

Lodewyk F A Wessels

List of Publications by Year in descending order

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Version: 2024-02-01

149
papers

25,720
citations

25034

57
h-index

7518

151
g-index

154
all docs

154
docs citations

154
times ranked

40044
citing authors

#	ARTICLE	IF	CITATIONS
1	Functional Genomic Identification of Predictors of Sensitivity and Mechanisms of Resistance to Multivalent Second-Generation TRAIL-R2 Agonists. <i>Molecular Cancer Therapeutics</i> , 2022, 21, 594-606.	4.1	1
2	Effective drug combinations in breast, colon and pancreatic cancer cells. <i>Nature</i> , 2022, 603, 166-173.	27.8	154
3	Differential Survival and Therapy Benefit of Patients with Breast Cancer Are Characterized by Distinct Epithelial and Immune Cell Microenvironments. <i>Clinical Cancer Research</i> , 2022, 28, 960-971.	7.0	4
4	Genomic analysis defines clonal relationships of ductal carcinoma in situ and recurrent invasive breast cancer. <i>Nature Genetics</i> , 2022, 54, 850-860.	21.4	34
5	Drug-Induced Epigenomic Plasticity Reprograms Circadian Rhythm Regulation to Drive Prostate Cancer toward Androgen Independence. <i>Cancer Discovery</i> , 2022, 12, 2074-2097.	9.4	22
6	Heterofusion: Fusing genomics data of different measurement scales. <i>Journal of Chemometrics</i> , 2021, 35, e3200.	1.3	5
7	Generalized simultaneous component analysis of binary and quantitative data. <i>Journal of Chemometrics</i> , 2021, 35, e3312.	1.3	3
8	Epigenetic and transcriptional analysis reveals a core transcriptional program conserved in clonal prostate cancer metastases. <i>Molecular Oncology</i> , 2021, 15, 1942-1955.	4.6	10
9	The Prognostic Potential of Human Prostate Cancer-Associated Macrophage Subtypes as Revealed by Single-Cell Transcriptomics. <i>Molecular Cancer Research</i> , 2021, 19, 1778-1791.	3.4	20
10	Limited evolution of the actionable metastatic cancer genome under therapeutic pressure. <i>Nature Medicine</i> , 2021, 27, 1553-1563.	30.7	41
11	Flexible coâ€data learning for highâ€dimensional prediction. <i>Statistics in Medicine</i> , 2021, 40, 5910-5925.	1.6	8
12	Ovarian Cancerâ€™Specific <i>BRCA</i>-like Copy-Number Aberration Classifiers Detect Mutations Associated with Homologous Recombination Deficiency in the AGO-TR1 Trial. <i>Clinical Cancer Research</i> , 2021, 27, 6559-6569.	7.0	9
13	Few-shot learning creates predictive models of drug response that translate from high-throughput screens to individual patients. <i>Nature Cancer</i> , 2021, 2, 233-244.	13.2	92
14	Contralateral parenchymal enhancement on MRI is associated with tumor proteasome pathway gene expression and overall survival of early ER+/HER2-breast cancer patients. <i>Breast</i> , 2021, 60, 230-237.	2.2	0
15	Predicting patient response with models trained on cell lines and patient-derived xenografts by nonlinear transfer learning. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	7.1	19
16	The Tumor Immune Landscape and Architecture of Tertiary Lymphoid Structures in Urothelial Cancer. <i>Frontiers in Immunology</i> , 2021, 12, 793964.	4.8	13
17	RUNX2/CBFB modulates the response to MEK inhibitors through activation of receptor tyrosine kinases in KRAS-mutant colorectal cancer. <i>Translational Oncology</i> , 2020, 13, 201-211.	3.7	7
18	Preoperative ipilimumab plus nivolumab in locoregionally advanced urothelial cancer: the NABUCCO trial. <i>Nature Medicine</i> , 2020, 26, 1839-1844.	30.7	245

