

Marc L Salit

List of Publications by Year in descending order

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Version: 2024-02-01

71
papers

6,038
citations

168829

31
h-index

107981

68
g-index

81
all docs

81
docs citations

81
times ranked

11679
citing authors

#	ARTICLE	IF	CITATIONS
1	Benchmarking challenging small variants with linked and long reads. <i>Cell Genomics</i> , 2022, 2, 100128.	3.0	77
2	LAMP Diagnostics at the Point-of-Care: Emerging Trends and Perspectives for the Developer Community. <i>Expert Review of Molecular Diagnostics</i> , 2021, 21, 43-61.	1.5	105
3	Testing at scale during the COVID-19 pandemic. <i>Nature Reviews Genetics</i> , 2021, 22, 415-426.	7.7	261
4	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.	1.1	40
5	The Environmental Microbiology Minimum Information (EMMI) Guidelines: qPCR and dPCR Quality and Reporting for Environmental Microbiology. <i>Environmental Science & Technology</i> , 2021, 55, 10210-10223.	4.6	117
6	MAQC and the era of genomic medicine. <i>Nature Biotechnology</i> , 2021, 39, 1066-1067.	9.4	8
7	A diploid assembly-based benchmark for variants in the major histocompatibility complex. <i>Nature Communications</i> , 2020, 11, 4794.	5.8	56
8	Cautionary Note on Contamination of Reagents Used for Molecular Detection of SARS-CoV-2. <i>Clinical Chemistry</i> , 2020, 66, 1369-1372.	1.5	46
9	The COVID-19 XPRIZE and the need for scalable, fast, and widespread testing. <i>Nature Biotechnology</i> , 2020, 38, 1021-1024.	9.4	71
10	A robust benchmark for detection of germline large deletions and insertions. <i>Nature Biotechnology</i> , 2020, 38, 1347-1355.	9.4	233
11	Assembly and annotation of an Ashkenazi human reference genome. <i>Genome Biology</i> , 2020, 21, 129.	3.8	42
12	A crowdsourced set of curated structural variants for the human genome. <i>PLoS Computational Biology</i> , 2020, 16, e1007933.	1.5	6
13	A crowdsourced set of curated structural variants for the human genome. , 2020, 16, e1007933.		0
14	A crowdsourced set of curated structural variants for the human genome. , 2020, 16, e1007933.		0
15	A crowdsourced set of curated structural variants for the human genome. , 2020, 16, e1007933.		0
16	A crowdsourced set of curated structural variants for the human genome. , 2020, 16, e1007933.		0
17	Simultaneous RNA purification and size selection using on-chip isotachopheresis with an ionic spacer. <i>Lab on A Chip</i> , 2019, 19, 2741-2749.	3.1	15
18	A Rigorous Interlaboratory Examination of the Need to Confirm Next-Generation Sequencingâ€œDetected Variants with an Orthogonal Methodâ€œin Clinical Genetic Testing. <i>Journal of Molecular Diagnostics</i> , 2019, 21, 318-329.	1.2	49

