

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	The consensus molecular subtypes of colorectal cancer. <i>Nature Medicine</i> , 2015, 21, 1350-1356.	30.7	3,596
2	Pancreatic cancer genomes reveal aberrations in axon guidance pathway genes. <i>Nature</i> , 2012, 491, 399-405.	27.8	1,741
3	Prospective Derivation of a Living Organoid Biobank of Colorectal Cancer Patients. <i>Cell</i> , 2015, 161, 933-945.	28.9	1,710
4	Domain organization of human chromosomes revealed by mapping of nuclear lamina interactions. <i>Nature</i> , 2008, 453, 948-951.	27.8	1,658
5	A Landscape of Pharmacogenomic Interactions in Cancer. <i>Cell</i> , 2016, 166, 740-754.	28.9	1,518
6	Concordance among Gene-Expression-Based Predictors for Breast Cancer. <i>New England Journal of Medicine</i> , 2006, 355, 560-569.	27.0	1,201
7	Large-scale genotyping identifies 41 new loci associated with breast cancer risk. <i>Nature Genetics</i> , 2013, 45, 353-361.	21.4	960
8	Molecular Maps of the Reorganization of Genome-Nuclear Lamina Interactions during Differentiation. <i>Molecular Cell</i> , 2010, 38, 603-613.	9.7	916
9	Reversible and adaptive resistance to BRAF(V600E) inhibition in melanoma. <i>Nature</i> , 2014, 508, 118-122.	27.8	702
10	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
11	Identification of CMTM6 and CMTM4 as PD-L1 protein regulators. <i>Nature</i> , 2017, 549, 106-110.	27.8	501
12	Converting a breast cancer microarray signature into a high-throughput diagnostic test. <i>BMC Genomics</i> , 2006, 7, 278.	2.8	429
13	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
14	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
15	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
16	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
17	MED12 Controls the Response to Multiple Cancer Drugs through Regulation of TGF- β Receptor Signaling. <i>Cell</i> , 2012, 151, 937-950.	28.9	371
18	MicroRNA Sequence and Expression Analysis in Breast Tumors by Deep Sequencing. <i>Cancer Research</i> , 2011, 71, 4443-4453.	0.9	331

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19	Loss of p53 triggers WNT-dependent systemic inflammation to drive breast cancer metastasis. <i>Nature</i> , 2019, 572, 538-542.	27.8	312
20	The deubiquitinase USP9X suppresses pancreatic ductal adenocarcinoma. <i>Nature</i> , 2012, 486, 266-270.	27.8	297
21	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
22	Chromatin Position Effects Assayed by Thousands of Reporters Integrated in Parallel. <i>Cell</i> , 2013, 154, 914-927.	28.9	283
23	Preoperative ipilimumab plus nivolumab in locoregionally advanced urothelial cancer: the NABUCCO trial. <i>Nature Medicine</i> , 2020, 26, 1839-1844.	30.7	245
24	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
25	Predicting a local recurrence after breast-conserving therapy by gene expression profiling. <i>Breast Cancer Research</i> , 2006, 8, R62.	5.0	184
26	MMTV insertional mutagenesis identifies genes, gene families and pathways involved in mammary cancer. <i>Nature Genetics</i> , 2007, 39, 759-769.	21.4	184
27	Insertional mutagenesis identifies multiple networks of cooperating genes driving intestinal tumorigenesis. <i>Nature Genetics</i> , 2011, 43, 1202-1209.	21.4	172
28	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
29	Random subspace method for multivariate feature selection. <i>Pattern Recognition Letters</i> , 2006, 27, 1067-1076.	4.2	163
30	Cross-validated Cox regression on microarray gene expression data. <i>Statistics in Medicine</i> , 2006, 25, 3201-3216.	1.6	158
31	Effective drug combinations in breast, colon and pancreatic cancer cells. <i>Nature</i> , 2022, 603, 166-173.	27.8	154
32	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
33	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
34	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
35	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
36	Elevated APOBEC3B Correlates with Poor Outcomes for Estrogen-Receptor-Positive Breast Cancers. <i>Hormones and Cancer</i> , 2014, 5, 405-413.	4.9	140

