

Amr H Sawalha

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

148
papers

6,477
citations

47
h-index

75
g-index

165
ext. papers

7,970
ext. citations

7.9
avg, IF

6.54
L-index

#	Paper	IF	Citations
148	Systemic lupus erythematosus as a genetic disease.. <i>Clinical Immunology</i> , 2022 , 236, 108953	9	1
147	Functional Characterization of Glycoprotein Nonmetastatic Melanoma Protein B in Scleroderma Fibrosis.. <i>Frontiers in Immunology</i> , 2022 , 13, 814533	8.4	0
146	Post-GWAS functional analysis identifies CUX1 as a regulator of p16INK4a and cellular senescence. <i>Nature Aging</i> , 2022 , 2, 140-154		1
145	COVID-19 and autoimmune diseases. <i>Current Opinion in Rheumatology</i> , 2021 , 33, 155-162	5.3	119
144	Genetic Association of a Gain-of-Function IFNGR1 Polymorphism and the Intergenic Region LNCAROD/DKK1 With Behçet Disease. <i>Arthritis and Rheumatology</i> , 2021 , 73, 1244-1252	9.5	6
143	Detection of immunoglobulin response to COVID-19 vaccination using a novel rapid fingerstick assay. <i>Clinical Immunology</i> , 2021 , 108791	9	2
142	Neutrophils in systemic lupus erythematosus 2021 , 139-142		
141	Patients with lupus are not protected from COVID-19. <i>Annals of the Rheumatic Diseases</i> , 2021 , 80, e21	2.4	8
140	COVID-19: A review of therapeutic strategies and vaccine candidates. <i>Clinical Immunology</i> , 2021 , 222, 108634	9	109
139	BCL-6 and EZH2 cooperate to epigenetically repress anti-inflammatory miR-142-3p/5p in lupus CD4+T cells. <i>Cellular and Molecular Immunology</i> , 2021 , 18, 504-505	15.4	1
138	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	11	8
137	Clinical Treatment Options in Scleroderma: Recommendations and Comprehensive Review. <i>Clinical Reviews in Allergy and Immunology</i> , 2021 , 1	12.3	9
136	SARS-CoV-2 and Systemic Lupus Erythematosus. <i>Current Rheumatology Reports</i> , 2021 , 23, 8	4.9	6
135	Genetics of Behçet Disease: Functional Genetic Analysis and Estimating Disease Heritability. <i>Frontiers in Medicine</i> , 2021 , 8, 625710	4.9	8
134	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	9.5	3
133	DNA methylation patterns in juvenile systemic sclerosis and localized scleroderma. <i>Clinical Immunology</i> , 2021 , 228, 108756	9	2
132	Guideline for the diagnosis, treatment and long-term management of cutaneous lupus erythematosus. <i>Journal of Autoimmunity</i> , 2021 , 123, 102707	15.5	2

131	HLA-DRB1 allelic epitopes that associate with autoimmune disease risk or protection activate reciprocal macrophage polarization. <i>Scientific Reports</i> , 2021 , 11, 2599	4.9	1
130	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	9	158
129	A longitudinal and transancestral analysis of DNA methylation patterns and disease activity in lupus patients. <i>JCI Insight</i> , 2020 , 5,	9.9	10
128	Increased Expression of EZH2 Is Mediated by Higher Glycolysis and mTORC1 Activation in Lupus CD4 T Cells. <i>Immunometabolism</i> , 2020 , 2,	4.1	7
127	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	1.7	22
126	Epigenetic dysregulation of ACE2 and interferon-regulated genes might suggest increased COVID-19 susceptibility and severity in lupus patients 2020 ,		8
125	Reply. <i>Arthritis and Rheumatology</i> , 2020 , 72, 373-374	9.5	
124	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	4.4	29
123	Clinical value of DNA methylation markers in autoimmune rheumatic diseases. <i>Nature Reviews Rheumatology</i> , 2020 , 16, 514-524	8.1	16
122	Glycoprotein nonmetastatic melanoma protein B: A key mediator and an emerging therapeutic target in autoimmune diseases. <i>FASEB Journal</i> , 2020 , 34, 8810-8823	0.9	8
121	Hypomethylation of and is associated with type-I interferon-dependent expression in lupus CD8+ T cells. <i>Annals of the Rheumatic Diseases</i> , 2019 , 78, 519-528	2.4	15
120	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	15.5	14
119	Inhibition of EZH2 Ameliorates Lupus-Like Disease in MRL/lpr Mice. <i>Arthritis and Rheumatology</i> , 2019 , 71, 1681-1690	9.5	22
118	Structural variation of centromeric endogenous retroviruses in human populations and their impact on cutaneous T-cell lymphoma, Sjögren syndrome, and HIV infection. <i>BMC Medical Genomics</i> , 2019 , 12, 58	3.7	4
117	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	9.5	10
116	Evaluating the Perception Among Rheumatologists of Maintenance of Board Certification in the US. <i>Arthritis Care and Research</i> , 2019 , 71, 337-342	4.7	1
115	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	11.5	44
114	Takayasu Arteritis. <i>Rare Diseases of the Immune System</i> , 2019 , 151-162	0.2	

