Graham Roy Ball

List of Publications by Year
in descending order

75 papers	3,892 citations	109137 35 h-index	123241 61 g-index
81 all docs	81 docs citations	81 times ranked	6164 citing authors

#	Article	IF	Citations
1	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. International Journal of Cancer, 2005, 116, 340-350.	2.3	500
2	MicroRNA signatures predict oestrogen receptor, progesterone receptor and HER2/neureceptor status in breast cancer. Breast Cancer Research, 2009, 11, R27.	2.2	375
3	Transferrin receptor (CD71) is a marker of poor prognosis in breast cancer and can predict response to tamoxifen. Breast Cancer Research and Treatment, 2010, 119, 283-293.	1.1	193
4	Network Inference Analysis Identifies an <i>APRR2-Like</i> Gene Linked to Pigment Accumulation in Tomato and Pepper Fruits Â Â. Plant Physiology, 2013, 161, 1476-1485.	2.3	166
5	NKG2D Ligand Expression in Human Colorectal Cancer Reveals Associations with Prognosis and Evidence for Immunoediting. Clinical Cancer Research, 2009, 15, 6993-7002.	3.2	161
6	Delayed Disease Progression after Allogeneic Cell Vaccination in Hormone-Resistant Prostate Cancer and Correlation with Immunologic Variables. Clinical Cancer Research, 2005, 11, 4469-4478.	3.2	125
7	Serum Proteomic Fingerprinting Discriminates Between Clinical Stages and Predicts Disease Progression in Melanoma Patients. Journal of Clinical Oncology, 2005, 23, 5088-5093.	0.8	109
8	Genomic and protein expression analysis reveals flap endonuclease 1 (FEN1) as a key biomarker in breast and ovarian cancer. Molecular Oncology, 2014, 8, 1326-1338.	2.1	109
9	A Case-Controlled Study of the Oncologic Safety of Fat Grafting. Plastic and Reconstructive Surgery, 2015, 135, 1263-1275.	0.7	108
10	Identification and Validation of Oncologic miRNA Biomarkers for Luminal A-like Breast Cancer. PLoS ONE, 2014, 9, e87032.	1.1	93
11	Targeting XRCC1 Deficiency in Breast Cancer for Personalized Therapy. Cancer Research, 2013, 73, 1621-1634.	0.4	88
12	The prognostic significance of PELP1 expression in invasive breast cancer with emphasis on the ER-positive luminal-like subtype. Breast Cancer Research and Treatment, 2010, 120, 603-612.	1.1	83
13	Forkhead-box A1 (FOXA1) expression in breast cancer and its prognostic significance. European Journal of Cancer, 2008, 44, 1541-1551.	1.3	79
14	Untangling the ATRâ€CHEK1 network for prognostication, prediction and therapeutic target validation in breast cancer. Molecular Oncology, 2015, 9, 569-585.	2.1	75
15	Targeting BRCA1â€BER deficient breast cancer by ATM or DNAâ€PKcs blockade either alone or in combination with cisplatin for personalized therapy. Molecular Oncology, 2015, 9, 204-217.	2.1	72
16	Risk factors for the development of invasive cancer in unresected ductal carcinoma in situ. European Journal of Surgical Oncology, 2018, 44, 429-435.	0.5	62
17	High throughput identification of clinical isolates of Staphylococcus aureus using MALDI-TOF-MS of intact cells. Infection, Genetics and Evolution, 2009, 9, 507-513.	1.0	57
18	Guidelines and considerations for conducting experiments using tissue microarrays. Histopathology, 2013, 62, 827-839.	1.6	57

