Nicholas K Hayward

List of Publications by Citations

329 papers	25,939 citations	80 h-index	152 g-index
346 ext. papers	29,531 ext. citations	8.5 avg, IF	6.25 L-index

#	Paper	IF	Citations
329	Genomic Classification of Cutaneous Melanoma. *Cell*, **2015**, 161, 1681-96	56.2	1807
328	High frequency of BRAF mutations in nevi. *Nature Genetics*, **2003**, 33, 19-20	36.3	1355
327	Meta-analysis identifies 29 additional ulcerative colitis risk loci, increasing the number of confirmed associations to 47. *Nature Genetics*, **2011**, 43, 246-52	36.3	1028
326	Exome sequencing identifies recurrent somatic RAC1 mutations in melanoma. *Nature Genetics*, **2012**, 44, 1006-14	36.3	887
325	Whole-genome landscapes of major melanoma subtypes. *Nature*, **2017**, 545, 175-180	50.4	662
324	Germline mutations in the p16INK4a binding domain of CDK4 in familial melanoma. *Nature Genetics* , **1996**, 12, 97-9	36.3	652
323	A versatile gene-based test for genome-wide association studies. *American Journal of Human Genetics*, **2010**, 87, 139-45	11	648
322	Menin associates with a trithorax family histone methyltransferase complex and with the hoxc8 locus. *Molecular Cell*, **2004**, 13, 587-97	17.6	506
321	Melanocortin-1 receptor polymorphisms and risk of melanoma: is the association explained solely by pigmentation phenotype?. *American Journal of Human Genetics*, **2000**, 66, 176-86	11	424
320	A genome-wide association study identifies novel alleles associated with hair color and skin pigmentation. *PLoS Genetics*, **2008**, 4, e1000074	6	373
319	Geographical variation in the penetrance of CDKN2A mutations for melanoma. *Journal of the National Cancer Institute*, **2002**, 94, 894-903	9.7	363
318	Genome-wide association study identifies three loci associated with melanoma risk. *Nature Genetics* , **2009**, 41, 920-5	36.3	360
317	A novel recurrent mutation in MITF predisposes to familial and sporadic melanoma. *Nature*, **2011**, 480, 99-103	50.4	335
316	Melanocytic nevi, solar keratoses, and divergent pathways to cutaneous melanoma. *Journal of the National Cancer Institute*, **2003**, 95, 806-12	9.7	327
315	High-risk melanoma susceptibility genes and pancreatic cancer, neural system tumors, and uveal melanoma across GenoMEL. *Cancer Research*, **2006**, 66, 9818-28	10.1	313
314	Features associated with germline CDKN2A mutations: a GenoMEL study of melanoma-prone families from three continents. *Journal of Medical Genetics*, **2007**, 44, 99-106	5.8	296
313	A single SNP in an evolutionary conserved region within intron 86 of the HERC2 gene determines human blue-brown eye color. *American Journal of Human Genetics*, **2008**, 82, 424-31	11	275

312	Genetics of melanoma predisposition. *Oncogene*, **2003**, 22, 3053-62	9.2	249
311	MC1R genotype modifies risk of melanoma in families segregating CDKN2A mutations. *American Journal of Human Genetics*, **2001**, 69, 765-73	11	247
310	POT1 loss-of-function variants predispose to familial melanoma. *Nature Genetics*, **2014**, 46, 478-481	36.3	241
309	Increased MAPK reactivation in early resistance to dabrafenib/trametinib combination therapy of BRAF-mutant metastatic melanoma. *Nature Communications*, **2014**, 5, 5694	17.4	223
308	Mice lacking the vascular endothelial growth factor-B gene (Vegfb) have smaller hearts, dysfunctional coronary vasculature, and impaired recovery from cardiac ischemia. *Circulation Research*, **2000**, 86, E29-35	15.7	214
307	Genome-wide association study identifies three new melanoma susceptibility loci. *Nature Genetics*, **2011**, 43, 1108-13	36.3	203