113	Takayasu arteritis risk locus in represses the anti-inflammatory gene through chromatin looping and recruiting MEF2-HDAC complex. <i>Annals of the Rheumatic Diseases</i> , 2019 , 78, 1388-1397	2.4	11
112	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 ,	11.5	30
111	Genetics of Antiphospholipid Syndrome. <i>Current Rheumatology Reports</i> , 2019 , 21, 65	4.9	8
110	Caffeine inhibits STAT1 signaling and downregulates inflammatory pathways involved in autoimmunity. <i>Clinical Immunology</i> , 2018 , 192, 68-77	9	21
109	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	11.5	26
108	Management of Behçet's disease. <i>Current Opinion in Rheumatology</i> , 2018 , 30, 238-242	5.3	12
107	Cross-phenotype analysis of Immunochip data identifies as a relevant for the development of systemic vasculitis. <i>Annals of the Rheumatic Diseases</i> , 2018 , 77, 589-595	2.4	16
106	Novel Transcriptional Activity and Extensive Allelic Imbalance in the Human MHC Region. <i>Journal of Immunology</i> , 2018 , 200, 1496-1503	5.3	13
105	Sex chromosome contributions to sex differences in multiple sclerosis susceptibility and progression. <i>Multiple Sclerosis Journal</i> , 2018 , 24, 22-31	5	33
104	CD4+CD28+KIR+CD11a 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	15.5	17
103	An update on the role of epigenetics in systemic vasculitis. <i>Current Opinion in Rheumatology</i> , 2018 , 30, 4-15	5.3	20
102	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	9.5	26
101	Deoxyribonucleic Acid Methylation in Systemic Lupus Erythematosus: Implications for Future Clinical Practice. <i>Frontiers in Immunology</i> , 2018 , 9, 875	8.4	24
100	Drug-induced lupus erythematosus: an update on drugs and mechanisms. <i>Current Opinion in Rheumatology</i> , 2018 , 30, 490-497	5.3	52
99	Genome-wide DNA methylation analysis in primary antiphospholipid syndrome neutrophils. <i>Clinical Immunology</i> , 2018 , 196, 110-116	9	17
98	Monogenic Lupus: A Developing Paradigm of Disease. <i>Frontiers in Immunology</i> , 2018 , 9, 2496	8.4	54
97	Methyl-CpG-binding protein 2 mediates antifibrotic effects in scleroderma fibroblasts. <i>Annals of the Rheumatic Diseases</i> , 2018 , 77, 1208-1218	2.4	25
96	Analysis of the common genetic component of large-vessel vasculitides through a meta-ImmunoChip strategy. <i>Scientific Reports</i> , 2017 , 7, 43953	4.9	34

