Alexander Dobrovic

List of Publications by Year
in descending order

211	12,142	27035	35168
papers	citations	58 h-index	102 g-index

219	219	219	20784
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Low Levels of Hepatocyteâ€Specific Methylation in Cellâ€Free DNA Are a Strong Negative Predictor for Acute T Cellâ€"Mediated Rejection Requiring Treatment Following Liver Transplantation. Liver Transplantation, 2022, 28, 1024-1038.	1.3	5
2	Evaluating DNA recovery efficiency following bisulphite modification from plasma samples submitted for cell-free DNA methylation analysis. Epigenetics, 2022, 17, 1956-1960.	1.3	2
3	Cerebrospinal fluid liquid biopsy for detecting somatic mosaicism in brain. Brain Communications, 2021, 3, fcaa235.	1.5	42
4	Comment on: â€œHypoxia differently modulates the release of mitochondrial and nuclear DNAâ€. British Journal of Cancer, 2021, 124, 2035-2036.	2.9	3
5	Ropporin-1 and 1B Are Widely Expressed in Human Melanoma and Evoke Strong Humoral Immune Responses. Cancers, 2021, 13, 1805.	1.7	2
6	Molecular and clinical determinants of response and resistance to rucaparib for recurrent ovarian cancer treatment in ARIEL2 (Parts 1 and 2). Nature Communications, 2021, 12, 2487.	5.8	116
7	A Synthetic DNA Construct to Evaluate the Recovery Efficiency of Cell-Free DNA Extraction and Bisulfite Modification. Clinical Chemistry, 2021, 67, 1201-1209.	1.5	6
8	Characterization of a RAD51C-silenced high-grade serous ovarian cancer model during development of PARP inhibitor resistance. NAR Cancer, 2021, 3, zcab028.	1.6	20
9	Acquired RAD51C Promoter Methylation Loss Causes PARP Inhibitor Resistance in High-Grade Serous Ovarian Carcinoma. Cancer Research, 2021, 81, 4709-4722.	0.4	42
10	Elevated levels of circulating mitochondrial DNA predict early allograft dysfunction in patients following liver transplantation. Journal of Gastroenterology and Hepatology (Australia), 2021, 36, 3500-3507.	1.4	8
11	Elevated Plasma Levels of Cellâ€Free DNA During Liver Transplantation Are Associated With Activation of Coagulation. Liver Transplantation, 2020, 26, 602-603.	1.3	1
12	High Speed Centrifugation Before Frozen Storage of Plasma Is Critical for Quantitative Analysis of Mitochondrial-Derived Cell-Free DNA. Clinical Chemistry, 2020, 66, 1111-1114.	1.5	9
13	NTRK and ALK rearrangements in malignant pleural mesothelioma, pulmonary neuroendocrine tumours and non-small cell lung cancer. Lung Cancer, 2020, 146, 154-159.	0.9	20
14	Donor-specific cell-free DNA as a biomarker in liver transplantation: A review. World Journal of Transplantation, 2020, 10, 307-319.	0.6	18
15	TERTgene: its function and dysregulation in cancer. Journal of Clinical Pathology, 2019, 72, 281-284.	1.0	63
16	Standard dose osimertinib for erlotinib refractory T790M-negative EGFR-mutant non-small cell lung cancer with leptomeningeal disease. Journal of Thoracic Disease, 2019, 11, 1756-1764.	0.6	8
17	A new normalization for Nanostring nCounter gene expression data. Nucleic Acids Research, 2019, 47, 6073-6083.	6.5	73
18	Molecular Genomic Profiling of MelanocyticÂNevi. Journal of Investigative Dermatology, 2019, 139, 1762-1768.	0.3	55

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19	BCL-XL and MCL-1 are the key BCL-2 family proteins in melanoma cell survival. Cell Death and Disease, 2019, 10, 342.	2.7	125
20	A reference collection of patient-derived cell line and xenograft models of proneural, classical and mesenchymal glioblastoma. Scientific Reports, 2019, 9, 4902.	1.6	127
21	Genomic Analysis of Circulating Tumor DNAÂUsing a Melanoma-Specific UltraSEEK Oncogene Panel. Journal of Molecular Diagnostics, 2019, 21, 418-426.	1.2	18
22	The Measurement of Donor-Specific Cell-Free DNA Identifies Recipients With Biopsy-Proven Acute Rejection Requiring Treatment After Liver Transplantation. Transplantation Direct, 2019, 5, e462.	0.8	29
23	Clinical Utility of Real-Time Targeted Molecular Profiling in the Clinical Management of Ovarian Cancer: The ALLOCATE Study. JCO Precision Oncology, 2019, 3, 1-18.	1.5	0
24	In Reply to Leone. Journal of Thoracic Oncology, 2018, 13, e22-e23.	0.5	0
25	Fresh Frozen Plasma Transfusion Can Confound the Analysis of Circulating Cell-Free DNA. Clinical Chemistry, 2018, 64, 749-751.	1.5	5
26	Optimizing Amplification of the GC-Rich TERT Promoter Region Using 7-Deaza-dGTP for Droplet Digital PCR Quantification of TERT Promoter Mutations. Clinical Chemistry, 2018, 64, 745-747.	1.5	18
