

Amr H Sawalha

List of Publications by Year in descending order

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Version: 2024-02-01

151
papers

8,909
citations

34076

52
h-index

49868

87
g-index

165
all docs

165
docs citations

165
times ranked

9885
citing authors

#	ARTICLE	IF	CITATIONS
1	Clinical Treatment Options in Scleroderma: Recommendations and Comprehensive Review. <i>Clinical Reviews in Allergy and Immunology</i> , 2022, 62, 273-291.	2.9	28
2	Detection of immunoglobulin response to COVID-19 vaccination using a novel rapid fingerstick assay. <i>Clinical Immunology</i> , 2022, 235, 108791.	1.4	2
3	Clinical subgroup clustering analysis in a systemic lupus erythematosus cohort from Western Pennsylvania. <i>European Journal of Rheumatology</i> , 2022, 9, 3-7.	1.3	4
4	The Role of Oxidative Stress in Epigenetic Changes Underlying Autoimmunity. <i>Antioxidants and Redox Signaling</i> , 2022, 36, 423-440.	2.5	7
5	Systemic lupus erythematosus as a genetic disease. <i>Clinical Immunology</i> , 2022, 236, 108953.	1.4	18
6	Functional Characterization of Glycoprotein Nonmetastatic Melanoma Protein B in Scleroderma Fibrosis. <i>Frontiers in Immunology</i> , 2022, 13, 814533.	2.2	5
7	Post-GWAS functional analysis identifies CUX1 as a regulator of p16INK4a and cellular senescence. <i>Nature Aging</i> , 2022, 2, 140-154.	5.3	4
8	Inhibition of bromodomain extraterminal histone readers alleviates skin fibrosis in experimental models of scleroderma. <i>JCI Insight</i> , 2022, 7, .	2.3	11
9	Hypomethylation of miR-17-92 cluster in lupus T cells and no significant role for genetic factors in the lupus-associated DNA methylation signature. <i>Annals of the Rheumatic Diseases</i> , 2022, 81, 1428-1437.	0.5	5
10	Neutrophils in systemic lupus erythematosus. , 2021, , 139-142.		0
11	Patients with lupus are not protected from COVID-19. <i>Annals of the Rheumatic Diseases</i> , 2021, 80, e21-e21.	0.5	10
12	COVID-19: A review of therapeutic strategies and vaccine candidates. <i>Clinical Immunology</i> , 2021, 222, 108634.	1.4	180
13	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.	4.8	3
14	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.	2.6	26
15	SARS-CoV-2 and Systemic Lupus Erythematosus. <i>Current Rheumatology Reports</i> , 2021, 23, 8.	2.1	18
16	Genetics of Behçet's Disease: Functional Genetic Analysis and Estimating Disease Heritability. <i>Frontiers in Medicine</i> , 2021, 8, 625710.	1.2	18
17	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.	2.9	21
18	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.	2.9	10

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19	DNA methylation patterns in juvenile systemic sclerosis and localized scleroderma. <i>Clinical Immunology</i> , 2021, 228, 108756.	1.4	4
20	Guideline for the diagnosis, treatment and long-term management of cutaneous lupus erythematosus. <i>Journal of Autoimmunity</i> , 2021, 123, 102707.	3.0	27
21	HLA-DRB1 allelic epitopes that associate with autoimmune disease risk or protection activate reciprocal macrophage polarization. <i>Scientific Reports</i> , 2021, 11, 2599.	1.6	13
22	COVID-19 and autoimmune diseases. <i>Current Opinion in Rheumatology</i> , 2021, 33, 155-162.	2.0	332
23	Reply. <i>Arthritis and Rheumatology</i> , 2020, 72, 373-374.	2.9	0
24	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.	2.2	40
25	Clinical value of DNA methylation markers in autoimmune rheumatic diseases. <i>Nature Reviews Rheumatology</i> , 2020, 16, 514-524.	3.5	48
26	Glycoprotein nonmetastatic melanoma protein B: A key mediator and an emerging therapeutic target in autoimmune diseases. <i>FASEB Journal</i> , 2020, 34, 8810-8823.	0.2	18
27	Medical Licensure: It Is Time to Eliminate Practice Borders Within the United States. <i>American Journal of Medicine</i> , 2020, 133, 1120-1121.	0.6	0
28	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.	1.4	217
29	A longitudinal and transancestral analysis of DNA methylation patterns and disease activity in lupus patients. <i>JCI Insight</i> , 2020, 5, .	2.3	36
30	Increased Expression of EZH2 Is Mediated by Higher Glycolysis and mTORC1 Activation in Lupus CD4+ T Cells. <i>Immunometabolism</i> , 2020, 2, .	0.7	17
31	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.	1.3	28
32	Takayasu Arteritis. <i>Rare Diseases of the Immune System</i> , 2019, , 151-162.	0.1	0
33	Takayasu arteritis risk locus in <i>IL6</i> represses the anti-inflammatory gene <i>GPNMB</i> through chromatin looping and recruiting MEF2 ² HDAC complex. <i>Annals of the Rheumatic Diseases</i> , 2019, 78, 1388-1397.	0.5	20
34	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.	0.5	29
35	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.	3.0	24
36	Inhibition of EZH2 Ameliorates Lupus-Like Disease in MRL- <i>lpr</i> Mice. <i>Arthritis and Rheumatology</i> , 2019, 71, 1681-1690.	2.9	48