95	Epigenetic Variability in Systemic Lupus Erythematosus: What We Learned from Genome-Wide DNA Methylation Studies. <i>Current Rheumatology Reports</i> , 2017 , 19, 32	4.9	33
94	A genome-wide association study identifies nucleotide variants at SIGLEC5 and DEFA1A3 as risk loci for periodontitis. <i>Human Molecular Genetics</i> , 2017 , 26, 2577-2588	5.6	55
93	Unfolding the pathogenesis of scleroderma through genomics and epigenomics. <i>Journal of Autoimmunity</i> , 2017 , 83, 73-94	15.5	59
92	Interview with Amr H Sawalha: epigenetics and autoimmunity. <i>Epigenomics</i> , 2017 , 9, 379-382	4.4	2
91	Age-associated DNA methylation changes in naive CD4 T cells suggest an evolving autoimmune epigenotype in aging T cells. <i>Epigenomics</i> , 2017 , 9, 429-445	4.4	30
90	Clinical Images: Black Esophagus in Antiphospholipid Syndrome. <i>Arthritis and Rheumatology</i> , 2017 , 69, 1460	9.5	6
89	Behçet disease in the United States: A single center descriptive and comparative study. <i>European Journal of Rheumatology</i> , 2017 , 4, 239-244	1.7	11
88	The genetics of Takayasu arteritis. <i>Presse Medicale</i> , 2017 , 46, e179-e187	2.2	30
87	Epigenetics of Rheumatic Diseases 2017 , 344-354		
86	Activated signature of antiphospholipid syndrome neutrophils reveals potential therapeutic target. <i>JCI Insight</i> , 2017 , 2,	9.9	43
85	Epigenomic functional characterization of genetic susceptibility variants in systemic vasculitis. <i>Journal of Autoimmunity</i> , 2016 , 67, 76-81	15.5	11
84	Epigenetics and Vasculitis: a Comprehensive Review. <i>Clinical Reviews in Allergy and Immunology</i> , 2016 , 50, 357-66	12.3	27
83	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	4.6	10
82	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. <i>Arthritis and Rheumatology</i> , 2016 , 68, 2200-9	9.5	63
81	Sequencing of 16S rRNA reveals a distinct salivary microbiome signature in Behçet disease. <i>Clinical Immunology</i> , 2016 , 169, 28-35	9	58
80	DNA methylation analysis of the temporal artery microenvironment in giant cell arteritis. <i>Annals of the Rheumatic Diseases</i> , 2016 , 75, 1196-202	2.4	37
79	IFI44L promoter methylation as a blood biomarker for systemic lupus erythematosus. <i>Annals of the Rheumatic Diseases</i> , 2016 , 75, 1998-2006	2.4	110
78	Whole Exome Sequencing Identifies Rare Protein-Coding Variants in Behçet Disease. <i>Arthritis and Rheumatology</i> , 2016 , 68, 1272-80	9.5	5

77	Neutrophils in Systemic Lupus Erythematosus 2016 , 127-130		2
76	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, 1403-14	9.5	32
75	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	4.6	30
74	Genetic heterogeneity within the HLA region in three distinct clinical subgroups of myasthenia gravis. <i>Clinical Immunology</i> , 2016 , 166-167, 81-8	9	30
73	Analysis of Systemic Sclerosis-associated Genes in a Turkish Population. <i>Journal of Rheumatology</i> , 2016 , 43, 1376-9	4.1	4
72	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	9.5	46
71	The human microbiome in rheumatic autoimmune diseases: A comprehensive review. <i>Clinical Immunology</i> , 2016 , 170, 70-9	9	27
70	T cell PKC ζ kinase inactivation induces lupus-like autoimmunity in mice. <i>Clinical Immunology</i> , 2015 , 158, 193-203	9	35
69	DNA methylation patterns in naïve CD4+ T cells identify epigenetic susceptibility loci for malar rash and discoid rash in systemic lupus erythematosus. <i>Lupus Science and Medicine</i> , 2015 , 2, e000101	4.6	65
68	Systemic lupus erythematosus complicated by diffuse alveolar haemorrhage: risk factors, therapy and survival. <i>Lupus Science and Medicine</i> , 2015 , 2, e000117	4.6	40
67	Renal involvement in lupus is characterized by unique DNA methylation changes in naïve CD4+ T cells. <i>Journal of Autoimmunity</i> , 2015 , 61, 29-35	15.5	82
66	The DNA methylation signature of human TCR α CD4-CD8- 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	9	17
65	Ethnicity-specific epigenetic variation in naïve CD4+ T cells and the susceptibility to autoimmunity. <i>Epigenetics and Chromatin</i> , 2015 , 8, 49	5.8	40
64	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, 1612-20	2.4	115
63	Hydroxychloroquine-induced hyperpigmentation of the skin. <i>Journal of Rheumatology</i> , 2015 , 42, 135-6	4.1	6
62	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 ¹	5.1	48
61	Epigenome profiling reveals significant DNA demethylation of interferon signature genes in lupus neutrophils. <i>Journal of Autoimmunity</i> , 2015 , 58, 59-66	15.5	112
60	Identification of Susceptibility Loci in IL6, RPS9/LILRB3, and an Intergenic Locus on Chromosome 21q22 in Takayasu Arteritis in a Genome-Wide Association Study. <i>Arthritis and Rheumatology</i> , 2015 , 67, 1361-8	9.5	60

