

Robert Clarke

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

338 papers	19,300 citations	61 h-index	132 g-index
380 ext. papers	21,237 ext. citations	6 avg, IF	6.15 L-index

#	Paper	IF	Citations
338	Comparative assessment and novel strategy on methods for imputing proteomics data.. <i>Scientific Reports</i> , 2022 , 12, 1067	4.9	2
337	CHIP-BIT2: a software tool to detect weak binding events using a Bayesian integration approach. <i>BMC Bioinformatics</i> , 2021 , 22, 193	3.6	
336	Inhibition of Antiestrogen-Promoted Pro-Survival Autophagy and Tamoxifen Resistance in Breast Cancer through Vitamin D Receptor. <i>Nutrients</i> , 2021 , 13,	6.7	3
335	CHIP-GSM: Inferring active transcription factor modules to predict functional regulatory elements. <i>PLoS Computational Biology</i> , 2021 , 17, e1009203	5	0
334	IntAPT: integrated assembly of phenotype-specific transcripts from multiple RNA-seq profiles. <i>Bioinformatics</i> , 2021 , 37, 650-658	7.2	0
333	Experimental models of endocrine responsive breast cancer: strengths, limitations, and use. <i>Cancer Drug Resistance (Alhambra, Calif)</i> , 2021 , 4, 762-783	4.5	2
332	Data-driven detection of subtype-specific differentially expressed genes. <i>Scientific Reports</i> , 2021 , 11, 332	4.9	1
331	Identifying intracellular signaling modules and exploring pathways associated with breast cancer recurrence. <i>Scientific Reports</i> , 2021 , 11, 385	4.9	1
330	BICORN: An R package for integrative inference of de novo cis-regulatory modules. <i>Scientific Reports</i> , 2020 , 10, 7960	4.9	1
329	RNA interference screening methods to identify proliferation determinants and mechanisms of resistance to immune attack. <i>Methods in Enzymology</i> , 2020 , 636, 299-322	1.7	1
328	Maternal obesity increases offspring's mammary cancer recurrence and impairs tumor immune response. <i>Endocrine-Related Cancer</i> , 2020 , 27, 469-482	5.7	5
327	Biomedical image characterization and radiogenomics 2020 , 585-613		0
326	IB kinase-mediated phosphorylation triggers IRF-1 degradation in breast cancer cells. <i>Neoplasia</i> , 2020 , 22, 459-469	6.4	1
325	A systems biology approach to discovering pathway signaling dysregulation in metastasis. <i>Cancer and Metastasis Reviews</i> , 2020 , 39, 903-918	9.6	3
324	Radiogenomic signatures reveal multiscale intratumour heterogeneity associated with biological functions and survival in breast cancer. <i>Nature Communications</i> , 2020 , 11, 4861	17.4	18
323	debCAM: a bioconductor R package for fully unsupervised deconvolution of complex tissues. <i>Bioinformatics</i> , 2020 , 36, 3927-3929	7.2	5
322	Poly-ADP-Ribosylation of Estrogen Receptor-Alpha by PARP1 Mediates Antiestrogen Resistance in Human Breast Cancer Cells. <i>Cancers</i> , 2019 , 11,	6.6	5

