

Andrew D Yates

List of Publications by Citations

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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 | Patterns of somatic mutation in human cancer genomes. <i>Nature</i> , 2007 , 446, 153-8 | 50.4 | 2400 |
| 43 | Ensembl 2018. <i>Nucleic Acids Research</i> , 2018 , 46, D754-D761 | 20.1 | 1822 |
| 42 | GENCODE reference annotation for the human and mouse genomes. <i>Nucleic Acids Research</i> , 2019 , 47, D766-D773 | 20.1 | 1140 |
| 41 | Ensembl 2016. <i>Nucleic Acids Research</i> , 2016 , 44, D710-6 | 20.1 | 1094 |
| 40 | Ensembl 2012. <i>Nucleic Acids Research</i> , 2012 , 40, D84-90 | 20.1 | 798 |
| 39 | Lung cancer: intragenic ERBB2 kinase mutations in tumours. <i>Nature</i> , 2004 , 431, 525-6 | 50.4 | 655 |
| 38 | Ensembl 2020. <i>Nucleic Acids Research</i> , 2020 , 48, D682-D688 | 20.1 | 645 |
| 37 | Ensembl 2019. <i>Nucleic Acids Research</i> , 2019 , 47, D745-D751 | 20.1 | 554 |
| 36 | Ensembl 2017. <i>Nucleic Acids Research</i> , 2017 , 45, D635-D642 | 20.1 | 404 |
| 35 | Somatic mutations of the protein kinase gene family in human lung cancer. <i>Cancer Research</i> , 2005 , 65, 7591-5 | 10.1 | 392 |
| 34 | Ensembl Genomes 2018: an integrated omics infrastructure for non-vertebrate species. <i>Nucleic Acids Research</i> , 2018 , 46, D802-D808 | 20.1 | 330 |
| 33 | 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 |
| 32 | Ensembl 2021. <i>Nucleic Acids Research</i> , 2021 , 49, D884-D891 | 20.1 | 324 |
| 31 | 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 |
| 30 | 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 |
| 29 | Ensembl Genomes 2020-enabling non-vertebrate genomic research. <i>Nucleic Acids Research</i> , 2020 , 48, D689-D695 | 20.1 | 214 |
| 28 | Ensembl comparative genomics resources. <i>Database: the Journal of Biological Databases and Curation</i> , 2016 , 2016, | 5 | 186 |

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|----|---|------|-----|
| 27 | 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 |
| 26 | BioJava: an open-source framework for bioinformatics in 2012. <i>Bioinformatics</i> , 2012 , 28, 2693-5 | 7.2 | 136 |
| 25 | The Ensembl REST API: Ensembl Data for Any Language. <i>Bioinformatics</i> , 2015 , 31, 143-5 | 7.2 | 108 |
| 24 | 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 |
| 23 | 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 |
| 22 | GENCODE 2021. <i>Nucleic Acids Research</i> , 2021 , 49, D916-D923 | 20.1 | 82 |
| 21 | Ensembl 2022. <i>Nucleic Acids Research</i> , 2021 , | 20.1 | 72 |
| 20 | PHI-base: the pathogen-host interactions database. <i>Nucleic Acids Research</i> , 2020 , 48, D613-D620 | 20.1 | 62 |
| 19 | 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 |
| 18 | The ELIXIR Core Data Resources: fundamental infrastructure for the life sciences. <i>Bioinformatics</i> , 2020 , 36, 2636-2642 | 7.2 | 29 |
| 17 | A compendium of uniformly processed human gene expression and splicing quantitative trait loci. <i>Nature Genetics</i> , 2021 , 53, 1290-1299 | 36.3 | 28 |
| 16 | Pervasive lesion segregation shapes cancer genome evolution. <i>Nature</i> , 2020 , 583, 265-270 | 50.4 | 20 |
| 15 | GA4GH: International policies and standards for data sharing across genomic research and healthcare.. <i>Cell Genomics</i> , 2021 , 1, 100029-100029 | | 20 |
| 14 | Ensembl Genomes 2022: an expanding genome resource for non-vertebrates. <i>Nucleic Acids Research</i> , 2021 , | 20.1 | 12 |
| 13 | ClinGen advancing genomic data-sharing standards as a GA4GH driver project. <i>Human Mutation</i> , 2018 , 39, 1686-1689 | 4.7 | 12 |
| 12 | Gene 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 | 7.9 | 11 |
| 11 | 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 |
| 10 | Eleven quick tips to build a usable REST API for life sciences. <i>PLoS Computational Biology</i> , 2018 , 14, e1006542 | | 7 |

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| 9 | Collaborative Annotation Redefines Gene Sets for Crucial Phytopathogens. <i>Frontiers in Microbiology</i> , 2019 , 10, 2477 | 5.7 | 6 |
| 8 | Sharing Programming Resources Between Bio* Projects. <i>Methods in Molecular Biology</i> , 2019 , 1910, 747-766 | 7.6 | 4 |
| 7 | The GA4GH Variation Representation Specification: A computational framework for variation representation and federated identification.. <i>Cell Genomics</i> , 2021 , 1, 100027-100027 | | 4 |
| 6 | Refget: standardised access to reference sequences. <i>Bioinformatics</i> , 2021 , | 7.2 | 4 |
| 5 | The Ensembl COVID-19 resource: ongoing integration of public SARS-CoV-2 data. <i>Nucleic Acids Research</i> , 2021 , | 20.1 | 3 |
| 4 | The GA4GH Variation Representation Specification (VRS): a Computational Framework for the Precise Representation and Federated Identification of Molecular Variation | | 3 |
| 3 | PHI-base in 2022: a multi-species phenotype database for Pathogen-Host Interactions. <i>Nucleic Acids Research</i> , 2021 , | 20.1 | 2 |
| 2 | 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 |
| 1 | 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 |