306	Interactive effects of MC1R and OCA2 on melanoma risk phenotypes. *Human Molecular Genetics*, **2004**, 13, 447-61	5.6	199
305	A major quantitative-trait locus for mole density is linked to the familial melanoma gene CDKN2A: a maximum-likelihood combined linkage and association analysis in twins and their sibs. *American Journal of Human Genetics*, **1999**, 65, 483-92	11	193
304	Genome-wide loss of heterozygosity and copy number analysis in melanoma using high-density single-nucleotide polymorphism arrays. *Cancer Research*, **2007**, 67, 2632-42	10.1	189
303	Common sequence variants on 20q11.22 confer melanoma susceptibility. *Nature Genetics*, **2008**, 40, 838-40	36.3	188
302	Genome-wide association study identifies variants at 9p21 and 22q13 associated with development of cutaneous nevi. *Nature Genetics*, **2009**, 41, 915-9	36.3	186
301	Transcriptional pathway signatures predict MEK addiction and response to selumetinib (AZD6244). *Cancer Research*, **2010**, 70, 2264-73	10.1	185
300	ZEB1 drives epithelial-to-mesenchymal transition in lung cancer. *Journal of Clinical Investigation*, **2016**, 126, 3219-35	15.9	183
299	A combined analysis of D22S278 marker alleles in affected sib-pairs: support for a susceptibility locus for schizophrenia at chromosome 22q12. Schizophrenia Collaborative Linkage Group (Chromosome 22). *American Journal of Medical Genetics Part A*, **1996**, 67, 40-5		180
298	Genomic catastrophes frequently arise in esophageal adenocarcinoma and drive tumorigenesis. *Nature Communications*, **2014**, 5, 5224	17.4	176
297	The CDKN2A (p16) Gene and Human Cancer. *Molecular Medicine*, **1997**, 3, 5-20	6.2	174
296	A three-single-nucleotide polymorphism haplotype in intron 1 of OCA2 explains most human eye-color variation. *American Journal of Human Genetics*, **2007**, 80, 241-52	11	174
295	Deep sequencing of uveal melanoma identifies a recurrent mutation in PLCB4. *Oncotarget*, **2016**, 7, 4624-31	5.3	168

294	Genome-wide association study identifies novel loci predisposing to cutaneous melanoma. *Human Molecular Genetics*, **2011**, 20, 5012-23	5.6	164
293	Genome-wide meta-analysis identifies five new susceptibility loci for cutaneous malignant melanoma. *Nature Genetics*, **2015**, 47, 987-995	36.3	162
292	Characterization of the Melanoma miRNAome by Deep Sequencing. *PLoS ONE*, **2010**, 5, e9685	3.7	162
291	Microarray expression profiling in melanoma reveals a BRAF mutation signature. *Oncogene*, **2004**, 23, 4060-7	9.2	159
290	A genome-wide association study identifies new susceptibility loci for esophageal adenocarcinoma and Barrett@ esophagus. *Nature Genetics*, **2013**, 45, 1487-93	36.3	151
289	Additional support for schizophrenia linkage on chromosomes 6 and 8: a multicenter study. Schizophrenia Linkage Collaborative Group for Chromosomes 3, 6 and 8. *American Journal of Medical Genetics Part A*, **1996**, 67, 580-94		147
288	Nuclear PTEN expression and clinicopathologic features in a population-based series of primary cutaneous melanoma. *International Journal of Cancer*, **2002**, 99, 63-7	7.5	146
287	Frequent somatic mutations in MAP3K5 and MAP3K9 in metastatic melanoma identified by exome sequencing. *Nature Genetics*, **2011**, 44, 165-9	36.3	145
286	Multiple pigmentation gene polymorphisms account for a substantial proportion of risk of cutaneous malignant melanoma. *Journal of Investigative Dermatology*, **2010**, 130, 520-8	4.3	144
285	Mutations of the CDKN2/p16INK4 gene in Australian melanoma kindreds. *Human Molecular Genetics*, **1995**, 4, 1845-52	5.6	135
