

# Miriam Potrony

## List of Publications by Year in descending order

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41  
papers

1,305  
citations

516710

16  
h-index

377865

34  
g-index

42  
all docs

42  
docs citations

42  
times ranked

2318  
citing authors

#	ARTICLE	IF	CITATIONS
1	TERT Promoter Mutation Status as an Independent Prognostic Factor in Cutaneous Melanoma. Journal of the National Cancer Institute, 2014, 106, .	6.3	204
2	Comprehensive Study of the Clinical Phenotype of Germline <i>BAP1</i> Variant-Carrying Families Worldwide. Journal of the National Cancer Institute, 2018, 110, 1328-1341.	6.3	164
3	Cross-cohort gut microbiome associations with immune checkpoint inhibitor response in advanced melanoma. Nature Medicine, 2022, 28, 535-544.	30.7	158
4	Genome-wide association meta-analyses combining multiple risk phenotypes provide insights into the genetic architecture of cutaneous melanoma susceptibility. Nature Genetics, 2020, 52, 494-504.	21.4	138
5	Update in genetic susceptibility in melanoma. Annals of Translational Medicine, 2015, 3, 210.	1.7	100
6	Increased prevalence of lung, breast, and pancreatic cancers in addition to melanoma risk in families bearing the cyclin-dependent kinase inhibitor 2A mutation: Implications for genetic counseling. Journal of the American Academy of Dermatology, 2014, 71, 888-895.	1.2	52
7	The <i>MC1R</i> melanoma risk variant p. <i>R160W</i> is associated with Parkinson disease. Annals of Neurology, 2015, 77, 889-894.	5.3	52
8	Prevalence of <i>MITF</i> p.E318K in Patients With Melanoma Independent of the Presence of <i>CDKN2A</i> Causative Mutations. JAMA Dermatology, 2016, 152, 405.	4.1	41
9	<i>POT1</i> germline mutations but not <i>TERT</i> promoter mutations are implicated in melanoma susceptibility in a large cohort of Spanish melanoma families. British Journal of Dermatology, 2019, 181, 105-113.	1.5	37
10	Association of the <i>POT1</i> Germline Missense Variant p.I78T With Familial Melanoma. JAMA Dermatology, 2019, 155, 604.	4.1	34
11	Efficacy of novel immunotherapy regimens in patients with metastatic melanoma with germline <i>CDKN2A</i> mutations. Journal of Medical Genetics, 2020, 57, 316-321.	3.2	33
12	Characterization of individuals at high risk of developing melanoma in Latin America: bases for genetic counseling in melanoma. Genetics in Medicine, 2016, 18, 727-736.	2.4	31
13	Melanocortin 1 receptor ( <i>MC1R</i> ) polymorphisms™ influence on size and dermoscopic features of nevi. Pigment Cell and Melanoma Research, 2018, 31, 39-50.	3.3	28
14	Role of <i>CPI-17</i> in restoring skin homeostasis in cutaneous field of cancerization: effects of topical application of a film-forming medical device containing photolyase and UV filters. Experimental Dermatology, 2013, 22, 494-496.	2.9	19
15	Germline ATM variants predispose to melanoma: a joint analysis across the GenoMEL and MelaNostrum consortia. Genetics in Medicine, 2021, 23, 2087-2095.	2.4	19
16	Genetic susceptibility to cutaneous melanoma in southern Switzerland: role of <i>CDKN2A</i> , <i>MC1R</i> and <i>MITF</i> . British Journal of Dermatology, 2016, 175, 1030-1037.	1.5	17
17	Association of Melanocortin-1 Receptor Variants with Pigmentary Traits in Humans: A Pooled Analysis from the M-Skip Project. Journal of Investigative Dermatology, 2016, 136, 1914-1917.	0.7	16
18	<i>MC1R</i> variants in childhood and adolescent melanoma: a retrospective pooled analysis of a multicentre cohort. The Lancet Child and Adolescent Health, 2019, 3, 332-342.	5.6	16