27	Homologous Recombination DNA Repair Pathway Disruption and Retinoblastoma Protein Loss Are Associated with Exceptional Survival in High-Grade Serous Ovarian Cancer. Clinical Cancer Research, 2018, 24, 569-580.	3.2	79
28	TERT structural rearrangements in metastatic pheochromocytomas. Endocrine-Related Cancer, 2018, 25, 1-9.	1.6	45
29	BRAF Mutations in Low-Grade Serous Ovarian Cancer and Response to BRAF Inhibition. JCO Precision Oncology, 2018, 2, 1-14.	1.5	19
30	Methylation of all BRCA1 copies predicts response to the PARP inhibitor rucaparib in ovarian carcinoma. Nature Communications, 2018, 9, 3970.	5.8	192
31	Mismatch Repair Protein Defects and Microsatellite Instability in Malignant Pleural Mesothelioma. Journal of Thoracic Oncology, 2018, 13, 1588-1594.	0.5	35
32	Fcâ€gamma receptor polymorphisms, cetuximab therapy, and overall survival in the CCTG CO.20 trial of metastatic colorectal cancer. Cancer Medicine, 2018, 7, 5478-5487.	1.3	19
33	DNA Methylation Profiling of Breast Cancer Cell Lines along the Epithelial Mesenchymal Spectrumâ€"Implications for the Choice of Circulating Tumour DNA Methylation Markers. International Journal of Molecular Sciences, 2018, 19, 2553.	1.8	15
34	White Blood Cell BRCA1 Promoter Methylation Status and Ovarian Cancer Risk: A Perspective. Annals of Internal Medicine, 2018, 168, 365.	2.0	3
35	Somatic GNAQ mutation in the forme fruste of Sturge-Weber syndrome. Neurology: Genetics, 2018, 4, e236.	0.9	29
36	Adapting an Established Clinical Chemistry Quality Control Measure for Droplet Generation Performance in Digital PCR. Clinical Chemistry, 2018, 64, 1255-1257.	1.5	2

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37	Probe-Free Digital PCR Quantitative Methodology to Measure Donor-Specific Cell-Free DNA after Solid-Organ Transplantation. Clinical Chemistry, 2017, 63, 742-750.	1.5	23
38	Germline polymorphisms as biomarkers of tumor response in colorectal cancer patients treated with anti-EGFR monoclonal antibodies: a systematic review and meta-analysis. Pharmacogenomics Journal, 2017, 17, 535-542.	0.9	3
39	Breast ductal carcinoma in situ carry mutational driver events representative of invasive breast cancer. Modern Pathology, 2017, 30, 952-963.	2.9	50
40	Evaluation of Different Oligonucleotide Base Substitutions at CpG Binding sites in Multiplex Bisulfite-PCR sequencing. Scientific Reports, 2017, 7, 45096.	1.6	0
41	DNA Breathing Enables Closed-Tube Mutant Allele Enrichment for Circulating Tumor DNA Analysis. Clinical Chemistry, 2017, 63, e1-e3.	1.5	2
42	Combination Osimertinib and Gefitinib in C797S and T790M EGFR-Mutated Nonâ€“Small Cell Lung Cancer. Journal of Thoracic Oncology, 2017, 12, 1728-1732.	0.5	143
43	EGFR and KRAS mutations do not enrich for the activation of IL-6, JAK1 or phosphorylated STAT3 in resected lung adenocarcinoma. Medical Oncology, 2017, 34, 175.	1.2	5
44	Reducing Artifactual EGFR T790M Mutations in DNA from Formalin-Fixed Paraffin-Embedded Tissue by Use of Thymine-DNA Glycosylase. Clinical Chemistry, 2017, 63, 1506-1514.	1.5	16
45	GRIDSS: sensitive and specific genomic rearrangement detection using positional de Bruijn graph assembly. Genome Research, 2017, 27, 2050-2060.	2.4	255
46	Assessing alternative base substitutions at primer CpG sites to optimise unbiased PCR amplification of methylated sequences. Clinical Epigenetics, 2017, 9, 31.	1.8	10
47	Epigenetic Basis of Human Cancer. , 2017, , 83-102.		1
48	Sensitive quantitative detection of somatic mosaic mutation in â€œdouble cortexâ€•syndrome. Epileptic Disorders, 2017, 19, 450-455.	0.7	13
49	BRCA2 carriers with male breast cancer show elevated tumour methylation. BMC Cancer, 2017, 17, 641.	1.1	10
50	LRH-1 expression patterns in breast cancer tissues are associated with tumour aggressiveness. Oncotarget, 2017, 8, 83626-83636.	0.8	13
51	Comparison of 3 Methodologies for Genotyping of Small Deletion and Insertion Polymorphisms. Clinical Chemistry, 2016, 62, 1012-1019.	1.5	6
52	Genome-scale methylation assessment did not identify prognostic biomarkers in oral tongue carcinomas. Clinical Epigenetics, 2016, 8, 74.	1.8	8
53	Analysis of DNA Methylation in Clinical Samples: Methods and Applications. , 2016, , 261-277.		1
54	Temporal changes of EGFR mutations and T790M levels in tumour and plasma DNA following AZD9291 treatment. Lung Cancer, 2016, 98, 29-32.	0.9	24

