaplotypes: Bio-Geographical Ancestry Inference and Expanded Reference Data. Frontiers in Genetics, 2020, 11, 581041.	2.3	17

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19	Evaluation of the VISAGE Basic Tool for Appearance and Ancestry Prediction Using PowerSeq Chemistry on the MiSeq FGx System. Genes, 2020, 11, 708.	2.4	27
20	Development and validation of the VISAGE AmpliSeq basic tool to predict appearance and ancestry from DNA. Forensic Science International: Genetics, 2020, 48, 102336.	3.1	43
21	A compilation of tri-allelic SNPs from 1000 Genomes and use of the most polymorphic loci for a large-scale human identification panel. Forensic Science International: Genetics, 2020, 46, 102232.	3.1	34
22	Development and validation of the EUROFORGEN NAME (North African and Middle Eastern) ancestry panel. Forensic Science International: Genetics, 2019, 42, 260-267.	3.1	46
23	MAPlex - A massively parallel sequencing ancestry analysis multiplex for Asia-Pacific populations. Forensic Science International: Genetics, 2019, 42, 213-226.	3.1	63
24	Performance of ancestry-informative SNP and microhaplotype markers. Forensic Science International: Genetics, 2019, 43, 102141.	3.1	55
25	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.	3.1	45
26	Methicillin-Resistant Staphylococcus aureus Meningitis from Transanal Migration of a Ventriculoperitoneal Shunt. Journal of Emergency Medicine, 2019, 57, e81-e84.	0.7	2
27	The EUROFORGEN NAME Ampliseqâ„¢ custom panel: A second tier panel developed for differentiation of individuals from the Middle East/North Africa. Forensic Science International: Genetics Supplement Series, 2019, 7, 846-848.	0.3	3
28	â€œThe devilâ€™s in the detailâ€: Release of an expanded, enhanced and dynamically revised forensic STR Sequence Guide. Forensic Science International: Genetics, 2018, 34, 162-169.	3.1	73
29	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.	3.1	64
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.	3.1	38
31	Ancestry analysis in rural Brazilian populations of African descent. Forensic Science International: Genetics, 2018, 36, 160-166.	3.1	9
32	Inferring biogeographic ancestry with compound markers of slow and fast evolving polymorphisms. European Journal of Human Genetics, 2018, 26, 1697-1707.	2.8	13
33	Dog breed affiliation with a forensically validated canine STR set. Forensic Science International: Genetics, 2018, 37, 126-134.	3.1	12
34	Global patterns of STR sequence variation: Sequencing the CEPH human genome diversity panel for 58 forensic STRs using the Illumina ForenSeq DNA Signature Prep Kit. Electrophoresis, 2018, 39, 2708-2724.	2.4	51
35	Tracking age-correlated DNA methylation markers in the young. Forensic Science International: Genetics, 2018, 36, 50-59.	3.1	41
36	Modified aging of elite athletes revealed by analysis of epigenetic age markers. Aging, 2018, 10, 241-252.	3.1	25

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37	Evaluation of the Qiagen 140-SNP forensic identification multiplex for massively parallel sequencing. Forensic Science International: Genetics, 2017, 28, 35-43.	3.1	33
38	A forensic multiplex of nine novel pentameric-repeat STRs. Forensic Science International: Genetics, 2017, 29, 154-164.	3.1	6
39	A genomic audit of newly-adopted autosomal STRs for forensic identification. Forensic Science International: Genetics, 2017, 29, 193-204.	3.1	32
40	Using EuroForMix to analyse complex SNP mixtures, up to six contributors. Forensic Science International: Genetics Supplement Series, 2017, 6, e277-e279.	0.3	4
41	Helping the identification of refugee shipwreck victims in the Straits of Sicily: An AIM-Indel reference database for the Tigray population of Ethiopia. Forensic Science International: Genetics Supplement Series, 2017, 6, e21-e23.	0.3	1
