

# Walther Parson

## List of Publications by Year in descending order

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335  
papers

15,409  
citations

13865

67  
h-index

30922

102  
g-index

344  
all docs

344  
docs citations

344  
times ranked

11580  
citing authors

#	ARTICLE	IF	CITATIONS
1	Lack of Antibody Production Following Immunization in Old Age: Association with CD8+CD28 <sup>hi</sup> T Cell Clonal Expansions and an Imbalance in the Production of Th1 and Th2 Cytokines. <i>Journal of Immunology</i> , 2002, 168, 5893-5899.	0.8	477
2	Correlation between Genetic and Geographic Structure in Europe. <i>Current Biology</i> , 2008, 18, 1241-1248.	3.9	449
3	EMPOP <sup>®</sup> A forensic mtDNA database. <i>Forensic Science International: Genetics</i> , 2007, 1, 88-92.	3.1	321
4	DNA Commission of the International Society for Forensic Genetics: Revised and extended guidelines for mitochondrial DNA typing. <i>Forensic Science International: Genetics</i> , 2014, 13, 134-142.	3.1	243
5	A global analysis of Y-chromosomal haplotype diversity for 23 STR loci. <i>Forensic Science International: Genetics</i> , 2014, 12, 12-23.	3.1	214
6	Publication of population data for forensic purposes. <i>Forensic Science International: Genetics</i> , 2010, 4, 145-147.	3.1	195
7	Massively parallel sequencing of forensic STRs: Considerations of the DNA commission of the International Society for Forensic Genetics (ISFG) on minimal nomenclature requirements. <i>Forensic Science International: Genetics</i> , 2016, 22, 54-63.	3.1	190
8	Inhibition of the Acetyltransferases p300 and CBP Reveals a Targetable Function for p300 in the Survival and Invasion Pathways of Prostate Cancer Cell Lines. <i>Molecular Cancer Therapeutics</i> , 2011, 10, 1644-1655.	4.1	188
9	ISFG: Recommendations regarding the use of non-human (animal) DNA in forensic genetic investigations. <i>Forensic Science International: Genetics</i> , 2011, 5, 501-505.	3.1	175
10	DNA commission of the International Society of Forensic Genetics: Recommendations on the evaluation of STR typing results that may include drop-out and/or drop-in using probabilistic methods. <i>Forensic Science International: Genetics</i> , 2012, 6, 679-688.	3.1	171
11	Rapid coastal spread of First Americans: Novel insights from South America's Southern Cone mitochondrial genomes. <i>Genome Research</i> , 2012, 22, 811-820.	5.5	167
12	GeneMarker <sup>®</sup> HID: A Reliable Software Tool for the Analysis of Forensic STR Data. <i>Journal of Forensic Sciences</i> , 2011, 56, 29-35.	1.6	165
13	DNA Extraction and Quantitation of Forensic Samples Using the Phenol-Chloroform Method and Real-Time PCR. , 2005, 297, 013-030.		163
14	Identification of the remains of King Richard III. <i>Nature Communications</i> , 2014, 5, 5631.	12.8	163
15	Inferring Continental Ancestry of Argentineans from Autosomal, Y-Chromosomal and Mitochondrial DNA. <i>Annals of Human Genetics</i> , 2010, 74, 65-76.	0.8	155
16	High-quality and high-throughput massively parallel sequencing of the human mitochondrial genome using the Illumina MiSeq. <i>Forensic Science International: Genetics</i> , 2014, 12, 128-135.	3.1	155
17	Toward Male Individualization with Rapidly Mutating Y-Chromosomal Short Tandem Repeats. <i>Human Mutation</i> , 2014, 35, 1021-1032.	2.5	151
18	Investigation of Heteroplasmy in the Human Mitochondrial DNA Control Region: A Synthesis of Observations from More Than 5000 Global Population Samples. <i>Journal of Molecular Evolution</i> , 2009, 68, 516-527.	1.8	149

