Ann-Marie Patch

List of Publications by Year
in descending order

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77 papers	20,005 citations	66234 42 h-index	69108 77 g-index
84 all docs	84 docs citations	84 times ranked	31059 citing authors

#	Article	IF	Citations
1	Genomic and Molecular Analyses Identify Molecular Subtypes of Pancreatic Cancer Recurrence. Gastroenterology, 2022, 162, 320-324.e4.	0.6	26
2	Patient-derived xenograft models capture genomic heterogeneity in endometrial cancer. Genome Medicine, 2022, 14, 3.	3.6	16
3	qmotif: determination of telomere content from whole-genome sequence data. Bioinformatics Advances, 2022, 2, .	0.9	5
4	Neoantigens â€“ the next frontier in precision immunotherapy for B-cell lymphoproliferative disorders. Blood Reviews, 2022, 56, 100969.	2.8	2
5	Comprehensive genomic and tumour immune profiling reveals potential therapeutic targets in malignant pleural mesothelioma. Genome Medicine, 2022, 14, .	3.6	24
6	Targeting DNA Damage Response and Replication Stress in Pancreatic Cancer. Gastroenterology, 2021, 160, 362-377.e13.	0.6	90
7	Injection site vaccinology of a recombinant vaccinia-based vector reveals diverse innate immune signatures. PLoS Pathogens, 2021, 17, e1009215.	2.1	13
8	DNA methylation patterns identify subgroups of pancreatic neuroendocrine tumors with clinical association. Communications Biology, 2021, 4, 155.	2.0	26
9	Identification of a Locus Near ULK1 Associated With Progression-Free Survival in Ovarian Cancer. Cancer Epidemiology Biomarkers and Prevention, 2021, 30, 1669-1680.	1.1	5
10	Evaluation of Crizotinib Treatment in a Patient With Unresectable GOPC-ROS1 Fusion Agminated Spitz Nevi. JAMA Dermatology, 2021, 157, 836-841.	2.0	9
11	ROR1 and ROR2 expression in pancreatic cancer. BMC Cancer, 2021, 21, 1199.	1.1	4
12	Whole-genome sequencing of acral melanoma reveals genomic complexity and diversity. Nature Communications, 2020, 11, 5259.	5.8	102
13	The Impact of Next Generation Sequencing in Cancer Research. Cancers, 2020, 12, 2928.	1.7	7
14	FGFR2c Mesenchymal Isoform Expression Is Associated with Poor Prognosis and Further Refines Risk Stratification within Endometrial Cancer Molecular Subtypes. Clinical Cancer Research, 2020, 26, 4569-4580.	3.2	10
15	APC Mutation Marks an Aggressive Subtype of BRAF Mutant Colorectal Cancers. Cancers, 2020, 12, 1171.	1.7	28
16	HNF4A and GATA6 Loss Reveals Therapeutically Actionable Subtypes in Pancreatic Cancer. Cell Reports, 2020, 31, 107625.	2.9	78
17	Alterations in signaling pathways that accompany spontaneous transition to malignancy in a mouse model of BRAF mutant microsatellite stable colorectal cancer. Neoplasia, 2020, 22, 120-128.	2.3	14
18	Neoantigens Are Typically Associated with Intact HLA Class I Presentation in Early-Stage Follicular Lymphoma. Blood, 2020, 136, 37-38.	0.6	1

