

Peter M Vallone

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

127
papers

3,347
citations

31
h-index

54
g-index

131
ext. papers

3,790
ext. citations

3
avg, IF

5.24
L-index

| # | Paper | IF | Citations |
|-----|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|------|-----------|
| 127 | RNA reference materials with defined viral RNA loads of SARS-CoV-2-A useful tool towards a better PCR assay harmonization.. <i>PLoS ONE</i> , 2022 , 17, e0262656 | 3.7 | 2 |
| 126 | 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, <i>PLoS One</i> 16(9):e0256714.. <i>Forensic Science International: Genetics</i> , 2022 , 102710 | 4.3 | 0 |
| 125 | Massively parallel sequencing data of 31 autosomal STR loci obtained using the Precision ID GlobalFiler NGS STR Panel v2 for 82 Japanese population samples.. <i>Legal Medicine</i> , 2022 , 58, 102082 | 1.9 | |
| 124 | A multi-dimensional evaluation of the 'NIST 1032' sample set across four forensic Y-STR multiplexes.. <i>Forensic Science International: Genetics</i> , 2021 , 57, 102655 | 4.3 | 2 |
| 123 | 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. <i>Genetics in Medicine</i> , 2021 , 23, 1673-1680 | 8.1 | 10 |
| 122 | Evidence for multi-copy Mega-NUMTs in the human genome. <i>Nucleic Acids Research</i> , 2021 , 49, 1517-1531 | 10.1 | 15 |
| 121 | Examining performance and likelihood ratios for two likelihood ratio systems using the PROVEDIT dataset. <i>PLoS ONE</i> , 2021 , 16, e0256714 | 3.7 | 3 |
| 120 | Sequence-based U.S. population data for 7 X-STR loci. <i>Forensic Science International: Reports</i> , 2020 , 2, 100160 | 1.9 | |
| 119 | Ethical publication of research on genetics and genomics of biological material: guidelines and recommendations. <i>Forensic Science International: Genetics</i> , 2020 , 48, 102299 | 4.3 | 13 |
| 118 | Results of the 2018 Rapid DNA Maturity Assessment. <i>Journal of Forensic Sciences</i> , 2020 , 65, 953-959 | 1.8 | 11 |
| 117 | Understanding the characteristics of sequence-based single-source DNA profiles. <i>Forensic Science International: Genetics</i> , 2020 , 44, 102192 | 4.3 | 7 |
| 116 | Classification of STR allelic variation using massively parallel sequencing and assessment of flanking region power. <i>Forensic Science International: Genetics</i> , 2020 , 48, 102356 | 4.3 | 8 |
| 115 | Platinum-Quality Mitogenome Haplotypes from United States Populations. <i>Genes</i> , 2020 , 11, | 4.2 | 7 |
| 114 | Affine analysis for quantitative PCR measurements. <i>Analytical and Bioanalytical Chemistry</i> , 2020 , 412, 7977-7988 | 4.4 | 2 |
| 113 | Cautionary Note on Contamination of Reagents Used for Molecular Detection of SARS-CoV-2. <i>Clinical Chemistry</i> , 2020 , 66, 1369-1372 | 5.5 | 20 |
| 112 | The impact of common PCR inhibitors on forensic MPS analysis. <i>Forensic Science International: Genetics</i> , 2019 , 40, 182-191 | 4.3 | 29 |
| 111 | Estimation of extraction efficiency by droplet digital PCR. <i>Forensic Science International: Genetics Supplement Series</i> , 2019 , 7, 515-517 | 0.5 | 1 |

