

Robert Clarke

List of Publications by Year in descending order

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Version: 2024-02-01

361
papers

22,611
citations

15504

65
h-index

9861

141
g-index

380
all docs

380
docs citations

380
times ranked

34222
citing authors

#	ARTICLE	IF	CITATIONS
1	Comparative assessment and novel strategy on methods for imputing proteomics data. Scientific Reports, 2022, 12, 1067.	3.3	8
2	swCAM: estimation of subtype-specific expressions in individual samples with unsupervised sample-wise deconvolution. Bioinformatics, 2022, 38, 1403-1410.	4.1	5
3	COT: an efficient and accurate method for detecting marker genes among many subtypes. Bioinformatics Advances, 2022, 2, .	2.4	5
4	IntAPT: integrated assembly of phenotype-specific transcripts from multiple RNA-seq profiles. Bioinformatics, 2021, 37, 650-658.	4.1	1
5	Experimental models of endocrine responsive breast cancer: strengths, limitations, and use. , 2021, 4, 762-783.		8
6	ChIP-BIT2: a software tool to detect weak binding events using a Bayesian integration approach. BMC Bioinformatics, 2021, 22, 193.	2.6	0
7	Inhibition of Antiestrogen-Promoted Pro-Survival Autophagy and Tamoxifen Resistance in Breast Cancer through Vitamin D Receptor. Nutrients, 2021, 13, 1715.	4.1	14
8	ChIP-GSM: Inferring active transcription factor modules to predict functional regulatory elements. PLoS Computational Biology, 2021, 17, e1009203.	3.2	2
9	Data-driven detection of subtype-specific differentially expressed genes. Scientific Reports, 2021, 11, 332.	3.3	9
10	Identifying intracellular signaling modules and exploring pathways associated with breast cancer recurrence. Scientific Reports, 2021, 11, 385.	3.3	6
11	Biomedical image characterization and radiogenomics. , 2020, , 585-613.		1
12	Î² kinase-Î¼-mediated phosphorylation triggers IRF-1 degradation in breast cancer cells. Neoplasia, 2020, 22, 459-469.	5.3	8
13	A systems biology approach to discovering pathway signaling dysregulation in metastasis. Cancer and Metastasis Reviews, 2020, 39, 903-918.	5.9	11
14	Radiogenomic signatures reveal multiscale intratumour heterogeneity associated with biological functions and survival in breast cancer. Nature Communications, 2020, 11, 4861.	12.8	57
15	Preface. Cancer and Metastasis Reviews, 2020, 39, 579-579.	5.9	0
16	BICORN: An R package for integrative inference of de novo cis-regulatory modules. Scientific Reports, 2020, 10, 7960.	3.3	2
17	RNA interference screening methods to identify proliferation determinants and mechanisms of resistance to immune attack. Methods in Enzymology, 2020, 636, 299-322.	1.0	3
18	debCAM: a bioconductor R package for fully unsupervised deconvolution of complex tissues. Bioinformatics, 2020, 36, 3927-3929.	4.1	14

