Andrew D Yates

List of Publications by Year
in descending order

Source: https://exaly.com/author-pdf/6647779/publications.pdf

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44	20,859	136740	233125
papers	citations	32 h-index	45 g-index

51	51	51	40803
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Patterns of somatic mutation in human cancer genomes. Nature, 2007, 446, 153-158.	13.7	2,802
2	Ensembl 2018. Nucleic Acids Research, 2018, 46, D754-D761.	6.5	2,710
3	GENCODE reference annotation for the human and mouse genomes. Nucleic Acids Research, 2019, 47, D766-D773.	6.5	2,350
4	Ensembl 2016. Nucleic Acids Research, 2016, 44, D710-D716.	6.5	1,372
5	Ensembl 2021. Nucleic Acids Research, 2021, 49, D884-D891.	6.5	1,231
6	Ensembl 2022. Nucleic Acids Research, 2022, 50, D988-D995.	6.5	1,103
7	Ensembl 2020. Nucleic Acids Research, 2020, 48, D682-D688.	6.5	1,076
8	Ensembl 2019. Nucleic Acids Research, 2019, 47, D745-D751.	6.5	879
9	Ensembl 2012. Nucleic Acids Research, 2012, 40, D84-D90.	6.5	840
10	Intragenic ERBB2 kinase mutations in tumours. Nature, 2004, 431, 525-526.	13.7	757
11	GENCODE 2021. Nucleic Acids Research, 2021, 49, D916-D923.	6.5	633
12	Ensembl 2017. Nucleic Acids Research, 2017, 45, D635-D642.	6.5	535
13	Ensembl Genomes 2018: an integrated omics infrastructure for non-vertebrate species. Nucleic Acids Research, 2018, 46, D802-D808.	6.5	489
14	Somatic Mutations of the Protein Kinase Gene Family in Human Lung Cancer. Cancer Research, 2005, 65, 7591-7595.	0.4	429
15	Ensembl Genomes 2020â€"enabling non-vertebrate genomic research. Nucleic Acids Research, 2020, 48, D689-D695.	6.5	416
16	A Hypermutation Phenotype and Somatic MSH6 Mutations in Recurrent Human Malignant Gliomas after Alkylator Chemotherapy. Cancer Research, 2006, 66, 3987-3991.	0.4	383
17	Mutation analysis of 24 known cancer genes in the NCI-60 cell line set. Molecular Cancer Therapeutics, 2006, 5, 2606-2612.	1.9	374
18	Ensembl comparative genomics resources. Database: the Journal of Biological Databases and Curation, 2016, 2016, bav096.	1.4	344

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19	A screen of the complete protein kinase gene family identifies diverse patterns of somatic mutations in human breast cancer. Nature Genetics, 2005, 37, 590-592.	9.4	318
20	A compendium of uniformly processed human gene expression and splicing quantitative trait loci. Nature Genetics, 2021, 53, 1290-1299.	9.4	193
21	Ensembl Genomes: an integrative resource for genome-scale data from non-vertebrate species. Nucleic Acids Research, 2012, 40, D91-D97.	6.5	179
22	The Ensembl REST API: Ensembl Data for Any Language. Bioinformatics, 2015, 31, 143-145.	1.8	161
23	BioJava: an open-source framework for bioinformatics in 2012. Bioinformatics, 2012, 28, 2693-2695.	1.8	160
24	PHI-base: the pathogenâ€“host interactions database. Nucleic Acids Research, 2020, 48, D613-D620.	6.5	145
25	Ensembl Genomes 2022: an expanding genome resource for non-vertebrates. Nucleic Acids Research, 2022, 50, D996-D1003.	6.5	141
26	Mutations in the Gene Encoding the Sigma 2 Subunit of the Adaptor Protein 1 Complex, AP1S2, Cause X-Linked Mental Retardation. American Journal of Human Genetics, 2006, 79, 1119-1124.	2.6	102
27	Sequence analysis of the protein kinase gene family in human testicular germ-cell tumors of adolescents and adults. Genes Chromosomes and Cancer, 2006, 45, 42-46.	1.5	96
28	GA4GH: International policies and standards for data sharing across genomic research and healthcare. Cell Genomics, 2021, 1, 100029.	3.0	94
29	Ensembl core software resources: storage and programmatic access for DNA sequence and genome annotation. Database: the Journal of Biological Databases and Curation, 2017, 2017, .	1.4	56
30	PHI-base in 2022: a multi-species phenotype database for Pathogenâ€“Host Interactions. Nucleic Acids Research, 2022, 50, D837-D847.	6.5	53
31	The ELIXIR Core Data Resources: fundamental infrastructure for the life sciences. Bioinformatics, 2020, 36, 2636-2642.	1.8	47
32	Pervasive lesion segregation shapes cancer genome evolution. Nature, 2020, 583, 265-270.	13.7	36
33	Annotating and prioritizing genomic variants using the Ensembl Variant Effect Predictorâ€”A tutorial. Human Mutation, 2022, 43, 986-997.	1.1	30
34	Eleven quick tips to build a usable REST API for life sciences. PLoS Computational Biology, 2018, 14, e1006542.	1.5	18
35	The GA4GH Variation Representation Specification: A computational framework for variation representation and federated identification. Cell Genomics, 2021, 1, 100027.	3.0	18
36	Gene Ã— smoking interactions on human brain gene expression: finding common mechanisms in adolescents and adults. Journal of Child Psychology and Psychiatry and Allied Disciplines, 2013, 54, 1109-1119.	3.1	15

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37	ClinGen advancing genomic dataâ€sharing standards as a GA4GH driver project. Human Mutation, 2018, 39, 1686-1689.	1.1	15
38	Past and future uses of text mining in ecology and evolution. Proceedings of the Royal Society B: Biological Sciences, 2022, 289, 20212721.	1.2	15
39	Structured reporting in portable chest radiographs: An essential tool in the diagnosis of COVID-19. European Journal of Radiology, 2021, 134, 109414.	1.2	12
40	The Ensembl COVID-19 resource: ongoing integration of public SARS-CoV-2 data. Nucleic Acids Research, 2022, 50, D765-D770.	6.5	10
41	Collaborative Annotation Redefines Gene Sets for Crucial Phytopathogens. Frontiers in Microbiology, 2019, 10, 2477.	1.5	9
42	Refget: standardized access to reference sequences. Bioinformatics, 2021, 38, 299-300.	1.8	8
43	Sharing Programming Resources Between Bio* Projects. Methods in Molecular Biology, 2019, 1910, 747-766.	0.4	6
44	Sharing Programming Resources Between Bio* Projects Through Remote Procedure Call and Native Call Stack Strategies. Methods in Molecular Biology, 2012, 856, 513-527.	0.4	1