Claus BÃ¸rsting

List of Publications by Year
in descending order

Source: https://exaly.com/author-pdf/7382590/publications.pdf

Version: 2024-02-01

147 papers	4,199 citations	109321 35 h-index	128289 60 g-index
151 all docs	151 docs citations	151 times ranked	2984 citing authors

#	Article	IF	Citations
1	Sequencing of human identification markers in an Uyghur population using the MiSeq FGx^{TM} Forensic Genomics System. Forensic Sciences Research, 2022, 7, 154-162.	1.6	7
2	Genetic analysis of sixteen autosomal STR loci in three Tunisian populations from Makthar, Nabeul and Sousse. Annals of Human Biology, 2022, , 1-22.	1.0	1
3	Testing the Ion AmpliSeqâ„¢ HID Y-SNP Research Panel v1 for performance and resolution in admixed South Americans of haplogroup Q. Forensic Science International: Genetics, 2022, 59, 102708.	3.1	3
4	Forensic application and genetic diversity of 21 autosomal STR loci in five major population groups of Pakistan. International Journal of Legal Medicine, 2021, 135, 775-777.	2.2	4
5	Evaluation of a custom GeneReadâ„¢ massively parallel sequencing assay with 210 ancestry informative SNPs using the Ion S5â„¢ and MiSeq platforms. Forensic Science International: Genetics, 2021, 50, 102411.	3.1	7
6	Gene expressions in cerebral palsy subjects reveal structural and functional changes in the gastrocnemius muscle that are closely associated with passive muscle stiffness. Cell and Tissue Research, 2021, 384, 513-526.	2.9	8
7	Prediction of Eye Colour in Scandinavians Using the EyeColour 11 (EC11) SNP Set. Genes, 2021, 12, 821.	2.4	12
8	Analysis of Skin Pigmentation and Genetic Ancestry in Three Subpopulations from Pakistan: Punjabi, Pashtun, and Baloch. Genes, 2021, 12, 733.	2.4	2
9	Ancestry prediction efficiency of the software GenoGeographer using a z-score method and the ancestry informative markers in the Precision ID Ancestry Panel. Forensic Science International: Genetics, 2020, 44, 102154.	3.1	19
10	Association between brown eye colour in rs12913832:GG individuals and SNPs in TYR, TYRP1, and SLC24A4. PLoS ONE, 2020, 15, e0239131.	2.5	14
11	Evaluation of the Precision of Ancestry Inferences in South American Admixed Populations. Frontiers in Genetics, 2020, 11, 966.	2.3	10
12	Skin pigmentation and genetic variants in an admixed Brazilian population of primarily European ancestry. International Journal of Legal Medicine, 2020, 134, 1569-1579.	2.2	4
13	Development of an automated AmpliSeqâ„¢ library building workflow for biological stain samples on the BiomekÂ® 3000. BioTechniques, 2020, 68, 342-344.	1.8	4
14	STRinNGS v2.0: Improved tool for analysis and reporting of STR sequencing data. Forensic Science International: Genetics, 2020, 48, 102331.	3.1	11
15	The Danish STR sequence database: duplicate typing of 363 Danes with the ForenSeqâ„¢ DNA Signature Prep Kit. International Journal of Legal Medicine, 2019, 133, 325-334.	2.2	34
16	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
17	Non-invasive prenatal paternity testing using a standard forensic genetic massively parallel sequencing assay for amplification of human identification SNPs. International Journal of Legal Medicine, 2019, 133, 1361-1368.	2.2	10
18	Perception of blue and brown eye colours for forensic DNA phenotyping. Forensic Science International: Genetics Supplement Series, 2019, 7, 476-477.	0.3	9