59	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, 1648-58	9.5	56
58	Epigenetics in the treatment of systemic lupus erythematosus: potential clinical application. <i>Clinical Immunology</i> , 2014 , 155, 79-90	9	27
57	Genome-wide DNA methylation patterns in naive CD4+ T cells from patients with primary Sjögren's syndrome. <i>Arthritis and Rheumatology</i> , 2014 , 66, 731-9	9.5	119
56	DNA methylation and mRNA and microRNA expression of SLE CD4+ T cells correlate with disease phenotype. <i>Journal of Autoimmunity</i> , 2014 , 54, 127-36	15.5	128
55	Genome-wide DNA methylation study identifies significant epigenomic changes in osteoarthritic cartilage. <i>Arthritis and Rheumatology</i> , 2014 , 66, 2804-15	9.5	112
54	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, 168-74	15.5	41
53	Identification of multiple genetic susceptibility loci in Takayasu arteritis. <i>American Journal of Human Genetics</i> , 2013 , 93, 298-305	11	115
52	Identification of multiple independent susceptibility loci in the HLA region in Behçet's disease. <i>Nature Genetics</i> , 2013 , 45, 319-24	36.3	108
51	Impaired DNA methylation and its mechanisms in CD4(+)T cells of systemic lupus erythematosus. <i>Journal of Autoimmunity</i> , 2013 , 41, 92-9	15.5	142
50	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, 1872-81		65
49	Genome-wide DNA methylation study suggests epigenetic accessibility and transcriptional poising of interferon-regulated genes in naive CD4+ T cells from lupus patients. <i>Journal of Autoimmunity</i> , 2013 , 43, 78-84	15.5	224
48	Trans-ancestral studies fine map the SLE-susceptibility locus TNFSF4. <i>PLoS Genetics</i> , 2013 , 9, e1003554	6	41
47	Epigenetics in the pathogenesis of systemic lupus erythematosus. <i>Current Opinion in Rheumatology</i> , 2013 , 25, 569-76	5.3	24
46	Fine mapping of Xq28: both MECP2 and IRAK1 contribute to risk for systemic lupus erythematosus in multiple ancestral groups. <i>Annals of the Rheumatic Diseases</i> , 2013 , 72, 437-44	2.4	80
45	GFP affects human T cell activation and cytokine production following in vitro stimulation. <i>PLoS ONE</i> , 2013 , 8, e50068	3.7	9
44	Evidence for gene-gene epistatic interactions among susceptibility loci for systemic lupus erythematosus. <i>Arthritis and Rheumatism</i> , 2012 , 64, 485-92		47
43	Variation in the ICAM1-ICAM4-ICAM5 locus is associated with systemic lupus erythematosus susceptibility in multiple ancestries. <i>Annals of the Rheumatic Diseases</i> , 2012 , 71, 1809-14	2.4	51
42	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, J135-43	15.5	63

41	Sex-specific differences in the relationship between genetic susceptibility, T cell DNA demethylation and lupus flare severity. <i>Journal of Autoimmunity</i> , 2012 , 38, J216-22	15.5	58
40	Analysis of autosomal genes reveals gene-sex interactions and higher total genetic risk in men with systemic lupus erythematosus. <i>Annals of the Rheumatic Diseases</i> , 2012 , 71, 694-9	2.4	63
39	Murine models of lupus induced by hypomethylated T cells (DNA hypomethylation and lupus) <i>Methods in Molecular Biology</i> , 2012 , 900, 169-80	1.4	16
38	Epigenetics in systemic lupus erythematosus: leading the way for specific therapeutic agents. <i>International Journal of Clinical Rheumatology</i> , 2011 , 6, 423-439	1.5	47
37	An update on belimumab for the treatment of lupus. <i>Biologics: Targets and Therapy</i> , 2011 , 5, 33-43	4.4	12
36	Noodling and <i>Mycobacterium marinum</i> infection mimicking seronegative rheumatoid arthritis complicated by anti-tumor necrosis factor α therapy. <i>Arthritis Care and Research</i> , 2011 , 63, 160-4	4.7	10
35	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, 1689-97		41
34	Identification of novel genetic susceptibility loci in African American lupus patients in a candidate gene association study. <i>Arthritis and Rheumatism</i> , 2011 , 63, 3493-501		86
33	A putative functional variant within the UBAC2 gene is associated with increased risk of Behçet's disease. <i>Arthritis and Rheumatism</i> , 2011 , 63, 3607-12		31
32	The role of epigenetic variation in the pathogenesis of systemic lupus erythematosus. <i>Arthritis Research and Therapy</i> , 2011 , 13, 245	5.7	30
31	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, 151-6	2.4	112
30	IL18 polymorphism is associated with Behçet's disease but not lupus in patients from Turkey. <i>Journal of Rheumatology</i> , 2011 , 38, 962-3	4.1	15
29	Genome-wide DNA methylation patterns in CD4+ T cells from patients with systemic lupus erythematosus. <i>Epigenetics</i> , 2011 , 6, 593-601	5.7	184
28	Phenotypic associations of genetic susceptibility loci in systemic lupus erythematosus. <i>Annals of the Rheumatic Diseases</i> , 2011 , 70, 1752-7	2.4	89
27	Genetic association between methyl-CpG binding protein 2 (MECP2) and primary Sjogren's syndrome. <i>Annals of the Rheumatic Diseases</i> , 2010 , 69, 1731-2	2.4	27
26	Changes in the pattern of DNA methylation associate with twin discordance in systemic lupus erythematosus. <i>Genome Research</i> , 2010 , 20, 170-9	9.7	486
25	Genetically determined Amerindian ancestry correlates with increased frequency of risk alleles for systemic lupus erythematosus. <i>Arthritis and Rheumatism</i> , 2010 , 62, 3722-9		61
24	Uric acid directly promotes human T-cell activation. <i>American Journal of the Medical Sciences</i> , 2009 , 337, 23-7	2.2	42

