Manuel Corpas

List of Publications by Year
in descending order

45 papers	2,615 citations	471509 17 h-index	254184 43 g-index
68 all docs	68 docs citations	68 times ranked	6906 citing authors

#	Article	IF	Citations
1	Transferability of genetic risk scores in African populations. Nature Medicine, 2022, 28, 1163-1166.	30.7	39
2	Whole Genome Interpretation for a Family of Five. Frontiers in Genetics, 2021, 12, 535123.	2.3	3
3	Editorial: Personal Genomes: Accessing, Sharing, and Interpretation. Frontiers in Genetics, 2021, 12, 687584.	2.3	1
4	A Key Action Plan for EDUCATION in a Global Crisis. Lecture Notes in Educational Technology, 2021, , 263-272.	0.8	0
5	Personal Genome Project UK (PGP-UK): a research and citizen science hybrid project in support of personalized medicine. BMC Medical Genomics, 2018, 11, 108.	1.5	34
6	Phenotype-loci associations in networks of patients with rare disorders: application to assist in the diagnosis of novel clinical cases. European Journal of Human Genetics, 2018, 26, 1451-1461.	2.8	8
7	APPLaUD: access for patients and participants to individual level uninterpreted genomic data. Human Genomics, 2018, 12, 7.	2.9	45
8	A FAIR guide for data providers to maximise sharing of human genomic data. PLoS Computational Biology, 2018, 14, e1005873.	3.2	25
9	BioCIDER: a Contextualisation InDEx for biological Resources discovery. Bioinformatics, 2017, 33, 2607-2608.	4.1	1
10	Genome sequencing of the staple food crop white Guinea yam enables the development of a molecular marker for sex determination. BMC Biology, 2017, 15, 86.	3.8	114
11	Four simple recommendations to encourage best practices in research software. F1000Research, 2017, 6, 876.	1.6	88
12	Systematic identification of phenotypically enriched loci using a patient network of genomic disorders. BMC Genomics, 2016, 17, 232.	2.8	7
13	Top 10 metrics for life science software good practices. F1000Research, 2016, 5, 2000.	1.6	14
14	Crowdsourced direct-to-consumer genomic analysis of a family quartet. BMC Genomics, 2015, 16, 910.	2.8	20
15	Future opportunities and trends for e-infrastructures and life sciences: going beyond the grid to enable life science data analysis. Frontiers in Genetics, 2015, 6, 197.	2.3	8
16	The GOBLET training portal: a global repository of bioinformatics training materials, courses and trainers. Bioinformatics, 2015, 31, 140-142.	4.1	34
17	GOBLET: The Global Organisation for Bioinformatics Learning, Education and Training. PLoS Computational Biology, 2015, 11, e1004143.	3.2	52
18	Ten Simple Rules for Organizing an Unconference. PLoS Computational Biology, 2015, 11, e1003905.	3.2	69

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19	A Quick Guide for Building a Successful Bioinformatics Community. PLoS Computational Biology, 2015, 11, e1003972.	3.2	23
20	Anatomy of BioJS, an open source community for the life sciences. ELife, 2015, 4, .	6.0	29
21	Lessons from Fraxinus, a crowd-sourced citizen science game in genomics. ELife, 2015, 4, e07460.	6.0	21
22	BioJS: an open source standard for biological visualisation â€" its status in 2014. F1000Research, 2014, 3, 55.	1.6	22
23	The BioJS article collection of open source components for biological data visualisation. F1000Research, 2014, 3, 56.	1.6	5
24	wigExplorer, a BioJS component to visualise wig data. F1000Research, 2014, 3, 53.	1.6	4
25	wigExplorer, a BioJS component to visualise wig data. F1000Research, 2014, 3, 53.	1.6	3
26	Crowdsourcing the Corpasome. Source Code for Biology and Medicine, 2013, 8, 13.	1.7	9
27	BioJS: an open source JavaScript framework for biological data visualization. Bioinformatics, 2013, 29, 1103-1104.	4.1	110
28	Bioinformatics Workflows and Web Services in Systems Biology Made Easy for Experimentalists. Methods in Molecular Biology, 2013, 1021, 299-310.	0.9	4
29	iAnn: an event sharing platform for the life sciences. Bioinformatics, 2013, 29, 1919-1921.	4.1	6
30	The Young PI Buzz: Learning from the Organizers of the Junior Principal Investigator Meeting at ISMB-ECCB 2013. PLoS Computational Biology, 2013, 9, e1003350.	3.2	2
31	Spanish cuts: More economic damage. Nature, 2012, 487, 38-38.	27.8	1
32	DECIPHER: web-based, community resource for clinical interpretation of rare variants in developmental disorders. Human Molecular Genetics, 2012, 21, R37-R44.	2.9	74
33	Interpretation of Genomic Copy Number Variants Using DECIPHER. Current Protocols in Human Genetics, 2012, 72, Unit 8.14.	3.5	12
34	How Not to Be a Bioinformatician. Source Code for Biology and Medicine, 2012, 7, 3.	1.7	6
35	A genome blogger manifesto. GigaScience, 2012, 1, 15.	6.4	1
36	A Family Experience of Personal Genomics. Journal of Genetic Counseling, 2012, 21, 386-391.	1.6	18

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37	Low budget analysis of Direct-To-Consumer genomic testing familial data. F1000Research, 2012, 1, 3.	1.6	10
38	myKaryoView: A Light-Weight Client for Visualization of Genomic Data. PLoS ONE, 2011, 6, e26345.	2.5	5
39	DECIPHER: Database of Chromosomal Imbalance and Phenotype in Humans Using Ensembl Resources. American Journal of Human Genetics, 2009, 84, 524-533.	6.2	1,614
40	Ten Simple Rules for Organizing a Scientific Meeting. PLoS Computational Biology, 2008, 4, e1000080.	3.2	23
41	ENFIN - An Integrative Structure for Systems Biology. Lecture Notes in Computer Science, 2008, , 132-143.	1.3	0
42	PFF â€" an integrated database of residues and fragments critical for protein folding. BMC Systems Biology, 2007, 1, .	3.0	0
43	Highlights from the Third International Society for Computational Biology Student Council Symposium at the Fifteenth Annual International Conference on Intelligent Systems for Molecular Biology. BMC Bioinformatics, 2007, 8, .	2.6	7
44	Scientists & societies. Nature, 2005, 436, 1204-1204.	27.8	9
45	DNAContentViewer a BioJS component to visualise GC/AT Content. F1000Research, 0, 3, 54.	1.6	1