James S Wilmott

List of Publications by Year
in descending order

145 papers	14,847 citations	43973 48 h-index	20900 115 g-index
151 all docs	151 docs citations	151 times ranked	22587 citing authors

#	Article	IF	Citations
1	Genetic drivers of nonâ€cutaneous melanomas: Challenges and opportunities in a heterogeneous landscape. Experimental Dermatology, 2022, 31, 13-30.	1.4	14
2	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.	7.7	64
3	Anatomic position determines oncogenic specificity in melanoma. Nature, 2022, 604, 354-361.	13.7	44
4	Elevated non-coding promoter mutations are associated with malignant transformation of melanocytic naevi to melanoma. Pathology, 2022, 54, 533-540.	0.3	3
5	Multiple eruptive squamoproliferative lesions during antiâ€PD1 immunotherapy for metastatic melanoma: Pathogenesis, immunohistochemical analysis and treatment. Dermatologic Therapy, 2022, , e15472.	0.8	1
6	Characterization of the treatment-naive immune microenvironment in melanoma with BRAF mutation. , 2022, 10, e004095.		7
7	Comprehensive Clinical, Histopathologic, and Molecular Analysis and Long-term Follow-up of Patients With Nodal Blue Nevi. American Journal of Surgical Pathology, 2022, 46, 1048-1059.	2.1	3
8	Validation of an Accurate Automated Multiplex Immunofluorescence Method for Immuno-Profiling Melanoma. Frontiers in Molecular Biosciences, 2022, 9, .	1.6	9
9	Higher proportions of CD39+ tumor-resident cytotoxic T cells predict recurrence-free survival in patients with stage III melanoma treated with adjuvant immunotherapy. , 2022, 10, e004771.		16
10	Association of baseline corticosteroid treatment with outcomes for patients (pts) with BRAF-mutant melanoma brain metastases (MBMs) in COMBI-MB treated with dabrafenib and trametinib (DT).. Journal of Clinical Oncology, 2022, 40, e21546-e21546.	0.8	1
11	A biomarker-guided Bayesian response-adaptive phase II trial for metastatic melanoma: The Personalized Immunotherapy Platform (PIP) trial design.. Journal of Clinical Oncology, 2022, 40, TPS9599-TPS9599.	0.8	0
12	The tumour immune landscape and its implications in cutaneous melanoma. Pigment Cell and Melanoma Research, 2021, 34, 529-549.	1.5	21
13	G9a Inhibition Enhances Checkpoint Inhibitor Blockade Response in Melanoma. Clinical Cancer Research, 2021, 27, 2624-2635.	3.2	22
14	Î³Î´ T Cells in Merkel Cell Carcinomas Have a Proinflammatory Profile Prognostic of Patient Survival. Cancer Immunology Research, 2021, 9, 612-623.	1.6	22
15	Evolution of late-stage metastatic melanoma is dominated by aneuploidy and whole genome doubling. Nature Communications, 2021, 12, 1434.	5.8	46
16	Targeting NK Cells to Enhance Melanoma Response to Immunotherapies. Cancers, 2021, 13, 1363.	1.7	24
17	Cryopreservation of human cancers conserves tumour heterogeneity for single-cell multi-omics analysis. Genome Medicine, 2021, 13, 81.	3.6	25
18	The deacylase SIRT5 supports melanoma viability by influencing chromatin dynamics. Journal of Clinical Investigation, 2021, 131, .	3.9	23

