

# Göran Jönsson

## List of Publications by Year in descending order

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Version: 2024-02-01

73  
papers

9,155  
citations

109137

35  
h-index

88477

70  
g-index

74  
all docs

74  
docs citations

74  
times ranked

17734  
citing authors

#	ARTICLE	IF	CITATIONS
1	B Cells and Tertiary Lymphoid Structures: Friends or Foes in Cancer Immunotherapy?. <i>Clinical Cancer Research</i> , 2022, 28, 1751-1758.	3.2	39
2	Efficacy of novel immunotherapy regimens in patients with metastatic melanoma with germline <i>CDKN2A</i> mutations. <i>Journal of Medical Genetics</i> , 2020, 57, 316-321.	1.5	33
3	Analysis of DNA methylation patterns in the tumor immune microenvironment of metastatic melanoma. <i>Molecular Oncology</i> , 2020, 14, 933-950.	2.1	29
4	Prime-boost vaccination strategy enhances immunogenicity compared to single pneumococcal conjugate vaccination in patients receiving conventional DMARDs, to some extent in abatacept but not in rituximab-treated patients. <i>Arthritis Research and Therapy</i> , 2020, 22, 36.	1.6	15
5	Tertiary lymphoid structures improve immunotherapy and survival in melanoma. <i>Nature</i> , 2020, 577, 561-565.	13.7	1,209
6	The Role of PTEN Loss in Immune Escape, Melanoma Prognosis and Therapy Response. <i>Cancers</i> , 2020, 12, 742.	1.7	38
7	Whole-genome landscape of mucosal melanoma reveals diverse drivers and therapeutic targets. <i>Nature Communications</i> , 2019, 10, 3163.	5.8	205
8	Transcriptomic Analysis Reveals Prognostic Molecular Signatures of Stage I Melanoma. <i>Clinical Cancer Research</i> , 2019, 25, 7424-7435.	3.2	27
9	The X-Linked DDX3X RNA Helicase Dictates Translation Reprogramming and Metastasis in Melanoma. <i>Cell Reports</i> , 2019, 27, 3573-3586.e7.	2.9	66
10	Evaluation of the contribution of germline variants in BRCA1 and BRCA2 to uveal and cutaneous melanoma. <i>Melanoma Research</i> , 2019, 29, 483-490.	0.6	13
11	Comparative genomics reveals that loss of lunatic fringe ( <i>LFNG</i> ) promotes melanoma metastasis. <i>Molecular Oncology</i> , 2018, 12, 239-255.	2.1	20
12	The Genetic Evolution of Melanoma. , 2018, , 105-114.		0
13	<i>NF1</i> mutated melanoma tumors harbor distinct clinical and biological characteristics. <i>Molecular Oncology</i> , 2017, 11, 438-451.	2.1	112
14	Mutational and putative neoantigen load predict clinical benefit of adoptive T cell therapy in melanoma. <i>Nature Communications</i> , 2017, 8, 1738.	5.8	310
15	Correlation of histopathologic characteristics to protein expression and function in malignant melanoma. <i>PLoS ONE</i> , 2017, 12, e0176167.	1.1	27
16	Melanoma Genetics and Genomics. , 2017, , 63-93.		0
17	Consensus of Melanoma Gene Expression Subtypes Converges on Biological Entities. <i>Journal of Investigative Dermatology</i> , 2016, 136, 2502-2505.	0.3	23
18	A Preclinical Model of Malignant Peripheral Nerve Sheath Tumor-like Melanoma Is Characterized by Infiltrating Mast Cells. <i>Cancer Research</i> , 2016, 76, 251-263.	0.4	33

