

# Evolution and Impact of Subclonal Mutations in Chroni

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Citation Report

#	ARTICLE	IF	CITATIONS
1	ecancermedalscience. Ecancermedalscience, 2014, 8, 453.	0.6	0
3	Clinical application of targeted and genome-wide technologies: can we predict treatment responses in chronic lymphocytic leukemia?. Personalized Medicine, 2013, 10, 361-376.	0.8	9
4	Cancer heterogeneityâ€™a multifaceted view. EMBO Reports, 2013, 14, 686-695.	2.0	208
5	SAMHD1-dependent retroviral control and escape in mice. EMBO Journal, 2013, 32, 2454-2462.	3.5	141
6	The genomic landscape of chronic lymphocytic leukemia: clinical implications. BMC Medicine, 2013, 11, 124.	2.3	35
7	Oral squamous cell carcinoma in relation to field precancerisation: pathobiology. Cancer Cell International, 2013, 13, 31.	1.8	62
8	The rise of the minority. Nature Reviews Cancer, 2013, 13, 225-225.	12.8	6
9	The genomic landscape of oesophagogastric junctional adenocarcinoma. Journal of Pathology, 2013, 231, 301-310.	2.1	42
10	Genomics of lymphoid malignancies reveal major activation pathways in lymphocytes. Journal of Autoimmunity, 2013, 45, 15-23.	3.0	3
11	A High-Throughput Splicing Assay Identifies New Classes of Inhibitors of Human and Yeast Spliceosomes. Journal of Biomolecular Screening, 2013, 18, 1110-1120.	2.6	31
12	Nanomedicine therapeutic approaches to overcome cancer drug resistance. Advanced Drug Delivery Reviews, 2013, 65, 1866-1879.	6.6	598
13	Next-Generation Sequencing in Chronic Lymphocytic Leukemia. Seminars in Hematology, 2013, 50, 286-295.	1.8	16
14	Pan-cancer patterns of somatic copy number alteration. Nature Genetics, 2013, 45, 1134-1140.	9.4	1,616
15	Computational optimisation of targeted DNA sequencing for cancer detection. Scientific Reports, 2013, 3, 3309.	1.6	20
16	Genetic lesions associated with chronic lymphocytic leukemia transformation to Richter syndrome. Journal of Experimental Medicine, 2013, 210, 2273-2288.	4.2	255
17	Genome sequencing of lymphoid malignancies. Blood, 2013, 122, 3899-3907.	0.6	60
18	The causes and consequences of genetic heterogeneity in cancer evolution. Nature, 2013, 501, 338-345.	13.7	1,969
19	How <scp>I</scp> treat patients with relapsed chronic lymphocytic leukaemia. British Journal of Haematology, 2013, 163, 423-435.	1.2	4

