

# Amr H Sawalha

## List of Publications by Year in descending order

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151  
papers

8,909  
citations

34105  
52  
h-index

49909  
87  
g-index

165  
all docs

165  
docs citations

165  
times ranked

9885  
citing authors

#	ARTICLE	IF	CITATIONS
1	Changes in the pattern of DNA methylation associate with twin discordance in systemic lupus erythematosus. <i>Genome Research</i> , 2010, 20, 170-179.	5.5	569
2	COVID-19 and autoimmune diseases. <i>Current Opinion in Rheumatology</i> , 2021, 33, 155-162.	4.3	332
3	Genome-wide DNA methylation study suggests epigenetic accessibility and transcriptional poising of interferon-regulated genes in naïve CD4+ T cells from lupus patients. <i>Journal of Autoimmunity</i> , 2013, 43, 78-84.	6.5	294
4	Genome-wide DNA methylation patterns in CD4+ T cells from patients with systemic lupus erythematosus. <i>Epigenetics</i> , 2011, 6, 593-601.	2.7	224
5	Epigenetic dysregulation of ACE2 and interferon-regulated genes might suggest increased COVID-19 susceptibility and severity in lupus patients. <i>Clinical Immunology</i> , 2020, 215, 108410.	3.2	217
6	Impaired DNA methylation and its mechanisms in CD4+T cells of systemic lupus erythematosus. <i>Journal of Autoimmunity</i> , 2013, 41, 92-99.	6.5	190
7	COVID-19: A review of therapeutic strategies and vaccine candidates. <i>Clinical Immunology</i> , 2021, 222, 108634.	3.2	180
8	DNA methylation and mRNA and microRNA expression of SLE CD4+ T cells correlate with disease phenotype. <i>Journal of Autoimmunity</i> , 2014, 54, 127-136.	6.5	172
9	IFI44L promoter methylation as a blood biomarker for systemic lupus erythematosus. <i>Annals of the Rheumatic Diseases</i> , 2016, 75, 1998-2006.	0.9	167
10	Impaired T Cell Protein Kinase C $\gamma$ Activation Decreases ERK Pathway Signaling in Idiopathic and Hydralazine-Induced Lupus. <i>Journal of Immunology</i> , 2007, 179, 5553-5563.	0.8	163
11	Epigenome profiling reveals significant DNA demethylation of interferon signature genes in lupus neutrophils. <i>Journal of Autoimmunity</i> , 2015, 58, 59-66.	6.5	161
12	Early disease onset is predicted by a higher genetic risk for lupus and is associated with a more severe phenotype in lupus patients. <i>Annals of the Rheumatic Diseases</i> , 2011, 70, 151-156.	0.9	155
13	Genome-wide DNA methylation analysis in dermal fibroblasts from patients with diffuse and limited systemic sclerosis reveals common and subset-specific DNA methylation aberrancies. <i>Annals of the Rheumatic Diseases</i> , 2015, 74, 1612-1620.	0.9	148
14	Genome-Wide DNA Methylation Patterns in Naive CD4+ T Cells From Patients With Primary Sjögren's Syndrome. <i>Arthritis and Rheumatology</i> , 2014, 66, 731-739.	5.6	147
15	Identification of Multiple Genetic Susceptibility Loci in Takayasu Arteritis. <i>American Journal of Human Genetics</i> , 2013, 93, 298-305.	6.2	143
16	Identification of multiple independent susceptibility loci in the HLA region in Behçet's disease. <i>Nature Genetics</i> , 2013, 45, 319-324.	21.4	130
17	Genome-Wide DNA Methylation Study Identifies Significant Epigenomic Changes in Osteoarthritic Cartilage. <i>Arthritis and Rheumatology</i> , 2014, 66, 2804-2815.	5.6	128
18	Autoimmunity and Klinefelter's syndrome: When men have two X chromosomes. <i>Journal of Autoimmunity</i> , 2009, 33, 31-34.	6.5	127