3 ²¹	Role of Protein Translation in Unfolded Protein Response. <i>Cancer Drug Discovery and Development</i> , 2019 , 109-120	0.3	
3 ²⁰	Glutamine Metabolism Drives Growth in Advanced Hormone Receptor Positive Breast Cancer. <i>Frontiers in Oncology</i> , 2019 , 9, 686	5.3	21
3 ¹⁹	Systems biology: perspectives on multiscale modeling in research on endocrine-related cancers. <i>Endocrine-Related Cancer</i> , 2019 , 26, R345-R368	5.7	9
3 ¹⁸	Introduction: The Unfolded Protein Response. <i>Cancer Drug Discovery and Development</i> , 2019 , 1-15	0.3	
3 ¹⁷	Roles of Spliced and Unspliced XBP1 in Breast Cancer. <i>Cancer Drug Discovery and Development</i> , 2019 , 121-132	0.3	
3 ¹⁶	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	0.3	
3 ¹⁵	Effects of Jaeumkanghwa-tang on tamoxifen responsiveness in preclinical ER+ breast cancer model. <i>Endocrine-Related Cancer</i> , 2019 , 26, 339-353	5.7	1
3 ¹⁴	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	6.6	11
3 ¹³	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	7.2	8
3 ¹²	Sparselso: a novel Bayesian approach to identify alternatively spliced isoforms from RNA-seq data. <i>Bioinformatics</i> , 2018 , 34, 56-63	7.2	6
3 ¹¹	Autophagy and unfolded protein response (UPR) regulate mammary gland involution by restraining apoptosis-driven irreversible changes. <i>Cell Death Discovery</i> , 2018 , 4, 40	6.9	17
3 ¹⁰	Dielectrophoretic properties distinguish responses to estrogen and fulvestrant in breast cancer cells. <i>Sensors and Actuators B: Chemical</i> , 2018 , 277, 186-194	8.5	2
3 ⁰⁹	Lifetime Genistein Intake Increases the Response of Mammary Tumors to Tamoxifen in Rats. <i>Clinical Cancer Research</i> , 2017 , 23, 814-824	12.9	35
3 ⁰⁸	Breast cancer cell obatoclax response characterization using passivated-electrode insulator-based dielectrophoresis. <i>Electrophoresis</i> , 2017 , 38, 1988-1995	3.6	21
3 ⁰⁷	Introduction: Cancer Gene Networks. <i>Methods in Molecular Biology</i> , 2017 , 1513, 1-9	1.4	2
3 ⁰⁶	DM-BLD: differential methylation detection using a hierarchical Bayesian model exploiting local dependency. <i>Bioinformatics</i> , 2017 , 33, 161-168	7.2	16
3 ⁰⁵	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,	9.7	18
3 ⁰⁴	PSSV: a novel pattern-based probabilistic approach for somatic structural variation identification. <i>Bioinformatics</i> , 2017 , 33, 177-183	7.2	2

303	EGR1 regulates cellular metabolism and survival in endocrine resistant breast cancer. <i>Oncotarget</i> , 2017 , 8, 96865-96884	3.3	23
302	Autophagy, Inflammation, and Breast Cancer Risk 2017 , 359-372		
301	CyNetSVM: A Cytoscape App for Cancer Biomarker Identification Using Network Constrained Support Vector Machines. <i>PLoS ONE</i> , 2017 , 12, e0170482	3.7	3
300	Linking autophagy with inflammation through IRF1 signaling in ER+ breast cancer. <i>Molecular and Cellular Oncology</i> , 2016 , 3, e1023928	1.2	3
299	Acquisition of estrogen independence induces TOB1-related mechanisms supporting breast cancer cell proliferation. <i>Oncogene</i> , 2016 , 35, 1643-56	9.2	22
298	Biologically inspired survival analysis based on integrating gene expression as mediator with genomic variants. <i>Computers in Biology and Medicine</i> , 2016 , 77, 231-9	7	1
297	G-DOC Plus - an integrative bioinformatics platform for precision medicine. <i>BMC Bioinformatics</i> , 2016 , 17, 193	3.6	29
296	Guidelines for the use and interpretation of assays for monitoring autophagy (3rd edition). <i>Autophagy</i> , 2016 , 12, 1-222	10.2	3838
295	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	20.1	6
294	Associations of Epicardial, Abdominal, and Overall Adiposity With Atrial Fibrillation. <i>Circulation: Arrhythmia and Electrophysiology</i> , 2016 , 9,	6.4	75
293	Mathematical modelling of transcriptional heterogeneity identifies novel markers and subpopulations in complex tissues. <i>Scientific Reports</i> , 2016 , 6, 18909	4.9	39
292	Social isolation induces autophagy in the mouse mammary gland: link to increased mammary cancer risk. <i>Endocrine-Related Cancer</i> , 2016 , 23, 839-56	5.7	12
291	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	10.1	74
290	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, 265-78	4.4	29
289	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, 1646-52	0.9	50
288	Molecular mechanisms of tamoxifen-associated endometrial cancer (Review). <i>Oncology Letters</i> , 2015 , 9, 1495-1501	2.6	81
287	The Changing Spectrum of Biomedical and Clinical Research 2015 , 137-148		
286	Endocrine resistance in breast cancer--An overview and update. <i>Molecular and Cellular Endocrinology</i> , 2015 , 418 Pt 3, 220-34	4.4	200