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19	Clinical and Molecular Heterogeneity in Patients with Innate Resistance to Anti-PD-1 +/â^' Anti-CTLA-4 Immunotherapy in Metastatic Melanoma Reveals Distinct Therapeutic Targets. Cancers, 2021, 13, 3186.	1.7	11
20	Evaluation of Crizotinib Treatment in a Patient With Unresectable GOPC-ROS1 Fusion Agminated Spitz Nevi. JAMA Dermatology, 2021, 157, 836-841.	2.0	9
21	Mucosal Melanoma. Surgical Pathology Clinics, 2021, 14, 293-307.	0.7	1
22	Melanoma with osseous or chondroid differentiation: a report of eight cases including SATB2 expression and mutation analysis. Pathology, 2021, 53, 830-835.	0.3	7
23	Acquired resistance to anti-MAPK targeted therapy confers an immune-evasive tumor microenvironment and cross-resistance to immunotherapy in melanoma. Nature Cancer, 2021, 2, 693-708.	5.7	102
24	Tumour gene expression signature in primary melanoma predicts long-term outcomes. Nature Communications, 2021, 12, 1137.	5.8	33
25	Combined presentation and immunogenicity analysis reveals a recurrent RAS.Q61K neoantigen in melanoma. Journal of Clinical Investigation, 2021, 131, .	3.9	15
26	High-Dimensional Single-Cell Transcriptomics in Melanoma and Cancer Immunotherapy. Genes, 2021, 12, 1629.	1.0	8
27	Close proximity of immune and tumor cells underlies response to anti-PD-1 based therapies in metastatic melanoma patients. OncoImmunology, 2020, 9, 1659093.	2.1	62
28	The prognostic value of tumor mitotic rate in children and adolescents with cutaneous melanoma: A retrospective cohort study. Journal of the American Academy of Dermatology, 2020, 82, 910-919.	0.6	10
29	Molecular Profiling of Noncoding Mutations Distinguishes Nevoid Melanomas From Mitotically Active Nevi in Pregnancy. American Journal of Surgical Pathology, 2020, 44, 357-367.	2.1	10
30	Whole-genome sequencing of acral melanoma reveals genomic complexity and diversity. Nature Communications, 2020, 11, 5259.	5.8	102
31	CD155 on Tumor Cells Drives Resistance to Immunotherapy by Inducing the Degradation of the Activating Receptor CD226 in CD8+ TÂCells. Immunity, 2020, 53, 805-823.e15.	6.6	79
32	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.	1.6	13
33	Whole genome landscapes of uveal melanoma show an ultraviolet radiation signature in iris tumours. Nature Communications, 2020, 11, 2408.	5.8	86
34	Integration of Digital Pathologic and Transcriptomic Analyses Connects Tumor-Infiltrating Lymphocyte Spatial Density With Clinical Response to BRAF Inhibitors. Frontiers in Oncology, 2020, 10, 757.	1.3	11
35	Temporal and spatial modulation of the tumor and systemic immune response in the murine Gl261 glioma model. PLoS ONE, 2020, 15, e0226444.	1.1	16
36	Molecular analysis of primary melanoma T cells identifies patients at risk for metastatic recurrence. Nature Cancer, 2020, 1, 197-209.	5.7	30

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37	Pan-cancer analysis of whole genomes. Nature, 2020, 578, 82-93.	13.7	1,966
38	Tumor CD155 Expression Is Associated with Resistance to Anti-PD1 Immunotherapy in Metastatic Melanoma. Clinical Cancer Research, 2020, 26, 3671-3681.	3.2	53
39	Replacement and desmoplastic histopathological growth patterns in cutaneous melanoma liver metastases: frequency, characteristics, and robust prognostic value. Journal of Pathology: Clinical Research, 2020, 6, 195-206.	1.3	35
40	Transcriptional downregulation of MHC class I and melanoma de- differentiation in resistance to PD-1 inhibition. Nature Communications, 2020, 11, 1897.	5.8	165
41	Macrophage-Derived CXCL9 and CXCL10 Are Required for Antitumor Immune Responses Following Immune Checkpoint Blockade. Clinical Cancer Research, 2020, 26, 487-504.	3.2	355
42	Abstract 5734: Gut microbiota predicts response and toxicity with neoadjuvant immunotherapy. , 2020, , .		6
43	Abstract 913: Defining melanoma patients unresponsive to single agent anti-PD-1 therapy but responsive to combination anti-PD-1 + anti-CTLA-4 therapy. Cancer Research, 2020, 80, 913-913.	0.4	1
44	Whole-genome landscape of mucosal melanoma reveals diverse drivers and therapeutic targets. Nature Communications, 2019, 10, 3163.	5.8	205
45	Neoadjuvant dabrafenib combined with trametinib for resectable, stage IIIBâ€“C, BRAFV600 mutation-positive melanoma (NeoCombi): a single-arm, open-label, single-centre, phase 2 trial. Lancet Oncology, The, 2019, 20, 961-971.	5.1	126
46	LNK suppresses interferon signaling in melanoma. Nature Communications, 2019, 10, 2230.	5.8	21
47	Molecular Genomic Profiling of MelanocyticÂNevi. Journal of Investigative Dermatology, 2019, 139, 1762-1768.	0.3	55
48	Distinct Immune Cell Populations Define Response to Anti-PD-1 Monotherapy and Anti-PD-1/Anti-CTLA-4 Combined Therapy. Cancer Cell, 2019, 35, 238-255.e6.	7.7	547
49	Prevalence and Cellular Distribution of Novel Immune Checkpoint Targets Across Longitudinal Specimens in Treatment-naÂ¨ve Melanoma Patients: Implications for Clinical Trials. Clinical Cancer Research, 2019, 25, 3247-3258.	3.2	27
50	Novel Immune Targets in Melanomaâ€”Response. Clinical Cancer Research, 2019, 25, 5424-5425.	3.2	1
51	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.	2.3	54
52	bcGSTâ€”an interactive bias-correction method to identify over-represented gene-sets in boutique arrays. Bioinformatics, 2019, 35, 1350-1357.	1.8	1
53	RAB27A promotes melanoma cell invasion and metastasis via regulation of proâ€invasive exosomes. International Journal of Cancer, 2019, 144, 3070-3085.	2.3	72
54	Tissue-resident memory CD8+ T cells promote melanomaâ€“immune equilibrium in skin. Nature, 2019, 565, 366-371.	13.7	266