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19	Common Variants within MECP2 Confer Risk of Systemic Lupus Erythematosus. PLoS ONE, 2008, 3, e1727.	2.5	125
20	Identification of novel genetic susceptibility loci for Behçet's disease using a genome-wide association study. Arthritis Research and Therapy, 2009, 11, R66.	3.5	123
21	Phenotypic associations of genetic susceptibility loci in systemic lupus erythematosus. Annals of the Rheumatic Diseases, 2011, 70, 1752-1757.	0.9	110
22	Identification of novel genetic susceptibility loci in African American lupus patients in a candidate gene association study. Arthritis and Rheumatism, 2011, 63, 3493-3501.	6.7	109
23	Renal involvement in lupus is characterized by unique DNA methylation changes in naïve CD4+ T cells. Journal of Autoimmunity, 2015, 61, 29-35.	6.5	109
24	A polymorphism within <i>IL21R</i> confers risk for systemic lupus erythematosus. Arthritis and Rheumatism, 2009, 60, 2402-2407.	6.7	108
25	Monogenic Lupus: A Developing Paradigm of Disease. Frontiers in Immunology, 2018, 9, 2496.	4.8	105
26	Fine mapping of Xq28: both <i>MECP2</i> and <i>IRAK1</i> contribute to risk for systemic lupus erythematosus in multiple ancestral groups. Annals of the Rheumatic Diseases, 2013, 72, 437-444.	0.9	97
27	Drug-induced lupus erythematosus: an update on drugs and mechanisms. Current Opinion in Rheumatology, 2018, 30, 490-497.	4.3	96
28	T cell CD40LG gene expression and the production of IgG by autologous B cells in systemic lupus erythematosus. Clinical Immunology, 2009, 132, 362-370.	3.2	90
29	Epigenetic Reprogramming in Naive CD4+ T Cells Favoring T Cell Activation and Non-Th1 Effector T Cell Immune Response as an Early Event in Lupus Flares. Arthritis and Rheumatology, 2016, 68, 2200-2209.	5.6	88
30	Sequencing of 16S rRNA reveals a distinct salivary microbiome signature in Behçet's disease. Clinical Immunology, 2016, 169, 28-35.	3.2	88
31	Analysis of autosomal genes reveals gene-sex interactions and higher total genetic risk in men with systemic lupus erythematosus. Annals of the Rheumatic Diseases, 2012, 71, 694-699.	0.9	87
32	A genome-wide association study identifies nucleotide variants at SIGLEC5 and DEFA1A3 as risk loci for periodontitis. Human Molecular Genetics, 2017, 26, 2577-2588.	2.9	87
33	Epigenetic regulation and the pathogenesis of systemic lupus erythematosus. Translational Research, 2009, 153, 4-10.	5.0	83
34	DNA methylation patterns in naïve CD4+ T cells identify epigenetic susceptibility loci for malar rash and discoid rash in systemic lupus erythematosus. Lupus Science and Medicine, 2015, 2, e000101.	2.7	83
35	Variants within <i>MECP2</i> , a key transcription regulator, are associated with increased susceptibility to lupus and differential gene expression in patients with systemic lupus erythematosus. Arthritis and Rheumatism, 2009, 60, 1076-1084.	6.7	80
36	Unfolding the pathogenesis of scleroderma through genomics and epigenomics. Journal of Autoimmunity, 2017, 83, 73-94.	6.5	80

