

Andrew D Yates

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

44
papers

13,017
citations

28
h-index

51
g-index

51
ext. papers

17,930
ext. citations

15.7
avg, IF

5.04
L-index

#	Paper	IF	Citations
44	Past and future uses of text mining in ecology and evolution.. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2022 , 289, 20212721	4.4	1
43	Ensembl Genomes 2022: an expanding genome resource for non-vertebrates. <i>Nucleic Acids Research</i> , 2021 ,	20.1	12
42	GA4GH: International policies and standards for data sharing across genomic research and healthcare.. <i>Cell Genomics</i> , 2021 , 1, 100029-100029		20
41	The GA4GH Variation Representation Specification: A computational framework for variation representation and federated identification.. <i>Cell Genomics</i> , 2021 , 1, 100027-100027		4
40	Ensembl 2022. <i>Nucleic Acids Research</i> , 2021 ,	20.1	72
39	Refget: standardised access to reference sequences. <i>Bioinformatics</i> , 2021 ,	7.2	4
38	Ensembl 2021. <i>Nucleic Acids Research</i> , 2021 , 49, D884-D891	20.1	324
37	GENCODE 2021. <i>Nucleic Acids Research</i> , 2021 , 49, D916-D923	20.1	82
36	Structured reporting in portable chest radiographs: An essential tool in the diagnosis of COVID-19. <i>European Journal of Radiology</i> , 2021 , 134, 109414	4.7	8
35	The Ensembl COVID-19 resource: ongoing integration of public SARS-CoV-2 data. <i>Nucleic Acids Research</i> , 2021 ,	20.1	3
34	A compendium of uniformly processed human gene expression and splicing quantitative trait loci. <i>Nature Genetics</i> , 2021 , 53, 1290-1299	36.3	28
33	PHI-base in 2022: a multi-species phenotype database for Pathogen-Host Interactions. <i>Nucleic Acids Research</i> , 2021 ,	20.1	2
32	Pervasive lesion segregation shapes cancer genome evolution. <i>Nature</i> , 2020 , 583, 265-270	50.4	20
31	The ELIXIR Core Data Resources: fundamental infrastructure for the life sciences. <i>Bioinformatics</i> , 2020 , 36, 2636-2642	7.2	29
30	Ensembl 2020. <i>Nucleic Acids Research</i> , 2020 , 48, D682-D688	20.1	645
29	PHI-base: the pathogen-host interactions database. <i>Nucleic Acids Research</i> , 2020 , 48, D613-D620	20.1	62
28	Ensembl Genomes 2020-enabling non-vertebrate genomic research. <i>Nucleic Acids Research</i> , 2020 , 48, D689-D695	20.1	214

27	Sharing Programming Resources Between Bio* Projects. <i>Methods in Molecular Biology</i> , 2019 , 1910, 747-766	4
26	Collaborative Annotation Redefines Gene Sets for Crucial Phytopathogens. <i>Frontiers in Microbiology</i> , 2019 , 10, 2477	5.7 6
25	GENCODE reference annotation for the human and mouse genomes. <i>Nucleic Acids Research</i> , 2019 , 47, D766-D773	20.1 1140
24	Ensembl 2019. <i>Nucleic Acids Research</i> , 2019 , 47, D745-D751	20.1 554
23	Ensembl Genomes 2018: an integrated omics infrastructure for non-vertebrate species. <i>Nucleic Acids Research</i> , 2018 , 46, D802-D808	20.1 330
22	Ensembl 2018. <i>Nucleic Acids Research</i> , 2018 , 46, D754-D761	20.1 1822
21	Eleven quick tips to build a usable REST API for life sciences. <i>PLoS Computational Biology</i> , 2018 , 14, e1006542	7
20	ClinGen advancing genomic data-sharing standards as a GA4GH driver project. <i>Human Mutation</i> , 2018 , 39, 1686-1689	4.7 12
19	Ensembl 2017. <i>Nucleic Acids Research</i> , 2017 , 45, D635-D642	20.1 404
18	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,	5 35
17	Ensembl 2016. <i>Nucleic Acids Research</i> , 2016 , 44, D710-6	20.1 1094
16	Ensembl comparative genomics resources. <i>Database: the Journal of Biological Databases and Curation</i> , 2016 , 2016,	5 186
15	The Ensembl REST API: Ensembl Data for Any Language. <i>Bioinformatics</i> , 2015 , 31, 143-5	7.2 108
14	Gene bookmarking 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	11
13	Ensembl 2012. <i>Nucleic Acids Research</i> , 2012 , 40, D84-90	20.1 798
12	Sharing programming resources between Bio* projects through remote procedure call and native call stack strategies. <i>Methods in Molecular Biology</i> , 2012 , 856, 513-27	1.4 1
11	Ensembl Genomes: an integrative resource for genome-scale data from non-vertebrate species. <i>Nucleic Acids Research</i> , 2012 , 40, D91-7	20.1 141
10	BioJava: an open-source framework for bioinformatics in 2012. <i>Bioinformatics</i> , 2012 , 28, 2693-5	7.2 136

9	Patterns of somatic mutation in human cancer genomes. <i>Nature</i> , 2007 , 446, 153-8	50.4	2400
8	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, 42-6	5	88
7	A hypermutation phenotype and somatic MSH6 mutations in recurrent human malignant gliomas after alkylator chemotherapy. <i>Cancer Research</i> , 2006 , 66, 3987-91	10.1	328
6	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, 1119-24	11	92
5	Mutation analysis of 24 known cancer genes in the NCI-60 cell line set. <i>Molecular Cancer Therapeutics</i> , 2006 , 5, 2606-12	6.1	322
4	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, 590-2	36.3	289
3	Somatic mutations of the protein kinase gene family in human lung cancer. <i>Cancer Research</i> , 2005 , 65, 7591-5	10.1	392
2	Lung cancer: intragenic ERBB2 kinase mutations in tumours. <i>Nature</i> , 2004 , 431, 525-6	50.4	655
1	The GA4GH Variation Representation Specification (VRS): a Computational Framework for the Precise Representation and Federated Identification of Molecular Variation		3