

# Peter A Johansson

## List of Publications by Year in descending order

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Version: 2024-02-01

59  
papers

4,587  
citations

159585

30  
h-index

144013

57  
g-index

60  
all docs

60  
docs citations

60  
times ranked

8327  
citing authors

#	ARTICLE	IF	CITATIONS
1	Whole-genome landscapes of major melanoma subtypes. <i>Nature</i> , 2017, 545, 175-180.	27.8	1,068
2	Poor prognosis in carcinoma is associated with a gene expression signature of aberrant PTEN tumor suppressor pathway activity. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 7564-7569.	7.1	445
3	POT1 loss-of-function variants predispose to familial melanoma. <i>Nature Genetics</i> , 2014, 46, 478-481.	21.4	319
4	Increased MAPK reactivation in early resistance to dabrafenib/trametinib combination therapy of BRAF-mutant metastatic melanoma. <i>Nature Communications</i> , 2014, 5, 5694.	12.8	295
5	Deep sequencing of uveal melanoma identifies a recurrent mutation in <i>PLCB4</i> . <i>Oncotarget</i> , 2016, 7, 4624-4631.	1.8	235
6	Whole-genome landscape of mucosal melanoma reveals diverse drivers and therapeutic targets. <i>Nature Communications</i> , 2019, 10, 3163.	12.8	205
7	Microarray expression profiling in melanoma reveals a BRAF mutation signature. <i>Oncogene</i> , 2004, 23, 4060-4067.	5.9	169
8	Comprehensive Study of the Clinical Phenotype of Germline <i>BAP1</i> Variant-Carrying Families Worldwide. <i>Journal of the National Cancer Institute</i> , 2018, 110, 1328-1341.	6.3	164
9	Nonsense Mutations in the Shelterin Complex Genes ACD and TERF2IP in Familial Melanoma. <i>Journal of the National Cancer Institute</i> , 2015, 107, .	6.3	134
10	Whole-genome sequencing of acral melanoma reveals genomic complexity and diversity. <i>Nature Communications</i> , 2020, 11, 5259.	12.8	102
11	Recurrent inactivating RASA2 mutations in melanoma. <i>Nature Genetics</i> , 2015, 47, 1408-1410.	21.4	90
12	Whole genome landscapes of uveal melanoma show an ultraviolet radiation signature in iris tumours. <i>Nature Communications</i> , 2020, 11, 2408.	12.8	86
13	A recurrent germline <i>BAP1</i> mutation and extension of the <i>BAP1</i> tumor predisposition spectrum to include basal cell carcinoma. <i>Clinical Genetics</i> , 2015, 88, 267-272.	2.0	81
14	Confirmation of a BRAF mutation-associated gene expression signature in melanoma. <i>Pigment Cell &amp; Melanoma Research</i> , 2007, 20, 216-221.	3.6	76
15	Detection and Identification of Protein Isoforms Using Cluster Analysis of MALDI-MS Mass Spectra. <i>Journal of Proteome Research</i> , 2006, 5, 785-792.	3.7	68
16	Multiomic profiling of checkpoint inhibitor-treated melanoma: Identifying predictors of response and resistance, and markers of biological discordance. <i>Cancer Cell</i> , 2022, 40, 88-102.e7.	16.8	64
17	Osteopontin is a downstream effector of the PI3-kinase pathway in melanomas that is inversely correlated with functional PTEN. <i>Carcinogenesis</i> , 2006, 27, 1778-1786.	2.8	55
18	Molecular Genomic Profiling of Melanocytic Nevi. <i>Journal of Investigative Dermatology</i> , 2019, 139, 1762-1768.	0.7	55

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19	Whole genome sequencing of melanomas in adolescent and young adults reveals distinct mutation landscapes and the potential role of germline variants in disease susceptibility. <i>International Journal of Cancer</i> , 2019, 144, 1049-1060.	5.1	54
20	Prolonged stable disease in a uveal melanoma patient with germline MBD4 nonsense mutation treated with pembrolizumab and ipilimumab. <i>Immunogenetics</i> , 2019, 71, 433-436.	2.4	51
21	microRNA Profiling Identifies Cancer-Specific and Prognostic Signatures in Pediatric Malignancies. <i>Clinical Cancer Research</i> , 2009, 15, 5560-5568.	7.0	49
22	Bone marrow transplantation generates T cell-dependent control of myeloma in mice. <i>Journal of Clinical Investigation</i> , 2018, 129, 106-121.	8.2	49
23	Melanomas of unknown primary have a mutation profile consistent with cutaneous sun-exposed melanoma. <i>Pigment Cell and Melanoma Research</i> , 2013, 26, 852-860.	3.3	48
24	Anatomic position determines oncogenic specificity in melanoma. <i>Nature</i> , 2022, 604, 354-361.	27.8	44
25	Medical and Surgical Care of Patients With Mesothelioma and Their Relatives Carrying Germline BAP1 Mutations. <i>Journal of Thoracic Oncology</i> , 2022, 17, 873-889.	1.1	44
26	POLE mutations in families predisposed to cutaneous melanoma. <i>Familial Cancer</i> , 2015, 14, 621-628.	1.9	43
27	Unexpected UVR and non-UVR mutation burden in some acral and cutaneous melanomas. <i>Laboratory Investigation</i> , 2017, 97, 130-145.	3.7	40
28	Telomere sequence content can be used to determine ALT activity in tumours. <i>Nucleic Acids Research</i> , 2018, 46, 4903-4918.	14.5	40
29	Comparison of whole-exome sequencing of matched fresh and formalin fixed paraffin embedded melanoma tumours: implications for clinical decision making. <i>Pathology</i> , 2016, 48, 261-266.	0.6	39
30	A p53 Drug Response Signature Identifies Prognostic Genes in High-Risk Neuroblastoma. <i>PLoS ONE</i> , 2013, 8, e79843.	2.5	34
31	Expression profiling identifies epoxy anthraquinone derivative as a DNA topoisomerase inhibitor. <i>Cancer Letters</i> , 2010, 293, 124-131.	7.2	30
32	Whole Exome Sequencing Identifies Candidate Genes Associated with Hereditary Predisposition to Uveal Melanoma. <i>Ophthalmology</i> , 2020, 127, 668-678.	5.2	27
33	Screening a panel of drugs with diverse mechanisms of action yields potential therapeutic agents against neuroblastoma. <i>Cancer Biology and Therapy</i> , 2009, 8, 2386-2395.	3.4	25
34	Improving missing value imputation of microarray data by using spot quality weights. <i>BMC Bioinformatics</i> , 2006, 7, 306.	2.6	24
35	Massively Parallel Sequencing Reveals an Accumulation of De Novo Mutations and an Activating Mutation of LPAR1 in a Patient with Metastatic Neuroblastoma. <i>PLoS ONE</i> , 2013, 8, e77731.	2.5	24
36	Prevalence of Germline BAP1, CDKN2A, and CDK4 Mutations in an Australian Population-Based Sample of Cutaneous Melanoma Cases. <i>Twin Research and Human Genetics</i> , 2015, 18, 126-133.	0.6	20