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37	Identification of Susceptibility Loci in <i>IL6</i> , <i>RPS9</i> , <i>LILRB3</i> , and an Intergenic Locus on Chromosome 21q22 in Takayasu Arteritis in a Genome-Wide Association Study. <i>Arthritis and Rheumatology</i> , 2015, 67, 1361-1368.	5.6	79
38	Inhibition of EZH2 prevents fibrosis and restores normal angiogenesis in scleroderma. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 3695-3702.	7.1	77
39	Epigenetics and T-cell immunity. <i>Autoimmunity</i> , 2008, 41, 245-252.	2.6	75
40	Activated signature of antiphospholipid syndrome neutrophils reveals potential therapeutic target. <i>JCI Insight</i> , 2017, 2, .	5.0	75
41	Environmental exposure, estrogen and two X chromosomes are required for disease development in an epigenetic model of lupus. <i>Journal of Autoimmunity</i> , 2012, 38, 1135-1143.	6.5	74
42	Diet Influences Expression of Autoimmune-Associated Genes and Disease Severity by Epigenetic Mechanisms in a Transgenic Mouse Model of Lupus. <i>Arthritis and Rheumatism</i> , 2013, 65, 1872-1881.	6.7	74
43	Antinuclear autoantibodies in systemic lupus erythematosus. <i>Current Opinion in Rheumatology</i> , 2004, 16, 534-540.	4.3	73
44	Epigenome-Wide Scan Identifies a Treatment-Responsive Pattern of Altered DNA Methylation Among Cytoskeletal Remodeling Genes in Monocytes and CD4+ T Cells From Patients With Behçet's Disease. <i>Arthritis and Rheumatology</i> , 2014, 66, 1648-1658.	5.6	72
45	Sex-specific differences in the relationship between genetic susceptibility, T cell DNA demethylation and lupus flare severity. <i>Journal of Autoimmunity</i> , 2012, 38, 1216-1222.	6.5	71
46	Genetically determined Amerindian ancestry correlates with increased frequency of risk alleles for systemic lupus erythematosus. <i>Arthritis and Rheumatism</i> , 2010, 62, 3722-3729.	6.7	70
47	Defective DNA methylation and CD70 overexpression in CD4+ T cells in MRL/lpr lupus-prone mice. <i>European Journal of Immunology</i> , 2007, 37, 1407-1413.	2.9	64
48	Histone Deacetylase 5 Is Overexpressed in Scleroderma Endothelial Cells and Impairs Angiogenesis via Repression of Proangiogenic Factors. <i>Arthritis and Rheumatology</i> , 2016, 68, 2975-2985.	5.6	62
49	Variation in the <i>ICAM1</i> - <i>ICAM4</i> - <i>ICAM5</i> locus is associated with systemic lupus erythematosus susceptibility in multiple ancestries. <i>Annals of the Rheumatic Diseases</i> , 2012, 71, 1809-1814.	0.9	60
50	Autoimmune disease in the epigenetic era: how has epigenetics changed our understanding of disease and how can we expect the field to evolve?. <i>Expert Review of Clinical Immunology</i> , 2015, 11, 45-58.	3.0	59
51	Systemic lupus erythematosus complicated by diffuse alveolar haemorrhage: risk factors, therapy and survival. <i>Lupus Science and Medicine</i> , 2015, 2, e000117.	2.7	59
52	Epigenetics in systemic lupus erythematosus: leading the way for specific therapeutic agents. <i>International Journal of Clinical Rheumatology</i> , 2011, 6, 423-438.	0.3	57
53	Functional characterization of the MECP2/IRAK1 lupus risk haplotype in human T cells and a human MECP2 transgenic mouse. <i>Journal of Autoimmunity</i> , 2013, 41, 168-174.	6.5	55
54	DNA methylation analysis of the temporal artery microenvironment in giant cell arteritis. <i>Annals of the Rheumatic Diseases</i> , 2016, 75, 1196-1202.	0.9	55