284	Loss of CDKN2A expression is a frequent event in primary invasive melanoma and correlates with sensitivity to the CDK4/6 inhibitor PD0332991 in melanoma cell lines. *Pigment Cell and Melanoma Research*, **2014**, 27, 590-600	4.5	133
283	Compilation of somatic mutations of the CDKN2 gene in human cancers: non-random distribution of base substitutions. *Genes Chromosomes and Cancer*, **1996**, 15, 77-88	5	133
282	Melanoma genetics. *Journal of Medical Genetics*, **2016**, 53, 1-14	5.8	130
281	Melanoma cell invasiveness is regulated by miR-211 suppression of the BRN2 transcription factor. *Pigment Cell and Melanoma Research*, **2011**, 24, 525-37	4.5	128
280	Whole-genome sequencing identifies a recurrent functional synonymous mutation in melanoma. *Proceedings of the National Academy of Sciences of the United States of America*, **2013**, 110, 13481-6	11.5	127
279	Genome-wide association study identifies a new melanoma susceptibility locus at 1q21.3. *Nature Genetics*, **2011**, 43, 1114-8	36.3	126
278	Characterization of the mouse Men1 gene and its expression during development. *Oncogene*, **1998**, 17, 2485-93	9.2	122
277	Conditional inactivation of the MEN1 gene leads to pancreatic and pituitary tumorigenesis but does not affect normal development of these tissues. *Molecular and Cellular Biology*, **2004**, 24, 3125-31	4.8	115

276	Whole-genome landscape of mucosal melanoma reveals diverse drivers and therapeutic targets. *Nature Communications*, **2019**, 10, 3163	17.4	113
275	Novel variants in growth differentiation factor 9 in mothers of dizygotic twins. *Journal of Clinical Endocrinology and Metabolism*, **2006**, 91, 4713-6	5.6	110
274	Cell cycle alterations in biopsied olfactory neuroepithelium in schizophrenia and bipolar I disorder using cell culture and gene expression analyses. *Schizophrenia Research*, **2006**, 82, 163-73	3.6	106
273	Vegfb gene knockout mice display reduced pathology and synovial angiogenesis in both antigen-induced and collagen-induced models of arthritis. *Arthritis and Rheumatism*, **2003**, 48, 2660-9		105
272	Analysis of gene amplification in head-and-neck squamous-cell carcinoma. *International Journal of Cancer*, **1991**, 48, 511-5	7.5	105
271	MC1R is a potent regulator of PTEN after UV exposure in melanocytes. *Molecular Cell*, **2013**, 51, 409-22	17.6	104
270	Localization of a novel melanoma susceptibility locus to 1p22. *American Journal of Human Genetics*, **2003**, 73, 301-13	11	103
269	Nonsense mutations in the shelterin complex genes ACD and TERF2IP in familial melanoma. *Journal of the National Cancer Institute*, **2015**, 107,	9.7	102
268	Association of Helicobacter pylori infection with reduced risk for esophageal cancer is independent of environmental and genetic modifiers. *Gastroenterology*, **2010**, 139, 73-83; quiz e11-2	13.3	101
267	IRF4 variants have age-specific effects on nevus count and predispose to melanoma. *American Journal of Human Genetics*, **2010**, 87, 6-16	11	100
266	The genomic landscape of cutaneous melanoma. *Pigment Cell and Melanoma Research*, **2016**, 29, 266-83	4.5	100
265	The effect on melanoma risk of genes previously associated with telomere length. *Journal of the National Cancer Institute*, **2014**, 106,	9.7	97
264	Comprehensive Study of the Clinical Phenotype of Germline BAP1 Variant-Carrying Families Worldwide. *Journal of the National Cancer Institute*, **2018**, 110, 1328-1341	9.7	97
263	A cryptic BAP1 splice mutation in a family with uveal and cutaneous melanoma, and paraganglioma. *Pigment Cell and Melanoma Research*, **2012**, 25, 815-8	4.5	96
