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List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/4294815/publications.pdf>

Version: 2024-02-01

25
papers

671
citations

567281

15
h-index

610901

24
g-index

28
all docs

28
docs citations

28
times ranked

1346
citing authors

#	ARTICLE	IF	CITATIONS
1	Relationship between genetically determined telomere length and glioma risk. <i>Neuro-Oncology</i> , 2022, 24, 171-181.	1.2	21
2	Signatures of TOP1 transcription-associated mutagenesis in cancer and germline. <i>Nature</i> , 2022, 602, 623-631.	27.8	38
3	Elongin C (<i>ELOC</i> / <i>TCEB1</i>)-associated von Hippel-Lindau disease. <i>Human Molecular Genetics</i> , 2022, 31, 2728-2737.	2.9	11
4	Frequency of pathogenic germline variants in cancer susceptibility genes in 1336 renal cell carcinoma cases. <i>Human Molecular Genetics</i> , 2022, 31, 3001-3011.	2.9	9
5	Searching for causal relationships of glioma: a phenome-wide Mendelian randomisation study. <i>British Journal of Cancer</i> , 2021, 124, 447-454.	6.4	9
6	Lack of an association between gallstone disease and bilirubin levels with risk of colorectal cancer: a Mendelian randomisation analysis. <i>British Journal of Cancer</i> , 2021, 124, 1169-1174.	6.4	6
7	Cancer drivers and clonal dynamics in acute lymphoblastic leukaemia subtypes. <i>Blood Cancer Journal</i> , 2021, 11, 177.	6.2	9
8	Lack of association between modifiable exposures and glioma risk: A Mendelian randomisation analysis. <i>Neuro-Oncology</i> , 2020, 22, 207-215.	1.2	19
9	Modifiable pathways for colorectal cancer: a mendelian randomisation analysis. <i>The Lancet Gastroenterology and Hepatology</i> , 2020, 5, 55-62.	8.1	79
10	An enhanced genetic model of relapsed IGH-translocated multiple myeloma evolutionary dynamics. <i>Blood Cancer Journal</i> , 2020, 10, 101.	6.2	11
11	Impact of mitochondrial DNA mutations in multiple myeloma. <i>Blood Cancer Journal</i> , 2020, 10, 46.	6.2	8
12	Search for multiple myeloma risk factors using Mendelian randomization. <i>Blood Advances</i> , 2020, 4, 2172-2179.	5.2	27
13	Genomic landscape of platinum resistant and sensitive testicular cancers. <i>Nature Communications</i> , 2020, 11, 2189.	12.8	43
14	Reference bias in the Illumina Isaac aligner. <i>Bioinformatics</i> , 2020, 36, 4671-4672.	4.1	5
15	Mutational processes contributing to the development of multiple myeloma. <i>Blood Cancer Journal</i> , 2019, 9, 60.	6.2	41
16	Phenome-wide association analysis of LDL-cholesterol lowering genetic variants in PCSK9. <i>BMC Cardiovascular Disorders</i> , 2019, 19, 240.	1.7	22
17	Mendelian randomization provides support for obesity as a risk factor for meningioma. <i>Scientific Reports</i> , 2019, 9, 309.	3.3	21
18	Mendelian randomisation: A powerful and inexpensive method for identifying and excluding non-genetic risk factors for colorectal cancer. <i>Molecular Aspects of Medicine</i> , 2019, 69, 41-47.	6.4	39

#	ARTICLE	IF	CITATIONS
19	Identification of recurrent noncoding mutations in B-cell lymphoma using capture Hi-C. <i>Blood Advances</i> , 2019, 3, 21-32.	5.2	20
20	Mendelian randomisation study of the relationship between vitamin D and risk of glioma. <i>Scientific Reports</i> , 2018, 8, 2339.	3.3	23
21	Impact of atopy on risk of glioma: a Mendelian randomisation study. <i>BMC Medicine</i> , 2018, 16, 42.	5.5	38
22	Influence of obesity-related risk factors in the aetiology of glioma. <i>British Journal of Cancer</i> , 2018, 118, 1020-1027.	6.4	32
23	Whole-genome sequencing of multiple myeloma reveals oncogenic pathways are targeted somatically through multiple mechanisms. <i>Leukemia</i> , 2018, 32, 2459-2470.	7.2	68
24	Promoter capture Hi-C-based identification of recurrent noncoding mutations in colorectal cancer. <i>Nature Genetics</i> , 2018, 50, 1375-1380.	21.4	49
25	Genome-wide association analysis identifies a meningioma risk locus at 11p15.5. <i>Neuro-Oncology</i> , 2018, 20, 1485-1493.	1.2	23