

Anthony T. Papenfuss

List of Publications by Year in descending order

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Version: 2024-02-01

154
papers

11,868
citations

34016

52
h-index

33814

99
g-index

175
all docs

175
docs citations

175
times ranked

19206
citing authors

#	ARTICLE	IF	CITATIONS
1	Development of plasmacytoid and conventional dendritic cell subtypes from single precursor cells derived in vitro and in vivo. <i>Nature Immunology</i> , 2007, 8, 1217-1226.	7.0	713
2	Genome of the marsupial <i>Monodelphis domestica</i> reveals innovation in non-coding sequences. <i>Nature</i> , 2007, 447, 167-177.	13.7	661
3	Genome analysis of the platypus reveals unique signatures of evolution. <i>Nature</i> , 2008, 453, 175-183.	13.7	657
4	BET inhibitor resistance emerges from leukaemia stem cells. <i>Nature</i> , 2015, 525, 538-542.	13.7	441
5	A newly discovered protein export machine in malaria parasites. <i>Nature</i> , 2009, 459, 945-949.	13.7	437
6	Genome Sequencing and Analysis of the Tasmanian Devil and Its Transmissible Cancer. <i>Cell</i> , 2012, 148, 780-791.	13.5	300
7	Analysis of the platypus genome suggests a transposon origin for mammalian imprinting. <i>Genome Biology</i> , 2009, 10, R1.	13.9	272
8	UV-Associated Mutations Underlie the Etiology of MCV-Negative Merkel Cell Carcinomas. <i>Cancer Research</i> , 2015, 75, 5228-5234.	0.4	270
9	GRIDSS: sensitive and specific genomic rearrangement detection using positional de Bruijn graph assembly. <i>Genome Research</i> , 2017, 27, 2050-2060.	2.4	255
10	The Tasmanian Devil Transcriptome Reveals Schwann Cell Origins of a Clonally Transmissible Cancer. <i>Science</i> , 2010, 327, 84-87.	6.0	222
11	Whole genome analysis of a schistosomiasis-transmitting freshwater snail. <i>Nature Communications</i> , 2017, 8, 15451.	5.8	216
12	Complementarity and redundancy of IL-22-producing innate lymphoid cells. <i>Nature Immunology</i> , 2016, 17, 179-186.	7.0	211
13	A phase I clinical trial with monoclonal antibody ch806 targeting transitional state and mutant epidermal growth factor receptors. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 4071-4076.	3.3	203
14	Targeting of the Tumor Suppressor GRHL3 by a miR-21-Dependent Proto-Oncogenic Network Results in PTEN Loss and Tumorigenesis. <i>Cancer Cell</i> , 2011, 20, 635-648.	7.7	203
15	IMGT/HighV QUEST paradigm for T cell receptor IMGT clonotype diversity and next generation repertoire immunoprofiling. <i>Nature Communications</i> , 2013, 4, 2333.	5.8	193
16	Comprehensive evaluation and characterisation of short read general-purpose structural variant calling software. <i>Nature Communications</i> , 2019, 10, 3240.	5.8	184
17	Epidermal Wound Repair Is Regulated by the Planar Cell Polarity Signaling Pathway. <i>Developmental Cell</i> , 2010, 19, 138-147.	3.1	180
18	Molecular genetics and comparative genomics reveal RNAi is not functional in malaria parasites. <i>Nucleic Acids Research</i> , 2009, 37, 3788-3798.	6.5	177

