Nelleke A Gruis

List of Publications by Year
in descending order

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132 papers	8,270 citations	71102 41 h-index	49909 87 g-index
135 all docs	135 docs citations	135 times ranked	8635 citing authors

#	Article	IF	Citations
1	Accurate Quantification of T Cells in Copy Number Stable and Unstable DNA Samples Using Multiplex Digital PCR. Journal of Molecular Diagnostics, 2022, 24, 88-100.	2.8	2
2	Association between a 46-SNP Polygenic Risk Score and melanoma risk in Dutch patients with familial melanoma. Journal of Medical Genetics, 2021, 58, 760-766.	3.2	8
3	MC1R variants in relation to naevi in melanoma cases and controls: a pooled analysis from the Mâ€SKIP project. Journal of the European Academy of Dermatology and Venereology, 2021, 35, e135-e138.	2.4	3
4	Birth cohort-specific trends of sun-related behaviors among individuals from an international consortium of melanoma-prone families. BMC Public Health, 2021, 21, 692.	2.9	4
5	The importance of motivation in selecting undergraduate medical students for extracurricular research programmes. PLoS ONE, 2021, 16, e0260193.	2.5	4
6	Loss of Wild-Type CDKN2A Is an Early Event in the Development of Melanoma in FAMMM Syndrome. Journal of Investigative Dermatology, 2020, 140, 2298-2301.e3.	0.7	11
7	Association of HERV-K and LINE-1 hypomethylation with reduced disease-free survival in melanoma patients. Epigenomics, 2020, 12, 1689-1706.	2.1	11
8	Genome-wide analysis of constitutional DNA methylation in familial melanoma. Clinical Epigenetics, 2020, 12, 43.	4.1	4
9	NEK11 as a candidate high-penetrance melanoma susceptibility gene. Journal of Medical Genetics, 2020, 57, 203-210.	3.2	9
10	Genomeâ€wide characterization of 5â€hydroxymethylcytosine in melanoma reveals major differences with nevus. Genes Chromosomes and Cancer, 2020, 59, 366-374.	2.8	8
11	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
12	Interplay between TERT promoter mutations and methylation culminates in chromatin accessibility and TERT expression. PLoS ONE, 2020, 15, e0231418.	2.5	15
13	Title is missing!. , 2020, 15, e0231418.		0
14	Title is missing!. , 2020, 15, e0231418.		0
15	Title is missing!. , 2020, 15, e0231418.		0
16	Title is missing!. , 2020, 15, e0231418.		0
17	Estimating CDKN2A mutation carrier probability among global familial melanoma cases using GenoMELPREDICT. Journal of the American Academy of Dermatology, 2019, 81, 386-394.	1.2	17
18	Progress report on the major clinical advances in patient-oriented research into familial melanoma (2013â€“2018). Familial Cancer, 2019, 18, 267-271.	1.9	4

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19	MC1R 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
20	A novel germline variant in the DOT1L gene co-segregating in a Dutch family with a history of melanoma. Melanoma Research, 2019, 29, 582-589.	1.2	7
21	Multigene panel sequencing of established and candidate melanoma susceptibility genes in a large cohort of Dutch nonâ€CDKN2A/CDK4 melanoma families. International Journal of Cancer, 2019, 144, 2453-2464.	5.1	33
22	CM-Score: a validated scoring system to predict CDKN2A germline mutations in melanoma families from Northern Europe. Journal of Medical Genetics, 2018, 55, 661-668.	3.2	13
23	High Growth Rate of Pancreatic Ductal Adenocarcinoma in CDKN2A-p16-Leiden Mutation Carriers. Cancer Prevention Research, 2018, 11, 551-556.	1.5	5
