Miriam V Dwek

List of Publications by Year
in descending order

67 papers	5,244 citations	147801 31 h-index	110387 64 g-index
73 all docs	73 docs citations	73 times ranked	8087 citing authors

#	Article	IF	Citations
1	Association analysis identifies 65 new breast cancer risk loci. Nature, 2017, 551, 92-94.	27.8	1,099
2	Polygenic Risk Scores for Prediction of Breast Cancer and Breast Cancer Subtypes. American Journal of Human Genetics, 2019, 104, 21-34.	6.2	711
3	Prediction of Breast Cancer Risk Based on Profiling With Common Genetic Variants. Journal of the National Cancer Institute, 2015, 107, .	6.3	428
4	Identification of ten variants associated with risk of estrogen-receptor-negative breast cancer. Nature Genetics, 2017, 49, 1767-1778.	21.4	289
5	Genome-wide association study identifies 32 novel breast cancer susceptibility loci from overall and subtype-specific analyses. Nature Genetics, 2020, 52, 572-581.	21.4	265
6	A transcriptome-wide association study of 229,000 women identifies new candidate susceptibility genes for breast cancer. Nature Genetics, 2018, 50, 968-978.	21.4	184
7	Genetic insights into biological mechanisms governing human ovarian ageing. Nature, 2021, 596, 393-397.	27.8	183
8	Fine-mapping of 150 breast cancer risk regions identifies 191 likely target genes. Nature Genetics, 2020, 52, 56-73.	21.4	120
9	19p13.1 Is a Triple-Negativeâ€"Specific Breast Cancer Susceptibility Locus. Cancer Research, 2012, 72, 1795-1803.	0.9	100
10	Refined histopathological predictors of BRCA1 and BRCA2mutation status: a large-scale analysis of breast cancer characteristics from the BCAC, CIMBA, and ENIGMA consortia. Breast Cancer Research, 2014, 16, 3419.	5.0	97
11	Genome-wide association and transcriptome studies identify target genes and risk loci for breast cancer. Nature Communications, 2019, 10, 1741.	12.8	90
12	Shared heritability and functional enrichment across six solid cancers. Nature Communications, 2019, 10, 431.	12.8	88
13	Proteome and glycosylation mapping identifies post-translational modifications associated with aggressive breast cancer. Proteomics, 2001, 1, 756-762.	2.2	82
14	Use of Proteomic Methodology for the Characterization of Human Milk Fat Globular Membrane Proteins. Analytical Biochemistry, 2002, 301, 314-324.	2.4	82
15	Associations of obesity and circulating insulin and glucose with breast cancer risk: a Mendelian randomization analysis. International Journal of Epidemiology, 2019, 48, 795-806.	1.9	81
16	The lectin Helix pomatia agglutinin recognizes O-GlcNAc containing glycoproteins in human breast cancer. Glycobiology, 2012, 22, 839-848.	2.5	76
17	Cell surface glycanâ€"lectin interactions in tumor metastasis. Acta Histochemica, 2011, 113, 591-600.	1.8	72
18	Cellular glycosylation affects Herceptin binding and sensitivity of breast cancer cells to doxorubicin and growth factors. Scientific Reports, 2017, 7, 43006.	3.3	70