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19	Genome sequence of an Australian kangaroo, <i>Macropus eugenii</i> , provides insight into the evolution of mammalian reproduction and development. <i>Genome Biology</i> , 2011, 12, R81.	13.9	167
20	The Architecture and Evolution of Cancer Neochromosomes. <i>Cancer Cell</i> , 2014, 26, 653-667.	7.7	161
21	Malaria parasite DNA-harboring vesicles activate cytosolic immune sensors. <i>Nature Communications</i> , 2017, 8, 1985.	5.8	160
22	A statistical framework for analyzing deep mutational scanning data. <i>Genome Biology</i> , 2017, 18, 150.	3.8	155
23	Regulation of apicomplexan actin-based motility. <i>Nature Reviews Microbiology</i> , 2006, 4, 621-628.	13.6	151
24	Reconstructing an Ancestral Mammalian Immune Supercomplex from a Marsupial Major Histocompatibility Complex. <i>PLoS Biology</i> , 2006, 4, e46.	2.6	150
25	Defensins and the convergent evolution of platypus and reptile venom genes. <i>Genome Research</i> , 2008, 18, 986-994.	2.4	137
26	Determination of RNA structural diversity and its role in HIV-1 RNA splicing. <i>Nature</i> , 2020, 582, 438-442.	13.7	136
27	MaveDB: an open-source platform to distribute and interpret data from multiplexed assays of variant effect. <i>Genome Biology</i> , 2019, 20, 223.	3.8	130
28	Targeting enhancer switching overcomes non-genetic drug resistance in acute myeloid leukaemia. <i>Nature Communications</i> , 2019, 10, 2723.	5.8	126
29	DNA repair processes are critical mediators of p53-dependent tumor suppression. <i>Nature Medicine</i> , 2018, 24, 947-953.	15.2	122
30	<i>BRAF/NRAS</i> Wild-Type Melanomas Have a High Mutation Load Correlating with Histologic and Molecular Signatures of UV Damage. <i>Clinical Cancer Research</i> , 2013, 19, 4589-4598.	3.2	115
31	The Tasmanian devil microbiome—implications for conservation and management. <i>Microbiome</i> , 2015, 3, 76.	4.9	114
32	A Phase I Trial of Humanized Monoclonal Antibody A33 in Patients with Colorectal Carcinoma: Biodistribution, Pharmacokinetics, and Quantitative Tumor Uptake. <i>Clinical Cancer Research</i> , 2005, 11, 4810-4817.	3.2	113
33	A Novel Family of Apicomplexan Glideosome-associated Proteins with an Inner Membrane-anchoring Role. <i>Journal of Biological Chemistry</i> , 2009, 284, 25353-25363.	1.6	105
34	The immune gene repertoire of an important viral reservoir, the Australian black flying fox. <i>BMC Genomics</i> , 2012, 13, 261.	1.2	104
35	Characterization of the opossum immune genome provides insights into the evolution of the mammalian immune system. <i>Genome Research</i> , 2007, 17, 982-991.	2.4	100
36	Diversity of Conotoxin Gene Superfamilies in the Venomous Snail, <i>Conus victoriae</i> . <i>PLoS ONE</i> , 2014, 9, e87648.	1.1	100

