Mateusz Maciejewski

List of Publications by Year
in descending order

18	544	840776	888059
papers	citations	11	17
		h-index	g-index

22	22	22	1032
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Prediction of response of methotrexate in patients with rheumatoid arthritis using serum lipidomics. Scientific Reports, 2021, 11, 7266.	3.3	21
2	Distinct clinical phenotypes for Crohn's disease derived from patient surveys. BMC Gastroenterology, 2021, 21, 160.	2.0	5
3	What Is the Persistence to Methotrexate in Rheumatoid Arthritis, and Does Machine Learning Outperform Hypothesis-Based Approaches to Its Prediction?. ACR Open Rheumatology, 2021, 3, 457-463.	2.1	11
4	P17 Prediction of response of methotrexate in patients with rheumatoid arthritis using serum lipidomics. Rheumatology, 2020, 59, .	1.9	0
5	Standard machine learning approaches outperform deep representation learning on phenotype prediction from transcriptomics data. BMC Bioinformatics, 2020, 21, 119.	2.6	41
6	Peptide-TLR-7/8a conjugate vaccines chemically programmed for nanoparticle self-assembly enhance CD8 T-cell immunity to tumor antigens. Nature Biotechnology, 2020, 38, 320-332.	17.5	210
7	018 Gene expression profiling identifies classifier of methotrexate non-response in patients with rheumatoid arthritis. Rheumatology, 2019, 58, .	1.9	1
8	Profiling of Gene Expression Biomarkers as a Classifier of Methotrexate Nonresponse in Patients With Rheumatoid Arthritis. Arthritis and Rheumatology, 2019, 71, 678-684.	5.6	50
9	Mendelian Disease Associations Reveal Novel Insights into Inflammatory Bowel Disease. Inflammatory Bowel Diseases, 2018, 24, 471-481.	1.9	5
10	A probabilistic pathway score (PROPS) for classification with applications to inflammatory bowel disease. Bioinformatics, 2018, 34, 985-993.	4.1	25
11	Reverse translation of adverse event reports paves the way for de-risking preclinical off-targets. ELife, 2017, 6, .	6.0	44
12	Experimental Design Strategy: Weak Reinforcement Leads to Increased Hit Rates and Enhanced Chemical Diversity. Journal of Chemical Information and Modeling, 2015, 55, 956-962.	5.4	16
13	Using Mutagenesis and Structural Biology to Map the Binding Site for the Plasmodium falciparum Merozoite Protein PfRh4 on the Human Immune Adherence Receptor. Journal of Biological Chemistry, 2014, 289, 450-463.	3.4	30
14	Decoding the components of dynamics in three-domain proteins. Journal of Computational Chemistry, 2014, 35, 518-525.	3.3	2
15	Translation of off-target effects: prediction of ADRs by integrated experimental and computational approach. Toxicology Research, 2014, 3, 433-444.	2.1	11
16	Diversity Selection of Compounds Based on 'Protein Affinity Fingerprints' Improves Sampling of Bioactive Chemical Space. Chemical Biology and Drug Design, 2013, 82, 252-266.	3.2	19
17	Solution Structure of CCP Modules 10-12 Illuminates Functional Architecture of the Complement Regulator, Factor H. Journal of Molecular Biology, 2012, 424, 295-312.	4.2	24
18	Estimation of Interdomain Flexibility of N-Terminus of Factor H Using Residual Dipolar Couplings. Biochemistry, 2011, 50, 8138-8149.	2.5	26