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37	Development of Peptide Nucleic Acid Probes for Detection of the HER2 Oncogene. PLoS ONE, 2013, 8, e58870.	2.5	19
38	Mutation load in melanoma is affected by <i>MC1R</i> genotype. Pigment Cell and Melanoma Research, 2017, 30, 255-258.	3.3	19
39	Meta-Analysis and Systematic Review of the Genomics of Mucosal Melanoma. Molecular Cancer Research, 2021, 19, 991-1004.	3.4	19
40	Germline mutations in candidate predisposition genes in individuals with cutaneous melanoma and at least two independent additional primary cancers. PLoS ONE, 2018, 13, e0194098.	2.5	16
41	Germline variants in oculocutaneous albinism genes and predisposition to familial cutaneous melanoma. Pigment Cell and Melanoma Research, 2019, 32, 854-863.	3.3	14
42	Tumor Mutation Burden and Structural Chromosomal Aberrations Are Not Associated with T-cell Density or Patient Survival in Acral, Mucosal, and Cutaneous Melanomas. Cancer Immunology Research, 2020, 8, 1346-1353.	3.4	13
43	Assessment of PALB2 as a Candidate Melanoma Susceptibility Gene. PLoS ONE, 2014, 9, e100683.	2.5	12
44	The Prognostic Impact of Circulating Tumour DNA in Melanoma Patients Treated with Systemic Therapies Beyond BRAF Mutant Detection. Cancers, 2020, 12, 3793.	3.7	12
45	Clinical significance of intronic variants in BRAF inhibitor resistant melanomas with altered BRAF transcript splicing. Biomarker Research, 2017, 5, 17.	6.8	11
46	Tumour procurement, DNA extraction, coverage analysis and optimisation of mutation-detection algorithms for human melanoma genomes. Pathology, 2015, 47, 683-693.	0.6	9
47	Multiplex melanoma families are enriched for polygenic risk. Human Molecular Genetics, 2020, 29, 2976-2985.	2.9	9
48	Microsimulation Model for Evaluating the Cost-Effectiveness of Surveillance in <i>BAP1</i> Pathogenic Variant Carriers. JCO Clinical Cancer Informatics, 2021, 5, 143-154.	2.1	7
49	Systematic review and meta-analysis of genomic alterations in acral melanoma. Pigment Cell and Melanoma Research, 2022, 35, 369-386.	3.3	6
50	Comment on "Physical Picture for Light Emission in Scanning Tunneling Microscopy". Physical Review Letters, 2000, 84, 2034-2034.	7.8	4
51	Classification of Genomic and Proteomic Data Using Support Vector Machines. , 2007, , 187-202.		4
52	A rare missense variant in protection of telomeres 1 ( <i>POT1</i> ) predisposes to a range of haematological malignancies. British Journal of Haematology, 2021, 192, e57-e60.	2.5	4
53	Loss-of-function variants in <i>POT1</i> predispose to uveal melanoma. Journal of Medical Genetics, 2021, 58, 234-236.	3.2	3
54	Comprehensive molecular profiling of metastatic melanoma to predict response to monotherapy and combination immunotherapy.. Journal of Clinical Oncology, 2019, 37, 9511-9511.	1.6	3

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55	Genomic analysis of adult case of ocular surface giant congenital melanocytic nevus and associated clinicopathological findings. <i>Ophthalmic Genetics</i> , 2020, 41, 616-620.	1.2	2
56	Attack of the Subclones: Accurate Detection of Mutational Heterogeneity in Bulk DNA from Tumors. <i>Journal of Investigative Dermatology</i> , 2020, 140, 1501-1503.	0.7	1
57	Choroidal melanoma with synchronous Fuchs's adenoma and novel ATRX mutation. <i>International Journal of Retina and Vitreous</i> , 2022, 8, 24.	1.9	1
58	Differences between acral and nonacral melanoma genomes. <i>British Journal of Dermatology</i> , 2020, 182, 1085-1085.	1.5	0
59	Initial Genomic Analysis of a Pure Erythroid Leukemia Developing in Association with Hydroxyurea Treatment for Sickle Cell Anemia. <i>Blood</i> , 2012, 120, 3254-3254.	1.4	0