

# Thomas Karn

## List of Publications by Year in descending order

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87  
papers

6,127  
citations

109321

35  
h-index

74163

75  
g-index

93  
all docs

93  
docs citations

93  
times ranked

9263  
citing authors

#	ARTICLE	IF	CITATIONS
1	Predictive Markers of Response to Neoadjuvant Durvalumab with Nab-Paclitaxel and Dose-Dense Doxorubicin/Cyclophosphamide in Basal-Like Triple-Negative Breast Cancer. <i>Clinical Cancer Research</i> , 2022, 28, 2587-2597.	7.0	16
2	Immune-related Gene Expression Predicts Response to Neoadjuvant Chemotherapy but not Additional Benefit from PD-L1 Inhibition in Women with Early Triple-negative Breast Cancer. <i>Clinical Cancer Research</i> , 2021, 27, 2584-2591.	7.0	27
3	Reconstructing tumor history in breast cancer: signatures of mutational processes and response to neoadjuvant chemotherapy. <i>Annals of Oncology</i> , 2021, 32, 500-511.	1.2	9
4	Association of RAD51 with homologous recombination deficiency (HRD) and clinical outcomes in untreated triple-negative breast cancer (TNBC): analysis of the GeparSixto randomized clinical trial. <i>Annals of Oncology</i> , 2021, 32, 1590-1596.	1.2	55
5	Differential effect on different immune subsets of neoadjuvant chemotherapy in patients with TNBC. <i>Annals of Oncology</i> , 2020, 31, e001261.		18
6	Cardiotoxicity and Cardiovascular Biomarkers in Patients With Breast Cancer: Data From the GeparOcto-ECBG 84 Trial. <i>Journal of the American Heart Association</i> , 2020, 9, e018143.	3.7	23
7	MGMT promoter methylation in triple negative breast cancer of the GeparSixto trial. <i>PLoS ONE</i> , 2020, 15, e0238021.	2.5	8
8	Synthetic lethal combination targeting BET uncovered intrinsic susceptibility of TNBC to ferroptosis. <i>Science Advances</i> , 2020, 6, .	10.3	85
9	A Small Hypoxia Signature Predicted pCR Response to Bevacizumab in the Neoadjuvant GeparQuinto Breast Cancer Trial. <i>Clinical Cancer Research</i> , 2020, 26, 1896-1904.	7.0	9
10	Tumor mutational burden and immune infiltration as independent predictors of response to neoadjuvant immune checkpoint inhibition in early TNBC in GeparNuevo. <i>Annals of Oncology</i> , 2020, 31, 1216-1222.	1.2	128
11	Identification and Validation of a Novel Biologics Target in Triple Negative Breast Cancer. <i>Scientific Reports</i> , 2019, 9, 14934.	3.3	19
12	Clinical Relevance of Collagen Protein Degradation Markers C3M and C4M in the Serum of Breast Cancer Patients Treated with Neoadjuvant Therapy in the GeparQuinto Trial. <i>Cancers</i> , 2019, 11, 1186.	3.7	7
13	Evaluation of soluble carbonic anhydrase IX as predictive marker for efficacy of bevacizumab: A biomarker analysis from the gearquinto phase III neoadjuvant breast cancer trial. <i>International Journal of Cancer</i> , 2019, 145, 857-868.	5.1	12
14	Relevance of tumour-infiltrating lymphocytes, PD-1 and PD-L1 in patients with high-risk, nodal-metastasised breast cancer of the German Adjuvant Intergroup Node-positiv study. <i>European Journal of Cancer</i> , 2019, 114, 76-88.	2.8	37
15	Mutational Diversity and Therapy Response in Breast Cancer: A Sequencing Analysis in the Neoadjuvant GeparSepto Trial. <i>Clinical Cancer Research</i> , 2019, 25, 3986-3995.	7.0	32
16	Androgen receptor expression and response to chemotherapy in breast cancer patients treated in the neoadjuvant TECHNO and PREPARE trial. <i>British Journal of Cancer</i> , 2019, 121, 1009-1015.	6.4	12
17	TFF3 Expression as Stratification Marker in Borderline Epithelial Tumors of the Ovary. <i>Pathology and Oncology Research</i> , 2018, 24, 277-282.	1.9	5
18	Outcome after neoadjuvant chemotherapy in estrogen receptor-positive and progesterone receptor-negative breast cancer patients: a pooled analysis of individual patient data from ten prospectively randomized controlled neoadjuvant trials. <i>Breast Cancer Research and Treatment</i> , 2018, 167, 59-71.	2.5	32