262	Melanoma in adolescents: a case-control study of risk factors in Queensland, Australia. *International Journal of Cancer*, **2002**, 98, 92-8	7.5	96
261	A variant in FTO shows association with melanoma risk not due to BMI. *Nature Genetics*, **2013**, 45, 428-32, 432e1	36.3	95
260	Gene expression signature predicts recurrence in lung adenocarcinoma. *Clinical Cancer Research*, **2007**, 13, 2946-54	12.9	95
259	Predictors of sun protection behaviors and severe sunburn in an international online study. *Cancer Epidemiology Biomarkers and Prevention*, **2010**, 19, 2199-210	4	91

258	Melanocortin 1 receptor and risk of cutaneous melanoma: a meta-analysis and estimates of population burden. *International Journal of Cancer*, **2011**, 129, 1730-40	7.5	90
257	MicroRNA-218 is deleted and downregulated in lung squamous cell carcinoma. *PLoS ONE*, **2010**, 5, e12560	3.7	90
256	Melanoma prone families with CDK4 germline mutation: phenotypic profile and associations with MC1R variants. *Journal of Medical Genetics*, **2013**, 50, 264-70	5.8	89
255	Genetics of familial melanoma: 20 years after CDKN2A. *Pigment Cell and Melanoma Research*, **2015**, 28, 148-60	4.5	88
254	A genome scan for eye color in 502 twin families: most variation is due to a QTL on chromosome 15q. *Twin Research and Human Genetics*, **2004**, 7, 197-210		88
253	Cutaneous melanoma susceptibility and progression genes. *Cancer Letters*, **2005**, 230, 153-86	9.9	87
252	A large Norwegian family with inherited malignant melanoma, multiple atypical nevi, and CDK4 mutation. *Genes Chromosomes and Cancer*, **2005**, 44, 10-8	5	84
251	A genetic model of melanoma tumorigenesis based on allelic losses. *Genes Chromosomes and Cancer*, **1995**, 12, 134-41	5	84
250	Genetic testing for melanoma. *Lancet Oncology, The*, **2002**, 3, 653-4	21.7	80
249	Genome-wide copy number analysis in esophageal adenocarcinoma using high-density single-nucleotide polymorphism arrays. *Cancer Research*, **2008**, 68, 4163-72	10.1	76
248	Broad tumor spectrum in a mouse model of multiple endocrine neoplasia type 1. *International Journal of Cancer*, **2007**, 120, 259-67	7.5	76
247	Most common ‘sporadic’ cancers have a significant germline genetic component. *Human Molecular Genetics*, **2014**, 23, 6112-8	5.6	74
246	Analysis of the CDKN2A, CDKN2B and CDK4 genes in 48 Australian melanoma kindreds. *Oncogene*, **1997**, 15, 2999-3005	9.2	74
245	NF1-mutated melanoma tumors harbor distinct clinical and biological characteristics. *Molecular Oncology*, **2017**, 11, 438-451	7.9	73
244	Recurrent inactivating RASA2 mutations in melanoma. *Nature Genetics*, **2015**, 47, 1408-10	36.3	73
243	A recurrent germline BAP1 mutation and extension of the BAP1 tumor predisposition spectrum to include basal cell carcinoma. *Clinical Genetics*, **2015**, 88, 267-72	4	73
242	High-risk human papillomavirus in esophageal squamous cell carcinoma. *Cancer Epidemiology Biomarkers and Prevention*, **2010**, 19, 2080-7	4	70
241	The association between MC1R genotype and BRAF mutation status in cutaneous melanoma: findings from an Australian population. *Journal of Investigative Dermatology*, **2010**, 130, 241-8	4.3	70

240	ATG16L1 T300A shows strong associations with disease subgroups in a large Australian IBD population: further support for significant disease heterogeneity. *American Journal of Gastroenterology*, **2008**, 103, 2519-26	0.7	69
239	The Prognostic and Predictive Value of Melanoma-related MicroRNAs Using Tissue and Serum: A MicroRNA Expression Analysis. *EBioMedicine*, **2015**, 2, 671-80	8.8	67