42	STRSeq: A catalog of sequence diversity at human identification Short Tandem Repeat loci. Forensic Science International: Genetics, 2017, 31, 111-117.	3.1	77
43	A collaborative EDNAP exercise on SNaPshotâ„¢-based mtDNA control region typing. Forensic Science International: Genetics, 2017, 26, 77-84.	3.1	5
44	Forensic SNP genotyping with SNaPshot: Technical considerations for the development and optimization of multiplexed SNP assays. Forensic Science Review, 2017, 29, 57-76.	0.6	21
45	Forensic individual age estimation with DNA: From initial approaches to methylation tests. Forensic Science Review, 2017, 29, 121-144.	0.6	50
46	D5S2500 is an ambiguously characterized STR: Identification and description of forensic microsatellites in the genomics age.. Forensic Science International: Genetics, 2016, 23, 19-24.	3.1	21
47	Inference of Ancestry in Forensic Analysis I: Autosomal Ancestry-Informative Marker Sets. Methods in Molecular Biology, 2016, 1420, 233-253.	0.9	20
48	Recommendations of the DNA Commission of the International Society for Forensic Genetics (ISFG) on quality control of autosomal Short Tandem Repeat allele frequency databasing (STRidER). Forensic Science International: Genetics, 2016, 24, 97-102.	3.1	130
49	Development of a methylation marker set for forensic age estimation using analysis of public methylation data and the Agena Bioscience EpiTYPER system. Forensic Science International: Genetics, 2016, 24, 65-74.	3.1	127
50	Inter-laboratory evaluation of the EUROFORGEN Global ancestry-informative SNP panel by massively parallel sequencing using the Ion PGMâ„¢. Forensic Science International: Genetics, 2016, 23, 178-189.	3.1	65
51	The Global AIMs Nano set: A 31-plex SNaPshot assay of ancestry-informative SNPs. Forensic Science International: Genetics, 2016, 22, 81-88.	3.1	57
52	Massively parallel sequencing of forensic STRs: Considerations of the DNA commission of the International Society for Forensic Genetics (ISFG) on minimal nomenclature requirements. Forensic Science International: Genetics, 2016, 22, 54-63.	3.1	190
53	Pacifiplex : an ancestry-informative SNP panel centred on Australia and the Pacific region. Forensic Science International: Genetics, 2016, 20, 71-80.	3.1	60
54	Inference of biogeographical ancestry across central regions of Eurasia. International Journal of Legal Medicine, 2016, 130, 73-79.	2.2	17

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55	Forensic genetic analysis of bio-geographical ancestry. Forensic Science International: Genetics, 2015, 18, 49-65.	3.1	191
56	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.	3.1	27
57	Exploration of SNP variants affecting hair colour prediction in Europeans. International Journal of Legal Medicine, 2015, 129, 963-975.	2.2	31
58	Tetra-allelic SNPs: Informative forensic markers compiled from public whole-genome sequence data. Forensic Science International: Genetics, 2015, 19, 100-106.	3.1	44
59	Inter-laboratory evaluation of SNP-based forensic identification by massively parallel sequencing using the Ion PGMâ„¢. Forensic Science International: Genetics, 2015, 17, 110-121.	3.1	105
60	Completion of a worldwide reference panel of samples for an ancestry informative Indel assay. Forensic Science International: Genetics, 2015, 17, 75-80.	3.1	30
61	Evaluation of the predictive capacity of DNA variants associated with straight hair in Europeans. Forensic Science International: Genetics, 2015, 19, 280-288.	3.1	36
62	Studies of East European populations with a 46-plex ancestry-informative indel set. Forensic Science International: Genetics Supplement Series, 2015, 5, e16-e18.	0.3	1
63	The open-source software LRmix can be used to analyse SNP mixtures. Forensic Science International: Genetics Supplement Series, 2015, 5, e50-e51.	0.3	13