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| 110 | Sequencing of full mitochondrial genomes for NIST population samples. <i>Forensic Science International: Genetics Supplement Series</i> , 2019 , 7, 452-453 | 0.5 | |
| 109 | Understanding the behavior of stutter through the sequencing of STR alleles. <i>Forensic Science International: Genetics Supplement Series</i> , 2019 , 7, 115-116 | 0.5 | 2 |
| 108 | Unleashing novel STRs via characterization of genome in a bottle reference samples. <i>Forensic Science International: Genetics Supplement Series</i> , 2019 , 7, 218-220 | 0.5 | 2 |
| 107 | Are reported likelihood ratios well calibrated?. <i>Forensic Science International: Genetics Supplement Series</i> , 2019 , 7, 572-574 | 0.5 | 2 |
| 106 | Exploring DNA interpretation software using the PROVEDIt dataset. <i>Forensic Science International: Genetics Supplement Series</i> , 2019 , 7, 724-726 | 0.5 | 2 |
| 105 | Developmental validation of the ANDErapid DNA system with FlexPlex assay for arrestee and reference buccal swab processing and database searching. <i>Forensic Science International: Genetics</i> , 2019 , 40, 120-130 | 4.3 | 31 |
| 104 | Sequence variation observed in 27 Y-STR markers with U.S. population samples. <i>Forensic Science International: Genetics Supplement Series</i> , 2019 , 7, 520-521 | 0.5 | 0 |
| 103 | Estimating number of contributors in massively parallel sequencing data of STR loci. <i>Forensic Science International: Genetics</i> , 2019 , 38, 15-22 | 4.3 | 9 |
| 102 | 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 | 4.4 | 66 |
| 101 | Determining Performance Metrics for Targeted Next-Generation Sequencing Panels Using Reference Materials. <i>Journal of Molecular Diagnostics</i> , 2018 , 20, 583-590 | 5.1 | 7 |
| 100 | Sequence-based U.S. population data for 27 autosomal STR loci. <i>Forensic Science International: Genetics</i> , 2018 , 37, 106-115 | 4.3 | 44 |
| 99 | Sequence-based US population data for the SE33 locus. <i>Electrophoresis</i> , 2018 , 39, 2694-2701 | 3.6 | 18 |
| 98 | Accurate Digital Polymerase Chain Reaction Quantification of Challenging Samples Applying Inhibitor-Tolerant DNA Polymerases. <i>Analytical Chemistry</i> , 2017 , 89, 1642-1649 | 7.8 | 17 |
| 97 | 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 | 4.3 | 15 |
| 96 | Performing a BLAST search of the STRSeq BioProject. <i>Forensic Science International: Genetics Supplement Series</i> , 2017 , 6, e372-e374 | 0.5 | |
| 95 | Initial assessment of the Precision ID Globalfiler Mixture ID panel on the Ion Torrent S5XL DNA sequencer and Converge v2.0 software. <i>Forensic Science International: Genetics Supplement Series</i> , 2017 , 6, e94-e95 | 0.5 | 1 |
| 94 | Sequencing of the highly polymorphic STR locus SE33. <i>Forensic Science International: Genetics Supplement Series</i> , 2017 , 6, e322-e323 | 0.5 | 4 |
| 93 | Investigating the effects of different library preparation protocols on STR sequencing. <i>Forensic Science International: Genetics Supplement Series</i> , 2017 , 6, e418-e420 | 0.5 | |

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| 92 | Beyond the STRs: A comprehensive view of current forensic DNA markers characterized in the PCR-based DNA profiling standard SRM 2391D. <i>Forensic Science International: Genetics Supplement Series</i> , 2017 , 6, e426-e427 | 0.5 | 2 |
| 91 | The tao of MPS: Common novel variants. <i>Forensic Science International: Genetics Supplement Series</i> , 2017 , 6, e579-e581 | 0.5 | 2 |
| 90 | STRSeq: A catalog of sequence diversity at human identification Short Tandem Repeat loci. <i>Forensic Science International: Genetics</i> , 2017 , 31, 111-117 | 4.3 | 52 |
| 89 | 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 ²² | 7.8 | 22 |
| 88 | Sequence variation of 22 autosomal STR loci detected by next generation sequencing. <i>Forensic Science International: Genetics</i> , 2016 , 21, 15-21 | 4.3 | 119 |
| 87 | 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 | 4.3 | 18 |
| 86 | Developmental validation of the DNAscan[Rapid DNA Analysis]instrument and expert system for reference sample processing. <i>Forensic Science International: Genetics</i> , 2016 , 25, 145-156 | 4.3 | 32 |
| 85 | Developmental validation of a fully integrated sample-to-profile rapid human identification system for processing single-source reference buccal samples. <i>Forensic Science International: Genetics</i> , 2015 , 16, 181-194 | 4.3 | 41 |
| 84 | 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 ³ | 4.3 | 18 |
| 83 | STR allele sequence variation: Current knowledge and future issues. <i>Forensic Science International: Genetics</i> , 2015 , 18, 118-30 | 4.3 | 114 |
| 82 | Performance of a next generation sequencing SNP assay on degraded DNA. <i>Forensic Science International: Genetics</i> , 2015 , 19, 1-9 | 4.3 | 76 |
| 81 | Rapid PCR of STR markers: Applications to human identification. <i>Forensic Science International: Genetics</i> , 2015 , 18, 90-9 | 4.3 | 33 |
| 80 | Establishing traceability to NIST SRM 2391c: PCR-Based DNA Profiling Standard. <i>Forensic Science International: Genetics Supplement Series</i> , 2015 , 5, e112-e113 | 0.5 | 2 |
| 79 | 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 | 0.5 | 14 |
| 78 | A Strategy for Characterization of Single Nucleotide Polymorphisms in a Reference Material. <i>Forensic Science International: Genetics Supplement Series</i> , 2015 , 5, e363-e364 | 0.5 | |
| 77 | Rapid DNA maturity assessment. <i>Forensic Science International: Genetics Supplement Series</i> , 2015 , 5, e1-e0.5 | 0.5 | 4 |
| 76 | Sequence-based analysis of stutter at STR loci: Characterization and utility. <i>Forensic Science International: Genetics Supplement Series</i> , 2015 , 5, e456-e458 | 0.5 | 14 |
| 75 | Collaborative EDNAP exercise on the IrisPlex system for DNA-based prediction of human eye colour. <i>Forensic Science International: Genetics</i> , 2014 , 11, 241-51 | 4.3 | 17 |