238	Molecular pathways: mitogen-activated protein kinase pathway mutations and drug resistance. *Clinical Cancer Research*, **2013**, 19, 2301-9	12.9	67
237	A genome-wide scan for naevus count: linkage to CDKN2A and to other chromosome regions. *European Journal of Human Genetics*, **2007**, 15, 94-102	5.3	67
236	Melanoma genetics: recent findings take us beyond well-traveled pathways. *Journal of Investigative Dermatology*, **2012**, 132, 1763-74	4.3	65
235	Confirmation of a BRAF mutation-associated gene expression signature in melanoma. *Pigment Cell & Melanoma Research*, **2007**, 20, 216-21		65
234	Secretome from senescent melanoma engages the STAT3 pathway to favor reprogramming of naive melanoma towards a tumor-initiating cell phenotype. *Oncotarget*, **2013**, 4, 2212-24	3.3	65
233	miR-514a regulates the tumour suppressor NF1 and modulates BRAFi sensitivity in melanoma. *Oncotarget*, **2015**, 6, 17753-63	3.3	65
232	Second stage of a genome scan of schizophrenia: Study of five positive regions in an expanded sample. *American Journal of Medical Genetics Part A*, **2000**, 96, 864-869		64
231	Polymorphisms in MGMT and DNA repair genes and the risk of esophageal adenocarcinoma. *International Journal of Cancer*, **2008**, 123, 174-80	7.5	63
230	InterSCOPE study: Associations between esophageal squamous cell carcinoma and human papillomavirus serological markers. *Journal of the National Cancer Institute*, **2012**, 104, 147-58	9.7	61
229	Schizophrenia susceptibility and chromosome 6p24-22. *Nature Genetics*, **1995**, 11, 233-4	36.3	60
228	MicroRNA-34c is associated with emphysema severity and modulates SERPINE1 expression. *BMC Genomics*, **2014**, 15, 88	4.5	59
227	Mixed lineage kinases activate MEK independently of RAF to mediate resistance to RAF inhibitors. *Nature Communications*, **2014**, 5, 3901	17.4	59
226	Identification of candidate tumor suppressor genes inactivated by promoter methylation in melanoma. *Genes Chromosomes and Cancer*, **2009**, 48, 10-21	5	58
225	Loss of alleles on the short arm of chromosome 11 in a hepatoblastoma from a child with Beckwith-Wiedemann syndrome. *Human Genetics*, **1988**, 79, 186-9	6.3	58
224	Targeting activating mutations of EZH2 leads to potent cell growth inhibition in human melanoma by derepression of tumor suppressor genes. *Oncotarget*, **2015**, 6, 27023-36	3.3	57
223	Pathways to melanoma development: lessons from the mouse. *Journal of Investigative Dermatology* , **2002**, 119, 783-92	4.3	57

222	Cross-platform array screening identifies COL1A2, THBS1, TNFRSF10D and UCHL1 as genes frequently silenced by methylation in melanoma. *PLoS ONE*, **2011**, 6, e26121	3.7	57
221	MicroRNA regulation of melanoma progression. *Melanoma Research*, **2012**, 22, 101-13	3.3	56
220	A linkage study of schizophrenia to markers within Xp11 near the MAOB gene. *Psychiatry Research*, **1997**, 70, 131-43	9.9	55
219	PI3-kinase subunits are infrequent somatic targets in melanoma. *Journal of Investigative Dermatology*, **2006**, 126, 1660-3	4.3	53
218	BRAF mutation status is an independent prognostic factor for resected stage IIIB and IIIC melanoma: implications for melanoma staging and adjuvant therapy. *European Journal of Cancer*, **2014**, 50, 2668-76	7.5	50
217	SOX10 ablation arrests cell cycle, induces senescence, and suppresses melanomagenesis. *Cancer Research*, **2013**, 73, 5709-18	10.1	49
216	KCNN4 gene variant is associated with ileal Crohn's Disease in the Australian and New Zealand population. *American Journal of Gastroenterology*, **2010**, 105, 2209-17	0.7	49