285	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, 285-97	4.4	15
284	Role of GRP78 in promoting therapeutic-resistant breast cancer. <i>Future Medicinal Chemistry</i> , 2015 , 7, 1529-34	4.1	29
283	UNDO: a Bioconductor R package for unsupervised deconvolution of mixed gene expressions in tumor samples. <i>Bioinformatics</i> , 2015 , 31, 137-9	7.2	42
282	ER α decreases breast cancer cell survival by regulating the IRE1/XBP-1 pathway. <i>Oncogene</i> , 2015 , 34, 4130-41	9.2	38
281	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, 379-90	4.8	54
280	KDDN: an open-source Cytoscape app for constructing differential dependency networks with significant rewiring. <i>Bioinformatics</i> , 2015 , 31, 287-9	7.2	16
279	Autophagy inhibitor 3-methyladenine potentiates apoptosis induced by dietary tocotrienols in breast cancer cells. <i>European Journal of Nutrition</i> , 2015 , 54, 265-72	5.2	35
278	Dynamic Modeling of the Interaction Between Autophagy and Apoptosis in Mammalian Cells. <i>CPT: Pharmacometrics and Systems Pharmacology</i> , 2015 , 4, 263-72	4.5	53
277	BACOM2.0 facilitates absolute normalization and quantification of somatic copy number alterations in heterogeneous tumor. <i>Scientific Reports</i> , 2015 , 5, 13955	4.9	5
276	S88 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	7.3	1
275	BMRF-MI: integrative identification of protein interaction network by modeling the gene dependency. <i>BMC Genomics</i> , 2015 , 16 Suppl 7, S10	4.5	3
274	Overcoming cancer resistance. <i>Future Medicinal Chemistry</i> , 2015 , 7, 1471	4.1	
273	Blockage of Lysosomal Degradation Is Detrimental to Cancer Cell Survival: Role of Autophagy Activation 2015 , 121-133		2
272	Application of metabolomics in drug resistant breast cancer research. <i>Metabolites</i> , 2015 , 5, 100-18	5.6	38
271	Unfolding the Role of Stress Response Signaling in Endocrine Resistant Breast Cancers. <i>Frontiers in Oncology</i> , 2015 , 5, 140	5.3	24
270	BMRF-Net: a software tool for identification of protein interaction subnetworks by a bagging Markov random field-based method. <i>Bioinformatics</i> , 2015 , 31, 2412-4	7.2	10
269	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, 122-32	4.6	13
268	Interferon regulatory factor-1 signaling regulates the switch between autophagy and apoptosis to determine breast cancer cell fate. <i>Cancer Research</i> , 2015 , 75, 1046-55	10.1	27

267	A new class of small molecule estrogen receptor-alpha antagonists that overcome anti-estrogen resistance. <i>Oncotarget</i> , 2015 , 6, 40388-404	3.3	2
266	Integrating Proteotoxic Stress Response Pathways for Induction of Cell Death in Cancer Cells: Molecular Mechanisms and Therapeutic Opportunities 2015 , 183-202		
265	Hydroxychloroquine inhibits autophagy to potentiate antiestrogen responsiveness in ER+ breast cancer. <i>Clinical Cancer Research</i> , 2014 , 20, 3222-32	12.9	136
264	Knowledge-fused differential dependency network models for detecting significant rewiring in biological networks. <i>BMC Systems Biology</i> , 2014 , 8, 87	3.5	23
263	Mitochondria directly donate their membrane to form autophagosomes during a novel mechanism of parkin-associated mitophagy. <i>Cell and Bioscience</i> , 2014 , 4, 16	9.8	45
262	Inhibiting glucose-regulated protein 78 modulates lipid metabolism through controlling stearyl-CoA desaturase 1. <i>Cancer & Metabolism</i> , 2014 , 2,	5.4	78
261	Glutamine metabolism and the unfolded protein response in MYC-driven breast cancer. <i>Cancer & Metabolism</i> , 2014 , 2,	5.4	78
260	Enhancing reproducibility in cancer drug screening: how do we move forward?. <i>Cancer Research</i> , 2014 , 74, 4016-23	10.1	64
259	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, 3891-905	0.9	67
258	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	4.1	23
257	Blockage of Lysosomal Degradation is Detrimental to Cancer Cell Survival 2014 , 269-281		
256	Integrative Analysis Workflow for Untargeted Metabolomics in Translational Research. <i>Metabolomics: Open Access</i> , 2014 , 04,		1
255	Aromatase inhibitor plus ovarian suppression as adjuvant therapy in premenopausal women with breast cancer. <i>Cancer Biology and Therapy</i> , 2014 , 15, 1586-7	4.6	13
254	BSSV: Bayesian based somatic structural variation identification with whole genome DNA-seq data. <i>Annual International Conference of the IEEE Engineering in Medicine and Biology Society IEEE Engineering in Medicine and Biology Society Annual International Conference</i> , 2014 , 2014, 3937-40	0.9	1
253	BADGE: a novel Bayesian model for accurate abundance quantification and differential analysis of RNA-Seq data. <i>BMC Bioinformatics</i> , 2014 , 15 Suppl 9, S6	3.6	7
252	Small-molecule "BRCA1-mimetics" are antagonists of estrogen receptor- α <i>Molecular Endocrinology</i> , 2014 , 28, 1971-86		4
251	AISAIC: a software suite for accurate identification of significant aberrations in cancers. <i>Bioinformatics</i> , 2014 , 30, 431-3	7.2	8
250	Integration of Network Biology and Imaging to Study Cancer Phenotypes and Responses. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2014 , 11, 1009-19	3	11

