Marc L Salit

List of Publications by Year
in descending order

71 papers	6,038 citations	147801 31 h-index	95266 68 g-index
81 all docs	81 docs citations	81 times ranked	10572 citing authors

#	Article	IF	Citations
1	Integrating human sequence data sets provides a resource of benchmark SNP and indel genotype calls. Nature Biotechnology, 2014, 32, 246-251.	17.5	722
2	Synthetic spike-in standards for RNA-seq experiments. Genome Research, 2011, 21, 1543-1551.	5.5	588
3	Extensive sequencing of seven human genomes to characterize benchmark reference materials. Scientific Data, 2016, 3, 160025.	5.3	575
4	The External RNA Controls Consortium: a progress report. Nature Methods, 2005, 2, 731-734.	19.0	328
5	An open resource for accurately benchmarking small variant and reference calls. Nature Biotechnology, 2019, 37, 561-566.	17.5	277
6	Best practices for benchmarking germline small-variant calls in human genomes. Nature Biotechnology, 2019, 37, 555-560.	17.5	273
7	The determination of stem cell fate by 3D scaffold structures through the control of cell shape. Biomaterials, 2011, 32, 9188-9196.	11.4	264
8	Testing at scale during the COVID-19 pandemic. Nature Reviews Genetics, 2021, 22, 415-426.	16.3	261
9	A robust benchmark for detection of germline large deletions and insertions. Nature Biotechnology, 2020, 38, 1347-1355.	17.5	233
10	Measurements of translation initiation from all 64 codons in E. coli. Nucleic Acids Research, 2017, 45, 3615-3626.	14.5	165
11	Best practices for evaluating single nucleotide variant calling methods for microbial genomics. Frontiers in Genetics, 2015, 6, 235.	2.3	160
12	Multiplexed precision genome editing with trackable genomic barcodes in yeast. Nature Biotechnology, 2018, 36, 512-520.	17.5	138
13	Good laboratory practice for clinical next-generation sequencing informatics pipelines. Nature Biotechnology, 2015, 33, 689-693.	17.5	134
14	Medical implications of technical accuracy in genome sequencing. Genome Medicine, 2016, 8, 24.	8.2	123
15	Assessing technical performance in differential gene expression experiments with external spike-in RNA control ratio mixtures. Nature Communications, 2014, 5, 5125.	12.8	122
16	The Environmental Microbiology Minimum Information (EMMI) Guidelines: qPCR and dPCR Quality and Reporting for Environmental Microbiology. Environmental Science & Technology, 2021, 55, 10210-10223.	10.0	117
17	LAMP Diagnostics at the Point-of-Care: Emerging Trends and Perspectives for the Developer Community. Expert Review of Molecular Diagnostics, 2021, 21, 43-61.	3.1	105
18	Genome-wide reconstruction of complex structural variants using read clouds. Nature Methods, 2017, 14, 915-920.	19.0	96

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19	In Vivo Site-Specific Protein Tagging with Diverse Amines Using an Engineered Sortase Variant. Journal of the American Chemical Society, 2016, 138, 7496-7499.	13.7	77
20	Benchmarking challenging small variants with linked and long reads. Cell Genomics, 2022, 2, 100128.	6.5	77
21	The COVID-19 XPRIZE and the need for scalable, fast, and widespread testing. Nature Biotechnology, 2020, 38, 1021-1024.	17.5	71
22	A Drift Correction Procedure. Analytical Chemistry, 1998, 70, 3184-3190.	6.5	68
23	Use of Cause-and-Effect Analysis to Design a High-Quality Nanocytotoxicology Assay. Chemical Research in Toxicology, 2015, 28, 21-30.	3.3	65
24	A diploid assembly-based benchmark for variants in the major histocompatibility complex. Nature Communications, 2020, 11, 4794.	12.8	56
25	Single-Element Solution Comparisons with a High-Performance Inductively Coupled Plasma Optical Emission Spectrometric Method. Analytical Chemistry, 2001, 73, 4821-4829.	6.5	55
26	A Rigorous Interlaboratory Examination of the Need to Confirm Next-Generation Sequencingâ€“Detected Variants with an Orthogonal MethodÂin Clinical Genetic Testing. Journal of Molecular Diagnostics, 2019, 21, 318-329.	2.8	49
27	svviz: a read viewer for validating structural variants. Bioinformatics, 2015, 31, 3994-3996.	4.1	46
28	Achieving high-sensitivity for clinical applications using augmented exome sequencing. Genome Medicine, 2015, 7, 71.	8.2	46
29	Cautionary Note on Contamination of Reagents Used for Molecular Detection of SARS-CoV-2. Clinical Chemistry, 2020, 66, 1369-1372.	3.2	46
30	Assembly and annotation of an Ashkenazi human reference genome. Genome Biology, 2020, 21, 129.	8.8	42
31	Evaluation of the External RNA Controls Consortium (ERCC) reference material using a modified Latin square design. BMC Biotechnology, 2016, 16, 54.	3.3	41
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.	2.4	40
33	A research roadmap for next-generation sequencing informatics. Science Translational Medicine, 2016, 8, 335ps10.	12.4	37
34	Ontology analysis of global gene expression differences of human bone marrow stromal cells cultured on 3D scaffolds or 2D films. Biomaterials, 2014, 35, 6716-6726.	11.4	32
35	When Wavelengths Collide: Bias in Cell Abundance Measurements Due to Expressed Fluorescent Proteins. ACS Synthetic Biology, 2016, 5, 1024-1027.	3.8	32
36	An ICP-OES Method with 0.2 Expanded Uncertainties for the Characterization of LiAlO2. Analytical Chemistry, 2000, 72, 3504-3511.	6.5	31