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19	The initial peopling of the Americas: A growing number of founding mitochondrial genomes from Beringia. <i>Genome Research</i> , 2010, 20, 1174-1179.	5.5	147
20	Similar qualitative and quantitative changes of mitochondrial respiration following strength and endurance training in normoxia and hypoxia in sedentary humans. <i>American Journal of Physiology - Regulatory Integrative and Comparative Physiology</i> , 2011, 301, R1078-R1087.	1.8	144
21	Update of the guidelines for the publication of genetic population data. <i>Forensic Science International: Genetics</i> , 2014, 10, A1-A2.	3.1	144
22	New guidelines for the publication of genetic population data. <i>Forensic Science International: Genetics</i> , 2013, 7, 217-220.	3.1	142
23	Characterization of the <i>Aspergillus nidulans</i> transporters for the siderophores enterobactin and triacetylfusarinine C. <i>Biochemical Journal</i> , 2003, 371, 505-513.	3.7	141
24	Evaluation of next generation mtGenome sequencing using the Ion Torrent Personal Genome Machine (PGM). <i>Forensic Science International: Genetics</i> , 2013, 7, 543-549.	3.1	141
25	Mystery Solved: The Identification of the Two Missing Romanov Children Using DNA Analysis. <i>PLoS ONE</i> , 2009, 4, e4838.	2.5	135
26	Revised guidelines for the publication of genetic population data. <i>Forensic Science International: Genetics</i> , 2017, 30, 160-163.	3.1	135
27	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). <i>Forensic Science International: Genetics</i> , 2016, 24, 97-102.	3.1	130
28	Consistent treatment of length variants in the human mtDNA control region: a reappraisal. <i>International Journal of Legal Medicine</i> , 2008, 122, 11-21.	2.2	129
29	Extended guidelines for mtDNA typing of population data in forensic science. <i>Forensic Science International: Genetics</i> , 2007, 1, 13-19.	3.1	126
30	Rapid screening of mtDNA coding region SNPs for the identification of west European Caucasian haplogroups. <i>International Journal of Legal Medicine</i> , 2003, 117, 291-298.	2.2	122
31	Recommendations for animal DNA forensic and identity testing. <i>International Journal of Legal Medicine</i> , 2005, 119, 295-302.	2.2	122
32	xylP Promoter-Based Expression System and Its Use for Antisense Downregulation of the <i>Penicillium chrysogenum</i> Nitrogen Regulator NRE. <i>Applied and Environmental Microbiology</i> , 2000, 66, 4810-4816.	3.1	121
33	Mitochondrial DNA heteroplasmy in the emerging field of massively parallel sequencing. <i>Forensic Science International: Genetics</i> , 2015, 18, 131-139.	3.1	118
34	Building a forensic ancestry panel from the ground up: The EUROFORGEN Global AIM-SNP set. <i>Forensic Science International: Genetics</i> , 2014, 11, 13-25.	3.1	116
35	T Regulatory Cells and TH17 Cells in Periâ€Silicone Implant Capsular Fibrosis. <i>Plastic and Reconstructive Surgery</i> , 2012, 129, 327e-337e.	1.4	114
36	Cancer cell line identification by short tandem repeat profiling: power and limitations. <i>FASEB Journal</i> , 2005, 19, 1-18.	0.5	112