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37	Structural variation of centromeric endogenous retroviruses in human populations and their impact on cutaneous T-cell lymphoma, SÅ©zary syndrome, and HIV infection. <i>BMC Medical Genomics</i> , 2019, 12, 58.	0.7	5
38	Identification of Cysteineâ€Rich Angiogenic Inducer 61 as a Potential Antifibrotic and Proangiogenic Mediator in Scleroderma. <i>Arthritis and Rheumatology</i> , 2019, 71, 1350-1359.	2.9	16
39	Evaluating the Perception Among Rheumatologists of Maintenance of Board Certification in the US. <i>Arthritis Care and Research</i> , 2019, 71, 337-342.	1.5	4
40	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.	3.3	77
41	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.	3.3	53
42	Genetics of Antiphospholipid Syndrome. <i>Current Rheumatology Reports</i> , 2019, 21, 65.	2.1	18
43	Caffeine inhibits STAT1 signaling and downregulates inflammatory pathways involved in autoimmunity. <i>Clinical Immunology</i> , 2018, 192, 68-77.	1.4	33
44	Shared epitopeâ€aryl hydrocarbon receptor crosstalk underlies the mechanism of geneâ€environment interaction in autoimmune arthritis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 4755-4760.	3.3	45
45	Management of BehÃ§et's disease. <i>Current Opinion in Rheumatology</i> , 2018, 30, 238-242.	2.0	23
46	Cross-phenotype analysis of ImmunoChip data identifies <i>KDM4C</i> as a relevant <i>locus</i> for the development of systemic vasculitis. <i>Annals of the Rheumatic Diseases</i> , 2018, 77, 589-595.	0.5	27
47	Novel Transcriptional Activity and Extensive Allelic Imbalance in the Human MHC Region. <i>Journal of Immunology</i> , 2018, 200, 1496-1503.	0.4	20
48	Sex chromosome contributions to sex differences in multiple sclerosis susceptibility and progression. <i>Multiple Sclerosis Journal</i> , 2018, 24, 22-31.	1.4	52
49	CD4+CD28+KIR+CD11ahi 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.	3.0	21
50	An update on the role of epigenetics in systemic vasculitis. <i>Current Opinion in Rheumatology</i> , 2018, 30, 4-15.	2.0	29
51	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.	2.9	44
52	Editorial: The Innate and Adaptive Immune Response Are Both Involved in Drugâ€Induced Autoimmunity. <i>Arthritis and Rheumatology</i> , 2018, 70, 330-333.	2.9	7
53	Clinical immunology: A special issue on epigenetics. <i>Clinical Immunology</i> , 2018, 196, 1-2.	1.4	1
54	Genome-wide DNA methylation analysis in primary antiphospholipid syndrome neutrophils. <i>Clinical Immunology</i> , 2018, 196, 110-116.	1.4	26