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19	Inherited functional variants of the lymphocyte receptor CD5 influence melanoma survival. <i>International Journal of Cancer</i> , 2016, 139, 1297-1302.	5.1	14
20	Association Between Confocal Morphologic Classification and Clinical Phenotypes of Multiple Primary and Familial Melanomas. <i>JAMA Dermatology</i> , 2016, 152, 1099.	4.1	13
21	Genomic analysis and clinical management of adolescent cutaneous melanoma. <i>Pigment Cell and Melanoma Research</i> , 2017, 30, 307-316.	3.3	12
22	Lack of Mutations in POT1 Gene in Selected Families with Familial Non-Medullary Thyroid Cancer. <i>Hormones and Cancer</i> , 2020, 11, 111-116.	4.9	12
23	<i>IRF4</i> rs12203592 functional variant and melanoma survival. <i>International Journal of Cancer</i> , 2017, 140, 1845-1849.	5.1	11
24	Inherited MC1R variants in patients with melanoma are associated with better survival in women. <i>British Journal of Dermatology</i> , 2020, 182, 138-146.	1.5	10
25	Sex as a predictor of response to cancer immunotherapy. <i>Lancet Oncology</i> , The, 2018, 19, e375.	10.7	9
26	Dermoscopy comparative approach for early diagnosis in familial melanoma: influence of <i>MC1R</i> genotype. <i>Journal of the European Academy of Dermatology and Venereology</i> , 2021, 35, 403-410.	2.4	8
27	Detection of cell-free circulating <i>BRAF</i> <sup>V</sup> <i>600E</i> <sup>600E</sup> by droplet digital polymerase chain reaction in patients with and without melanoma under dermatological surveillance. <i>British Journal of Dermatology</i> , 2020, 182, 382-389.	1.5	7
28	Efficacy of BRAF and MEK Inhibition in Patients with BRAF-Mutant Advanced Melanoma and Germline CDKN2A Pathogenic Variants. <i>Cancers</i> , 2021, 13, 2440.	3.7	6
29	Common genetic variants associated with melanoma risk or naevus count in patients with wildtype MC1R melanoma. <i>British Journal of Dermatology</i> , 2022, 187, 753-764.	1.5	6
30	A Common Variant in the MC1R Gene (p.V92M) is associated with Alzheimer's Disease Risk. <i>Journal of Alzheimer's Disease</i> , 2017, 56, 1065-1074.	2.6	5
31	The p. R151C Polymorphism in MC1R Gene Modifies the Age of Onset in Spanish Huntington's Disease Patients. <i>Molecular Neurobiology</i> , 2017, 54, 3906-3910.	4.0	5
32	Melanocortin-1 receptor ( <i>MC1R</i> ) genotypes do not correlate with size in two cohorts of medium-to-giant congenital melanocytic nevi. <i>Pigment Cell and Melanoma Research</i> , 2020, 33, 685-694.	3.3	5
33	Histologic features of melanoma associated with germline mutations of CDKN2A, CDK4, and POT1 in melanoma-prone families from the United States, Italy, and Spain. <i>Journal of the American Academy of Dermatology</i> , 2020, 83, 860-869.	1.2	5
34	Genome-wide linkage analysis in Spanish melanoma-prone families identifies a new familial melanoma susceptibility locus at 11q. <i>European Journal of Human Genetics</i> , 2018, 26, 1188-1193.	2.8	4
35	Genetic markers for characterization and prediction of prognosis of melanoma subtypes: a 2021 update. <i>Italian Journal of Dermatology and Venereology</i> , 2021, 156, 322-330.	0.2	4
36	Reply. <i>Annals of Neurology</i> , 2016, 79, 161-163.	5.3	3

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37	Time and tumor type (primary or metastatic) do not influence the detection of BRAF/NRAS mutations in formalin fixed paraffin embedded samples from melanomas. <i>Clinical Chemistry and Laboratory Medicine</i> , 2016, 54, 1733-1738.	2.3	2
38	DNA Repair and Immune Response Pathways Are Deregulated in Melanocyte-Keratinocyte Co-cultures Derived From the Healthy Skin of Familial Melanoma Patients. <i>Frontiers in Medicine</i> , 2021, 8, 692341.	2.6	2
39	Influence of germline genetic variants on dermoscopic features of melanoma. <i>Pigment Cell and Melanoma Research</i> , 2021, 34, 618-628.	3.3	2
40	Reply. <i>Annals of Neurology</i> , 2015, 78, 153-154.	5.3	1
41	Reply. <i>Annals of Neurology</i> , 2016, 79, 868-868.	5.3	0