

Peter M Vallone

List of Publications by Year in descending order

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126
papers

4,275
citations

126708

33
h-index

133063

59
g-index

131
all docs

131
docs citations

131
times ranked

3651
citing authors

#	ARTICLE	IF	CITATIONS
1	AutoDimer: a screening tool for primer-dimer and hairpin structures. <i>BioTechniques</i> , 2004, 37, 226-231.	0.8	411
2	Predicting sequence-dependent melting stability of short duplex DNA oligomers. , 1997, 44, 217-239.		173
3	A novel multiplex for simultaneous amplification of 20 Y chromosome STR markers. <i>Forensic Science International</i> , 2002, 129, 10-24.	1.3	167
4	Inferring Continental Ancestry of Argentineans from Autosomal, Y-Chromosomal and Mitochondrial DNA. <i>Annals of Human Genetics</i> , 2010, 74, 65-76.	0.3	155
5	STR allele sequence variation: Current knowledge and future issues. <i>Forensic Science International: Genetics</i> , 2015, 18, 118-130.	1.6	155
6	STRs vs. SNPs: thoughts on the future of forensic DNA testing. <i>Forensic Science, Medicine, and Pathology</i> , 2007, 3, 200-205.	0.6	140
7	Sequence variation of 22 autosomal STR loci detected by next generation sequencing. <i>Forensic Science International: Genetics</i> , 2016, 21, 15-21.	1.6	140
8	Inhibition mechanisms of hemoglobin, immunoglobulin G, and whole blood in digital and real-time PCR. <i>Analytical and Bioanalytical Chemistry</i> , 2018, 410, 2569-2583.	1.9	129
9	A multiplex allele-specific primer extension assay for forensically informative SNPs distributed throughout the mitochondrial genome. <i>International Journal of Legal Medicine</i> , 2004, 118, 147-157.	1.2	125
10	Allele Frequencies for 15 Autosomal STR Loci on U.S. Caucasian, African American, and Hispanic Populations*. <i>Journal of Forensic Sciences</i> , 2003, 48, 1-4.	0.9	124
11	Revision of the SNPforID 34-plex forensic ancestry test: Assay enhancements, standard reference sample genotypes and extended population studies. <i>Forensic Science International: Genetics</i> , 2013, 7, 63-74.	1.6	102
12	Performance of a next generation sequencing SNP assay on degraded DNA. <i>Forensic Science International: Genetics</i> , 2015, 19, 1-9.	1.6	99
13	Evaluating self-declared ancestry of U.S. Americans with autosomal, Y-chromosomal and mitochondrial DNA. <i>Human Mutation</i> , 2010, 31, E1875-E1893.	1.1	86
14	A 26plex Autosomal STR Assay to Aid Human Identity Testing*. <i>Journal of Forensic Sciences</i> , 2009, 54, 1008-1015.	0.9	83
15	STRSeq: A catalog of sequence diversity at human identification Short Tandem Repeat loci. <i>Forensic Science International: Genetics</i> , 2017, 31, 111-117.	1.6	77
16	Sequence-based U.S. population data for 27 autosomal STR loci. <i>Forensic Science International: Genetics</i> , 2018, 37, 106-115.	1.6	75
17	Forensic performance of two insertion-deletion marker assays. <i>International Journal of Legal Medicine</i> , 2012, 126, 725-737.	1.2	70
18	High-throughput Y-STR typing of U.S. populations with 27 regions of the Y chromosome using two multiplex PCR assays. <i>Forensic Science International</i> , 2004, 139, 107-121.	1.3	67