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55	Monogenic Lupus: A Developing Paradigm of Disease. <i>Frontiers in Immunology</i> , 2018, 9, 2496.	2.2	105
56	Methyl-CpG-binding protein 2 mediates antifibrotic effects in scleroderma fibroblasts. <i>Annals of the Rheumatic Diseases</i> , 2018, 77, annrheumdis-2018-213022.	0.5	36
57	Deoxyribonucleic Acid Methylation in Systemic Lupus Erythematosus: Implications for Future Clinical Practice. <i>Frontiers in Immunology</i> , 2018, 9, 875.	2.2	32
58	Drug-induced lupus erythematosus: an update on drugs and mechanisms. <i>Current Opinion in Rheumatology</i> , 2018, 30, 490-497.	2.0	96
59	Analysis of the common genetic component of large-vessel vasculitides through a meta-immunochip strategy. <i>Scientific Reports</i> , 2017, 7, 43953.	1.6	52
60	Epigenetic Variability in Systemic Lupus Erythematosus: What We Learned from Genome-Wide DNA Methylation Studies. <i>Current Rheumatology Reports</i> , 2017, 19, 32.	2.1	54
61	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.	1.4	87
62	Unfolding the pathogenesis of scleroderma through genomics and epigenomics. <i>Journal of Autoimmunity</i> , 2017, 83, 73-94.	3.0	80
63	Interview with Amr H Sawalha: epigenetics and autoimmunity. <i>Epigenomics</i> , 2017, 9, 379-382.	1.0	2
64	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.	1.0	47
65	Clinical Images: Black Esophagus in Antiphospholipid Syndrome. <i>Arthritis and Rheumatology</i> , 2017, 69, 1460-1460.	2.9	8
66	The genetics of Takayasu arteritis. <i>Presse Medicale</i> , 2017, 46, e179-e187.	0.8	42
67	Epigenetics of Rheumatic Diseases. , 2017, , 344-354.		0
68	Behçet's disease in the United States: A single center descriptive and comparative study. <i>European Journal of Rheumatology</i> , 2017, 4, 239-244.	1.3	13
69	Activated signature of antiphospholipid syndrome neutrophils reveals potential therapeutic target. <i>JCI Insight</i> , 2017, 2, .	2.3	75
70	Neutrophils in Systemic Lupus Erythematosus. , 2016, , 127-130.		3
71	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.	2.9	50
72	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.	1.1	54

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73	Genetic heterogeneity within the HLA region in three distinct clinical subgroups of myasthenia gravis. <i>Clinical Immunology</i> , 2016, 166-167, 81-88.	1.4	38
74	Analysis of Systemic Sclerosis-associated Genes in a Turkish Population. <i>Journal of Rheumatology</i> , 2016, 43, 1376-1379.	1.0	5
75	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.	2.9	62
76	The human microbiome in rheumatic autoimmune diseases: A comprehensive review. <i>Clinical Immunology</i> , 2016, 170, 70-79.	1.4	35
77	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.	1.1	15
78	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, 2200-2209.	2.9	88
79	Sequencing of 16S rRNA reveals a distinct salivary microbiome signature in Behçet's disease. <i>Clinical Immunology</i> , 2016, 169, 28-35.	1.4	88
80	DNA methylation analysis of the temporal artery microenvironment in giant cell arteritis. <i>Annals of the Rheumatic Diseases</i> , 2016, 75, 1196-1202.	0.5	55
81	<i>IFI44L</i> promoter methylation as a blood biomarker for systemic lupus erythematosus. <i>Annals of the Rheumatic Diseases</i> , 2016, 75, 1998-2006.	0.5	167
82	Epigenomic functional characterization of genetic susceptibility variants in systemic vasculitis. <i>Journal of Autoimmunity</i> , 2016, 67, 76-81.	3.0	12
83	Epigenetics and Vasculitis: a Comprehensive Review. <i>Clinical Reviews in Allergy and Immunology</i> , 2016, 50, 357-366.	2.9	33
84	Ethnicity-specific epigenetic variation in naive CD4+ T cells and the susceptibility to autoimmunity. <i>Epigenetics and Chromatin</i> , 2015, 8, 49.	1.8	49
85	Whole exome sequencing identifies rare protein-coding variants in Behçet's disease. <i>Arthritis and Rheumatology</i> , 2015, 68, n/a-n/a.	2.9	9
86	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.	0.5	148
87	Hydroxychloroquine-induced Hyperpigmentation of the Skin. <i>Journal of Rheumatology</i> , 2015, 42, 135-136.	1.0	7
88	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.	1.3	59
89	Epigenome profiling reveals significant DNA demethylation of interferon signature genes in lupus neutrophils. <i>Journal of Autoimmunity</i> , 2015, 58, 59-66.	3.0	161
90	Identification of Susceptibility Loci in <i>IL6</i> , <i>RPS9</i> , and <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.	2.9	79