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19	Deep sequencing of uveal melanoma identifies a recurrent mutation in <i>PLCB4</i> . <i>Oncotarget</i> , 2016, 7, 4624-4631.	0.8	235
20	<i>CDKN2a</i> mutation-negative melanoma families have increased risk exclusively for skin cancers but not for other malignancies. <i>International Journal of Cancer</i> , 2015, 137, 2220-2226.	2.3	19
21	DNA methylation subgroups in melanoma are associated with proliferative and immunological processes. <i>BMC Medical Genomics</i> , 2015, 8, 73.	0.7	29
22	A Protein Deep Sequencing Evaluation of Metastatic Melanoma Tissues. <i>PLoS ONE</i> , 2015, 10, e0123661.	1.1	19
23	Genome-Wide DNA Methylation Analysis in Melanoma Reveals the Importance of CpG Methylation in MITF Regulation. <i>Journal of Investigative Dermatology</i> , 2015, 135, 1820-1828.	0.3	46
24	The association between antibody levels before and after 7-valent pneumococcal conjugate vaccine immunization and subsequent pneumococcal infection in chronic arthritis patients. <i>Arthritis Research and Therapy</i> , 2015, 17, 124.	1.6	14
25	Immune responses following meningococcal serogroups A, C, Y and W polysaccharide vaccination in C2-deficient persons: Evidence for increased levels of serum bactericidal antibodies. <i>Vaccine</i> , 2015, 33, 1839-1845.	1.7	9
26	MITF and c-Jun antagonism interconnects melanoma dedifferentiation with pro-inflammatory cytokine responsiveness and myeloid cell recruitment. <i>Nature Communications</i> , 2015, 6, 8755.	5.8	175
27	Molecular Characterization of Melanoma Cases in Denmark Suspected of Genetic Predisposition. <i>PLoS ONE</i> , 2015, 10, e0122662.	1.1	21
28	Molecular stratification of metastatic melanoma using gene expression profiling : Prediction of survival outcome and benefit from molecular targeted therapy. <i>Oncotarget</i> , 2015, 6, 12297-12309.	0.8	148
29	Loss of CITED1, an MITF regulator, drives a phenotype switch <i>in vitro</i> and can predict clinical outcome in primary melanoma tumours. <i>PeerJ</i> , 2015, 3, e788.	0.9	20
30	High risk of tobacco-related cancers in <i>CDKN2A</i> mutation-positive melanoma families. <i>Journal of Medical Genetics</i> , 2014, 51, 545-552.	1.5	73
31	Molecular and genetic diversity in the metastatic process of melanoma. <i>Journal of Pathology</i> , 2014, 233, 39-50.	2.1	58
32	Immune Cell-Poor Melanomas Benefit from PD-1 Blockade after Targeted Type I IFN Activation. <i>Cancer Discovery</i> , 2014, 4, 674-687.	7.7	226
33	Genome-wide DNA Methylation Analysis of Lung Carcinoma Reveals One Neuroendocrine and Four Adenocarcinoma Epitypes Associated with Patient Outcome. <i>Clinical Cancer Research</i> , 2014, 20, 6127-6140.	3.2	91
34	Feasibility Study on Measuring Selected Proteins in Malignant Melanoma Tissue by SRM Quantification. <i>Journal of Proteome Research</i> , 2014, 13, 1315-1326.	1.8	9
35	Primary Melanoma Tumors from <i>CDKN2A</i> Mutation Carriers Do Not Belong to a Distinct Molecular Subclass. <i>Journal of Investigative Dermatology</i> , 2014, 134, 3000-3003.	0.3	8
36	WNT5A induces release of exosomes containing pro-angiogenic and immunosuppressive factors from malignant melanoma cells. <i>Molecular Cancer</i> , 2014, 13, 88.	7.9	213

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37	Advances in molecular profiling of malignant melanoma: ready for clinical practice?. Melanoma Management, 2014, 1, 3-6.	0.1	0
38	Establishing a Southern Swedish Malignant Melanoma OMICS and biobank clinical capability. Clinical and Translational Medicine, 2013, 2, 7.	1.7	15
39	Low BRAF and NRAS expression levels are associated with clinical benefit from DTIC therapy and prognosis in metastatic melanoma. Clinical and Experimental Metastasis, 2013, 30, 867-876.	1.7	16
40	Gain of chromosomal region 20q and loss of 18 discriminates between Lynch syndrome and familial colorectal cancer. European Journal of Cancer, 2013, 49, 1226-1235.	1.3	23
41	Nonfamilial Breast Cancer Subtypes. Methods in Molecular Biology, 2013, 973, 279-295.	0.4	5
42	Monitoring of Technical Variation in Quantitative High-Throughput Datasets. Cancer Informatics, 2013, 12, CIN.S12862.	0.9	47
43	The Retinoblastoma Gene Undergoes Rearrangements in BRCA1-Deficient Basal-like Breast Cancer. Cancer Research, 2012, 72, 4028-4036.	0.4	41
44	Molecular Profiling Reveals Low- and High-Grade Forms of Primary Melanoma. Clinical Cancer Research, 2012, 18, 4026-4036.	3.2	96
45	Vaccination against encapsulated bacteria in hereditary C2 deficiency results in antibody response and opsonization due to antibody-dependent complement activation. Clinical Immunology, 2012, 144, 214-227.	1.4	24
46	Mutational Processes Molding the Genomes of 21 Breast Cancers. Cell, 2012, 149, 979-993.	13.5	1,673
47	The Life History of 21 Breast Cancers. Cell, 2012, 149, 994-1007.	13.5	1,249
48	Relation between smoking history and gene expression profiles in lung adenocarcinomas. BMC Medical Genomics, 2012, 5, 22.	0.7	41
49	Characterisation of amplification patterns and target genes at chromosome 11q13 in CCND1-amplified sporadic and familial breast tumours. Breast Cancer Research and Treatment, 2012, 133, 583-594.	1.1	44
50	Genome-wide association study identifies three new melanoma susceptibility loci. Nature Genetics, 2011, 43, 1108-1113.	9.4	230
51	Landscape of somatic allelic imbalances and copy number alterations in HER2-amplified breast cancer. Breast Cancer Research, 2011, 13, R129.	2.2	25
52	High-resolution genomic profiling of male breast cancer reveals differences hidden behind the similarities with female breast cancer. Breast Cancer Research and Treatment, 2011, 129, 747-760.	1.1	70
53	Melanoma Genetics and Genomics. , 2011, , 57-77.		0
54	Gene Expression Profiling-Based Identification of Molecular Subtypes in Stage IV Melanomas with Different Clinical Outcome. Clinical Cancer Research, 2010, 16, 3356-3367.	3.2	235

