

Andrew D Yates

List of Publications by Year in descending order

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Version: 2024-02-01

44
papers

20,859
citations

136740

32
h-index

233125

45
g-index

51
all docs

51
docs citations

51
times ranked

40803
citing authors

#	ARTICLE	IF	CITATIONS
1	The Ensembl COVID-19 resource: ongoing integration of public SARS-CoV-2 data. <i>Nucleic Acids Research</i> , 2022, 50, D765-D770.	6.5	10
2	Ensembl 2022. <i>Nucleic Acids Research</i> , 2022, 50, D988-D995.	6.5	1,103
3	Ensembl Genomes 2022: an expanding genome resource for non-vertebrates. <i>Nucleic Acids Research</i> , 2022, 50, D996-D1003.	6.5	141
4	PHI-base in 2022: a multi-species phenotype database for Pathogen-Host Interactions. <i>Nucleic Acids Research</i> , 2022, 50, D837-D847.	6.5	53
5	Annotating and prioritizing genomic variants using the Ensembl Variant Effect Predictor—A tutorial. <i>Human Mutation</i> , 2022, 43, 986-997.	1.1	30
6	Past and future uses of text mining in ecology and evolution. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2022, 289, 20212721.	1.2	15
7	Ensembl 2021. <i>Nucleic Acids Research</i> , 2021, 49, D884-D891.	6.5	1,231
8	GENCODE 2021. <i>Nucleic Acids Research</i> , 2021, 49, D916-D923.	6.5	633
9	Structured reporting in portable chest radiographs: An essential tool in the diagnosis of COVID-19. <i>European Journal of Radiology</i> , 2021, 134, 109414.	1.2	12
10	Refget: standardized access to reference sequences. <i>Bioinformatics</i> , 2021, 38, 299-300.	1.8	8
11	A compendium of uniformly processed human gene expression and splicing quantitative trait loci. <i>Nature Genetics</i> , 2021, 53, 1290-1299.	9.4	193
12	GA4GH: International policies and standards for data sharing across genomic research and healthcare. <i>Cell Genomics</i> , 2021, 1, 100029.	3.0	94
13	The GA4GH Variation Representation Specification: A computational framework for variation representation and federated identification. <i>Cell Genomics</i> , 2021, 1, 100027.	3.0	18
14	Ensembl 2020. <i>Nucleic Acids Research</i> , 2020, 48, D682-D688.	6.5	1,076
15	PHI-base: the pathogen-host interactions database. <i>Nucleic Acids Research</i> , 2020, 48, D613-D620.	6.5	145
16	Ensembl Genomes 2020—enabling non-vertebrate genomic research. <i>Nucleic Acids Research</i> , 2020, 48, D689-D695.	6.5	416
17	Pervasive lesion segregation shapes cancer genome evolution. <i>Nature</i> , 2020, 583, 265-270.	13.7	36
18	The ELIXIR Core Data Resources: fundamental infrastructure for the life sciences. <i>Bioinformatics</i> , 2020, 36, 2636-2642.	1.8	47

#	ARTICLE	IF	CITATIONS
19	Sharing Programming Resources Between Bio* Projects. <i>Methods in Molecular Biology</i> , 2019, 1910, 747-766.	0.4	6
20	Collaborative Annotation Redefines Gene Sets for Crucial Phytopathogens. <i>Frontiers in Microbiology</i> , 2019, 10, 2477.	1.5	9
21	GENCODE reference annotation for the human and mouse genomes. <i>Nucleic Acids Research</i> , 2019, 47, D766-D773.	6.5	2,350
22	Ensembl 2019. <i>Nucleic Acids Research</i> , 2019, 47, D745-D751.	6.5	879
23	Ensembl Genomes 2018: an integrated omics infrastructure for non-vertebrate species. <i>Nucleic Acids Research</i> , 2018, 46, D802-D808.	6.5	489
24	Ensembl 2018. <i>Nucleic Acids Research</i> , 2018, 46, D754-D761.	6.5	2,710
25	Eleven quick tips to build a usable REST API for life sciences. <i>PLoS Computational Biology</i> , 2018, 14, e1006542.	1.5	18
26	ClinGen advancing genomic dataâ€™sharing standards as a GA4GH driver project. <i>Human Mutation</i> , 2018, 39, 1686-1689.	1.1	15
27	Ensembl 2017. <i>Nucleic Acids Research</i> , 2017, 45, D635-D642.	6.5	535
28	Ensembl core software resources: storage and programmatic access for DNA sequence and genome annotation. <i>Database: the Journal of Biological Databases and Curation</i> , 2017, 2017, .	1.4	56
29	Ensembl comparative genomics resources. <i>Database: the Journal of Biological Databases and Curation</i> , 2016, 2016, bav096.	1.4	344
30	Ensembl 2016. <i>Nucleic Acids Research</i> , 2016, 44, D710-D716.	6.5	1,372
31	The Ensembl REST API: Ensembl Data for Any Language. <i>Bioinformatics</i> , 2015, 31, 143-145.	1.8	161
32	Gene Ã– smoking interactions on human brain gene expression: finding common mechanisms in adolescents and adults. <i>Journal of Child Psychology and Psychiatry and Allied Disciplines</i> , 2013, 54, 1109-1119.	3.1	15
33	Ensembl Genomes: an integrative resource for genome-scale data from non-vertebrate species. <i>Nucleic Acids Research</i> , 2012, 40, D91-D97.	6.5	179
34	BioJava: an open-source framework for bioinformatics in 2012. <i>Bioinformatics</i> , 2012, 28, 2693-2695.	1.8	160
35	Ensembl 2012. <i>Nucleic Acids Research</i> , 2012, 40, D84-D90.	6.5	840
36	Sharing Programming Resources Between Bio* Projects Through Remote Procedure Call and Native Call Stack Strategies. <i>Methods in Molecular Biology</i> , 2012, 856, 513-527.	0.4	1

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37	Patterns of somatic mutation in human cancer genomes. <i>Nature</i> , 2007, 446, 153-158.	13.7	2,802
38	Mutations in the Gene Encoding the Sigma 2 Subunit of the Adaptor Protein 1 Complex, AP1S2, Cause X-Linked Mental Retardation. <i>American Journal of Human Genetics</i> , 2006, 79, 1119-1124.	2.6	102
39	Mutation analysis of 24 known cancer genes in the NCI-60 cell line set. <i>Molecular Cancer Therapeutics</i> , 2006, 5, 2606-2612.	1.9	374
40	Sequence analysis of the protein kinase gene family in human testicular germ-cell tumors of adolescents and adults. <i>Genes Chromosomes and Cancer</i> , 2006, 45, 42-46.	1.5	96
41	A Hypermutation Phenotype and Somatic MSH6 Mutations in Recurrent Human Malignant Gliomas after Alkylator Chemotherapy. <i>Cancer Research</i> , 2006, 66, 3987-3991.	0.4	383
42	A screen of the complete protein kinase gene family identifies diverse patterns of somatic mutations in human breast cancer. <i>Nature Genetics</i> , 2005, 37, 590-592.	9.4	318
43	Somatic Mutations of the Protein Kinase Gene Family in Human Lung Cancer. <i>Cancer Research</i> , 2005, 65, 7591-7595.	0.4	429
44	Intragenic ERBB2 kinase mutations in tumours. <i>Nature</i> , 2004, 431, 525-526.	13.7	757