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55	Fc-Î³ Receptor Polymorphisms, Cetuximab Therapy, and Survival in the NCIC CTG CO.17 Trial of Colorectal Cancer. Clinical Cancer Research, 2016, 22, 2435-2444.	3.2	33
56	Digital PCR of Genomic Rearrangements for Monitoring Circulating Tumour DNA. Advances in Experimental Medicine and Biology, 2016, 924, 139-146.	0.8	6
57	Associations between the IASLC/ATS/ERS lung adenocarcinoma classification and EGFR and KRAS mutations. Pathology, 2016, 48, 17-24.	0.3	10
58	MethPat: a tool for the analysis and visualisation of complex methylation patterns obtained by massively parallel sequencing. BMC Bioinformatics, 2016, 17, 98.	1.2	22
59	Clustered somatic mutations are frequent in transcription factor binding motifs within proximal promoter regions in melanoma and other cutaneous malignancies. Oncotarget, 2016, 7, 66569-66585.	0.8	21
60	Appraisal of the technologies and review of the genomic landscape of ductal carcinoma in situ of the breast. Breast Cancer Research, 2015, 17, 80.	2.2	5
61	An optimised direct lysis method for gene expression studies on low cell numbers. Scientific Reports, 2015, 5, 12859.	1.6	25
62	Assessment of DNA methylation profiling and copy number variation as indications of clonal relationship in ipsilateral and contralateral breast cancers to distinguish recurrent breast cancer from a second primary tumour. BMC Cancer, 2015, 15, 669.	1.1	14
63	Exemplary multiplex bisulfite amplicon data used to demonstrate the utility of Methpat. GigaScience, 2015, 4, 55.	3.3	3
64	The role ofBRAFmutations in primary melanoma growth rate and survival. British Journal of Dermatology, 2015, 173, 76-82.	1.4	35
65	â€œCancer 2015â€• A Prospective, Population-Based Cancer Cohortâ€”Phase 1: Feasibility of Genomics-Guided Precision Medicine in the Clinic. Journal of Personalized Medicine, 2015, 5, 354-369.	1.1	8
66	Methylome sequencing in triple-negative breast cancer reveals distinct methylation clusters with prognostic value. Nature Communications, 2015, 6, 5899.	5.8	162
67	Sequence Artifacts in DNA from Formalin-Fixed Tissues: Causes and Strategies for Minimization. Clinical Chemistry, 2015, 61, 64-71.	1.5	412
68	Assessing the clinical value of targeted massively parallel sequencing in a longitudinal, prospective population-based study of cancer patients. British Journal of Cancer, 2015, 112, 1411-1420.	2.9	51
69	Heterozygosity for the common perforin mutation, p.A91V, impairs the cytotoxicity of primary natural killer cells from healthy individuals. Immunology and Cell Biology, 2015, 93, 575-580.	1.0	42
70	Monitoring response to therapy in melanoma by quantifying circulating tumour DNA with droplet digital PCR for BRAF and NRAS mutations. Scientific Reports, 2015, 5, 11198.	1.6	150
71	High-Resolution Assessment of Copy Number Variation. Clinical Chemistry, 2015, 61, 684-685.	1.5	2
72	Copy number analysis of ductal carcinoma in situ with and without recurrence. Modern Pathology, 2015, 28, 1174-1184.	2.9	40

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73	Multicenter randomized, open-label phase II trial of sequential erlotinib and gemcitabine compared with gemcitabine monotherapy as first-line therapy in elderly or ECOG PS two patients with advanced NSCLC. Asia-Pacific Journal of Clinical Oncology, 2015, 11, 4-14.	0.7	15
74	DNA Ligase-Based Strategy for Quantifying Heterogeneous DNA Methylation without Sequencing. Clinical Chemistry, 2015, 61, 163-171.	1.5	24
75	Whole exome sequencing identifies a recurrentRQCD1P131L mutation in cutaneous melanoma. Oncotarget, 2015, 6, 1115-1127.	0.8	40
76	Bioinformatics Pipelines for Targeted Resequencing and Whole-Exome Sequencing of Human and Mouse Genomes: A Virtual Appliance Approach for Instant Deployment. PLoS ONE, 2014, 9, e95217.	1.1	17
77	Role of p53 in the progression of gastric cancer. Oncotarget, 2014, 5, 12016-12026.	0.8	64
78	Mapping of actionable mutations to histological subtype domains in lung adenocarcinoma: implications for precision medicine. Oncotarget, 2014, 5, 2107-2115.	0.8	18
79	Genomic Classification of Serous Ovarian Cancer with Adjacent Borderline Differentiates RAS Pathway and TP53-Mutant Tumors and Identifies NRAS as an Oncogenic Driver. Clinical Cancer Research, 2014, 20, 6618-6630.	3.2	96