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37	Gene Expression Profiles from Formalin Fixed Paraffin Embedded Breast Cancer Tissue Are Largely Comparable to Fresh Frozen Matched Tissue. PLoS ONE, 2011, 6, e17163.	2.5	130
38	Prediction of BRCA1-association in hereditary non-BRCA1/2 breast carcinomas with array-CGH. Breast Cancer Research and Treatment, 2009, 116, 479-489.	2.5	124
39	Molecular classification of breast carcinomas by comparative genomic hybridization: a specific somatic genetic profile for BRCA1 tumors. Cancer Research, 2002, 62, 7110-7.	0.9	123
40	Detecting Statistically Significant Common Insertion Sites in Retroviral Insertional Mutagenesis Screens. PLoS Computational Biology, 2006, 2, e166.	3.2	111
41	Transposon mutagenesis identifies genes driving hepatocellular carcinoma in a chronic hepatitis B mouse model. Nature Genetics, 2014, 46, 24-32.	21.4	105
42	MAP3K1 and MAP2K4 mutations are associated with sensitivity to MEK inhibitors in multiple cancer models. Cell Research, 2018, 28, 719-729.	12.0	105
43	A comparison of univariate and multivariate gene selection techniques for classification of cancer datasets. BMC Bioinformatics, 2006, 7, 235.	2.6	97
44	Ubiquitin E3 Ligase Ring1b/Rnf2 of Polycomb Repressive Complex 1 Contributes to Stable Maintenance of Mouse Embryonic Stem Cells. PLoS ONE, 2008, 3, e2235.	2.5	97
45	Comparative genomic hybridization profiles in human BRCA1 and BRCA2 breast tumors highlight differential sets of genomic aberrations. Cancer Research, 2005, 65, 822-7.	0.9	97
46	Few-shot learning creates predictive models of drug response that translate from high-throughput screens to individual patients. Nature Cancer, 2021, 2, 233-244.	13.2	92
47	Mammary tumor-derived CCL2 enhances pro-metastatic systemic inflammation through upregulation of IL1 β in tumor-associated macrophages. Oncoimmunology, 2017, 6, e1334744.	4.6	81
48	Identifying Epistasis in Cancer Genomes: A Delicate Affair. Cell, 2019, 177, 1375-1383.	28.9	81
49	Chromatin Landscapes of Retroviral and Transposon Integration Profiles. PLoS Genetics, 2014, 10, e1004250.	3.5	80
50	Hallmarks of Aromatase Inhibitor Drug Resistance Revealed by Epigenetic Profiling in Breast Cancer. Cancer Research, 2013, 73, 6632-6641.	0.9	79
51	Loss of androgen receptor signaling in prostate cancer-associated fibroblasts (CAFs) promotes CCL2- and CXCL8-mediated cancer cell migration. Molecular Oncology, 2018, 12, 1308-1323.	4.6	79
52	A conditional piggyBac transposition system for genetic screening in mice identifies oncogenic networks in pancreatic cancer. Nature Genetics, 2015, 47, 47-56.	21.4	77
53	A Vulnerability of a Subset of Colon Cancers with Potential Clinical Utility. Cell, 2016, 165, 317-330.	28.9	70
54	Classification in the presence of class noise using a probabilistic Kernel Fisher method. Pattern Recognition, 2007, 40, 3349-3357.	8.1	68

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55	Androgen receptor profiling predicts prostate cancer outcome. <i>EMBO Molecular Medicine</i> , 2015, 7, 1450-1464.	6.9	67
56	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
57	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
58	Chemical profiling of the genome with anti-cancer drugs defines target specificities. <i>Nature Chemical Biology</i> , 2015, 11, 472-480.	8.0	62
59	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
60	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
61	Do predictive signatures really predict response to cancer chemotherapy? <i>Cell Cycle</i> , 2010, 9, 4836-4840.	2.6	58
62	Multilevel models improve precision and speed of IC_{50} estimates. <i>Pharmacogenomics</i> , 2016, 17, 691-700.	1.3	57
63	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
64	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
65	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
66	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
67	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
68	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
69	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
70	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
71	Biclustering Sparse Binary Genomic Data. <i>Journal of Computational Biology</i> , 2008, 15, 1329-1345.	1.6	48
72	Impact of Intertumoral Heterogeneity on Predicting Chemotherapy Response of BRCA1-Deficient Mammary Tumors. <i>Cancer Research</i> , 2012, 72, 2350-2361.	0.9	48