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20	Signaling the end of chronic lymphocytic leukemia: new frontline treatment strategies. Hematology American Society of Hematology Education Program, 2013, 2013, 138-150.	0.9	33
21	THetA: inferring intra-tumor heterogeneity from high-throughput DNA sequencing data. Genome Biology, 2013, 14, R80.	13.9	209
22	Detecting somatic point mutations in cancer genome sequencing data: a comparison of mutation callers. Genome Medicine, 2013, 5, 91.	3.6	146
23	Tumour heterogeneity and cancer cell plasticity. Nature, 2013, 501, 328-337.	13.7	2,043
24	Genetic sequencing studies in Burkitt's lymphoma: what can we learn about tumorigenesis?. Expert Review of Hematology, 2013, 6, 219-221.	1.0	0
25	Targeted resequencing for analysis of clonal composition of recurrent gene mutations in chronic lymphocytic leukaemia. British Journal of Haematology, 2013, 163, 496-500.	1.2	42
26	Chronic lymphocytic leukemia: molecular heterogeneity revealed by high-throughput genomics. Genome Medicine, 2013, 5, 47.	3.6	41
27	Intra-tumor heterogeneity: lessons from microbial evolution and clinical implications. Genome Medicine, 2013, 5, 101.	3.6	38
28	SF3B1 mutations in chronic lymphocytic leukemia. Blood, 2013, 121, 4627-4634.	0.6	103
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39	Punctuated Evolution of Prostate Cancer Genomes. <i>Cell</i> , 2013, 153, 666-677.	13.5	1,107
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41	Cancer chromosomes going to POT1. <i>Nature Genetics</i> , 2013, 45, 473-475.	9.4	50
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48	How Variability in Clinical Phenotypes Should Guide Research into Disease Mechanisms in Asthma. <i>Annals of the American Thoracic Society</i> , 2013, 10, S109-S117.	1.5	34
49	Landscape of somatic mutations and clonal evolution in mantle cell lymphoma. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 18250-18255.	3.3	488
50	Clonal Evolution, Genomic Drivers, and Effects of Therapy in Chronic Lymphocytic Leukemia. <i>Clinical Cancer Research</i> , 2013, 19, 2893-2904.	3.2	56
51	At the Bench: Preclinical rationale for exploiting NK cells and T lymphocytes for the treatment of high-risk leukemias. <i>Journal of Leukocyte Biology</i> , 2013, 94, 1123-1139.	1.5	43
53	Identification of novel point mutations in splicing sites integrating whole-exome and RNA-seq data in myeloproliferative diseases. <i>Molecular Genetics &amp; Genomic Medicine</i> , 2013, 1, 246-259.	0.6	17
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58	The genetic basis of myelodysplasia and its clinical relevance. <i>Blood</i> , 2013, 122, 4021-4034.	0.6	294
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60	Using Network Biology to Bridge Pharmacokinetics and Pharmacodynamics in Oncology. <i>CPT: Pharmacometrics and Systems Pharmacology</i> , 2013, 2, 1-7.	1.3	27
61	Myeloma: a subclonal disease?. <i>Hematologie</i> , 2013, 19, 383-387.	0.0	0
62	Endothelin-1 Promotes Survival and Chemoresistance in Chronic Lymphocytic Leukemia B Cells through ETA Receptor. <i>PLoS ONE</i> , 2014, 9, e98818.	1.1	33
63	Highly Adaptable Triple-Negative Breast Cancer Cells as a Functional Model for Testing Anticancer Agents. <i>PLoS ONE</i> , 2014, 9, e109487.	1.1	17
64	Genetic Abnormalities in Chronic Lymphocytic Leukemia: Where We Are and Where We Go. <i>BioMed Research International</i> , 2014, 2014, 1-13.	0.9	106
66	Accuracy of Next Generation Sequencing Platforms. <i>Journal of Next Generation Sequencing &amp; Applications</i> , 2014, 01, .	0.3	100
67	Novel Treatments for Chronic Lymphocytic Leukemia and Moving Forward. <i>American Society of Clinical Oncology Educational Book / ASCO American Society of Clinical Oncology Meeting</i> , 2014, , e317-e325.	1.8	17
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70	SubcloneSeeker: a computational framework for reconstructing tumor clone structure for cancer variant interpretation and prioritization. <i>Genome Biology</i> , 2014, 15, 443.	3.8	59
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73	CpG Oligonucleotide and Interleukin 2 stimulation enables higher cytogenetic abnormality detection rates than 12-o-tetradecanolyphorbol-13-acetate in Asian patients with B-cell chronic lymphocytic leukemia (B-CLL). <i>International Journal of Hematology</i> , 2014, 100, 545-553.	0.7	6
74	APOBEC3 signature mutations in chronic lymphocytic leukemia. <i>Leukemia</i> , 2014, 28, 1929-1932.	3.3	20
