Nicholas K Hayward

List of Publications by Year in Descending Order

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	Anatomic position determines oncogenic specificity in melanoma.. *Nature*, **2022**,	50.4	3
328	Choroidal melanoma with synchronous FuchsQadenoma and novel ATRX mutation.. *International Journal of Retina and Vitreous*, **2022**, 8, 24	2.9	
327	Multiomic profiling of checkpoint inhibitor-treated melanoma: Identifying predictors of response and resistance, and markers of biological discordance.. *Cancer Cell*, **2021**,	24.3	6
326	Germline variants are associated with increased primary melanoma tumor thickness at diagnosis. *Human Molecular Genetics*, **2021**, 29, 3578-3587	5.6	1
325	FRAMe: Familial Risk Assessment of Melanoma-a risk prediction tool to guide CDKN2A germline mutation testing in Australian familial melanoma. *Familial Cancer*, **2021**, 20, 231-239	3	0
324	Evolution of late-stage metastatic melanoma is dominated by aneuploidy and whole genome doubling. *Nature Communications*, **2021**, 12, 1434	17.4	5
323	Meta-Analysis and Systematic Review of the Genomics of Mucosal Melanoma. *Molecular Cancer Research*, **2021**, 19, 991-1004	6.6	5
322	Evaluation of Crizotinib Treatment in a Patient With Unresectable GOPC-ROS1 Fusion Agminated Spitz Nevi. *JAMA Dermatology*, **2021**, 157, 836-841	5.1	2
321	Novel MAPK/AKT-impairing germline NRAS variant identified in a melanoma-prone family. *Familial Cancer*, **2021**, 1	3	0
320	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	4.5	0
319	Loss-of-function variants in predispose to uveal melanoma. *Journal of Medical Genetics*, **2021**, 58, 234-236	5.8	1
318	G9a Inhibition Enhances Checkpoint Inhibitor Blockade Response in Melanoma. *Clinical Cancer Research*, **2021**, 27, 2624-2635	12.9	4
317	Microsimulation Model for Evaluating the Cost-Effectiveness of Surveillance in Pathogenic Variant Carriers. *JCO Clinical Cancer Informatics*, **2021**, 5, 143-154	5.2	1
316	Whole genome landscapes of uveal melanoma show an ultraviolet radiation signature in iris tumours. *Nature Communications*, **2020**, 11, 2408	17.4	42
315	EZH2 Cooperates with DNA Methylation to Downregulate Key Tumor Suppressors and IFN Gene Signatures in Melanoma. *Journal of Investigative Dermatology*, **2020**, 140, 2442-2454.e5	4.3	23
314	Cluster of pregnancy-associated melanoma: A case report and brief update. *Journal of Dermatology* , **2020**, 47, 1054-1057	1.6	2
313	as a candidate high-penetrance melanoma susceptibility gene. *Journal of Medical Genetics*, **2020**, 57, 203-210	5.8	6

