Vincent Ferretti

List of Publications by Year
in descending order

24 papers	4,778 citations	361413 20 h-index	610901 24 g-index
25 all docs	25 docs citations	25 times ranked	10639 citing authors

#	Article	IF	Citations
1	The NCI Genomic Data Commons. Nature Genetics, 2021, 53, 257-262.	21.4	52
2	A user guide for the online exploration and visualization of PCAWG data. Nature Communications, 2020, 11, 3400.	12.8	23
3	The landscape of viral associations in human cancers. Nature Genetics, 2020, 52, 320-330.	21.4	261
4	The International Cancer Genome Consortium Data Portal. Nature Biotechnology, 2019, 37, 367-369.	17.5	332
5	Fostering population-based cohort data discovery: The Maelstrom Research cataloguing toolkit. PLoS ONE, 2018, 13, e0200926.	2.5	33
6	Maelstrom Research guidelines for rigorous retrospective data harmonization. International Journal of Epidemiology, 2017, 46, dyw075.	1.9	116
7	The NCI Genomic Data Commons as an engine for precision medicine. Blood, 2017, 130, 453-459.	1.4	226
8	Developing Cancer Informatics Applications and Tools Using the NCI Genomic Data Commons API. Cancer Research, 2017, 77, e15-e18.	0.9	32
9	Association of Distinct Mutational Signatures With Correlates of Increased Immune Activity in Pancreatic Ductal Adenocarcinoma. JAMA Oncology, 2017, 3, 774.	7.1	221
10	Toward a Shared Vision for Cancer Genomic Data. New England Journal of Medicine, 2016, 375, 1109-1112.	27.0	1,242
11	DataSHIELD: taking the analysis to the data, not the data to the analysis. International Journal of Epidemiology, 2014, 43, 1929-1944.	1.9	188
12	Feasibility of real time next generation sequencing of cancer genes linked to drug response: Results from a clinical trial. International Journal of Cancer, 2013, 132, 1547-1555.	5.1	76
13	Clinical genomics information management software linking cancer genome sequence and clinical decisions. Genomics, 2013, 102, 140-147.	2.9	14
14	Evaluation of Alignment Algorithms for Discovery and Identification of Pathogens Using RNA-Seq. PLoS ONE, 2013, 8, e76935.	2.5	37
15	Observ-OM and Observ-TAB: Universal syntax solutions for the integration, search, and exchange of phenotype and genotype information. Human Mutation, 2012, 33, 867-873.	2.5	18
16	Is rigorous retrospective harmonization possible? Application of the DataSHaPER approach across 53 large studies. International Journal of Epidemiology, 2011, 40, 1314-1328.	1.9	84
17	Quality, quantity and harmony: the DataSHaPER approach to integrating data across bioclinical studies. International Journal of Epidemiology, 2010, 39, 1383-1393.	1.9	148
18	DataSHIELD: resolving a conflict in contemporary bioscience--performing a pooled analysis of individual-level data without sharing the data. International Journal of Epidemiology, 2010, 39, 1372-1382.	1.9	150

#	Article	IF	Citations
19	Analyses of associations with asthma in four asthma population samples from Canada and Australia. Human Genetics, 2009, 125, 445-459.	3.8	95
20	Germline EPHB2 Receptor Variants in Familial Colorectal Cancer. PLoS ONE, 2008, 3, e2885.	2.5	16
21	Genome-wide association scan identifies a colorectal cancer susceptibility locus on chromosome 8q24. Nature Genetics, 2007, 39, 989-994.	21.4	676
22	Genome-wide computational prediction of transcriptional regulatory modules reveals new insights into human gene expression. Genome Research, 2006, 16, 656-668.	5.5	229
23	A predominant role for the HLA class II region in the association of the MHC region with multiple sclerosis. Nature Genetics, 2005, 37, 1108-1112.	21.4	295
24	Antimicrobial drug discovery through bacteriophage genomics. Nature Biotechnology, 2004, 22, 185-191.	17.5	210