80	Loss of <scp>CDKN</scp>2A expression is a frequent event in primary invasive melanoma and correlates with sensitivity to the <scp>CDK</scp>4/6 inhibitor <scp>PD</scp>0332991 in melanoma cell lines. Pigment Cell and Melanoma Research, 2014, 27, 590-600.	1.5	165
81	Mutational profiling of familial male breast cancers reveals similarities with luminal A female breast cancer with rare TP53 mutations. British Journal of Cancer, 2014, 111, 2351-2360.	2.9	22
82	Quantitative methodology is critical for assessing DNA methylation and impacts on correlation with patient outcome. Clinical Epigenetics, 2014, 6, 22.	1.8	19
83	Methylation profiling of ductal carcinoma in situand its relationship to histopathological features. Breast Cancer Research, 2014, 16, 423.	2.2	18
84	EGFR gene copy number alterations are not a useful screening tool for predicting EGFR mutation status in lung adenocarcinoma. Pathology, 2014, 46, 32-36.	0.3	0
85	The Clinical Relevance of Pathologic Subtypes in Metastatic Lung Adenocarcinoma. Journal of Thoracic Oncology, 2014, 9, 654-663.	0.5	20
86	Prevalence and natural history of ALK positive non-small-cell lung cancer and the clinical impact of targeted therapy with ALK inhibitors. Clinical Epidemiology, 2014, 6, 423.	1.5	139
87	Clinical and pathological associations of the activating <scp>RAC</scp>1 P29S mutation in primary cutaneous melanoma. Pigment Cell and Melanoma Research, 2014, 27, 1117-1125.	1.5	51
88	Characterization of a Novel Tumorigenic Esophageal Adenocarcinoma Cell Line: OANC1. Digestive Diseases and Sciences, 2014, 59, 78-88.	1.1	10
89	Nuclear HIF1A expression is strongly prognostic in sporadic but not familial male breast cancer. Modern Pathology, 2014, 27, 1223-1230.	2.9	23
90	Differential mechanisms of CDKN2A (p16) alteration in oral tongue squamous cell carcinomas and correlation with patient outcome. International Journal of Cancer, 2014, 135, 887-895.	2.3	53

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91	Sequence artefacts in a prospective series of formalin-fixed tumours tested for mutations in hotspot regions by massively parallel sequencing. BMC Medical Genomics, 2014, 7, 23.	0.7	200
92	A critical re-assessment of DNA repair gene promoter methylation in non-small cell lung carcinoma. Scientific Reports, 2014, 4, 4186.	1.6	37
93	No evidence for PALB2 methylation in high-grade serous ovarian cancer. Journal of Ovarian Research, 2013, 6, 26.	1.3	8
94	Quantitative threefold allele-specific PCR (QuanTAS-PCR) for highly sensitive JAK2V617F mutant allele detection. BMC Cancer, 2013, 13, 206.	1.1	14
95	The fusion partner specifies the oncogenic potential of NUP98 fusion proteins. Leukemia Research, 2013, 37, 1668-1673.	0.4	12
96	BRAF Inhibitorâ€"Driven Tumor Proliferation in a KRAS-Mutated Colon Carcinoma Is Not Overcome by MEK1/2 Inhibition. Journal of Clinical Oncology, 2013, 31, e448-e451.	0.8	51
97	Intratumoral genetic heterogeneity in metastatic melanoma is accompanied by variation in malignant behaviors. BMC Medical Genomics, 2013, 6, 40.	0.7	28
98	PIK3CA mutations are frequently observed in BRCAX but not BRCA2-associated male breast cancer. Breast Cancer Research, 2013, 15, R69.	2.2	22
99	DNA methylation in ductal carcinoma in situof the breast. Breast Cancer Research, 2013, 15, 206.	2.2	19
100	A critical review of the role of Fc gamma receptor polymorphisms in the response to monoclonal antibodies in cancer. Journal of Hematology and Oncology, 2013, 6, 1.	6.9	301
101	Reducing Sequence Artifacts in Amplicon-Based Massively Parallel Sequencing of Formalin-Fixed Paraffin-Embedded DNA by Enzymatic Depletion of Uracil-Containing Templates. Clinical Chemistry, 2013, 59, 1376-1383.	1.5	94
102	Nonequivalent Gene Expression and Copy Number Alterations in High-Grade Serous Ovarian Cancers with BRCA1 and BRCA2 Mutations. Clinical Cancer Research, 2013, 19, 3474-3484.	3.2	76
103	BRAF/NRAS Wild-Type Melanomas Have a High Mutation Load Correlating with Histologic and Molecular Signatures of UV Damage. Clinical Cancer Research, 2013, 19, 4589-4598.	3.2	115
104	Docetaxel plus cetuximab as second-line treatment for docetaxel-refractory oesophagogastric cancer: the AGITG ATTAX2 trial. British Journal of Cancer, 2013, 108, 771-774.	2.9	17
105	Targeted-capture massively-parallel sequencing enables robust detection of clinically informative mutations from formalin-fixed tumours. Scientific Reports, 2013, 3, 3494.	1.6	44
