Cyprien Mbogning

List of Publications by Year
in descending order

12 papers	**232** citations	1307594 **7** h-index	1281871 **11** g-index
12 all docs	**12** docs citations	**12** times ranked	**459** citing authors

#	ARTICLE	IF	CITATIONS
1	Risk stratification integrating genetic data for factor VIII inhibitor development in patients with severe hemophilia A. PLoS ONE, 2019, 14, e0218258.	2.5	12
2	Incidence and risk factors for adalimumab and infliximab anti-drug antibodies in rheumatoid arthritis: A European retrospective multicohort analysis. Seminars in Arthritis and Rheumatism, 2019, 48, 967-975.	3.4	46
3	Monocyte NOTCH2 expression predicts IFN-Î² immunogenicity in multiple sclerosis patients. JCI Insight, 2018, 3, .	5.0	46
4	A test for comparing current status survival data with crossing hazard functions and its application to immunogenicity of biotherapeutics. Statistics in Medicine, 2017, 36, 4364-4377.	1.6	0
5	A score test for comparing cross-sectional survival data with a fraction of non-susceptible patients and its application in clinical immunology. PLoS ONE, 2017, 12, e0179896.	2.5	1
6	Clinical practice of analysis of anti-drug antibodies against interferon beta and natalizumab in multiple sclerosis patients in Europe: A descriptive study of test results. PLoS ONE, 2017, 12, e0170395.	2.5	34
7	Occurrence of Anti-Drug Antibodies against Interferon-Beta and Natalizumab in Multiple Sclerosis: A Collaborative Cohort Analysis. PLoS ONE, 2016, 11, e0162752.	2.5	41
8	Bagging survival tree procedure for variable selection and prediction in the presence of nonsusceptible patients. BMC Bioinformatics, 2016, 17, 230.	2.6	7
9	A Bagged, Partially Linear, Tree-Based Regression Procedure for Prediction and Variable Selection. Human Heredity, 2015, 79, 182-193.	0.8	5
10	Joint modelling of longitudinal and repeated time-to-event data using nonlinear mixed-effects models and the stochastic approximation expectationâ€"maximization algorithm. Journal of Statistical Computation and Simulation, 2015, 85, 1512-1528.	1.2	18
11	A novel tree-based procedure for deciphering the genomic spectrum of clinical disease entities. Journal of Clinical Bioinformatics, 2014, 4, 6.	1.2	6
12	An improved SAEM algorithm for maximum likelihood estimation in mixtures of non linear mixed effects models. Statistics and Computing, 2014, 24, 693-707.	1.5	16