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19	Tumour-infiltrating lymphocytes and prognosis in different subtypes of breast cancer: a pooled analysis of 3771 patients treated with neoadjuvant therapy. <i>Lancet Oncology</i> , The, 2018, 19, 40-50.	10.7	1,327
20	Claudin-1 is linked to presence of implants and micropapillary pattern in serous borderline epithelial tumours of the ovary. <i>Journal of Clinical Pathology</i> , 2018, 71, 1060-1064.	2.0	7
21	Immune Gene Expression Is Associated with Genomic Aberrations in Breast Cancer. <i>Cancer Research</i> , 2017, 77, 3317-3324.	0.9	117
22	BRCA1-like profile is not significantly associated with survival benefit of non-myeloablative intensified chemotherapy in the GAIN randomized controlled trial. <i>Breast Cancer Research and Treatment</i> , 2017, 166, 775-785.	2.5	2
23	Germline Mutation Status, Pathological Complete Response, and Disease-Free Survival in Triple-Negative Breast Cancer. <i>JAMA Oncology</i> , 2017, 3, 1378.	7.1	300
24	Association Between Genomic Metrics and Immune Infiltration in Triple-Negative Breast Cancer. <i>JAMA Oncology</i> , 2017, 3, 1707.	7.1	129
25	Targeting of PYK2 Synergizes with EGFR Antagonists in Basal-like TNBC and Circumvents HER3-Associated Resistance via the NEDD4-NDRG1 Axis. <i>Cancer Research</i> , 2017, 77, 86-99.	0.9	63
26	Abstract S1-07: Immune sculpting of the triple negative breast cancer genome. , 2017, , .		1
27	IMP3 Expression in Borderline Tumors of the Ovary. <i>Anticancer Research</i> , 2017, 37, 583-588.	1.1	4
28	Abstract P1-09-11: Outcome after neoadjuvant chemotherapy in progesterone receptor negative breast cancer patients – A pooled analysis of individual patient data from ten prospectively randomized controlled neoadjuvant trials. , 2017, , .		0
29	Fascin-1 expression as stratification marker in borderline epithelial tumours of the ovary. <i>Journal of Clinical Pathology</i> , 2016, 69, 142-148.	2.0	8
30	Subtype-Specific Metagene-Based Prediction of Outcome after Neoadjuvant and Adjuvant Treatment in Breast Cancer. <i>Clinical Cancer Research</i> , 2016, 22, 337-345.	7.0	58
31	Serum carbonic anhydrase IX as predictive marker for efficacy of bevacizumab: A biomarker analysis from the GeparQuinto phase III neoadjuvant breast cancer trial.. <i>Journal of Clinical Oncology</i> , 2016, 34, 11505-11505.	1.6	1
32	Abstract P3-07-28: BRCA1-like profile as predictive biomarker in non myeloablative chemotherapy (GAIN) Tj ETQq0 0 0 rgBT /Qverlock 10		
33	Abstract 3233: Macrophages orchestrate early dissemination of HER2+ cancer cells. , 2016, , .		0
34	Dynamic classification using case-specific training cohorts outperforms static gene expression signatures in breast cancer. <i>International Journal of Cancer</i> , 2015, 136, 2091-2098.	5.1	11
35	Expression of secreted protein acidic and rich in cysteine (SPARC) in breast cancer and response to neoadjuvant chemotherapy. <i>Annals of Oncology</i> , 2015, 26, 95-100.	1.2	64
36	Relevance of glycosylation-associated genes for tumor progression and metastasis localization in breast cancer. <i>Annals of Oncology</i> , 2015, 26, iii15.	1.2	1