312	Co-targeting bromodomain and extra-terminal proteins and MCL1 induces synergistic cell death in melanoma. *International Journal of Cancer*, **2020**, 147, 2176-2189	7.5	10
311	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
310	Whole Exome Sequencing Identifies Candidate Genes Associated with Hereditary Predisposition to Uveal Melanoma. *Ophthalmology*, **2020**, 127, 668-678	7.3	16
309	Whole-genome sequencing of acral melanoma reveals genomic complexity and diversity. *Nature Communications*, **2020**, 11, 5259	17.4	28
308	Multiplex melanoma families are enriched for polygenic risk. *Human Molecular Genetics*, **2020**, 29, 2976-2985	5.6	3
307	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	12.5	4
306	Genomic analysis of adult case of ocular surface giant congenital melanocytic nevus and associated clinicopathological findings. *Ophthalmic Genetics*, **2020**, 41, 616-620	1.2	1
305	The Prognostic Impact of Circulating Tumour DNA in Melanoma Patients Treated with Systemic Therapies-Beyond Mutant Detection. *Cancers*, **2020**, 12,	6.6	5
304	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
303	Molecular Genomic Profiling of Melanocytic Nevi. *Journal of Investigative Dermatology*, **2019**, 139, 1762-1768	4.3	36
302	Somatic Hypermutation of the Oncogene in a Human Cutaneous Melanoma. *Molecular Cancer Research*, **2019**, 17, 1435-1449	6.6	15
301	Whole-genome landscape of mucosal melanoma reveals diverse drivers and therapeutic targets. *Nature Communications*, **2019**, 10, 3163	17.4	113
300	Germline variants in oculocutaneous albinism genes and predisposition to familial cutaneous melanoma. *Pigment Cell and Melanoma Research*, **2019**, 32, 854-863	4.5	13
299	Estimating CDKN2A mutation carrier probability among global familial melanoma cases using GenoMELPREDICT. *Journal of the American Academy of Dermatology*, **2019**, 81, 386-394	4.5	9
298	Genetic Heterogeneity of BRAF Fusion Kinases in Melanoma Affects Drug Responses. *Cell Reports*, **2019**, 29, 573-588.e7	10.6	30
297	Recurrent hotspot SF3B1 mutations at codon 625 in vulvovaginal mucosal melanoma identified in a study of 27 Australian mucosal melanomas. *Oncotarget*, **2019**, 10, 930-941	3.3	18
296	A Panel of Circulating MicroRNAs Detects Uveal Melanoma With High Precision. *Translational Vision Science and Technology*, **2019**, 8, 12	3.3	20
295	Evaluation of the contribution of germline variants in BRCA1 and BRCA2 to uveal and cutaneous melanoma. *Melanoma Research*, **2019**, 29, 483-490	3.3	7

294	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	7.5	27
293	Locus-specific concordance of genomic alterations between tissue and plasma circulating tumor DNA in metastatic melanoma. *Molecular Oncology*, **2019**, 13, 171-184	7.9	27
292	The Prognostic Significance of Low-Frequency Somatic Mutations in Metastatic Cutaneous Melanoma. *Frontiers in Oncology*, **2018**, 8, 584	5.3	9
291	The protective role of DOT1L in UV-induced melanomagenesis. *Nature Communications*, **2018**, 9, 259	17.4	42
290	RGS7 is recurrently mutated in melanoma and promotes migration and invasion of human cancer cells. *Scientific Reports*, **2018**, 8, 653	4.9	8
289	Telomere sequence content can be used to determine ALT activity in tumours. *Nucleic Acids Research*, **2018**, 46, 4903-4918	20.1	26
288	Proteomic phenotyping of metastatic melanoma reveals putative signatures of MEK inhibitor response and prognosis. *British Journal of Cancer*, **2018**, 119, 713-723	8.7	2
287	Germline mutations in candidate predisposition genes in individuals with cutaneous melanoma and at least two independent additional primary cancers. *PLoS ONE*, **2018**, 13, e0194098	3.7	12
286	Novel pleiotropic risk loci for melanoma and nevus density implicate multiple biological pathways. *Nature Communications*, **2018**, 9, 4774	17.4	47
285	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
284	Somatic inactivating PTPRJ mutations and dysregulated pathways identified in canine malignant melanoma by integrated comparative genomic analysis. *PLoS Genetics*, **2018**, 14, e1007589	6	30
283	Promoter Mutations Ablate GABP Transcription Factor Binding in Melanoma. *Cancer Research*, **2017**, 77, 1649-1661	10.1	6
282	UVB represses melanocyte cell migration and acts through Ecatenin. *Experimental Dermatology*, **2017**, 26, 875-882	4	8
281	Unexpected UVR and non-UVR mutation burden in some acral and cutaneous melanomas. *Laboratory Investigation*, **2017**, 97, 130-145	5.9	25
280	Whole-genome landscapes of major melanoma subtypes. *Nature*, **2017**, 545, 175-180	50.4	662
279	NF1-mutated melanoma tumors harbor distinct clinical and biological characteristics. *Molecular Oncology*, **2017**, 11, 438-451	7.9	73
278	Mutation load in melanoma is affected by MC1R genotype. *Pigment Cell and Melanoma Research*, **2017**, 30, 255-258	4.5	15
277	Germline Variation at CDKN2A and Associations with Nevus Phenotypes among Members of Melanoma Families. *Journal of Investigative Dermatology*, **2017**, 137, 2606-2612	4.3	10