#	Article	IF	Citations
19	Analysis of 16 autosomal STR loci in Uyghur and Kazakh populations from Xinjiang, China. Forensic Science International: Genetics, 2019, 40, e262-e263.	3.1	3
20	Presentation of the Human Pigmentation (HuPi) AmpliSeqâ„¢ custom panel. Forensic Science International: Genetics Supplement Series, 2019, 7, 478-479.	0.3	3
21	Optimization of the collection and analysis of touch DNA traces. Forensic Science International: Genetics Supplement Series, 2019, 7, 98-99.	0.3	9
22	Sequence variants in muscle tissueâ€related genes may determine the severity of muscle contractures in cerebral palsy. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2019, 180, 12-24.	1.7	4
23	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
24	GENETIC PORTRAIT OF THE PUNJABI POPULATION FROM PAKISTAN USING THE PRECISION ID ANCESTRY PANEL. Forensic Science International: Genetics Supplement Series, 2019, 7, 87-89.	0.3	1
25	Quantification of massively parallel sequencing libraries â€“ a comparative study of eight methods. Scientific Reports, 2018, 8, 1110.	3.3	30
26	Analysis of mainland Japanese and Okinawan Japanese populations using the precision ID Ancestry Panel. Forensic Science International: Genetics, 2018, 33, 106-109.	3.1	16
27	Sequencing of 231 forensic genetic markers using the MiSeq FGxâ„¢ forensic genomics systemÂâ€“Âan evaluation of the assay and software. Forensic Sciences Research, 2018, 3, 111-123.	1.6	37
28	Modelling allelic drop-outs in STR sequencing data generated by MPS. Forensic Science International: Genetics, 2018, 37, 6-12.	3.1	7
29	Sequencing of mitochondrial genomes using the Precision ID mtDNA Whole Genome Panel. Electrophoresis, 2018, 39, 2766-2775.	2.4	25
30	Evaluation of the Precision ID Ancestry Panel for crime case work: A SNP typing assay developed for typing of 165 ancestral informative markers. Forensic Science International: Genetics, 2017, 28, 138-145.	3.1	82
31	Comparison of manual and automated AmpliSeqâ„¢ workflows in the typing of a Somali population with the Precision ID Identity Panel. Forensic Science International: Genetics, 2017, 31, 118-125.	3.1	22
32	Typing of two Middle Eastern populations with the Precision ID Ancestry Panel. Forensic Science International: Genetics Supplement Series, 2017, 6, e301-e302.	0.3	9
33	Analysis of 16 autosomal STR loci in Uyghur and Kazakh populations from Xinjiang, China. Forensic Science International: Genetics Supplement Series, 2017, 6, e537-e538.	0.3	0
34	Decrease DNA contamination in the laboratories. Forensic Science International: Genetics Supplement Series, 2017, 6, e577-e578.	0.3	21
35	Reproducibility of methylated CpG typing with the Illumina MiSeq. Forensic Science International: Genetics Supplement Series, 2017, 6, e430-e432.	0.3	0
36	Analysis of ancestry informative markers in three main ethnic groups from Ecuador supports a trihybrid origin of Ecuadorians. Forensic Science International: Genetics, 2017, 31, 29-33.	3.1	40

#	Article	IF	Citations
37	A collaborative EDNAP exercise on SNaPshotâ„¢-based mtDNA control region typing. Forensic Science International: Genetics, 2017, 26, 77-84.	3.1	5
38	High-throughput sequencing of forensic genetic samples using punches of FTA cards with buccal swabs. BioTechniques, 2016, 61, 149-151.	1.8	23
39	Thirty autosomal insertion-deletion polymorphisms analyzed using the Investigator Â® DIPplex Kit in populations from Iraq, Lithuania, Slovenia, and Turkey. Forensic Science International: Genetics, 2016, 25, 142-144.	3.1	11
40	Frequencies of HID-ion ampliseq ancestry panel markers among greenlanders. Forensic Science International: Genetics, 2016, 24, 60-64.	3.1	26
41	Importance of nonsynonymous <scp>OCA</scp>2 variants in human eye color prediction. Molecular Genetics & Genomic Medicine, 2016, 4, 420-430.	1.2	31
42	Evaluation of the iPLEXÂ® ADME PGx Pro Panel and allele frequencies of pharmacogenetic markers in Danes. Clinical Biochemistry, 2016, 49, 1299-1301.	1.9	10
43	A study of the peopling of Greenland using next generation sequencing of complete mitochondrial genomes. American Journal of Physical Anthropology, 2016, 161, 698-704.	2.1	15
44	ISO 17025 validation of a nextâ€generation sequencing assay for relationship testing. Electrophoresis, 2016, 37, 2822-2831.	2.4	52
45	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
46	Introduction of the Python script STRinNGS for analysis of STR regions in FASTQ or BAM files and expansion of the Danish STR sequence database to 11 STRs. Forensic Science International: Genetics, 2016, 21, 68-75.	3.1	34
47	Pigmentary Markers in Danes â€“ Associations with Quantitative Skin Colour, Nevi Count, Familial Atypical Multiple-Mole, and Melanoma Syndrome. PLoS ONE, 2016, 11, e0150381.	2.5	5
48	Typing of 111 ancestry informative markers in an Albanian population. Forensic Science International: Genetics Supplement Series, 2015, 5, e124-e125.	0.3	0
49	Peopling of the North Circumpolar Region â€“ Insights from Y Chromosome STR and SNP Typing of Greenlanders. PLoS ONE, 2015, 10, e0116573.	2.5	16
50	Evaluation of DNA Variants Associated with Androgenetic Alopecia and Their Potential to Predict Male Pattern Baldness. PLoS ONE, 2015, 10, e0127852.	2.5	51
51	Forensic and population genetic analyses of Danes, Greenlanders and Somalis typed with the Yfiler Â® Plus PCR amplification kit. Forensic Science International: Genetics, 2015, 16, 232-236.	3.1	48
52	Testing of the Illumina Â® ForenSeqâ„¢ kit. Forensic Science International: Genetics Supplement Series, 2015, 5, e449-e450.	0.3	11
53	Next generation sequencing and its applications in forensic genetics. Forensic Science International: Genetics, 2015, 18, 78-89.	3.1	338
54	Results for five sets of forensic genetic markers studied in a Greek population sample. Forensic Science International: Genetics, 2015, 16, 132-137.	3.1	21