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37	A modular real-time PCR concept for determining the quantity and quality of human nuclear and mitochondrial DNA. <i>Forensic Science International: Genetics</i> , 2007, 1, 29-34.	3.1	106
38	The EDNAP mitochondrial DNA population database (EMPOP) collaborative exercises: organisation, results and perspectives. <i>Forensic Science International</i> , 2004, 139, 215-226.	2.2	105
39	Inter-laboratory evaluation of SNP-based forensic identification by massively parallel sequencing using the Ion PGM <sup>®</sup> . <i>Forensic Science International: Genetics</i> , 2015, 17, 110-121.	3.1	105
40	Mitochondrial DNA control region sequences from Nairobi (Kenya): inferring phylogenetic parameters for the establishment of a forensic database. <i>International Journal of Legal Medicine</i> , 2004, 118, 294-306.	2.2	104
41	RNA/DNA co-analysis from human saliva and semen stains – Results of a third collaborative EDNAP exercise. <i>Forensic Science International: Genetics</i> , 2013, 7, 230-239.	3.1	97
42	Human Bone Marrow Hosts Polyfunctional Memory CD4+ and CD8+ T Cells with Close Contact to IL-15 <sup>+</sup> Producing Cells. <i>Journal of Immunology</i> , 2011, 186, 6965-6971.	0.8	95
43	Naive T Cells in the Elderly: Are They Still There?. <i>Annals of the New York Academy of Sciences</i> , 2006, 1067, 152-157.	3.8	94
44	RNA/DNA co-analysis from human menstrual blood and vaginal secretion stains: Results of a fourth and fifth collaborative EDNAP exercise. <i>Forensic Science International: Genetics</i> , 2014, 8, 203-212.	3.1	94
45	mRNA profiling for the identification of blood – Results of a collaborative EDNAP exercise. <i>Forensic Science International: Genetics</i> , 2011, 5, 21-26.	3.1	93
46	Analysis of Polymerase Chain Reaction Products by On-Line Liquid Chromatography <sup>~</sup> Mass Spectrometry for Genotyping of Polymorphic Short Tandem Repeat Loci. <i>Analytical Chemistry</i> , 2001, 73, 5109-5115.	6.5	92
47	RNA/DNA co-analysis from blood stains – Results of a second collaborative EDNAP exercise. <i>Forensic Science International: Genetics</i> , 2012, 6, 70-80.	3.1	92
48	Generating population data for the EMPOP database – An overview of the mtDNA sequencing and data evaluation processes considering 273 Austrian control region sequences as example. <i>Forensic Science International</i> , 2007, 166, 164-175.	2.2	88
49	Massively parallel sequencing of complete mitochondrial genomes from hair shaft samples. <i>Forensic Science International: Genetics</i> , 2015, 15, 8-15.	3.1	85
50	Evaluation of the Illumina ForenSeq <sup>®</sup> DNA Signature Prep Kit – MPS forensic application for the MiSeq FG <sup>®</sup> benchtop sequencer. <i>Forensic Science International: Genetics</i> , 2017, 28, 188-194.	3.1	84
51	Evidence for frequent and tissue-specific sequence heteroplasmy in human mitochondrial DNA. <i>Mitochondrion</i> , 2015, 20, 82-94.	3.4	83
52	DNA commission of the International society for forensic genetics: Assessing the value of forensic biological evidence - Guidelines highlighting the importance of propositions. <i>Forensic Science International: Genetics</i> , 2018, 36, 189-202.	3.1	83
53	Phantom mutation hotspots in human mitochondrial DNA. <i>Electrophoresis</i> , 2005, 26, 3414-3429.	2.4	81
54	Concept for estimating mitochondrial DNA haplogroups using a maximum likelihood approach (EMMA). <i>Forensic Science International: Genetics</i> , 2013, 7, 601-609.	3.1	80