24	Telomere length and survival in primary cutaneous melanoma patients. Scientific Reports, 2018, 8, 10947.	3.3	23
25	MC1R variants as melanoma risk factors independent of at-risk phenotypic characteristics: a pooled analysis from the M-SKIP project. Cancer Management and Research, 2018, Volume 10, 1143-1154.	1.9	57
26	Genomic analysis and clinical management of adolescent cutaneous melanoma. Pigment Cell and Melanoma Research, 2017, 30, 307-316.	3.3	12
27	GermlineCDKN2A/P16INK4A mutations contribute to genetic determinism of sarcoma. Journal of Medical Genetics, 2017, 54, 607-612.	3.2	19
28	Germline Variation at CDKN2A and Associations with Nevus Phenotypes amongÂMembers of Melanoma Families. Journal of Investigative Dermatology, 2017, 137, 2606-2612.	0.7	18
29	The absence of multiple atypical nevi in germline CDKN2A mutations: Comment on â€œHereditary melanoma: Update on syndromes and management: Genetics of familial atypical multiple mole melanoma syndromeâ€. Journal of the American Academy of Dermatology, 2016, 75, e157.	1.2	6
30	Multiple rare variants in high-risk pancreatic cancer-related genes may increase risk for pancreatic cancer in a subset of patients with and without germline CDKN2A mutations. Human Genetics, 2016, 135, 1241-1249.	3.8	24
31	Association of Melanocortin-1 Receptor Variants with Pigmentary Traits in Humans: AÂPooled Analysis from the M-Skip Project. Journal of Investigative Dermatology, 2016, 136, 1914-1917.	0.7	16
32	Phenotypic and Histopathological Tumor Characteristics According to CDKN2A Mutation Status among Affected Members ofÂMelanoma Families. Journal of Investigative Dermatology, 2016, 136, 1066-1069.	0.7	13
33	Germline TERT promoter mutations are rare in familial melanoma. Familial Cancer, 2016, 15, 139-144.	1.9	51
34	MC1R variants increased the risk of sporadic cutaneous melanoma in darkerâ€pigmented <scp>C</scp>aucasians: A pooledâ€analysis from the Mâ€SKIP project. International Journal of Cancer, 2015, 136, 618-631.	5.1	92
35	Development and Validation of a Melanoma Risk Score Based on Pooled Data from 16 Caseâ€“Control Studies. Cancer Epidemiology Biomarkers and Prevention, 2015, 24, 817-824.	2.5	25
36	Histologic features of melanoma associated with CDKN2A genotype. Journal of the American Academy of Dermatology, 2015, 72, 496-507.e7.	1.2	19

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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	Genome-wide meta-analysis identifies five new susceptibility loci for cutaneous malignant melanoma. Nature Genetics, 2015, 47, 987-995.	21.4	218
39	Fine mapping of genetic susceptibility loci for melanoma reveals a mixture of single variant and multiple variant regions. International Journal of Cancer, 2015, 136, 1351-1360.	5.1	30
40	Prognostic Significance of Promoter Hypermethylation and Diminished Gene Expression of SYNPO2 in Melanoma. Journal of Investigative Dermatology, 2015, 135, 2328-2331.	0.7	13
41	Somatic BRAF and NRAS Mutations in Familial Melanomas with Known Germline CDKN2A Status: A GenoMEL Study. Journal of Investigative Dermatology, 2014, 134, 287-290.	0.7	18
42	An inherited variant in the gene coding for vitamin <scp>D</scp>â€binding protein and survival from cutaneous melanoma: a <scp>B</scp>io<scp>G</scp>eno<scp>MEL</scp> study. Pigment Cell and Melanoma Research, 2014, 27, 234-243.	3.3	25
43	In-vitro melanoma models. Melanoma Research, 2014, 24, 305-314.	1.2	8