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19	Melting studies of short DNA hairpins: Influence of loop sequence and adjoining base pair identity on hairpin thermodynamic stability. , 1999, 50, 425-442.		66
20	Multiplex PCR design strategy used for the simultaneous amplification of 10Å chromosome short tandem repeat (STR) loci. Analytical and Bioanalytical Chemistry, 2003, 375, 333-343.	1.9	63
21	Forensic typing of autosomal SNPs with a 29 SNP-multiplexâ€”Results of a collaborative EDNAP exercise. Forensic Science International: Genetics, 2008, 2, 176-183.	1.6	53
22	Demonstration of rapid multiplex PCR amplification involving 16 genetic loci. Forensic Science International: Genetics, 2008, 3, 42-45.	1.6	52
23	Developmental validation of a fully integrated sample-to-profile rapid human identification system for processing single-source reference buccal samples. Forensic Science International: Genetics, 2015, 16, 181-194.	1.6	50
24	Rapid PCR of STR markers: Applications to human identification. Forensic Science International: Genetics, 2015, 18, 90-99.	1.6	46
25	Cautionary Note on Contamination of Reagents Used for Molecular Detection of SARS-CoV-2. Clinical Chemistry, 2020, 66, 1369-1372.	1.5	46
26	Allele frequencies for 27 Y-STR loci with U.S. Caucasian, African American, and Hispanic samples. Forensic Science International, 2006, 156, 250-260.	1.3	45
27	Developmental validation of the ANDEâ„¢ rapid DNA system with FlexPlexâ„¢ assay for arrestee and reference buccal swab processing and database searching. Forensic Science International: Genetics, 2019, 40, 120-130.	1.6	45
28	Capillary electrophoresis as a tool for optimization of multiplex PCR reactions. Fresenius' Journal of Analytical Chemistry, 2001, 369, 200-205.	1.5	42
29	Evidence for multi-copy Mega-NUMT<i>s</i></i> in the human genome. Nucleic Acids Research, 2021, 49, 1517-1531.	6.5	42
30	The impact of common PCR inhibitors on forensic MPS analysis. Forensic Science International: Genetics, 2019, 40, 182-191.	1.6	41
31	Genotyping of Two Mutations in the HFE Gene Using Single-Base Extension and High-Performance Liquid Chromatography. Analytical Chemistry, 2001, 73, 620-624.	3.2	40
32	One in seven pathogenic variants can be challenging to detect by NGS: an analysis of 450,000 patients with implications for clinical sensitivity and genetic test implementation. Genetics in Medicine, 2021, 23, 1673-1680.	1.1	40
33	Production and certification of NIST Standard Reference Material 2372 Human DNA Quantitation Standard. Analytical and Bioanalytical Chemistry, 2009, 394, 1183-1192.	1.9	38
34	Studies of DNA dumbbells VII: Evaluation of the next-nearest-neighbor sequence-dependent interactions in duplex DNA. , 1999, 52, 29-56.		37
35	Developmental validation of the DNAscanâ„¢ Rapid DNA Analysisâ„¢ instrument and expert system for reference sample processing. Forensic Science International: Genetics, 2016, 25, 145-156.	1.6	37
36	Y-SNP Typing of U.S. African American and Caucasian Samples Using Allele-Specific Hybridization and Primer Extension. Journal of Forensic Sciences, 2004, 49, 1-10.	0.9	37