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37	Barcoding reveals complex clonal behavior in patient-derived xenografts of metastatic triple negative breast cancer. <i>Nature Communications</i> , 2019, 10, 766.	5.8	99
38	Dual Plasmepsin-Targeting Antimalarial Agents Disrupt Multiple Stages of the Malaria Parasite Life Cycle. <i>Cell Host and Microbe</i> , 2020, 27, 642-658.e12.	5.1	94
39	Genomic Restructuring in the Tasmanian Devil Facial Tumour: Chromosome Painting and Gene Mapping Provide Clues to Evolution of a Transmissible Tumour. <i>PLoS Genetics</i> , 2012, 8, e1002483.	1.5	92
40	How the evolution of multicellularity set the stage for cancer. <i>British Journal of Cancer</i> , 2018, 118, 145-152.	2.9	89
41	Gut microbiome dysbiosis and increased intestinal permeability in children with islet autoimmunity and type 1 diabetes: A prospective cohort study. <i>Pediatric Diabetes</i> , 2019, 20, 574-583.	1.2	86
42	MTOR signaling orchestrates stress-induced mutagenesis, facilitating adaptive evolution in cancer. <i>Science</i> , 2020, 368, 1127-1131.	6.0	83
43	NLRP1 restricts butyrate producing commensals to exacerbate inflammatory bowel disease. <i>Nature Communications</i> , 2018, 9, 3728.	5.8	81
44	Regulation of PRMT5â€“MDM4 axis is critical in the response to CDK4/6 inhibitors in melanoma. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 17990-18000.	3.3	81
45	Socrates: identification of genomic rearrangements in tumour genomes by re-aligning soft clipped reads. <i>Bioinformatics</i> , 2014, 30, 1064-1072.	1.8	75
46	Phase I Trial of 131I-huA33 in Patients with Advanced Colorectal Carcinoma. <i>Clinical Cancer Research</i> , 2005, 11, 4818-4826.	3.2	73
47	Novel venom gene discovery in the platypus. <i>Genome Biology</i> , 2010, 11, R95.	13.9	72
48	Circulating tumour DNA reflects treatment response and clonal evolution in chronic lymphocytic leukaemia. <i>Nature Communications</i> , 2017, 8, 14756.	5.8	70
49	CD8+ T Cells from a Novel T Cell Receptor Transgenic Mouse Induce Liver-Stage Immunity That Can Be Boosted by Blood-Stage Infection in Rodent Malaria. <i>PLoS Pathogens</i> , 2014, 10, e1004135.	2.1	68
50	The Plasmodium falciparum transcriptome in severe malaria reveals altered expression of genes involved in important processes including surface antigenâ€“encoding var genes. <i>PLoS Biology</i> , 2018, 16, e2004328.	2.6	67
51	A community-based model of rapid autopsy in end-stage cancer patients. <i>Nature Biotechnology</i> , 2016, 34, 1010-1014.	9.4	66
52	Regression of devil facial tumour disease following immunotherapy in immunised Tasmanian devils. <i>Scientific Reports</i> , 2017, 7, 43827.	1.6	64
53	A Phase I Biodistribution and Pharmacokinetic Trial of Humanized Monoclonal Antibody Hu3s193 in Patients with Advanced Epithelial Cancers that Express the Lewis-Y Antigen. <i>Clinical Cancer Research</i> , 2007, 13, 3286-3292.	3.2	63
54	Hormone-like peptides in the venoms of marine cone snails. <i>General and Comparative Endocrinology</i> , 2017, 244, 11-18.	0.8	63

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55	Tumor-Specific Diagnostic Marker for Transmissible Facial Tumors of Tasmanian Devils. <i>Veterinary Pathology</i> , 2011, 48, 1195-1203.	0.8	60
56	Evolution and comparative analysis of the MHC Class III inflammatory region. <i>BMC Genomics</i> , 2006, 7, 281.	1.2	54
57	The Hippo pathway oncoprotein YAP promotes melanoma cell invasion and spontaneous metastasis. <i>Oncogene</i> , 2020, 39, 5267-5281.	2.6	53
58	Interfacing Seurat with the R tidy universe. <i>Bioinformatics</i> , 2021, 37, 4100-4107.	1.8	50
59	Somatic mutations in early metazoan genes disrupt regulatory links between unicellular and multicellular genes in cancer. <i>ELife</i> , 2019, 8, .	2.8	50
60	The inner ear proteome of fish. <i>FEBS Journal</i> , 2019, 286, 66-81.	2.2	48
61	Evolution of coding and non-coding genes in HOX clusters of a marsupial. <i>BMC Genomics</i> , 2012, 13, 251.	1.2	47
62	Inositol polyphosphate 4-phosphatase II (INPP4B) is associated with chemoresistance and poor outcome in AML. <i>Blood</i> , 2015, 125, 2815-2824.	0.6	47
63	Influence of fecal collection conditions and 16S rRNA gene sequencing at two centers on human gut microbiota analysis. <i>Scientific Reports</i> , 2018, 8, 4386.	1.6	46
64	Evolution of late-stage metastatic melanoma is dominated by aneuploidy and whole genome doubling. <i>Nature Communications</i> , 2021, 12, 1434.	5.8	46
65	TERT structural rearrangements in metastatic pheochromocytomas. <i>Endocrine-Related Cancer</i> , 2018, 25, 1-9.	1.6	45
66	Blood-Stage Plasmodium berghei Infection Generates a Potent, Specific CD8+ T-Cell Response Despite Residence Largely in Cells Lacking MHC I Processing Machinery. <i>Journal of Infectious Diseases</i> , 2011, 204, 1989-1996.	1.9	41
67	PD-L1 Is Not Constitutively Expressed on Tasmanian Devil Facial Tumor Cells but Is Strongly Upregulated in Response to IFN- γ and Can Be Expressed in the Tumor Microenvironment. <i>Frontiers in Immunology</i> , 2016, 7, 581.	2.2	41
68	Optical mapping reveals a higher level of genomic architecture of chained fusions in cancer. <i>Genome Research</i> , 2018, 28, 726-738.	2.4	41
69	Understanding and utilising mammalian venom via a platypus venom transcriptome. <i>Journal of Proteomics</i> , 2009, 72, 155-164.	1.2	40
70	The transcription factor Nerfin-1 prevents reversion of neurons into neural stem cells. <i>Genes and Development</i> , 2015, 29, 129-143.	2.7	40
71	Investigation of hypoxia and carbonic anhydrase IX expression in a renal cell carcinoma xenograft model with oxygen tension measurements and 124I-cG250 PET/CT. <i>Urologic Oncology: Seminars and Original Investigations</i> , 2011, 29, 411-420.	0.8	39
72	Proteomics and Deep Sequencing Comparison of Seasonally Active Venom Glands in the Platypus Reveals Novel Venom Peptides and Distinct Expression Profiles. <i>Molecular and Cellular Proteomics</i> , 2012, 11, 1354-1364.	2.5	39