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19	A sensitive assay to measure biomarker glycosylation demonstrates increased fucosylation of prostate specific antigen (PSA) in patients with prostate cancer compared with benign prostatic hyperplasia. Clinica Chimica Acta, 2010, 411, 1935-1939.	1.1	60
20	Conjugation of quantum dots on carbon nanotubes for medical diagnosis and treatment. International Journal of Nanomedicine, 2013, 8, 941.	6.7	59
21	A Detailed Analysis of Neutral and Acidic Carbohydrates in Human Milk. Analytical Biochemistry, 1999, 273, 261-277.	2.4	53
22	Genome-wide association study of germline variants and breast cancer-specific mortality. British Journal of Cancer, 2019, 120, 647-657.	6.4	52
23	Proteome analysis enables separate clustering of normal breast, benign breast and breast cancer tissues. British Journal of Cancer, 2003, 89, 305-307.	6.4	51
24	Functionalization of single-walled carbon nanotubes and their binding to cancer cells. International Journal of Nanomedicine, 2012, 7, 905.	6.7	51
25	Helix pomatia agglutinin lectin-binding oligosaccharides of aggressive breast cancer. International Journal of Cancer, 2001, 95, 79-85.	5.1	45
26	Harnessing Changes in Cellular Glycosylation in New Cancer Treatment Strategies. Current Cancer Drug Targets, 2004, 4, 425-442.	1.6	45
27	Genetic Predisposition to In Situ and Invasive Lobular Carcinoma of the Breast. PLoS Genetics, 2014, 10, e1004285.	3.5	39
28	Breast Cancer Polygenic Risk Score and Contralateral Breast Cancer Risk. American Journal of Human Genetics, 2020, 107, 837-848.	6.2	39
29	A targeted glycoproteomic approach identifies cadherin-5 as a novel biomarker of metastatic breast cancer. Cancer Letters, 2013, 328, 335-344.	7.2	36
30	Cadherin-5: a biomarker for metastatic breast cancer with optimum efficacy in oestrogen receptor-positive breast cancers with vascular invasion. British Journal of Cancer, 2016, 114, 1019-1026.	6.4	36
31	Proteome analysis of metastatic colorectal cancer cells recognized by the lectin <i>Helix pomatia</i> agglutinin (HPA). Proteomics, 2007, 7, 4082-4089.	2.2	34
32	Transcriptome€wide association study of breast cancer risk by estrogen€receptor status. Genetic Epidemiology, 2020, 44, 442-468.	1.3	32
33	Identification of independent association signals and putative functional variants for breast cancer risk through fine-scale mapping of the 12p11 locus. Breast Cancer Research, 2016, 18, 64.	5.0	31
34	A novel approach to determining the affinity of protein€"carbohydrate interactions employing adherent cancer cells grown on a biosensor surface. Biosensors and Bioelectronics, 2012, 35, 160-166.	10.1	30
35	A network analysis to identify mediators of germline-driven differences in breast cancer prognosis. Nature Communications, 2020, 11, 312.	12.8	30
36	MiR-21 Is Required for the Epithelial€"Mesenchymal Transition in MDA-MB-231 Breast Cancer Cells. International Journal of Molecular Sciences, 2021, 22, 1557.	4.1	29