106	A multisite blinded study for the detection of BRAF mutations in formalin-fixed, paraffin-embedded malignant melanoma. Scientific Reports, 2013, 3, 1659.	1.6	36
107	High Frequency of Germline TP53 Mutations in a Prospective Adult-Onset Sarcoma Cohort. PLoS ONE, 2013, 8, e69026.	1.1	51
108	Abstract 4693: Characterization of the differential mechanisms ofCDKN2Ainactivation in oral tongue squamous cell carcinomas and correlation with patient outcome.. , 2013, , .		0

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109	Rapid detection of FLT3 exon 20 tyrosine kinase domain mutations in patients with acute myeloid leukemia by high-resolution melting analysis. Leukemia and Lymphoma, 2012, 53, 1225-1229.	0.6	3
110	Mapping the regulatory sequences controlling 93 breast cancer-associated miRNA genes leads to the identification of two functional promoters of the Hsa-mir-200b cluster, methylation of which is associated with metastasis or hormone receptor status in advanced breast cancer. Oncogene, 2012, 31, 4182-4195.	2.6	75
111	Detection of BRAF mutations in patients with hairy cell leukemia and related lymphoproliferative disorders. Haematologica, 2012, 97, 780-783.	1.7	63
112	Using tumour pathology to identify people at high genetic risk of breast and colorectal cancers. Pathology, 2012, 44, 89-98.	0.3	7
113	No evidence for DNA methylation of theATMpromoter CpG island in chronic lymphocytic leukemia. Leukemia and Lymphoma, 2012, 53, 1420-1422.	0.6	4
114	Dual Targeting of the Epidermal Growth Factor Receptor Using the Combination of Cetuximab and Erlotinib: Preclinical Evaluation and Results of the Phase II DUX Study in Chemotherapy-Refractory, Advanced Colorectal Cancer. Journal of Clinical Oncology, 2012, 30, 1505-1512.	0.8	95
115	DNA methylation biomarkers in cancer: progress towards clinical implementation. Expert Review of Molecular Diagnostics, 2012, 12, 473-487.	1.5	146
116	BRCA Mutation Frequency and Patterns of Treatment Response in BRCA Mutationâ€“Positive Women With Ovarian Cancer: A Report From the Australian Ovarian Cancer Study Group. Journal of Clinical Oncology, 2012, 30, 2654-2663.	0.8	1,018
117	Methylation profiling of normal individuals reveals mosaic promoter methylation of cancer-associated genes. Oncotarget, 2012, 3, 450-461.	0.8	33
118	Dramatic reduction of sequence artefacts from DNA isolated from formalin-fixed cancer biopsies by treatment with uracil-DNA glycosylase. Oncotarget, 2012, 3, 546-558.	0.8	147
119	Sensitive Quantification of Somatic Mutations Using Molecular Inversion Probes. Analytical Chemistry, 2011, 83, 8215-8221.	3.2	6
120	1.29 Development of Highly Accurate RT-qPCR Assays for Profiling the Expression of DNA Repair and Apoptosis Genes in CLL. Clinical Lymphoma, Myeloma and Leukemia, 2011, 11, S158-S159.	0.2	0
121	1.31 Investigating Methylation of the Pro-Apoptotic CLL Tumour Suppressor Gene, Death Associated Protein Kinase 1 (DAPK1). Clinical Lymphoma, Myeloma and Leukemia, 2011, 11, S159.	0.2	0
122	Analysing DNA Methylation Using Bisulphite Pyrosequencing. Methods in Molecular Biology, 2011, 791, 33-53.	0.4	61
123	Closed-Tube PCR Methods for Locus-Specific DNA Methylation Analysis. Methods in Molecular Biology, 2011, 791, 55-71.	0.4	12
124	Assessing Gene-Specific Methylation Using HRM-Based Analysis. Methods in Molecular Biology, 2011, 687, 207-217.	0.4	9
125	Clinical outcome and pathological features associated with NRAS mutation in cutaneous melanoma. Pigment Cell and Melanoma Research, 2011, 24, 666-672.	1.5	211
126	The expression of the ubiquitin ligase SIAH2 (seven in absentia homolog 2) is mediated through gene copy number in breast cancer and is associated with a basal-like phenotype and p53 expression. Breast Cancer Research, 2011, 13, R19.	2.2	45

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127	Integrated mutation, copy number and expression profiling in resectable non-small cell lung cancer. BMC Cancer, 2011, 11, 93.	1.1	16
128	Aberrant DNA methylation but not mutation of CITED4 is associated with alteration of HIF-regulated genes in breast cancer. Breast Cancer Research and Treatment, 2011, 130, 319-329.	1.1	16
129	A high-throughput protocol for mutation scanning of the BRCA1 and BRCA2genes. BMC Cancer, 2011, 11, 265.	1.1	27
130	Constitutional Methylation of the BRCA1 Promoter Is Specifically Associated with BRCA1 Mutation-Associated Pathology in Early-Onset Breast Cancer. Cancer Prevention Research, 2011, 4, 23-33.	0.7	147