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37	Effective strategies for forensic analysis in the mitochondrial DNA coding region. <i>International Journal of Legal Medicine</i> , 2006, 120, 27-32.	1.2	34
38	Thermodynamic, Spectroscopic, and Equilibrium Binding Studies of DNA Sequence Context Effects in Four 40 Base Pair Deoxyoligonucleotides. <i>Biochemistry</i> , 2000, 39, 7835-7846.	1.2	33
39	International Comparison of Enumeration-Based Quantification of DNA Copy-Concentration Using Flow Cytometric Counting and Digital Polymerase Chain Reaction. <i>Analytical Chemistry</i> , 2016, 88, 12169-12176.	3.2	32
40	Linkage disequilibrium analysis of D12S391 and vWA in U.S. population and paternity samples. <i>Forensic Science International: Genetics</i> , 2011, 5, 538-540.	1.6	30
41	Toward increased utility of mtDNA in forensic identifications. <i>Forensic Science International</i> , 2004, 146, S147-S149.	1.3	29
42	RNA reference materials with defined viral RNA loads of SARS-CoV-2â€”A useful tool towards a better PCR assay harmonization. <i>PLoS ONE</i> , 2022, 17, e0262656.	1.1	29
43	Melting studies of short DNA hairpins containing the universal base 5-nitroindole. <i>Nucleic Acids Research</i> , 1999, 27, 3589-3596.	6.5	27
44	Thermodynamic, Spectroscopic, and Equilibrium Binding Studies of DNA Sequence Context Effects in Six 22-Base Pair Deoxyoligonucleotides. <i>Biochemistry</i> , 1999, 38, 11197-11208.	1.2	27
45	Developmental validation of the PowerPlexÂ® 18D System, a rapid STR multiplex for analysis of reference samples. <i>Forensic Science International: Genetics</i> , 2013, 7, 129-135.	1.6	27
46	Forensic ancestry analysis with two capillary electrophoresis ancestry informative marker (AIM) panels: Results of a collaborative EDNAP exercise. <i>Forensic Science International: Genetics</i> , 2015, 19, 56-67.	1.6	27
47	Accurate Digital Polymerase Chain Reaction Quantification of Challenging Samples Applying Inhibitor-Tolerant DNA Polymerases. <i>Analytical Chemistry</i> , 2017, 89, 1642-1649.	3.2	27
48	Sequenceâ€”based US population data for the SE33 locus. <i>Electrophoresis</i> , 2018, 39, 2694-2701.	1.3	27
49	Report on ISFG SNP Panel Discussion. <i>Forensic Science International: Genetics Supplement Series</i> , 2008, 1, 471-472.	0.1	26
50	The Role of the Loop in Binding of an Actinomycin D Analog to Hairpins Formed by Single-Stranded DNA. <i>Archives of Biochemistry and Biophysics</i> , 2000, 384, 199-203.	1.4	24
51	Allele frequencies for 70 autosomal SNP loci with U.S. Caucasian, African-American, and Hispanic samples. <i>Forensic Science International</i> , 2005, 149, 279-286.	1.3	24
52	Allele frequencies for 15 autosomal STR loci on U.S. Caucasian, African American, and Hispanic populations. <i>Journal of Forensic Sciences</i> , 2003, 48, 908-11.	0.9	24
53	Collaborative EDNAP exercise on the IrisPlex system for DNA-based prediction of human eye colour. <i>Forensic Science International: Genetics</i> , 2014, 11, 241-251.	1.6	23
54	D5S2500 is an ambiguously characterized STR: Identification and description of forensic microsatellites in the genomics age.. <i>Forensic Science International: Genetics</i> , 2016, 23, 19-24.	1.6	21