276	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
275	Clinical significance of intronic variants in BRAF inhibitor resistant melanomas with altered transcript splicing. *Biomarker Research*, **2017**, 5, 17	8	6
274	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
273	Melanoma genetics. *Journal of Medical Genetics*, **2016**, 53, 1-14	5.8	130
272	Histologic and Phenotypic Factors and MC1R Status Associated with BRAF(V600E), BRAF(V600K), and NRAS Mutations in a Community-Based Sample of 414 Cutaneous Melanomas. *Journal of Investigative Dermatology*, **2016**, 136, 829-837	4.3	17
271	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
270	Comparison of whole-exome sequencing of matched fresh and formalin fixed paraffin embedded melanoma tumours: implications for clinical decision making. *Pathology*, **2016**, 48, 261-6	1.6	28
269	Phenotypic and Histopathological Tumor Characteristics According to CDKN2A Mutation Status among Affected Members of Melanoma Families. *Journal of Investigative Dermatology*, **2016**, 136, 1066-1069	4.3	9
268	Germline TERT promoter mutations are rare in familial melanoma. *Familial Cancer*, **2016**, 15, 139-44	3	34
267	ZEB1 drives epithelial-to-mesenchymal transition in lung cancer. *Journal of Clinical Investigation*, **2016**, 126, 3219-35	15.9	183
266	The "melanoma-enriched" microRNA miR-4731-5p acts as a tumour suppressor. *Oncotarget*, **2016**, 7, 49677-49687	3.3	18
265	Deep sequencing of uveal melanoma identifies a recurrent mutation in PLCB4. *Oncotarget*, **2016**, 7, 4624-31	5.31	168
264	Molecular markers to complement sentinel node status in predicting survival in patients with high-risk locally invasive melanoma. *International Journal of Cancer*, **2016**, 139, 664-72	7.5	6
263	Increased incidence of bladder cancer, lymphoid leukaemia, and myeloma in a cohort of Queensland melanoma families. *Familial Cancer*, **2016**, 15, 651-63	3	3
262	A Transcriptionally Inactive ATF2 Variant Drives Melanomagenesis. *Cell Reports*, **2016**, 15, 1884-92	10.6	10
261	The genomic landscape of cutaneous melanoma. *Pigment Cell and Melanoma Research*, **2016**, 29, 266-83	4.5	100
260	Nonsense mutations in the shelterin complex genes ACD and TERF2IP in familial melanoma. *Journal of the National Cancer Institute*, **2015**, 107,	9.7	102
259	Genomic Classification of Cutaneous Melanoma. *Cell*, **2015**, 161, 1681-96	56.2	1807