131	Assessing combined methylationâ€“sensitive high resolution melting and pyrosequencing for the analysis of heterogeneous DNA methylation. Epigenetics, 2011, 6, 500-507.	1.3	61
132	Investigating the Potential Role of Genetic and Epigenetic Variation of DNA Methyltransferase Genes in Hyperplastic Polyposis Syndrome. PLoS ONE, 2011, 6, e16831.	1.1	11
133	DNA methylation profiling of phyllodes and fibroadenoma tumours of the breast. Breast Cancer Research and Treatment, 2010, 124, 555-565.	1.1	33
134	No evidence for DNA methylation of von Hippel-Lindau ubiquitin ligase complex genes in breast cancer. Breast Cancer Research and Treatment, 2010, 124, 853-856.	1.1	2
135	A multiplex endpoint RT-PCR assay for quality assessment of RNA extracted from formalin-fixed paraffin-embedded tissues. BMC Biotechnology, 2010, 10, 89.	1.7	17
136	DNA methylation analysis of the HIFâ€1Î± prolyl hydroxylase domain genes PHD1, PHD2, PHD3 and the factor inhibiting HIF gene FIH in invasive breast carcinomas. Histopathology, 2010, 57, 451-460.	1.6	15
137	Clinical responses observed with imatinib or sorafenib in melanoma patients expressing mutations in KIT. British Journal of Cancer, 2010, 102, 1219-1223.	2.9	120
138	The implications of heterogeneous DNA methylation for the accurate quantification of methylation. Epigenomics, 2010, 2, 561-573.	1.0	126
139	Rarity ofAKT1andAKT3E17K mutations in squamous cell carcinoma of lung. Cell Cycle, 2010, 9, 4411-4412.	1.3	23
140	Mutations in KIT occur at low frequency in melanomas arising from anatomical sites associated with chronic and intermittent sun exposure. Pigment Cell and Melanoma Research, 2010, 23, 210-215.	1.5	101
141	HER3 and downstream pathways are involved in colonization of brain metastases from breast cancer. Breast Cancer Research, 2010, 12, R46.	2.2	122
142	TP53 Mutations In Relapsed/Refractory Multiple Myeloma (MM) Treated with Thalidomide (Thal) or Thalidomide Combination Therapy. Blood, 2010, 116, 4046-4046.	0.6	0
143	DNA Methylation of the ABO Promoter Underlies Loss of ABO Allelic Expression in a Significant Proportion of Leukemic Patients. PLoS ONE, 2009, 4, e4788.	1.1	59
144	Validation of a primer optimisation matrix to improve the performance of reverse transcription â€“ quantitative real-time PCR assays. BMC Research Notes, 2009, 2, 112.	0.6	31

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145	No evidence for promoter region methylation of the succinate dehydrogenase and fumarate hydratase tumour suppressor genes in breast cancer. BMC Research Notes, 2009, 2, 194.	0.6	13
146	Selective inhibition of proliferation in colorectal carcinoma cell lines expressing mutant APC or activated Bâ€Raf. International Journal of Cancer, 2009, 125, 297-307.	2.3	36
147	DNA methylation, epimutations and cancer predisposition. International Journal of Biochemistry and Cell Biology, 2009, 41, 34-39.	1.2	63
148	Limited copy number - high resolution melting (LCN-HRM) enables the detection and identification by sequencing of low level mutations in cancer biopsies. Molecular Cancer, 2009, 8, 82.	7.9	65
149	Identification of circulating tumour cells in early stage breast cancer patients using multi marker immunobead RT-PCR. Journal of Hematology and Oncology, 2009, 2, 24.	6.9	28
150	Melting Curve Assays for DNA Methylation Analysis. Methods in Molecular Biology, 2009, 507, 229-240.	0.4	18
151	A Multicenter Blinded Study to Evaluate KRAS Mutation Testing Methodologies in the Clinical Setting. Journal of Molecular Diagnostics, 2009, 11, 543-552.	1.2	107
152	Detection of MGMT Promoter Methylation in Normal Individuals Is Strongly Associated with the T Allele of the rs16906252 MGMT Promoter Single Nucleotide Polymorphism. Cancer Prevention Research, 2009, 2, 862-867.	0.7	62
153	Wnt inhibitory factor 1 is epigenetically silenced in human osteosarcoma, and targeted disruption accelerates osteosarcomagenesis in mice. Journal of Clinical Investigation, 2009, 119, 837-851.	3.9	244
154	G1738R is a BRCA1 founder mutation in Greek breast/ovarian cancer patients: evaluation of its pathogenicity and inferences on its genealogical history. Breast Cancer Research and Treatment, 2008, 110, 377-385.	1.1	37
155	Negative selection of chronic lymphocytic leukaemia cells using a bifunctional rosette-based antibody cocktail. BMC Biotechnology, 2008, 8, 6.	1.7	7