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19	Maternal obesity increases offspring's mammary cancer recurrence and impairs tumor immune response. <i>Endocrine-Related Cancer</i> , 2020, 27, 469-482.	3.1	10
20	Glutamine Metabolism Drives Growth in Advanced Hormone Receptor Positive Breast Cancer. <i>Frontiers in Oncology</i> , 2019, 9, 686.	2.8	41
21	Poly-ADP-Ribosylation of Estrogen Receptor-Alpha by PARP1 Mediates Antiestrogen Resistance in Human Breast Cancer Cells. <i>Cancers</i> , 2019, 11, 43.	3.7	9
22	Role of Protein Translation in Unfolded Protein Response. <i>Cancer Drug Discovery and Development</i> , 2019, , 109-120.	0.4	0
23	Estrogen-Induced Apoptosis in Breast Cancers Is Phenocopied by Blocking Dephosphorylation of Eukaryotic Initiation Factor 2 Alpha (eIF2 α) Protein. <i>Molecular Cancer Research</i> , 2019, 17, 918-928.	3.4	15
24	Systems biology: perspectives on multiscale modeling in research on endocrine-related cancers. <i>Endocrine-Related Cancer</i> , 2019, 26, R345-R368.	3.1	14
25	Introduction: The Unfolded Protein Response. <i>Cancer Drug Discovery and Development</i> , 2019, , 1-15.	0.4	0
26	Roles of Spliced and Unspliced XBP1 in Breast Cancer. <i>Cancer Drug Discovery and Development</i> , 2019, , 121-132.	0.4	0
27	The Unfolded Protein Response as an Integrator of Response to Endocrine Therapy in Estrogen Receptor Positive Breast Cancer. <i>Cancer Drug Discovery and Development</i> , 2019, , 163-180.	0.4	0
28	Effects of Jaeumkanghwa-tang on tamoxifen responsiveness in preclinical ER+ breast cancer model. <i>Endocrine-Related Cancer</i> , 2019, 26, 339-353.	3.1	2
29	CRNET: an efficient sampling approach to infer functional regulatory networks by integrating large-scale ChIP-seq and time-course RNA-seq data. <i>Bioinformatics</i> , 2018, 34, 1733-1740.	4.1	20
30	Sparselso: a novel Bayesian approach to identify alternatively spliced isoforms from RNA-seq data. <i>Bioinformatics</i> , 2018, 34, 56-63.	4.1	7
31	Autophagy and unfolded protein response (UPR) regulate mammary gland involution by restraining apoptosis-driven irreversible changes. <i>Cell Death Discovery</i> , 2018, 4, 40.	4.7	30
32	Dielectrophoretic properties distinguish responses to estrogen and fulvestrant in breast cancer cells. <i>Sensors and Actuators B: Chemical</i> , 2018, 277, 186-194.	7.8	3
33	Lifetime Genistein Intake Increases the Response of Mammary Tumors to Tamoxifen in Rats. <i>Clinical Cancer Research</i> , 2017, 23, 814-824.	7.0	45
34	Breast cancer cell obatoclax response characterization using passivated electrode insulator-based dielectrophoresis. <i>Electrophoresis</i> , 2017, 38, 1988-1995.	2.4	23
35	Introduction: Cancer Gene Networks. <i>Methods in Molecular Biology</i> , 2017, 1513, 1-9.	0.9	7
36	DM-BLD: differential methylation detection using a hierarchical Bayesian model exploiting local dependency. <i>Bioinformatics</i> , 2017, 33, 161-168.	4.1	17