64	Ancestry informative markers: Inference of ancestry in aged bone samples using an autosomal AIM-Indel multiplex. Forensic Science International: Genetics, 2015, 16, 58-63.	3.1	27
65	A SNaPshot of next generation sequencing for forensic SNP analysis. Forensic Science International: Genetics, 2015, 14, 50-60.	3.1	85
66	The genetics of skin, hair, and eye color variation and its relevance to forensic pigmentation predictive tests. Forensic Science Review, 2015, 27, 13-40.	0.6	17
67	â€œNew turns from old STaRsâ€• Enhancing the capabilities of forensic short tandem repeat analysis. Electrophoresis, 2014, 35, 3173-3187.	2.4	31
68	SNP variation with latitude: Analysis of the SNPforID 52-plex markers in north, mid-region and south Chilean populations. Forensic Science International: Genetics, 2014, 10, 12-16.	3.1	10
69	Building a forensic ancestry panel from the ground up: The EUROFORGEN Global AIM-SNP set. Forensic Science International: Genetics, 2014, 11, 13-25.	3.1	116
70	Allele frequencies of the five new European Standard Set (ESS) STRs and 15 established STRs in a Turkish population. Forensic Science International: Genetics, 2014, 9, e26.	3.1	13
71	A global analysis of Y-chromosomal haplotype diversity for 23 STR loci. Forensic Science International: Genetics, 2014, 12, 12-23.	3.1	214
72	Collaborative EDNAP exercise on the IrisPlex system for DNA-based prediction of human eye colour. Forensic Science International: Genetics, 2014, 11, 241-251.	3.1	23

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73	Exploring iris colour prediction and ancestry inference in admixed populations of South America. Forensic Science International: Genetics, 2014, 13, 3-9.	3.1	32
74	Development of a forensic skin colour predictive test. Forensic Science International: Genetics, 2014, 13, 34-44.	3.1	69
75	Global population variability in Qiagen Investigator HDplex STRs. Forensic Science International: Genetics, 2014, 8, 36-43.	3.1	19
76	Gauging the impact of Forensic Science International: Geneticsâ€"Citation metrics for top articles in the journal. Forensic Science International: Genetics, 2014, 11, e1-e6.	3.1	2
77	RNA/DNA co-analysis from human menstrual blood and vaginal secretion stains: Results of a fourth and fifth collaborative EDNAP exercise. Forensic Science International: Genetics, 2014, 8, 203-212.	3.1	94
78	Toward Male Individualization with Rapidly Mutating Y-Chromosomal Short Tandem Repeats. Human Mutation, 2014, 35, 1021-1032.	2.5	151
79	Ancestry Informative Markers. , 2013, , 323-331.		3
80	Global population variability in Promega PowerPlex CS7, D6S1043, and Penta B STRs. International Journal of Legal Medicine, 2013, 127, 901-906.	2.2	11
81	Comparative analysis of two indel-based ancestry informative multiplex PCR typing kits. Forensic Science International: Genetics Supplement Series, 2013, 4, e21-e22.	0.3	0
82	Revision of the SNPforID 34-plex forensic ancestry test: Assay enhancements, standard reference sample genotypes and extended population studies. Forensic Science International: Genetics, 2013, 7, 63-74.	3.1	102
83	Further development of forensic eye color predictive tests. Forensic Science International: Genetics, 2013, 7, 28-40.	3.1	119
84	An assessment of Bayesian and multinomial logistic regression classification systems to analyse admixed individuals. Forensic Science International: Genetics Supplement Series, 2013, 4, e63-e64.	0.3	10
85	Eurasiaplex: A forensic SNP assay for differentiating European and South Asian ancestries. Forensic Science International: Genetics, 2013, 7, 359-366.	3.1	102
86	Casework application of a stand-alone pentaplex assay of extended-ESS STRs. Legal Medicine, 2013, 15, 217-221.	1.3	0