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19	High-coverage, long-read sequencing of Han Chinese trio reference samples. <i>Scientific Data</i> , 2019, 6, 91.	2.4	13
20	Best practices for benchmarking germline small-variant calls in human genomes. <i>Nature Biotechnology</i> , 2019, 37, 555-560.	9.4	273
21	An open resource for accurately benchmarking small variant and reference calls. <i>Nature Biotechnology</i> , 2019, 37, 561-566.	9.4	277
22	CrowdVariant: a crowdsourcing approach to classify copy number variants. <i>Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing</i> , 2019, 24, 224-235.	0.7	2
23	Cell-based reference samples designed with specific differences in microRNA biomarkers. <i>BMC Biotechnology</i> , 2018, 18, 17.	1.7	2
24	Proffered Papers and Posters Presented at the Seventh International Symposium on Hereditary Breast and Ovarian Cancer—BrCA: From the Personal to the Population. <i>Current Oncology</i> , 2018, 25, 224-262.	0.9	2
25	Unbiased Fitness Estimation of Pooled Barcode or Amplicon Sequencing Studies. <i>Cell Systems</i> , 2018, 7, 521-525.e4.	2.9	27
26	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
27	Summarizing performance for genome scale measurement of miRNA: reference samples and metrics. <i>BMC Genomics</i> , 2018, 19, 180.	1.2	5
28	Multiplexed precision genome editing with trackable genomic barcodes in yeast. <i>Nature Biotechnology</i> , 2018, 36, 512-520.	9.4	138
29	Measurements of translation initiation from all 64 codons in <i>E. coli</i> . <i>Nucleic Acids Research</i> , 2017, 45, 3615-3626.	6.5	165
30	Genome-wide reconstruction of complex structural variants using read clouds. <i>Nature Methods</i> , 2017, 14, 915-920.	9.0	96
31	External RNA Controls Consortium Beta Version Update. <i>Journal of Genomics</i> , 2016, 4, 19-22.	0.6	28
32	Development and Characterization of Reference Materials for Genetic Testing: Focus on Public Partnerships. <i>Annals of Laboratory Medicine</i> , 2016, 36, 513-520.	1.2	21
33	Medical implications of technical accuracy in genome sequencing. <i>Genome Medicine</i> , 2016, 8, 24.	3.6	123
34	An international comparability study on quantification of mRNA gene expression ratios: CCQM-P103.1. <i>Biomolecular Detection and Quantification</i> , 2016, 8, 15-28.	7.0	15
35	Extensive sequencing of seven human genomes to characterize benchmark reference materials. <i>Scientific Data</i> , 2016, 3, 160025.	2.4	575
36	A research roadmap for next-generation sequencing informatics. <i>Science Translational Medicine</i> , 2016, 8, 335ps10.	5.8	37

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37	Gradient Elution Moving Boundary Electrophoresis Enables Rapid Analysis of Acids in Complex Biomass-Derived Streams. <i>ACS Sustainable Chemistry and Engineering</i> , 2016, 4, 7175-7185.	3.2	8
38	Evaluation of the External RNA Controls Consortium (ERCC) reference material using a modified Latin square design. <i>BMC Biotechnology</i> , 2016, 16, 54.	1.7	41
39	In Vivo Site-Specific Protein Tagging with Diverse Amines Using an Engineered Sortase Variant. <i>Journal of the American Chemical Society</i> , 2016, 138, 7496-7499.	6.6	77
40	PEPR: pipelines for evaluating prokaryotic references. <i>Analytical and Bioanalytical Chemistry</i> , 2016, 408, 2975-2983.	1.9	5
41	When Wavelengths Collide: Bias in Cell Abundance Measurements Due to Expressed Fluorescent Proteins. <i>ACS Synthetic Biology</i> , 2016, 5, 1024-1027.	1.9	32
42	Best practices for evaluating single nucleotide variant calling methods for microbial genomics. <i>Frontiers in Genetics</i> , 2015, 6, 235.	1.1	160
43	Unmet needs: Research helps regulators do their jobs. <i>Science Translational Medicine</i> , 2015, 7, 315ps22.	5.8	15
44	Advancing Benchmarks for Genome Sequencing. <i>Cell Systems</i> , 2015, 1, 176-177.	2.9	6
45	Good laboratory practice for clinical next-generation sequencing informatics pipelines. <i>Nature Biotechnology</i> , 2015, 33, 689-693.	9.4	134
46	Minimum information for reporting next generation sequence genotyping (MIRING): Guidelines for reporting HLA and KIR genotyping via next generation sequencing. <i>Human Immunology</i> , 2015, 76, 954-962.	1.2	28
47	svviz: a read viewer for validating structural variants. <i>Bioinformatics</i> , 2015, 31, 3994-3996.	1.8	46
48	Achieving high-sensitivity for clinical applications using augmented exome sequencing. <i>Genome Medicine</i> , 2015, 7, 71.	3.6	46
49	Use of Cause-and-Effect Analysis to Design a High-Quality Nanocytotoxicology Assay. <i>Chemical Research in Toxicology</i> , 2015, 28, 21-30.	1.7	65
50	Integrating human sequence data sets provides a resource of benchmark SNP and indel genotype calls. <i>Nature Biotechnology</i> , 2014, 32, 246-251.	9.4	722
51	Assessing technical performance in differential gene expression experiments with external spike-in RNA control ratio mixtures. <i>Nature Communications</i> , 2014, 5, 5125.	5.8	122
52	Ontology analysis of global gene expression differences of human bone marrow stromal cells cultured on 3D scaffolds or 2D films. <i>Biomaterials</i> , 2014, 35, 6716-6726.	5.7	32
53	Characterization of in vitro transcription amplification linearity and variability in the low copy number regime using External RNA Control Consortium (ERCC) spike-ins. <i>Analytical and Bioanalytical Chemistry</i> , 2013, 405, 315-320.	1.9	10
54	Wave numbers and pressure-induced shifts of Ar I atomic lines measured by Fourier transform spectroscopy. <i>Journal of Physics B: Atomic, Molecular and Optical Physics</i> , 2012, 45, 115001.	0.6	3