44	The Effect on Melanoma Risk of Genes Previously Associated With Telomere Length. Journal of the National Cancer Institute, 2014, 106, .	6.3	109
45	Cutaneous melanoma: Medical specialists' opinions onÂfollow-up and sentinel lymph node biopsy. European Journal of Surgical Oncology, 2014, 40, 1276-1283.	1.0	8
46	POT1 loss-of-function variants predispose to familial melanoma. Nature Genetics, 2014, 46, 478-481.	21.4	319
47	Promoter CpG Island Hypermethylation in Dysplastic Nevus and Melanoma: CLDN11 as an Epigenetic Biomarker for Malignancy. Journal of Investigative Dermatology, 2014, 134, 2957-2966.	0.7	38
48	Primary Melanoma Tumors from CDKN2A Mutation Carriers Do Not Belong to a Distinct Molecular Subclass. Journal of Investigative Dermatology, 2014, 134, 3000-3003.	0.7	8
49	Acquired Melanocytic Nevi in Childhood and Familial Melanoma. JAMA Dermatology, 2014, 150, 35.	4.1	11
50	Abstract 20: POT1 mutations predispose to familial melanoma. , 2014, , .		0
51	Class III Î²-tubulin, a novel biomarker in the human melanocyte lineage. Differentiation, 2013, 85, 173-181.	1.9	18
52	Increasing First Year Studentâ€™s Attitude and Understanding towards Biomedical Research. Medical Science Educator, 2013, 23, 148-153.	1.5	3
53	A variant in FTO shows association with melanoma risk not due to BMI. Nature Genetics, 2013, 45, 428-432.	21.4	111
54	Genomeâ€wide promoter methylation analysis identifies epigenetic silencing of <scp>MAPK</scp>13 in primary cutaneous melanoma. Pigment Cell and Melanoma Research, 2013, 26, 542-554.	3.3	52

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55	Surveillance of Second-Degree Relatives from Melanoma Families with a CDKN2A Germline Mutation. Cancer Epidemiology Biomarkers and Prevention, 2013, 22, 1771-1777.	2.5	6
56	Melanocortin 1 Receptor (MC1R) Variants in High Melanoma Risk Patients are Associated with Specific Dermoscopic ABCD Features. Acta Dermato-Venereologica, 2012, 92, 587-592.	1.3	17
57	Melanocortin 1 Receptor Function: Shifting Gears from Determining Skin and Nevus Phenotype to Fetal Growth. Journal of Investigative Dermatology, 2012, 132, 1953-1955.	0.7	4
58	Skin Examination Behavior. Archives of Dermatology, 2012, 148, 1142.	1.4	36
59	Genome-Wide Analysis of Gene and Protein Expression of Dysplastic Naevus Cells. Journal of Skin Cancer, 2012, 2012, 1-13.	1.2	8
60	Inherited variants in the MC1R gene and survival from cutaneous melanoma: a BioGenoMEL study. Pigment Cell and Melanoma Research, 2012, 25, 384-394.	3.3	61
61	Perceptions of genetic research and testing among members of families with an increased risk of malignant melanoma. European Journal of Cancer, 2012, 48, 3052-3062.	2.8	17
62	Melanocortin-1 receptor, skin cancer and phenotypic characteristics (M-SKIP) project: study design and methods for pooling results of genetic epidemiological studies. BMC Medical Research Methodology, 2012, 12, 116.	3.1	12
63	Magnetic Resonance Imaging Surveillance Detects Early-Stage Pancreatic Cancer in Carriers of a p16-Leiden Mutation. Gastroenterology, 2011, 140, 850-856.	1.3	148
64	Genome-wide association study identifies three new melanoma susceptibility loci. Nature Genetics, 2011, 43, 1108-1113.	21.4	230
65	Clinical and histologic characteristics of malignant melanoma in families with a germline mutation in CDKN2A. Journal of the American Academy of Dermatology, 2011, 65, 281-288.	1.2	45
