

# Miriam V Dwek

## List of Publications by Year in descending order

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Version: 2024-02-01

67  
papers

5,244  
citations

147566

31  
h-index

110170

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. <i>Nature</i> , 2017, 551, 92-94.	13.7	1,099
2	Polygenic Risk Scores for Prediction of Breast Cancer and Breast Cancer Subtypes. <i>American Journal of Human Genetics</i> , 2019, 104, 21-34.	2.6	711
3	Prediction of Breast Cancer Risk Based on Profiling With Common Genetic Variants. <i>Journal of the National Cancer Institute</i> , 2015, 107, .	3.0	428
4	Identification of ten variants associated with risk of estrogen-receptor-negative breast cancer. <i>Nature Genetics</i> , 2017, 49, 1767-1778.	9.4	289
5	Genome-wide association study identifies 32 novel breast cancer susceptibility loci from overall and subtype-specific analyses. <i>Nature Genetics</i> , 2020, 52, 572-581.	9.4	265
6	A transcriptome-wide association study of 229,000 women identifies new candidate susceptibility genes for breast cancer. <i>Nature Genetics</i> , 2018, 50, 968-978.	9.4	184
7	Genetic insights into biological mechanisms governing human ovarian ageing. <i>Nature</i> , 2021, 596, 393-397.	13.7	183
8	Fine-mapping of 150 breast cancer risk regions identifies 191 likely target genes. <i>Nature Genetics</i> , 2020, 52, 56-73.	9.4	120
9	19p13.1 Is a Triple-Negative-Specific Breast Cancer Susceptibility Locus. <i>Cancer Research</i> , 2012, 72, 1795-1803.	0.4	100
10	Refined histopathological predictors of BRCA1 and BRCA2 mutation status: a large-scale analysis of breast cancer characteristics from the BCAC, CIMBA, and ENIGMA consortia. <i>Breast Cancer Research</i> , 2014, 16, 3419.	2.2	97
11	Genome-wide association and transcriptome studies identify target genes and risk loci for breast cancer. <i>Nature Communications</i> , 2019, 10, 1741.	5.8	90
12	Shared heritability and functional enrichment across six solid cancers. <i>Nature Communications</i> , 2019, 10, 431.	5.8	88
13	Proteome and glycosylation mapping identifies post-translational modifications associated with aggressive breast cancer. <i>Proteomics</i> , 2001, 1, 756-762.	1.3	82
14	Use of Proteomic Methodology for the Characterization of Human Milk Fat Globular Membrane Proteins. <i>Analytical Biochemistry</i> , 2002, 301, 314-324.	1.1	82
15	Associations of obesity and circulating insulin and glucose with breast cancer risk: a Mendelian randomization analysis. <i>International Journal of Epidemiology</i> , 2019, 48, 795-806.	0.9	81
16	The lectin <i>Helix pomatia</i> agglutinin recognizes O-GlcNAc containing glycoproteins in human breast cancer. <i>Glycobiology</i> , 2012, 22, 839-848.	1.3	76
17	Cell surface glycan-lectin interactions in tumor metastasis. <i>Acta Histochemica</i> , 2011, 113, 591-600.	0.9	72
18	Cellular glycosylation affects Herceptin binding and sensitivity of breast cancer cells to doxorubicin and growth factors. <i>Scientific Reports</i> , 2017, 7, 43006.	1.6	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. <i>Clinica Chimica Acta</i> , 2010, 411, 1935-1939.	0.5	60
20	Conjugation of quantum dots on carbon nanotubes for medical diagnosis and treatment. <i>International Journal of Nanomedicine</i> , 2013, 8, 941.	3.3	59
21	A Detailed Analysis of Neutral and Acidic Carbohydrates in Human Milk. <i>Analytical Biochemistry</i> , 1999, 273, 261-277.	1.1	53
22	Genome-wide association study of germline variants and breast cancer-specific mortality. <i>British Journal of Cancer</i> , 2019, 120, 647-657.	2.9	52
23	Proteome analysis enables separate clustering of normal breast, benign breast and breast cancer tissues. <i>British Journal of Cancer</i> , 2003, 89, 305-307.	2.9	51
24	Functionalization of single-walled carbon nanotubes and their binding to cancer cells. <i>International Journal of Nanomedicine</i> , 2012, 7, 905.	3.3	51
25	Helix pomatia agglutinin lectin-binding oligosaccharides of aggressive breast cancer. <i>International Journal of Cancer</i> , 2001, 95, 79-85.	2.3	45
26	Harnessing Changes in Cellular Glycosylation in New Cancer Treatment Strategies. <i>Current Cancer Drug Targets</i> , 2004, 4, 425-442.	0.8	45
27	Genetic Predisposition to In Situ and Invasive Lobular Carcinoma of the Breast. <i>PLoS Genetics</i> , 2014, 10, e1004285.	1.5	39
28	Breast Cancer Polygenic Risk Score and Contralateral Breast Cancer Risk. <i>American Journal of Human Genetics</i> , 2020, 107, 837-848.	2.6	39
29	A targeted glycoproteomic approach identifies cadherin-5 as a novel biomarker of metastatic breast cancer. <i>Cancer Letters</i> , 2013, 328, 335-344.	3.2	36
30	Cadherin-5: a biomarker for metastatic breast cancer with optimum efficacy in oestrogen receptor-positive breast cancers with vascular invasion. <i>British Journal of Cancer</i> , 2016, 114, 1019-1026.	2.9	36
31	Proteome analysis of metastatic colorectal cancer cells recognized by the lectin <i>Helix pomatia</i> agglutinin (HPA). <i>Proteomics</i> , 2007, 7, 4082-4089.	1.3	34
32	Transcriptome-wide association study of breast cancer risk by estrogen receptor status. <i>Genetic Epidemiology</i> , 2020, 44, 442-468.	0.6	32
33	Identification of independent association signals and putative functional variants for breast cancer risk through fine-scale mapping of the 12p11 locus. <i>Breast Cancer Research</i> , 2016, 18, 64.	2.2	31
34	A novel approach to determining the affinity of protein-carbohydrate interactions employing adherent cancer cells grown on a biosensor surface. <i>Biosensors and Bioelectronics</i> , 2012, 35, 160-166.	5.3	30
35	A network analysis to identify mediators of germline-driven differences in breast cancer prognosis. <i>Nature Communications</i> , 2020, 11, 312.	5.8	30
36	MIR-21 Is Required for the Epithelial-Mesenchymal Transition in MDA-MB-231 Breast Cancer Cells. <i>International Journal of Molecular Sciences</i> , 2021, 22, 1557.	1.8	29