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19	ATM, ATR and DNA-PKcs expressions correlate to adverse clinical outcomes in epithelial ovarian cancers. BBA Clinical, 2014, 2, 10-17.	4.1	57
20	An Artificial Neural Network Integrated Pipeline for Biomarker Discovery Using Alzheimer's Disease as a Case Study. Computational and Structural Biotechnology Journal, 2018, 16, 77-87.	1.9	56
21	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. Proteomics, 2003, 3, 1725-1737.	1.3	55
22	A methodology to identify consensus classes from clustering algorithms applied to immunohistochemical data from breast cancer patients. Computers in Biology and Medicine, 2010, 40, 318-330.	3.9	55
23	Management and 5-year outcomes in 9938 women with screen-detected ductal carcinoma in situ: the UK Sloane Project. European Journal of Cancer, 2018, 101, 210-219.	1.3	52
24	Identification of SPARC-like 1 Protein as Part of a Biomarker Panel for Alzheimer's Disease in Cerebrospinal Fluid. Journal of Alzheimer's Disease, 2012, 28, 625-636.	1.2	50
25	Diagnostic biomarkers differentiating metastatic melanoma patients from healthy controls identified by an integrated MALDI-TOF mass spectrometry/bioinformatic approach. Proteomics - Clinical Applications, 2007, 1, 605-620.	0.8	44
26	<scp>RECQL4</scp> helicase has oncogenic potential in sporadic breast cancers. Journal of Pathology, 2016, 238, 495-501.	2.1	43
27	KI67 and DLX2 predict increased risk of metastasis formation in prostate cancer—a targeted molecular approach. British Journal of Cancer, 2016, 115, 236-242.	2.9	43
28	Transcriptomic and Protein Expression Analysis Reveals Clinicopathological Significance of Bloom Syndrome Helicase (BLM) in Breast Cancer. Molecular Cancer Therapeutics, 2015, 14, 1057-1065.	1.9	42
29	Tracing the transition of methicillin resistance in sub-populations of Staphylococcus aureus, using SELDI-TOF Mass Spectrometry and Artificial Neural Network Analysis. Systematic and Applied Microbiology, 2011, 34, 81-86.	1.2	41
30	RERG (Ras-like, oestrogen-regulated, growth-inhibitor) expression in breast cancer: a marker of ER-positive luminal-like subtype. Breast Cancer Research and Treatment, 2011, 128, 315-326.	1.1	41
31	Proteomic Profiling Reveals the Transglutaminase-2 Externalization Pathway in Kidneys after Unilateral Ureteric Obstruction. Journal of the American Society of Nephrology: JASN, 2018, 29, 880-905.	3.0	40
32	Camptothecin targets WRN protein: mechanism and relevance in clinical breast cancer. Oncotarget, 2016, 7, 13269-13284.	0.8	38
33	Proposal for a modified grading system based on mitotic index and Bcl2 provides objective determination of clinical outcome for patients with breast cancer. Journal of Pathology, 2010, 222, 388-399.	2.1	37
34	Clinicopathological Significance of ATM-Chk2 Expression in Sporadic Breast Cancers: a Comprehensive Analysis in Large Cohorts. Neoplasia, 2014, 16, 982-991.	2.3	37
35	MTSS1 and SCAMP1 cooperate to prevent invasion in breast cancer. Cell Death and Disease, 2018, 9, 344.	2.7	37
36	Single-strand selective monofunctional uracil-DNA glycosylase (SMUG1) deficiency is linked to aggressive breast cancer and predicts response to adjuvant therapy. Breast Cancer Research and Treatment, 2013, 142, 515-527.	1.1	35

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37	Breast cancer histologic grading using digital microscopy: concordance and outcome association. Journal of Clinical Pathology, 2018, 71, 680-686.	1.0	35
38	Low expression of G protein-coupled oestrogen receptor 1 (GPER) is associated with adverse survival of breast cancer patients. Oncotarget, 2018, 9, 25946-25956.	0.8	34
39	DNA polymerase Î² deficiency is linked to aggressive breast cancer: A comprehensive analysis of gene copy number, mRNA and protein expression in multiple cohorts. Molecular Oncology, 2014, 8, 520-532.	2.1	33
40	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 Neisseria gonorrhoeae. Journal of Medical Microbiology, 2005, 54, 1205-1211.	0.7	31
41	Clinicopathological and prognostic significance of RECQL5 helicase expression in breast cancers. Carcinogenesis, 2016, 37, 63-71.	1.3	31
42	Prognostic stratification of oestrogen receptorâ€positive <scp>HER</scp>2â€negative lymph nodeâ€negative class of breast cancer. Histopathology, 2017, 70, 622-631.	1.6	30
43	Analysis of Gene Regulatory Networks of Maize in Response to Nitrogen. Genes, 2018, 9, 151.	1.0	30
44	The prognostic significance of STAT3 in invasive breast cancer: analysis of protein and mRNA expressions in large cohorts. Breast Cancer Research and Treatment, 2016, 156, 9-20.	1.1	29
45	Identification of Enterobacter sakazakii from closely related species: the use of artificial neural networks in the analysis of biochemical and 16S rDNA data. BMC Microbiology, 2006, 6, 28.	1.3	27
46	Clinical proteomics: Discovery of cancer biomarkers using mass spectrometry and bioinformatics approachesâ€"A prostate cancer perspective. Vaccine, 2007, 25, B110-B121.	1.7	26
47	Artificial neural networks and player recruitment in professional soccer. PLoS ONE, 2018, 13, e0205818.	1.1	25
48	Current Developments in the Analysis of Proteomic Data: Artificial Neural Network Data Mining Techniques for the Identification of Proteomic Biomarkers Related to Breast Cancer. Current Proteomics, 2005, 2, 15-29.	0.1	22
49	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. PLoS ONE, 2016, 11, e0154320.	1.1	19
50	Adverse surgical outcomes in screen-detected ductal carcinoma in situ of the breast. European Journal of Cancer, 2014, 50, 1880-1890.	1.3	17
51	Nottingham Clinico-Pathological Response Index (NPRI) after Neoadjuvant Chemotherapy (Neo-ACT) Accurately Predicts Clinical Outcome in Locally Advanced Breast Cancer. Clinical Cancer Research, 2015, 21, 1052-1062.	3.2	17
52	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. Frontiers in Immunology, 2020, 11, 380.	2.2	17
53	Correlation between Phylogroups and Intracellular Proteomes of <i>Propionibacterium acnes</i> and Differences in the Protein Expression Profiles between Anaerobically and Aerobically Grown Cells. BioMed Research International, 2013, 2013, 1-9.	0.9	16
54	Prognostic significance of nucleolar assessment in invasive breast cancer. Histopathology, 2020, 76, 671-684.	1.6	14

