

Signatures of mutation and selection in the cancer genome

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Citation Report

#	ARTICLE	IF	CITATIONS
1	Discovering Tumor Suppressor Genes Through Genome-Wide Copy Number Analysis. <i>Current Genomics</i> , 2010, 11, 297-310.	0.7	15
2	Molecular aspects of cyclophilins mediating therapeutic actions of their ligands. <i>Cellular and Molecular Life Sciences</i> , 2010, 67, 3467-3488.	2.4	44
3	Passenger mutations as a marker of clonal cell lineages in emerging neoplasia. <i>Seminars in Cancer Biology</i> , 2010, 20, 294-303.	4.3	27
4	Characterization of FRA7B, a human common fragile site mapped at the 7p chromosome terminal region. <i>Cancer Genetics and Cytogenetics</i> , 2010, 202, 47-52.	1.0	31
5	The "omics" of cancer. <i>Cancer Genetics and Cytogenetics</i> , 2010, 203, 37-42.	1.0	3
6	CAM: A web tool for combining array CGH and microarray gene expression data from multiple samples. <i>Computers in Biology and Medicine</i> , 2010, 40, 781-785.	3.9	2
7	Merotelic attachments and non-homologous end joining are the basis of chromosomal instability. <i>Cell Division</i> , 2010, 5, 13.	1.1	24
8	History of leukemia-lymphoma cell lines. <i>Human Cell</i> , 2010, 23, 75-82.	1.2	33
9	Guidelines for the welfare and use of animals in cancer research. <i>British Journal of Cancer</i> , 2010, 102, 1555-1577.	2.9	1,167
10	ANO1 amplification and expression in HNSCC with a high propensity for future distant metastasis and its functions in HNSCC cell lines. <i>British Journal of Cancer</i> , 2010, 103, 715-726.	2.9	124
11	Distant metastasis occurs late during the genetic evolution of pancreatic cancer. <i>Nature</i> , 2010, 467, 1114-1117.	13.7	2,184
12	How accurate are cancer cell lines?. <i>Nature</i> , 2010, 463, 858-858.	13.7	60
13	Advances in understanding cancer genomes through second-generation sequencing. <i>Nature Reviews Genetics</i> , 2010, 11, 685-696.	7.7	1,014
14	Fractal-like Distributions over the Rational Numbers in High-throughput Biological and Clinical Data. <i>Nature Precedings</i> , 2010, , .	0.1	0
16	Analysis of next-generation genomic data in cancer: accomplishments and challenges. <i>Human Molecular Genetics</i> , 2010, 19, R188-R196.	1.4	122
17	The Use of DNA Transposons for Cancer Gene Discovery in Mice. <i>Methods in Enzymology</i> , 2010, 477, 91-106.	0.4	1
18	Histone deacetylase inhibitor induces DNA damage, which normal but not transformed cells can repair. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 14639-14644.	3.3	320
19	<i>PARK2</i> deletions occur frequently in sporadic colorectal cancer and accelerate adenoma development in <i>Apc</i> mutant mice. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 15145-15150.	3.3	202