258	POLE mutations in families predisposed to cutaneous melanoma. *Familial Cancer*, **2015**, 14, 621-8	3	38
257	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
256	Genome-wide meta-analysis identifies five new susceptibility loci for cutaneous malignant melanoma. *Nature Genetics*, **2015**, 47, 987-995	36.3	162
255	Prevalence of Germline BAP1, CDKN2A, and CDK4 Mutations in an Australian Population-Based Sample of Cutaneous Melanoma Cases. *Twin Research and Human Genetics*, **2015**, 18, 126-33	2.2	12
254	Fine mapping of genetic susceptibility loci for melanoma reveals a mixture of single variant and multiple variant regions. *International Journal of Cancer*, **2015**, 136, 1351-60	7.5	26
253	Recurrent inactivating RASA2 mutations in melanoma. *Nature Genetics*, **2015**, 47, 1408-10	36.3	73
252	BRAF/NRAS wild-type melanoma, NF1 status and sensitivity to trametinib. *Pigment Cell and Melanoma Research*, **2015**, 28, 117-9	4.5	35
251	Survival outcomes in patients with multiple primary melanomas. *Journal of the European Academy of Dermatology and Venereology*, **2015**, 29, 2120-7	4.6	18
250	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
249	Genetics of familial melanoma: 20 years after CDKN2A. *Pigment Cell and Melanoma Research*, **2015**, 28, 148-60	4.5	88
248	PARP1 polymorphisms play opposing roles in melanoma occurrence and survival. *International Journal of Cancer*, **2015**, 136, 2488-9	7.5	6
247	Tumour procurement, DNA extraction, coverage analysis and optimisation of mutation-detection algorithms for human melanoma genomes. *Pathology*, **2015**, 47, 683-93	1.6	6
246	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
245	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
244	Exome Sequencing to Predict Neoantigens in Melanoma. *Cancer Immunology Research*, **2015**, 3, 992-8	12.5	41
243	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
242	Histologic features of melanoma associated with CDKN2A genotype. *Journal of the American Academy of Dermatology*, **2015**, 72, 496-507.e7	4.5	16
241	Exploration of peptides bound to MHC class I molecules in melanoma. *Pigment Cell and Melanoma Research*, **2015**, 28, 281-94	4.5	19

240	Telomere-regulating genes and the telomere interactome in familial cancers. *Molecular Cancer Research*, **2015**, 13, 211-22	6.6	26
239	Germline RAD51B truncating mutation in a family with cutaneous melanoma. *Familial Cancer*, **2015**, 14, 337-40	3	11
238	Molecular characterization of melanoma cases in Denmark suspected of genetic predisposition. *PLoS ONE*, **2015**, 10, e0122662	3.7	16
237	miR-514a regulates the tumour suppressor NF1 and modulates BRAFi sensitivity in melanoma. *Oncotarget*, **2015**, 6, 17753-63	3.3	65
236	POT1 loss-of-function variants predispose to familial melanoma. *Nature Genetics*, **2014**, 46, 478-481	36.3	241
235	MicroRNA-34c is associated with emphysema severity and modulates SERPINE1 expression. *BMC Genomics*, **2014**, 15, 88	4.5	59
234	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
233	Genomic catastrophes frequently arise in esophageal adenocarcinoma and drive tumorigenesis. *Nature Communications*, **2014**, 5, 5224	17.4	176
232	Primary melanoma tumors from CDKN2A mutation carriers do not belong to a distinct molecular subclass. *Journal of Investigative Dermatology*, **2014**, 134, 3000-3003	4.3	5
231	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
230	Assessment of PALB2 as a candidate melanoma susceptibility gene. *PLoS ONE*, **2014**, 9, e100683	3.7	9
229	Mixed lineage kinases activate MEK independently of RAF to mediate resistance to RAF inhibitors. *Nature Communications*, **2014**, 5, 3901	17.4	59
228	Most common ‘sporadic’ cancers have a significant germline genetic component. *Human Molecular Genetics*, **2014**, 23, 6112-8	5.6	74
227	Identification of a melanoma susceptibility locus and somatic mutation in TET2. *Carcinogenesis*, **2014**, 35, 2097-101	4.6	38
226	Somatic BRAF and NRAS mutations in familial melanomas with known germline CDKN2A status: a GenoMEL study. *Journal of Investigative Dermatology*, **2014**, 134, 287-290	4.3	15
225	Increased MAPK reactivation in early resistance to dabrafenib/trametinib combination therapy of BRAF-mutant metastatic melanoma. *Nature Communications*, **2014**, 5, 5694	17.4	223
224	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
223	The effect on melanoma risk of genes previously associated with telomere length. *Journal of the National Cancer Institute*, **2014**, 106,	9.7	97