87	Development of a novel forensic STR multiplex for ancestry analysis and extended identity testing. Electrophoresis, 2013, 34, 1151-1162.	2.4	34
88	An overview of STRUCTURE: applications, parameter settings, and supporting software. Frontiers in Genetics, 2013, 4, 98.	2.3	432
89	Differentiation of African Components of Ancestry to Stratify Groups in a Caseâ€"Control Study of a Brazilian Urban Population. Genetic Testing and Molecular Biomarkers, 2012, 16, 524-530.	0.7	5
90	Typing short amplicon binary polymorphisms: Supplementary SNP and Indel genetic information in the analysis of highly degraded skeletal remains. Forensic Science International: Genetics, 2012, 6, 469-476.	3.1	60

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91	Forensic performance of two insertionâ€“deletion marker assays. International Journal of Legal Medicine, 2012, 126, 725-737.	2.2	70
92	Evaluation of PRDM9 variation as a risk factor for recurrent genomic disorders and chromosomal non-disjunction. Human Genetics, 2012, 131, 1519-1524.	3.8	15
93	A new SNP assay for identification of highly degraded human DNA. Forensic Science International: Genetics, 2012, 6, 341-349.	3.1	82
94	Analysis of a claimed distant relationship in a deficient pedigree using high density SNP data. Forensic Science International: Genetics, 2012, 6, 350-353.	3.1	22
95	The recombination landscape around forensic STRs: Accurate measurement of genetic distances between syntenic STR pairs using HapMap high density SNP data. Forensic Science International: Genetics, 2012, 6, 354-365.	3.1	73
96	An evaluation of potential allelic association between the STRs vWA and D12S391: Implications in criminal casework and applications to short pedigrees. Forensic Science International: Genetics, 2012, 6, 477-486.	3.1	59
97	Distribution of allele frequencies of 20 STRs loci in a population sample from Calabria, Southern Italy. Forensic Science International: Genetics, 2012, 6, e137-e138.	3.1	5
98	Analysis of the SNPforID 52-plex markers in four Native American populations from Venezuela. Forensic Science International: Genetics, 2012, 6, e142-e145.	3.1	7
99	Allele frequencies of 20 STRs from Northwest Spain (Galicia). Forensic Science International: Genetics, 2012, 6, e149-e150.	3.1	9
100	European Network of Forensic Science Institutes (ENFSI): Evaluation of new commercial STR multiplexes that include the European Standard Set (ESS) of markers. Forensic Science International: Genetics, 2012, 6, 819-826.	3.1	53
101	Genetic variability of the SNPforID 52-plex identification SNP panel in Italian population samples. Forensic Science International: Genetics, 2012, 6, e185-e186.	3.1	3
102	SNPs as Supplements in Simple Kinship Analysis or as Core Markers in Distant Pairwise Relationship Tests: When Do SNPs Add Value or Replace Well-Established and Powerful STR Tests?. Transfusion Medicine and Hemotherapy, 2012, 39, 202-210.	1.6	52
103	A 34-plex Autosomal SNP Single Base Extension Assay for Ancestry Investigations. Methods in Molecular Biology, 2012, 830, 109-126.	0.9	20
104	Straightforward Inference of Ancestry and Admixture Proportions through Ancestry-Informative Insertion Deletion Multiplexing. PLoS ONE, 2012, 7, e29684.	2.5	211
105	Evaluation of forensic and anthropological potential of D9S1120 in Mestizos and Amerindian populations from Mexico. Croatian Medical Journal, 2012, 53, 423-431.	0.7	3
106	Application of Autosomal SNPs and Indels in Forensic Analysis. Forensic Science Review, 2012, 24, 43-62.	0.6	3
107	A SNP multiplex for the simultaneous prediction of biogeographic ancestry and pigmentation type. Forensic Science International: Genetics Supplement Series, 2011, 3, e500-e501.	0.3	10
108	Characterization of U.S. population samples using a 34plex ancestry informative SNP multiplex. Forensic Science International: Genetics Supplement Series, 2011, 3, e182-e183.	0.3	2