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55	Characterization of NIST human mitochondrial DNA SRM-2392 and SRM-2392-I standard reference materials by next generation sequencing. <i>Forensic Science International: Genetics</i> , 2017, 29, 181-192.	1.6	21
56	Ethical publication of research on genetics and genomics of biological material: guidelines and recommendations. <i>Forensic Science International: Genetics</i> , 2020, 48, 102299.	1.6	21
57	Results of the 2018 Rapid DNA Maturity Assessment. <i>Journal of Forensic Sciences</i> , 2020, 65, 953-959.	0.9	21
58	Quality control of PCR primers used in multiplex STR amplification reactions. <i>Forensic Science International</i> , 2001, 119, 87-96.	1.3	20
59	Examining performance and likelihood ratios for two likelihood ratio systems using the PROVEDIt dataset. <i>PLoS ONE</i> , 2021, 16, e0256714.	1.1	20
60	Calculating sequence-dependent melting stability of duplex DNA oligomers and multiplex sequence analysis by graphs. <i>Methods in Enzymology</i> , 2001, 340, 165-192.	0.4	18
61	Autosomal SNP typing of forensic samples with the GenPlex [®] , [®] HID System: Results of a collaborative study. <i>Forensic Science International: Genetics</i> , 2011, 5, 369-375.	1.6	17
62	Sequence-based analysis of stutter at STR loci: Characterization and utility. <i>Forensic Science International: Genetics Supplement Series</i> , 2015, 5, e456-e458.	0.1	17
63	Classification of STR allelic variation using massively parallel sequencing and assessment of flanking region power. <i>Forensic Science International: Genetics</i> , 2020, 48, 102356.	1.6	17
64	Platinum-Quality Mitogenome Haplotypes from United States Populations. <i>Genes</i> , 2020, 11, 1290.	1.0	17
65	The impact of additional Y-STR loci on resolving common haplotypes and closely related individuals. <i>Forensic Science International: Genetics</i> , 2007, 1, 215-217.	1.6	16
66	Forensic application of the affymetrix human mitochondrial resequencing array. <i>Forensic Science International: Genetics</i> , 2007, 1, 196-198.	1.6	15
67	SNP Genotyping Using Multiplex Single Base Primer Extension Assays. <i>Methods in Molecular Biology</i> , 2009, 578, 379-391.	0.4	15
68	Rapid PCR protocols for forensic DNA typing on six thermal cycling platforms. <i>Electrophoresis</i> , 2014, 35, 3053-3061.	1.3	15
69	The next dimension in STR sequencing: Polymorphisms in flanking regions and their allelic associations. <i>Forensic Science International: Genetics Supplement Series</i> , 2015, 5, e121-e123.	0.1	15
70	Estimating number of contributors in massively parallel sequencing data of STR loci. <i>Forensic Science International: Genetics</i> , 2019, 38, 15-22.	1.6	15
71	NIST validation studies on the 3500 Genetic Analyzer. <i>Forensic Science International: Genetics Supplement Series</i> , 2011, 3, e184-e185.	0.1	14
72	Understanding the characteristics of sequence-based single-source DNA profiles. <i>Forensic Science International: Genetics</i> , 2020, 44, 102192.	1.6	14

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73	Identification of West Eurasian mitochondrial haplogroups by mtDNA SNP screening: Results of the 2006-2007 EDNAP collaborative exercise. <i>Forensic Science International: Genetics</i> , 2008, 2, 61-68.	1.6	13
74	A Strategy for Examining Complex Mixtures of Deoxyoligonucleotides Using Ion-Pair-Reverse-Phase High-Performance Liquid Chromatography, Matrix-Assisted Laser Desorption Ionization Time-of-Flight Mass Spectrometry, and Informatics. <i>Analytical Biochemistry</i> , 2002, 304, 257-265.	1.1	12
75	Rapid amplification of commercial STR typing kits. <i>Forensic Science International: Genetics Supplement Series</i> , 2009, 2, 111-112.	0.1	12
76	Allele frequency distribution of twelve X-chromosomal short tandem repeat markers in four U.S. population groups. <i>Forensic Science International: Genetics Supplement Series</i> , 2011, 3, e481-e483.	0.1	12
77	Forensic performance of insertion-deletion marker systems. <i>Forensic Science International: Genetics Supplement Series</i> , 2011, 3, e443-e444.	0.1	11
78	A multi-dimensional evaluation of the NIST 1032 sample set across four forensic Y-STR multiplexes. <i>Forensic Science International: Genetics</i> , 2022, 57, 102655.	1.6	11
79	Development and usage of a NIST standard reference material for real time PCR quantitation of human DNA. <i>Forensic Science International: Genetics Supplement Series</i> , 2008, 1, 80-82.	0.1	10
80	Determining Performance Metrics for Targeted Next-Generation Sequencing Panels Using Reference Materials. <i>Journal of Molecular Diagnostics</i> , 2018, 20, 583-590.	1.2	10
81	Mitochondrial DNA typing screens with control region and coding region SNPs. <i>Journal of Forensic Sciences</i> , 2005, 50, 377-85.	0.9	9
82	Studies of DNA dumbbells VIII. Melting analysis of DNA dumbbells with dinucleotide repeat stem sequences. <i>Biopolymers</i> , 2006, 82, 199-221.	1.2	8
83	Corrigendum to "Linkage disequilibrium analysis of D12S391 and vWA in U.S. population and paternity samples" [<i>Forensic Sci. Int.: Genet.</i> (in press), doi:10.1016/j.fsigen.2010.09.003]. <i>Forensic Science International: Genetics</i> , 2011, 5, 541-542.	1.6	8
84	Y-SNP typing of U.S. African American and Caucasian samples using allele-specific hybridization and primer extension. <i>Journal of Forensic Sciences</i> , 2004, 49, 723-32.	0.9	8
85	DNA purification from crude samples for human identification using gradient elution isotachopheresis. <i>Electrophoresis</i> , 2013, 34, 2522-2530.	1.3	7
86	Affine analysis for quantitative PCR measurements. <i>Analytical and Bioanalytical Chemistry</i> , 2020, 412, 7977-7988.	1.9	6
87	An Introductory Overview of Open-Source and Commercial Software Options for the Analysis of Forensic Sequencing Data. <i>Genes</i> , 2021, 12, 1739.	1.0	6
88	Concordance study of direct PCR kits: PowerPlex 18D and Identifiler Direct. <i>Forensic Science International: Genetics Supplement Series</i> , 2011, 3, e353-e354.	0.1	5
89	Allele frequencies for 40 autosomal SNP loci typed for US population samples using electrospray ionization mass spectrometry. <i>Croatian Medical Journal</i> , 2013, 54, 225-231.	0.2	5
90	Rapid DNA maturity assessment. <i>Forensic Science International: Genetics Supplement Series</i> , 2015, 5, e1-e2.	0.1	5

