

# Estimating abundances of retroviral insertion sites from

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Citation Report

#	ARTICLE	IF	CITATIONS
1	Extended Survival of Glioblastoma Patients After Chemoprotective HSC Gene Therapy. <i>Science Translational Medicine</i> , 2012, 4, 133ra57.	5.8	91
2	Special features of <scp>RAD</scp> Sequencing data: implications for genotyping. <i>Molecular Ecology</i> , 2013, 22, 3151-3164.	2.0	318
3	Evaluating a Ligation-Mediated PCR and Pyrosequencing Method for the Detection of Clonal Contribution in Polyclonal Retrovirally Transduced Samples. <i>Human Gene Therapy Methods</i> , 2013, 24, 68-79.	2.1	21
4	Strongyloidiasis and Infective Dermatitis Alter Human T Lymphotropic Virus-1 Clonality in vivo. <i>PLoS Pathogens</i> , 2013, 9, e1003263.	2.1	51
5	Massive Depletion of Bovine Leukemia Virus Proviral Clones Located in Genomic Transcriptionally Active Sites during Primary Infection. <i>PLoS Pathogens</i> , 2013, 9, e1003687.	2.1	78
6	Cancer Gene Discovery: Exploiting Insertional Mutagenesis. <i>Molecular Cancer Research</i> , 2013, 11, 1141-1158.	1.5	59
7	Integration Site and Clonal Expansion in Human Chronic Retroviral Infection and Gene Therapy. <i>Viruses</i> , 2014, 6, 4140-4164.	1.5	16
8	Quantification of HTLV-1 Clonality and TCR Diversity. <i>PLoS Computational Biology</i> , 2014, 10, e1003646.	1.5	71
9	Engineering the Human Genome: Reflections on the Beginning. <i>Human Gene Therapy</i> , 2014, 25, 395-400.	1.4	0
10	Development and validation of a new high-throughput method to investigate the clonality of HTLV-1-infected cells based on provirus integration sites. <i>Genome Medicine</i> , 2014, 6, 46.	3.6	56
11	HTLV-1 clonality in adult T-cell leukaemia and non-malignant HTLV-1 infection. <i>Seminars in Cancer Biology</i> , 2014, 26, 89-98.	4.3	87
12	Vector Integration and Tumorigenesis. <i>Human Gene Therapy</i> , 2014, 25, 475-481.	1.4	22
13	Specific HIV integration sites are linked to clonal expansion and persistence of infected cells. <i>Science</i> , 2014, 345, 179-183.	6.0	722
14	A Modified $\hat{\beta}$ -Retrovirus Vector for X-Linked Severe Combined Immunodeficiency. <i>New England Journal of Medicine</i> , 2014, 371, 1407-1417.	13.9	358
15	Clonal Tracking of Rhesus Macaque Hematopoiesis Highlights a Distinct Lineage Origin for Natural Killer Cells. <i>Cell Stem Cell</i> , 2014, 14, 486-499.	5.2	149
16	The role of HTLV-1 clonality, proviral structure, and genomic integration site in adult T-cell leukemia/lymphoma. <i>Blood</i> , 2014, 123, 3925-3931.	0.6	112
17	Common Viral Integration Sites Identified in Avian Leukosis Virus-Induced B-Cell Lymphomas. <i>MBio</i> , 2015, 6, e01863-15.	1.8	25
18	Estimating T-cell repertoire diversity: limitations of classical estimators and a new approach. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2015, 370, 20140291.	1.8	156