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19	Radiogenomic Analysis of Breast Cancer by Linking MRI Phenotypes with Tumor Gene Expression. <i>Radiology</i> , 2020, 296, 277-287.	7.3	37
20	Functional Categorization of <i>BRCA1</i> Variants of Uncertain Clinical Significance in Homologous Recombination Repair Complementation Assays. <i>Clinical Cancer Research</i> , 2020, 26, 4559-4568.	7.0	19
21	Endonuclease FEN1 Coregulates ER \pm Activity and Provides a Novel Drug Interface in Tamoxifen-Resistant Breast Cancer. <i>Cancer Research</i> , 2020, 80, 1914-1926.	0.9	23
22	Integrative analysis of genomic amplification-dependent expression and loss-of-function screen identifies ASAP1 as a driver gene in triple-negative breast cancer progression. <i>Oncogene</i> , 2020, 39, 4118-4131.	5.9	19
23	Approximating multivariate posterior distribution functions from Monte Carlo samples for sequential Bayesian inference. <i>PLoS ONE</i> , 2020, 15, e0230101.	2.5	5
24	Response of metastatic mouse invasive lobular carcinoma to mTOR inhibition is partly mediated by the adaptive immune system. <i>Oncoimmunology</i> , 2020, 9, 1724049.	4.6	12
25	<i>In situ</i> CRISPR-Cas9 base editing for the development of genetically engineered mouse models of breast cancer. <i>EMBO Journal</i> , 2020, 39, e102169.	7.8	40
26	Androgen modulation of XBP1 is functionally driving part of the AR transcriptional program. <i>Endocrine-Related Cancer</i> , 2020, 27, 67-79.	3.1	7
27	PRECISE: a domain adaptation approach to transfer predictors of drug response from pre-clinical models to tumors. <i>Bioinformatics</i> , 2019, 35, i510-i519.	4.1	53
28	Loss of p53 triggers WNT-dependent systemic inflammation to drive breast cancer metastasis. <i>Nature</i> , 2019, 572, 538-542.	27.8	312
29	Genomic data integration by WON-PARAFAC identifies interpretable factors for predicting drug-sensitivity in vivo. <i>Nature Communications</i> , 2019, 10, 5034.	12.8	12
30	Are contralateral parenchymal enhancement on dynamic contrast-enhanced MRI and genomic ER-pathway activity in ER-positive/HER2-negative breast cancer related?. <i>European Journal of Radiology</i> , 2019, 121, 108705.	2.6	9
31	Identifying Epistasis in Cancer Genomes: A Delicate Affair. <i>Cell</i> , 2019, 177, 1375-1383.	28.9	81
32	Immune induction strategies in metastatic triple-negative breast cancer to enhance the sensitivity to PD-1 blockade: the TONIC trial. <i>Nature Medicine</i> , 2019, 25, 920-928.	30.7	589
33	Inhibition of the Replication Stress Response Is a Synthetic Vulnerability in SCLC That Acts Synergistically in Combination with Cisplatin. <i>Molecular Cancer Therapeutics</i> , 2019, 18, 762-770.	4.1	25
34	Lysine specific demethylase 1 inactivation enhances differentiation and promotes cytotoxic response when combined with all-trans retinoic acid in acute myeloid leukemia across subtypes. <i>Haematologica</i> , 2019, 104, 1156-1167.	3.5	50
35	Principal component analysis of binary genomics data. <i>Briefings in Bioinformatics</i> , 2019, 20, 317-329.	6.5	21
36	Role of variant allele fraction and rare SNP filtering to improve cellular DNA repair endpoint association. <i>PLoS ONE</i> , 2018, 13, e0206632.	2.5	2