215	Haplotype analysis of two recurrent CDKN2A mutations in 10 melanoma families: evidence for common founders and independent mutations. *Human Mutation*, **1998**, 11, 424-31	4.7	49
214	Osteopontin is a downstream effector of the PI3-kinase pathway in melanomas that is inversely correlated with functional PTEN. *Carcinogenesis*, **2006**, 27, 1778-86	4.6	49
213	High intake of folate from food sources is associated with reduced risk of esophageal cancer in an Australian population. *Journal of Nutrition*, **2011**, 141, 274-83	4.1	48
212	The phospholipase C beta 3 gene located in the MEN1 region shows loss of expression in endocrine tumours. *Human Molecular Genetics*, **1994**, 3, 1775-81	5.6	48
211	A BAP1 mutation in a Danish family predisposes to uveal melanoma and other cancers. *PLoS ONE*, **2013**, 8, e72144	3.7	48
210	MicroRNA and mRNA expression profiling in metastatic melanoma reveal associations with BRAF mutation and patient prognosis. *Pigment Cell and Melanoma Research*, **2015**, 28, 254-66	4.5	47
209	Prevalence of germline BAP1 mutation in a population-based sample of uveal melanoma cases. *Pigment Cell and Melanoma Research*, **2013**, 26, 278-9	4.5	47
208	Helicobacter pylori infection and the risks of Barrett's oesophagus: a population-based case-control study. *International Journal of Cancer*, **2012**, 130, 2407-16	7.5	47
207	Spontaneous and UV radiation-induced multiple metastatic melanomas in Cdk4R24C/R24C/TPras mice. *Cancer Research*, **2006**, 66, 2946-52	10.1	47
206	Exclusion of the familial melanoma locus (MLM) from the PND/D1S47 and MYCL1 regions of chromosome arm 1p in 7 Australian pedigrees. *Genomics*, **1992**, 12, 18-25	4.3	47
205	Novel pleiotropic risk loci for melanoma and nevus density implicate multiple biological pathways. *Nature Communications*, **2018**, 9, 4774	17.4	47

204	H-cadherin expression reduces invasion of malignant melanoma. *Pigment Cell and Melanoma Research*, **2009**, 22, 296-306	4.5	45
203	Similarity of aberrant DNA methylation in Barrett@ esophagus and esophageal adenocarcinoma. *Molecular Cancer*, **2008**, 7, 75	42.1	45
202	Expression and localization of mutant p16 proteins in melanocytic lesions from familial melanoma patients. *Human Pathology*, **2004**, 35, 25-33	3.7	45
201	Functional reassessment of P16 variants using a transfection-based assay. *International Journal of Cancer*, **1999**, 82, 305-12	7.5	45
200	Hepatocellular carcinoma mutation. *Nature*, **1991**, 352, 764	50.4	45
199	A highly recurrent RPS27 5@UTR mutation in melanoma. *Oncotarget*, **2014**, 5, 2912-7	3.3	45
198	Reviewing the somatic genetics of melanoma: from current to future analytical approaches. *Pigment Cell and Melanoma Research*, **2012**, 25, 144-54	4.5	44
197	A high-throughput panel for identifying clinically relevant mutation profiles in melanoma. *Molecular Cancer Therapeutics*, **2012**, 11, 888-97	6.1	44
196	Fibroblast and lymphoblast gene expression profiles in schizophrenia: are non-neural cells informative?. *PLoS ONE*, **2008**, 3, e2412	3.7	44
195	New developments in melanoma genetics. *Current Oncology Reports*, **2000**, 2, 300-6	6.3	43
194	Whole genome landscapes of uveal melanoma show an ultraviolet radiation signature in iris tumours. *Nature Communications*, **2020**, 11, 2408	17.4	42
193	The protective role of DOT1L in UV-induced melanomagenesis. *Nature Communications*, **2018**, 9, 259	17.4	42
192	Localization of multiple melanoma tumor-suppressor genes on chromosome 11 by use of homozygosity mapping-of-deletions analysis. *American Journal of Human Genetics*, **2000**, 67, 417-31	11	42
