

# 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	Mutational Processes Molding the Genomes of 21 Breast Cancers. <i>Cell</i> , 2012, 149, 979-993.	13.5	1,673
2	The Life History of 21 Breast Cancers. <i>Cell</i> , 2012, 149, 994-1007.	13.5	1,249
3	Tertiary lymphoid structures improve immunotherapy and survival in melanoma. <i>Nature</i> , 2020, 577, 561-565.	13.7	1,209
4	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
5	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
6	Molecular subtypes of breast cancer are associated with characteristic DNA methylation patterns. <i>Breast Cancer Research</i> , 2010, 12, R36.	2.2	251
7	Gene Expression Profiling-Based Identification of Molecular Subtypes in Stage IV Melanomas with Different Clinical Outcome. <i>Clinical Cancer Research</i> , 2010, 16, 3356-3367.	3.2	235
8	Deep sequencing of uveal melanoma identifies a recurrent mutation in <i>PLCB4</i> . <i>Oncotarget</i> , 2016, 7, 4624-4631.	0.8	235
9	Genome-wide association study identifies three new melanoma susceptibility loci. <i>Nature Genetics</i> , 2011, 43, 1108-1113.	9.4	230
10	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
11	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
12	Whole-genome landscape of mucosal melanoma reveals diverse drivers and therapeutic targets. <i>Nature Communications</i> , 2019, 10, 3163.	5.8	205
13	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
14	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
15	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
16	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
17	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
18	Identification of Subtypes in Human Epidermal Growth Factor Receptor 2-Positive Breast Cancer Reveals a Gene Signature Prognostic of Outcome. <i>Journal of Clinical Oncology</i> , 2010, 28, 1813-1820.	0.8	145

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19	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
20	CDKN2A-mutated melanoma tumors harbor distinct clinical and biological characteristics. <i>Molecular Oncology</i> , 2017, 11, 438-451.	2.1	112
21	Molecular Profiling Reveals Low- and High-Grade Forms of Primary Melanoma. <i>Clinical Cancer Research</i> , 2012, 18, 4026-4036.	3.2	96
22	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
23	Prognostic Impact of Array-based Genomic Profiles in Esophageal Squamous Cell Cancer. <i>BMC Cancer</i> , 2008, 8, 98.	1.1	77
24	High risk of tobacco-related cancers in CDKN2A-mutation-positive melanoma families. <i>Journal of Medical Genetics</i> , 2014, 51, 545-552.	1.5	73
25	High-resolution genomic profiling of male breast cancer reveals differences hidden behind the similarities with female breast cancer. <i>Breast Cancer Research and Treatment</i> , 2011, 129, 747-760.	1.1	70
26	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
27	Mapping of a Novel Ocular and Cutaneous Malignant Melanoma Susceptibility Locus to Chromosome 9q21.32. <i>Journal of the National Cancer Institute</i> , 2005, 97, 1377-1382.	3.0	63
28	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
29	Molecular and genetic diversity in the metastatic process of melanoma. <i>Journal of Pathology</i> , 2014, 233, 39-50.	2.1	58
30	Normalization of array-CGH data: influence of copy number imbalances. <i>BMC Genomics</i> , 2007, 8, 382.	1.2	57
31	Monitoring of Technical Variation in Quantitative High-Throughput Datasets. <i>Cancer Informatics</i> , 2013, 12, CIN.S12862.	0.9	47
32	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
33	Characterisation of amplification patterns and target genes at chromosome 11q13 in CCND1-amplified sporadic and familial breast tumours. <i>Breast Cancer Research and Treatment</i> , 2012, 133, 583-594.	1.1	44
34	The Retinoblastoma Gene Undergoes Rearrangements in BRCA1-Deficient Basal-like Breast Cancer. <i>Cancer Research</i> , 2012, 72, 4028-4036.	0.4	41
35	Relation between smoking history and gene expression profiles in lung adenocarcinomas. <i>BMC Medical Genomics</i> , 2012, 5, 22.	0.7	41
36	B Cells and Tertiary Lymphoid Structures: Friends or Foes in Cancer Immunotherapy?. <i>Clinical Cancer Research</i> , 2022, 28, 1751-1758.	3.2	39

