Irina M Armean

List of Publications by Year
in descending order

15	12,585	623734 14	940533 16
papers	citations	h-index	g-index

20	20	20	28514
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Ensembl 2022. Nucleic Acids Research, 2022, 50, D988-D995.	14.5	1,103
2	Annotating and prioritizing genomic variants using the Ensembl Variant Effect Predictorâ€”A tutorial. Human Mutation, 2022, 43, 986-997.	2.5	30
3	Ensembl 2021. Nucleic Acids Research, 2021, 49, D884-D891.	14.5	1,231
4	The value of primary transcripts to the clinical and nonâ€clinical genomics community: Survey results and roadmap for improvements. Molecular Genetics & Genomic Medicine, 2021, 9, e1786.	1.2	5
5	Addendum: The mutational constraint spectrum quantified from variation in 141,456 humans. Nature, 2021, 597, E3-E4.	27.8	45
6	Ensembl 2020. Nucleic Acids Research, 2020, 48, D682-D688.	14.5	1,076
7	Evaluating drug targets through human loss-of-function genetic variation. Nature, 2020, 581, 459-464.	27.8	115
8	The mutational constraint spectrum quantified from variation in 141,456 humans. Nature, 2020, 581, 434-443.	27.8	6,140
9	The effect of LRRK2 loss-of-function variants in humans. Nature Medicine, 2020, 26, 869-877.	30.7	79
10	The ELIXIR Human Copy Number Variations Community: building bioinformatics infrastructure for research. F1000Research, 2020, 9, 1229.	1.6	5
11	A plugin for the Ensembl Variant Effect Predictor that uses MaxEntScan to predict variant spliceogenicity. Bioinformatics, 2019, 35, 2315-2317.	4.1	52
12	Ensembl 2019. Nucleic Acids Research, 2019, 47, D745-D751.	14.5	879
13	Ensembl variation resources. Database: the Journal of Biological Databases and Curation, 2018, 2018, .	3.0	377
14	Human knockouts and phenotypic analysis in a cohort with a high rate of consanguinity. Nature, 2017, 544, 235-239.	27.8	292
15	Ensembl Genomes 2016: more genomes, more complexity. Nucleic Acids Research, 2016, 44, D574-D580.	14.5	530