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37	Minimum information for reporting next generation sequence genotyping (MIRING): Guidelines for reporting HLA and KIR genotyping via next generation sequencing. Human Immunology, 2015, 76, 954-962.	2.4	28
38	External RNA Controls Consortium Beta Version Update. Journal of Genomics, 2016, 4, 19-22.	0.9	28
39	Unbiased Fitness Estimation of Pooled Barcode or Amplicon Sequencing Studies. Cell Systems, 2018, 7, 521-525.e4.	6.2	27
40	Development and Characterization of Reference Materials for Genetic Testing: Focus on Public Partnerships. Annals of Laboratory Medicine, 2016, 36, 513-520.	2.5	21
41	Traceability of Single-Element Calibration Solutions. Analytical Chemistry, 2005, 77, 136 A-141 A.	6.5	20
42	[5] Standards in Gene Expression Microarray Experiments. Methods in Enzymology, 2006, 411, 63-78.	1.0	17
43	Unmet needs: Research helps regulators do their jobs. Science Translational Medicine, 2015, 7, 315ps22.	12.4	15
44	An international comparability study on quantification of mRNA gene expression ratios: CCQM-P103.1. Biomolecular Detection and Quantification, 2016, 8, 15-28.	7.0	15
45	Simultaneous RNA purification and size selection using on-chip isotachophoresis with an ionic spacer. Lab on A Chip, 2019, 19, 2741-2749.	6.0	15
46	Image-based feedback control for real-time sorting of microspheres in a microfluidic device. Lab on A Chip, 2010, 10, 2402.	6.0	14
47	High-coverage, long-read sequencing of Han Chinese trio reference samples. Scientific Data, 2019, 6, 91.	5.3	13
48	Using inductively coupled plasma-mass spectrometry for calibration transfer between environmental CRMs. Fresenius' Journal of Analytical Chemistry, 2001, 370, 259-263.	1.5	12
49	Design and initial characterization of a glow discharge atomic emission instrument for macro-scale elemental composition mapping of solid surfaces. Spectrochimica Acta, Part B: Atomic Spectroscopy, 1995, 50, 1045-1058.	2.9	11
50	Wave numbers and Ar pressure-induced shifts of198Hg atomic lines measured by Fourier transform spectroscopy. Journal of Physics B: Atomic, Molecular and Optical Physics, 2005, 38, 3739-3753.	1.5	11
51	Characterization of in vitro transcription amplification linearity and variability in the low copy number regime using External RNA Control Consortium (ERCC) spike-ins. Analytical and Bioanalytical Chemistry, 2013, 405, 315-320.	3.7	10
52	Determining Performance Metrics for Targeted Next-Generation Sequencing Panels Using Reference Materials. Journal of Molecular Diagnostics, 2018, 20, 583-590.	2.8	10
53	Preparation and certification of a rhodium standard reference material solution. Analytical Chemistry, 1993, 65, 2899-2902.	6.5	9
54	Gradient Elution Moving Boundary Electrophoresis Enables Rapid Analysis of Acids in Complex Biomass-Derived Streams. ACS Sustainable Chemistry and Engineering, 2016, 4, 7175-7185.	6.7	8

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55	MAQC and the era of genomic medicine. Nature Biotechnology, 2021, 39, 1066-1067.	17.5	8
56	Fourier transform atomic emission studies using a glow discharge as the emission source. Spectrochimica Acta, Part B: Atomic Spectroscopy, 1993, 48, 1325-1337.	2.9	7
57	Integrating Automated Systems With Modular Architecture. Analytical Chemistry, 1994, 66, 361A-367A.	6.5	7
58	Advancing Benchmarks for Genome Sequencing. Cell Systems, 2015, 1, 176-177.	6.2	6
59	A crowdsourced set of curated structural variants for the human genome. PLoS Computational Biology, 2020, 16, e1007933.	3.2	6
60	PEPR: pipelines for evaluating prokaryotic references. Analytical and Bioanalytical Chemistry, 2016, 408, 2975-2983.	3.7	5
61	Summarizing performance for genome scale measurement of miRNA: reference samples and metrics. BMC Genomics, 2018, 19, 180.	2.8	5
62	Wave numbers and pressure-induced shifts of Ar I atomic lines measured by Fourier transform spectroscopy. Journal of Physics B: Atomic, Molecular and Optical Physics, 2012, 45, 115001.	1.5	3
63	Cell-based reference samples designed with specific differences in microRNA biomarkers. BMC Biotechnology, 2018, 18, 17.	3.3	2
64	Proffered Papers and Posters Presented at the Seventh International Symposium on Hereditary Breast and Ovarian Cancerâ€"BrcA: From the Personal to the Population. Current Oncology, 2018, 25, 224-262.	2.2	2
65	CrowdVariant: a crowdsourcing approach to classify copy number variants. Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing, 2019, 24, 224-235.	0.7	2
66	Use of Standard Reference Material 2242 (Relative Intensity Correction Standard for Raman) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 302 T	1.8	1
67	System-ready behaviors for integration. Laboratory Robotics and Automation, 1997, 9, 113-118.	0.2	0
68	A crowdsourced set of curated structural variants for the human genome. , 2020, 16, e1007933.		0
69	A crowdsourced set of curated structural variants for the human genome. , 2020, 16, e1007933.		0
70	A crowdsourced set of curated structural variants for the human genome. , 2020, 16, e1007933.		0
71	A crowdsourced set of curated structural variants for the human genome. , 2020, 16, e1007933.		0