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37	Effects of In Utero Exposure to Ethinyl Estradiol on Tamoxifen Resistance and Breast Cancer Recurrence in a Preclinical Model. <i>Journal of the National Cancer Institute</i> , 2017, 109, djw188.	6.3	28
38	PSSV: a novel pattern-based probabilistic approach for somatic structural variation identification. <i>Bioinformatics</i> , 2017, 33, 177-183.	4.1	5
39	EGR1 regulates cellular metabolism and survival in endocrine resistant breast cancer. <i>Oncotarget</i> , 2017, 8, 96865-96884.	1.8	29
40	Autophagy, Inflammation, and Breast Cancer Risk. , 2017, , 359-372.		0
41	CyNetSVM: A Cytoscape App for Cancer Biomarker Identification Using Network Constrained Support Vector Machines. <i>PLoS ONE</i> , 2017, 12, e0170482.	2.5	5
42	RNA Interference Screening to Identify Proliferation Determinants in Breast Cancer Cells. <i>Bio-protocol</i> , 2017, 7, .	0.4	0
43	Abstract P3-04-12: Both spliced and unspliced XBP1 regulates breast cancer cell fate response to antiestrogen via NFkappaB signaling. , 2017, , .		0
44	Abstract P4-10-01: Estrogen induced apoptosis can be mimicked by targeting unfolded protein response. , 2017, , .		0
45	Abstract P4-10-02: Transmembrane protein 33 (TMEM33) induces apoptosis via UPR signaling and autophagy in breast cancer cells. , 2017, , .		0
46	Abstract 2164: BLID is a novel drug-inducible apoptotic molecule: Identification of an integrative mechanism of chemosensitivity in breast cancer cells. , 2017, , .		0
47	Abstract 2604: The Georgetown Database of Cancer (G-DOC): A web-based data sharing platform for precision medicine. , 2017, , .		2
48	Abstract 2329: TMEM33 induces apoptosis via UPR signaling and autophagy in breast cancer cells. , 2017, , .		0
49	Associations of Epicardial, Abdominal, and Overall Adiposity With Atrial Fibrillation. <i>Circulation: Arrhythmia and Electrophysiology</i> , 2016, 9, .	4.8	141
50	Mathematical modelling of transcriptional heterogeneity identifies novel markers and subpopulations in complex tissues. <i>Scientific Reports</i> , 2016, 6, 18909.	3.3	57
51	Social isolation induces autophagy in the mouse mammary gland: link to increased mammary cancer risk. <i>Endocrine-Related Cancer</i> , 2016, 23, 839-856.	3.1	17
52	Endoplasmic Reticulum Stress Protein GRP78 Modulates Lipid Metabolism to Control Drug Sensitivity and Antitumor Immunity in Breast Cancer. <i>Cancer Research</i> , 2016, 76, 5657-5670.	0.9	91
53	Biologically inspired survival analysis based on integrating gene expression as mediator with genomic variants. <i>Computers in Biology and Medicine</i> , 2016, 77, 231-239.	7.0	1
54	G-DOC Plus “an integrative bioinformatics platform for precision medicine. <i>BMC Bioinformatics</i> , 2016, 17, 193.	2.6	39

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55	Guidelines for the use and interpretation of assays for monitoring autophagy (3rd edition). <i>Autophagy</i> , 2016, 12, 1-222.	9.1	4,701
56	ChIP-BIT: Bayesian inference of target genes using a novel joint probabilistic model of ChIP-seq profiles. <i>Nucleic Acids Research</i> , 2016, 44, e65-e65.	14.5	15
57	Linking autophagy with inflammation through IRF1 signaling in ER+ breast cancer. <i>Molecular and Cellular Oncology</i> , 2016, 3, e1023928.	0.7	4
58	Acquisition of estrogen independence induces TOB1-related mechanisms supporting breast cancer cell proliferation. <i>Oncogene</i> , 2016, 35, 1643-1656.	5.9	29
59	Fat saturation has no effect on glycaemic or satiety response to a high GI carbohydrate meal in healthy women. <i>Proceedings of the Nutrition Society</i> , 2015, 74, .	1.0	0
60	Dynamic Modeling of the Interaction Between Autophagy and Apoptosis in Mammalian Cells. <i>CPT: Pharmacometrics and Systems Pharmacology</i> , 2015, 4, 263-272.	2.5	67
61	BACOM2.0 facilitates absolute normalization and quantification of somatic copy number alterations in heterogeneous tumor. <i>Scientific Reports</i> , 2015, 5, 13955.	3.3	6
62	S88â€¦The viral mimic polyinosinic: polycytidylic acid (Poly I:C) induces TRPA1 channel hyper-responsiveness in an adult human stem cell-derived sensory neuronal model. <i>Thorax</i> , 2015, 70, A50.2-A51.	5.6	1
63	BMRF-MI: integrative identification of protein interaction network by modeling the gene dependency. <i>BMC Genomics</i> , 2015, 16, S10.	2.8	4
64	Overcoming cancer resistance. <i>Future Medicinal Chemistry</i> , 2015, 7, 1471-1471.	2.3	0
65	Blockage of Lysosomal Degradation Is Detrimental to Cancer Cell Survival. , 2015, , 121-133.		2
66	Application of Metabolomics in Drug Resistant Breast Cancer Research. <i>Metabolites</i> , 2015, 5, 100-118.	2.9	50
67	Unfolding the Role of Stress Response Signaling in Endocrine Resistant Breast Cancers. <i>Frontiers in Oncology</i> , 2015, 5, 140.	2.8	27
68	BMRF-Net: a software tool for identification of protein interaction subnetworks by a bagging Markov random field-based method. <i>Bioinformatics</i> , 2015, 31, 2412-2414.	4.1	30
69	Comparison of tamoxifen and letrozole response in mammary preneoplasia of ER and aromatase overexpressing mice defines an immune-associated gene signature linked to tamoxifen resistance. <i>Carcinogenesis</i> , 2015, 36, 122-132.	2.8	16
70	Interferon Regulatory Factor-1 Signaling Regulates the Switch between Autophagy and Apoptosis to Determine Breast Cancer Cell Fate. <i>Cancer Research</i> , 2015, 75, 1046-1055.	0.9	31
71	Inhibition of BET proteins impairs estrogen-mediated growth and transcription in breast cancers by pausing RNA polymerase advancement. <i>Breast Cancer Research and Treatment</i> , 2015, 150, 265-278.	2.5	30
72	Recommendations concerning the new U.S. National Institutes of Health initiative to balance the sex of cells and animals in preclinical research. <i>FASEB Journal</i> , 2015, 29, 1646-1652.	0.5	63