#	Article	IF	Citations
55	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
56	Population and forensic data for three sets of forensic genetic markers in four ethnic groups from Iran: Persians, Lurs, Kurds and Azeris. Forensic Science International: Genetics, 2015, 17, 43-46.	3.1	16
57	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
58	Template preparation of AmpliSeqâ„¢ libraries using the Ion Chefâ„¢. Forensic Science International: Genetics Supplement Series, 2015, 5, e368-e369.	0.3	2
59	Comparison of techniques for quantification of next-generation sequencing libraries. Forensic Science International: Genetics Supplement Series, 2015, 5, e276-e278.	0.3	9
60	Second-generation sequencing of forensic STRs using the Ion Torrentâ„¢ HID STR 10-plex and the Ion PGMâ„¢. Forensic Science International: Genetics, 2015, 14, 132-140.	3.1	112
61	Next-generation sequencing of multiple individuals per barcoded library by deconvolution of sequenced amplicons using endonuclease fragment analysis. BioTechniques, 2014, 57, 91-4.	1.8	5
62	Non-uniform phenotyping of D12S391 resolved by second generation sequencing. Forensic Science International: Genetics, 2014, 8, 195-199.	3.1	35
63	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
64	Characterization of mutations and sequence variants in the D21S11 locus by next generation sequencing. Forensic Science International: Genetics, 2014, 8, 68-72.	3.1	70
65	The effect of gender on eye colour variation in European populations and an evaluation of the IrisPlex prediction model. Forensic Science International: Genetics, 2014, 11, 1-6.	3.1	29
66	Evaluation of the Ion Torrentâ„¢ HID SNP 169-plex: A SNP typing assay developed for human identification by second generation sequencing. Forensic Science International: Genetics, 2014, 12, 144-154.	3.1	95
67	Second generation sequencing of three STRs D3S1358, D12S391 and D21S11 in Danes and a new nomenclature for sequenced STR alleles. Forensic Science International: Genetics, 2014, 12, 38-41.	3.1	70
68	Genetic analyses of the human eye colours using a novel objective method for eye colour classification. Forensic Science International: Genetics, 2013, 7, 508-515.	3.1	31
69	Characterization of sequence variations in the D21S11 locus in Danes, Somalis and Greenlanders by second generation sequencing. Forensic Science International: Genetics Supplement Series, 2013, 4, e302-e303.	0.3	5
70	Assessing the potential application of X-chromosomal haploblocks in population genetics and forensic studies. Forensic Science International: Genetics Supplement Series, 2013, 4, e9-e10.	0.3	1
71	Distribution of Y chromosome haplogroup Q in Greenlanders. Forensic Science International: Genetics Supplement Series, 2013, 4, e220-e221.	0.3	2
72	Forensic genetic SNP typing of low-template DNA and highly degraded DNA from crime case samples. Forensic Science International: Genetics, 2013, 7, 345-352.	3.1	53