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91	T cell PKC ζ kinase inactivation induces lupus-like autoimmunity in mice. <i>Clinical Immunology</i> , 2015, 158, 193-203.	1.4	47
92	DNA methylation patterns in na ζ -ve 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.	1.1	83
93	Systemic lupus erythematosus complicated by diffuse alveolar haemorrhage: risk factors, therapy and survival. <i>Lupus Science and Medicine</i> , 2015, 2, e000117.	1.1	59
94	Renal involvement in lupus is characterized by unique DNA methylation changes in na ζ -ve CD4+ T cells. <i>Journal of Autoimmunity</i> , 2015, 61, 29-35.	3.0	109
95	The DNA methylation signature of human TCR β ^{hi} CD4 ^{hi} CD8 ^{lo} 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.	1.4	25
96	Genome-Wide DNA Methylation Study Identifies Significant Epigenomic Changes in Osteoarthritic Cartilage. <i>Arthritis and Rheumatology</i> , 2014, 66, 2804-2815.	2.9	128
97	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 Beh ζ 's Disease. <i>Arthritis and Rheumatology</i> , 2014, 66, 1648-1658.	2.9	72
98	Epigenetics in the treatment of systemic lupus erythematosus: Potential clinical application. <i>Clinical Immunology</i> , 2014, 155, 79-90.	1.4	31
99	Genome-Wide DNA Methylation Patterns in Naive CD4+ T Cells From Patients With Primary Sj ζ gren's Syndrome. <i>Arthritis and Rheumatology</i> , 2014, 66, 731-739.	2.9	147
100	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.	3.0	172
101	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.	3.0	55
102	Identification of Multiple Genetic Susceptibility Loci in Takayasu Arteritis. <i>American Journal of Human Genetics</i> , 2013, 93, 298-305.	2.6	143
103	Identification of multiple independent susceptibility loci in the HLA region in Beh ζ 's disease. <i>Nature Genetics</i> , 2013, 45, 319-324.	9.4	130
104	Impaired DNA methylation and its mechanisms in CD4+T cells of systemic lupus erythematosus. <i>Journal of Autoimmunity</i> , 2013, 41, 92-99.	3.0	190
105	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
106	Genome-wide DNA methylation study suggests epigenetic accessibility and transcriptional poisoning of interferon-regulated genes in na ζ -ve CD4+ T cells from lupus patients. <i>Journal of Autoimmunity</i> , 2013, 43, 78-84.	3.0	294
107	Trans-Ancestral Studies Fine Map the SLE-Susceptibility Locus TNFSF4. <i>PLoS Genetics</i> , 2013, 9, e1003554.	1.5	50
108	Epigenetics in the pathogenesis of systemic lupus erythematosus. <i>Current Opinion in Rheumatology</i> , 2013, 25, 569-576.	2.0	26

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109	Fine mapping of Xq28: both <i>MECP2</i> and <i>IRAK1</i> contribute to risk for systemic lupus erythematosus in multiple ancestral groups. <i>Annals of the Rheumatic Diseases</i> , 2013, 72, 437-444.	0.5	97
110	GFP Affects Human T Cell Activation and Cytokine Production following In Vitro Stimulation. <i>PLoS ONE</i> , 2013, 8, e50068.	1.1	15
111	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, 694-699.	0.5	87
112	Variation in the <i>ICAM1-ICAM4-ICAM5</i> locus is associated with systemic lupus erythematosus susceptibility in multiple ancestries. <i>Annals of the Rheumatic Diseases</i> , 2012, 71, 1809-1814.	0.5	60
113	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-J143.	3.0	74
114	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-J222.	3.0	71
115	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
116	Murine Models of Lupus Induced by Hypomethylated T Cells (DNA Hypomethylation and Lupus). <i>Methods in Molecular Biology</i> , 2012, 900, 169-180.	0.4	16
117	The role of epigenetic variation in the pathogenesis of systemic lupus erythematosus. <i>Arthritis Research and Therapy</i> , 2011, 13, 245.	1.6	34
118	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
119	An update on belimumab for the treatment of lupus. <i>Biologics: Targets and Therapy</i> , 2011, 5, 33.	3.0	18
120	Noodling and <i>Mycobacterium marinum</i> infection mimicking seronegative rheumatoid arthritis complicated by anti-tumor necrosis factor therapy. <i>Arthritis Care and Research</i> , 2011, 63, 160-164.	1.5	12
121	Fine-mapping and transethnic genotyping establish <i>IL2/IL21</i> genetic association with lupus and localize this genetic effect to <i>IL21</i> . <i>Arthritis and Rheumatism</i> , 2011, 63, 1689-1697.	6.7	49
122	Identification of novel genetic susceptibility loci in African American lupus patients in a candidate gene association study. <i>Arthritis and Rheumatism</i> , 2011, 63, 3493-3501.	6.7	109
123	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
124	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.	0.5	155
125	<i>IL18</i> Polymorphism Is Associated with Behçet's Disease But Not Lupus in Patients from Turkey. <i>Journal of Rheumatology</i> , 2011, 38, 962-963.	1.0	17
126	Genome-wide DNA methylation patterns in CD4+ T cells from patients with systemic lupus erythematosus. <i>Epigenetics</i> , 2011, 6, 593-601.	1.3	224