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20	Mutagenesis as a Genetic Research Strategy. <i>Genetics</i> , 2010, 185, 1135-1139.	1.2	9
21	Gain of MYC underlies recurrent trisomy of the MYC chromosome in acute promyelocytic leukemia. <i>Journal of Experimental Medicine</i> , 2010, 207, 2581-2594.	4.2	58
22	Are aneuploidy and chromosome breakage caused by a CINgle mechanism?. <i>Cell Cycle</i> , 2010, 9, 2275-2280.	1.3	22
23	Epigenetic regulation of the <i>INK4b-ARF-INK4a</i> locus. <i>Epigenetics</i> , 2010, 5, 685-690.	1.3	211
26	Epigenetic Alterations as Cancer Diagnostic, Prognostic, and Predictive Biomarkers. <i>Advances in Genetics</i> , 2010, 71, 125-176.	0.8	85
27	Induction of Human Epithelial Stem/Progenitor Expansion by FOXM1. <i>Cancer Research</i> , 2010, 70, 9515-9526.	0.4	92
28	Germline copy number variation and cancer risk. <i>Current Opinion in Genetics and Development</i> , 2010, 20, 282-289.	1.5	115
29	Synthetic lethal approaches to breast cancer therapy. <i>Nature Reviews Clinical Oncology</i> , 2010, 7, 718-724.	12.5	86
30	Systematic detection of putative tumor suppressor genes through the combined use of exome and transcriptome sequencing. <i>Genome Biology</i> , 2010, 11, R114.	13.9	35
31	Somatic structural rearrangements in genetically engineered mouse mammary tumors. <i>Genome Biology</i> , 2010, 11, R100.	13.9	24
32	A statistical approach for detecting genomic aberrations in heterogeneous tumor samples from single nucleotide polymorphism genotyping data. <i>Genome Biology</i> , 2010, 11, R92.	3.8	125
33	Mutant proteins as cancer-specific biomarkers. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 2444-2449.	3.3	157
34	<i>Drosophila</i> Duplication Hotspots Are Associated with Late-Replicating Regions of the Genome. <i>PLoS Genetics</i> , 2011, 7, e1002340.	1.5	31
35	A continuum model for tumour suppression. <i>Nature</i> , 2011, 476, 163-169.	13.7	432
36	Studies of genomic copy number changes in human cancers reveal signatures of DNA replication stress. <i>Molecular Oncology</i> , 2011, 5, 308-314.	2.1	69
37	Large-scale analysis of chromosomal aberrations in cancer karyotypes reveals two distinct paths to aneuploidy. <i>Genome Biology</i> , 2011, 12, R61.	13.9	49
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42	Mutant onco-proteins as drug targets: successes, failures, and future prospects. <i>Current Opinion in Genetics and Development</i> , 2011, 21, 29-33.	1.5	10
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44	Failure of Origin Activation in Response to Fork Stalling Leads to Chromosomal Instability at Fragile Sites. <i>Molecular Cell</i> , 2011, 43, 122-131.	4.5	157
45	Collisions between Replication and Transcription Complexes Cause Common Fragile Site Instability at the Longest Human Genes. <i>Molecular Cell</i> , 2011, 44, 966-977.	4.5	470
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47	Somatic <i>SF3B1</i> Mutation in Myelodysplasia with Ring Sideroblasts. <i>New England Journal of Medicine</i> , 2011, 365, 1384-1395.	13.9	1,094
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55	A model for random genetic damage directing selection of diploid or aneuploid tumours. <i>Cell Proliferation</i> , 2011, 44, 212-223.	2.4	3
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59	The genomic complexity of primary human prostate cancer. <i>Nature</i> , 2011, 470, 214-220.	13.7	1,107

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61	Charting a course for genomic medicine from base pairs to bedside. <i>Nature</i> , 2011, 470, 204-213.	13.7	823
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73	Genome profiling of pancreatic adenocarcinoma. <i>Genes Chromosomes and Cancer</i> , 2011, 50, 456-465.	1.5	107
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82	Losing balance: Hardy-Weinberg disequilibrium as a marker for recurrent loss-of-heterozygosity in cancer. <i>Human Molecular Genetics</i> , 2011, 20, 4831-4839.	1.4	6
83	Prognostic Significance of <i>p14ARF</i> , <i>p15INK4b</i> , and <i>p16INK4a</i> Inactivation in Malignant Peripheral Nerve Sheath Tumors. <i>Clinical Cancer Research</i> , 2011, 17, 3771-3782.	3.2	53
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102	The Role of Fragile Sites in Sporadic Papillary Thyroid Carcinoma. <i>Journal of Thyroid Research</i> , 2012, 2012, 1-12.	0.5	8
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115	Identification of novel CHD1-associated collaborative alterations of genomic structure and functional assessment of CHD1 in prostate cancer. <i>Oncogene</i> , 2012, 31, 3939-3948.	2.6	87
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160	Common chromosomal fragile site <i>FRA16D</i> tumor suppressor <i>WWOX</i> gene expression and metabolic reprogramming in cells. Genes Chromosomes and Cancer, 2013, 52, 823-831.	1.5	27
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