156	Rapid analysis of heterogeneously methylated DNA using digital methylation-sensitive high resolution melting: application to the CDKN2B (p15) gene. Epigenetics and Chromatin, 2008, 1, 7.	1.8	65
157	Rapid detection of methylation change at H19 in human imprinting disorders using methylation-sensitive high-resolution melting. Human Mutation, 2008, 29, 1255-1260.	1.1	51
158	In vitro sensitivity testing of minimally passaged and uncultured gliomas with TRAIL and/or chemotherapy drugs. British Journal of Cancer, 2008, 99, 294-304.	2.9	17
159	Methylation-sensitive high-resolution melting. Nature Protocols, 2008, 3, 1903-1908.	5.5	262
160	High resolution melting analysis for rapid and sensitive EGFR and KRAS mutation detection in formalin fixed paraffin embedded biopsies. BMC Cancer, 2008, 8, 142.	1.1	184
161	Rapid detection of carriers with BRCA1 and BRCA2mutations using high resolution melting analysis. BMC Cancer, 2008, 8, 59.	1.1	69
162	Detection of the transforming AKT1 mutation E17K in non-small cell lung cancer by high resolution melting. BMC Research Notes, 2008, 1, 14.	0.6	42

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163	A new approach to primer design for the control of PCR bias in methylation studies. BMC Research Notes, 2008, 1, 54.	0.6	117
164	Detection of NPM1 exon 12 mutations and FLT3 â€“ internal tandem duplications by high resolution melting analysis in normal karyotype acute myeloid leukemia. Journal of Hematology and Oncology, 2008, 1, 10.	6.9	39
165	BRCA1 promoter methylation in peripheral blood DNA of mutation negative familial breast cancer patients with a BRCA1tumour phenotype. Breast Cancer Research, 2008, 10, R12.	2.2	123
166	Direct Genotyping of Single Nucleotide Polymorphisms in Methyl Metabolism Genes Using Probe-Free High-Resolution Melting Analysis. Cancer Epidemiology Biomarkers and Prevention, 2008, 17, 1240-1247.	1.1	34
167	Sensitive Melting Analysis after Real Time- Methylation Specific PCR (SMART-MSP): high-throughput and probe-free quantitative DNA methylation detection. Nucleic Acids Research, 2008, 36, e42-e42.	6.5	159
168	Complete molecular response of e6a2 BCR-ABLâ€“positive acute myeloid leukemia to imatinib then dasatinib. Blood, 2008, 111, 2896-2898.	0.6	25
169	A Simple, Rapid, and Sensitive Method for the Detection of theJAK2V617F Mutation. American Journal of Clinical Pathology, 2007, 127, 977-981.	0.4	25
170	Methylation-sensitive high resolution melting (MS-HRM): a new approach for sensitive and high-throughput assessment of methylation. Nucleic Acids Research, 2007, 35, e41-e41.	6.5	460
171	Distinct Clinical and Pathological Features Are Associated with the BRAFT1799A(V600E) Mutation in Primary Melanoma. Journal of Investigative Dermatology, 2007, 127, 900-905.	0.3	169
172	High resolution melting for mutation scanning of TP53exons 5â€“8. BMC Cancer, 2007, 7, 168.	1.1	119
173	Incorporation of somatic BRAF mutation testing into an algorithm for the investigation of hereditary non-polyposis colorectal cancer. Familial Cancer, 2007, 6, 301-310.	0.9	153
174	P3-002: High resolution melting analysis for rapid and sensitive EGFR mutation detection. Journal of Thoracic Oncology, 2007, 2, S500.	0.5	0
175	DNA repair gene inactivation in non-Hodgkin's lymphoma. Leukemia and Lymphoma, 2006, 47, 1728-1729.	0.6	1
176	Pathological response of gastrointestinal stromal tumour to imatinib treatment correlates with tumourKITmutational status in individual tumour clones. Histopathology, 2006, 49, 99-100.	1.6	6
177	KIT immunohistochemistry and mutation status in gastrointestinal stromal tumours (GISTs) evaluated for treatment with imatinib. Histopathology, 2006, 49, 52-65.	1.6	12
178	High resolution melting analysis for the rapid and sensitive detection of mutations in clinical samples: KRAS codon 12 and 13 mutations in non-small cell lung cancer. BMC Cancer, 2006, 6, 295.	1.1	254
179	Empirical array quality weights in the analysis of microarray data. BMC Bioinformatics, 2006, 7, 261.	1.2	259
180	Mutations in theMYB intron I regulatory sequence increase transcription in colon cancers. Genes Chromosomes and Cancer, 2006, 45, 1143-1154.	1.5	73

#	Article	IF	Citations
181	Sensitive Detection of KIT D816V in Patients with Mastocytosis. Clinical Chemistry, 2006, 52, 2250-2257.	1.5	32