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55	Genome-wide profiling identifies associations between lupus nephritis and differential methylation of genes regulating tissue hypoxia and type 1 interferon responses. <i>Lupus Science and Medicine</i> , 2016, 3, e000183.	2.7	54
56	Epigenetic Variability in Systemic Lupus Erythematosus: What We Learned from Genome-Wide DNA Methylation Studies. <i>Current Rheumatology Reports</i> , 2017, 19, 32.	4.7	54
57	Evidence for gene–gene epistatic interactions among susceptibility loci for systemic lupus erythematosus. <i>Arthritis and Rheumatism</i> , 2012, 64, 485-492.	6.7	53
58	Parent-of-origin differences in DNA methylation of X chromosome genes in T lymphocytes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 26779-26787.	7.1	53
59	Analysis of the common genetic component of large-vessel vasculitides through a meta-immunochip strategy. <i>Scientific Reports</i> , 2017, 7, 43953.	3.3	52
60	Sex chromosome contributions to sex differences in multiple sclerosis susceptibility and progression. <i>Multiple Sclerosis Journal</i> , 2018, 24, 22-31.	3.0	52
61	Uric Acid Directly Promotes Human T-Cell Activation. <i>American Journal of the Medical Sciences</i> , 2009, 337, 23-27.	1.1	51
62	Trans-Ancestral Studies Fine Map the SLE-Susceptibility Locus TNFSF4. <i>PLoS Genetics</i> , 2013, 9, e1003554.	3.5	50
63	Genome-Wide DNA Methylation Study Identifies Significant Epigenomic Changes in Osteoarthritic Subchondral Bone and Similarity to Overlying Cartilage. <i>Arthritis and Rheumatology</i> , 2016, 68, 1403-1414.	5.6	50
64	Fine-mapping and transethnic genotyping establish IL2/IL21 genetic association with lupus and localize this genetic effect to IL21. <i>Arthritis and Rheumatism</i> , 2011, 63, 1689-1697.	6.7	49
65	Ethnicity-specific epigenetic variation in naïve CD4 <sup>+</sup> T cells and the susceptibility to autoimmunity. <i>Epigenetics and Chromatin</i> , 2015, 8, 49.	3.9	49
66	Inhibition of EZH2 Ameliorates Lupus-Like Disease in MRL <sup>lpr</sup> Mice. <i>Arthritis and Rheumatology</i> , 2019, 71, 1681-1690.	5.6	48
67	Clinical value of DNA methylation markers in autoimmune rheumatic diseases. <i>Nature Reviews Rheumatology</i> , 2020, 16, 514-524.	8.0	48
68	T cell PKC $\delta$ kinase inactivation induces lupus-like autoimmunity in mice. <i>Clinical Immunology</i> , 2015, 158, 193-203.	3.2	47
69	Age-associated DNA methylation changes in naïve CD4 <sup>+</sup> T cells suggest an evolving autoimmune epigenotype in aging T cells. <i>Epigenomics</i> , 2017, 9, 429-445.	2.1	47
70	Association between systemic lupus erythematosus and <i>Helicobacter pylori</i> seronegativity. <i>Journal of Rheumatology</i> , 2004, 31, 1546-50.	2.0	47
71	Shared epitope–aryl hydrocarbon receptor crosstalk underlies the mechanism of gene–environment interaction in autoimmune arthritis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 4755-4760.	7.1	45
72	EZH2 Modulates the DNA Methylome and Controls T Cell Adhesion Through Junctional Adhesion Molecule A in Lupus Patients. <i>Arthritis and Rheumatology</i> , 2018, 70, 98-108.	5.6	44

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73	The genetics of Takayasu arteritis. <i>Presse Medicale</i> , 2017, 46, e179-e187.	1.9	42
74	Dehydroepiandrosterone in systemic lupus erythematosus. <i>Current Rheumatology Reports</i> , 2008, 10, 286-291.	4.7	40
75	Genetic variability in the expression of the SARS-CoV-2 host cell entry factors across populations. <i>Genes and Immunity</i> , 2020, 21, 269-272.	4.1	40
76	A putative functional variant within the <i>UBAC2</i> gene is associated with increased risk of Behçet's disease. <i>Arthritis and Rheumatism</i> , 2011, 63, 3607-3612.	6.7	39
77	Genetic heterogeneity within the HLA region in three distinct clinical subgroups of myasthenia gravis. <i>Clinical Immunology</i> , 2016, 166-167, 81-88.	3.2	38
78	Methyl-CpG-binding protein 2 mediates antifibrotic effects in scleroderma fibroblasts. <i>Annals of the Rheumatic Diseases</i> , 2018, 77, annrheumdis-2018-213022.	0.9	36
79	A longitudinal and transancestral analysis of DNA methylation patterns and disease activity in lupus patients. <i>JCI Insight</i> , 2020, 5, .	5.0	36
80	The human microbiome in rheumatic autoimmune diseases: A comprehensive review. <i>Clinical Immunology</i> , 2016, 170, 70-79.	3.2	35
81	The role of epigenetic variation in the pathogenesis of systemic lupus erythematosus. <i>Arthritis Research and Therapy</i> , 2011, 13, 245.	3.5	34
82	Epigenetics and Vasculitis: a Comprehensive Review. <i>Clinical Reviews in Allergy and Immunology</i> , 2016, 50, 357-366.	6.5	33
83	Caffeine inhibits STAT1 signaling and downregulates inflammatory pathways involved in autoimmunity. <i>Clinical Immunology</i> , 2018, 192, 68-77.	3.2	33
84	Deoxyribonucleic Acid Methylation in Systemic Lupus Erythematosus: Implications for Future Clinical Practice. <i>Frontiers in Immunology</i> , 2018, 9, 875.	4.8	32
85	Genetic association between methyl-CpG binding protein 2 (MECP2) and primary Sjogren's syndrome. <i>Annals of the Rheumatic Diseases</i> , 2010, 69, 1731-1732.	0.9	31
86	Epigenetics in the treatment of systemic lupus erythematosus: Potential clinical application. <i>Clinical Immunology</i> , 2014, 155, 79-90.	3.2	31
87	Aberrant DNA methylation in skin diseases. <i>Journal of Dermatological Science</i> , 2009, 54, 143-149.	1.9	29
88	An update on the role of epigenetics in systemic vasculitis. <i>Current Opinion in Rheumatology</i> , 2018, 30, 4-15.	4.3	29
89	Hypomethylation of <i>STAT1</i> and <i>HLA-DRB1</i> is associated with type-I interferon-dependent <i>HLA-DRB1</i> expression in lupus CD8+ T cells. <i>Annals of the Rheumatic Diseases</i> , 2019, 78, 519-528.	0.9	29
90	Clinical Treatment Options in Scleroderma: Recommendations and Comprehensive Review. <i>Clinical Reviews in Allergy and Immunology</i> , 2022, 62, 273-291.	6.5	28