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19	HIV-1 Integration Landscape during Latent and Active Infection. <i>Cell</i> , 2015, 160, 420-432.	13.5	393
20	Quantitative Shearing Linear Amplification Polymerase Chain Reaction: An Improved Method for Quantifying Lentiviral Vector Insertion Sites in Transplanted Hematopoietic Cell Systems. <i>Human Gene Therapy Methods</i> , 2015, 26, 4-12.	2.1	13
21	Outcomes Following Gene Therapy in Patients With Severe Wiskott-Aldrich Syndrome. <i>JAMA - Journal of the American Medical Association</i> , 2015, 313, 1550.	3.8	327
22	TheMETGene Is a Common Integration Target in Avian Leukosis Virus Subgroup J-Induced Chicken Hemangiomas. <i>Journal of Virology</i> , 2015, 89, 4712-4719.	1.5	28
23	The Latent Reservoir for HIV-1: How Immunologic Memory and Clonal Expansion Contribute to HIV-1 Persistence. <i>Journal of Immunology</i> , 2016, 197, 407-417.	0.4	121
24	Amplification, Next-generation Sequencing, and Genomic DNA Mapping of Retroviral Integration Sites. <i>Journal of Visualized Experiments</i> , 2016, , .	0.2	36
25	Gene Therapy for X-Linked Severe Combined Immunodeficiency: Where Do We Stand?. <i>Human Gene Therapy</i> , 2016, 27, 108-116.	1.4	92
26	INSPIRED: A Pipeline for Quantitative Analysis of Sites of New DNA Integration in Cellular Genomes. <i>Molecular Therapy - Methods and Clinical Development</i> , 2017, 4, 39-49.	1.8	81
27	INSPIRED: Quantification and Visualization Tools for Analyzing Integration Site Distributions. <i>Molecular Therapy - Methods and Clinical Development</i> , 2017, 4, 17-26.	1.8	60
28	Integration site selection by retroviruses and transposable elements in eukaryotes. <i>Nature Reviews Genetics</i> , 2017, 18, 292-308.	7.7	215
29	Quantitative stability of hematopoietic stem and progenitor cell clonal output in rhesus macaques receiving transplants. <i>Blood</i> , 2017, 129, 1448-1457.	0.6	53
30	Serological and Molecular Methods to Study Epidemiological Aspects of Human T-Cell Lymphotropic Virus Type 1 Infection. <i>Methods in Molecular Biology</i> , 2017, 1582, 3-24.	0.4	28
31	High-Throughput Mapping and Clonal Quantification of Retroviral Integration Sites. <i>Methods in Molecular Biology</i> , 2017, 1582, 127-141.	0.4	9
32	Integrating Vectors for Gene Therapy and Clonal Tracking of Engineered Hematopoiesis. <i>Hematology/Oncology Clinics of North America</i> , 2017, 31, 737-752.	0.9	16
33	Gene therapy for Wiskott-Aldrich syndrome in a severely affected adult. <i>Blood</i> , 2017, 130, 1327-1335.	0.6	83
34	Dynamics and mechanisms of clonal expansion of HIV-1-infected cells in a humanized mouse model. <i>Scientific Reports</i> , 2017, 7, 6913.	1.6	24
35	Integration Site Analysis in Gene Therapy Patients: Expectations and Reality. <i>Human Gene Therapy</i> , 2017, 28, 1122-1129.	1.4	12
36	Multidisciplinary insight into clonal expansion of HTLV-1-infected cells in adult T-cell leukemia via modeling by deterministic finite automata coupled with high-throughput sequencing. <i>BMC Medical Genomics</i> , 2017, 10, 4.	0.7	10