222	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
221	Somatic mutations in MAP3K5 attenuate its proapoptotic function in melanoma through increased binding to thioredoxin. *Journal of Investigative Dermatology*, **2014**, 134, 452-460	4.3	14
220	A highly recurrent RPS27 5′UTR mutation in melanoma. *Oncotarget*, **2014**, 5, 2912-7	3.3	45
219	MC1R is a potent regulator of PTEN after UV exposure in melanocytes. *Molecular Cell*, **2013**, 51, 409-22	17.6	104
218	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
217	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
216	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
215	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
214	Molecular pathways: mitogen-activated protein kinase pathway mutations and drug resistance. *Clinical Cancer Research*, **2013**, 19, 2301-9	12.9	67
213	SOX10 ablation arrests cell cycle, induces senescence, and suppresses melanomagenesis. *Cancer Research*, **2013**, 73, 5709-18	10.1	49
212	A variant in FTO shows association with melanoma risk not due to BMI. *Nature Genetics*, **2013**, 45, 428-32, 432e1	36.3	95
211	Association between putative functional variants in the PSMB9 gene and risk of melanoma--re-analysis of published melanoma genome-wide association studies. *Pigment Cell and Melanoma Research*, **2013**, 26, 392-401	4.5	4
210	Prevalence of BRAF and NRAS mutations in fast-growing melanomas. *Pigment Cell and Melanoma Research*, **2013**, 26, 429-31	4.5	10
209	A genome-wide association study identifies new susceptibility loci for esophageal adenocarcinoma and Barrett's esophagus. *Nature Genetics*, **2013**, 45, 1487-93	36.3	151
208	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
207	Association between functional polymorphisms in genes involved in the MAPK signaling pathways and cutaneous melanoma risk. *Carcinogenesis*, **2013**, 34, 885-92	4.6	6
206	The effect of MC1R variants and sunscreen on the response of human melanocytes in vivo to ultraviolet radiation and implications for melanoma. *Pigment Cell and Melanoma Research*, **2013**, 26, 835-44	4.5	18
205	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

204	A BAP1 mutation in a Danish family predisposes to uveal melanoma and other cancers. *PLoS ONE*, **2013**, 8, e72144	3.7	48
203	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
202	Brca1 is involved in establishing murine pigmentation in a p53 and developmentally specific manner. *Pigment Cell and Melanoma Research*, **2012**, 25, 530-2	4.5	2
201	Prevalence and determinants of frequent gastroesophageal reflux symptoms in the Australian community. *Ecological Management and Restoration*, **2012**, 25, 573-83	3	29
200	Identification of TFG (TRK-fused gene) as a putative metastatic melanoma tumor suppressor gene. *Genes Chromosomes and Cancer*, **2012**, 51, 452-61	5	22
199	Duplication of CXC chemokine genes on chromosome 4q13 in a melanoma-prone family. *Pigment Cell and Melanoma Research*, **2012**, 25, 243-7	4.5	11
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	Whole genome and exome sequencing of melanoma: a step toward personalized targeted therapy. *Advances in Pharmacology*, **2012**, 65, 399-435	5.7	8
196	Exome sequencing identifies recurrent somatic RAC1 mutations in melanoma. *Nature Genetics*, **2012**, 44, 1006-14	36.3	887
195	Menin and p53 have non-synergistic effects on tumorigenesis in mice. *BMC Cancer*, **2012**, 12, 252	4.8	9
194	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
193	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
192	A high-throughput panel for identifying clinically relevant mutation profiles in melanoma. *Molecular Cancer Therapeutics*, **2012**, 11, 888-97	6.1	44
191	Melanoma genetics: recent findings take us beyond well-traveled pathways. *Journal of Investigative Dermatology*, **2012**, 132, 1763-74	4.3	65
190	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
189	Skin examination behavior: the role of melanoma history, skin type, psychosocial factors, and region of residence in determining clinical and self-conducted skin examination. *Archives of Dermatology*, **2012**, 148, 1142-51		28
188	MicroRNA regulation of melanoma progression. *Melanoma Research*, **2012**, 22, 101-13	3.3	56
187	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

