Jordi Rambla de Argila

List of Publications by Year in descending order

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24 946 12 23
papers citations h-index g-index

26 26 26 2457
all docs docs citations times ranked citing authors

#	Article	IF	Citations
1	The European Genome-phenome Archive of human data consented for biomedical research. Nature Genetics, 2015, 47, 692-695.	21.4	338
2	GA4GH: International policies and standards for data sharing across genomic research and healthcare. Cell Genomics, 2021, 1, 100029.	6.5	94
3	Federated discovery and sharing of genomic data using Beacons. Nature Biotechnology, 2019, 37, 220-224.	17.5	75
4	Leveraging European infrastructures to access 1 million human genomes by 2022. Nature Reviews Genetics, 2019, 20, 693-701.	16.3	69
5	Consent Codes: Upholding Standard Data Use Conditions. PLoS Genetics, 2016, 12, e1005772.	3.5	65
6	The European Genome-phenome Archive in 2021. Nucleic Acids Research, 2022, 50, D980-D987.	14.5	55
7	The ELIXIR Core Data Resources: fundamental infrastructure for the life sciences. Bioinformatics, 2020, 36, 2636-2642.	4.1	47
8	Registered access: authorizing data access. European Journal of Human Genetics, 2018, 26, 1721-1731.	2.8	33
9	The Data Use Ontology to streamline responsible access to human biomedical datasets. Cell Genomics, 2021, 1, 100028.	6.5	31
10	International federation of genomic medicine databases using GA4GH standards. Cell Genomics, 2021, 1, 100032.	6.5	22
11	Ready-to-use public infrastructure for global SARS-CoV-2 monitoring. Nature Biotechnology, 2021, 39, 1178-1179.	17.5	21
12	ELIXIRâ€EXCELERATE: establishing Europe's data infrastructure for the life science research of the future. EMBO Journal, 2021, 40, e107409.	7.8	18
13	The RDâ€Connect Genomeâ€Phenome Analysis Platform: Accelerating diagnosis, research, and gene discovery for rare diseases. Human Mutation, 2022, , .	2.5	18
14	Beacon v2 and Beacon networks: A "lingua franca―for federated data discovery in biomedical genomics, and beyond. Human Mutation, 2022, , .	2.5	10
15	Systematically linking tranSMART, Galaxy and EGA for reusing human translational research data. F1000Research, 2017, 6, 1488.	1.6	8
16	Inversions and genomic differentiation after secondary contact: When drift contributes to maintenance, not loss, of differentiation. Evolution; International Journal of Organic Evolution, 2021, 75, 1288-1303.	2.3	7
17	Integration of EGA secure data access into Galaxy. F1000Research, 2016, 5, 2841.	1.6	7
18	FaST-LMM for Two-Way Epistasis Tests on High-Performance Clusters. Journal of Computational Biology, 2018, 25, 862-870.	1.6	6

#	Article	IF	CITATIONS
19	iASiS: Towards Heterogeneous Big Data Analysis for Personalized Medicine. , 2019, , .		6
20	European Genome-Phenome Archive (EGA) - Granular Solutions for the Next 10 Years. , 2019, , .		4
21	Genome-phenome explorer (GePhEx): a tool for the visualization and interpretation of phenotypic relationships supported by genetic evidence. Bioinformatics, 2019, 36, 890-896.	4.1	3
22	Accelerating FaST-LMM for Epistasis Tests. Lecture Notes in Computer Science, 2017, , 548-557.	1.3	2
23	Analysis of Five Gene Sets in Chimpanzees Suggests Decoupling between the Action of Selection on Protein-Coding and on Noncoding Elements. Genome Biology and Evolution, 2015, 7, 1490-1505.	2.5	1
24	A quality control portal for sequencing data deposited at the European genome–phenome archive. Briefings in Bioinformatics, 2022, , .	6.5	0