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73	Somatic Hypermutation of the <i>YAP</i> Oncogene in a Human Cutaneous Melanoma. <i>Molecular Cancer Research</i> , 2019, 17, 1435-1449.	1.5	39
74	De novo transcriptome assembly for the spiny mouse (<i>Acomys cahirinus</i>). <i>Scientific Reports</i> , 2017, 7, 8996.	1.6	37
75	Identification of dendritic cells, B cell and T cell subsets in Tasmanian devil lymphoid tissue; evidence for poor immune cell infiltration into devil facial tumors. <i>Anatomical Record</i> , 2014, 297, 925-938.	0.8	35
76	A Limited Role for Gene Duplications in the Evolution of Platypus Venom. <i>Molecular Biology and Evolution</i> , 2012, 29, 167-177.	3.5	33
77	Genomic characterisation of E14-Myc mouse lymphomas identifies Bcor as a Myc co-operative tumour-suppressor gene. <i>Nature Communications</i> , 2017, 8, 14581.	5.8	33
78	Inferring structural variant cancer cell fraction. <i>Nature Communications</i> , 2020, 11, 730.	5.8	33
79	Distinct Gut Virome Profile of Pregnant Women With Type 1 Diabetes in the ENDIA Study. <i>Open Forum Infectious Diseases</i> , 2019, 6, ofz025.	0.4	32
80	Discovery by proteogenomics and characterization of an RF-amide neuropeptide from cone snail venom. <i>Journal of Proteomics</i> , 2015, 114, 38-47.	1.2	31
81	The Scalloped and Nerfin-1 Transcription Factors Cooperate to Maintain Neuronal Cell Fate. <i>Cell Reports</i> , 2018, 25, 1561-1576.e7.	2.9	31
82	Mitochondrial Genome Sequence of the Scabies Mite Provides Insight into the Genetic Diversity of Individual Scabies Infections. <i>PLoS Neglected Tropical Diseases</i> , 2016, 10, e0004384.	1.3	30
83	Expression patterns of platypus defensin and related venom genes across a range of tissue types reveal the possibility of broader functions for OvDLPs than previously suspected. <i>Toxicon</i> , 2008, 52, 559-565.	0.8	28
84	Genomic resources and draft assemblies of the human and porcine varieties of scabies mites, <i>Sarcoptes scabiei</i> var. <i>hominis</i> and var. <i>suis</i> . <i>GigaScience</i> , 2016, 5, 23.	3.3	28
85	Two of a kind: transmissible Schwann cell cancers in the endangered Tasmanian devil (<i>Sarcophilus</i>) Tj ETQq1 1 0.784314 rgBT /Overlo 2.4 28	2.4	28
86	Histone modifications associated with gene expression and genome accessibility are dynamically enriched at <i>Plasmodium falciparum</i> regulatory sequences. <i>Epigenetics and Chromatin</i> , 2020, 13, 50.	1.8	28
87	Immunome database for marsupials and monotremes. <i>BMC Immunology</i> , 2011, 12, 48.	0.9	27
88	A forward genetic screen identifies a negative regulator of rapid Ca ²⁺ -dependent cell egress (MS1) in the intracellular parasite <i>Toxoplasma gondii</i> . <i>Journal of Biological Chemistry</i> , 2017, 292, 7662-7674.	1.6	27
89	CD271 Expression on Patient Melanoma Cells Is Unstable and Unlinked to Tumorigenicity. <i>Cancer Research</i> , 2016, 76, 3965-3977.	0.4	26
90	Deep multi-region whole-genome sequencing reveals heterogeneity and gene-by-environment interactions in treatment-naive, metastatic lung cancer. <i>Oncogene</i> , 2019, 38, 1661-1675.	2.6	26