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91	Unleashing novel STRS via characterization of genome in a bottle reference samples. Forensic Science International: Genetics Supplement Series, 2019, 7, 218-220.	0.1	5
92	Are reported likelihood ratios well calibrated?. Forensic Science International: Genetics Supplement Series, 2019, 7, 572-574.	0.1	5
93	Genotyping SNPs Using a UV-Photocleavable Oligonucleotide in MALDI-TOF MS. , 2005, 297, 169-178.		4
94	New autosomal STR loci. Forensic Science International: Genetics Supplement Series, 2008, 1, 95-96.	0.1	4
95	Comparison of base composition analysis and Sanger sequencing of mitochondrial DNA for four U.S. population groups. Forensic Science International: Genetics, 2014, 8, 226-232.	1.6	4
96	Sequencing of the highly polymorphic STR locus SE33. Forensic Science International: Genetics Supplement Series, 2017, 6, e322-e323.	0.1	4
97	Characterization and performance of new MiniSTR loci for typing degraded samples. International Congress Series, 2006, 1288, 504-506.	0.2	3
98	Beyond the STRs: A comprehensive view of current forensic DNA markers characterized in the PCR-based DNA profiling standard SRM 2391D. Forensic Science International: Genetics Supplement Series, 2017, 6, e426-e427.	0.1	3
99	The tao of MPS: Common novel variants. Forensic Science International: Genetics Supplement Series, 2017, 6, e579-e581.	0.1	3
100	Capillary Electrophoresis of an 11-Plex mtDNA Coding Region SNP Single Base Extension Assay for Discrimination of the Most Common Caucasian HV1/HV2 Mitotype. Methods in Molecular Biology, 2012, 830, 159-167.	0.4	3
101	Exploring DNA interpretation software using the PROVEDIt dataset. Forensic Science International: Genetics Supplement Series, 2019, 7, 724-726.	0.1	3
102	Setting standards and developing technology to aid the human identity testing community. International Congress Series, 2006, 1288, 628-635.	0.2	2
103	Characterization of U.S. population samples using a 34plex ancestry informative SNP multiplex. Forensic Science International: Genetics Supplement Series, 2011, 3, e182-e183.	0.1	2
104	Recertification of the NIST Standard Reference Material [®] 2372, human DNA quantitation standard. Forensic Science International: Genetics Supplement Series, 2013, 4, e256-e257.	0.1	2
105	Establishing traceability to NIST SRM 2391c: PCR-Based DNA Profiling Standard. Forensic Science International: Genetics Supplement Series, 2015, 5, e112-e113.	0.1	2
106	Sequence variation observed in 27 Y-STR markers with U.S. population samples. Forensic Science International: Genetics Supplement Series, 2019, 7, 520-521.	0.1	2
107	Predicting sequence-dependent melting stability of short duplex DNA oligomers. , 0, .		2
108	Predicting sequence-dependent melting stability of short duplex DNA oligomers. , 1997, 44, 217.		2