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37	The Role of PTEN Loss in Immune Escape, Melanoma Prognosis and Therapy Response. <i>Cancers</i> , 2020, 12, 742.	1.7	38
38	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
39	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
40	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
41	DNA methylation subgroups in melanoma are associated with proliferative and immunological processes. <i>BMC Medical Genomics</i> , 2015, 8, 73.	0.7	29
42	Analysis of DNA methylation patterns in the tumor immune microenvironment of metastatic melanoma. <i>Molecular Oncology</i> , 2020, 14, 933-950.	2.1	29
43	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
44	Transcriptomic Analysis Reveals Prognostic Molecular Signatures of Stage I Melanoma. <i>Clinical Cancer Research</i> , 2019, 25, 7424-7435.	3.2	27
45	Correlation of histopathologic characteristics to protein expression and function in malignant melanoma. <i>PLoS ONE</i> , 2017, 12, e0176167.	1.1	27
46	Landscape of somatic allelic imbalances and copy number alterations in HER2-amplified breast cancer. <i>Breast Cancer Research</i> , 2011, 13, R129.	2.2	25
47	Vaccination against encapsulated bacteria in hereditary C2 deficiency results in antibody response and opsonization due to antibody-dependent complement activation. <i>Clinical Immunology</i> , 2012, 144, 214-227.	1.4	24
48	Gain of chromosomal region 20q and loss of 18 discriminates between Lynch syndrome and familial colorectal cancer. <i>European Journal of Cancer</i> , 2013, 49, 1226-1235.	1.3	23
49	Consensus of Melanoma Gene Expression Subtypes Converges on Biological Entities. <i>Journal of Investigative Dermatology</i> , 2016, 136, 2502-2505.	0.3	23
50	Molecular Characterization of Melanoma Cases in Denmark Suspected of Genetic Predisposition. <i>PLoS ONE</i> , 2015, 10, e0122662.	1.1	21
51	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
52	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
53	<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
54	A Protein Deep Sequencing Evaluation of Metastatic Melanoma Tissues. <i>PLoS ONE</i> , 2015, 10, e0123661.	1.1	19

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55	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
56	Low BRAF and NRAS expression levels are associated with clinical benefit from DTIC therapy and prognosis in metastatic melanoma. <i>Clinical and Experimental Metastasis</i> , 2013, 30, 867-876.	1.7	16
57	Establishing a Southern Swedish Malignant Melanoma OMICS and biobank clinical capability. <i>Clinical and Translational Medicine</i> , 2013, 2, 7.	1.7	15
58	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
59	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
60	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
61	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
62	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
63	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
64	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
65	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
66	Primary Melanoma Tumors from CDKN2A Mutation Carriers Do Not Belong to a Distinct Molecular Subclass. <i>Journal of Investigative Dermatology</i> , 2014, 134, 3000-3003.	0.3	8
67	Effect of polyamine deficiency on proteins involved in Okazaki fragment maturation. <i>Cell Biology International</i> , 2008, 32, 1467-1477.	1.4	7
68	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
69	Nonfamilial Breast Cancer Subtypes. <i>Methods in Molecular Biology</i> , 2013, 973, 279-295.	0.4	5
70	Advances in molecular profiling of malignant melanoma: ready for clinical practice?. <i>Melanoma Management</i> , 2014, 1, 3-6.	0.1	0
71	The Genetic Evolution of Melanoma. , 2018, , 105-114.		0
72	Melanoma Genetics and Genomics. , 2011, , 57-77.		0

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73	Melanoma Genetics and Genomics. , 2017, , 63-93.		0