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91	PathOS: a decision support system for reporting high throughput sequencing of cancers in clinical diagnostic laboratories. <i>Genome Medicine</i> , 2017, 9, 38.	3.6	25
92	Significant decline in anticancer immune capacity during puberty in the Tasmanian devil. <i>Scientific Reports</i> , 2017, 7, 44716.	1.6	25
93	High-quality nuclear genome for <i>Sarcoptes scabiei</i> —A critical resource for a neglected parasite. <i>PLoS Neglected Tropical Diseases</i> , 2020, 14, e0008720.	1.3	25
94	tidybulk: an R tidy framework for modular transcriptomic data analysis. <i>Genome Biology</i> , 2021, 22, 42.	3.8	25
95	Identification of natural killer cell receptor clusters in the platypus genome reveals an expansion of C-type lectin genes. <i>Immunogenetics</i> , 2009, 61, 565-579.	1.2	24
96	Transmissible cancers in an evolutionary context. <i>BioEssays</i> , 2016, 38, S14-23.	1.2	24
97	Differences in PfEMP1s recognized by antibodies from patients with uncomplicated or severe malaria. <i>Malaria Journal</i> , 2016, 15, 258.	0.8	23
98	The site of breast cancer metastases dictates their clonal composition and reversible transcriptomic profile. <i>Science Advances</i> , 2021, 7, .	4.7	23
99	Genome sequence of an Australian kangaroo, <i>Macropus eugenii</i> , provides insight into the evolution of mammalian reproduction and development. <i>Genome Biology</i> , 2011, 12, 414.	13.9	22
100	Telomere Dynamics and Homeostasis in a Transmissible Cancer. <i>PLoS ONE</i> , 2012, 7, e44085.	1.1	22
101	Marsupials and monotremes possess a novel family of MHC class I genes that is lost from the eutherian lineage. <i>BMC Genomics</i> , 2015, 16, 535.	1.2	22
102	Eggs, embryos and the evolution of imprinting: insights from the platypus genome. <i>Reproduction, Fertility and Development</i> , 2009, 21, 935.	0.1	21
103	Transcriptomic analysis supports similar functional roles for the two thymuses of the tammar wallaby. <i>BMC Genomics</i> , 2011, 12, 420.	1.2	21
104	Clustered somatic mutations are frequent in transcription factor binding motifs within proximal promoter regions in melanoma and other cutaneous malignancies. <i>Oncotarget</i> , 2016, 7, 66569-66585.	0.8	21
105	tidyHeatmap: an R package for modular heatmap production based on tidy principles. <i>Journal of Open Source Software</i> , 2020, 5, 2472.	2.0	21
106	A phase I radioimmunolocalization trial of humanized monoclonal antibody huA33 in patients with gastric carcinoma. <i>Cancer Science</i> , 2006, 97, 1248-1254.	1.7	20
107	The Use of Imaging Mass Spectrometry to Study Peptide Toxin Distribution in Australian Sea Anemones. <i>Australian Journal of Chemistry</i> , 2017, 70, 1235.	0.5	20
108	A 4-cyano-3-methylisoquinoline inhibitor of <i>Plasmodium falciparum</i> growth targets the sodium efflux pump PfATP4. <i>Scientific Reports</i> , 2019, 9, 10292.	1.6	20

