

Graham Roy Ball

List of Publications by Citations

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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.

74
papers

3,034
citations

29
h-index

54
g-index

81
ext. papers

3,535
ext. citations

5.3
avg, IF

4.53
L-index

#	Paper	IF	Citations
74	High-throughput protein expression analysis using tissue microarray technology of a large well-characterised series identifies biologically distinct classes of breast cancer confirming recent cDNA expression analyses. <i>International Journal of Cancer</i> , 2005 , 116, 340-50	7.5	443
73	MicroRNA signatures predict oestrogen receptor, progesterone receptor and HER2/neu receptor status in breast cancer. <i>Breast Cancer Research</i> , 2009 , 11, R27	8.3	332
72	Transferrin receptor (CD71) is a marker of poor prognosis in breast cancer and can predict response to tamoxifen. <i>Breast Cancer Research and Treatment</i> , 2010 , 119, 283-93	4.4	155
71	NKG2D ligand expression in human colorectal cancer reveals associations with prognosis and evidence for immunoediting. <i>Clinical Cancer Research</i> , 2009 , 15, 6993-7002	12.9	122
70	Delayed disease progression after allogeneic cell vaccination in hormone-resistant prostate cancer and correlation with immunologic variables. <i>Clinical Cancer Research</i> , 2005 , 11, 4469-78	12.9	111
69	Network inference analysis identifies an APRR2-like gene linked to pigment accumulation in tomato and pepper fruits. <i>Plant Physiology</i> , 2013 , 161, 1476-85	6.6	106
68	Serum proteomic fingerprinting discriminates between clinical stages and predicts disease progression in melanoma patients. <i>Journal of Clinical Oncology</i> , 2005 , 23, 5088-93	2.2	96
67	A case-controlled study of the oncologic safety of fat grafting. <i>Plastic and Reconstructive Surgery</i> , 2015 , 135, 1263-1275	2.7	87
66	Genomic and protein expression analysis reveals flap endonuclease 1 (FEN1) as a key biomarker in breast and ovarian cancer. <i>Molecular Oncology</i> , 2014 , 8, 1326-38	7.9	77
65	Forkhead-box A1 (FOXA1) expression in breast cancer and its prognostic significance. <i>European Journal of Cancer</i> , 2008 , 44, 1541-51	7.5	74
64	Identification and validation of oncologic miRNA biomarkers for luminal A-like breast cancer. <i>PLoS ONE</i> , 2014 , 9, e87032	3.7	73
63	Targeting XRCC1 deficiency in breast cancer for personalized therapy. <i>Cancer Research</i> , 2013 , 73, 1621-34	10.1	71
62	The prognostic significance of PELP1 expression in invasive breast cancer with emphasis on the ER-positive luminal-like subtype. <i>Breast Cancer Research and Treatment</i> , 2010 , 120, 603-12	4.4	66
61	Untangling the ATR-CHEK1 network for prognostication, prediction and therapeutic target validation in breast cancer. <i>Molecular Oncology</i> , 2015 , 9, 569-85	7.9	57
60	Targeting BRCA1-BER deficient breast cancer by ATM or DNA-PKcs blockade either alone or in combination with cisplatin for personalized therapy. <i>Molecular Oncology</i> , 2015 , 9, 204-17	7.9	55
59	High throughput identification of clinical isolates of <i>Staphylococcus aureus</i> using MALDI-TOF-MS of intact cells. <i>Infection, Genetics and Evolution</i> , 2009 , 9, 507-13	4.5	53
58	Guidelines and considerations for conducting experiments using tissue microarrays. <i>Histopathology</i> , 2013 , 62, 827-39	7.3	50