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37	Molecular characterization of breast and lung tumors by integration of multiple data types with functional sparse-factor analysis. <i>PLoS Computational Biology</i> , 2018, 14, e1006520.	3.2	13
38	MAP3K1 and MAP2K4 mutations are associated with sensitivity to MEK inhibitors in multiple cancer models. <i>Cell Research</i> , 2018, 28, 719-729.	12.0	105
39	Loss of androgen receptor signaling in prostate cancer-associated fibroblasts (CAFs) promotes CCL2- and CXCL8-mediated cancer cell migration. <i>Molecular Oncology</i> , 2018, 12, 1308-1323.	4.6	79
40	Integrative Modeling Identifies Key Determinants of Inhibitor Sensitivity in Breast Cancer Cell Lines. <i>Cancer Research</i> , 2018, 78, 4396-4410.	0.9	14
41	A System-wide Approach to Monitor Responses to Synergistic BRAF and EGFR Inhibition in Colorectal Cancer Cells. <i>Molecular and Cellular Proteomics</i> , 2018, 17, 1892-1908.	3.8	13
42	Transcriptomics and Transposon Mutagenesis Identify Multiple Mechanisms of Resistance to the FGFR Inhibitor AZD4547. <i>Cancer Research</i> , 2018, 78, 5668-5679.	0.9	35
43	Fanconi anemia and homologous recombination gene variants are associated with functional DNA repair defects <i>in vitro</i> and poor outcome in patients with advanced head and neck squamous cell carcinoma. <i>Oncotarget</i> , 2018, 9, 18198-18213.	1.8	37
44	Estrogen receptor β yields treatment-specific enhancers between morphologically similar endometrial tumors. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E1316-E1325.	7.1	25
45	Mammary tumor-derived CCL2 enhances pro-metastatic systemic inflammation through upregulation of IL1 β in tumor-associated macrophages. <i>Oncolmmunology</i> , 2017, 6, e1334744.	4.6	81
46	Identifying transposon insertions and their effects from RNA-sequencing data. <i>Nucleic Acids Research</i> , 2017, 45, 7064-7077.	14.5	9
47	Complementary Value of Contralateral Parenchymal Enhancement on DCE-MRI to Prognostic Models and Molecular Assays in High-risk ER+/HER2 ⁺ Breast Cancer. <i>Clinical Cancer Research</i> , 2017, 23, 6505-6515.	7.0	18
48	Identification of CMTM6 and CMTM4 as PD-L1 protein regulators. <i>Nature</i> , 2017, 549, 106-110.	27.8	501
49	Insertional mutagenesis identifies drivers of a novel oncogenic pathway in invasive lobular breast carcinoma. <i>Nature Genetics</i> , 2017, 49, 1219-1230.	21.4	64
50	Predicting clinical benefit from everolimus in patients with advanced solid tumors, the CPCT-03 study. <i>Oncotarget</i> , 2017, 8, 55582-55592.	1.8	9
51	Systematic functional perturbations uncover a prognostic genetic network driving human breast cancer. <i>Oncotarget</i> , 2017, 8, 20572-20587.	1.8	28
52	A Landscape of Pharmacogenomic Interactions in Cancer. <i>Cell</i> , 2016, 166, 740-754.	28.9	1,518
53	Integration of genomic, transcriptomic and proteomic data identifies two biologically distinct subtypes of invasive lobular breast cancer. <i>Scientific Reports</i> , 2016, 6, 18517.	3.3	143
54	Sensitizing Triple-Negative Breast Cancer to PI3K Inhibition by Cotargeting IGF1R. <i>Molecular Cancer Therapeutics</i> , 2016, 15, 1545-1556.	4.1	30