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91	Coronavirus Disease-2019: Implication for the care and management of patients with systemic lupus erythematosus. <i>European Journal of Rheumatology</i> , 2020, 7, S117-S120.	0.6	28
92	Cross-phenotype analysis of ImmunoChip data identifies <i>KDM4C</i> as a relevant locus for the development of systemic vasculitis. <i>Annals of the Rheumatic Diseases</i> , 2018, 77, 589-595.	0.9	27
93	Guideline for the diagnosis, treatment and long-term management of cutaneous lupus erythematosus. <i>Journal of Autoimmunity</i> , 2021, 123, 102707.	6.5	27
94	The genetics of primary Sjögren's syndrome. <i>Current Rheumatology Reports</i> , 2003, 5, 324-332.	4.7	26
95	Epigenetics in the pathogenesis of systemic lupus erythematosus. <i>Current Opinion in Rheumatology</i> , 2013, 25, 569-576.	4.3	26
96	Genome-wide DNA methylation analysis in primary antiphospholipid syndrome neutrophils. <i>Clinical Immunology</i> , 2018, 196, 110-116.	3.2	26
97	Identification of susceptibility loci for Takayasu arteritis through a large multi-ancestral genome-wide association study. <i>American Journal of Human Genetics</i> , 2021, 108, 84-99.	6.2	26
98	The DNA methylation signature of human TCR $\beta$ <sup>hi</sup> CD4 <sup>hi</sup> CD8 <sup>lo</sup> double negative T cells reveals CG demethylation and a unique epigenetic architecture permissive to a broad stimulatory immune response. <i>Clinical Immunology</i> , 2015, 156, 19-27.	3.2	25
99	Genome-wide DNA methylation analysis in ankylosing spondylitis identifies HLA-B*27 dependent and independent DNA methylation changes in whole blood. <i>Journal of Autoimmunity</i> , 2019, 102, 126-132.	6.5	24
100	Management of Behçet's disease. <i>Current Opinion in Rheumatology</i> , 2018, 30, 238-242.	4.3	23
101	CD4 <sup>+</sup> CD28 <sup>+</sup> KIR <sup>+</sup> CD11a <sup>hi</sup> T cells correlate with disease activity and are characterized by a pro-inflammatory epigenetic and transcriptional profile in lupus patients. <i>Journal of Autoimmunity</i> , 2018, 86, 19-28.	6.5	21
102	Genetic Association of a Gain-of-Function <i>IFNGR1</i> Polymorphism and the Intergenic Region <i>LNCAROD/DKK1</i> With Behçet's Disease. <i>Arthritis and Rheumatology</i> , 2021, 73, 1244-1252.	5.6	21
103	DNA Methylation in the Pathogenesis of Systemic Lupus Erythematosus. <i>Current Pharmacogenomics and Personalized Medicine: the International Journal for Expert Reviews in Pharmacogenomics</i> , 2005, 3, 73-78.	0.3	20
104	Novel Transcriptional Activity and Extensive Allelic Imbalance in the Human MHC Region. <i>Journal of Immunology</i> , 2018, 200, 1496-1503.	0.8	20
105	Takayasu arteritis risk locus in <i>IL6</i> represses the anti-inflammatory gene <i>GPNUMB</i> through chromatin looping and recruiting MEF2 <sup>hi</sup> HDAC complex. <i>Annals of the Rheumatic Diseases</i> , 2019, 78, 1388-1397.	0.9	20
106	An update on belimumab for the treatment of lupus. <i>Biologics: Targets and Therapy</i> , 2011, 5, 33.	3.2	18
107	Genetics of Antiphospholipid Syndrome. <i>Current Rheumatology Reports</i> , 2019, 21, 65.	4.7	18
108	Glycoprotein nonmetastatic melanoma protein B: A key mediator and an emerging therapeutic target in autoimmune diseases. <i>FASEB Journal</i> , 2020, 34, 8810-8823.	0.5	18



