Peter A Johansson

List of Publications by Year
in descending order

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	Multiomic profiling of checkpoint inhibitor-treated melanoma: Identifying predictors of response and resistance, and markers of biological discordance. Cancer Cell, 2022, 40, 88-102.e7.	16.8	64
2	Systematic review and metaâ€analysis of genomic alterations in acral melanoma. Pigment Cell and Melanoma Research, 2022, 35, 369-386.	3.3	6
3	Anatomic position determines oncogenic specificity in melanoma. Nature, 2022, 604, 354-361.	27.8	44
4	Choroidal melanoma with synchronous Fuchsâ€™ adenoma and novel ATRX mutation. International Journal of Retina and Vitreous, 2022, 8, 24.	1.9	1
5	Medical and Surgical Care of Patients With Mesothelioma and Their Relatives Carrying Germline BAP1 Mutations. Journal of Thoracic Oncology, 2022, 17, 873-889.	1.1	44
6	A rare missense variant in protection of telomeres 1 (POT1) predisposes to a range of haematological malignancies. British Journal of Haematology, 2021, 192, e57-e60.	2.5	4
7	Loss-of-function variants in POT1 predispose to uveal melanoma. Journal of Medical Genetics, 2021, 58, 234-236.	3.2	3
8	Microsimulation Model for Evaluating the Cost-Effectiveness of Surveillance in BAP1 Pathogenic Variant Carriers. JCO Clinical Cancer Informatics, 2021, 5, 143-154.	2.1	7
9	Meta-Analysis and Systematic Review of the Genomics of Mucosal Melanoma. Molecular Cancer Research, 2021, 19, 991-1004.	3.4	19
10	Differences between acral and nonacral melanoma genomes. British Journal of Dermatology, 2020, 182, 1085-1085.	1.5	0
11	Whole Exome Sequencing Identifies Candidate Genes Associated with Hereditary Predisposition to Uveal Melanoma. Ophthalmology, 2020, 127, 668-678.	5.2	27
12	Whole-genome sequencing of acral melanoma reveals genomic complexity and diversity. Nature Communications, 2020, 11, 5259.	12.8	102
13	Multiplex melanoma families are enriched for polygenic risk. Human Molecular Genetics, 2020, 29, 2976-2985.	2.9	9
14	Attack of the Subclones: Accurate Detection of Mutational Heterogeneity in Bulk DNA from Tumors. Journal of Investigative Dermatology, 2020, 140, 1501-1503.	0.7	1
15	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
16	Genomic analysis of adult case of ocular surface giant congenital melanocytic nevus and associated clinicopathological findings. Ophthalmic Genetics, 2020, 41, 616-620.	1.2	2
17	The Prognostic Impact of Circulating Tumour DNA in Melanoma Patients Treated with Systemic Therapiesâ€”Beyond BRAF Mutant Detection. Cancers, 2020, 12, 3793.	3.7	12
18	Whole genome landscapes of uveal melanoma show an ultraviolet radiation signature in iris tumours. Nature Communications, 2020, 11, 2408.	12.8	86

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19	Whole-genome landscape of mucosal melanoma reveals diverse drivers and therapeutic targets. Nature Communications, 2019, 10, 3163.	12.8	205
20	Germline variants in oculocutaneous albinism genes and predisposition to familial cutaneous melanoma. Pigment Cell and Melanoma Research, 2019, 32, 854-863.	3.3	14
21	Prolonged stable disease in a uveal melanoma patient with germline MBD4 nonsense mutation treated with pembrolizumab and ipilimumab. Immunogenetics, 2019, 71, 433-436.	2.4	51
22	Molecular Genomic Profiling of MelanocyticÂNevi. Journal of Investigative Dermatology, 2019, 139, 1762-1768.	0.7	55
23	Whole genome sequencing of melanomas in adolescent and young adults reveals distinct mutation landscapes and the potential role of germline variants in disease susceptibility. International Journal of Cancer, 2019, 144, 1049-1060.	5.1	54
24	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
25	Telomere sequence content can be used to determine ALT activity in tumours. Nucleic Acids Research, 2018, 46, 4903-4918.	14.5	40
26	Comprehensive Study of the Clinical Phenotype of GermlineBAP1Variant-Carrying Families Worldwide. Journal of the National Cancer Institute, 2018, 110, 1328-1341.	6.3	164
27	Bone marrow transplantation generates T cellâ€“dependent control of myeloma in mice. Journal of Clinical Investigation, 2018, 129, 106-121.	8.2	49
28	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
29	Unexpected UVR and non-UVR mutation burden in some acral and cutaneous melanomas. Laboratory Investigation, 2017, 97, 130-145.	3.7	40
30	Whole-genome landscapes of major melanoma subtypes. Nature, 2017, 545, 175-180.	27.8	1,068
31	Mutation load in melanoma is affected by <scp>MC</scp>1R genotype. Pigment Cell and Melanoma Research, 2017, 30, 255-258.	3.3	19
32	Clinical significance of intronic variants in BRAF inhibitor resistant melanomas with altered BRAF transcript splicing. Biomarker Research, 2017, 5, 17.	6.8	11
33	Comparison of whole-exome sequencing of matched fresh and formalin fixed paraffin embedded melanoma tumours: implications for clinical decision making. Pathology, 2016, 48, 261-266.	0.6	39
34	Deep sequencing of uveal melanoma identifies a recurrent mutation in PLCB4. Oncotarget, 2016, 7, 4624-4631.	1.8	235
35	Tumour procurement, DNA extraction, coverage analysis and optimisation of mutation-detection algorithms for human melanoma genomes. Pathology, 2015, 47, 683-693.	0.6	9
36	A recurrent germline <scp>BAP1</scp> mutation and extension of the <scp>BAP1</scp> tumor predisposition spectrum to include basal cell carcinoma. Clinical Genetics, 2015, 88, 267-272.	2.0	81