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55	Multilevel models improve precision and speed of IC ₅₀ estimates. <i>Pharmacogenomics</i> , 2016, 17, 691-700.	1.3	57
56	A Vulnerability of a Subset of Colon Cancers with Potential Clinical Utility. <i>Cell</i> , 2016, 165, 317-330.	28.9	70
57	Comparative Cistromics Reveals Genomic Cross-talk between FOXA1 and ER \pm in Tamoxifen-Associated Endometrial Carcinomas. <i>Cancer Research</i> , 2016, 76, 3773-3784.	0.9	30
58	Loss of <i>ARID1A</i> Activates <i>ANXA1</i> , which Serves as a Predictive Biomarker for Trastuzumab Resistance. <i>Clinical Cancer Research</i> , 2016, 22, 5238-5248.	7.0	43
59	Defining chromosomal translocation risks in cancer. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, E3649-56.	7.1	15
60	Androgen receptor DNA binding and chromatin accessibility profiling in prostate cancer. <i>Genomics Data</i> , 2016, 7, 124-126.	1.3	13
61	Large variety in a panel of human colon cancer organoids in response to EZH2 inhibition. <i>Oncotarget</i> , 2016, 7, 69816-69828.	1.8	23
62	Comparative analysis of human and mouse transcriptomes of Th17 cell priming. <i>Oncotarget</i> , 2016, 7, 13416-13428.	1.8	43
63	Neoadjuvant tamoxifen synchronizes ER \pm binding and gene expression profiles related to outcome and proliferation. <i>Oncotarget</i> , 2016, 7, 33901-33918.	1.8	13
64	Androgen receptor profiling predicts prostate cancer outcome. <i>EMBO Molecular Medicine</i> , 2015, 7, 1450-1464.	6.9	67
65	BRCA1-like signature in triple negative breast cancer: Molecular and clinical characterization reveals subgroups with therapeutic potential. <i>Molecular Oncology</i> , 2015, 9, 1528-1538.	4.6	54
66	Quantitative imaging of focal adhesion dynamics and their regulation by HGF and Rap1 signaling. <i>Experimental Cell Research</i> , 2015, 330, 382-397.	2.6	13
67	BRCA2-Deficient Sarcomatoid Mammary Tumors Exhibit Multidrug Resistance. <i>Cancer Research</i> , 2015, 75, 732-741.	0.9	47
68	Chemical profiling of the genome with anti-cancer drugs defines target specificities. <i>Nature Chemical Biology</i> , 2015, 11, 472-480.	8.0	62
69	Prospective Derivation of a Living Organoid Biobank of Colorectal Cancer Patients. <i>Cell</i> , 2015, 161, 933-945.	28.9	1,710
70	SMARCE1 suppresses EGFR expression and controls responses to MET and ALK inhibitors in lung cancer. <i>Cell Research</i> , 2015, 25, 445-458.	12.0	36
71	Genome-Wide Identification and Characterization of Novel Factors Conferring Resistance to Topoisomerase II Poisons in Cancer. <i>Cancer Research</i> , 2015, 75, 4176-4187.	0.9	59
72	The consensus molecular subtypes of colorectal cancer. <i>Nature Medicine</i> , 2015, 21, 1350-1356.	30.7	3,596

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73	A conditional piggyBac transposition system for genetic screening in mice identifies oncogenic networks in pancreatic cancer. <i>Nature Genetics</i> , 2015, 47, 47-56.	21.4	77
74	Fra-1 is a key driver of colon cancer metastasis and a Fra-1 classifier predicts disease-free survival. <i>Oncotarget</i> , 2015, 6, 43146-43161.	1.8	45
75	Lack of Genomic Heterogeneity at High-Resolution aCGH between Primary Breast Cancers and Their Paired Lymph Node Metastases. <i>PLoS ONE</i> , 2014, 9, e103177.	2.5	9
76	Chromatin Landscapes of Retroviral and Transposon Integration Profiles. <i>PLoS Genetics</i> , 2014, 10, e1004250.	3.5	80
77	Complex Formation and Function of Estrogen Receptor β in Transcription Requires RIP140. <i>Cancer Research</i> , 2014, 74, 5469-5479.	0.9	28
78	Identifying regulatory mechanisms underlying tumorigenesis using locus expression signature analysis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 5747-5752.	7.1	7
79	Colorectal cancer intrinsic subtypes predict chemotherapy benefit, deficient mismatch repair and epithelial-to-mesenchymal transition. <i>International Journal of Cancer</i> , 2014, 134, 552-562.	5.1	286
80	Reversible and adaptive resistance to BRAF(V600E) inhibition in melanoma. <i>Nature</i> , 2014, 508, 118-122.	27.8	702
81	Transposon mutagenesis identifies genes driving hepatocellular carcinoma in a chronic hepatitis B mouse model. <i>Nature Genetics</i> , 2014, 46, 24-32.	21.4	105
82	Elevated APOBEC3B Correlates with Poor Outcomes for Estrogen-Receptor-Positive Breast Cancers. <i>Hormones and Cancer</i> , 2014, 5, 405-413.	4.9	140
83	Genome-wide epigenetic profiling of breast cancer tumors treated with aromatase inhibitors. <i>Genomics Data</i> , 2014, 2, 195-198.	1.3	4
84	USP9X Downregulation Renders Breast Cancer Cells Resistant to Tamoxifen. <i>Cancer Research</i> , 2014, 74, 3810-3820.	0.9	38
85	Multiscale representation of genomic signals. <i>Nature Methods</i> , 2014, 11, 689-694.	19.0	31
86	Using TRIP for genome-wide position effect analysis in cultured cells. <i>Nature Protocols</i> , 2014, 9, 1255-1281.	12.0	34
87	Breast Cancer Subtype Specific Classifiers of Response to Neoadjuvant Chemotherapy Do Not Outperform Classifiers Trained on All Subtypes. <i>PLoS ONE</i> , 2014, 9, e88551.	2.5	8
88	Chromatin Position Effects Assayed by Thousands of Reporters Integrated in Parallel. <i>Cell</i> , 2013, 154, 914-927.	28.9	283
89	Platform comparisons for identification of breast cancers with a BRCA-like copy number profile. <i>Breast Cancer Research and Treatment</i> , 2013, 139, 317-327.	2.5	20
90	SERPINA6, BEX1, AGTR1, SLC26A3, and LAPTM4B are markers of resistance to neoadjuvant chemotherapy in HER2-negative breast cancer. <i>Breast Cancer Research and Treatment</i> , 2013, 137, 213-223.	2.5	52