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73	BRCA2-Deficient Sarcomatoid Mammary Tumors Exhibit Multidrug Resistance. <i>Cancer Research</i> , 2015, 75, 732-741.	0.9	47
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	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
76	Comparative analysis of human and mouse transcriptomes of Th17 cell priming. <i>Oncotarget</i> , 2016, 7, 13416-13428.	1.8	43
77	Exploiting combinatorial cultivation conditions to infer transcriptional regulation. <i>BMC Genomics</i> , 2007, 8, 25.	2.8	42
78	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
79	Limited evolution of the actionable metastatic cancer genome under therapeutic pressure. <i>Nature Medicine</i> , 2021, 27, 1553-1563.	30.7	41
80	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
81	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
82	<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
83	High-throughput semiquantitative analysis of insertional mutations in heterogeneous tumors. <i>Genome Research</i> , 2011, 21, 2181-2189.	5.5	39
84	USP9X Downregulation Renders Breast Cancer Cells Resistant to Tamoxifen. <i>Cancer Research</i> , 2014, 74, 3810-3820.	0.9	38
85	Radiogenomic Analysis of Breast Cancer by Linking MRI Phenotypes with Tumor Gene Expression. <i>Radiology</i> , 2020, 296, 277-287.	7.3	37
86	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
87	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
88	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
89	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
90	Using TRIP for genome-wide position effect analysis in cultured cells. <i>Nature Protocols</i> , 2014, 9, 1255-1281.	12.0	34

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91	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
92	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
93	Multiscale representation of genomic signals. <i>Nature Methods</i> , 2014, 11, 689-694.	19.0	31
94	Sensitizing Triple-Negative Breast Cancer to PI3K Inhibition by Cotargeting IGF1R. <i>Molecular Cancer Therapeutics</i> , 2016, 15, 1545-1556.	4.1	30
95	Comparative Cistromics Reveals Genomic Cross-talk between FOXA1 and ER α in Tamoxifen-Associated Endometrial Carcinomas. <i>Cancer Research</i> , 2016, 76, 3773-3784.	0.9	30
96	Complex Formation and Function of Estrogen Receptor α in Transcription Requires RIP140. <i>Cancer Research</i> , 2014, 74, 5469-5479.	0.9	28
97	Systematic functional perturbations uncover a prognostic genetic network driving human breast cancer. <i>Oncotarget</i> , 2017, 8, 20572-20587.	1.8	28
98	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
99	Estrogen receptor α wields 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
100	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
101	Somatic structural rearrangements in genetically engineered mouse mammary tumors. <i>Genome Biology</i> , 2010, 11, R100.	9.6	24
102	Computational identification of insertional mutagenesis targets for cancer gene discovery. <i>Nucleic Acids Research</i> , 2011, 39, e105-e105.	14.5	24
103	Module-Based Outcome Prediction Using Breast Cancer Compendia. <i>PLoS ONE</i> , 2007, 2, e1047.	2.5	23
104	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
105	Endonuclease FEN1 Coregulates ER α Activity and Provides a Novel Drug Interface in Tamoxifen-Resistant Breast Cancer. <i>Cancer Research</i> , 2020, 80, 1914-1926.	0.9	23
106	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
107	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
108	Identifying subgroup markers in heterogeneous populations. <i>Nucleic Acids Research</i> , 2013, 41, e200-e200.	14.5	21

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109	Principal component analysis of binary genomics data. <i>Briefings in Bioinformatics</i> , 2019, 20, 317-329.	6.5	21
110	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
111	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
112	Functional Categorization of BRCA1 Variants of Uncertain Clinical Significance in Homologous Recombination Repair Complementation Assays. <i>Clinical Cancer Research</i> , 2020, 26, 4559-4568.	7.0	19
113	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
114	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
115	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
116	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
117	Molecular subtyping of breast cancer: ready to use?. <i>Lancet Oncology</i> , The, 2010, 11, 306-307.	10.7	14
118	Integrative Modeling Identifies Key Determinants of Inhibitor Sensitivity in Breast Cancer Cell Lines. <i>Cancer Research</i> , 2018, 78, 4396-4410.	0.9	14
119	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
120	Androgen receptor DNA binding and chromatin accessibility profiling in prostate cancer. <i>Genomics Data</i> , 2016, 7, 124-126.	1.3	13
121	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
122	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
123	Neoadjuvant tamoxifen synchronizes ER± binding and gene expression profiles related to outcome and proliferation. <i>Oncotarget</i> , 2016, 7, 33901-33918.	1.8	13
124	The Tumor Immune Landscape and Architecture of Tertiary Lymphoid Structures in Urothelial Cancer. <i>Frontiers in Immunology</i> , 2021, 12, 793964.	4.8	13
125	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
126	Response of metastatic mouse invasive lobular carcinoma to mTOR inhibition is partly mediated by the adaptive immune system. <i>Oncotarget</i> , 2020, 9, 1724049.	4.6	12