23	T cell CD40LG gene expression and the production of IgG by autologous B cells in systemic lupus erythematosus. <i>Clinical Immunology</i> , 2009 , 132, 362-70	9	79
22	Variants within MECP2, a key transcription regulator, are associated with increased susceptibility to lupus and differential gene expression in patients with systemic lupus erythematosus. <i>Arthritis and Rheumatism</i> , 2009 , 60, 1076-84		69
21	A polymorphism within IL21R confers risk for systemic lupus erythematosus. <i>Arthritis and Rheumatism</i> , 2009 , 60, 2402-7		97
20	Autoimmunity and Klinefelter's syndrome: when men have two X chromosomes. <i>Journal of Autoimmunity</i> , 2009 , 33, 31-4	15.5	103
19	Aberrant DNA methylation in skin diseases. <i>Journal of Dermatological Science</i> , 2009 , 54, 143-9	4.3	25
18	Epigenetic regulation and the pathogenesis of systemic lupus erythematosus. <i>Translational Research</i> , 2009 , 153, 4-10	11	69
17	Identification of novel genetic susceptibility loci for Behçet's disease using a genome-wide association study. <i>Arthritis Research and Therapy</i> , 2009 , 11, R66	5.7	102
16	Epigenetics and T-cell immunity. <i>Autoimmunity</i> , 2008 , 41, 245-52	3	59
15	Dehydroepiandrosterone in systemic lupus erythematosus. <i>Current Rheumatology Reports</i> , 2008 , 10, 286-91	4.9	34
14	Common variants within MECP2 confer risk of systemic lupus erythematosus. <i>PLoS ONE</i> , 2008 , 3, e1727	3.7	112
13	Defective DNA methylation and CD70 overexpression in CD4+ T cells in MRL/lpr lupus-prone mice. <i>European Journal of Immunology</i> , 2007 , 37, 1407-13	6.1	54
12	Horizons in Sjögren's syndrome genetics. <i>Clinical Reviews in Allergy and Immunology</i> , 2007 , 32, 201-9	12.3	11
11	Impaired T cell protein kinase C delta activation decreases ERK pathway signaling in idiopathic and hydralazine-induced lupus. <i>Journal of Immunology</i> , 2007 , 179, 5553-63	5.3	143
10	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		16
9	Clinical problem-solving. Still consider the source. <i>New England Journal of Medicine</i> , 2005 , 353, 1503-7	59.2	2
8	Antinuclear autoantibodies in systemic lupus erythematosus. <i>Current Opinion in Rheumatology</i> , 2004 , 16, 534-40	5.3	66
7	Association between systemic lupus erythematosus and Helicobacter pylori seronegativity. <i>Journal of Rheumatology</i> , 2004 , 31, 1546-50	4.1	40
6	Clinical problem-solving. Step by step. <i>New England Journal of Medicine</i> , 2003 , 349, 2253-7	59.2	2

5	Panniculitis: a presenting manifestation of disseminated histoplasmosis in a patient with rheumatoid arthritis. <i>Journal of Clinical Rheumatology</i> , 2003 , 9, 259-62	1.1	13
4	The genetics of primary Sjögren's syndrome. <i>Current Rheumatology Reports</i> , 2003 , 5, 324-32	4.9	22
3	Genome-wide reduction in chromatin accessibility and unique transcription factor footprints in endothelial cells and fibroblasts in scleroderma skin		1
2	Genetic variability in the expression of the SARS-CoV-2 host cell entry factors across populations		3
1	Inhibition of histone readers bromodomain extra-terminal proteins alleviates scleroderma fibrosis		1