191	Exome Sequencing to Predict Neoantigens in Melanoma. *Cancer Immunology Research*, **2015**, 3, 992-8	12.5	41
190	Melanoma risk factors, perceived threat and intentional tanning: an international online survey. *European Journal of Cancer Prevention*, **2010**, 19, 216-26	2	41
189	Vascular endothelial growth factor-B-deficient mice show impaired development of hypoxic pulmonary hypertension. *Cardiovascular Research*, **2002**, 55, 361-8	9.9	41
188	Melanomas of unknown primary have a mutation profile consistent with cutaneous sun-exposed melanoma. *Pigment Cell and Melanoma Research*, **2013**, 26, 852-60	4.5	40
187	Murine neonatal melanocytes exhibit a heightened proliferative response to ultraviolet radiation and migrate to the epidermal basal layer. *Journal of Investigative Dermatology*, **2009**, 129, 184-93	4.3	40

186	Nevi, family history, and fair skin increase the risk of second primary melanoma. *Journal of Investigative Dermatology*, **2011**, 131, 461-7	4.3	40
185	Transgenic overexpression of vascular endothelial growth factor-B isoforms by endothelial cells potentiates postnatal vessel growth in vivo and in vitro. *Circulation Research*, **2005**, 97, e60-70	15.7	40
184	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	36.3	39
183	Analysis of the promoter region of the human VEGF-related factor gene. *Biochemical and Biophysical Research Communications*, **1997**, 230, 413-8	3.4	39
182	No evidence for the H133Y mutation in SONIC HEDGEHOG in a collection of common tumour types. *Oncogene*, **1998**, 16, 1091-3	9.2	39
181	Epidermal growth factor gene (EGF) polymorphism and risk of melanocytic neoplasia. *Journal of Investigative Dermatology*, **2004**, 123, 760-2	4.3	39
180	Allelic losses on chromosome band 11q13 in aldosterone-producing adrenal tumors. *Genes Chromosomes and Cancer*, **1995**, 12, 73-5	5	39
179	Sensitive droplet digital PCR method for detection of promoter mutations in cell free DNA from patients with metastatic melanoma. *Oncotarget*, **2017**, 8, 78890-78900	3.3	39
178	POLE mutations in families predisposed to cutaneous melanoma. *Familial Cancer*, **2015**, 14, 621-8	3	38
177	Identification of a melanoma susceptibility locus and somatic mutation in TET2. *Carcinogenesis*, **2014**, 35, 2097-101	4.6	38
176	Meta-analysis combining new and existing data sets confirms that the TERT-CLPTM1L locus influences melanoma risk. *Journal of Investigative Dermatology*, **2012**, 132, 485-7	4.3	38
175	The Queensland Study of Melanoma: environmental and genetic associations (Q-MEGA); study design, baseline characteristics, and repeatability of phenotype and sun exposure measures. *Twin Research and Human Genetics*, **2008**, 11, 183-96	2.2	38
174	Simple tandem repeat allelic deletions confirm the preferential loss of distal chromosome 6q in melanoma. *International Journal of Cancer*, **1994**, 58, 203-6	7.5	38
173	Downregulation of the Ubiquitin Ligase RNF125 Underlies Resistance of Melanoma Cells to BRAF Inhibitors via JAK1 Deregulation. *Cell Reports*, **2015**, 11, 1458-73	10.6	37
172	Loss of heterozygosity of chromosome 13 in Merkel cell carcinoma. *Genes Chromosomes and Cancer* , **1997**, 20, 93-7	5	37
171	CDKN2A mutation in a non-FAMMM kindred with cancers at multiple sites results in a functionally abnormal protein. *International Journal of Cancer*, **1997**, 73, 531-6	7.5	37
170	Single nucleotide polymorphisms in obesity-related genes and the risk of esophageal cancers. *Cancer Epidemiology Biomarkers and Prevention*, **2008**, 17, 1007-12	4	37
169	Expression of Wnt5a and its downstream effector beta-catenin in uveal melanoma. *Melanoma Research*, **2007**, 17, 380-6	3.3	37

