

# Patrick Coit

## List of Publications by Year in descending order

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Version: 2024-02-01

32  
papers

1,977  
citations

279798

23  
h-index

454955

30  
g-index

33  
all docs

33  
docs citations

33  
times ranked

2757  
citing authors

#	ARTICLE	IF	CITATIONS
1	Clinical subgroup clustering analysis in a systemic lupus erythematosus cohort from Western Pennsylvania. <i>European Journal of Rheumatology</i> , 2022, 9, 3-7.	0.6	4
2	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.	0.9	5
3	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
4	DNA methylation patterns in juvenile systemic sclerosis and localized scleroderma. <i>Clinical Immunology</i> , 2021, 228, 108756.	3.2	4
5	1507â€¦The relationship between DNA methylation patterns and disease activity in a longitudinal multi-ancestral cohort of lupus patients. , 2021, , .		0
6	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
7	A longitudinal and transancestral analysis of DNA methylation patterns and disease activity in lupus patients. <i>JCI Insight</i> , 2020, 5, .	5.0	36
8	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
9	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
10	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
11	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
12	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.	7.1	45
13	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.	6.5	21
14	An update on the role of epigenetics in systemic vasculitis. <i>Current Opinion in Rheumatology</i> , 2018, 30, 4-15.	4.3	29
15	CG-01â€¦Hypomethylation of <i>STAT1</i> and <i>HLA-DRB1</i> in CD8+ T cells is associated with type-I interferon-dependent <i>HLA-DRB1</i> overexpression and activation of autologous CD4+ T cells in systemic lupus erythematosus. , 2018, , .		0
16	Genome-wide DNA methylation analysis in primary antiphospholipid syndrome neutrophils. <i>Clinical Immunology</i> , 2018, 196, 110-116.	3.2	26
17	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
18	Age-associated DNA methylation changes in naive CD4 <sup>+</sup> T cells suggest an evolving autoimmune epigenotype in aging T cells. <i>Epigenomics</i> , 2017, 9, 429-445.	2.1	47

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19	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
20	The human microbiome in rheumatic autoimmune diseases: A comprehensive review. <i>Clinical Immunology</i> , 2016, 170, 70-79.	3.2	35
21	Epigenetic Reprogramming in Naive CD4+ T Cells Favoring T Cell Activation and Non- $\text{Th1}$ Effector T Cell Immune Response as an Early Event in Lupus Flares. <i>Arthritis and Rheumatology</i> , 2016, 68, 2200-2209.	5.6	88
22	Sequencing of 16S rRNA reveals a distinct salivary microbiome signature in Behçet's disease. <i>Clinical Immunology</i> , 2016, 169, 28-35.	3.2	88
23	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
24	Epigenetics and Vasculitis: a Comprehensive Review. <i>Clinical Reviews in Allergy and Immunology</i> , 2016, 50, 357-366.	6.5	33
25	Ethnicity-specific epigenetic variation in naive CD4+ T cells and the susceptibility to autoimmunity. <i>Epigenetics and Chromatin</i> , 2015, 8, 49.	3.9	49
26	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
27	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
28	DNA methylation patterns in naive 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.	2.7	83
29	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
30	Renal involvement in lupus is characterized by unique DNA methylation changes in naive CD4+ T cells. <i>Journal of Autoimmunity</i> , 2015, 61, 29-35.	6.5	109
31	The DNA methylation signature of human $\text{TCR}^{\text{hi}}\text{CD4}^{\text{hi}}\text{CD8}^{\text{lo}}$ 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.	3.2	25
32	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.	6.5	294