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55	Identification of Subtypes in Human Epidermal Growth Factor Receptor 2â€“Positive Breast Cancer Reveals a Gene Signature Prognostic of Outcome. <i>Journal of Clinical Oncology</i> , 2010, 28, 1813-1820.	0.8	145
56	High-resolution genomic and expression analyses of copy number alterations in HER2-amplified breast cancer. <i>Breast Cancer Research</i> , 2010, 12, R25.	2.2	123
57	Genome-wide search for breast cancer linkage in large Icelandic non-BRCA1/2 families. <i>Breast Cancer Research</i> , 2010, 12, R50.	2.2	18
58	Molecular subtypes of breast cancer are associated with characteristic DNA methylation patterns. <i>Breast Cancer Research</i> , 2010, 12, R36.	2.2	251
59	Genomic subtypes of breast cancer identified by array-comparative genomic hybridization display distinct molecular and clinical characteristics. <i>Breast Cancer Research</i> , 2010, 12, R42.	2.2	167
60	Multiple metastases from cutaneous malignant melanoma patients may display heterogeneous genomic and epigenomic patterns. <i>Melanoma Research</i> , 2010, 20, 381-391.	0.6	30
61	Tiling array-CGH for the assessment of genomic similarities among synchronous unilateral and bilateral invasive breast cancer tumor pairs. <i>BMC Clinical Pathology</i> , 2008, 8, 6.	1.8	28
62	Effect of polyamine deficiency on proteins involved in Okazaki fragment maturation. <i>Cell Biology International</i> , 2008, 32, 1467-1477.	1.4	7
63	Recurrent gross mutations of the PTEN tumor suppressor gene in breast cancers with deficient DSB repair. <i>Nature Genetics</i> , 2008, 40, 102-107.	9.4	316
64	Prognostic Impact of Array-based Genomic Profiles in Esophageal Squamous Cell Cancer. <i>BMC Cancer</i> , 2008, 8, 98.	1.1	77
65	Molecular mechanisms underlying N 1, N 11-diethylnorspermine-induced apoptosis in a human breast cancer cell line. <i>Anti-Cancer Drugs</i> , 2008, 19, 871-883.	0.7	9
66	Different cell cycle kinetic effects of N 1,N 11-diethylnorspermine-induced polyamine depletion in four human breast cancer cell lines. <i>Anti-Cancer Drugs</i> , 2008, 19, 359-368.	0.7	14
67	Tumor Genome Wide DNA Alterations Assessed by Array CGH in Patients with Poor and Excellent Survival following Operation for Colorectal Cancer. <i>Cancer Informatics</i> , 2007, 3, 117693510700300.	0.9	13
68	High-resolution genomic profiles of breast cancer cell lines assessed by tiling BAC array comparative genomic hybridization. <i>Genes Chromosomes and Cancer</i> , 2007, 46, 543-558.	1.5	176
69	Normalization of array-CGH data: influence of copy number imbalances. <i>BMC Genomics</i> , 2007, 8, 382.	1.2	57
70	Tumor genome wide DNA alterations assessed by array CGH in patients with poor and excellent survival following operation for colorectal cancer. <i>Cancer Informatics</i> , 2007, 3, 341-55.	0.9	7
71	Chromosome 5 imbalance mapping in breast tumors from BRCA1 and BRCA2 mutation carriers and sporadic breast tumors. <i>International Journal of Cancer</i> , 2006, 119, 1052-1060.	2.3	59
72	Distinct Genomic Profiles in Hereditary Breast Tumors Identified by Array-Based Comparative Genomic Hybridization. <i>Cancer Research</i> , 2005, 65, 7612-7621.	0.4	147

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73	Mapping of a Novel Ocular and Cutaneous Malignant Melanoma Susceptibility Locus to Chromosome 9q21.32. Journal of the National Cancer Institute, 2005, 97, 1377-1382.	3.0	63