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55	Full mtGenome reference data: Development and characterization of 588 forensic-quality haplotypes representing three U.S. populations. <i>Forensic Science International: Genetics</i> , 2015, 14, 141-155.	3.1	78
56	Sequencing strategy for the whole mitochondrial genome resulting in high quality sequences. <i>BMC Genomics</i> , 2009, 10, 139.	2.8	77
57	The impact of aging on memory T cell phenotype and function in the human bone marrow. <i>Journal of Leukocyte Biology</i> , 2011, 91, 197-205.	3.3	77
58	STRSeq: A catalog of sequence diversity at human identification Short Tandem Repeat loci. <i>Forensic Science International: Genetics</i> , 2017, 31, 111-117.	3.1	77
59	Publication of population data of linearly inherited DNA markers in the <i>International Journal of Legal Medicine</i> . <i>International Journal of Legal Medicine</i> , 2010, 124, 505-509.	2.2	75
60	The side population of ovarian cancer cells defines a heterogeneous compartment exhibiting stem cell characteristics. <i>Oncotarget</i> , 2014, 5, 7027-7039.	1.8	75
61	CD25-Expressing CD8+T Cells Are Potent Memory Cells in Old Age. <i>Journal of Immunology</i> , 2005, 175, 1566-1574.	0.8	74
62	Forensic validation of the SNPforID 52-plex assay. <i>Forensic Science International: Genetics</i> , 2007, 1, 186-190.	3.1	74
63	â€œMitominisâ€™: multiplex PCR analysis of reduced size amplicons for compound sequence analysis of the entire mtDNA control region in highly degraded samples. <i>International Journal of Legal Medicine</i> , 2008, 122, 385-388.	2.2	74
64	T-cells from advanced atherosclerotic lesions recognize hHSP60 and have a restricted T-cell receptor repertoire. <i>Experimental Gerontology</i> , 2008, 43, 229-237.	2.8	74
65	â€œThe devilâ€™s in the detailâ€– Release of an expanded, enhanced and dynamically revised forensic STR Sequence Guide. <i>Forensic Science International: Genetics</i> , 2018, 34, 162-169.	3.1	73
66	Localization and quantification of Cd- and Cu-specific metallothionein isoform mRNA in cells and organs of the terrestrial gastropod <i>Helix pomatia</i> . <i>Toxicology and Applied Pharmacology</i> , 2003, 190, 25-36.	2.8	72
67	DNA Commission of the International Society for Forensic Genetics: Recommendations on the validation of software programs performing biostatistical calculations for forensic genetics applications. <i>Forensic Science International: Genetics</i> , 2016, 25, 191-197.	3.1	72
68	Next generation database search algorithm for forensic mitogenome analyses. <i>Forensic Science International: Genetics</i> , 2018, 37, 204-214.	3.1	72
69	STR analysis of artificially degraded DNAâ€”results of a collaborative European exercise. <i>Forensic Science International</i> , 2004, 139, 123-134.	2.2	71
70	A collaborative European exercise on mRNA-based body fluid/skin typing and interpretation of DNA and RNA results. <i>Forensic Science International: Genetics</i> , 2014, 10, 40-48.	3.1	71
71	DNA Commission of the International Society for Forensic Genetics (ISFG): Guidelines on the use of X-STRs in kinship analysis. <i>Forensic Science International: Genetics</i> , 2017, 29, 269-275.	3.1	71
72	Dissection of mitochondrial superhaplogroup H using coding region SNPs. <i>Electrophoresis</i> , 2006, 27, 2541-2550.	2.4	70

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73	Evaluation of the precision ID whole MtDNA genome panel for forensic analyses. <i>Forensic Science International: Genetics</i> , 2018, 35, 21-25.	3.1	70
74	Building a custom large-scale panel of novel microhaplotypes for forensic identification using MiSeq and Ion S5 massively parallel sequencing systems. <i>Forensic Science International: Genetics</i> , 2020, 45, 102213.	3.1	70
75	Current state-of-art of STR sequencing in forensic genetics. <i>Electrophoresis</i> , 2018, 39, 2655-2668.	2.4	68
76	Phylogeography of the vairone ( <i>Leuciscus souffia</i> , Risso 1826) in Central Europe. <i>Molecular Ecology</i> , 2003, 12, 2371-2386.	3.9	67
77	Colour-assortative mating among populations of <i>Tropheus moorii</i> , a cichlid fish from Lake Tanganyika, East Africa. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2006, 273, 257-266.	2.6	66
78	Inter-laboratory evaluation of the EUROFORGEN Global ancestry-informative SNP panel by massively parallel sequencing using the Ion PGM, c. <i>Forensic Science International: Genetics</i> , 2016, 23, 178-189.	3.1	65
79	Body fluid identification using a targeted mRNA massively parallel sequencing approach – results of a EUROFORGEN/EDNAP collaborative exercise. <i>Forensic Science International: Genetics</i> , 2018, 34, 105-115.	3.1	64
80	Age Estimation with DNA: From Forensic DNA Fingerprinting to Forensic (Epi)Genomics: A Mini-Review. <i>Gerontology</i> , 2018, 64, 326-332.	2.8	63
81	MAPlex - A massively parallel sequencing ancestry analysis multiplex for Asia-Pacific populations. <i>Forensic Science International: Genetics</i> , 2019, 42, 213-226.	3.1	63
82	Glucocorticoid resistance in two key models of acute lymphoblastic leukemia occurs at the level of the glucocorticoid receptor. <i>FASEB Journal</i> , 2006, 20, 2600-2602.	0.5	62
83	Mitochondrial Haplogroup U5b3: A Distant Echo of the Epipaleolithic in Italy and the Legacy of the Early Sardinians. <i>American Journal of Human Genetics</i> , 2009, 84, 814-821.	6.2	62
84	Reconstructing the Indian Origin and Dispersal of the European Roma: A Maternal Genetic Perspective. <i>PLoS ONE</i> , 2011, 6, e15988.	2.5	61
85	No further evidence for paternal leakage of mitochondrial DNA in humans yet. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 1821-1822.	7.1	60
86	DNA commission of the International society for forensic genetics: Assessing the value of forensic biological evidence - Guidelines highlighting the importance of propositions. Part II: Evaluation of biological traces considering activity level propositions. <i>Forensic Science International: Genetics</i> , 2020, 44, 102186.	3.1	59
87	Y-STR typing of an Austrian population sample using a 17-loci multiplex PCR assay. <i>International Journal of Legal Medicine</i> , 2005, 119, 241-246.	2.2	58
88	Arrival of Paleo-Indians to the Southern Cone of South America: New Clues from Mitogenomes. <i>PLoS ONE</i> , 2012, 7, e51311.	2.5	57
89	On-Line Liquid Chromatography Mass Spectrometry: A Useful Tool for the Detection of DNA Sequence Variation. <i>Angewandte Chemie - International Edition</i> , 2001, 40, 3828-3830.	13.8	54
90	Comparison of five DNA quantification methods. <i>Forensic Science International: Genetics</i> , 2008, 2, 226-230.	3.1	54

