

Matthew Anthony Care

List of Publications by Year in descending order

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36
papers

1,514
citations

393982

19
h-index

377514

34
g-index

43
all docs

43
docs citations

43
times ranked

3399
citing authors

#	ARTICLE	IF	CITATIONS
1	A System for In Vitro Generation of Mature Murine Plasma Cells Uncovers Differential Blimp-1 Promoter Usage. <i>Journal of Immunology</i> , 2022, 208, 514-525.	0.4	1
2	Comparative analysis of gene expression platforms for cell-of-origin classification of diffuse large B-cell lymphoma shows high concordance. <i>British Journal of Haematology</i> , 2021, 192, 599-604.	1.2	7
3	Distinct genetic changes reveal evolutionary history and heterogeneous molecular grade of DLBCL with MYC/BCL2 double-hit. <i>Leukemia</i> , 2020, 34, 1329-1341.	3.3	66
4	TLR-mediated activation of Waldenström macroglobulinemia B cells reveals an uncoupling from plasma cell differentiation. <i>Blood Advances</i> , 2020, 4, 2821-2836.	2.5	5
5	A dichotomy of gene regulatory associations during the activated B-cell to plasmablast transition. <i>Life Science Alliance</i> , 2020, 3, e202000654.	1.3	4
6	Chromatin remodelling to facilitate treatment resistance in glioblastoma. <i>Neuro-Oncology</i> , 2019, 21, iv7-iv7.	0.6	1
7	Regulation of S1PR2 by the EBV oncogene LMP1 in aggressive ABC subtype diffuse large B-cell lymphoma. <i>Journal of Pathology</i> , 2019, 248, 142-154.	2.1	8
8	Sphingosine-1-phosphate signalling drives an angiogenic transcriptional programme in diffuse large B cell lymphoma. <i>Leukemia</i> , 2019, 33, 2884-2897.	3.3	26
9	Parsimonious Gene Correlation Network Analysis (PGCNA): a tool to define modular gene co-expression for refined molecular stratification in cancer. <i>Npj Systems Biology and Applications</i> , 2019, 5, 13.	1.4	22
10	Gene-expression profiling of bortezomib added to standard chemoimmunotherapy for diffuse large B-cell lymphoma (REMoDL-B): an open-label, randomised, phase 3 trial. <i>Lancet Oncology</i> , The, 2019, 20, 649-662.	5.1	187
11	Molecular High-Grade B-Cell Lymphoma: Defining a Poor-Risk Group That Requires Different Approaches to Therapy. <i>Journal of Clinical Oncology</i> , 2019, 37, 202-212.	0.8	187
12	Growth Factor-like Gene Regulation Is Separable from Survival and Maturation in Antibody-Secreting Cells. <i>Journal of Immunology</i> , 2019, 202, 1287-1300.	0.4	11
13	Biallelic interferon regulatory factor 8 mutation: A complex immunodeficiency syndrome with dendritic cell deficiency, monocytopenia, and immune dysregulation. <i>Journal of Allergy and Clinical Immunology</i> , 2018, 141, 2234-2248.	1.5	63
14	Site-1 protease function is essential for the generation of antibody secreting cells and reprogramming for secretory activity. <i>Scientific Reports</i> , 2018, 8, 14338.	1.6	24
15	An ultra-deep sequencing strategy to detect sub-clonal TP53 mutations in presentation chronic lymphocytic leukaemia cases using multiple polymerases. <i>Oncogene</i> , 2016, 35, 5328-5336.	2.6	9
16	Network Analysis Identifies Proinflammatory Plasma Cell Polarization for Secretion of ISG15 in Human Autoimmunity. <i>Journal of Immunology</i> , 2016, 197, 1447-1459.	0.4	52
17	TLR Adaptor Protein MYD88 Mediates Sensitivity to HDAC Inhibitors via a Cytokine-Dependent Mechanism. <i>Cancer Research</i> , 2016, 76, 6975-6987.	0.4	21
18	Biallelic mutations in IRF8 impair human NK cell maturation and function. <i>Journal of Clinical Investigation</i> , 2016, 127, 306-320.	3.9	76