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| 74 | Comparison of base composition analysis and Sanger sequencing of mitochondrial DNA for four U.S. population groups. <i>Forensic Science International: Genetics</i> , 2014 , 8, 226-32 | 4.3 | 4 |
| 73 | Rapid PCR protocols for forensic DNA typing on six thermal cycling platforms. <i>Electrophoresis</i> , 2014 , 35, 3053-61 | 3.6 | 13 |
| 72 | DNA purification from crude samples for human identification using gradient elution isotachopheresis. <i>Electrophoresis</i> , 2013 , 34, 2522-30 | 3.6 | 6 |
| 71 | Additional sequence characterization of NIST SRM 2391c: PCR-Based DNA Profiling Standard. <i>Forensic Science International: Genetics Supplement Series</i> , 2013 , 4, e133-e134 | 0.5 | |
| 70 | Characterization of NIST standard reference materials by next generation sequencing. <i>Forensic Science International: Genetics Supplement Series</i> , 2013 , 4, e97-e98 | 0.5 | 1 |
| 69 | 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 | 4.3 | 87 |
| 68 | Developmental validation of the PowerPlex [®] 18D System, a rapid STR multiplex for analysis of reference samples. <i>Forensic Science International: Genetics</i> , 2013 , 7, 129-35 | 4.3 | 25 |
| 67 | Recertification of the NIST Standard Reference Material [®] 2372, human DNA quantitation standard. <i>Forensic Science International: Genetics Supplement Series</i> , 2013 , 4, e256-e257 | 0.5 | 1 |
| 66 | Allele frequencies for 40 autosomal SNP loci typed for US population samples using electrospray ionization mass spectrometry. <i>Croatian Medical Journal</i> , 2013 , 54, 225-31 | 1.6 | 5 |
| 65 | Forensic performance of two insertion-deletion marker assays. <i>International Journal of Legal Medicine</i> , 2012 , 126, 725-37 | 3.1 | 56 |
| 64 | Capillary electrophoresis of an 11-plex mtDNA coding region SNP single base extension assay for discrimination of the most common Caucasian HV1/HV2 mitotype. <i>Methods in Molecular Biology</i> , 2012 , 830, 159-67 | 1.4 | 1 |
| 63 | Concordance study of direct PCR kits: PowerPlex 18D and Identifiler Direct. <i>Forensic Science International: Genetics Supplement Series</i> , 2011 , 3, e353-e354 | 0.5 | 5 |
| 62 | 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 | 0.5 | 12 |
| 61 | NIST validation studies on the 3500 Genetic Analyzer. <i>Forensic Science International: Genetics Supplement Series</i> , 2011 , 3, e184-e185 | 0.5 | 13 |
| 60 | Forensic performance of insertion-deletion marker systems. <i>Forensic Science International: Genetics Supplement Series</i> , 2011 , 3, e443-e444 | 0.5 | 7 |
| 59 | Autosomal SNP typing of forensic samples with the GenPlex [®] HID System: results of a collaborative study. <i>Forensic Science International: Genetics</i> , 2011 , 5, 369-75 | 4.3 | 16 |
| 58 | Linkage disequilibrium analysis of D12S391 and vWA in U.S. population and paternity samples. <i>Forensic Science International: Genetics</i> , 2011 , 5, 538-40 | 4.3 | 28 |
| 57 | 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 | 4.3 | 7 |