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109	Evolution of cnidarian <i>defensins</i> : Sequence, structure and exploration of chemical space. <i>Proteins: Structure, Function and Bioinformatics</i> , 2019, 87, 551-560.	1.5	20
110	Evolutionary analyses of the major variant surface antigen-encoding genes reveal population structure of <i>Plasmodium falciparum</i> within and between continents. <i>PLoS Genetics</i> , 2021, 17, e1009269.	1.5	20
111	RAF1 rearrangements are common in pancreatic acinar cell carcinomas. <i>Modern Pathology</i> , 2020, 33, 1811-1821.	2.9	19
112	Tentacle Transcriptomes of the Speckled Anemone (<i>Actiniaria: Actiniidae: Oulactis sp.</i>): Venom-Related Components and Their Domain Structure. <i>Marine Biotechnology</i> , 2020, 22, 207-219.	1.1	19
113	Evolution of a contagious cancer: epigenetic variation in Devil Facial Tumour Disease. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2013, 280, 20121720.	1.2	18
114	Bioinformatics Pipelines for Targeted Resequencing and Whole-Exome Sequencing of Human and Mouse Genomes: A Virtual Appliance Approach for Instant Deployment. <i>PLoS ONE</i> , 2014, 9, e95217.	1.1	17
115	CNSpector: a web-based tool for visualisation and clinical diagnosis of copy number variation from next generation sequencing. <i>Scientific Reports</i> , 2019, 9, 6426.	1.6	17
116	A Naturally Occurring Peptide with an Elementary Single Disulfide-Directed β^2 -Hairpin Fold. <i>Structure</i> , 2016, 24, 293-299.	1.6	16
117	Androgen deprivation therapy promotes an obesity-like microenvironment in periprostatic fat. <i>Endocrine Connections</i> , 2019, 8, 547-558.	0.8	16
118	The identification of immune genes in the milk transcriptome of the Tasmanian devil (<i>Sarcophilus tjarringtonii</i>). <i>PLoS ONE</i> , 2016, 11, e0160000.	0.9	16
119	VIRUSBreakend: Viral Integration Recognition Using Single Breakends. <i>Bioinformatics</i> , 2021, 37, 3115-3119.	1.8	15
120	Analysis of a set of Australian northern brown bandicoot expressed sequence tags with comparison to the genome sequence of the South American grey short tailed opossum. <i>BMC Genomics</i> , 2007, 8, 50.	1.2	14
121	A recombination hotspot leads to sequence variability within a novel gene (AK005651) and contributes to type 1 diabetes susceptibility. <i>Genome Research</i> , 2010, 20, 1629-1638.	2.4	14
122	Identification and analysis of divergent immune gene families within the Tasmanian devil genome. <i>BMC Genomics</i> , 2015, 16, 1017.	1.2	14
123	HYSYS: have you swapped your samples?. <i>Bioinformatics</i> , 2017, 33, 596-598.	1.8	14
124	Tasmanian devils with contagious cancer exhibit a constricted T-cell repertoire diversity. <i>Communications Biology</i> , 2019, 2, 99.	2.0	14
125	Embryonic Lethality in Homozygous Human Her-2 Transgenic Mice Due to Disruption of the Pds5b Gene. <i>PLoS ONE</i> , 2015, 10, e0136817.	1.1	14
126	Expression of a Chimeric Antigen Receptor in Multiple Leukocyte Lineages in Transgenic Mice. <i>PLoS ONE</i> , 2015, 10, e0140543.	1.1	12