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19	Similarity Search Methods As an Alternative to Sub-Type Characterisation in Aggressive Lymphomas. <i>Blood</i> , 2016, 128, 3052-3052.	0.6	2
20	Transferring genomics to the clinic: distinguishing Burkitt and diffuse large B cell lymphomas. <i>Genome Medicine</i> , 2015, 7, 64.	3.6	20
21	Gene expression meta-analysis reveals immune response convergence on the IFN ³ -STAT1-IRF1 axis and adaptive immune resistance mechanisms in lymphoma. <i>Genome Medicine</i> , 2015, 7, 96.	3.6	24
22	A Prospective Randomised Trial of Targeted Therapy for Diffuse Large B-Cell Lymphoma (DLBCL) Based upon Real-Time Gene Expression Profiling: The Remodl-B Study of the UK NCRI and SAKK Lymphoma Groups (ISRCTN51837425). <i>Blood</i> , 2015, 126, 812-812.	0.6	20
23	Real-Time Molecular Classification of Diffuse Large B-Cell Lymphoma (DLBCL) By Gene Expression Profiling (GEP): Successful Delivery of a Routine Service for Randomization of Patients Onto the Multicenter Remodl-B Trial (ISRCTN 51837425). <i>Blood</i> , 2015, 126, 331-331.	0.6	0
24	SPIB and BATF provide alternate determinants of IRF4 occupancy in diffuse large B-cell lymphoma linked to disease heterogeneity. <i>Nucleic Acids Research</i> , 2014, 42, 7591-7610.	6.5	43
25	A Microarray Platform-Independent Classification Tool for Cell of Origin Class Allows Comparative Analysis of Gene Expression in Diffuse Large B-cell Lymphoma. <i>PLoS ONE</i> , 2013, 8, e55895.	1.1	64
26	Whole genome expression profiling based on paraffin embedded tissue can be used to classify diffuse large <sc>B</sc>-cell lymphoma and predict clinical outcome. <i>British Journal of Haematology</i> , 2012, 159, 441-453.	1.2	81
27	In Vitro Generation of Long-lived Human Plasma Cells. <i>Journal of Immunology</i> , 2012, 189, 5773-5785.	0.4	111
28	Depletion of RUNX1/ETO in t(8;21) AML cells leads to genome-wide changes in chromatin structure and transcription factor binding. <i>Leukemia</i> , 2012, 26, 1829-1841.	3.3	161
29	GO-At–in silicoprediction of gene function inArabidopsis thalianaby combining heterogeneous data. <i>Plant Journal</i> , 2010, 61, 713-721.	2.8	17
30	An extended set of PRDM1/BLIMP1 target genes links binding motif type to dynamic repression. <i>Nucleic Acids Research</i> , 2010, 38, 5336-5350.	6.5	52
31	Gene Expression Profiling Using the Illumina –DASL– Platform on RNA Extracted From Formalin Fixed Paraffin Embedded (FFPE) Tissue Identifies Distinct Prognostic Groups In CHOP-R Treated DLBCL. <i>Blood</i> , 2010, 116, 2485-2485.	0.6	1
32	RQ-PCR Provides a Superior Alternative to Immunohistochemistry In Defining Prognostic Groups In DLBCL, and Predicts Treatment Failure with CHOP-R. <i>Blood</i> , 2010, 116, 2484-2484.	0.6	8
33	Combining the interactome and deleterious SNP predictions to improve disease gene identification. <i>Human Mutation</i> , 2009, 30, 485-492.	1.1	18
34	A sequence–anchored genetic linkage map for the moss, <i>Physcomitrella patens</i>. <i>Plant Journal</i> , 2008, 56, 855-866.	2.8	42
35	Deleterious SNP prediction: be mindful of your training data!. <i>Bioinformatics</i> , 2007, 23, 664-672.	1.8	54
36	Predicting the effect of missense mutations on protein function: analysis with Bayesian networks. <i>BMC Bioinformatics</i> , 2006, 7, 405.	1.2	21