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109	Forensic performance of insertionâ€“deletion marker systems. Forensic Science International: Genetics Supplement Series, 2011, 3, e443-e444.	0.3	11
110	A study of East Timor variability using the SNPforID 52-plex SNP panel. Forensic Science International: Genetics, 2011, 5, e25-e26.	3.1	13
111	Genetic analysis of the SNPforID 34-plex ancestry informative SNP panel in Tunisian and Libyan populations. Forensic Science International: Genetics, 2011, 5, e45-e47.	3.1	10
112	Validation of a Cost-Efficient Multi-Purpose SNP Panel for Disease Based Research. PLoS ONE, 2011, 6, e19699.	2.5	6
113	Analysis of global variability in 15 established and 5 new European Standard Set (ESS) STRs using the CEPH human genome diversity panel. Forensic Science International: Genetics, 2011, 5, 155-169.	3.1	103
114	ENGINES: exploring single nucleotide variation in entire human genomes. BMC Bioinformatics, 2011, 12, 105.	2.6	34
115	Pharmacogenetics of OATP Transporters Reveals That SLCO1B1 c.388A>G Variant Is Determinant of Increased Atorvastatin Response. International Journal of Molecular Sciences, 2011, 12, 5815-5827.	4.1	49
116	Association study of 44 candidate genes with depressive and anxiety symptoms in post-partum women. Journal of Psychiatric Research, 2010, 44, 717-724.	3.1	69
117	Ancestry Analysis in the 11-M Madrid Bomb Attack Investigation. PLoS ONE, 2009, 4, e6583.	2.5	110
118	A new multiplex for human identification using insertion/deletion polymorphisms. Electrophoresis, 2009, 30, 3682-3690.	2.4	197
119	Viability of in-house datamarting approaches for population genetics analysis of SNP genotypes. BMC Bioinformatics, 2009, 10, S5.	2.6	17
120	SNP Databases. Methods in Molecular Biology, 2009, 578, 43-71.	0.9	16
121	Genetic variability of the SNPforID 52-plex identification-SNP panel in Central West Colombia. Forensic Science International: Genetics, 2009, 4, e9-e10.	3.1	15
122	Population data of 5 next generation STRs in Southern Italy. Forensic Science International: Genetics Supplement Series, 2009, 2, 386-387.	0.3	0
123	Population data of 52 autosomal SNPs in Italian population. Forensic Science International: Genetics Supplement Series, 2009, 2, 351-352.	0.3	1
124	pop.STRâ€”An online population frequency browser for established and new forensic STRs. Forensic Science International: Genetics Supplement Series, 2009, 2, 361-362.	0.3	38
125	Development and validation of a next generation STR ESS-pentaplex. Forensic Science International: Genetics Supplement Series, 2009, 2, 25-26.	0.3	4
126	Internal validation of 29 autosomal SNP multiplex using a ABI 310 genetic analyser. Forensic Science International: Genetics Supplement Series, 2009, 2, 129-130.	0.3	5

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127	Insertion/deletion polymorphisms: A multiplex assay and forensic applications. Forensic Science International: Genetics Supplement Series, 2009, 2, 513-515.	0.3	50
128	Supplementary markers for deficient immigration cases: Additional STRs or SNPs?. Forensic Science International: Genetics Supplement Series, 2009, 2, 153-154.	0.3	1
129	The SNPforID browser: an online tool for query and display of frequency data from the SNPforID project. International Journal of Legal Medicine, 2008, 122, 435-440.	2.2	47
130	The mtDNA ancestry of admixed Colombian populations. American Journal of Human Biology, 2008, 20, 584-591.	1.6	44
131	SPSmart: adapting population based SNP genotype databases for fast and comprehensive web access. BMC Bioinformatics, 2008, 9, 428.	2.6	95
132	Association of schizophrenia with DTNBP1 but not with DAO, DAOA, NRG1 and RGS4 nor their genetic interaction. Journal of Psychiatric Research, 2008, 42, 278-288.	3.1	80