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37	Nonsense Mutations in the Shelterin Complex Genes ACD and TERF2IP in Familial Melanoma. Journal of the National Cancer Institute, 2015, 107, .	6.3	134
38	POLE mutations in families predisposed to cutaneous melanoma. Familial Cancer, 2015, 14, 621-628.	1.9	43
39	Prevalence of GermlineBAP1, CDKN2A, andCDK4Mutations in an Australian Population-Based Sample of Cutaneous Melanoma Cases. Twin Research and Human Genetics, 2015, 18, 126-133.	0.6	20
40	Recurrent inactivating RASA2 mutations in melanoma. Nature Genetics, 2015, 47, 1408-1410.	21.4	90
41	Assessment of PALB2 as a Candidate Melanoma Susceptibility Gene. PLoS ONE, 2014, 9, e100683.	2.5	12
42	Increased MAPK reactivation in early resistance to dabrafenib/trametinib combination therapy of BRAF-mutant metastatic melanoma. Nature Communications, 2014, 5, 5694.	12.8	295
43	POT1 loss-of-function variants predispose to familial melanoma. Nature Genetics, 2014, 46, 478-481.	21.4	319
44	Melanomas of unknown primary have a mutation profile consistent with cutaneous sunâ€exposed melanoma. Pigment Cell and Melanoma Research, 2013, 26, 852-860.	3.3	48
45	A p53 Drug Response Signature Identifies Prognostic Genes in High-Risk Neuroblastoma. PLoS ONE, 2013, 8, e79843.	2.5	34
46	Development of Peptide Nucleic Acid Probes for Detection of the HER2 Oncogene. PLoS ONE, 2013, 8, e58870.	2.5	19
47	Massively Parallel Sequencing Reveals an Accumulation of De Novo Mutations and an Activating Mutation of LPAR1 in a Patient with Metastatic Neuroblastoma. PLoS ONE, 2013, 8, e77731.	2.5	24
48	Initial Genomic Analysis of a Pure Erythroid Leukemia Developing in Association with Hydroyurea Treatment for Sickle Cell Anemia. Blood, 2012, 120, 3254-3254.	1.4	0
49	Expression profiling identifies epoxy anthraquinone derivative as a DNA topoisomerase inhibitor. Cancer Letters, 2010, 293, 124-131.	7.2	30
50	Screening a panel of drugs with diverse mechanisms of action yields potential therapeutic agents against neuroblastoma. Cancer Biology and Therapy, 2009, 8, 2386-2395.	3.4	25
51	microRNA Profiling Identifies Cancer-Specific and Prognostic Signatures in Pediatric Malignancies. Clinical Cancer Research, 2009, 15, 5560-5568.	7.0	49
52	Poor prognosis in carcinoma is associated with a gene expression signature of aberrant PTEN tumor suppressor pathway activity. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 7564-7569.	7.1	445
53	Classification of Genomic and Proteomic Data Using Support Vector Machines. , 2007, , 187-202.		4
54	Confirmation of a BRAF mutation-associated gene expression signature in melanoma. Pigment Cell & Melanoma Research, 2007, 20, 216-221.	3.6	76

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55	Detection and Identification of Protein Isoforms Using Cluster Analysis of MALDIâˆ’MS Mass Spectra. Journal of Proteome Research, 2006, 5, 785-792.	3.7	68
56	Improving missing value imputation of microarray data by using spot quality weights. BMC Bioinformatics, 2006, 7, 306.	2.6	24
57	Osteopontin is a downstream effector of the PI3-kinase pathway in melanomas that is inversely correlated with functional PTEN. Carcinogenesis, 2006, 27, 1778-1786.	2.8	55
58	Microarray expression profiling in melanoma reveals a BRAF mutation signature. Oncogene, 2004, 23, 4060-4067.	5.9	169
59	Comment on â€œPhysical Picture for Light Emission in Scanning Tunneling Microscopyâ€• Physical Review Letters, 2000, 84, 2034-2034.	7.8	4