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77	Emergence of New <i>ALK</i> Mutations at Relapse of Neuroblastoma. <i>Journal of Clinical Oncology</i> , 2014, 32, 2727-2734.	0.8	176
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84	<i>EGFR</i> Variant Heterogeneity in Glioblastoma Resolved through Single-Nucleus Sequencing. <i>Cancer Discovery</i> , 2014, 4, 956-971.	7.7	251
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86	Clonal evolution in <i>CLL</i> patients as detected by <i>FISH</i> versus chromosome banding analysis, and its clinical significance. <i>European Journal of Haematology</i> , 2014, 92, 91-101.	1.1	20
87	Integrated Genomic Characterization of Papillary Thyroid Carcinoma. <i>Cell</i> , 2014, 159, 676-690.	13.5	2,318
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94	Deciphering clonality in aneuploid breast tumors using SNP array and sequencing data. <i>Genome Biology</i> , 2014, 15, 470.	3.8	11
95	A Preclinical Assay for Chemosensitivity in Multiple Myeloma. <i>Cancer Research</i> , 2014, 74, 56-67.	0.4	43
96	Synthetic Lethality in ATM-Deficient <i>RAD50</i> -Mutant Tumors Underlies Outlier Response to Cancer Therapy. <i>Cancer Discovery</i> , 2014, 4, 1014-1021.	7.7	114
97	Molecular Subtypes of High-Grade Serous Ovarian Cancer: The Holy Grail?. <i>Journal of the National Cancer Institute</i> , 2014, 106, .	3.0	18
98	The Genomic Landscape of Pediatric Ewing Sarcoma. <i>Cancer Discovery</i> , 2014, 4, 1326-1341.	7.7	415
99	Systematic identification of personal tumor-specific neoantigens in chronic lymphocytic leukemia. <i>Blood</i> , 2014, 124, 453-462.	0.6	286
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110	Tumor Heterogeneity Confounds and Illuminates: A case for Darwinian tumor evolution. <i>Nature Medicine</i> , 2014, 20, 344-346.	15.2	57
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121	Defining Phenotypes in Asthma: A Step Towards Personalized Medicine. <i>Drugs</i> , 2014, 74, 719-728.	4.9	67
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124	Feasibility of targeted next-generation sequencing of the TP53 and ATM genes in chronic lymphocytic leukemia. <i>Leukemia</i> , 2014, 28, 694-696.	3.3	9
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131	Exome sequencing identifies BRAF mutations in papillary craniopharyngiomas. <i>Nature Genetics</i> , 2014, 46, 161-165.	9.4	408
132	Single-Cell RNA-Seq Reveals Dynamic, Random Monoallelic Gene Expression in Mammalian Cells. <i>Science</i> , 2014, 343, 193-196.	6.0	1,164
133	Mutational Analysis Reveals the Origin and Therapy-Driven Evolution of Recurrent Glioma. <i>Science</i> , 2014, 343, 189-193.	6.0	1,147
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143	Age-related mutations associated with clonal hematopoietic expansion and malignancies. <i>Nature Medicine</i> , 2014, 20, 1472-1478.	15.2	1,533
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151	Monoclonal B-cell lymphocytosis is characterized by mutations in CLL putative driver genes and clonal heterogeneity many years before disease progression. <i>Leukemia</i> , 2014, 28, 2395-2398.	3.3	43
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165	Expanding the computational toolbox for mining cancer genomes. <i>Nature Reviews Genetics</i> , 2014, 15, 556-570.	7.7	166

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167	Comparison of somatic mutation calling methods in amplicon and whole exome sequence data. <i>BMC Genomics</i> , 2014, 15, 244.	1.2	136
168	t(14;18) Translocation: A Predictive Blood Biomarker for Follicular Lymphoma. <i>Journal of Clinical Oncology</i> , 2014, 32, 1347-1355.	0.8	115
169	Zebrafish as a model to assess cancer heterogeneity, progression and relapse. <i>DMM Disease Models and Mechanisms</i> , 2014, 7, 755-762.	1.2	42
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171	Clonal Evolution Enhances Leukemia-Propagating Cell Frequency in T Cell Acute Lymphoblastic Leukemia through Akt/mTORC1 Pathway Activation. <i>Cancer Cell</i> , 2014, 25, 366-378.	7.7	98
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173	Heterogeneity in immune responses: from populations to single cells. <i>Trends in Immunology</i> , 2014, 35, 219-229.	2.9	166
174	Evolution of DNA Methylation Is Linked to Genetic Aberrations in Chronic Lymphocytic Leukemia. <i>Cancer Discovery</i> , 2014, 4, 348-361.	7.7	135
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