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127	SIRAC: Supervised Identification of Regions of Aberration in aCGH datasets. BMC Bioinformatics, 2007, 8, 422.	2.6	10
128	Epigenetic and transcriptional analysis reveals a core transcriptional program conserved in clonal prostate cancer metastases. Molecular Oncology, 2021, 15, 1942-1955.	4.6	10
129	PROTEIN COMPLEX PREDICTION USING AN INTEGRATIVE BIOINFORMATICS APPROACH. Journal of Bioinformatics and Computational Biology, 2007, 05, 839-864.	0.8	9
130	Lack of Genomic Heterogeneity at High-Resolution aCGH between Primary Breast Cancers and Their Paired Lymph Node Metastases. PLoS ONE, 2014, 9, e103177.	2.5	9
131	Identifying transposon insertions and their effects from RNA-sequencing data. Nucleic Acids Research, 2017, 45, 7064-7077.	14.5	9
132	Are contralateral parenchymal enhancement on dynamic contrast-enhanced MRI and genomic ER-pathway activity in ER-positive/HER2-negative breast cancer related?. European Journal of Radiology, 2019, 121, 108705.	2.6	9
133	Ovarian Cancer-Specific BRCA-like Copy-Number Aberration Classifiers Detect Mutations Associated with Homologous Recombination Deficiency in the AGO-TR1 Trial. Clinical Cancer Research, 2021, 27, 6559-6569.	7.0	9
134	Predicting clinical benefit from everolimus in patients with advanced solid tumors, the CPCT-03 study. Oncotarget, 2017, 8, 55582-55592.	1.8	9
135	Flexible co-data learning for high-dimensional prediction. Statistics in Medicine, 2021, 40, 5910-5925.	1.6	8
136	Breast Cancer Subtype Specific Classifiers of Response to Neoadjuvant Chemotherapy Do Not Outperform Classifiers Trained on All Subtypes. PLoS ONE, 2014, 9, e88551.	2.5	8
137	Artifacts of Markov blanket filtering based on discretized features in small sample size applications. Pattern Recognition Letters, 2006, 27, 709-714.	4.2	7
138	Identifying regulatory mechanisms underlying tumorigenesis using locus expression signature analysis. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 5747-5752.	7.1	7
139	RUNX2/CBFB modulates the response to MEK inhibitors through activation of receptor tyrosine kinases in KRAS-mutant colorectal cancer. Translational Oncology, 2020, 13, 201-211.	3.7	7
140	Androgen modulation of XBP1 is functionally driving part of the AR transcriptional program. Endocrine-Related Cancer, 2020, 27, 67-79.	3.1	7
141	Approximating multivariate posterior distribution functions from Monte Carlo samples for sequential Bayesian inference. PLoS ONE, 2020, 15, e0230101.	2.5	5
142	Heterofusion: Fusing genomics data of different measurement scales. Journal of Chemometrics, 2021, 35, e3200.	1.3	5
143	Genome-wide epigenetic profiling of breast cancer tumors treated with aromatase inhibitors. Genomics Data, 2014, 2, 195-198.	1.3	4
144	Differential Survival and Therapy Benefit of Patients with Breast Cancer Are Characterized by Distinct Epithelial and Immune Cell Microenvironments. Clinical Cancer Research, 2022, 28, 960-971.	7.0	4

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145	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
146	Generalized simultaneous component analysis of binary and quantitative data. <i>Journal of Chemometrics</i> , 2021, 35, e3312.	1.3	3
147	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
148	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
149	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