

Pierre D'Ágnes

List of Publications by Year in descending order

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Version: 2024-02-01

34
papers

1,814
citations

331670

21
h-index

377865

34
g-index

36
all docs

36
docs citations

36
times ranked

2640
citing authors

#	ARTICLE	IF	CITATIONS
1	Robust humoral and cellular immune responses and low risk for reinfection at least 8 months following asymptomatic to mild COVID-19. <i>Journal of Internal Medicine</i> , 2022, 291, 72-80.	6.0	47
2	Long-term SARS-CoV-2-specific and cross-reactive cellular immune responses correlate with humoral responses, disease severity, and symptomatology. <i>Immunity, Inflammation and Disease</i> , 2022, 10, e595.	2.7	6
3	Longitudinal analysis of anti-drug antibody development in multiple sclerosis patients treated with interferon beta-1a (Rebif [®]) using B cell receptor repertoire analysis. <i>Journal of Neuroimmunology</i> , 2022, 370, 577932.	2.3	2
4	Serum Metabolomic Signatures Can Predict Subclinical Atherosclerosis in Patients With Systemic Lupus Erythematosus. <i>Arteriosclerosis, Thrombosis, and Vascular Biology</i> , 2021, 41, 1446-1458.	2.4	26
5	Protein interaction, monocyte toxicity and immunogenic properties of cerium oxide crystals with 5% or 14% gadolinium, cobalt oxide and iron oxide nanoparticles – an interdisciplinary approach. <i>Nanotoxicology</i> , 2021, 15, 1035-1058.	3.0	1
6	Machine Learning Techniques for Personalised Medicine Approaches in Immune-Mediated Chronic Inflammatory Diseases: Applications and Challenges. <i>Frontiers in Pharmacology</i> , 2021, 12, 720694.	3.5	37
7	An evaluation of a FluoroSpot assay as a diagnostic tool to determine SARS-CoV-2 specific T cell responses. <i>PLoS ONE</i> , 2021, 16, e0258041.	2.5	10
8	Using Serum Metabolomics to Predict Development of Anti-drug Antibodies in Multiple Sclerosis Patients Treated With IFN ² . <i>Frontiers in Immunology</i> , 2020, 11, 1527.	4.8	24
9	Disease-associated and patient-specific immune cell signatures in juvenile-onset systemic lupus erythematosus: patient stratification using a machine-learning approach. <i>Lancet Rheumatology</i> , The, 2020, 2, e485-e496.	3.9	52
10	Clinicogenomic factors of biotherapy immunogenicity in autoimmune disease: A prospective multicohort study of the ABIRISK consortium. <i>PLoS Medicine</i> , 2020, 17, e1003348.	8.4	31
11	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
12	Detection and kinetics of persistent neutralizing anti-interferon-beta antibodies in patients with multiple sclerosis. Results from the ABIRISK prospective cohort study. <i>Journal of Neuroimmunology</i> , 2019, 326, 19-27.	2.3	22
13	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
14	Barrier Properties and Transcriptome Expression in Human iPSC-Derived Models of the Blood-Brain Barrier. <i>Stem Cells</i> , 2018, 36, 1816-1827.	3.2	81
15	Methotrexate and BAFF interaction prevents immunization against TNF inhibitors. <i>Annals of the Rheumatic Diseases</i> , 2018, 77, 1463-1470.	0.9	25
16	Monocyte NOTCH2 expression predicts IFN- ² immunogenicity in multiple sclerosis patients. <i>JCI Insight</i> , 2018, 3, .	5.0	46
17	Population-specific design of de-immunized protein biotherapeutics. <i>PLoS Computational Biology</i> , 2018, 14, e1005983.	3.2	16
18	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

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19	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
20	WIPI proteins: essential PtdIns3<i>P</i> effectors at the nascent autophagosome. <i>Journal of Cell Science</i> , 2015, 128, 207-17.	2.0	214
21	Fluorescence-based imaging of autophagy progression by human WIPI protein detection. <i>Methods</i> , 2015, 75, 69-78.	3.8	17
22	miHA-Match: Computational detection of tissue-specific minor histocompatibility antigens. <i>Journal of Immunological Methods</i> , 2012, 386, 94-100.	1.4	7
23	FREDâ€”a framework for T-cell epitope detection. <i>Bioinformatics</i> , 2009, 25, 2758-2759.	4.1	20
24	A Mathematical Framework for the Selection of an Optimal Set of Peptides for Epitope-Based Vaccines. <i>PLoS Computational Biology</i> , 2008, 4, e1000246.	3.2	32
25	SherLoc: high-accuracy prediction of protein subcellular localization by integrating text and protein sequence data. <i>Bioinformatics</i> , 2007, 23, 1410-1417.	4.1	113
26	Support Vector Machine-Based Prediction of MHC-Binding Peptides. <i>Methods in Molecular Biology</i> , 2007, 409, 273-282.	0.9	2
27	MultiLoc: prediction of protein subcellular localization using N-terminal targeting sequences, sequence motifs and amino acid composition. <i>Bioinformatics</i> , 2006, 22, 1158-1165.	4.1	290
28	SVMHC: a server for prediction of MHC-binding peptides. <i>Nucleic Acids Research</i> , 2006, 34, W194-W197.	14.5	79
29	Integrated modeling of the major events in the MHC class I antigen processing pathway. <i>Protein Science</i> , 2005, 14, 2132-2140.	7.6	76
30	SNEP: SNP-derived Epitope Prediction program for minor H antigens. <i>Immunogenetics</i> , 2005, 57, 816-820.	2.4	26
31	Analysis of MHC-Peptide Binding Using Amino Acid Property-Based Decision Rules. <i>Lecture Notes in Computer Science</i> , 2005, , 446-453.	1.3	2
32	Integrative analysis of cancerâ€”related data using CAP. <i>FASEB Journal</i> , 2004, 18, 1465-1467.	0.5	9
33	Predicting Protein Subcellular Localization: Past, Present, and Future. <i>Genomics, Proteomics and Bioinformatics</i> , 2004, 2, 209-215.	6.9	95
34	Prediction of MHC class I binding peptides, using SVMHC. <i>BMC Bioinformatics</i> , 2002, 3, 25.	2.6	271