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127	Type 1 diabetes: a disease of developmental origins. <i>Pediatric Diabetes</i> , 2017, 18, 417-421.	1.2	12
128	Combined BRAF, MEK, and CDK4/6 Inhibition Depletes Intratumoral Immune-Potentiating Myeloid Populations in Melanoma. <i>Cancer Immunology Research</i> , 2021, 9, 136-146.	1.6	12
129	Hatching time for monotreme immunology. <i>Australian Journal of Zoology</i> , 2009, 57, 185.	0.6	11
130	Genomic Identification of Chemokines and Cytokines in Opossum. <i>Journal of Interferon and Cytokine Research</i> , 2011, 31, 317-330.	0.5	10
131	Higher frequency of vertebrate-infecting viruses in the gut of infants born to mothers with type 1 diabetes. <i>Pediatric Diabetes</i> , 2020, 21, 271-279.	1.2	10
132	Phylogenetic relationships, stage-specific expression and localisation of a unique family of inactive cysteine proteases in <i>Sarcoptes scabiei</i> . <i>Parasites and Vectors</i> , 2018, 11, 301.	1.0	9
133	Probabilistic outlier identification for RNA sequencing generalized linear models. <i>NAR Genomics and Bioinformatics</i> , 2021, 3, lqab005.	1.5	9
134	CLOVE: classification of genomic fusions into structural variation events. <i>BMC Bioinformatics</i> , 2017, 18, 346.	1.2	8
135	Detection of clinically relevant early genomic lesions in B-cell malignancies from circulating tumour <sc>DNA</sc> using a single hybridisation-based next generation sequencing assay. <i>British Journal of Haematology</i> , 2018, 183, 146-149.	1.2	8
136	The UT family of MHC class I loci unique to non-eutherian mammals has limited polymorphism and tissue specific patterns of expression in the opossum. <i>BMC Immunology</i> , 2016, 17, 43.	0.9	7
137	Molecular diagnosis of scabies using a novel probe-based polymerase chain reaction assay targeting high-copy number repetitive sequences in the <i>Sarcoptes scabiei</i> genome. <i>PLoS Neglected Tropical Diseases</i> , 2021, 15, e0009149.	1.3	7
138	Unifying package managers, workflow engines, and containers: Computational reproducibility with BioNix. <i>GigaScience</i> , 2020, 9, .	3.3	7
139	Digital PCR of Genomic Rearrangements for Monitoring Circulating Tumour DNA. <i>Advances in Experimental Medicine and Biology</i> , 2016, 924, 139-146.	0.8	6
140	No evidence of expression of two classes of natural antibiotics (cathelicidins and defensins) in a sample of platypus milk. <i>Australian Journal of Zoology</i> , 2009, 57, 211.	0.6	6
141	Improving the Power of Structural Variation Detection by Augmenting the Reference. <i>PLoS ONE</i> , 2015, 10, e0136771.	1.1	6
142	Clinical cancer genomic analysis: data engineering required. <i>Lancet Oncology</i> , The, 2015, 16, 1015-1017.	5.1	5
143	Crystal structure of the <i>Leishmania major</i> MIX protein: A scaffold protein that mediates protein-protein interactions. <i>Protein Science</i> , 2011, 20, 1060-1068.	3.1	4
144	Canary: an atomic pipeline for clinical amplicon assays. <i>BMC Bioinformatics</i> , 2017, 18, 555.	1.2	4

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145	StructuralVariantAnnotation: a R/Bioconductor foundation for a caller-agnostic structural variant software ecosystem. <i>Bioinformatics</i> , 2022, 38, 2046-2048.	1.8	4
146	Transcriptome sequencing and multi-plex imaging of prostate cancer microenvironment reveals a dominant role for monocytic cells in progression. <i>BMC Cancer</i> , 2021, 21, 846.	1.1	3
147	Gut Microbiome Dysbiosis and Increased Intestinal Permeability in Australian Children with Islet Autoimmunity and Type 1 Diabetes. <i>Diabetes</i> , 2018, 67, .	0.3	3
148	Epidermal Wound Repair Is Regulated by the Planar Cell Polarity Signaling Pathway. <i>Developmental Cell</i> , 2010, 19, 353.	3.1	2
149	Marsupial Sequencing Projects and Bioinformatics Challenges. , 2010, , 121-132.		1
150	Elementary: breast cancer culprits leave their signatures on the double helix. <i>Cell Death and Differentiation</i> , 2016, 23, 1577-1578.	5.0	0
151	Peptide toxins in australian sea anemones: Transcriptomics, peptidomics and distribution. <i>Toxicon</i> , 2019, 158, S47.	0.8	0
152	1079MO Progression of BRAF mutant CNS metastases are associated with a transcriptional network bearing similarities with the innate PD-1 resistant signature (IPRES). <i>Annals of Oncology</i> , 2020, 31, S733.	0.6	0
153	Insight into Evolution of Gene Regulation Networks from the Opossum Genome. , 2010, , 133-146.		0
154	Cnspectorx - Copy Number Assessment at a Genome Level from Targeted Sequence Data Optimized for Hematological Malignancy. <i>Blood</i> , 2019, 134, 3378-3378.	0.6	0