57	Identification of SPARC-like 1 protein as part of a biomarker panel for Alzheimer's disease in cerebrospinal fluid. <i>Journal of Alzheimer's Disease</i> , 2012 , 28, 625-36	4.3	49
56	A prototype methodology combining surface-enhanced laser desorption/ionization protein chip technology and artificial neural network algorithms to predict the chemoresponsiveness of breast cancer cell lines exposed to Paclitaxel and Doxorubicin under in vitro conditions. <i>Proteomics</i> , 2003 , 3, 1785-97	4.8	47
55	A methodology to identify consensus classes from clustering algorithms applied to immunohistochemical data from breast cancer patients. <i>Computers in Biology and Medicine</i> , 2010 , 40, 318-30	7	42
54	Risk factors for the development of invasive cancer in unresected ductal carcinoma in situ. <i>European Journal of Surgical Oncology</i> , 2018 , 44, 429-435	3.6	41
53	ATM, ATR and DNA-PKcs expressions correlate to adverse clinical outcomes in epithelial ovarian cancers. <i>BBA Clinical</i> , 2014 , 2, 10-7		41
52	Management and 5-year outcomes in 9938 women with screen-detected ductal carcinoma in situ: the UK Sloane Project. <i>European Journal of Cancer</i> , 2018 , 101, 210-219	7.5	34
51	Proposal for a modified grading system based on mitotic index and Bcl2 provides objective determination of clinical outcome for patients with breast cancer. <i>Journal of Pathology</i> , 2010 , 222, 388-99	8.4	34
50	Tracing the transition of methicillin resistance in sub-populations of <i>Staphylococcus aureus</i> , using SELDI-TOF Mass Spectrometry and Artificial Neural Network Analysis. <i>Systematic and Applied Microbiology</i> , 2011 , 34, 81-6	4.2	33
49	RERG (Ras-like, oestrogen-regulated, growth-inhibitor) expression in breast cancer: a marker of ER-positive luminal-like subtype. <i>Breast Cancer Research and Treatment</i> , 2011 , 128, 315-26	4.4	33
48	Transcriptomic and Protein Expression Analysis Reveals Clinicopathological Significance of Bloom Syndrome Helicase (BLM) in Breast Cancer. <i>Molecular Cancer Therapeutics</i> , 2015 , 14, 1057-65	6.1	32
47	Camptothecin targets WRN protein: mechanism and relevance in clinical breast cancer. <i>Oncotarget</i> , 2016 , 7, 13269-84	3.3	31
46	Clinicopathological significance of ATM-Chk2 expression in sporadic breast cancers: a comprehensive analysis in large cohorts. <i>Neoplasia</i> , 2014 , 16, 982-91	6.4	30
45	RECQL4 helicase has oncogenic potential in sporadic breast cancers. <i>Journal of Pathology</i> , 2016 , 238, 495-501	9.4	29
44	New approaches to identification of bacterial pathogens by surface enhanced laser desorption/ionization time of flight mass spectrometry in concert with artificial neural networks, with special reference to <i>Neisseria gonorrhoeae</i> . <i>Journal of Medical Microbiology</i> , 2005 , 54, 1205-1211	3.2	28
43	An Artificial Neural Network Integrated Pipeline for Biomarker Discovery Using Alzheimer's Disease as a Case Study. <i>Computational and Structural Biotechnology Journal</i> , 2018 , 16, 77-87	6.8	27
42	DNA polymerase β deficiency is linked to aggressive breast cancer: a comprehensive analysis of gene copy number, mRNA and protein expression in multiple cohorts. <i>Molecular Oncology</i> , 2014 , 8, 520-32	7.9	27
41	Diagnostic biomarkers differentiating metastatic melanoma patients from healthy controls identified by an integrated MALDI-TOF mass spectrometry/bioinformatic approach. <i>Proteomics - Clinical Applications</i> , 2007 , 1, 605-20	3.1	26
40	KI67 and DLX2 predict increased risk of metastasis formation in prostate cancer-a targeted molecular approach. <i>British Journal of Cancer</i> , 2016 , 115, 236-42	8.7	25

39	Clinicopathological and prognostic significance of RECQL5 helicase expression in breast cancers. <i>Carcinogenesis</i> , 2016 , 37, 63-71	4.6	25
38	Low expression of G protein-coupled oestrogen receptor 1 (GPER) is associated with adverse survival of breast cancer patients. <i>Oncotarget</i> , 2018 , 9, 25946-25956	3.3	25
37	Clinical proteomics: discovery of cancer biomarkers using mass spectrometry and bioinformatics approaches--a prostate cancer perspective. <i>Vaccine</i> , 2007 , 25 Suppl 2, B110-21	4.1	23
36	Proteomic Profiling Reveals the Transglutaminase-2 Externalization Pathway in Kidneys after Unilateral Ureteric Obstruction. <i>Journal of the American Society of Nephrology: JASN</i> , 2018 , 29, 880-905	12.7	22
35	The prognostic significance of STAT3 in invasive breast cancer: analysis of protein and mRNA expressions in large cohorts. <i>Breast Cancer Research and Treatment</i> , 2016 , 156, 9-20	4.4	22
34	Single-strand selective monofunctional uracil-DNA glycosylase (SMUG1) deficiency is linked to aggressive breast cancer and predicts response to adjuvant therapy. <i>Breast Cancer Research and Treatment</i> , 2013 , 142, 515-27	4.4	22
33	Identification of <i>Enterobacter sakazakii</i> from closely related species: the use of artificial neural networks in the analysis of biochemical and 16S rDNA data. <i>BMC Microbiology</i> , 2006 , 6, 28	4.5	21
32	Breast cancer histologic grading using digital microscopy: concordance and outcome association. <i>Journal of Clinical Pathology</i> , 2018 , 71, 680-686	3.9	20
31	MTSS1 and SCAMP1 cooperate to prevent invasion in breast cancer. <i>Cell Death and Disease</i> , 2018 , 9, 3449.8		19
30	Current Developments in the Analysis of Proteomic Data: Artificial Neural Network Data Mining Techniques for the Identification of Proteomic Biomarkers Related to Breast Cancer. <i>Current Proteomics</i> , 2005 , 2, 15-29	0.7	19
29	Prognostic stratification of oestrogen receptor-positive HER2-negative lymph node-negative class of breast cancer. <i>Histopathology</i> , 2017 , 70, 622-631	7.3	18
28	Analysis of Gene Regulatory Networks of Maize in Response to Nitrogen. <i>Genes</i> , 2018 , 9,	4.2	18
27	Nottingham Clinico-Pathological Response Index (NPRI) after neoadjuvant chemotherapy (Neo-ACT) accurately predicts clinical outcome in locally advanced breast cancer. <i>Clinical Cancer Research</i> , 2015 , 21, 1052-62	12.9	14
26	Correlation between phylogroups and intracellular proteomes of <i>Propionibacterium acnes</i> and differences in the protein expression profiles between anaerobically and aerobically grown cells. <i>BioMed Research International</i> , 2013 , 2013, 151797	3	14
25	Adverse surgical outcomes in screen-detected ductal carcinoma in situ of the breast. <i>European Journal of Cancer</i> , 2014 , 50, 1880-90	7.5	13
24	Artificial neural networks and player recruitment in professional soccer. <i>PLoS ONE</i> , 2018 , 13, e0205818	3.7	13
23	Adverse prognostic and predictive significance of low DNA-dependent protein kinase catalytic subunit (DNA-PKcs) expression in early-stage breast cancers. <i>Breast Cancer Research and Treatment</i> , 2014 , 146, 309-20	4.4	10
22	Development of a Bioinformatics Framework for Identification and Validation of Genomic Biomarkers and Key Immunopathology Processes and Controllers in Infectious and Non-infectious Severe Inflammatory Response Syndrome. <i>Frontiers in Immunology</i> , 2020 , 11, 380	8.4	8