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55	Interâ€•and intrapatient heterogeneity of indoleamine 2,3â€•dioxygenase expression in primary and metastatic melanoma cells and the tumour microenvironment. Histopathology, 2019, 74, 817-828.	1.6	16
56	Distinct Molecular Profiles and Immunotherapy Treatment Outcomes of V600E and V600K BRAF-Mutant Melanoma. Clinical Cancer Research, 2019, 25, 1272-1279.	3.2	57
57	Integrated molecular and immunophenotypic analysis of NK cells in anti-PD-1 treated metastatic melanoma patients. OncoImmunology, 2019, 8, e1537581.	2.1	61
58	Primary anorectal melanoma: clinical, immunohistology and DNA analysis of 43 cases. Pathology, 2019, 51, 39-45.	0.3	25
59	Abstract 975: Liver metastases (mets) induce systemic immunosuppression and immunotherapy resistance in metastatic melanoma. , 2019, , .		2
60	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.	0.8	31
61	Abstract 2822: Low intestinal microbial diversity is associated with severe immune-related adverse events and lack of response to neoadjuvant combination antiPD1, anti-CTLA4 immunotherapy. , 2019, , .		2
62	Abstract 3246: Dynamics of T-cell checkpoint receptor profiles during melanoma progression. , 2019, , .		0
63	Telomere sequence content can be used to determine ALT activity in tumours. Nucleic Acids Research, 2018, 46, 4903-4918.	6.5	40
64	CD103+ Tumor-Resident CD8+ T Cells Are Associated with Improved Survival in Immunotherapy-NaÃ¯ve Melanoma Patients and Expand Significantly During Antiâ€“PD-1 Treatment. Clinical Cancer Research, 2018, 24, 3036-3045.	3.2	297
65	Combination nivolumab and ipilimumab or nivolumab alone in melanoma brain metastases: a multicentre randomised phase 2 study. Lancet Oncology, The, 2018, 19, 672-681.	5.1	732
66	HDAC inhibitors restore BRAFâ€•inhibitor sensitivity by altering PI3K and survival signalling in a subset of melanoma. International Journal of Cancer, 2018, 142, 1926-1937.	2.3	48
67	Primary and Acquired Resistance to Immune Checkpoint Inhibitors in Metastatic Melanoma. Clinical Cancer Research, 2018, 24, 1260-1270.	3.2	289
68	Epigenetic profiling for the molecular classification of metastatic brain tumors. Nature Communications, 2018, 9, 4627.	5.8	79
69	Differences in LC3B expression and prognostic implications in oropharyngeal and oral cavity squamous cell carcinoma patients. BMC Cancer, 2018, 18, 624.	1.1	12
70	Melanoma protective antitumor immunity activated by catalytic DNA. Oncogene, 2018, 37, 5115-5126.	2.6	15
71	Proteomic phenotyping of metastatic melanoma reveals putative signatures of MEK inhibitor response and prognosis. British Journal of Cancer, 2018, 119, 713-723.	2.9	9
72	The Prognostic Significance of Low-Frequency Somatic Mutations in Metastatic Cutaneous Melanoma. Frontiers in Oncology, 2018, 8, 584.	1.3	14