168	Molecular Genomic Profiling of Melanocytic Nevi. *Journal of Investigative Dermatology*, **2019**, 139, 1762-1768	4.5	36
167	A common intronic variant of PARP1 confers melanoma risk and mediates melanocyte growth via regulation of MITF. *Nature Genetics*, **2017**, 49, 1326-1335	36.3	36
166	The risk of Barrett's esophagus associated with abdominal obesity in males and females. *International Journal of Cancer*, **2013**, 132, 2192-9	7.5	36
165	Deletion mapping suggests that the 1p22 melanoma susceptibility gene is a tumor suppressor localized to a 9-Mb interval. *Genes Chromosomes and Cancer*, **2004**, 41, 56-64	5	36
164	BRAF/NRAS wild-type melanoma, NF1 status and sensitivity to trametinib. *Pigment Cell and Melanoma Research*, **2015**, 28, 117-9	4.5	35
163	NRAS and BRAF mutations in cutaneous melanoma and the association with MC1R genotype: findings from Spanish and Austrian populations. *Journal of Investigative Dermatology*, **2013**, 133, 1027-33	4.3	35
162	Generation of homozygosity at the c-Ha-ras-1 locus on chromosome 11p in an adrenal adenoma from an adult with Wiedemann-Beckwith syndrome. *Cancer Genetics and Cytogenetics*, **1988**, 30, 127-32		35
161	Germline TERT promoter mutations are rare in familial melanoma. *Familial Cancer*, **2016**, 15, 139-44	3	34
160	Polymorphisms in nevus-associated genes MTAP, PLA2G6, and IRF4 and the risk of invasive cutaneous melanoma. *Twin Research and Human Genetics*, **2011**, 14, 422-32	2.2	34
159	Genome-wide analysis of esophageal adenocarcinoma yields specific copy number aberrations that correlate with prognosis. *Genes Chromosomes and Cancer*, **2014**, 53, 324-38	5	33
158	Coexisting NRAS and BRAF mutations in primary familial melanomas with specific CDKN2A germline alterations. *Journal of Investigative Dermatology*, **2010**, 130, 618-20	4.3	33
157	Prolonged stable disease in a uveal melanoma patient with germline MBD4 nonsense mutation treated with pembrolizumab and ipilimumab. *Immunogenetics*, **2019**, 71, 433-436	3.2	32
156	Expression profiling identifies genes involved in emphysema severity. *Respiratory Research*, **2009**, 10, 81	7.3	32
155	Linkage analysis in familial melanoma kindreds to markers on chromosome 6p. *International Journal of Cancer*, **1994**, 59, 771-5	7.5	31
154	Identification of the CIMP-like subtype and aberrant methylation of members of the chromosomal segregation and spindle assembly pathways in esophageal adenocarcinoma. *Carcinogenesis*, **2016**, 37, 356-65	4.6	30
153	Genetic Heterogeneity of BRAF Fusion Kinases in Melanoma Affects Drug Responses. *Cell Reports*, **2019**, 29, 573-588.e7	10.6	30
152	SiDCoN: a tool to aid scoring of DNA copy number changes in SNP chip data. *PLoS ONE*, **2007**, 2, e1093	3.7	30
151	Chromosomal gains and losses in ocular melanoma detected by comparative genomic hybridization in an Australian population-based study. *Cancer Genetics and Cytogenetics*, **2003**, 144, 12-7		30

150	Somatic inactivating PTPRJ mutations and dysregulated pathways identified in canine malignant melanoma by integrated comparative genomic analysis. *PLoS Genetics*, **2018**, 14, e1007589	6	30
149	Prevalence and determinants of frequent gastroesophageal reflux symptoms in the Australian community. *Ecological Management and Restoration*, **2012**, 25, 573-83	3	29
148	Prognostic value of BRAF mutations in localized cutaneous melanoma. *Journal of the American Academy of Dermatology*, **2014**, 70, 858-62.e1-2	4.5	29
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