

# Cyprien Mbogning

## List of Publications by Year in descending order

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Version: 2024-02-01

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