182	Polyclonal Resistance in Gastrointestinal Stromal Tumor Treated with Sequential Kinase Inhibitors: Fig. 1.. Clinical Cancer Research, 2006, 12, 6205-6206.	3.2	17
183	A novel duplication polymorphism in the FANCApromoter and its association with breast and ovarian cancer. BMC Cancer, 2005, 5, 43.	1.1	17
184	Novel Methods for the Sensitive Detection of c-KIT D816V and Other Exon 17 Mutations in Patients with Mastocytosis.. Blood, 2005, 106, 3273-3273.	0.6	2
185	Variable promoter region CpG island methylation of the putative tumor suppressor gene Connexin 26 in breast cancer. Carcinogenesis, 2002, 23, 231-236.	1.3	76
186	Recurrent coiled-coil motifs in NUP98 fusion partners provide a clue to leukemogenesis. Blood, 2002, 99, 1097-1097.	0.6	25
187	Screening for and analysis of methylation differences using methylation-sensitive single-strand conformation analysis. Methods, 2002, 27, 134-138.	1.9	17
188	Optimisation of the RT-PCR detection of immunomagnetically enriched carcinoma cells. BMC Cancer, 2002, 2, 14.	1.1	29
189	Methylation Analysis of Formalin-Fixed, Paraffin-Embedded Sections Using a Nontoxic DNA Extraction Protocol. BioTechniques, 2001, 31, 1354-1357.	0.8	8
190	Loss of red cell A, B, and H antigens is frequent in myeloid malignancies. Blood, 2001, 97, 3633-3639.	0.6	88
191	Clustering of 1p36 breakpoints distal to 1p36.2 in hematological malignancies. Cancer Genetics and Cytogenetics, 2001, 125, 78-79.	1.0	6
192	Fusion of the NUP98 gene with the LEDGF/p52 gene defines a recurrent acute myeloid leukemia translocation. BMC Genetics, 2001, 2, 20.	2.7	38
193	Molecular detection of blood-borne epithelial cells in colorectal cancer patients and in patients with benign bowel disease. International Journal of Cancer, 2000, 89, 8-13.	2.3	138
194	Promoter region methylation does not account for the frequent loss of expression of the Fas gene in colorectal carcinoma. British Journal of Cancer, 2000, 82, 131-135.	2.9	29
195	Tumour-specific distribution of BRCA1 promoter region methylation supports a pathogenetic role in breast and ovarian cancer. Carcinogenesis, 2000, 21, 147-151.	1.3	108
196	Molecular detection of blood-borne epithelial cells in colorectal cancer patients and in patients with benign bowel disease. , 2000, 89, 8.		4
197	Methylation-sensitive, single-strand conformation analysis (MS-SSCA): A rapid method to screen for and analyze methylation. , 1999, 14, 289-293.		43
198	The (4;11)(q21;p15) Translocation Fuses the NUP98 andRAP1GDS1 Genes and Is Recurrent in T-Cell Acute Lymphocytic Leukemia. Blood, 1999, 94, 2072-2079.	0.6	81

#	Article	IF	Citations
199	The (4;11)(q21;p15) Translocation Fuses the NUP98 andRAP1GDS1 Genes and Is Recurrent in T-Cell Acute Lymphocytic Leukemia. Blood, 1999, 94, 2072-2079.	0.6	0
200	Characterization of a KRAB Family Zinc Finger Gene,ZNF195,Mapping to Chromosome Band 11p15.5. Genomics, 1997, 45, 451-455.	1.3	12
201	Immunobead RT-PCR: A Sensitive Method for Detection of Circulating Tumor Cells. BioTechniques, 1997, 22, 100-105.	0.8	58
202	A rapid and reliable PCR method for genotyping the ABO blood group. II: A2 and O2 alleles. , 1996, 8, 358-361.		16
203	A rapid and reliable PCR method for genotyping the ABO blood group. Human Mutation, 1993, 2, 67-70.	1.1	43
204	Localization of the human growth arrest-specific gene (GAS1) to chromosome bands 9q21.3-q22, a region frequently deleted in myeloid malignancies. Genomics, 1993, 18, 731-733.	1.3	29
205	Mapping of the chromosome 11 breakpoint of the t(4;11)(q21;p14â€“15) translocation. Cancer Genetics and Cytogenetics, 1993, 69, 122-125.	1.0	2
206	A rare translocation (4;11)(q21;p14â€“15) in an acute lymphoblastic leukemia expressing T-cell and myeloid markers. Cancer Genetics and Cytogenetics, 1991, 56, 255-262.	1.0	13
207	Review: Molecular analysis of the Philadelphia chromosome. Chromosoma, 1991, 100, 479-486.	1.0	7
208	The significance of oncogene amplification in primary breast cancer. International Journal of Cancer, 1989, 43, 270-272.	2.3	87
209	DNA methylation and genetic inactivation at thymidine kinase locus: Two different mechanisms for silencing autosomal genes. Somatic Cell and Molecular Genetics, 1988, 14, 55-68.	0.7	22
210	A frequent HindIII RFLP on chromosome 3p21â€“25 detected by a genomicerbAÎ² sequence. Nucleic Acids Research, 1988, 16, 1223-1223.	6.5	23
211	AHindIII RFLP for the HPRT pseudogene on chromosome 3 (HPRTP1). Nucleic Acids Research, 1987, 15, 1346-1346.	6.5	2