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91	European Network of Forensic Science Institutes (ENFSI): Evaluation of new commercial STR multiplexes that include the European Standard Set (ESS) of markers. <i>Forensic Science International: Genetics</i> , 2012, 6, 819-826.	3.1	53
92	RNA/DNA co-analysis from human skin and contact traces – results of a sixth collaborative EDNAP exercise. <i>Forensic Science International: Genetics</i> , 2015, 16, 139-147.	3.1	53
93	Critical role of androgen receptor level in prostate cancer cell resistance to new generation antiandrogen enzalutamide. <i>Oncotarget</i> , 2016, 7, 59781-59794.	1.8	52
94	Evaluation of DNA Variants Associated with Androgenetic Alopecia and Their Potential to Predict Male Pattern Baldness. <i>PLoS ONE</i> , 2015, 10, e0127852.	2.5	51
95	Optimized mtDNA Control Region Primer Extension Capture Analysis for Forensically Relevant Samples and Highly Compromised mtDNA of Different Age and Origin. <i>Genes</i> , 2017, 8, 237.	2.4	51
96	Inter-laboratory validation study of the ForenSeq™ DNA Signature Prep Kit. <i>Forensic Science International: Genetics</i> , 2018, 36, 77-85.	3.1	50
97	Preparation and evaluation of packed capillary columns for the separation of nucleic acids by ion-pair reversed-phase high-performance liquid chromatography. <i>Journal of Chromatography A</i> , 2000, 893, 23-35.	3.7	49
98	Canine-specific STR typing of saliva traces on dog bite wounds. <i>International Journal of Legal Medicine</i> , 2004, 118, 337-342.	2.2	49
99	Development and expansion of high-quality control region databases to improve forensic mtDNA evidence interpretation. <i>Forensic Science International: Genetics</i> , 2007, 1, 154-157.	3.1	49
100	Human evolution in Siberia: from frozen bodies to ancient DNA. <i>BMC Evolutionary Biology</i> , 2010, 10, 25.	3.2	49
101	Development of the VISAGE enhanced tool and statistical models for epigenetic age estimation in blood, buccal cells and bones. <i>Aging</i> , 2021, 13, 6459-6484.	3.1	49
102	Monitoring the inheritance of heteroplasmy by computer-assisted detection of mixed basecalls in the entire human mitochondrial DNA control region. <i>International Journal of Legal Medicine</i> , 2004, 118, 47-54.	2.2	48
103	Italian mitochondrial DNA database: results of a collaborative exercise and proficiency testing. <i>International Journal of Legal Medicine</i> , 2008, 122, 199-204.	2.2	48
104	Assessing various Infrared (IR) microscopic imaging techniques for post-mortem interval evaluation of human skeletal remains. <i>PLoS ONE</i> , 2017, 12, e0174552.	2.5	48
105	A Proposal for Standardization in Forensic Canine DNA Typing: Allele Nomenclature of Six Canine-Specific STR Loci. <i>Journal of Forensic Sciences</i> , 2006, 51, 274-281.	1.6	47
106	Mitochondrial control region sequences from northern Greece and Greek Cypriots. <i>International Journal of Legal Medicine</i> , 2008, 122, 87-89.	2.2	47
107	Amerindian mitochondrial DNA haplogroups predominate in the population of Argentina: towards a first nationwide forensic mitochondrial DNA sequence database. <i>International Journal of Legal Medicine</i> , 2010, 124, 263-268.	2.2	47
108	The mtDNA composition of Uzbekistan: a microcosm of Central Asian patterns. <i>International Journal of Legal Medicine</i> , 2010, 124, 195-204.	2.2	47