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19	Whole-genome landscape of mucosal melanoma reveals diverse drivers and therapeutic targets. Nature Communications, 2019, 10, 3163.	5.8	205
20	Whole-genome sequencing reveals clinically relevant insights into the aetiology of familial breast cancers. Annals of Oncology, 2019, 30, 1071-1079.	0.6	64
21	Integrative Genome-Scale DNA Methylation Analysis of a Large and Unselected Cohort Reveals 5 Distinct Subtypes of Colorectal Adenocarcinomas. Cellular and Molecular Gastroenterology and Hepatology, 2019, 8, 269-290.	2.3	42
22	Complex structural rearrangements are present in high-grade dysplastic Barrettâ€™s oesophagus samples. BMC Medical Genomics, 2019, 12, 31.	0.7	19
23	Intratumoural Heterogeneity Underlies Distinct Therapy Responses and Treatment Resistance in Glioblastoma. Cancers, 2019, 11, 190.	1.7	39
24	Evaluation of the contribution of germline variants in BRCA1 and BRCA2 to uveal and cutaneous melanoma. Melanoma Research, 2019, 29, 483-490.	0.6	13
25	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
26	Homozygosity mapping provides supporting evidence of pathogenicity in recessive Mendelian disease. Genetics in Medicine, 2019, 21, 982-986.	1.1	22
27	Telomere sequence content can be used to determine ALT activity in tumours. Nucleic Acids Research, 2018, 46, 4903-4918.	6.5	40
28	Malignant cells from pleural fluids in malignant mesothelioma patients reveal novel mutations. Lung Cancer, 2018, 119, 64-70.	0.9	23
29	Homologous Recombination DNA Repair Pathway Disruption and Retinoblastoma Protein Loss Are Associated with Exceptional Survival in High-Grade Serous Ovarian Cancer. Clinical Cancer Research, 2018, 24, 569-580.	3.2	79
30	A2AR Adenosine Signaling Suppresses Natural Killer Cell Maturation in the Tumor Microenvironment. Cancer Research, 2018, 78, 1003-1016.	0.4	269
31	BRAF Mutations in Low-Grade Serous Ovarian Cancer and Response to BRAF Inhibition. JCO Precision Oncology, 2018, 2, 1-14.	1.5	19
32	Germline and somatic variant identification using BGISEQ-500 and HiSeq X Ten whole genome sequencing. PLoS ONE, 2018, 13, e0190264.	1.1	57
33	Copy number profiles of paired primary and metastatic colorectal cancers. Oncotarget, 2018, 9, 3394-3405.	0.8	14
34	Whole-genome landscape of pancreatic neuroendocrine tumours. Nature, 2017, 543, 65-71.	13.7	716
35	Unexpected UVR and non-UVR mutation burden in some acral and cutaneous melanomas. Laboratory Investigation, 2017, 97, 130-145.	1.7	40
36	Whole-genome landscapes of major melanoma subtypes. Nature, 2017, 545, 175-180.	13.7	1,068

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37	Mutation load in melanoma is affected by <scp>MC</scp>1R genotype. Pigment Cell and Melanoma Research, 2017, 30, 255-258.	1.5	19
38	Long Noncoding RNAs CUPID1 and CUPID2 Mediate Breast Cancer Risk at 11q13 by Modulating the Response to DNA Damage. American Journal of Human Genetics, 2017, 101, 255-266.	2.6	77
39	EIF1AX and NRAS Mutations Co-occur and Cooperate in Low-Grade Serous Ovarian Carcinomas. Cancer Research, 2017, 77, 4268-4278.	0.4	56
40	Whole exome sequencing of an asbestos-induced wild-type murine model of malignant mesothelioma. BMC Cancer, 2017, 17, 396.	1.1	30
41	Lost in translation: returning germline genetic results in genome-scale cancer research. Genome Medicine, 2017, 9, 41.	3.6	27
42	Hypermutation In Pancreatic Cancer. Gastroenterology, 2017, 152, 68-74.e2.	0.6	174
43	Point Mutations in Exon 1B of APC Reveal Gastric Adenocarcinoma and Proximal Polyposis of the Stomach as a Familial Adenomatous Polyposis Variant. American Journal of Human Genetics, 2016, 98, 830-842.	2.6	201
44	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, 356-365.	1.3	46
45	Genomic analyses identify molecular subtypes of pancreatic cancer. Nature, 2016, 531, 47-52.	13.7	2,700
46	Integrated genomic and transcriptomic analysis of human brain metastases identifies alterations of potential clinical significance. Journal of Pathology, 2015, 237, 363-378.	2.1	98
47	Wholeâ€“genome characterization of chemoresistant ovarian cancer. Nature, 2015, 521, 489-494.	13.7	1,206
48	A comprehensive assessment of somatic mutation detection in cancer using whole-genome sequencing. Nature Communications, 2015, 6, 10001.	5.8	266
49	Whole genomes redefine the mutational landscape of pancreatic cancer. Nature, 2015, 518, 495-501.	13.7	2,132
50	A workflow to increase verification rate of chromosomal structural rearrangements using high-throughput next-generation sequencing. BioTechniques, 2014, 57, 31-38.	0.8	0
51	Genomeâ€wide DNA methylation patterns in pancreatic ductal adenocarcinoma reveal epigenetic deregulation of SLITâ€ROBO, ITGA2 and MET signaling. International Journal of Cancer, 2014, 135, 1110-1118.	2.3	192
52	Recessive mutations in a distal PTF1A enhancer cause isolated pancreatic agenesis. Nature Genetics, 2014, 46, 61-64.	9.4	255
53	Genomic catastrophes frequently arise in esophageal adenocarcinoma and drive tumorigenesis. Nature Communications, 2014, 5, 5224.	5.8	236
54	Analysis of Transcription Factors Key for Mouse Pancreatic Development Establishes NKX2-2 and MNX1 Mutations as Causes of Neonatal Diabetes in Man. Cell Metabolism, 2014, 19, 146-154.	7.2	123