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73	Molecular mechanisms of tamoxifen-associated endometrial cancer (Review). <i>Oncology Letters</i> , 2015, 9, 1495-1501.	1.8	102
74	The Changing Spectrum of Biomedical and Clinical Research. , 2015, , 137-148.		0
75	Endocrine resistance in breast cancer – An overview and update. <i>Molecular and Cellular Endocrinology</i> , 2015, 418, 220-234.	3.2	280
76	TMEM33: a new stress-inducible endoplasmic reticulum transmembrane protein and modulator of the unfolded protein response signaling. <i>Breast Cancer Research and Treatment</i> , 2015, 153, 285-297.	2.5	26
77	Role of GRP78 in promoting therapeutic-resistant breast cancer. <i>Future Medicinal Chemistry</i> , 2015, 7, 1529-1534.	2.3	35
78	UNDO: a Bioconductor R package for unsupervised deconvolution of mixed gene expressions in tumor samples. <i>Bioinformatics</i> , 2015, 31, 137-139.	4.1	60
79	ER ² decreases breast cancer cell survival by regulating the IRE1/XBP-1 pathway. <i>Oncogene</i> , 2015, 34, 4130-4141.	5.9	45
80	NF- κ B Signaling Is Required for XBP1 (Unspliced and Spliced)-Mediated Effects on Antiestrogen Responsiveness and Cell Fate Decisions in Breast Cancer. <i>Molecular and Cellular Biology</i> , 2015, 35, 379-390.	2.3	80
81	KDDN: an open-source Cytoscape app for constructing differential dependency networks with significant rewiring. <i>Bioinformatics</i> , 2015, 31, 287-289.	4.1	17
82	Autophagy inhibitor 3-methyladenine potentiates apoptosis induced by dietary tocotrienols in breast cancer cells. <i>European Journal of Nutrition</i> , 2015, 54, 265-272.	3.9	51
83	A new class of small molecule estrogen receptor-alpha antagonists that overcome anti-estrogen resistance. <i>Oncotarget</i> , 2015, 6, 40388-40404.	1.8	4
84	Integrating Proteotoxic Stress Response Pathways for Induction of Cell Death in Cancer Cells: Molecular Mechanisms and Therapeutic Opportunities. , 2015, , 183-202.		0
85	Blockage of Lysosomal Degradation is Detrimental to Cancer Cell Survival. , 2014, , 269-281.		0
86	Integrative Analysis Workflow for Untargeted Metabolomics in Translational Research. <i>Metabolomics: Open Access</i> , 2014, 04, .	0.1	3
87	Aromatase inhibitor plus ovarian suppression as adjuvant therapy in premenopausal women with breast cancer. <i>Cancer Biology and Therapy</i> , 2014, 15, 1586-1587.	3.4	15
88	BSSV: Bayesian based somatic structural variation identification with whole genome DNA-seq data. , 2014, 2014, 3937-40.		2
89	BADGE: A novel Bayesian model for accurate abundance quantification and differential analysis of RNA-Seq data. <i>BMC Bioinformatics</i> , 2014, 15, S6.	2.6	11
90	Small-Molecule –BRCA1-Mimetics– Are Antagonists of Estrogen Receptor- α . <i>Molecular Endocrinology</i> , 2014, 28, 1971-1986.	3.7	4