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91	Constitutive nuclear lamina genome interactions are highly conserved and associated with A/T-rich sequence. <i>Genome Research</i> , 2013, 23, 270-280.	5.5	377
92	Large-scale genotyping identifies 41 new loci associated with breast cancer risk. <i>Nature Genetics</i> , 2013, 45, 353-361.	21.4	960
93	A scale-space method for detecting recurrent DNA copy number changes with analytical false discovery rate control. <i>Nucleic Acids Research</i> , 2013, 41, e100-e100.	14.5	23
94	Hallmarks of Aromatase Inhibitor Drug Resistance Revealed by Epigenetic Profiling in Breast Cancer. <i>Cancer Research</i> , 2013, 73, 6632-6641.	0.9	79
95	Timely deposition of macromolecular structures is necessary for peer review. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2013, 69, 2293-2295.	2.5	3
96	Identification of a pharmacologically tractable Fra-1/ADORA2B axis promoting breast cancer metastasis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 5139-5144.	7.1	150
97	Identifying subgroup markers in heterogeneous populations. <i>Nucleic Acids Research</i> , 2013, 41, e200-e200.	14.5	21
98	Analysis of Tumor Heterogeneity and Cancer Gene Networks Using Deep Sequencing of MMTV-Induced Mouse Mammary Tumors. <i>PLoS ONE</i> , 2013, 8, e62113.	2.5	40
99	Current composite-feature classification methods do not outperform simple single-genes classifiers in breast cancer prognosis. <i>Frontiers in Genetics</i> , 2013, 4, 289.	2.3	41
100	The deubiquitinase USP9X suppresses pancreatic ductal adenocarcinoma. <i>Nature</i> , 2012, 486, 266-270.	27.8	297
101	Impact of Intertumoral Heterogeneity on Predicting Chemotherapy Response of BRCA1-Deficient Mammary Tumors. <i>Cancer Research</i> , 2012, 72, 2350-2361.	0.9	48
102	MED12 Controls the Response to Multiple Cancer Drugs through Regulation of TGF- β 2 Receptor Signaling. <i>Cell</i> , 2012, 151, 937-950.	28.9	371
103	Pancreatic cancer genomes reveal aberrations in axon guidance pathway genes. <i>Nature</i> , 2012, 491, 399-405.	27.8	1,741
104	A Critical Evaluation of Network and Pathway-Based Classifiers for Outcome Prediction in Breast Cancer. <i>PLoS ONE</i> , 2012, 7, e34796.	2.5	56
105	Integration of Clinical and Gene Expression Data Has a Synergetic Effect on Predicting Breast Cancer Outcome. <i>PLoS ONE</i> , 2012, 7, e40358.	2.5	35
106	PKA-induced phosphorylation of ER α at serine 305 and high PAK1 levels is associated with sensitivity to tamoxifen in ER-positive breast cancer. <i>Breast Cancer Research and Treatment</i> , 2011, 125, 1-12.	2.5	49
107	Insertional mutagenesis identifies multiple networks of cooperating genes driving intestinal tumorigenesis. <i>Nature Genetics</i> , 2011, 43, 1202-1209.	21.4	172
108	High-throughput semiquantitative analysis of insertional mutations in heterogeneous tumors. <i>Genome Research</i> , 2011, 21, 2181-2189.	5.5	39

