

Göran Jönsson

List of Publications by Year in descending order

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Version: 2024-02-01

66
papers

4,918
citations

172207

29
h-index

114278

63
g-index

69
all docs

69
docs citations

69
times ranked

9501
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	Incidence and predictors of severe infections in ANCA-associated vasculitis: a population-based cohort study. <i>Rheumatology</i> , 2021, 60, 2745-2754.	0.9	30
3	Infections Are Associated With Increased Risk of Giant Cell Arteritis: A Population-based Case-control Study from Southern Sweden. <i>Journal of Rheumatology</i> , 2021, 48, 251-257.	1.0	16
4	Increased serum bactericidal activity of autologous serum in C2 deficiency after vaccination against <i>Haemophilus influenzae</i> type b, and further support for an MBL-dependent C2 bypass mechanism. <i>Vaccine</i> , 2021, 39, 1297-1302.	1.7	1
5	Midkine – A potential therapeutic target in melanoma. <i>Pigment Cell and Melanoma Research</i> , 2021, 34, 834-835.	1.5	0
6	Methotrexate reduces circulating Th17 cells and impairs plasmablast and memory B cell expansions following pneumococcal conjugate immunization in RA patients. <i>Scientific Reports</i> , 2021, 11, 9199.	1.6	13
7	Clinical efficacy of T-cell therapy after short-term BRAF-inhibitor priming in patients with checkpoint inhibitor-resistant metastatic melanoma. , 2021, 9, e002703.		9
8	Transcriptomic signatures of tumors undergoing T cell attack. <i>Cancer Immunology, Immunotherapy</i> , 2021, , 1.	2.0	6
9	Rapid Identification of the Tumor-Specific Reactive TIL Repertoire via Combined Detection of CD137, TNF, and IFN γ , Following Recognition of Autologous Tumor-Antigens. <i>Frontiers in Immunology</i> , 2021, 12, 705422.	2.2	10
10	Tumor genetic heterogeneity analysis of chronic sun-damaged melanoma. <i>Pigment Cell and Melanoma Research</i> , 2020, 33, 480-489.	1.5	22
11	Clinical Utility of Targeted Sequencing in Lung Cancer: Experience From an Autonomous Swedish Health Care Center. <i>JTO Clinical and Research Reports</i> , 2020, 1, 100013.	0.6	4
12	Qualitative Analysis of Tumor-Infiltrating Lymphocytes across Human Tumor Types Reveals a Higher Proportion of Bystander CD8+ T Cells in Non-Melanoma Cancers Compared to Melanoma. <i>Cancers</i> , 2020, 12, 3344.	1.7	19
13	Escape from nonsense-mediated decay associates with anti-tumor immunogenicity. <i>Nature Communications</i> , 2020, 11, 3800.	5.8	61
14	Analysis of DNA methylation patterns in the tumor immune microenvironment of metastatic melanoma. <i>Molecular Oncology</i> , 2020, 14, 933-950.	2.1	29
15	CTLA-4 blockade boosts the expansion of tumor-reactive CD8+ tumor-infiltrating lymphocytes in ovarian cancer. <i>Scientific Reports</i> , 2020, 10, 3914.	1.6	50
16	Tertiary lymphoid structures improve immunotherapy and survival in melanoma. <i>Nature</i> , 2020, 577, 561-565.	13.7	1,209
17	The Role of PTEN Loss in Immune Escape, Melanoma Prognosis and Therapy Response. <i>Cancers</i> , 2020, 12, 742.	1.7	38
18	Whole-genome landscape of mucosal melanoma reveals diverse drivers and therapeutic targets. <i>Nature Communications</i> , 2019, 10, 3163.	5.8	205

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19	Germline variants in oculocutaneous albinism genes and predisposition to familial cutaneous melanoma. <i>Pigment Cell and Melanoma Research</i> , 2019, 32, 854-863.	1.5	14
20	165.â€¦INFECTIONS ARE ASSOCIATED WITH INCREASED RISK OF GIANT CELL ARTERITIS - A POPULATION-BASED CASE-CONTROL STUDY FROM SOUTHERN SWEDEN. <i>Rheumatology</i> , 2019, 58, .	0.9	0
21	Transcriptomic Analysis Reveals Prognostic Molecular Signatures of Stage I Melanoma. <i>Clinical Cancer Research</i> , 2019, 25, 7424-7435.	3.2	27
22	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
23	Clinical protein science in translational medicine targeting malignant melanoma. <i>Cell Biology and Toxicology</i> , 2019, 35, 293-332.	2.4	33
24	The Hidden Story of Heterogeneous B-raf V600E Mutation Quantitative Protein Expression in Metastatic Melanomaâ€”Association with Clinical Outcome and Tumor Phenotypes. <i>Cancers</i> , 2019, 11, 1981.	1.7	16
25	Immunoprofiles of colorectal cancer from Lynch syndrome. <i>Oncolmmunology</i> , 2019, 8, e1515612.	2.1	14
26	Pseudouridylation of tRNA-Derived Fragments Steers Translational Control in Stem Cells. <i>Cell</i> , 2018, 173, 1204-1216.e26.	13.5	332
27	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
28	KITD816V Induces SRC-Mediated Tyrosine Phosphorylation of MITF and Altered Transcription Program in Melanoma. <i>Molecular Cancer Research</i> , 2017, 15, 1265-1274.	1.5	15
29	Immune response to pneumococcal conjugate vaccine in patients with systemic vasculitis receiving standard of care therapy. <i>Vaccine</i> , 2017, 35, 3639-3646.	1.7	21
30	Rare Variant, Gene-Based Association Study of Hereditary Melanoma Using Whole-Exome Sequencing. <i>Journal of the National Cancer Institute</i> , 2017, 109, .	3.0	32
31	Targeted sequencing may facilitate differential diagnostics of pulmonary tumours: a case series. <i>Diagnostic Pathology</i> , 2017, 12, 31.	0.9	7
32	<i>NF1</i> mutated melanoma tumors harbor distinct clinical and biological characteristics. <i>Molecular Oncology</i> , 2017, 11, 438-451.	2.1	112
33	Acquired Immune Resistance Follows Complete Tumor Regression without Loss of Target Antigens or IFN β Signaling. <i>Cancer Research</i> , 2017, 77, 4562-4566.	0.4	39
34	Clinical framework for next generation sequencing based analysis of treatment predictive mutations and multiplexed gene fusion detection in non-small cell lung cancer. <i>Oncotarget</i> , 2017, 8, 34796-34810.	0.8	45
35	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
36	Correlation of histopathologic characteristics to protein expression and function in malignant melanoma. <i>PLoS ONE</i> , 2017, 12, e0176167.	1.1	27