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91	AISAIC: a software suite for accurate identification of significant aberrations in cancers. <i>Bioinformatics</i> , 2014, 30, 431-433.	4.1	10
92	Integration of Network Biology and Imaging to Study Cancer Phenotypes and Responses. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2014, 11, 1009-1019.	3.0	15
93	Robust identification of transcriptional regulatory networks using a Gibbs sampler on outlier sum statistic. <i>Bioinformatics</i> , 2014, 30, 2242-2242.	4.1	0
94	MYC regulates the unfolded protein response and glucose and glutamine uptake in endocrine resistant breast cancer. <i>Molecular Cancer</i> , 2014, 13, 239.	19.2	74
95	When is a vesicle not just a vesicle: mitochondrial spheroids and mitochondrial autophagosomes. <i>Cell and Bioscience</i> , 2014, 4, 66.	4.8	7
96	VAV3 mediates resistance to breast cancer endocrine therapy. <i>Breast Cancer Research</i> , 2014, 16, R53.	5.0	28
97	Soluble E-cadherin activates HER and IAP family members in HER2+ and TNBC human breast cancers. <i>Molecular Carcinogenesis</i> , 2014, 53, 893-906.	2.7	28
98	Chloroquine Inhibits Autophagy to Potentiate Antiestrogen Responsiveness in ER+ Breast Cancer. <i>Clinical Cancer Research</i> , 2014, 20, 3222-3232.	7.0	176
99	A Markov random field-based Bayesian model to identify genes with differential methylation. , 2014, , .		0
100	Knowledge-fused differential dependency network models for detecting significant rewiring in biological networks. <i>BMC Systems Biology</i> , 2014, 8, 87.	3.0	26
101	Mitochondria directly donate their membrane to form autophagosomes during a novel mechanism of parkin-associated mitophagy. <i>Cell and Bioscience</i> , 2014, 4, 16.	4.8	54
102	Inhibiting glucose-regulated protein 78 modulates lipid metabolism through controlling stearyl-CoA desaturase 1. <i>Cancer & Metabolism</i> , 2014, 2, .	5.0	0
103	Glutamine metabolism and the unfolded protein response in MYC-driven breast cancer. <i>Cancer & Metabolism</i> , 2014, 2, .	5.0	1
104	Enhancing Reproducibility in Cancer Drug Screening: How Do We Move Forward?. <i>Cancer Research</i> , 2014, 74, 4016-4023.	0.9	90
105	Knockdown of estrogen receptor α induces autophagy and inhibits antiestrogen-mediated unfolded protein response activation, promoting ROS-induced breast cancer cell death. <i>FASEB Journal</i> , 2014, 28, 3891-3905.	0.5	78
106	Mathematical models of the transitions between endocrine therapy responsive and resistant states in breast cancer. <i>Journal of the Royal Society Interface</i> , 2014, 11, 20140206.	3.4	30
107	Unsupervised Deconvolution of Dynamic Imaging Reveals Intratumor Vascular Heterogeneity and Repopulation Dynamics. <i>PLoS ONE</i> , 2014, 9, e112143.	2.5	15
108	Do conditionally reprogrammed cell cultures represent the tumors they have been isolated from with high fidelity?. <i>Journal of Clinical Oncology</i> , 2014, 32, e22140-e22140.	1.6	0