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55	Clinical and molecular characterization of HER2 amplified-pancreatic cancer. Genome Medicine, 2013, 5, 78.	3.6	97
56	Somatic Point Mutation Calling in Low Cellularity Tumors. PLoS ONE, 2013, 8, e74380.	1.1	67
57	Pancreatic cancer genomes reveal aberrations in axon guidance pathway genes. Nature, 2012, 491, 399-405.	13.7	1,741
58	Recessive SLC19A2 mutations are a cause ofÂneonatal diabetes mellitus inÂthiamine-responsive megaloblastic anaemia. Pediatric Diabetes, 2012, 13, 314-321.	1.2	57
59	Genome-Wide Homozygosity Analysis Reveals HADH Mutations as a Common Cause of Diazoxide-Responsive Hyperinsulinemic-Hypoglycemia in Consanguineous Pedigrees. Journal of Clinical Endocrinology and Metabolism, 2011, 96, E498-E502.	1.8	51
60	Novel GLIS3 mutations demonstrate an extended multisystem phenotype. European Journal of Endocrinology, 2011, 164, 437-443.	1.9	86
61	Rfx6 directs islet formation and insulin production in mice and humans. Nature, 2010, 463, 775-780.	13.7	300
62	Recessive mutations in the INS gene result in neonatal diabetes through reduced insulin biosynthesis. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 3105-3110.	3.3	185
63	In vitro expression of NGN3 identifies RAB3B as the predominant Ras-associated GTP-binding protein 3 family member in human islets. Journal of Endocrinology, 2010, 207, 151-161.	1.2	22
64	Using SIFT and PolyPhen to Predict Loss-of-Function and Gain-of-Function Mutations. Genetic Testing and Molecular Biomarkers, 2010, 14, 533-537.	0.3	330
65	Sequencing of candidate genes selected by beta cell experts in monogenic diabetes of unknown aetiology. JOP: Journal of the Pancreas, 2010, 11, 14-7.	1.5	8
66	Wolcott-Rallison Syndrome Is the Most Common Genetic Cause of Permanent Neonatal Diabetes in Consanguineous Families. Journal of Clinical Endocrinology and Metabolism, 2009, 94, 4162-4170.	1.8	127
67	Partial lipodystrophy and insulin resistant diabetes in a patient with a homozygous nonsense mutation in CIDEC. EMBO Molecular Medicine, 2009, 1, 280-287.	3.3	235
68	Mutations in the ABCC8 (SUR1 subunit of the K_{ATP} channel) gene are associated with a variable clinical phenotype. Clinical Endocrinology, 2009, 71, 358-362.	1.2	35
69	Neonatal diabetes mellitus due to pancreas agenesis: a new case report and review of the literature. Pediatric Diabetes, 2009, 10, 487-491.	1.2	10
70	Effective Treatment With Oral Sulfonylureas in Patients With Diabetes Due to Sulfonylurea Receptor 1 (SUR1) Mutations. Diabetes Care, 2008, 31, 204-209.	4.3	239
71	Insulin Mutation Screening in 1,044 Patients With Diabetes. Diabetes, 2008, 57, 1034-1042.	0.3	347
72	Mutations in ATP-Sensitive K+ Channel Genes Cause Transient Neonatal Diabetes and Permanent Diabetes in Childhood or Adulthood. Diabetes, 2007, 56, 1930-1937.	0.3	320

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73	Fingerprinting fission yeast: polymorphic markers for molecular genetic analysis of Schizosaccharomyces pombe strains. Microbiology (United Kingdom), 2007, 153, 887-897.	0.7	6
74	Increased ATPase activity produced by mutations at arginine-1380 in nucleotide-binding domain 2 of ABCC8 causes neonatal diabetes. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 18988-18992.	3.3	51
75	Insulin gene mutations as a cause of permanent neonatal diabetes. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 15040-15044.	3.3	494
76	Permanent Neonatal Diabetes Caused by Dominant, Recessive, or Compound Heterozygous SUR1 Mutations with Opposite Functional Effects. American Journal of Human Genetics, 2007, 81, 375-382.	2.6	194
77	A Common Variant in the FTO Gene Is Associated with Body Mass Index and Predisposes to Childhood and Adult Obesity. Science, 2007, 316, 889-894.	6.0	3,884