249	Robust identification of transcriptional regulatory networks using a Gibbs sampler on outlier sum statistic. <i>Bioinformatics</i> , 2014 , 30, 2242-2242	7.2	78
248	MYC regulates the unfolded protein response and glucose and glutamine uptake in endocrine resistant breast cancer. <i>Molecular Cancer</i> , 2014 , 13, 239	42.1	58
247	When is a vesicle not just a vesicle: mitochondrial spheroids and mitochondrial autophagosomes. <i>Cell and Bioscience</i> , 2014 , 4, 66	9.8	6
246	VAV3 mediates resistance to breast cancer endocrine therapy. <i>Breast Cancer Research</i> , 2014 , 16, R53	8.3	21
245	Soluble-E-cadherin activates HER and IAP family members in HER2+ and TNBC human breast cancers. <i>Molecular Carcinogenesis</i> , 2014 , 53, 893-906	5	24
244	Unsupervised deconvolution of dynamic imaging reveals intratumor vascular heterogeneity and repopulation dynamics. <i>PLoS ONE</i> , 2014 , 9, e112143	3.7	9
243	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	2.2	
242	Estrogen receptor- β signaling and localization regulates autophagy and unfolded protein response activation in ER+ breast cancer. <i>Receptors & Clinical Investigation</i> , 2014 , 1,		8
241	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, 3234-46	12.9	30
240	mAPC-GibbsOS: an integrated approach for robust identification of gene regulatory networks. <i>BMC Systems Biology</i> , 2013 , 7 Suppl 5, S4	3.5	3
239	Reconstruction of transcriptional regulatory networks by stability-based network component analysis. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2013 , 10, 1347-58	3	7
238	Modelling the effect of GRP78 on anti-oestrogen sensitivity and resistance in breast cancer. <i>Interface Focus</i> , 2013 , 3, 20130012	3.9	24
237	Modeling the estrogen receptor to growth factor receptor signaling switch in human breast cancer cells. <i>FEBS Letters</i> , 2013 , 587, 3327-34	3.8	20
236	Identifying early events of gene expression in breast cancer with systems biology phylogenetics. <i>Cytogenetic and Genome Research</i> , 2013 , 139, 206-14	1.9	11
235	Targeting GRP78 and antiestrogen resistance in breast cancer. <i>Future Medicinal Chemistry</i> , 2013 , 5, 1047-57	4.7	21
234	Module-based breast cancer classification. <i>International Journal of Data Mining and Bioinformatics</i> , 2013 , 7, 284-302	0.5	13
233	Reconstructing transcriptional regulatory networks by probabilistic network component analysis 2013 ,		1
232	Advancing Translational Research through Facility Design in Non-AMC Hospitals. <i>Herd</i> , 2013 , 6, 126-37	2.4	2