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109	SARS-CoV-2 and Systemic Lupus Erythematosus. <i>Current Rheumatology Reports</i> , 2021, 23, 8.	4.7	18
110	Genetics of Behçet's Disease: Functional Genetic Analysis and Estimating Disease Heritability. <i>Frontiers in Medicine</i> , 2021, 8, 625710.	2.6	18
111	Systemic lupus erythematosus as a genetic disease. <i>Clinical Immunology</i> , 2022, 236, 108953.	3.2	18
112	IL18 Polymorphism Is Associated with Behçet's Disease But Not Lupus in Patients from Turkey. <i>Journal of Rheumatology</i> , 2011, 38, 962-963.	2.0	17
113	Increased Expression of EZH2 Is Mediated by Higher Glycolysis and mTORC1 Activation in Lupus CD4+ T Cells. <i>Immunometabolism</i> , 2020, 2, .	1.6	17
114	Identification of Cysteine-Rich Angiogenic Inducer 61 as a Potential Antifibrotic and Proangiogenic Mediator in Scleroderma. <i>Arthritis and Rheumatology</i> , 2019, 71, 1350-1359.	5.6	16
115	Murine Models of Lupus Induced by Hypomethylated T Cells (DNA Hypomethylation and Lupus). <i>Methods in Molecular Biology</i> , 2012, 900, 169-180.	0.9	16
116	GFP Affects Human T Cell Activation and Cytokine Production following In Vitro Stimulation. <i>PLoS ONE</i> , 2013, 8, e50068.	2.5	15
117	Histone H2AX phosphorylation as a measure of DNA double-strand breaks and a marker of environmental stress and disease activity in lupus. <i>Lupus Science and Medicine</i> , 2016, 3, e000148.	2.7	15
118	Panniculitis. <i>Journal of Clinical Rheumatology</i> , 2003, 9, 259-262.	0.9	14
119	Horizons in Sjögren's Syndrome Genetics. <i>Clinical Reviews in Allergy and Immunology</i> , 2007, 32, 201-209.	6.5	14
120	Behçet's disease in the United States: A single center descriptive and comparative study. <i>European Journal of Rheumatology</i> , 2017, 4, 239-244.	0.6	13
121	HLA-DRB1 allelic epitopes that associate with autoimmune disease risk or protection activate reciprocal macrophage polarization. <i>Scientific Reports</i> , 2021, 11, 2599.	3.3	13
122	Noodling and <i>Mycobacterium marinum</i> infection mimicking seronegative rheumatoid arthritis complicated by anti-tumor necrosis factor $\alpha$ therapy. <i>Arthritis Care and Research</i> , 2011, 63, 160-164.	3.4	12
123	Epigenomic functional characterization of genetic susceptibility variants in systemic vasculitis. <i>Journal of Autoimmunity</i> , 2016, 67, 76-81.	6.5	12
124	Inhibition of bromodomain extraterminal histone readers alleviates skin fibrosis in experimental models of scleroderma. <i>JCI Insight</i> , 2022, 7, .	5.0	11
125	Patients with lupus are not protected from COVID-19. <i>Annals of the Rheumatic Diseases</i> , 2021, 80, e21-e21.	0.9	10
126	Genome-Wide Reduction in Chromatin Accessibility and Unique Transcription Factor Footprints in Endothelial Cells and Fibroblasts in Scleroderma Skin. <i>Arthritis and Rheumatology</i> , 2021, 73, 1501-1513.	5.6	10