133	Analyses of variants located in estrogen metabolism genes (ESR1, ESR2, COMT and APOE) and schizophrenia. Schizophrenia Research, 2008, 100, 308-315.	2.0	23
134	Forensic typing of autosomal SNPs with a 29 SNP-multiplexâ€"Results of a collaborative EDNAP exercise. Forensic Science International: Genetics, 2008, 2, 176-183.	3.1	53
135	Resolving relationship tests that show ambiguous STR results using autosomal SNPs as supplementary markers. Forensic Science International: Genetics, 2008, 2, 198-204.	3.1	100
136	Case report: Identification of skeletal remains using short-amplicon marker analysis of severely degraded DNA extracted from a decomposed and charred femur. Forensic Science International: Genetics, 2008, 2, 212-218.	3.1	66
137	D9S1120, a simple STR with a common Native American-specific allele: Forensic optimization, locus characterization and allele frequency studies. Forensic Science International: Genetics, 2008, 3, 7-13.	3.1	25
138	Challenging DNA: Assessment of a range of genotyping approaches for highly degraded forensic samples. Forensic Science International: Genetics Supplement Series, 2008, 1, 26-28.	0.3	38
139	Genetic characterization of 52 autosomal SNPs in two sub-Saharan African populations. Forensic Science International: Genetics Supplement Series, 2008, 1, 361-363.	0.3	1
140	Report on ISFG SNP Panel Discussion. Forensic Science International: Genetics Supplement Series, 2008, 1, 471-472.	0.3	26
141	Genetic characterization of 52 autosomal SNPs in the Portuguese population. Forensic Science International: Genetics Supplement Series, 2008, 1, 358-360.	0.3	3
142	Differentiating European and South Asian individuals using SNPs and pyrosequencing technology. Forensic Science International: Genetics Supplement Series, 2008, 1, 476-478.	0.3	2
143	Forensic validation of the Genplex SNP typing systemâ€"Results of an inter-laboratory study. Forensic Science International: Genetics Supplement Series, 2008, 1, 389-393.	0.3	4
144	Viability of in-house datamarting approaches for population genetics analysis of snp genotypes. , 2008, , .		0

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145	Forensic validation of the SNPforID 52-plex assay. Forensic Science International: Genetics, 2007, 1, 186-190.	3.1	74
146	Evaluation of the Genplex SNP typing system and a 49plex forensic marker panel. Forensic Science International: Genetics, 2007, 1, 180-185.	3.1	85
147	Finding genes that underlie physical traits of forensic interest using genetic tools. Forensic Science International: Genetics, 2007, 1, 100-104.	3.1	19
148	Inferring ancestral origin using a single multiplex assay of ancestry-informative marker SNPs. Forensic Science International: Genetics, 2007, 1, 273-280.	3.1	332
149	Online Resources for SNP Analysis: A Review and Route Map. Molecular Biotechnology, 2007, 35, 65-98.	2.4	22
150	Initial study of candidate genes on chromosome two for relative hand skill. International Congress Series, 2006, 1288, 798-800.	0.2	0
151	A compact population analysis test using 32 SNPs with highly diverse allele frequency distributions. International Congress Series, 2006, 1288, 58-60.	0.2	0
152	Development of a multiplex PCR assay detecting 52 autosomal SNPs. International Congress Series, 2006, 1288, 67-69.	0.2	4
153	Mixture analysis using SWaPâ„¢ SNPs and non-biallelic SNPs. International Congress Series, 2006, 1288, 34-36.	0.2	0
154	Y chromosome STR haplotype data for an Irish population. Forensic Science International, 2006, 161, 64-68.	2.2	6
155	Ancestry vs physical traits: the search for ancestry informative markers (AIMs). International Journal of Legal Medicine, 2006, 120, 188-189.	2.2	7