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73	Brain metastasis DNA methylomes, a novel resource for the identification of biological and clinical features. Scientific Data, 2018, 5, 180245.	2.4	18
74	Abstract LB-146: T cell receptor immunosequencing improves prediction of melanoma recurrence. , 2018, , .		0
75	Abstract 2420: Skp2-mediated stabilization of MTH1 promotes survival of melanoma cells upon oxidative stress. , 2018, , .		0
76	Unexpected UVR and non-UVR mutation burden in some acral and cutaneous melanomas. Laboratory Investigation, 2017, 97, 130-145.	1.7	40
77	Dynamic Changes in PD-L1 Expression and Immune Infiltrates Early During Treatment Predict Response to PD-1 Blockade in Melanoma. Clinical Cancer Research, 2017, 23, 5024-5033.	3.2	192
78	Whole-genome landscapes of major melanoma subtypes. Nature, 2017, 545, 175-180.	13.7	1,068
79	The â€œTricky Businessâ€•of Identifying Mechanisms of Resistance to Antiâ€“PD-1. Clinical Cancer Research, 2017, 23, 2921-2923.	3.2	5
80	Mutation load in melanoma is affected by <scp>MC</scp>1R genotype. Pigment Cell and Melanoma Research, 2017, 30, 255-258.	1.5	19
81	Skp2-Mediated Stabilization of MTH1 Promotes Survival of Melanoma Cells upon Oxidative Stress. Cancer Research, 2017, 77, 6226-6239.	0.4	43
82	PD-L1 Expression and Immune Escape in Melanoma Resistance to MAPK Inhibitors. Clinical Cancer Research, 2017, 23, 6054-6061.	3.2	75
83	Negative immune checkpoint regulation by VISTA: a mechanism of acquired resistance to anti-PD-1 therapy in metastatic melanoma patients. Modern Pathology, 2017, 30, 1666-1676.	2.9	150
84	Reply to comment on: Detailed Pathological Examination of Completion Node Dissection Specimens and Outcome in Melanoma Patients with Minimal (<Â0.1Âmm) Sentinel Lymph Node Metastases. Annals of Surgical Oncology, 2017, 24, 660-660.	0.7	1
85	Advantages of whole-genome sequencing for identification of tumor etiology and clinically actionable genomic aberrations: lessons from the Australian Melanoma Genome Project. Melanoma Management, 2017, 4, 147-149.	0.1	1
86	Distinct gene expression, mutational profile and clinical outcomes of V600E and V600K/R BRAF-mutant metastatic melanoma (MM).. Journal of Clinical Oncology, 2017, 35, 9541-9541.	0.8	2
87	Differences in immune profiles of metastatic melanoma patients treated with anti-CTLA-4 and anti-PD-1 combined immunotherapy.. Journal of Clinical Oncology, 2017, 35, 51-51.	0.8	0
88	Abstract 2206: Proteome phenotype of stage III metastatic melanoma and response to MEK inhibition. , 2017, , .		0
89	Multiparameter analysis of naevi and primary melanomas identifies a subset of naevi with elevated markers of transformation. Pigment Cell and Melanoma Research, 2016, 29, 444-452.	1.5	3
90	The protein phosphatase 2A regulatory subunit PR70 is a gonosomal melanoma tumor suppressor gene. Science Translational Medicine, 2016, 8, 369ra177.	5.8	33