21	Cross-species gene expression analysis of species specific differences in the preclinical assessment of pharmaceutical compounds. <i>PLoS ONE</i> , 2014 , 9, e96853	3.7	8
20	Prognostic significance of nucleolar assessment in invasive breast cancer. <i>Histopathology</i> , 2020 , 76, 671-684	3.4	7
19	Relationship between preparation of cells for therapy and cell quality using artificial neural network analysis. <i>Artificial Intelligence in Medicine</i> , 2014 , 62, 119-27	7.4	6
18	Serum biomarkers which correlate with failure to respond to immunotherapy and tumor progression in a murine colorectal cancer model. <i>Proteomics - Clinical Applications</i> , 2010 , 4, 682-96	3.1	6
17	Temporal Expression of Peripheral Blood Leukocyte Biomarkers in a Macaca fascicularis Infection Model of Tuberculosis; Comparison with Human Datasets and Analysis with Parametric/Non-parametric Tools for Improved Diagnostic Biomarker Identification. <i>PLoS ONE</i> , 2016 , 11, e0154320	3.7	6
16	New Insights into the Anti-pathogenic Potential of against Based on RNA Sequencing Profiling. <i>Frontiers in Microbiology</i> , 2017 , 8, 359	5.7	5
15	A proteomic approach combining MS and bioinformatic analysis for the detection and identification of biomarkers of administration of exogenous human growth hormone in humans. <i>Proteomics - Clinical Applications</i> , 2009 , 3, 912-22	3.1	5
14	Comprehending Meningioma Signaling Cascades Using Multipronged Proteomics Approaches & Targeted Validation of Potential Markers. <i>Frontiers in Oncology</i> , 2020 , 10, 1600	5.3	5
13	Dopamine and cAMP-regulated phosphoprotein 32 kDa (DARPP-32) and survival in breast cancer: a retrospective analysis of protein and mRNA expression. <i>Scientific Reports</i> , 2019 , 9, 16987	4.9	5
12	Discovery and application of immune biomarkers for hematological malignancies. <i>Expert Review of Molecular Diagnostics</i> , 2017 , 17, 983-1000	3.8	4
11	Identifying playing talent in professional football using artificial neural networks. <i>Journal of Sports Sciences</i> , 2020 , 38, 1211-1220	3.6	3
10	Comprehensive proteomic analysis reveals distinct functional modules associated with skull base and supratentorial meningiomas and perturbations in collagen pathway components. <i>Journal of Proteomics</i> , 2021 , 246, 104303	3.9	2
9	Current Approaches to Identify and Evaluate Cancer Biomarkers for Patient Stratification 2012 , 452-463		1
8	Visual assessment of mitotic figures in breast cancer: a comparative study between light microscopy and whole slide images. <i>Histopathology</i> , 2021 , 79, 913-925	7.3	1
7	Interactomic Analysis of the Stem Cell Marker NANOG in a Prostate Cancer Setting 2015 , 317-352		
6	Data Mining for Predictive Proteomics 2010 , 409-422		
5	Computational & Statistical Methodologies to Identify Biomarkers in Cancer. <i>Current Cancer Therapy Reviews</i> , 2008 , 4, 157-160	0.4	
4	Biomarkers for development of cancer vaccines. <i>Personalized Medicine</i> , 2006 , 3, 79-88	2.2	

- 3 Computational and Statistical Methodologies for Data Mining in Bioinformatics **2010**, 337-350
- 2 The Future Role of Biomarkers in Alzheimer's Disease Diagnostics **2013**, 231-248
- 1 Selecting Lung Cancer Patients from UK Primary Care Data: A Longitudinal Study of Feature Trends. *Communications in Computer and Information Science*, **2021**, 43-59 0.3