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109	Estrogen receptor- α signaling and localization regulates autophagy and unfolded protein response activation in ER+ breast cancer. <i>Receptors & Clinical Investigation</i> , 2014, 1, .	0.9	9
110	Monoclonal Antibody against the Ectodomain of E-Cadherin (DECMA-1) Suppresses Breast Carcinogenesis: Involvement of the HER/PI3K/Akt/mTOR and IAP Pathways. <i>Clinical Cancer Research</i> , 2013, 19, 3234-3246.	7.0	42
111	mAPC-GibbsOS: an integrated approach for robust identification of gene regulatory networks. <i>BMC Systems Biology</i> , 2013, 7, S4.	3.0	8
112	Reconstruction of Transcriptional Regulatory Networks by Stability-Based Network Component Analysis. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2013, 10, 1347-1358.	3.0	12
113	Modelling the effect of GRP78 on anti-oestrogen sensitivity and resistance in breast cancer. <i>Interface Focus</i> , 2013, 3, 20130012.	3.0	26
114	Modeling the estrogen receptor to growth factor receptor signaling switch in human breast cancer cells. <i>FEBS Letters</i> , 2013, 587, 3327-3334.	2.8	24
115	Identifying Early Events of Gene Expression in Breast Cancer with Systems Biology Phylogenetics. <i>Cytogenetic and Genome Research</i> , 2013, 139, 206-214.	1.1	13
116	Targeting GRP78 and antiestrogen resistance in breast cancer. <i>Future Medicinal Chemistry</i> , 2013, 5, 1047-1057.	2.3	26
117	Module-based breast cancer classification. <i>International Journal of Data Mining and Bioinformatics</i> , 2013, 7, 284.	0.1	16
118	Reconstructing transcriptional regulatory networks by probabilistic network component analysis. , 2013, , .		1
119	Advancing Translational Research through Facility Design in Non-AMC Hospitals. <i>Herd</i> , 2013, 6, 126-137.	1.5	3
120	Identifying protein interaction subnetworks by a bagging Markov random field-based method. <i>Nucleic Acids Research</i> , 2013, 41, e42-e42.	14.5	34
121	GX15-070 (Obatoclox) Induces Apoptosis and Inhibits Cathepsin D- and L α -Mediated Autophagosomal Lysis in Antiestrogen-Resistant Breast Cancer Cells. <i>Molecular Cancer Therapeutics</i> , 2013, 12, 448-459.	4.1	49
122	In Silico Discovery of Mitosis Regulation Networks Associated with Early Distant Metastases in Estrogen Receptor Positive Breast Cancers. <i>Cancer Informatics</i> , 2013, 12, CIN.S10329.	1.9	15
123	A novel statistical approach to identify co-regulatory gene modules. , 2013, , .		2
124	Genomic and network analysis to study the origin of ovarian cancer. <i>Systems Biomedicine (Austin, Tex)</i> Tj ETQq0 0 0,rgBT /Overlock 10	0.7	1
125	ANTI-HORMONE DRUG RESISTANCE. , 2013, , 295-323.		0
126	Tyrosine-phosphorylated Caveolin-1 (Tyr-14) Increases Sensitivity to Paclitaxel by Inhibiting BCL2 and BCLxL Proteins via c-Jun N-terminal Kinase (JNK). <i>Journal of Biological Chemistry</i> , 2012, 287, 17682-17692.	3.4	58