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37	PYK2 sustains endosomal-derived receptor signalling and enhances epithelial-to-mesenchymal transition. <i>Nature Communications</i> , 2015, 6, 6064.	12.8	64
38	Genomic predictor of residual risk of recurrence after adjuvant chemotherapy and endocrine therapy in high risk estrogen receptor-positive breast cancers. <i>Breast Cancer Research and Treatment</i> , 2015, 149, 789-797.	2.5	4
39	The prognostic impact of age in different molecular subtypes of breast cancer. <i>Breast Cancer Research and Treatment</i> , 2015, 152, 667-673.	2.5	74
40	CD73 Is Associated with Poor Prognosis in High-Grade Serous Ovarian Cancer. <i>Cancer Research</i> , 2015, 75, 4494-4503.	0.9	186
41	Acid ceramidase is associated with an improved prognosis in both DCIS and invasive breast cancer. <i>Molecular Oncology</i> , 2015, 9, 58-67.	4.6	31
42	The Influence of Host Factors on the Prognosis of Breast Cancer: Stroma and Immune Cell Components as Cancer Biomarkers. <i>Current Cancer Drug Targets</i> , 2015, 15, 652-664.	1.6	33
43	Abstract P2-05-04: Gene expression associated with poor prognosis of young TNBC patients. , 2015, , .		0
44	Abstract P2-03-05: The heterogeneous clinical behavior of luminal breast cancers is associated with different mutational landscapes. , 2015, , .		0
45	Control of dataset bias in combined Affymetrix cohorts of triple negative breast cancer. <i>Genomics Data</i> , 2014, 2, 354-356.	1.3	9
46	The lipid-transfer protein Nir2 enhances epithelial-mesenchymal transition and facilitates breast cancer metastasis. <i>Journal of Cell Science</i> , 2014, 127, 4740-9.	2.0	32
47	OPG and PgR show similar cohort specific effects as prognostic factors in ER positive breast cancer. <i>Molecular Oncology</i> , 2014, 8, 1196-1207.	4.6	17
48	Prognostic relevance of glycosylation-associated genes in breast cancer. <i>Breast Cancer Research and Treatment</i> , 2014, 145, 295-305.	2.5	77
49	OPG and PGR Show Similar Cohort Specific Effects as Prognostic Factors in ER Positive Breast Cancer. <i>Annals of Oncology</i> , 2014, 25, i5.	1.2	0
50	Validity of the proliferation markers Ki67, TOP2A, and RacGAP1 in molecular subgroups of breast cancer. <i>Breast Cancer Research and Treatment</i> , 2013, 137, 57-67.	2.5	75
51	Prognostic evaluation of the B cell/IL-8 metagene in different intrinsic breast cancer subtypes. <i>Breast Cancer Research and Treatment</i> , 2013, 137, 407-416.	2.5	30
52	Androgen receptor expression is a predictive marker in chemotherapy-treated patients with endocrine receptor-positive primary breast cancers. <i>Journal of Cancer Research and Clinical Oncology</i> , 2013, 139, 809-816.	2.5	30
53	High-Throughput Gene Expression and Mutation Profiling: Current Methods and Future Perspectives. <i>Breast Care</i> , 2013, 8, 401-406.	1.4	14
54	Predictive value of sphingosine kinase 1 expression in neoadjuvant treatment of breast cancer. <i>Journal of Cancer Research and Clinical Oncology</i> , 2013, 139, 1681-1689.	2.5	13

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55	Acid Ceramidase (AC)â€™ A Key Enzyme of Sphingolipid Metabolismâ€™ Correlates With Better Prognosis in Epithelial Ovarian Cancer. <i>International Journal of Gynecological Pathology</i> , 2013, 32, 249-257.	1.4	18
56	Ki67 Measured after Neoadjuvant Chemotherapy for Primary Breast Cancer. <i>Clinical Cancer Research</i> , 2013, 19, 4521-4531.	7.0	137
57	Proliferation and estrogen signaling can distinguish patients at risk for early versus late relapse among estrogen receptor positive breast cancers. <i>Breast Cancer Research</i> , 2013, 15, R86.	5.0	44
58	Predictive value of HER2 serum levels in patients treated with lapatinib or trastuzumab â€™ a translational project in the neoadjuvant GeparQuinto trial. <i>British Journal of Cancer</i> , 2012, 107, 956-960.	6.4	33
59	Thymosin beta 15A (TMSB15A) is a predictor of chemotherapy response in triple-negative breast cancer. <i>British Journal of Cancer</i> , 2012, 107, 1892-1900.	6.4	20
60	A Comprehensive Analysis of Human Gene Expression Profiles Identifies Stromal Immunoglobulin Î² C as a Compatible Prognostic Marker in Human Solid Tumors. <i>Clinical Cancer Research</i> , 2012, 18, 2695-2703.	7.0	237
61	The role of genetic breast cancer susceptibility variants as prognostic factors. <i>Human Molecular Genetics</i> , 2012, 21, 3926-3939.	2.9	80
62	Melanoma antigen family A identified by the bimodality index defines a subset of triple negative breast cancers as candidates for immune response augmentation. <i>European Journal of Cancer</i> , 2012, 48, 12-23.	2.8	43
63	Controversies Concerning the Use of Neoadjuvant Systemic Therapy for Primary Breast Cancer. <i>World Journal of Surgery</i> , 2012, 36, 1480-1485.	1.6	6
64	Recommendations from an International Consensus Conference on the Current Status and Future of Neoadjuvant Systemic Therapy in Primary Breast Cancer. <i>Annals of Surgical Oncology</i> , 2012, 19, 1508-1516.	1.5	401
65	A clinically relevant gene signature in triple negative and basal-like breast cancer. <i>Breast Cancer Research</i> , 2011, 13, R97.	5.0	286
66	Homogeneous Datasets of Triple Negative Breast Cancers Enable the Identification of Novel Prognostic and Predictive Signatures. <i>PLoS ONE</i> , 2011, 6, e28403.	2.5	93
67	SATB1 gene expression and breast cancer prognosis. <i>Breast</i> , 2011, 20, 309-313.	2.2	41
68	Gene expression profiling of luminal B breast cancers reveals NHERF1 as a new marker of endocrine resistance. <i>Breast Cancer Research and Treatment</i> , 2011, 130, 409-420.	2.5	29
69	Data driven derivation of cutoffs from a pool of 3,030 Affymetrix arrays to stratify distinct clinical types of breast cancer. <i>Breast Cancer Research and Treatment</i> , 2010, 120, 567-579.	2.5	53
70	Clinical relevance of the putative stem cell marker p63 in breast cancer. <i>Breast Cancer Research and Treatment</i> , 2010, 122, 765-775.	2.5	27
71	Breast Cancer Proteomics â€™ Differences in Protein Expression between Estrogen Receptor-Positive and -Negative Tumors Identified by Tandem Mass Tag Technology. <i>Breast Care</i> , 2010, 5, 7-10.	1.4	4
72	Prognostic impact of thymidine phosphorylase expression in breast cancer â€™ Comparison of microarray and immunohistochemical data. <i>European Journal of Cancer</i> , 2010, 46, 549-557.	2.8	17