231	Identifying protein interaction subnetworks by a bagging Markov random field-based method. <i>Nucleic Acids Research</i> , 2013 , 41, e42	20.1	30
230	GX15-070 (obatoclox) induces apoptosis and inhibits cathepsin D- and L-mediated autophagosomal lysis in antiestrogen-resistant breast cancer cells. <i>Molecular Cancer Therapeutics</i> , 2013 , 12, 448-59	6.1	47
229	In silico discovery of mitosis regulation networks associated with early distant metastases in estrogen receptor positive breast cancers. <i>Cancer Informatics</i> , 2013 , 12, 31-51	2.4	13
228	A novel statistical approach to identify co-regulatory gene modules 2013 ,		2
227	Genomic and network analysis to study the origin of ovarian cancer. <i>Systems Biomedicine (Austin, Tex)</i> , 2013 , 1, 55-64		1
226	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	4.4	4
225	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	6.3	50
224	Vitamin E succinate inhibits survivin and induces apoptosis in pancreatic cancer cells. <i>Genes and Nutrition</i> , 2012 , 7, 83-9	4.3	14
223	Glucose-regulated protein 78 controls cross-talk between apoptosis and autophagy to determine antiestrogen responsiveness. <i>Cancer Research</i> , 2012 , 72, 3337-49	10.1	123
222	Antiestrogen Resistance and the Application of Systems Biology. <i>Drug Discovery Today Disease Mechanisms</i> , 2012 , 9, e11-e17		2
221	Genome-wide identification of significant aberrations in cancer genome. <i>BMC Genomics</i> , 2012 , 13, 342	4.5	27
220	Heat shock 70 kDa protein 5/glucose-regulated protein 78 "AMP"ing up autophagy. <i>Autophagy</i> , 2012 , 8, 1827-9	10.2	21
219	Guidelines for the use and interpretation of assays for monitoring autophagy. <i>Autophagy</i> , 2012 , 8, 445-544	16.2	2783
218	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, 5693-708	5.7	93
217	Robust identification of transcriptional regulatory networks using a Gibbs sampler on outlier sum statistic. <i>Bioinformatics</i> , 2012 , 28, 1990-7	7.2	8
216	Endoplasmic reticulum stress, the unfolded protein response, autophagy, and the integrated regulation of breast cancer cell fate. <i>Cancer Research</i> , 2012 , 72, 1321-31	10.1	153
215	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	5.4	45
214	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, 147828	2.3	5

213	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	1.3	8
212	Reconstruction of Transcription Regulatory Networks by Stability-Based Network Component Analysis. <i>Lecture Notes in Computer Science</i> , 2012 , 36-47	0.9	
211	G-DOC: a systems medicine platform for personalized oncology. <i>Neoplasia</i> , 2011 , 13, 771-83	6.4	42
210	G-CODE: enabling systems medicine through innovative informatics 2011 , 12, P38		4
209	Cannibalism, cell survival, and endocrine resistance in breast cancer. <i>Breast Cancer Research</i> , 2011 , 13, 311	8.3	6
208	Dynamic modelling of oestrogen signalling and cell fate in breast cancer cells. <i>Nature Reviews Cancer</i> , 2011 , 11, 523-32	31.3	154
207	Autophagy and endocrine resistance in breast cancer. <i>Expert Review of Anticancer Therapy</i> , 2011 , 11, 1283-94	3.5	113
206	Identifying cancer biomarkers by network-constrained support vector machines. <i>BMC Systems Biology</i> , 2011 , 5, 161	3.5	61
205	Motif-guided sparse decomposition of gene expression data for regulatory module identification. <i>BMC Bioinformatics</i> , 2011 , 12, 82	3.6	13
204	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, 421-68		69
203	DDN: a caBIG analytical tool for differential network analysis. <i>Bioinformatics</i> , 2011 , 27, 1036-8	7.2	33
202	GIST: a Gibbs sampler to identify intracellular signal transduction pathways. <i>Annual International Conference of the IEEE Engineering in Medicine and Biology Society IEEE Engineering in Medicine and Biology Society Annual International Conference</i> , 2011 , 2011, 2434-7	0.9	1
201	Therapeutically activating RB: reestablishing cell cycle control in endocrine therapy-resistant breast cancer. <i>Endocrine-Related Cancer</i> , 2011 , 18, 333-45	5.7	202
200	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, 8329-41	6.6	21
199	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	1.3	39
198	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, 912102	2.3	31
197	PUGSVM: a caBIG analytical tool for multiclass gene selection and predictive classification. <i>Bioinformatics</i> , 2011 , 27, 736-8	7.2	15
196	IFNgamma restores breast cancer sensitivity to fulvestrant by regulating STAT1, IFN regulatory factor 1, NF-kappaB, BCL2 family members, and signaling to caspase-dependent apoptosis. <i>Molecular Cancer Therapeutics</i> , 2010 , 9, 1274-85	6.1	62