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91	BRAF^{V600E} and NRAS^{Q61L/Q61R} mutation analysis in metastatic melanoma using immunohistochemistry: a study of 754 cases highlighting potential pitfalls and guidelines for interpretation and reporting. Histopathology, 2016, 69, 680-686.	1.6	28
92	Programmed death ligand 1 expression in tripleâ€negative breast cancer is associated with tumourâ€infiltrating lymphocytes and improved outcome. Histopathology, 2016, 69, 25-34.	1.6	177
93	PD-L1 Negative Status is Associated with Lower Mutation Burden, Differential Expression of Immune-Related Genes, and Worse Survival in Stage III Melanoma. Clinical Cancer Research, 2016, 22, 3915-3923.	3.2	91
94	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.	0.3	39
95	Plasma cells in primary melanoma. Prognostic significance and possible role of IgA. Modern Pathology, 2016, 29, 347-358.	2.9	43
96	Targeted therapies and immune checkpoint inhibitors in the treatment of metastatic melanoma patients: a guide and update for pathologists. Pathology, 2016, 48, 194-202.	0.3	19
97	Tumour procurement, DNA extraction, coverage analysis and optimisation of mutation-detection algorithms for human melanoma genomes. Pathology, 2015, 47, 683-693.	0.3	9
98	Clinicopathologic features associated with efficacy and longâ€term survival in metastatic melanoma patients treated with <scp>BRAF</scp> or combined <scp>BRAF</scp> and MEK inhibitors. Cancer, 2015, 121, 3826-3835.	2.0	40
99	Synergistic effects of MAPK and immune checkpoint inhibitors in melanoma: what is the best combination strategy?. Melanoma Management, 2015, 2, 15-19.	0.1	4
100	Detailed Pathological Examination of Completion Node Dissection Specimens and Outcome in Melanoma Patients with Minimal (<0.1Âmm) Sentinel Lymph Node Metastases. Annals of Surgical Oncology, 2015, 22, 2972-2977.	0.7	13
101	RIP1 Kinase Is an Oncogenic Driver in Melanoma. Cancer Research, 2015, 75, 1736-1748.	0.4	63
102	UV-Associated Mutations Underlie the Etiology of MCV-Negative Merkel Cell Carcinomas. Cancer Research, 2015, 75, 5228-5234.	0.4	270
103	Genomic Classification of Cutaneous Melanoma. Cell, 2015, 161, 1681-1696.	13.5	2,562
104	PD-L1 Expression and Tumor-Infiltrating Lymphocytes Define Different Subsets of MAPK Inhibitorâ€“Treated Melanoma Patients. Clinical Cancer Research, 2015, 21, 3140-3148.	3.2	120
105	Expression of the class 1 histone deacetylases HDAC8 and 3 are associated with improved survival of patients with metastatic melanoma. Modern Pathology, 2015, 28, 884-894.	2.9	37
106	<scp>PD</scp>â€L1 expression in melanoma shows marked heterogeneity within and between patients: implications for antiâ€<scp>PD</scp>â€1/<scp>PD</scp>â€<scp>L</scp>1 clinical trials. Pigment Cell and Melanoma Research, 2015, 28, 245-253.	1.5	356
107	Tumor PD-L1 expression, immune cell correlates and PD-1+ lymphocytes in sentinel lymph node melanoma metastases. Modern Pathology, 2015, 28, 1535-1544.	2.9	76
108	Recurrent inactivating RASA2 mutations in melanoma. Nature Genetics, 2015, 47, 1408-1410.	9.4	90

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109	Phylogenetic analyses of melanoma reveal complex patterns of metastatic dissemination. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 10995-11000.	3.3	146
110	Endosialin Expression in Metastatic Melanoma Tumor Microenvironment Vasculature: Potential Therapeutic Implications. Cancer Microenvironment, 2015, 8, 111-118.	3.1	17
111	Combining BET and HDAC inhibitors synergistically induces apoptosis of melanoma and suppresses AKT and YAP signaling. Oncotarget, 2015, 6, 21507-21521.	0.8	72
112	INPP4B is upregulated and functions as an oncogenic driver through SGK3 in a subset of melanomas. Oncotarget, 2015, 6, 39891-39907.	0.8	40
113	PD-L1 expression, immune cell correlates, and PD-1+ lymphocytes in sentinel lymph node positive melanoma patients: Implications for adjuvant PD-1 clinical trials.. Journal of Clinical Oncology, 2015, 33, e20011-e20011.	0.8	0
114	Abstract 56: Receptor-Interacting protein kinase 1 functions as an oncogenic regulator in human melanoma. , 2015, , .		0
115	Abstract 5025: Immune expression profiling of MAPK inhibitor resistant tumors based upon mechanisms of resistance. , 2015, , .		0
116	Abstract 4718: Inositol polyphosphate 4-phosphatase II activates PI3K/SGK3 signaling to promote proliferation of human melanoma cells. , 2015, , .		0
117	Oncogenic suppression of PHLPP1 in human melanoma. Oncogene, 2014, 33, 4756-4766.	2.6	29
118	Intra-patient heterogeneity of BRAF mutation status: fact or fiction?. British Journal of Cancer, 2014, 111, 1678-1679.	2.9	9
119	Intrapatient Homogeneity of BRAFV600E Expression in Melanoma. American Journal of Surgical Pathology, 2014, 38, 377-382.	2.1	66
120	Concordant BRAFV600E mutation status in primary melanomas and associated naevi: implications for mutation testing of primary melanomas. Pathology, 2014, 46, 193-198.	0.3	19
121	Dynamics of Chemokine, Cytokine, and Growth Factor Serum Levels in BRAF-Mutant Melanoma Patients during BRAF Inhibitor Treatment. Journal of Immunology, 2014, 192, 2505-2513.	0.4	69
122	A light shines on melanoma metastagenesis. Pigment Cell and Melanoma Research, 2014, 27, 696-697.	1.5	0
123	Epigenome-wide DNA methylation landscape of melanoma progression to brain metastasis reveals aberrations on homeobox D cluster associated with prognosis. Human Molecular Genetics, 2014, 23, 226-238.	1.4	96
124	DNA methylation and gene deletion analysis of brain metastases in melanoma patients identifies mutually exclusive molecular alterations. Neuro-Oncology, 2014, 16, 1499-1509.	0.6	65
125	How anti-PD1 treatments are changing the management of melanoma. Melanoma Management, 2014, 1, 165-172.	0.1	5
126	TRIM16 inhibits proliferation and migration through regulation of interferon beta 1 in melanoma cells. Oncotarget, 2014, 5, 10127-10139.	0.8	31