66	Effectiveness and causes for failure of surveillance of CDKN2A-mutated melanoma families. Journal of the American Academy of Dermatology, 2011, 65, 289-296.	1.2	16
67	A Flexible Multiplex Bead-Based Assay for Detecting Germline CDKN2A and CDK4 Variants in Melanoma-Prone Kindreds. Journal of Investigative Dermatology, 2011, 131, 480-486.	0.7	11
68	Genome-wide association study identifies a new melanoma susceptibility locus at 1q21.3. Nature Genetics, 2011, 43, 1114-1118.	21.4	140
69	Familial melanoma. Atlas of Genetics and Cytogenetics in Oncology and Haematology, 2011, , .	0.1	0
70	Melanoma susceptibility genes. Melanoma Research, 2010, 20, 161-162.	1.2	5
71	High and low penetrance genes in melanoma. Melanoma Research, 2010, 20, e7.	1.2	0
72	Melanoma risk factors, perceived threat and intentional tanning: an international online survey. European Journal of Cancer Prevention, 2010, 19, 216-226.	1.3	47

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73	Management of Melanoma Families. Cancers, 2010, 2, 549-566.	3.7	5
74	Predictors of Sun Protection Behaviors and Severe Sunburn in an International Online Study. Cancer Epidemiology Biomarkers and Prevention, 2010, 19, 2199-2210.	2.5	106
75	Sun exposure and melanoma risk at different latitudes: a pooled analysis of 5700 cases and 7216 controls. International Journal of Epidemiology, 2009, 38, 814-830.	1.9	219
76	A pooled analysis of melanocytic nevus phenotype and the risk of cutaneous melanoma at different latitudes. International Journal of Cancer, 2009, 124, 420-428.	5.1	84
77	Absence of Germline Epimutation of the CDKN2A Gene in Familial Melanoma. Journal of Investigative Dermatology, 2009, 129, 781-784.	0.7	7
78	Genome-wide association study identifies three loci associated with melanoma risk. Nature Genetics, 2009, 41, 920-925.	21.4	422
79	The emergence of networks in human genome epidemiology: challenges and opportunities. , 2009, , 120-134.		0
80	Genetic testing in familial melanoma: uptake and implications. Psycho-Oncology, 2008, 17, 790-796.	2.3	25
81	Genome-wide linkage scan for atypical nevi in p16-Leiden melanoma families. European Journal of Human Genetics, 2008, 16, 1135-1141.	2.8	17
82	Common sequence variants on 20q11.22 confer melanoma susceptibility. Nature Genetics, 2008, 40, 838-840.	21.4	209
83	A comparison of CDKN2A mutation detection within the Melanoma Genetics Consortium (GenoMEL). European Journal of Cancer, 2008, 44, 1269-1274.	2.8	26
84	Increased Risk of Cancer Other Than Melanoma in CDKN2A Founder Mutation (p16-Leiden)-Positive Melanoma Families. Clinical Cancer Research, 2008, 14, 7151-7157.	7.0	161
85	Pyrophosphorolysis DetectsB-RAFMutations in Primary Uveal Melanoma. , 2008, 49, 23.		41
86	Epigenetic Regulation IdentifiesRASEFas a Tumor-Suppressor Gene in Uveal Melanoma. , 2008, 49, 1291.		43
87	Epigenetic Inactivation of RASSF1a in Uveal Melanoma. , 2007, 48, 486.		67
88	Phenotypic Variation in Familial Melanoma. Archives of Dermatology, 2007, 143, 525-6.	1.4	2
89	Gene-specific fluorescence in-situ hybridization analysis on tissue microarray to refine the region of chromosome 20q amplification in melanoma. Melanoma Research, 2007, 17, 37-41.	1.2	33
90	The Emergence of Networks in Human Genome Epidemiology. Epidemiology, 2007, 18, 1-8.	2.7	102