#	Article	IF	Citations
73	Analysis of 49 autosomal SNPs in three ethnic groups from Iran: Persians, Lurs and Kurds. Forensic Science International: Genetics, 2013, 7, 471-473.	3.1	6
74	The genetics of eye colours in an Italian population measured with an objective method for eye colour quantification. Forensic Science International: Genetics Supplement Series, 2013, 4, e23-e24.	0.3	1
75	Analysis of 49 autosomal SNPs in an Iraqi population. Forensic Science International: Genetics, 2013, 7, 198-199.	3.1	8
76	Development and optimisation of five multiplex assays with 115 of the AIM SNPs from the EUROFORGEN AIMs set on the SequenomÂ® MassARRAYÂ® system. Forensic Science International: Genetics Supplement Series, 2013, 4, e182-e183.	0.3	0
77	Drop-out probabilities of IrisPlex SNP alleles. Forensic Science International: Genetics Supplement Series, 2013, 4, e238-e239.	0.3	0
78	Characterization of mutations and sequence variations in complex STR loci by second generation sequencing. Forensic Science International: Genetics Supplement Series, 2013, 4, e218-e219.	0.3	16
79	Evaluation of the iPLEXÂ® Sample ID Plus Panel designed for the Sequenom MassARRAYÂ® system. A SNP typing assay developed for human identification and sample tracking based on the SNPforID panel. Forensic Science International: Genetics, 2013, 7, 482-487.	3.1	43
80	Understanding geographic origins and history of admixture among chimpanzees in European zoos, with implications for future breeding programmes. Heredity, 2013, 110, 586-593.	2.6	39
81	Correlation of iris biometrics and DNA. , 2013, , .		1
82	Evaluation of Four Automated Protocols for Extraction of DNA from FTA Cards. Journal of the Association for Laboratory Automation, 2013, 18, 404-410.	2.8	25
83	What Genes Tell about Iris Appearance. Lecture Notes in Computer Science, 2013, , 244-253.	1.3	2
84	Kinship Analysis with Diallelic SNPs Â– Experiences with the SNPforID Multiplex in an ISO17025 Accreditated Laboratory. Transfusion Medicine and Hemotherapy, 2012, 39, 195-201.	1.6	23
85	Typing of 49 Autosomal SNPs by Single Base Extension and Capillary Electrophoresis for Forensic Genetic Testing. Methods in Molecular Biology, 2012, 830, 87-107.	0.9	5
86	Typing of 30 insertion/deletions in Danes using the first commercial indel kitâ€"MentypeÂ® DIPplex. Forensic Science International: Genetics, 2012, 6, e72-e74.	3.1	77
87	Biomek 3000. Journal of the Association for Laboratory Automation, 2012, 17, 378-386.	2.8	4
88	Reinvestigations of six unusual paternity cases by typing of autosomal singleâ€nucleotide polymorphisms. Transfusion, 2012, 52, 425-430.	1.6	12
89	A 48-plex Autosomal SNP GenPlexâ„¢ Assay for Human Individualization and Relationship Testing. Methods in Molecular Biology, 2012, 830, 73-85.	0.9	0
90	Validation of the AmpFlSTRÂ® IdentifilerÂ® Direct PCR Amplification kit in a laboratory accredited according to the ISO17025 standard. Forensic Science International: Genetics Supplement Series, 2011, 3, e165-e166.	0.3	8