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37	High <i>TERT</i> promoter mutation frequency in non-actinic cutaneous metastatic melanoma. <i>Pigment Cell and Melanoma Research</i> , 2016, 29, 598-600.	1.5	22
38	Multiregion Whole-Exome Sequencing Uncovers the Genetic Evolution and Mutational Heterogeneity of Early-Stage Metastatic Melanoma. <i>Cancer Research</i> , 2016, 76, 4765-4774.	0.4	86
39	Germline <i>CDKN2A</i> Mutation Status and Survival in Familial Melanoma Cases. <i>Journal of the National Cancer Institute</i> , 2016, 108, djw135.	3.0	47
40	An integrated genomics analysis of epigenetic subtypes in human breast tumors links DNA methylation patterns to chromatin states in normal mammary cells. <i>Breast Cancer Research</i> , 2016, 18, 27.	2.2	67
41	Consensus of Melanoma Gene Expression Subtypes Converges on Biological Entities. <i>Journal of Investigative Dermatology</i> , 2016, 136, 2502-2505.	0.3	23
42	Promoter Methylation of <i>PTEN</i> Is a Significant Prognostic Factor in Melanoma Survival. <i>Journal of Investigative Dermatology</i> , 2016, 136, 1002-1011.	0.3	51
43	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
44	Prognostic and Chemotherapy Predictive Value of Gene-Expression Phenotypes in Primary Lung Adenocarcinoma. <i>Clinical Cancer Research</i> , 2016, 22, 218-229.	3.2	29
45	DNA methylation subgroups in melanoma are associated with proliferative and immunological processes. <i>BMC Medical Genomics</i> , 2015, 8, 73.	0.7	29
46	A Protein Deep Sequencing Evaluation of Metastatic Melanoma Tissues. <i>PLoS ONE</i> , 2015, 10, e0123661.	1.1	19
47	Mutational and gene fusion analyses of primary large cell and large cell neuroendocrine lung cancer. <i>Oncotarget</i> , 2015, 6, 22028-22037.	0.8	61
48	Genome-Wide DNA Methylation Analysis in Melanoma Reveals the Importance of CpG Methylation in <i>MITF</i> Regulation. <i>Journal of Investigative Dermatology</i> , 2015, 135, 1820-1828.	0.3	46
49	<i>MITF</i> Modulates Therapeutic Resistance through <i>EGFR</i> Signaling. <i>Journal of Investigative Dermatology</i> , 2015, 135, 1863-1872.	0.3	76
50	<i>MITF</i> and <i>c-Jun</i> antagonism interconnects melanoma dedifferentiation with pro-inflammatory cytokine responsiveness and myeloid cell recruitment. <i>Nature Communications</i> , 2015, 6, 8755.	5.8	175
51	Recurrent fever caused by <i>Candidatus Neoehrlichia mikurensis</i> in a rheumatoid arthritis patient treated with rituximab. <i>Rheumatology</i> , 2015, 54, 369-371.	0.9	23
52	<i>BAP1</i> Has a Survival Role in Cutaneous Melanoma. <i>Journal of Investigative Dermatology</i> , 2015, 135, 1089-1097.	0.3	31
53	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
54	Loss of <i>CITED1</i> , an <i>MITF</i> 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

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55	Somatic BRAF and NRAS Mutations in Familial Melanomas with Known Germline CDKN2A Status: A GenoMEL Study. <i>Journal of Investigative Dermatology</i> , 2014, 134, 287-290.	0.3	18
56	Molecular and genetic diversity in the metastatic process of melanoma. <i>Journal of Pathology</i> , 2014, 233, 39-50.	2.1	58
57	Immune Cellâ€“Poor Melanomas Benefit from PD-1 Blockade after Targeted Type I IFN Activation. <i>Cancer Discovery</i> , 2014, 4, 674-687.	7.7	226
58	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
59	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
60	Investigation of a putative melanoma susceptibility locus at chromosome 3q29. <i>Cancer Genetics</i> , 2014, 207, 70-74.	0.2	3
61	Immune escape mechanisms associated with tumor recurrence after adoptive cell transfer immunotherapy.. <i>Journal of Clinical Oncology</i> , 2014, 32, 3054-3054.	0.8	0
62	Risk of tobacco-related cancers in <i>CDKN2A</i> mutation-positive melanoma families.. <i>Journal of Clinical Oncology</i> , 2014, 32, 1513-1513.	0.8	0
63	The Retinoblastoma Gene Undergoes Rearrangements in <i>BRCA1</i>-Deficient Basal-like Breast Cancer. <i>Cancer Research</i> , 2012, 72, 4028-4036.	0.4	41
64	Gene Expression Profilingâ€“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
65	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
66	Hereditary C2 Deficiency in Sweden. <i>Medicine (United States)</i> , 2005, 84, 23-34.	0.4	153