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55	Adverse prognostic and predictive significance of low DNA-dependent protein kinase catalytic subunit (DNA-PKcs) expression in early-stage breast cancers. Breast Cancer Research and Treatment, 2014, 146, 309-320.	1.1	12
56	Visual assessment of mitotic figures in breast cancer: a comparative study between light microscopy and whole slide images. Histopathology, 2021, 79, 913-925.	1.6	12
57	Dopamine and cAMP-regulated phosphoprotein 32â€‰kDa (DARPP-32) and survival in breast cancer: a retrospective analysis of protein and mRNA expression. Scientific Reports, 2019, 9, 16987.	1.6	11
58	New Insights into the Anti-pathogenic Potential of Lactococcus garvieae against Staphylococcus aureus Based on RNA Sequencing Profiling. Frontiers in Microbiology, 2017, 08, 359.	1.5	10
59	Comprehending Meningioma Signaling Cascades Using Multipronged Proteomics Approaches & Targeted Validation of Potential Markers. Frontiers in Oncology, 2020, 10, 1600.	1.3	10
60	Cross-Species Gene Expression Analysis of Species Specific Differences in the Preclinical Assessment of Pharmaceutical Compounds. PLoS ONE, 2014, 9, e96853.	1.1	9
61	Defining the area of mitoses counting in invasive breast cancer using whole slide image. Modern Pathology, 2022, 35, 739-748.	2.9	9
62	A proteomic approach combining MS and bioinformatic analysis for the detection and identification of biomarkers of administration of exogenous human growth hormone in humans. Proteomics - Clinical Applications, 2009, 3, 912-922.	0.8	8
63	Serum biomarkers which correlate with failure to respond to immunotherapy and tumor progression in a murine colorectal cancer model. Proteomics - Clinical Applications, 2010, 4, 682-696.	0.8	8
64	Issues in biomarker identification, validation and development for disease diagnostics in Public Health. Expert Review of Molecular Diagnostics, 2016, 16, 383-386.	1.5	8
65	Relationship between preparation of cells for therapy and cell quality using artificial neural network analysis. Artificial Intelligence in Medicine, 2014, 62, 119-127.	3.8	7
66	Discovery and application of immune biomarkers for hematological malignancies. Expert Review of Molecular Diagnostics, 2017, 17, 983-1000.	1.5	6
67	Identifying playing talent in professional football using artificial neural networks. Journal of Sports Sciences, 2020, 38, 1211-1220.	1.0	6
68	Comprehensive proteomic analysis reveals distinct functional modules associated with skull base and supratentorial meningiomas and perturbations in collagen pathway components. Journal of Proteomics, 2021, 246, 104303.	1.2	4
69	Prognostic significance of heat shock protein 90AA1 (HSP90Î±) in invasive breast cancer. Journal of Clinical Pathology, 2022, 75, 263-269.	1.0	1
70	Biomarkers for development of cancer vaccines. Personalized Medicine, 2006, 3, 79-88.	0.8	0
71	Computational & Statistical Methodologies to Identify Biomarkers in Cancer. Current Cancer Therapy Reviews, 2008, 4, 157-160.	0.2	0
72	Selecting Lung Cancer Patients from UK Primary Care Data: A Longitudinal Study of Feature Trends. Communications in Computer and Information Science, 2021, , 43-59.	0.4	0

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73	Emerging Breast Cancer Biomarkers. Current Cancer Therapy Reviews, 2008, 4, 79-85.	0.2	0
74	Computational and Statistical Methodologies for Data Mining in Bioinformatics. , 2010, , 337-350.		0
75	The Future Role of Biomarkers in Alzheimer's Disease Diagnostics. , 2013, , 231-248.		0