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127	Noxa upregulation by oncogenic activation of MEK/ERK through CREB promotes autophagy in human melanoma cells. Oncotarget, 2014, 5, 11237-11251.	0.8	34
128	Effects of <scp>BRAF</scp> inhibitors on human melanoma tissue before treatment, early during treatment, and on progression. Pigment Cell and Melanoma Research, 2013, 26, 499-508.	1.5	37
129	BRAFV600E protein expression and outcome from BRAF inhibitor treatment in BRAFV600E metastatic melanoma. British Journal of Cancer, 2013, 108, 924-931.	2.9	55
130	BAP1 expression in cutaneous melanoma: a pilot study. Pathology, 2013, 45, 606-609.	0.3	30
131	PI(4,5)P2 5-phosphatase A regulates PI3K/Akt signalling and has a tumour suppressive role in human melanoma. Nature Communications, 2013, 4, 1508.	5.8	67
132	BRAF Mutation, NRAS Mutation, and the Absence of an Immune-Related Expressed Gene Profile Predict Poor Outcome in Patients with Stage III Melanoma. Journal of Investigative Dermatology, 2013, 133, 509-517.	0.3	156
133	Immunohistochemistry Is Highly Sensitive and Specific for the Detection of V600E BRAF Mutation in Melanoma. American Journal of Surgical Pathology, 2013, 37, 61-65.	2.1	289
134	Abstract B67: Galectin-1 expression related to hypoxia in primary human melanoma as a driver for metastatic progression. A target to promote anticancer immunotherapy.. , 2013, , .		0
135	Abstract B8: Galectin-1 expressed in human melanoma is bound to cancer stem cells: A driver for metastatic progression and target for antimetastatic cancer therapy. , 2013, , .		0
136	Selective BRAF Inhibitors Induce Marked T-cell Infiltration into Human Metastatic Melanoma. Clinical Cancer Research, 2012, 18, 1386-1394.	3.2	589
137	Combined targeted therapy and immunotherapy in the treatment of advanced melanoma. OncoImmunology, 2012, 1, 997-999.	2.1	27
138	Intratumoral Molecular Heterogeneity in a BRAF-Mutant, BRAF Inhibitor-Resistant Melanoma: A Case Illustrating the Challenges for Personalized Medicine. Molecular Cancer Therapeutics, 2012, 11, 2704-2708.	1.9	78
139	The retinoid signalling molecule, TRIM16, is repressed during squamous cell carcinoma skin carcinogenesis in vivo and reduces skin cancer cell migration in vitro. Journal of Pathology, 2012, 226, 451-462.	2.1	36
140	Angiotropism is an independent predictor of microscopic satellites in primary cutaneous melanoma. Histopathology, 2012, 61, 889-898.	1.6	42
141	Lymphatic vessel density in primary melanomas predicts sentinel lymph node status and risk of metastasis. Histopathology, 2012, 61, 702-710.	1.6	29
142	The emerging important role of microRNAs in the pathogenesis, diagnosis and treatment of human cancers. Pathology, 2011, 43, 657-671.	0.3	40
143	MicroRNA-149*, a p53-responsive microRNA, functions as an oncogenic regulator in human melanoma. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 15840-15845.	3.3	168
144	Sentinel Lymph Node Biopsy in Pediatric and Adolescent Cutaneous Melanoma Patients. Annals of Surgical Oncology, 2010, 17, 138-143.	0.7	68

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145	Atypical Spitzoid Melanocytic Tumors With Positive Sentinel Lymph Nodes in Children and Teenagers, and Comparison With Histologically Unambiguous and Lethal Melanomas. American Journal of Surgical Pathology, 2009, 33, 1386-1395.	2.1	95