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37	VISPA2: a scalable pipeline for high-throughput identification and annotation of vector integration sites. <i>BMC Bioinformatics</i> , 2017, 18, 520.	1.2	23
38	Analyzing the Genotoxicity of Retroviral Vectors in Hematopoietic Cell Gene Therapy. <i>Molecular Therapy - Methods and Clinical Development</i> , 2018, 8, 21-30.	1.8	34
39	Long-term remission despite clonal expansion of replication-competent HIV-1 isolates. <i>JCI Insight</i> , 2018, 3, .	2.3	39
40	Induction of resistance to chimeric antigen receptor T cell therapy by transduction of a single leukemic B cell. <i>Nature Medicine</i> , 2018, 24, 1499-1503.	15.2	459
41	T cell dynamics and response of the microbiota after gene therapy to treat X-linked severe combined immunodeficiency. <i>Genome Medicine</i> , 2018, 10, 70.	3.6	28
42	The role of integration and clonal expansion in HIV infection: live long and prosper. <i>Retrovirology</i> , 2018, 15, 71.	0.9	54
43	Disruption of TET2 promotes the therapeutic efficacy of CD19-targeted T cells. <i>Nature</i> , 2018, 558, 307-312.	13.7	574
44	The Nature of the HTLV-1 Provirus in Naturally Infected Individuals Analyzed by the Viral DNA-Capture-Seq Approach. <i>Cell Reports</i> , 2019, 29, 724-735.e4.	2.9	46
45	HIV-1 DNA-capture-seq is a useful tool for the comprehensive characterization of HIV-1 provirus. <i>Scientific Reports</i> , 2019, 9, 12326.	1.6	33
46	A quantitative approach for measuring the reservoir of latent HIV-1 proviruses. <i>Nature</i> , 2019, 566, 120-125.	13.7	471
47	Gorillas have been infected with the HERV-K (HML-2) endogenous retrovirus much more recently than humans and chimpanzees. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 1337-1346.	3.3	27
48	The forces driving clonal expansion of the HIV-1 latent reservoir. <i>Virology Journal</i> , 2020, 17, 4.	1.4	53
49	The relative contributions of infectious and mitotic spread to HTLV-1 persistence. <i>PLoS Computational Biology</i> , 2020, 16, e1007470.	1.5	22
50	DNA Barcoding in Nonhuman Primates Reveals Important Limitations in Retrovirus Integration Site Analysis. <i>Molecular Therapy - Methods and Clinical Development</i> , 2020, 17, 796-809.	1.8	15
51	The Chimeric Antigen Receptor Detection Toolkit. <i>Frontiers in Immunology</i> , 2020, 11, 1770.	2.2	34
52	Lentiviral gene therapy for X-linked chronic granulomatous disease. <i>Nature Medicine</i> , 2020, 26, 200-206.	15.2	175
53	Clonal tracking in gene therapy patients reveals a diversity of human hematopoietic differentiation programs. <i>Blood</i> , 2020, 135, 1219-1231.	0.6	50
54	HIV Genetic Diversity â€“ Superpower of a Formidable Virus. <i>Current HIV Research</i> , 2020, 18, 69-73.	0.2	1

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55	Hematopoietic Tumors in a Mouse Model of X-linked Chronic Granulomatous Disease after Lentiviral Vector-Mediated Gene Therapy. <i>Molecular Therapy</i> , 2021, 29, 86-102.	3.7	17
56	A long-term study of AAV gene therapy in dogs with hemophilia A identifies clonal expansions of transduced liver cells. <i>Nature Biotechnology</i> , 2021, 39, 47-55.	9.4	238
57	iGUIDE Method for CRISPR Off-Target Detection. <i>Methods in Molecular Biology</i> , 2021, 2189, 71-80.	0.4	3
58	NPM <sup>1</sup> -ALK-Induced Reprogramming of Mature TCR-Stimulated T Cells Results in Dedifferentiation and Malignant Transformation. <i>Cancer Research</i> , 2021, 81, 3241-3254.	0.4	10
59	Antigen-driven clonal selection shapes the persistence of HIV-1 <sup>+</sup> infected CD4 <sup>+</sup> T cells in vivo. <i>Journal of Clinical Investigation</i> , 2021, 131, .	3.9	103
60	Integration in oncogenes plays only a minor role in determining the in vivo distribution of HIV integration sites before or during suppressive antiretroviral therapy. <i>PLoS Pathogens</i> , 2021, 17, e1009141.	2.1	36
61	Early Emergence and Long-Term Persistence of HIV-Infected T-Cell Clones in Children. <i>MBio</i> , 2021, 12, .	1.8	7
62	Lentiviral vector ALS20 yields high hemoglobin levels with low genomic integrations for treatment of beta-globinopathies. <i>Molecular Therapy</i> , 2021, 29, 1625-1638.	3.7	10
64	Long-term outcomes after gene therapy for adenosine deaminase severe combined immune deficiency. <i>Blood</i> , 2021, 138, 1304-1316.	0.6	28
65	Retrieval of vector integration sites from cell-free DNA. <i>Nature Medicine</i> , 2021, 27, 1458-1470.	15.2	26
67	Forward and Reverse Genetics of B Cell Malignancies: From Insertional Mutagenesis to CRISPR-Cas. <i>Frontiers in Immunology</i> , 2021, 12, 670280.	2.2	1
68	The Clonal Expansion Dynamics of the HIV-1 Reservoir: Mechanisms of Integration Site-Dependent Proliferation and HIV-1 Persistence. <i>Viruses</i> , 2021, 13, 1858.	1.5	17
69	Safety and Efficacy of Retroviral and Lentiviral Vectors for Gene Therapy. , 2017, , 9-35.		6
70	Clones of infected cells arise early in HIV-infected individuals. <i>JCI Insight</i> , 2019, 4, .	2.3	59
71	CD19-targeting CAR T cell immunotherapy outcomes correlate with genomic modification by vector integration. <i>Journal of Clinical Investigation</i> , 2019, 130, 673-685.	3.9	78
72	Sleeping Beauty <sup>2</sup> -engineered CAR T cells achieve antileukemic activity without severe toxicities. <i>Journal of Clinical Investigation</i> , 2020, 130, 6021-6033.	3.9	102
73	LUMI-PCR: an Illumina platform ligation-mediated PCR protocol for integration site cloning, provides molecular quantitation of integration sites. <i>Mobile DNA</i> , 2020, 11, 7.	1.3	4
74	Selection for avian leukosis virus integration sites determines the clonal progression of B-cell lymphomas. <i>PLoS Pathogens</i> , 2017, 13, e1006708.	2.1	15