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127	Whole exome sequencing identifies rare protein-coding variants in Behçet's disease. Arthritis and Rheumatology, 2015, 68, n/a-n/a.	5.6	9
128	Clinical Images: Black Esophagus in Antiphospholipid Syndrome. Arthritis and Rheumatology, 2017, 69, 1460-1460.	5.6	8
129	Hydroxychloroquine-induced Hyperpigmentation of the Skin. Journal of Rheumatology, 2015, 42, 135-136.	2.0	7
130	Editorial: The Innate and Adaptive Immune Response Are Both Involved in Drug-Induced Autoimmunity. Arthritis and Rheumatology, 2018, 70, 330-333.	5.6	7
131	The Role of Oxidative Stress in Epigenetic Changes Underlying Autoimmunity. Antioxidants and Redox Signaling, 2022, 36, 423-440.	5.4	7
132	Analysis of Systemic Sclerosis-associated Genes in a Turkish Population. Journal of Rheumatology, 2016, 43, 1376-1379.	2.0	5
133	Structural variation of centromeric endogenous retroviruses in human populations and their impact on cutaneous T-cell lymphoma, SÅ©zary syndrome, and HIV infection. BMC Medical Genomics, 2019, 12, 58.	1.5	5
134	Functional Characterization of Glycoprotein Nonmetastatic Melanoma Protein B in Scleroderma Fibrosis. Frontiers in Immunology, 2022, 13, 814533.	4.8	5
135	Hypomethylation of miR-17-92 cluster in lupus T cells and no significant role for genetic factors in the lupus-associated DNA methylation signature. Annals of the Rheumatic Diseases, 2022, 81, 1428-1437.	0.9	5
136	Evaluating the Perception Among Rheumatologists of Maintenance of Board Certification in the US. Arthritis Care and Research, 2019, 71, 337-342.	3.4	4
137	DNA methylation patterns in juvenile systemic sclerosis and localized scleroderma. Clinical Immunology, 2021, 228, 108756.	3.2	4
138	Clinical subgroup clustering analysis in a systemic lupus erythematosus cohort from Western Pennsylvania. European Journal of Rheumatology, 2022, 9, 3-7.	0.6	4
139	Post-GWAS functional analysis identifies CUX1 as a regulator of p16INK4a and cellular senescence. Nature Aging, 2022, 2, 140-154.	11.6	4
140	Neutrophils in Systemic Lupus Erythematosus. , 2016, , 127-130.		3
141	BCL-6 and EZH2 cooperate to epigenetically repress anti-inflammatory miR-142-3p/5p in lupus CD4+T cells. Cellular and Molecular Immunology, 2021, 18, 504-505.	10.5	3
142	Step by Step. New England Journal of Medicine, 2003, 349, 2253-2257.	27.0	2
143	Still Consider the Source. New England Journal of Medicine, 2005, 353, 1503-1507.	27.0	2
144	Interview with Amr H Sawalha: epigenetics and autoimmunity. Epigenomics, 2017, 9, 379-382.	2.1	2

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145	Detection of immunoglobulin response to COVID-19 vaccination using a novel rapid fingerstick assay. Clinical Immunology, 2022, 235, 108791.	3.2	2
146	Clinical immunology: A special issue on epigenetics. Clinical Immunology, 2018, 196, 1-2.	3.2	1
147	Epigenetics of Rheumatic Diseases. , 2017, , 344-354.		0
148	Takayasu Arteritis. Rare Diseases of the Immune System, 2019, , 151-162.	0.1	0
149	Reply. Arthritis and Rheumatology, 2020, 72, 373-374.	5.6	0
150	Medical Licensure: It Is Time to Eliminate Practice Borders Within the United States. American Journal of Medicine, 2020, 133, 1120-1121.	1.5	0
151	Neutrophils in systemic lupus erythematosus. , 2021, , 139-142.		0