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127	Phenotypic associations of genetic susceptibility loci in systemic lupus erythematosus. <i>Annals of the Rheumatic Diseases</i> , 2011, 70, 1752-1757.	0.5	110
128	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
129	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.	0.5	31
130	Changes in the pattern of DNA methylation associate with twin discordance in systemic lupus erythematosus. <i>Genome Research</i> , 2010, 20, 170-179.	2.4	569
131	Uric Acid Directly Promotes Human T-Cell Activation. <i>American Journal of the Medical Sciences</i> , 2009, 337, 23-27.	0.4	51
132	T cell CD40LG gene expression and the production of IgG by autologous B cells in systemic lupus erythematosus. <i>Clinical Immunology</i> , 2009, 132, 362-370.	1.4	90
133	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. <i>Arthritis and Rheumatism</i> , 2009, 60, 1076-1084.	6.7	80
134	A polymorphism within <i>IL21R</i> confers risk for systemic lupus erythematosus. <i>Arthritis and Rheumatism</i> , 2009, 60, 2402-2407.	6.7	108
135	Autoimmunity and Klinefelter's syndrome: When men have two X chromosomes. <i>Journal of Autoimmunity</i> , 2009, 33, 31-34.	3.0	127
136	Aberrant DNA methylation in skin diseases. <i>Journal of Dermatological Science</i> , 2009, 54, 143-149.	1.0	29
137	Epigenetic regulation and the pathogenesis of systemic lupus erythematosus. <i>Translational Research</i> , 2009, 153, 4-10.	2.2	83
138	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.	1.6	123
139	Dehydroepiandrosterone in systemic lupus erythematosus. <i>Current Rheumatology Reports</i> , 2008, 10, 286-291.	2.1	40
140	Epigenetics and T-cell immunity. <i>Autoimmunity</i> , 2008, 41, 245-252.	1.2	75
141	Common Variants within MECP2 Confer Risk of Systemic Lupus Erythematosus. <i>PLoS ONE</i> , 2008, 3, e1727.	1.1	125
142	Impaired T Cell Protein Kinase C γ Activation Decreases ERK Pathway Signaling in Idiopathic and Hydralazine-Induced Lupus. <i>Journal of Immunology</i> , 2007, 179, 5553-5563.	0.4	163
143	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.	1.6	64
144	Horizons in Sjögren's Syndrome Genetics. <i>Clinical Reviews in Allergy and Immunology</i> , 2007, 32, 201-209.	2.9	14

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145	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
146	Still Consider the Source. <i>New England Journal of Medicine</i> , 2005, 353, 1503-1507.	13.9	2
147	Antinuclear autoantibodies in systemic lupus erythematosus. <i>Current Opinion in Rheumatology</i> , 2004, 16, 534-540.	2.0	73
148	Association between systemic lupus erythematosus and <i>Helicobacter pylori</i> seronegativity. <i>Journal of Rheumatology</i> , 2004, 31, 1546-50.	1.0	47
149	The genetics of primary Sjögren's syndrome. <i>Current Rheumatology Reports</i> , 2003, 5, 324-332.	2.1	26
150	Step by Step. <i>New England Journal of Medicine</i> , 2003, 349, 2253-2257.	13.9	2
151	Panniculitis. <i>Journal of Clinical Rheumatology</i> , 2003, 9, 259-262.	0.5	14