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37	The FANCM:p.Arg658* truncating variant is associated with risk of triple-negative breast cancer. <i>Npj Breast Cancer</i> , 2019, 5, 38.	2.3	28
38	Cancer cells grown in 3D under fluid flow exhibit an aggressive phenotype and reduced responsiveness to the anti-cancer treatment doxorubicin. <i>Scientific Reports</i> , 2020, 10, 12020.	1.6	27
39	Beyond the genome and proteome: targeting protein modifications in cancer. <i>Current Opinion in Pharmacology</i> , 2012, 12, 408-413.	1.7	26
40	The DietCompLyf study: A prospective cohort study of breast cancer survival and phytoestrogen consumption. <i>Maturitas</i> , 2013, 75, 232-240.	1.0	25
41	Identification, Cloning, and Characterization of Two N-Acetylgalactosamine-binding Lectins from the Albumen Gland of <i>Helix pomatia</i> . <i>Journal of Biological Chemistry</i> , 2011, 286, 20260-20266.	1.6	21
42	A case-only study to identify genetic modifiers of breast cancer risk for BRCA1/BRCA2 mutation carriers. <i>Nature Communications</i> , 2021, 12, 1078.	5.8	19
43	Breast Cancer Risk Factors and Survival by Tumor Subtype: Pooled Analyses from the Breast Cancer Association Consortium. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2021, 30, 623-642.	1.1	19
44	Breast cancer progression is associated with a reduction in the diversity of sialylated and neutral oligosaccharides. <i>Clinica Chimica Acta</i> , 1998, 271, 191-202.	0.5	18
45	Serum IgA1 shows increased levels of $\alpha$ 2,6-linked sialic acid in breast cancer. <i>Interface Focus</i> , 2019, 9, 20180079.	1.5	18
46	Identification of O-Linked Glycoproteins Binding to the Lectin <i>Helix pomatia</i> Agglutinin as Markers of Metastatic Colorectal Cancer. <i>PLoS ONE</i> , 2015, 10, e0138345.	1.1	17
47	Common variants in breast cancer risk loci predispose to distinct tumor subtypes. <i>Breast Cancer Research</i> , 2022, 24, 2.	2.2	15
48	Identification, purification and analysis of a 55 kDa lectin binding glycoprotein present in breast cancer tissue. <i>Clinica Chimica Acta</i> , 1996, 254, 47-61.	0.5	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. <i>BioTechniques</i> , 2007, 43, 458-464.	0.8	13
50	Lectin Array-Based Strategies for Identifying Metastasis-Associated Changes in Glycosylation. <i>Methods in Molecular Biology</i> , 2012, 878, 267-272.	0.4	13
51	Current Perspectives in Cancer Proteomics. <i>Molecular Biotechnology</i> , 2002, 22, 139-152.	1.3	12
52	Oligosaccharide Release from Frozen and Paraffin-Wax-Embedded Archival Tissues. <i>Analytical Biochemistry</i> , 1996, 242, 8-14.	1.1	10
53	Preferential Lectin Binding of Cancer Cells upon Sialic Acid Treatment Under Nutrient Deprivation. <i>Applied Biochemistry and Biotechnology</i> , 2013, 171, 963-974.	1.4	10
54	Mendelian randomisation study of smoking exposure in relation to breast cancer risk. <i>British Journal of Cancer</i> , 2021, 125, 1135-1145.	2.9	9