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109	Characterization of synthetic nucleic acids by electrospray ionization quadrupole time-of-flight mass spectrometry. <i>Journal of Mass Spectrometry</i> , 2005, 40, 932-945.	1.6	46
110	Mini-midi-mito: Adapting the amplification and sequencing strategy of mtDNA to the degradation state of crime scene samples. <i>Forensic Science International: Genetics</i> , 2009, 3, 149-153.	3.1	46
111	Mitochondrial DNA heteroplasmy or artefacts—a matter of the amplification strategy?. <i>International Journal of Legal Medicine</i> , 2003, 117, 180-184.	2.2	45
112	HlrisPlex-S system for eye, hair, and skin color prediction from DNA: Massively parallel sequencing solutions for two common forensically used platforms. <i>Forensic Science International: Genetics</i> , 2019, 43, 102152.	3.1	45
113	A common nonsense mutation in the repetitive Kringle IV-2 domain of human apolipoprotein(a) results in a truncated protein and low plasma Lp(a). <i>Human Mutation</i> , 2004, 24, 474-480.	2.5	44
114	PopAffiliator: online calculator for individual affiliation to a major population group based on 17 autosomal short tandem repeat genotype profile. <i>International Journal of Legal Medicine</i> , 2011, 125, 629-636.	2.2	44
115	Differentiation of human iPSCs into functional podocytes. <i>PLoS ONE</i> , 2018, 13, e0203869.	2.5	44
116	Development and validation of the VISAGE AmpliSeq basic tool to predict appearance and ancestry from DNA. <i>Forensic Science International: Genetics</i> , 2020, 48, 102336.	3.1	43
117	Post-mortem interval estimation of human skeletal remains by micro-computed tomography, mid-infrared microscopic imaging and energy dispersive X-ray mapping. <i>Analytical Methods</i> , 2015, 7, 2917-2927.	2.7	42
118	DNA commission of the International Society of Forensic Genetics (ISFG): Recommendations on the interpretation of Y-STR results in forensic analysis. <i>Forensic Science International: Genetics</i> , 2020, 48, 102308.	3.1	42
119	Evidence for multi-copy Mega-NUMT in the human genome. <i>Nucleic Acids Research</i> , 2021, 49, 1517-1531.	14.5	42
120	The GHEP—EMPOP collaboration on mtDNA population data—A new resource for forensic casework. <i>Forensic Science International: Genetics</i> , 2011, 5, 146-151.	3.1	41
121	Accumulation of mutations over the entire mitochondrial genome of breast cancer cells obtained by tissue microdissection. <i>Breast Cancer Research and Treatment</i> , 2011, 128, 327-336.	2.5	40
122	Mapping human dispersals into the Horn of Africa from Arabian Ice Age refugia using mitogenomes. <i>Scientific Reports</i> , 2016, 6, 25472.	3.3	40
123	Migration Rates and Genetic Structure of two Hungarian Ethnic Groups in Transylvania, Romania. <i>Annals of Human Genetics</i> , 2007, 71, 791-803.	0.8	39
124	Differential effect of catechol-O-methyltransferase Val158Met genotype on emotional recognition abilities in healthy men and women. <i>Journal of the International Neuropsychological Society</i> , 2007, 13, 881-7.	1.8	39
125	Age-related appearance of a CMV-specific high-avidity CD8+ T cell clonotype which does not occur in young adults. <i>Immunity and Ageing</i> , 2008, 5, 14.	4.2	39
126	Splice variant transcripts of the anterior gradient 2 gene as a marker of prostate cancer. <i>Oncotarget</i> , 2014, 5, 8681-8689.	1.8	39