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109	Melting studies of short DNA hairpins: Influence of loop sequence and adjoining base pair identity on hairpin thermodynamic stability. , 1999, 50, 425.		2
110	Understanding the behavior of stutter through the sequencing of STR alleles. Forensic Science International: Genetics Supplement Series, 2019, 7, 115-116.	0.1	2
111	A response to a correspondence letter by Buckleton et al. on: Riman et al. (2021) Examining performance and likelihood ratios for two likelihood ratio systems using the PROVEDIt dataset, PLoS One 16(9):e0256714. Forensic Science International: Genetics, 2022, 59, 102710.	1.6	2
112	Multiplexed assays for evaluation of Y-SNP markers in US populations. International Congress Series, 2004, 1261, 85-87.	0.2	1
113	The evaluation of an autosomal SNP 12-plex assay. International Congress Series, 2006, 1288, 61-63.	0.2	1
114	SNP typing of forensic samples with the GenPlexâ„¢ HID system: A collaborative study. Forensic Science International: Genetics Supplement Series, 2009, 2, 508-509.	0.1	1
115	Characterization of NIST standard reference materials by next generation sequencing. Forensic Science International: Genetics Supplement Series, 2013, 4, e97-e98.	0.1	1
116	Initial assessment of the Precision ID Globalfiler Mixture ID panel on the Ion Torrent S5XL DNA sequencer and Converge v2.0 software. Forensic Science International: Genetics Supplement Series, 2017, 6, e94-e95.	0.1	1
117	Estimation of extraction efficiency by droplet digital PCR. Forensic Science International: Genetics Supplement Series, 2019, 7, 515-517.	0.1	1
118	Highly multiplexed assays for measuring polymorphisms on the Y-chromosome. International Congress Series, 2003, 1239, 301-305.	0.2	0
119	Uses of the NIST 26plex STR assay for human identity testing. Forensic Science International: Genetics Supplement Series, 2009, 2, 29-30.	0.1	0
120	Additional sequence characterization of NIST SRM 2391c: PCR-Based DNA Profiling Standard. Forensic Science International: Genetics Supplement Series, 2013, 4, e133-e134.	0.1	0
121	A Strategy for Characterization of Single Nucleotide Polymorphisms in a Reference Material. Forensic Science International: Genetics Supplement Series, 2015, 5, e363-e364.	0.1	0
122	Performing a BLAST search of the STRSeq BioProject. Forensic Science International: Genetics Supplement Series, 2017, 6, e372-e374.	0.1	0
123	Investigating the effects of different library preparation protocols on STR sequencing. Forensic Science International: Genetics Supplement Series, 2017, 6, e418-e420.	0.1	0
124	Sequence-based U.S. population data for 7 X-STR loci. Forensic Science International: Reports, 2020, 2, 100160.	0.4	0
125	Sequencing of full mitochondrial genomes for NIST population samples. Forensic Science International: Genetics Supplement Series, 2019, 7, 452-453.	0.1	0
126	Massively parallel sequencing data of 31 autosomal STR loci obtained using the Precision ID GlobalFiler NGS STR Panel v2 for 82 Japanese population samples. Legal Medicine, 2022, 58, 102082.	0.6	0