## Logan C Brooks

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Comparing trained and untrained probabilistic ensemble forecasts of COVID-19 cases and deaths in the United States. International Journal of Forecasting, 2023, 39, 1366-1383.	6.5	23
2	An open repository of real-time COVID-19 indicators. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	7.1	27
3	Collaborative efforts to forecast seasonal influenza in the United States, 2015–2016. Scientific Reports, 2019, 9, 683.	3.3	90
4	An open challenge to advance probabilistic forecasting for dengue epidemics. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 24268-24274.	7.1	136
5	Accuracy of real-time multi-model ensemble forecasts for seasonal influenza in the U.S PLoS Computational Biology, 2019, 15, e1007486.	3.2	119
6	A collaborative multiyear, multimodel assessment of seasonal influenza forecasting in the United States. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 3146-3154.	7.1	199
7	Accuracy of real-time multi-model ensemble forecasts for seasonal influenza in the U.S , 2019, 15, e1007486.		0
8	Accuracy of real-time multi-model ensemble forecasts for seasonal influenza in the U.S , 2019, 15, e1007486.		0
9	Accuracy of real-time multi-model ensemble forecasts for seasonal influenza in the U.S , 2019, 15, e1007486.		0
10	Accuracy of real-time multi-model ensemble forecasts for seasonal influenza in the U.S , 2019, 15, e1007486.		0
11	Results from the second year of a collaborative effort to forecast influenza seasons in the United States. Epidemics, 2018, 24, 26-33.	3.0	83
12	Nonmechanistic forecasts of seasonal influenza with iterative one-week-ahead distributions. PLoS Computational Biology, 2018, 14, e1006134.	3.2	55
13	A human judgment approach to epidemiological forecasting. PLoS Computational Biology, 2017, 13, e1005248.	3.2	50
14	Flexible Modeling of Epidemics with an Empirical Bayes Framework. PLoS Computational Biology, 2015, 11, e1004382.	3.2	92