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| 56 | Characterization of U.S. population samples using a 34plex ancestry informative SNP multiplex. <i>Forensic Science International: Genetics Supplement Series</i> , 2011 , 3, e182-e183 | 0.5 | 2 |
| 55 | Inferring continental ancestry of argentineans from Autosomal, Y-chromosomal and mitochondrial DNA. <i>Annals of Human Genetics</i> , 2010 , 74, 65-76 | 2.2 | 122 |
| 54 | Evaluating self-declared ancestry of U.S. Americans with autosomal, Y-chromosomal and mitochondrial DNA. <i>Human Mutation</i> , 2010 , 31, E1875-93 | 4.7 | 74 |
| 53 | Production and certification of NIST Standard Reference Material 2372 Human DNA Quantitation Standard. <i>Analytical and Bioanalytical Chemistry</i> , 2009 , 394, 1183-92 | 4.4 | 34 |
| 52 | A 26plex autosomal STR assay to aid human identity testing*. <i>Journal of Forensic Sciences</i> , 2009 , 54, 1008-85 | 8.5 | 72 |
| 51 | SNP genotyping using multiplex single base primer extension assays. <i>Methods in Molecular Biology</i> , 2009 , 578, 379-91 | 1.4 | 9 |
| 50 | SNP typing of forensic samples with the GenPlex [®] HID system: A collaborative study. <i>Forensic Science International: Genetics Supplement Series</i> , 2009 , 2, 508-509 | 0.5 | 1 |
| 49 | Rapid amplification of commercial STR typing kits. <i>Forensic Science International: Genetics Supplement Series</i> , 2009 , 2, 111-112 | 0.5 | 12 |
| 48 | Uses of the NIST 26plex STR assay for human identity testing. <i>Forensic Science International: Genetics Supplement Series</i> , 2009 , 2, 29-30 | 0.5 | |
| 47 | 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, 61-8 | 4.3 | 13 |
| 46 | Forensic typing of autosomal SNPs with a 29 SNP-multiplex--results of a collaborative EDNAP exercise. <i>Forensic Science International: Genetics</i> , 2008 , 2, 176-83 | 4.3 | 53 |
| 45 | Demonstration of rapid multiplex PCR amplification involving 16 genetic loci. <i>Forensic Science International: Genetics</i> , 2008 , 3, 42-5 | 4.3 | 46 |
| 44 | Report on ISFG SNP Panel Discussion. <i>Forensic Science International: Genetics Supplement Series</i> , 2008 , 1, 471-472 | 0.5 | 20 |
| 43 | New autosomal STR loci. <i>Forensic Science International: Genetics Supplement Series</i> , 2008 , 1, 95-96 | 0.5 | 2 |
| 42 | 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 | 0.5 | 7 |
| 41 | STRs vs. SNPs: thoughts on the future of forensic DNA testing. <i>Forensic Science, Medicine, and Pathology</i> , 2007 , 3, 200-5 | 1.5 | 108 |
| 40 | The impact of additional Y-STR loci on resolving common haplotypes and closely related individuals. <i>Forensic Science International: Genetics</i> , 2007 , 1, 215-7 | 4.3 | 14 |
| 39 | Forensic application of the Affymetrix human mitochondrial resequencing array. <i>Forensic Science International: Genetics</i> , 2007 , 1, 196-8 | 4.3 | 14 |

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| 38 | Studies of DNA dumbbells VIII. Melting analysis of DNA dumbbells with dinucleotide repeat stem sequences. <i>Biopolymers</i> , 2006 , 82, 199-221 | 2.2 | 8 |
| 37 | Characterization and performance of new MiniSTR loci for typing degraded samples. <i>International Congress Series</i> , 2006 , 1288, 504-506 | | 3 |
| 36 | Setting standards and developing technology to aid the human identity testing community. <i>International Congress Series</i> , 2006 , 1288, 628-635 | | 2 |
| 35 | The evaluation of an autosomal SNP 12-plex assay. <i>International Congress Series</i> , 2006 , 1288, 61-63 | | 1 |
| 34 | Allele frequencies for 27 Y-STR loci with U.S. Caucasian, African American, and Hispanic samples. <i>Forensic Science International</i> , 2006 , 156, 250-60 | 2.6 | 43 |
| 33 | Effective strategies for forensic analysis in the mitochondrial DNA coding region. <i>International Journal of Legal Medicine</i> , 2006 , 120, 27-32 | 3.1 | 31 |
| 32 | Genotyping SNPs using a UV-photocleavable oligonucleotide in MALDI-TOF MS. <i>Methods in Molecular Biology</i> , 2005 , 297, 169-78 | 1.4 | 4 |
| 31 | Allele frequencies for 70 autosomal SNP loci with U.S. Caucasian, African-American, and Hispanic samples. <i>Forensic Science International</i> , 2005 , 149, 279-86 | 2.6 | 23 |
| 30 | Mitochondrial DNA typing screens with control region and coding region SNPs. <i>Journal of Forensic Sciences</i> , 2005 , 50, 377-85 | 1.8 | 9 |
| 29 | AutoDimer: a screening tool for primer-dimer and hairpin structures. <i>BioTechniques</i> , 2004 , 37, 226-31 | 2.5 | 346 |
| 28 | 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, 147-57 | 3.1 | 112 |
| 27 | Toward increased utility of mtDNA in forensic identifications. <i>Forensic Science International</i> , 2004 , 146 Suppl, S147-9 | 2.6 | 24 |
| 26 | 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, 107-21 | 2.6 | 63 |
| 25 | Multiplexed assays for evaluation of Y-SNP markers in US populations. <i>International Congress Series</i> , 2004 , 1261, 85-87 | | 1 |
| 24 | 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, 1-10 | 1.8 | 32 |
| 23 | 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 | 1.8 | 7 |
| 22 | Multiplex PCR design strategy used for the simultaneous amplification of 10 Y chromosome short tandem repeat (STR) loci. <i>Analytical and Bioanalytical Chemistry</i> , 2003 , 375, 333-43 | 4.4 | 54 |
| 21 | Highly multiplexed assays for measuring polymorphisms on the Y-chromosome. <i>International Congress Series</i> , 2003 , 1239, 301-305 | | |