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127	Effect of Berry Extracts and Bioactive Compounds on Fulvestrant (ICI 182,780) Sensitive and Resistant Cell Lines. <i>International Journal of Breast Cancer</i> , 2012, 2012, 1-11.	1.2	7
128	Interaction of dietary polyphenols with molecular signaling pathways of antiestrogen resistance: possible role in breast cancer recurrence. <i>Hormone Molecular Biology and Clinical Investigation</i> , 2012, 9, 127-41.	0.7	9
129	Glucose-Regulated Protein 78 Controls Cross-talk between Apoptosis and Autophagy to Determine Antiestrogen Responsiveness. <i>Cancer Research</i> , 2012, 72, 3337-3349.	0.9	133
130	Antiestrogen resistance and the application of systems biology. <i>Drug Discovery Today Disease Mechanisms</i> , 2012, 9, e11-e17.	0.8	3
131	Sampling-Based Subnetwork Identification from Microarray Data and Protein-Protein Interaction Network. , 2012, , .		0
132	Accurate identification of significant aberrations in contaminated cancer genome. , 2012, , .		0
133	Genome-wide identification of significant aberrations in cancer genome. <i>BMC Genomics</i> , 2012, 13, 342.	2.8	34
134	Heat shock 70 kDa protein 5/glucose-regulated protein 78 α -AMP α ing up autophagy. <i>Autophagy</i> , 2012, 8, 1827-1829.	9.1	27
135	Guidelines for the use and interpretation of assays for monitoring autophagy. <i>Autophagy</i> , 2012, 8, 445-544.	9.1	3,122
136	Influence of Berry Polyphenols on Receptor Signaling and Cell-Death Pathways: Implications for Breast Cancer Prevention. <i>Journal of Agricultural and Food Chemistry</i> , 2012, 60, 5693-5708.	5.2	106
137	Robust identification of transcriptional regulatory networks using a Gibbs sampler on outlier sum statistic. <i>Bioinformatics</i> , 2012, 28, 1990-1997.	4.1	8
138	Endoplasmic Reticulum Stress, the Unfolded Protein Response, Autophagy, and the Integrated Regulation of Breast Cancer Cell Fate. <i>Cancer Research</i> , 2012, 72, 1321-1331.	0.9	183
139	Regulatory component analysis: A semi-blind extraction approach to infer gene regulatory networks with imperfect biological knowledge. <i>Signal Processing</i> , 2012, 92, 1902-1915.	3.7	4
140	Gamma-tocotrienol induced apoptosis is associated with unfolded protein response in human breast cancer cells. <i>Journal of Nutritional Biochemistry</i> , 2012, 23, 93-100.	4.2	57
141	Vitamin E succinate inhibits survivin and induces apoptosis in pancreatic cancer cells. <i>Genes and Nutrition</i> , 2012, 7, 83-89.	2.5	19
142	Reconstruction of Transcription Regulatory Networks by Stability-Based Network Component Analysis. <i>Lecture Notes in Computer Science</i> , 2012, , 36-47.	1.3	0
143	G-DOC: A Systems Medicine Platform for Personalized Oncology. <i>Neoplasia</i> , 2011, 13, 771-783.	5.3	58
144	G-CODE: enabling systems medicine through innovative informatics. <i>Genome Biology</i> , 2011, 12, .	9.6	4