156	A multiplex assay with 52 single nucleotide polymorphisms for human identification. Electrophoresis, 2006, 27, 1713-1724.	2.4	462
157	Using Online Databases for Developing SNP Markers of Forensic Interest. , 2005, 297, 083-106.		5
158	Y chromosome STR haplotypes in three UK populations. Forensic Science International, 2005, 152, 289-305.	2.2	19
159	A study of mutation rates and the characterisation of intermediate, null and duplicated alleles for 13 Y chromosome STRs. Forensic Science International, 2005, 155, 65-70.	2.2	35
160	Human genome-wide screen of haplotype-like blocks of reduced diversity. Gene, 2005, 349, 219-225.	2.2	43
161	Relative efficiency of the linkage disequilibrium mapping approach in detecting candidate genes for schizophrenia in different European populations. Genomics, 2005, 86, 280-286.	2.9	9
162	Large-scale single nucleotide polymorphism analysis of candidates for low-penetrance breast cancer genes. Breast Cancer Research, 2005, 7, 1.	5.0	2

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163	High-density screening of the Zbtb7gene in breast cancer patients. Breast Cancer Research, 2005, 7, 1.	5.0	1
164	ZBTB7 HapMap in a worldwide population study. Breast Cancer Research, 2005, 7, 1.	5.0	1
165	Typing of mitochondrial DNA coding region SNPs of forensic and anthropological interest using SNaPshot minisequencing. Forensic Science International, 2004, 140, 251-257.	2.2	161
166	Selecting single nucleotide polymorphisms for forensic applications. International Congress Series, 2004, 1261, 18-20.	0.2	11
167	Nonbinary single-nucleotide polymorphism markers. International Congress Series, 2004, 1261, 27-29.	0.2	21
168	Population specific single nucleotide polymorphisms. International Congress Series, 2004, 1261, 233-235.	0.2	4
169	Population studies using single nucleotide polymorphismsâ€"how important is detailed sample origin information?. International Congress Series, 2004, 1261, 30-32.	0.2	0
170	Haplotype discrimination amongst three UK population groups using three multiplexes to type eleven Y chromosome STRs. International Congress Series, 2003, 1239, 435-437.	0.2	2
171	Typing Y-chromosome single nucleotide polymorphisms with DNA microarray technology. International Congress Series, 2003, 1239, 21-25.	0.2	5
172	Haplotype Combinations of Calpain 10 Gene Polymorphisms Associate With Increased Risk of Impaired Glucose Tolerance and Type 2 Diabetes in South Indians. Diabetes, 2002, 51, 1622-1628.	0.6	77
173	Results of a collaborative study of the EDNAP group regarding the reproducibility and robustness of the Y-chromosome STRs DYS19, DYS389 I and II, DYS390 and DYS393 in a PCR pentaplex format. Forensic Science International, 2001, 119, 28-41.	2.2	41
174	Normal and anomalous electrophoretic behavior of polymerase chain reaction-based DNA polymorphisms in polyacrylamide gels. Electrophoresis, 1998, 19, 1566-1572.	2.4	14
175	Band shift analysis of three base-pair repeat alleles in the short tandem repeat locus D12S391. Forensic Science International, 1998, 93, 79-88.	2.2	15
176	Report of the European DNA profiling group (EDNAP)-an investigation of the hypervariable STR loci ACTBP2, APOAI1 and D11S554 and the compound loci D12S391 and D1S1656. Forensic Science International, 1998, 98, 193-200.	2.2	12
177	Report of the European DNA profiling group (EDNAP): an investigation of the complex STR loci D21S11 and HUMFIBRA (FGA). Forensic Science International, 1997, 86, 25-33.	2.2	25
178	Report on the third EDNAP collaborative STR exercise. Forensic Science International, 1996, 78, 83-93.	2.2	29
179	Report on the second EDNAP collaborative STR exercise. Forensic Science International, 1995, 71, 137-152.	2.2	64
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#	Article	IF	Citations
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