#	Article	IF	Citations
91	Eye colour and SNPs in Danes. Forensic Science International: Genetics Supplement Series, 2011, 3, e151-e152.	0.3	2
92	SNP typing of crime case samples with the SNPforID multiplex assay. Forensic Science International: Genetics Supplement Series, 2011, 3, e99-e100.	0.3	0
93	Implementation of the SNPforID multiplex on the SequenomÂ® MassARRAYÂ® analyzer 4 system. Forensic Science International: Genetics Supplement Series, 2011, 3, e496-e497.	0.3	0
94	Repeated extraction of DNA from FTA cards. Forensic Science International: Genetics Supplement Series, 2011, 3, e345-e346.	0.3	6
95	Genetic variants and skin colour in Danes. Forensic Science International: Genetics Supplement Series, 2011, 3, e153-e154.	0.3	3
96	Sequences of microvariant/â€œoff-ladderâ€•STR alleles. Forensic Science International: Genetics Supplement Series, 2011, 3, e204-e205.	0.3	4
97	Mutations and/or close relatives? Six case work examples where 49 autosomal SNPs were used as supplementary markers. Forensic Science International: Genetics, 2011, 5, 236-241.	3.1	50
98	Autosomal SNP typing of forensic samples with the GenPlexâ„¢ HID System: Results of a collaborative study. Forensic Science International: Genetics, 2011, 5, 369-375.	3.1	17
99	SNP typing of the reference materials SRM 2391b 1â€“10, K562, XY1, XX74, and 007 with the SNPforID multiplex. Forensic Science International: Genetics, 2011, 5, e81-e82.	3.1	7
100	Frequencies of 33 coding region mitochondrial SNPs in a Danish and a Turkish population. Forensic Science International: Genetics, 2011, 5, 559-560.	3.1	3
101	Typing of Amerindian Kichwas and Mestizos from Ecuador with the SNPforID multiplex. Forensic Science International: Genetics, 2011, 5, e105-e107.	3.1	12
102	High-throughput sequencing of core STR loci for forensic genetic investigations using the Roche Genome Sequencer FLX platform. BioTechniques, 2011, 51, 127-133.	1.8	98
103	Forensic usefulness of a 25 Xâ€chromosome singleâ€nucleotide polymorphism marker set. Transfusion, 2010, 50, 2258-2265.	1.6	27
104	Human eye colour and HERC2, OCA2 and MATP. Forensic Science International: Genetics, 2010, 4, 323-328.	3.1	70
105	Typing of 49 autosomal SNPs by SNaPshotÂ® in the Slovenian population. Forensic Science International: Genetics, 2010, 4, e125-e127.	3.1	9
106	Validation of a single nucleotide polymorphism (SNP) typing assay with 49 SNPs for forensic genetic testing in a laboratory accredited according to the ISO 17025 standard. Forensic Science International: Genetics, 2009, 4, 34-42.	3.1	67
107	Customizing a commercial laboratory information management system for a forensic genetic laboratory. Forensic Science International: Genetics Supplement Series, 2009, 2, 77-79.	0.3	2
108	Successful STR and SNP typing of FTA Card samples with low amounts of DNA after DNA extraction using a Qiagen BioRobotÂ® EZ1 Workstation. Forensic Science International: Genetics Supplement Series, 2009, 2, 83-84.	0.3	9

#	Article	IF	Citations
109	SNP typing of forensic samples with the GenPlexâ„¢ HID system: A collaborative study. Forensic Science International: Genetics Supplement Series, 2009, 2, 508-509.	0.3	1
110	Determination of cis/trans phase of variations in the MC1R gene with alleleâ€specific PCR and single base extension. Electrophoresis, 2008, 29, 4780-4787.	2.4	10
111	Identification of West Eurasian mitochondrial haplogroups by mtDNA SNP screening: Results of the 2006â€“2007 EDNAP collaborative exercise. Forensic Science International: Genetics, 2008, 2, 61-68.	3.1	13
112	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
113	Performance of the SNPforID 52 SNP-plex assay in paternity testing. Forensic Science International: Genetics, 2008, 2, 292-300.	3.1	82
114	Typing of 48 autosomal SNPs and amelogenin with GenPlex SNP genotyping system in forensic genetics. Forensic Science International: Genetics, 2008, 3, 1-6.	3.1	18
115	Utility of X-chromosome SNPs in relationship testing. Forensic Science International: Genetics Supplement Series, 2008, 1, 528-530.	0.3	2
116	A 50 SNP-multiplex mass spectrometry assay for human identification. Forensic Science International: Genetics Supplement Series, 2008, 1, 487-489.	0.3	2
117	A mitochondrial DNA SNP multiplex assigning Caucasians into 36 haplo- and subhaplogroups. Forensic Science International: Genetics Supplement Series, 2008, 1, 287-289.	0.3	5
118	Associations between Î±+â€Thalassemia andPlasmodium falciparumMalarial Infection in Northeastern Tanzania. Journal of Infectious Diseases, 2007, 196, 451-459.	4.0	44
119	Forensic validation of the SNPforID 52-plex assay. Forensic Science International: Genetics, 2007, 1, 186-190.	3.1	74
120	Multiplex PCR with minisequencing as an effective high-throughput SNP typing method for formalin-fixed tissue. Electrophoresis, 2007, 28, 2361-2367.	2.4	31
121	Carrier Frequency of a Nonsense Mutation in the Adenosine Deaminase (ADA) Gene Implies a High Incidence of ADA-deficient Severe Combined Immunodeficiency (SCID) in Somalia and a Single, Common Haplotype Indicates Common Ancestry. Annals of Human Genetics, 2007, 71, 336-347.	0.8	44
122	Comparison of paternity indices based on typing of 15 STRs, 7 VNTRs and 52 SNPs in 50 Danish motherâ€“childâ€“father trios. International Congress Series, 2006, 1288, 436-438.	0.2	1
123	Semi-automatic preparation of biological database samples for STR typing. International Congress Series, 2006, 1288, 663-665.	0.2	3
124	Analysis of 29 Y-chromosome SNPs in a single multiplex useful to predict the geographic origin of male lineages. International Congress Series, 2006, 1288, 13-15.	0.2	3
125	The effect of whole genome amplification on samples originating from more than one donor. International Congress Series, 2006, 1288, 722-724.	0.2	1
126	Development of a multiplex PCR assay detecting 52 autosomal SNPs. International Congress Series, 2006, 1288, 67-69.	0.2	4