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145	Cannibalism, cell survival, and endocrine resistance in breast cancer. <i>Breast Cancer Research</i> , 2011, 13, 311.	5.0	9
146	Dynamic modelling of oestrogen signalling and cell fate in breast cancer cells. <i>Nature Reviews Cancer</i> , 2011, 11, 523-532.	28.4	179
147	Autophagy and endocrine resistance in breast cancer. <i>Expert Review of Anticancer Therapy</i> , 2011, 11, 1283-1294.	2.4	137
148	Identifying cancer biomarkers by network-constrained support vector machines. <i>BMC Systems Biology</i> , 2011, 5, 161.	3.0	76
149	Motif-guided sparse decomposition of gene expression data for regulatory module identification. <i>BMC Bioinformatics</i> , 2011, 12, 82.	2.6	13
150	NTP&CERHR expert panel report on the developmental toxicity of soy infant formula. <i>Birth Defects Research Part B: Developmental and Reproductive Toxicology</i> , 2011, 92, 421-468.	1.4	81
151	DDN: a caBIG&A analytical tool for differential network analysis. <i>Bioinformatics</i> , 2011, 27, 1036-1038.	4.1	39
152	GIST: A Gibbs sampler to identify intracellular signal transduction pathways. , 2011, 2011, 2434-7.		1
153	Therapeutically activating RB: reestablishing cell cycle control in endocrine therapy-resistant breast cancer. <i>Endocrine-Related Cancer</i> , 2011, 18, 333-345.	3.1	256
154	Overexpression of the Dominant-Negative Form of Interferon Regulatory Factor 1 in Oligodendrocytes Protects against Experimental Autoimmune Encephalomyelitis. <i>Journal of Neuroscience</i> , 2011, 31, 8329-8341.	3.6	26
155	Endoplasmic reticulum stress, the unfolded protein response, and gene network modeling in antiestrogen resistant breast cancer. <i>Hormone Molecular Biology and Clinical Investigation</i> , 2011, 5, 35-44.	0.7	49
156	The Role of Interferon Regulatory Factor-1 (IRF1) in Overcoming Antiestrogen Resistance in the Treatment of Breast Cancer. <i>International Journal of Breast Cancer</i> , 2011, 2011, 1-9.	1.2	36
157	PUGSVM: a caBIGTM analytical tool for multiclass gene selection and predictive classification. <i>Bioinformatics</i> , 2011, 27, 736-738.	4.1	19
158	BCL2 and CASP8 regulation by NF&CkB differentially affect mitochondrial function and cell fate in antiestrogen&Cnsensitive and &Cresistant breast cancer cells. <i>FASEB Journal</i> , 2010, 24, 2040-2055.	0.5	76
159	Frequent loss of heterozygosity at the interferon regulatory factor-1 gene locus in breast cancer. <i>Breast Cancer Research and Treatment</i> , 2010, 121, 227-231.	2.5	33
160	Knowledge-guided gene ranking by coordinative component analysis. <i>BMC Bioinformatics</i> , 2010, 11, 162.	2.6	8
161	IFN&I3 Restores Breast Cancer Sensitivity to Fulvestrant by Regulating STAT1, IFN Regulatory Factor 1, NF-&I3B, BCL2 Family Members, and Signaling to Caspase-Dependent Apoptosis. <i>Molecular Cancer Therapeutics</i> , 2010, 9, 1274-1285.	4.1	66
162	Changes in mammary caveolin-1 signaling pathways are associated with breast cancer risk in rats exposed to estradiol in utero or during prepuberty. <i>Hormone Molecular Biology and Clinical Investigation</i> , 2010, 2, 227-234.	0.7	3

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163	Multilevel support vector regression analysis to identify condition-specific regulatory networks. <i>Bioinformatics</i> , 2010, 26, 1416-1422.	4.1	20
164	Module-based biomarker discovery in breast cancer. , 2010, , .		2
165	The Proapoptotic Molecule BLID Interacts with Bcl-XL and Its Downregulation in Breast Cancer Correlates with Poor Disease-Free and Overall Survival. <i>Clinical Cancer Research</i> , 2010, 16, 2939-2948.	7.0	18
166	Orphan nuclear receptors in breast cancer pathogenesis and therapeutic response. <i>Endocrine-Related Cancer</i> , 2010, 17, R213-R231.	3.1	43
167	DBC-1 mediates endocrine resistant breast cancer cell survival. <i>Cell Cycle</i> , 2010, 9, 1218-1219.	2.6	14
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