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109	MicroRNA Sequence and Expression Analysis in Breast Tumors by Deep Sequencing. <i>Cancer Research</i> , 2011, 71, 4443-4453.	0.9	331
110	Computational identification of insertional mutagenesis targets for cancer gene discovery. <i>Nucleic Acids Research</i> , 2011, 39, e105-e105.	14.5	24
111	Gene Expression Profiles from Formalin Fixed Paraffin Embedded Breast Cancer Tissue Are Largely Comparable to Fresh Frozen Matched Tissue. <i>PLoS ONE</i> , 2011, 6, e17163.	2.5	130
112	Concordance of clinical and molecular breast cancer subtyping in the context of preoperative chemotherapy response. <i>Breast Cancer Research and Treatment</i> , 2010, 119, 119-126.	2.5	142
113	Integration of DNA Copy Number Alterations and Prognostic Gene Expression Signatures in Breast Cancer Patients. <i>Clinical Cancer Research</i> , 2010, 16, 651-663.	7.0	61
114	Insertional Mutagenesis in Mice Deficient for <i>p15Ink4b</i> , <i>p16Ink4a</i> , <i>p21Cip1</i> , and <i>p27Kip1</i> Reveals Cancer Gene Interactions and Correlations with Tumor Phenotypes. <i>Cancer Research</i> , 2010, 70, 520-531.	0.9	31
115	Identification of Networks of Co-Occurring, Tumor-Related DNA Copy Number Changes Using a Genome-Wide Scoring Approach. <i>PLoS Computational Biology</i> , 2010, 6, e1000631.	3.2	27
116	Do predictive signatures really predict response to cancer chemotherapy? <i>Cell Cycle</i> , 2010, 9, 4836-4840.	2.6	58
117	Novel Candidate Cancer Genes Identified by a Large-Scale Cross-Species Comparative Oncogenomics Approach. <i>Cancer Research</i> , 2010, 70, 883-895.	0.9	40
118	Molecular Maps of the Reorganization of Genome-Nuclear Lamina Interactions during Differentiation. <i>Molecular Cell</i> , 2010, 38, 603-613.	9.7	916
119	Molecular subtyping of breast cancer: ready to use?. <i>Lancet Oncology</i> , The, 2010, 11, 306-307.	10.7	14
120	Somatic structural rearrangements in genetically engineered mouse mammary tumors. <i>Genome Biology</i> , 2010, 11, R100.	9.6	24
121	Combinatorial effects of environmental parameters on transcriptional regulation in <i>Saccharomyces cerevisiae</i> : A quantitative analysis of a compendium of chemostat-based transcriptome data. <i>BMC Genomics</i> , 2009, 10, 53.	2.8	55
122	Prediction of BRCA1-association in hereditary non-BRCA1/2 breast carcinomas with array-CGH. <i>Breast Cancer Research and Treatment</i> , 2009, 116, 479-489.	2.5	124
123	Comparison of gene expression profiles predicting progression in breast cancer patients treated with tamoxifen. <i>Breast Cancer Research and Treatment</i> , 2009, 113, 275-283.	2.5	56
124	Domain organization of human chromosomes revealed by mapping of nuclear lamina interactions. <i>Nature</i> , 2008, 453, 948-951.	27.8	1,658
125	Large-Scale Mutagenesis in p19ARF- and p53-Deficient Mice Identifies Cancer Genes and Their Collaborative Networks. <i>Cell</i> , 2008, 133, 727-741.	28.9	167
126	Identification of cancer genes using a statistical framework for multiexperiment analysis of nondiscretized array CGH data. <i>Nucleic Acids Research</i> , 2008, 36, e13-e13.	14.5	62