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| 20 | Allele Frequencies for 15 Autosomal STR Loci on U.S. Caucasian, African American, and Hispanic Populations. <i>Journal of Forensic Sciences</i> , 2003 , 48, 2003045 | 1.8 | 94 |
| 19 | 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 | 1.8 | 20 |
| 18 | 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, 257-65 | 3.1 | 8 |
| 17 | A novel multiplex for simultaneous amplification of 20 Y chromosome STR markers. <i>Forensic Science International</i> , 2002 , 129, 10-24 | 2.6 | 154 |
| 16 | Capillary electrophoresis as a tool for optimization of multiplex PCR reactions. <i>Fresenius Journal of Analytical Chemistry</i> , 2001 , 369, 200-5 | | 33 |
| 15 | Quality control of PCR primers used in multiplex STR amplification reactions. <i>Forensic Science International</i> , 2001 , 119, 87-96 | 2.6 | 16 |
| 14 | Calculating sequence-dependent melting stability of duplex DNA oligomers and multiplex sequence analysis by graphs. <i>Methods in Enzymology</i> , 2001 , 340, 165-92 | 1.7 | 14 |
| 13 | Genotyping of two mutations in the HFE gene using single-base extension and high-performance liquid chromatography. <i>Analytical Chemistry</i> , 2001 , 73, 620-4 | 7.8 | 37 |
| 12 | 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 | 4.1 | 21 |
| 11 | Thermodynamic, spectroscopic, and equilibrium binding studies of DNA sequence context effects in four 40 base pair deoxyoligonucleotides. <i>Biochemistry</i> , 2000 , 39, 7835-46 | 3.2 | 31 |
| 10 | Melting studies of short DNA hairpins containing the universal base 5-nitroindole. <i>Nucleic Acids Research</i> , 1999 , 27, 3589-96 | 20.1 | 26 |
| 9 | Studies of DNA dumbbells VII: evaluation of the next-nearest-neighbor sequence-dependent interactions in duplex DNA. <i>Biopolymers</i> , 1999 , 52, 29-56 | 2.2 | 34 |
| 8 | Melting studies of short DNA hairpins: influence of loop sequence and adjoining base pair identity on hairpin thermodynamic stability. <i>Biopolymers</i> , 1999 , 50, 425-42 | 2.2 | 60 |
| 7 | Thermodynamic, spectroscopic, and equilibrium binding studies of DNA sequence context effects in six 22-base pair deoxyoligonucleotides. <i>Biochemistry</i> , 1999 , 38, 11197-208 | 3.2 | 26 |
| 6 | Melting studies of short DNA hairpins: Influence of loop sequence and adjoining base pair identity on hairpin thermodynamic stability 1999 , 50, 425 | | 1 |
| 5 | Predicting sequence-dependent melting stability of short duplex DNA oligomers. <i>Biopolymers</i> , 1997 , 44, 217-39 | 2.2 | 153 |
| 4 | Predicting sequence-dependent melting stability of short duplex DNA oligomers 1997 , 44, 217 | | 2 |
| 3 | 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 | | 3 |

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| 2 | An interlaboratory study of complex variant detection | 4 |
| 1 | Predicting sequence-dependent melting stability of short duplex DNA oligomers | 2 |