186	Array-comparative genomic hybridization reveals loss of SOCS6 is associated with poor prognosis in primary lung squamous cell carcinoma. *PLoS ONE*, **2012**, 7, e30398	3.7	23
185	MS4A1 dysregulation in asbestos-related lung squamous cell carcinoma is due to CD20 stromal lymphocyte expression. *PLoS ONE*, **2012**, 7, e34943	3.7	12
184	Frequent somatic mutations in MAP3K5 and MAP3K9 in metastatic melanoma identified by exome sequencing. *Nature Genetics*, **2011**, 44, 165-9	36.3	145
183	Genome-wide association study identifies three new melanoma susceptibility loci. *Nature Genetics*, **2011**, 43, 1108-13	36.3	203
182	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
181	Genes and gene ontologies common to airflow obstruction and emphysema in the lungs of patients with COPD. *PLoS ONE*, **2011**, 6, e17442	3.7	21
180	Pathway-based analysis of a melanoma genome-wide association study: analysis of genes related to tumour-immunosuppression. *PLoS ONE*, **2011**, 6, e29451	3.7	16
179	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
178	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
177	Genome-wide association study identifies novel loci predisposing to cutaneous melanoma. *Human Molecular Genetics*, **2011**, 20, 5012-23	5.6	164
176	Nevi, family history, and fair skin increase the risk of second primary melanoma. *Journal of Investigative Dermatology*, **2011**, 131, 461-7	4.3	40
175	A flexible multiplex bead-based assay for detecting germline CDKN2A and CDK4 variants in melanoma-prone kindreds. *Journal of Investigative Dermatology*, **2011**, 131, 480-6	4.3	10
174	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
173	High-Risk Human Papillomavirus in Esophageal Squamous Cell Carcinoma Response. *Cancer Epidemiology Biomarkers and Prevention*, **2011**, 20, 409-410	4	2
172	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
171	A novel recurrent mutation in MITF predisposes to familial and sporadic melanoma. *Nature*, **2011**, 480, 99-103	50.4	335
170	Genome-wide association study identifies a new melanoma susceptibility locus at 1q21.3. *Nature Genetics*, **2011**, 43, 1114-8	36.3	126
169	Whole genome expression array profiling highlights differences in mucosal defense genes in Barrett's esophagus and esophageal adenocarcinoma. *PLoS ONE*, **2011**, 6, e22513	3.7	29

168	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
167	MicroRNA-218 is deleted and downregulated in lung squamous cell carcinoma. *PLoS ONE*, **2010**, 5, e12560	3.7	90
166	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
165	High-risk human papillomavirus in esophageal squamous cell carcinoma. *Cancer Epidemiology Biomarkers and Prevention*, **2010**, 19, 2080-7	4	70
164	Predictors of sun protection behaviors and severe sunburn in an international online study. *Cancer Epidemiology Biomarkers and Prevention*, **2010**, 19, 2199-210	4	91
163	Transcriptional pathway signatures predict MEK addiction and response to selumetinib (AZD6244). *Cancer Research*, **2010**, 70, 2264-73	10.1	185
162	KCNN4 gene variant is associated with ileal Crohn¢ Disease in the Australian and New Zealand population. *American Journal of Gastroenterology*, **2010**, 105, 2209-17	0.7	49
161	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
160	Gene expression alterations in formalin-fixed, paraffin-embedded Barrett esophagus and esophageal adenocarcinoma tissues. *Cancer Biology and Therapy*, **2010**, 10, 172-9	4.6	16
159	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
158	Dual loss of rb1 and Trp53 in the adrenal medulla leads to spontaneous pheochromocytoma. *Neoplasia*, **2010**, 12, 235-43	6.4	8
157	Characterization of the Melanoma miRNAome by Deep Sequencing. *PLoS ONE*, **2010**, 5, e9685	3.7	162
156	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
155	webFOG: A web tool to map genomic features onto genes. *Biochemical and Biophysical Research Communications*, **2010**, 401, 447-50	3.4	
154	Enhancement of DNA repair using topical T4 endonuclease V does not inhibit melanoma formation in Cdk4(R24C/R24C)/Tyr-Nras(Q61K) mice following neonatal UVR. *Pigment Cell and Melanoma Research*, **2010**, 23, 121-8	4.5	12
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