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55	Synthetic spike-in standards for RNA-seq experiments. <i>Genome Research</i> , 2011, 21, 1543-1551.	2.4	588
56	The determination of stem cell fate by 3D scaffold structures through the control of cell shape. <i>Biomaterials</i> , 2011, 32, 9188-9196.	5.7	264
57	Image-based feedback control for real-time sorting of microspheres in a microfluidic device. <i>Lab on A Chip</i> , 2010, 10, 2402.	3.1	14
58	Use of Standard Reference Material 2242 (Relative Intensity Correction Standard for Raman) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 622	0.8	1
59	[5] Standards in Gene Expression Microarray Experiments. <i>Methods in Enzymology</i> , 2006, 411, 63-78.	0.4	17
60	The External RNA Controls Consortium: a progress report. <i>Nature Methods</i> , 2005, 2, 731-734.	9.0	328
61	Wave numbers and Ar pressure-induced shifts of 198Hg atomic lines measured by Fourier transform spectroscopy. <i>Journal of Physics B: Atomic, Molecular and Optical Physics</i> , 2005, 38, 3739-3753.	0.6	11
62	Traceability of Single-Element Calibration Solutions. <i>Analytical Chemistry</i> , 2005, 77, 136 A-141 A.	3.2	20
63	Single-Element Solution Comparisons with a High-Performance Inductively Coupled Plasma Optical Emission Spectrometric Method. <i>Analytical Chemistry</i> , 2001, 73, 4821-4829.	3.2	55
64	Using inductively coupled plasma-mass spectrometry for calibration transfer between environmental CRMs. <i>Fresenius' Journal of Analytical Chemistry</i> , 2001, 370, 259-263.	1.5	12
65	An ICP-OES Method with 0.2 Expanded Uncertainties for the Characterization of LiAlO ₂ . <i>Analytical Chemistry</i> , 2000, 72, 3504-3511.	3.2	31
66	A Drift Correction Procedure. <i>Analytical Chemistry</i> , 1998, 70, 3184-3190.	3.2	68
67	System-ready behaviors for integration. <i>Laboratory Robotics and Automation</i> , 1997, 9, 113-118.	0.3	0
68	Design and initial characterization of a glow discharge atomic emission instrument for macro-scale elemental composition mapping of solid surfaces. <i>Spectrochimica Acta, Part B: Atomic Spectroscopy</i> , 1995, 50, 1045-1058.	1.5	11
69	Integrating Automated Systems With Modular Architecture. <i>Analytical Chemistry</i> , 1994, 66, 361A-367A.	3.2	7
70	Fourier transform atomic emission studies using a glow discharge as the emission source. <i>Spectrochimica Acta, Part B: Atomic Spectroscopy</i> , 1993, 48, 1325-1337.	1.5	7
71	Preparation and certification of a rhodium standard reference material solution. <i>Analytical Chemistry</i> , 1993, 65, 2899-2902.	3.2	9