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55	Release and analysis of polypeptides and glycopolypeptides from formalin-fixed, paraffin wax-embedded tissue. <i>The Histochemical Journal</i> , 1998, 30, 609-615.	0.6	8
56	Clinical relevance assessment of animal preclinical research (RAA) tool: development and explanation. <i>PeerJ</i> , 2021, 9, e10673.	0.9	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. <i>Health and Technology</i> , 2020, 10, 925-944.	2.1	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. <i>Breast Cancer Research</i> , 2021, 23, 86.	2.2	7
60	Functional annotation of the 2q35 breast cancer risk locus implicates a structural variant in influencing activity of a long-range enhancer element. <i>American Journal of Human Genetics</i> , 2021, 108, 1190-1203.	2.6	6
61	Two truncating variants in FANCC and breast cancer risk. <i>Scientific Reports</i> , 2019, 9, 12524.	1.6	5
62	A data science approach for early-stage prediction of Patient's susceptibility to acute side effects of advanced radiotherapy. <i>Computers in Biology and Medicine</i> , 2021, 135, 104624.	3.9	3
63	Germline HOXB13 mutations p.G84E and p.R217C do not confer an increased breast cancer risk. <i>Scientific Reports</i> , 2020, 10, 9688.	1.6	2
64	Altered expression of N-acetyl galactosamine glycoproteins by breast cancers. <i>Biochemical Society Transactions</i> , 1994, 22, 95S-95S.	1.6	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. <i>Methods in Molecular Biology</i> , 2012, 878, 111-120.	0.4	1
67	Machine Learning Classification of Females Susceptibility to Visceral Fat Associated Diseases. <i>IFMBE Proceedings</i> , 2020, , 679-693.	0.2	0