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127	Molecular characterization of the canine mitochondrial DNA control region for forensic applications. <i>International Journal of Legal Medicine</i> , 2007, 121, 411-416.	2.2	38
128	Towards broadening Forensic DNA Phenotyping beyond pigmentation: Improving the prediction of head hair shape from DNA. <i>Forensic Science International: Genetics</i> , 2018, 37, 241-251.	3.1	38
129	Estimating the probability of identity in a random dog population using 15 highly polymorphic canine STR markers. <i>Forensic Science International</i> , 2005, 151, 37-44.	2.2	37
130	Detection of DNA Sequence Variations in Homo- and Heterozygous Samples via Molecular Mass Measurements by Electrospray Ionization Time-of-Flight Mass Spectrometry. <i>Analytical Chemistry</i> , 2005, 77, 4999-5008.	6.5	37
131	Comparison of morphological and molecular genetic sex-typing on mediaeval human skeletal remains. <i>Forensic Science International: Genetics</i> , 2013, 7, 581-586.	3.1	37
132	Open source software EuroForMix can be used to analyse complex SNP mixtures. <i>Forensic Science International: Genetics</i> , 2017, 31, 105-110.	3.1	37
133	Evaluation of mitogenome sequence concordance, heteroplasmy detection, and haplogrouping in a worldwide lineage study using the Precision ID mtDNA Whole Genome Panel. <i>Forensic Science International: Genetics</i> , 2019, 42, 244-251.	3.1	37
134	Identification of atherosclerosis-associated conformational heat shock protein 60 epitopes by phage display and structural alignment. <i>Atherosclerosis</i> , 2007, 194, 79-87.	0.8	36
135	Timing and deciphering mitochondrial DNA macro-haplogroup R0 variability in Central Europe and Middle East. <i>BMC Evolutionary Biology</i> , 2008, 8, 191.	3.2	36
136	Evaluation of the predictive capacity of DNA variants associated with straight hair in Europeans. <i>Forensic Science International: Genetics</i> , 2015, 19, 280-288.	3.1	36
137	SOCS3 Modulates the Response to Enzalutamide and Is Regulated by Androgen Receptor Signaling and CpG Methylation in Prostate Cancer Cells. <i>Molecular Cancer Research</i> , 2016, 14, 574-585.	3.4	36
138	Considering DNA damage when interpreting mtDNA heteroplasmy in deep sequencing data. <i>Forensic Science International: Genetics</i> , 2017, 26, 1-11.	3.1	36
139	Improved specificity of Y-STR typing in DNA mixture samples. <i>International Journal of Legal Medicine</i> , 2003, 117, 109-114.	2.2	35
140	Increased forensic efficiency of DNA fingerprints through simultaneous resolution of length and nucleotide variability by high-performance mass spectrometry. <i>Human Mutation</i> , 2008, 29, 427-432.	2.5	35
141	GenderPlex: a PCR multiplex for reliable gender determination of degraded human DNA samples and complex gender constellations. <i>International Journal of Legal Medicine</i> , 2009, 123, 459-464.	2.2	35
142	Southeast Asian diversity: first insights into the complex mtDNA structure of Laos. <i>BMC Evolutionary Biology</i> , 2011, 11, 49.	3.2	35
143	Massively parallel sequence data of 31 autosomal STR loci from 496 Spanish individuals revealed concordance with CE-STR technology and enhanced discrimination power. <i>Forensic Science International: Genetics</i> , 2019, 42, 49-55.	3.1	34
144	Serotonin transporter genotype (5-HTTLPR) and electrocortical responses indicating the sensitivity to negative emotional cues. <i>Emotion</i> , 2013, 13, 1173-1181.	1.8	34

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145	Forensic and phylogeographic characterization of mtDNA lineages from northern Thailand (Chiang Tj ETQq1 1 0.784314 rgBTJ/Overlock	2.2	33
146	Oxidative stress can alter the antigenicity of immunodominant peptides. <i>Journal of Leukocyte Biology</i> , 2009, 87, 165-172.	3.3	33
147	mtGenome reference population databases and the future of forensic mtDNA analysis. <i>Forensic Science International: Genetics</i> , 2011, 5, 222-225.	3.1	33
148	Reprint of: Evaluation of next generation mtGenome sequencing using the Ion Torrent Personal Genome Machine (PGM). <i>Forensic Science International: Genetics</i> , 2013, 7, 632-639.	3.1	33
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