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37	The FANCM:p.Arg658* truncating variant is associated with risk of triple-negative breast cancer. Npj Breast Cancer, 2019, 5, 38.	5.2	28
38	Cancer cells grown in 3D under fluid flow exhibit an aggressive phenotype and reduced responsiveness to the anti-cancer treatment doxorubicin. Scientific Reports, 2020, 10, 12020.	3.3	27
39	Beyond the genome and proteome: targeting protein modifications in cancer. Current Opinion in Pharmacology, 2012, 12, 408-413.	3.5	26
40	The DietCompLyf study: A prospective cohort study of breast cancer survival and phytoestrogen consumption. Maturitas, 2013, 75, 232-240.	2.4	25
41	Identification, Cloning, and Characterization of Two N-Acetylgalactosamine-binding Lectins from the Albumen Gland of Helix pomatia. Journal of Biological Chemistry, 2011, 286, 20260-20266.	3.4	21
42	A case-only study to identify genetic modifiers of breast cancer risk for BRCA1/BRCA2 mutation carriers. Nature Communications, 2021, 12, 1078.	12.8	19
43	Breast Cancer Risk Factors and Survival by Tumor Subtype: Pooled Analyses from the Breast Cancer Association Consortium. Cancer Epidemiology Biomarkers and Prevention, 2021, 30, 623-642.	2.5	19
44	Breast cancer progression is associated with a reduction in the diversity of sialylated and neutral oligosaccharides. Clinica Chimica Acta, 1998, 271, 191-202.	1.1	18
45	Serum IgA1 shows increased levels of α2,6-linked sialic acid in breast cancer. Interface Focus, 2019, 9, 20180079.	3.0	18
46	Identification of O-Linked Glycoproteins Binding to the Lectin Helix pomatia Agglutinin as Markers of Metastatic Colorectal Cancer. PLoS ONE, 2015, 10, e0138345.	2.5	17
47	Common variants in breast cancer risk loci predispose to distinct tumor subtypes. Breast Cancer Research, 2022, 24, 2.	5.0	15
48	Identification, purification and analysis of a 55 kDa lectin binding glycoprotein present in breast cancer tissue. Clinica Chimica Acta, 1996, 254, 47-61.	1.1	14
49	Identification and elimination of false-positives in an ELISA-based system for qualitative assessment of glycoconjugate binding using a selection of plant lectins. BioTechniques, 2007, 43, 458-464.	1.8	13
50	Lectin Array-Based Strategies for Identifying Metastasis-Associated Changes in Glycosylation. Methods in Molecular Biology, 2012, 878, 267-272.	0.9	13
51	Current Perspectives in Cancer Proteomics. Molecular Biotechnology, 2002, 22, 139-152.	2.4	12
52	Oligosaccharide Release from Frozen and Paraffin-Wax-Embedded Archival Tissues. Analytical Biochemistry, 1996, 242, 8-14.	2.4	10
53	Preferential Lectin Binding of Cancer Cells upon Sialic Acid Treatment Under Nutrient Deprivation. Applied Biochemistry and Biotechnology, 2013, 171, 963-974.	2.9	10
54	Mendelian randomisation study of smoking exposure in relation to breast cancer risk. British Journal of Cancer, 2021, 125, 1135-1145.	6.4	9

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55	Release and analysis of polypeptides and glycopolypeptides from formalin-fixed, paraffin wax-embedded tissue. The Histochemical Journal, 1998, 30, 609-615.	0.6	8
56	Clinical relevance assessment of animal preclinical research (RAA) tool: development and explanation. PeerJ, 2021, 9, e10673.	2.0	8
57	PhytoCloud: A Gamified Mobile Web Application to Modulate Diet and Physical Activity of Women with Breast Cancer. , 2017, , .		7
58	Machine learning prediction of susceptibility to visceral fat associated diseases. Health and Technology, 2020, 10, 925-944.	3.6	7
59	Association of germline genetic variants with breast cancer-specific survival in patient subgroups defined by clinic-pathological variables related to tumor biology and type of systemic treatment. Breast Cancer Research, 2021, 23, 86.	5.0	7
60	Functional annotation of the 2q35 breast cancer risk locus implicates a structural variant in influencing activity of a long-range enhancer element. American Journal of Human Genetics, 2021, 108, 1190-1203.	6.2	6
61	Two truncating variants in FANCC and breast cancer risk. Scientific Reports, 2019, 9, 12524.	3.3	5
62	A data science approach for early-stage prediction of Patient's susceptibility to acute side effects of advanced radiotherapy. Computers in Biology and Medicine, 2021, 135, 104624.	7.0	3
63	Germline HOXB13 mutations p.G84E and p.R217C do not confer an increased breast cancer risk. Scientific Reports, 2020, 10, 9688.	3.3	2
64	Altered expression of N-acetyl galactosamine glycoproteins by breast cancers. Biochemical Society Transactions, 1994, 22, 95S-95S.	3.4	1
65	Breast Cancer Proteomics Using Two-Dimensional Electrophoresis : Studying the Breast Cancer Proteome. , 2006, 120, 231-244.		1
66	2-DE-Based Proteomics for the Analysis of Metastasis-Associated Proteins. Methods in Molecular Biology, 2012, 878, 111-120.	0.9	1
67	Machine Learning Classification of Females Susceptibility to Visceral Fat Associated Diseases. IFMBE Proceedings, 2020, , 679-693.	0.3	0