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91	From sporadic atypical nevi to familial melanoma: Risk analysis for melanoma in sporadic atypical nevus patients. Journal of the American Academy of Dermatology, 2007, 56, 748-752.	1.2	28
92	Genetics: What Advice for Patients Who Present With a Family History of Melanoma?. Seminars in Oncology, 2007, 34, 452-459.	2.2	21
93	Increased C-MYC copy numbers on the background of CDKN2A loss is associated with improved survival in nodular melanoma. Journal of Cancer Research and Clinical Oncology, 2007, 133, 117-123.	2.5	9
94	High-risk Melanoma Susceptibility Genes and Pancreatic Cancer, Neural System Tumors, and Uveal Melanoma across GenoMEL. Cancer Research, 2006, 66, 9818-9828.	0.9	373
95	Increased p21-activated kinase-1 expression is associated with invasive potential in uveal melanoma. Melanoma Research, 2006, 16, 285-296.	1.2	24
96	A road map for efficient and reliable human genome epidemiology. Nature Genetics, 2006, 38, 3-5.	21.4	244
97	Features associated with germline CDKN2A mutations: a GenoMEL study of melanoma-prone families from three continents. Journal of Medical Genetics, 2006, 44, 99-106.	3.2	350
98	Proteomic Analysis of Uveal Melanoma Reveals Novel Potential Markers Involved in Tumor Progression. , 2006, 47, 786.		32
99	A mutation hotspot at the p14ARF splice site. Oncogene, 2005, 24, 4604-4608.	5.9	70
100	Aberrant DNA Methylation in Cutaneous Malignancies. Seminars in Oncology, 2005, 32, 479-487.	2.2	69
101	p16INK4A-independence of Epsteinâ€“Barr virus-induced cell proliferation and virus latency. Journal of General Virology, 2004, 85, 1381-1386.	2.9	6
102	Familial melanoma: a complex disorder leading to controversy on DNA testing. Familial Cancer, 2003, 2, 109-116.	1.9	41
103	Expression profiling reveals that methylation of TIMP3 is involved in uveal melanoma development. International Journal of Cancer, 2003, 106, 472-479.	5.1	86
104	Localization of a Novel Melanoma Susceptibility Locus to 1p22. American Journal of Human Genetics, 2003, 73, 301-313.	6.2	113
105	Homozygous germline mutation of CDKN2A/p16 and glucose-6-phosphate dehydrogenase deficiency in a multiple melanoma case. Melanoma Research, 2003, 13, 171-178.	1.2	20
106	Pancreatic carcinoma in carriers of a specific 19 base pair deletion of CDKN2A/p16 (p16-leiden). Clinical Cancer Research, 2003, 9, 3598-605.	7.0	22
107	Geographical Variation in the Penetrance of CDKN2A Mutations for Melanoma. Journal of the National Cancer Institute, 2002, 94, 894-903.	6.3	435
108	MICA Gene Polymorphism is Not Associated With an Increased Risk for Skin Cancer. Journal of Investigative Dermatology, 2002, 118, 686-691.	0.7	14

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109	INK4a-deficient human diploid fibroblasts are resistant to RAS-induced senescence. EMBO Journal, 2002, 21, 2936-2945.	7.8	173
110	Melanocortin-1 Receptor Gene Variants Determine the Risk of Nonmelanoma Skin Cancer Independently of Fair Skin and Red Hair. American Journal of Human Genetics, 2001, 68, 884-894.	6.2	221
111	Melanocortin-1 Receptor Variant R151C Modifies Melanoma Risk in Dutch Families with Melanoma. American Journal of Human Genetics, 2001, 69, 774-779.	6.2	162
112	Melanocortin 1 Receptor (MC1R) Gene Variants are Associated with an Increased Risk for Cutaneous Melanoma Which is Largely Independent of Skin Type and Hair Color. Journal of Investigative Dermatology, 2001, 117, 294-300.	0.7	351
113	Cutaneous squamous cell carcinoma andp53 codon 72 polymorphism: A need for screening?. Molecular Carcinogenesis, 2001, 30, 56-61.	2.7	41