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127	Biclustering Sparse Binary Genomic Data. <i>Journal of Computational Biology</i> , 2008, 15, 1329-1345.	1.6	48
128	Ubiquitin E3 Ligase Ring1b/Rnf2 of Polycomb Repressive Complex 1 Contributes to Stable Maintenance of Mouse Embryonic Stem Cells. <i>PLoS ONE</i> , 2008, 3, e2235.	2.5	97
129	PROTEIN COMPLEX PREDICTION USING AN INTEGRATIVE BIOINFORMATICS APPROACH. <i>Journal of Bioinformatics and Computational Biology</i> , 2007, 05, 839-864.	0.8	9
130	Somatic loss of BRCA1 and p53 in mice induces mammary tumors with features of human <i>BRCA1</i> -mutated basal-like breast cancer. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 12111-12116.	7.1	428
131	Module-Based Outcome Prediction Using Breast Cancer Compendia. <i>PLoS ONE</i> , 2007, 2, e1047.	2.5	23
132	Classification in the presence of class noise using a probabilistic Kernel Fisher method. <i>Pattern Recognition</i> , 2007, 40, 3349-3357.	8.1	68
133	MMTV insertional mutagenesis identifies genes, gene families and pathways involved in mammary cancer. <i>Nature Genetics</i> , 2007, 39, 759-769.	21.4	184
134	SIRAC: Supervised Identification of Regions of Aberration in aCGH datasets. <i>BMC Bioinformatics</i> , 2007, 8, 422.	2.6	10
135	Exploiting combinatorial cultivation conditions to infer transcriptional regulation. <i>BMC Genomics</i> , 2007, 8, 25.	2.8	42
136	Predicting a local recurrence after breast-conserving therapy by gene expression profiling. <i>Breast Cancer Research</i> , 2006, 8, R62.	5.0	184
137	Concordance among Gene-Expression-Based Predictors for Breast Cancer. <i>New England Journal of Medicine</i> , 2006, 355, 560-569.	27.0	1,201
138	Cross-validated Cox regression on microarray gene expression data. <i>Statistics in Medicine</i> , 2006, 25, 3201-3216.	1.6	158
139	Artifacts of Markov blanket filtering based on discretized features in small sample size applications. <i>Pattern Recognition Letters</i> , 2006, 27, 709-714.	4.2	7
140	Random subspace method for multivariate feature selection. <i>Pattern Recognition Letters</i> , 2006, 27, 1067-1076.	4.2	163
141	A comparison of univariate and multivariate gene selection techniques for classification of cancer datasets. <i>BMC Bioinformatics</i> , 2006, 7, 235.	2.6	97
142	Converting a breast cancer microarray signature into a high-throughput diagnostic test. <i>BMC Genomics</i> , 2006, 7, 278.	2.8	429
143	Detecting Statistically Significant Common Insertion Sites in Retroviral Insertional Mutagenesis Screens. <i>PLoS Computational Biology</i> , 2006, 2, e166.	3.2	111
144	Gene expression profiling in follicular lymphoma to assess clinical aggressiveness and to guide the choice of treatment. <i>Blood</i> , 2005, 105, 301-307.	1.4	208

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145	An expression profile for diagnosis of lymph node metastases from primary head and neck squamous cell carcinomas. <i>Nature Genetics</i> , 2005, 37, 182-186.	21.4	383
146	Changes in Gene Expression Associated With Response to Neoadjuvant Chemotherapy in Breast Cancer. <i>Journal of Clinical Oncology</i> , 2005, 23, 3331-3342.	1.6	152
147	Comparative genomic hybridization profiles in human BRCA1 and BRCA2 breast tumors highlight differential sets of genomic aberrations. <i>Cancer Research</i> , 2005, 65, 822-7.	0.9	97
148	Gene expression profiles of primary breast tumors maintained in distant metastases. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 15901-15905.	7.1	404
149	Molecular classification of breast carcinomas by comparative genomic hybridization: a specific somatic genetic profile for BRCA1 tumors. <i>Cancer Research</i> , 2002, 62, 7110-7.	0.9	123