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75	Characterizing the Latent HIV-1 Reservoir in Patients with Viremia Suppressed on cART: Progress, Challenges, and Opportunities. <i>Current HIV Research</i> , 2020, 18, 99-113.	0.2	6
76	Clonal Expansion of Infected CD4+ T Cells in People Living with HIV. <i>Viruses</i> , 2021, 13, 2078.	1.5	11
79	Challenges in estimating numbers of vectors integrated in gene-modified cells using DNA sequence information. <i>Molecular Therapy</i> , 2021, 29, 3328-3331.	3.7	7
81	Efficient and safe correction of hemophilia A by lentiviral vector-transduced BOECs in an implantable device. <i>Molecular Therapy - Methods and Clinical Development</i> , 2021, 23, 551-566.	1.8	11
85	Lentiviral globin gene therapy with reduced-intensity conditioning in adults with $\beta^0$ -thalassemia: a phase 1 trial. <i>Nature Medicine</i> , 2022, 28, 63-70.	15.2	18
86	Decade-long leukaemia remissions with persistence of CD4+ CAR T cells. <i>Nature</i> , 2022, 602, 503-509.	13.7	369
87	Lentiviral standards to determine the sensitivity of assays that quantify lentiviral vector copy numbers and genomic insertion sites in cells. <i>Gene Therapy</i> , 2022, 29, 536-543.	2.3	6
88	Rapid manufacturing of non-activated potent CAR T cells. <i>Nature Biomedical Engineering</i> , 2022, 6, 118-128.	11.6	92
89	PSMA-targeting TGF $\beta$ -insensitive armored CAR T cells in metastatic castration-resistant prostate cancer: a phase 1 trial. <i>Nature Medicine</i> , 2022, 28, 724-734.	15.2	171
90	Normalization of clonal diversity in gene therapy studies using shape constrained splines. <i>Scientific Reports</i> , 2022, 12, 3836.	1.6	8
91	Selective clonal persistence of human retroviruses in vivo: Radial chromatin organization, integration site, and host transcription. <i>Science Advances</i> , 2022, 8, eabm6210.	4.7	15
92	Comprehensive Comparison of Novel Bovine Leukemia Virus (BLV) Integration Sites between B-Cell Lymphoma Lines BLSC-KU1 and BLSC-KU17 Using the Viral DNA Capture High-Throughput Sequencing Method. <i>Viruses</i> , 2022, 14, 995.	1.5	4
94	Evaluating the state of the science for adeno-associated virus integration: An integrated perspective. <i>Molecular Therapy</i> , 2022, 30, 2646-2663.	3.7	65
95	Clonal reconstruction from co-occurrence of vector integration sites accurately quantifies expanding clones in vivo. <i>Nature Communications</i> , 2022, 13, .	5.8	0
96	ISAnalytics enables longitudinal and high-throughput clonal tracking studies in hematopoietic stem cell gene therapy applications. <i>Briefings in Bioinformatics</i> , 2023, 24, .	3.2	2