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73	Acid ceramidase 1 expression correlates with a better prognosis in ER-positive breast cancer. <i>Climacteric</i> , 2009, 12, 502-513.	2.4	43
74	Prognostic relevance of glucosylceramide synthase (GCS) expression in breast cancer. <i>Journal of Cancer Research and Clinical Oncology</i> , 2009, 135, 81-90.	2.5	32
75	Gene expression of ceramide kinase, galactosyl ceramide synthase and ganglioside CD3 synthase is associated with prognosis in breast cancer. <i>Journal of Cancer Research and Clinical Oncology</i> , 2009, 135, 1005-1013.	2.5	86
76	Gene expression of topoisomerase II alpha (TOP2A) by microarray analysis is highly prognostic in estrogen receptor (ER) positive breast cancer. <i>Breast Cancer Research and Treatment</i> , 2009, 113, 457-466.	2.5	57
77	Loss of Plexin B1 is highly prognostic in low proliferating ER positive breast cancers – Results of a large scale microarray analysis. <i>European Journal of Cancer</i> , 2009, 45, 405-413.	2.8	35
78	T-cell metagene predicts a favorable prognosis in estrogen receptor-negative and HER2-positive breast cancers. <i>Breast Cancer Research</i> , 2009, 11, R15.	5.0	380
79	Microarray analysis of altered sphingolipid metabolism reveals prognostic significance of sphingosine kinase 1 in breast cancer. <i>Breast Cancer Research and Treatment</i> , 2008, 112, 41-52.	2.5	280
80	Differentially expressed genes of reprogrammed human pluripotent stem cells in breast cancer. <i>European Journal of Cancer</i> , 2008, 44, 1789-1792.	2.8	9
81	Differential expression of claudins in human endometrium and endometriosis. <i>Gynecological Endocrinology</i> , 2008, 24, 442-449.	1.7	32
82	Poor Outcome in Estrogen Receptor-Positive Breast Cancers Predicted by Loss of Plexin B1. <i>Clinical Cancer Research</i> , 2007, 13, 1115-1122.	7.0	66
83	Gene expression profiling of breast cancer patients treated with docetaxel, doxorubicin, and cyclophosphamide within the GEPARTRIO trial: HER-2, but not topoisomerase II alpha and microtubule-associated protein tau, is highly predictive of tumor response. <i>Breast</i> , 2007, 16, 86-93.	2.2	70
84	The erbB2+ cluster of the intrinsic gene set predicts tumor response of breast cancer patients receiving neoadjuvant chemotherapy with docetaxel, doxorubicin and cyclophosphamide within the GEPARTRIO trial. <i>Breast</i> , 2007, 16, 235-240.	2.2	58
85	Predictive and Prognostic Markers in Breast Cancer Treatment – Presentations at the 28th San Antonio Breast Cancer Symposium 2005. <i>Breast Care</i> , 2006, 1, 118-122.	1.4	0
86	Gene Expression Profiles of Breast Cancer Obtained from Core Cut Biopsies Before Neoadjuvant Docetaxel, Adriamycin, and Cyclophosphamide Chemotherapy Correlate with Routine Prognostic Markers and Could Be Used to Identify Predictive Signatures. <i>Zentralblatt Fur Gynakologie</i> , 2006, 128, 76-81.	0.6	21
87	Methylation of estrogen receptor $\beta$ promoter correlates with loss of ER- $\beta$ expression in mammary carcinoma and is an early indication marker in premalignant lesions. <i>Endocrine-Related Cancer</i> , 2005, 12, 903-916.	3.1	70