114	Risk of developing pancreatic cancer in families with familial atypical multiple mole melanoma associated with a specific 19 deletion ofp16 (p16-Leiden). International Journal of Cancer, 2000, 87, 809-811.	5.1	362
115	The risk of developing pancreatic cancer in families with familial atypical multiple mole melanoma (FAMMM) associated with a specific 19 BP deletion of P16 (P16 Leiden). Gastroenterology, 2000, 118, A641.	1.3	1
116	Risk of developing pancreatic cancer in families with familial atypical multiple mole melanoma associated with a specific 19 deletion of p16 p16Leiden. International Journal of Cancer, 2000, 87, 809-811.	5.1	67
117	Familial Melanoma; CDKN2A and Beyond. Journal of Investigative Dermatology Symposium Proceedings, 1999, 4, 50-54.	0.8	19
118	Risk of cutaneous malignant melanoma in patients with nonfamilial atypical nevi from a pigmented lesions clinic. Journal of the American Academy of Dermatology, 1999, 40, 686-693.	1.2	27
119	A Locus Linked to p16 Modifies Melanoma Risk in Dutch Familial Atypical Multiple Mole Melanoma (FAMMM) Syndrome Families. Genome Research, 1999, 9, 575-580.	5.5	19
120	Haplotype analysis of two recurrentCDKN2A mutations in 10 melanoma families: Evidence for common founders and independent mutations. , 1998, 11, 424-431.		61
121	Excess Cancer Mortality in Six Dutch Pedigrees with the Familial Atypical Multiple Mole-Melanoma Syndrome from 1830 to 1994. Journal of Investigative Dermatology, 1998, 110, 788-792.	0.7	42
122	Affected members of melanoma-prone families with linkage to 9p21 but lacking mutations in CDKN2A do not harbor mutations in the coding regions of either CDKN2B or p19ARF. Genes Chromosomes and Cancer, 1997, 19, 52-54.	2.8	43
123	Homozygotes for CDKN2 (p16) germline mutation in Dutch familial melanoma kindreds. Nature Genetics, 1995, 10, 351-353.	21.4	288
124	Infrequent CDKN2 (MTS1/p16) gene alterations in human primary breast cancer. British Journal of Cancer, 1995, 72, 964-967.	6.4	36
125	Genetics of Seven Dutch Familial Atypcial Multiple Mole-Menaloma Syndrome Families: A Review of Linkage Results Including Chromosomes 1 and 9.. Journal of Investigative Dermatology, 1994, 103, 122S-125S.	0.7	12
126	Localization of the 9p Melanoma Susceptibility Locus (MLM) to a 2-cM Region between D9S736 and D9S171. Genomics, 1994, 23, 265-268.	2.9	55

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127	Genetics of Seven Dutch Familial Atypical Multiple Mole-Melanoma Syndrome Families: A Review of Linkage Results Including Chromosomes 1 and 9. Journal of Investigative Dermatology, 1994, 103, S122-S125.	0.7	21
128	PCR-based microsatellite polymorphisms in the detection of loss of heterozygosity in fresh and archival tumour tissue. British Journal of Cancer, 1993, 68, 308-313.	6.4	63
129	The Dutch FAMMM family material: Clinical and genetic data. Cytogenetic and Genome Research, 1992, 59, 161-164.	1.1	25
130	Genetic Linkage Between the Collagen VII (COL7A1) Gene and the Autosomal Dominant Form of Dystrophic Epidermolysis Bullosa in Two Dutch Kindreds. Journal of Investigative Dermatology, 1992, 99, 528-530.	0.7	27
131	Dinucleotide repeat polymorphism at the D17S513 locus. Nucleic Acids Research, 1991, 19, 4794-4794.	14.5	8
132	Dinucleotide repeat polymorphism at the D17S514 locus. Nucleic Acids Research, 1991, 19, 4794-4794.	14.5	4