#	Article	IF	Citations
127	Genetic screening of 15 SNPs in the MC1R gene in relation to hair colour in Danes. International Congress Series, 2006, 1288, 55-57.	0.2	2
128	Multiple displacement amplification of blood and saliva samples placed on FTAÂ® cards. International Congress Series, 2006, 1288, 716-718.	0.2	1
129	Application of whole genome amplification for forensic analysis. International Congress Series, 2006, 1288, 725-727.	0.2	8
130	A multiplex assay with 52 single nucleotide polymorphisms for human identification. Electrophoresis, 2006, 27, 1713-1724.	2.4	462
131	SNP Typing on the NanoChip Electronic Microarray. , 2005, 297, 155-168.		8
132	Typing of Y Chromosome SNPs With Multiplex PCR Methods. , 2005, 297, 209-228.		26
133	High frequencies of Y chromosome lineages characterized by E3b1, DYS19-11, DYS392-12 in Somali males. European Journal of Human Genetics, 2005, 13, 856-866.	2.8	45
134	Introduction of an single nucleodite polymorphism-based â€œMajor Y-chromosome haplogroup typing kitâ€•suitable for predicting the geographical origin of male lineages. Electrophoresis, 2005, 26, 4411-4420.	2.4	73
135	Typing of Multiple Single-Nucleotide Polymorphisms Using Ribonuclease Cleavage of DNA/RNA Chimeric Single-Base Extension Primers and Detection by MALDI-TOF Mass Spectrometry. Analytical Chemistry, 2005, 77, 5229-5235.	6.5	24
136	Multiplex PCR, amplicon size and hybridization efficiency on the NanoChip electronic microarray. International Journal of Legal Medicine, 2004, 118, 75-82.	2.2	14
137	Duplications of the Y-chromosome specific loci P25 and 92R7 and forensic implications. Forensic Science International, 2004, 140, 241-250.	2.2	24
138	MALDI-TOF Mass Spectrometric Detection of Multiplex Single Base Extended Primers. A Study of 17 Y-Chromosome Single-Nucleotide Polymorphisms. Analytical Chemistry, 2004, 76, 6039-6045.	6.5	32
139	Multiplex Y chromosome SNP genotyping using MALDI-TOF mass spectrometry. International Congress Series, 2004, 1261, 15-17.	0.2	2
140	SNP and STR Y chromosome markers in the Canary Islands population. International Congress Series, 2004, 1261, 328-330.	0.2	0
141	Y chromosome SNP haplogroups in Danes, Greenlanders and Somalis. International Congress Series, 2004, 1261, 347-349.	0.2	8
142	Multiplex PCR and minisequencing of SNPsâ€”a model with 35 Y chromosome SNPs. Forensic Science International, 2003, 137, 74-84.	2.2	114
143	Vectorial Acylation in Saccharomyces cerevisiae. Journal of Biological Chemistry, 2003, 278, 16414-16422.	3.4	108
144	Saccharomyces carlsbergensis contains two functional genes encoding the Acyl-CoA binding protein, one similar to theACB1 gene fromS. cerevisiae and one identical to theACB1 gene fromS. monacensis. Yeast, 1997, 13, 1409-1421.	1.7	44

#	Article	IF	Citations
145	Saccharomyces carlsbergensis contains two functional genes encoding the Acyl-CoA binding protein, one similar to the ACB1 gene from S. cerevisiae and one identical to the ACB1 gene from S. monacensis. Yeast, 1997, 13, 1409-1421.	1.7	2
146	Disruption of the Gene Encoding the Acyl-CoA-binding Protein ( ) Perturbs Acyl-CoA Metabolism in. Journal of Biological Chemistry, 1996, 271, 22514-22521.	3.4	125
147	Anthropological analyses of 30 insertion/deletion autosomal markers in five major ethnic groups of Pakistan. Forensic Sciences Research, 0, , 1-5.	1.6	1