195	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	1.3	3
194	Multilevel support vector regression analysis to identify condition-specific regulatory networks. <i>Bioinformatics</i> , 2010 , 26, 1416-22	7.2	18
193	Module-Based Biomarker Discovery in Breast Cancer 2010 ,		1
192	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, 2939-48	12.9	15
191	Orphan nuclear receptors in breast cancer pathogenesis and therapeutic response. <i>Endocrine-Related Cancer</i> , 2010 , 17, R213-31	5.7	35
190	DBC-1 mediates endocrine resistant breast cancer cell survival. <i>Cell Cycle</i> , 2010 , 9, 1218-9	4.7	13
189	Differential Dependency Network Analysis to Identify Topological Changes in Biological Networks 2010 , 185-203		
188	BCL2 and CASP8 regulation by NF-kappaB differentially affect mitochondrial function and cell fate in antiestrogen-sensitive and -resistant breast cancer cells. <i>FASEB Journal</i> , 2010 , 24, 2040-55	0.9	71
187	Frequent loss of heterozygosity at the interferon regulatory factor-1 gene locus in breast cancer. <i>Breast Cancer Research and Treatment</i> , 2010 , 121, 227-31	4.4	27
186	Knowledge-guided gene ranking by coordinative component analysis. <i>BMC Bioinformatics</i> , 2010 , 11, 1623.6	3.6	6
185	Co-inhibition of BCL-W and BCL2 restores antiestrogen sensitivity through BECN1 and promotes an autophagy-associated necrosis. <i>PLoS ONE</i> , 2010 , 5, e8604	3.7	56
184	Reconstruction of gene regulatory modules in cancer cell cycle by multi-source data integration. <i>PLoS ONE</i> , 2010 , 5, e10268	3.7	9
183	Cross phenotype normalization of microarray data. <i>Frontiers in Bioscience - Elite</i> , 2010 , 2, 171-86	1.6	1
182	Signaling Pathways in the Normal and Neoplastic Breast 2010 , 2699-2706		
181	Differential dependency network analysis to identify condition-specific topological changes in biological networks. <i>Bioinformatics</i> , 2009 , 25, 526-32	7.2	97
180	Reverse engineering module networks by PSO-RNN hybrid modeling. <i>BMC Genomics</i> , 2009 , 10 Suppl 1, S15	4.5	28
179	Gene network signaling in hormone responsiveness modifies apoptosis and autophagy in breast cancer cells. <i>Journal of Steroid Biochemistry and Molecular Biology</i> , 2009 , 114, 8-20	5.1	63
178	The role of preclinical animal models in breast cancer drug development. <i>Breast Cancer Research</i> , 2009 , 11 Suppl 3, S22	8.3	16

177	Identification of condition-specific regulatory modules through multi-level motif and mRNA expression analysis. <i>International Journal of Computational Biology and Drug Design</i> , 2009 , 2, 1-20	0.4	
176	Biomarker identification by knowledge-driven multilevel ICA and motif analysis. <i>International Journal of Data Mining and Bioinformatics</i> , 2009 , 3, 365-81	0.5	8
175	The role of X-box binding protein-1 in tumorigenicity. <i>Drug News and Perspectives</i> , 2009 , 22, 241-6		59
174	Approaches to working in high-dimensional data spaces: gene expression microarrays. <i>British Journal of Cancer</i> , 2008 , 98, 1023-8	8.7	45
173	The properties of high-dimensional data spaces: implications for exploring gene and protein expression data. <i>Nature Reviews Cancer</i> , 2008 , 8, 37-49	31.3	370
172	Network motif-based identification of transcription factor-target gene relationships by integrating multi-source biological data. <i>BMC Bioinformatics</i> , 2008 , 9, 203	3.6	30
171	caBIG VISDA: modeling, visualization, and discovery for cluster analysis of genomic data. <i>BMC Bioinformatics</i> , 2008 , 9, 383	3.6	11
170	Knowledge-guided multi-scale independent component analysis for biomarker identification. <i>BMC Bioinformatics</i> , 2008 , 9, 416	3.6	20
169	Motif-directed network component analysis for regulatory network inference. <i>BMC Bioinformatics</i> , 2008 , 9 Suppl 1, S21	3.6	17
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1	swCAM: estimation of subtype-specific expressions in individual samples with unsupervised sample-wise deconvolution		1