James E Peters

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.

26 papers	1,208 citations	13 h-index	34 g-index
38 ext. papers	2,118 ext. citations	13.9 avg, IF	3.57 L-index

#	Paper	IF	Citations
26	Immuno-proteomic profiling reveals aberrant immune cell regulation in the airways of individuals with ongoing post-COVID-19 respiratory disease.. *Immunity*, **2022**,	32.3	9
25	Elucidating mechanisms of genetic cross-disease associations at the PROCR vascular disease locus.. *Nature Communications*, **2022**, 13, 1222	17.4	0
24	Longitudinal proteomic profiling of dialysis patients with COVID-19 reveals markers of severity and predictors of death. *ELife*, **2021**, 10,	8.9	17
23	Actionable druggable genome-wide Mendelian randomization identifies repurposing opportunities for COVID-19. *Nature Medicine*, **2021**, 27, 668-676	50.5	19
22	A critical beat in eosinophilic granulomatosis with polyangiitis. *Rheumatology*, **2021**, 60, iii28-iii31	3.9	1
21	Autoimmunity Due to Unicentric Castleman Disease Cured by Resection of a Hepatic Mass. *Journal of Clinical Rheumatology*, **2021**, 27, e32-e33	1.1	
20	A genome-wide meta-analysis yields 46 new loci associating with biomarkers of iron homeostasis. *Communications Biology*, **2021**, 4, 156	6.7	11
19	Novel Approach to Imaging Active Takayasu Arteritis Using Somatostatin Receptor Positron Emission Tomography/Magnetic Resonance Imaging. *Circulation: Cardiovascular Imaging*, **2020**, 13, e010389	3.9	8
18	Genomic and drug target evaluation of 90 cardiovascular proteins in 30,931 individuals. *Nature Metabolism*, **2020**, 2, 1135-1148	14.6	61
17	Temporal changes in complement activation in haemodialysis patients with COVID-19 as a predictor of disease progression. *CKJ: Clinical Kidney Journal*, **2020**, 13, 889-896	4.5	13
16	Discovery of rare variants associated with blood pressure regulation through meta-analysis of 1.3 million individuals. *Nature Genetics*, **2020**, 52, 1314-1332	36.3	26
15	Interleukin-6 Receptor Signaling and Abdominal Aortic Aneurysm Growth Rates. *Circulation Genomic and Precision Medicine*, **2019**, 12, e002413	5.2	25
14	Genome-wide association study of eosinophilic granulomatosis with polyangiitis reveals genomic loci stratified by ANCA status. *Nature Communications*, **2019**, 10, 5120	17.4	71
13	Genetic Determinants of Lipids and Cardiovascular Disease Outcomes: A Wide-Angled Mendelian Randomization Investigation. *Circulation Genomic and Precision Medicine*, **2019**, 12, e002711	5.2	41
12	Severe localised granulomatosis with polyangiitis (Wegener\'s granulomatosis) manifesting with extensive cranial nerve palsies and cranial diabetes insipidus: a case report and literature review. *BMC Neurology*, **2018**, 18, 59	3.1	11
11	Genomic atlas of the human plasma proteome. *Nature*, **2018**, 558, 73-79	50.4	529
10	Association of LPA Variants With Risk of Coronary Disease and the Implications for Lipoprotein(a)-Lowering Therapies: A Mendelian Randomization Analysis. *JAMA Cardiology*, **2018**, 3, 619-627	16.2	235

9	Reduced monocyte and macrophage TNFSF15/TL1A expression is associated with susceptibility to inflammatory bowel disease. *PLoS Genetics*, **2018**, 14, e1007458	6	18
8	MT-HESS: an efficient Bayesian approach for simultaneous association detection in OMICS datasets, with application to eQTL mapping in multiple tissues. *Bioinformatics*, **2016**, 32, 523-32	7.2	20
7	Insight into Genotype-Phenotype Associations through eQTL Mapping in Multiple Cell Types in Health and Immune-Mediated Disease. *PLoS Genetics*, **2016**, 12, e1005908	6	58
6	Targeted genomic analysis reveals widespread autoimmune disease association with regulatory variants in the TNF superfamily cytokine signalling network. *Genome Medicine*, **2016**, 8, 76	14.4	10
5	Three cases of rheumatoid arthritis with laryngeal stridor. *Clinical Rheumatology*, **2011**, 30, 723-7	3.9	14
4	Genetic Analyses of Blood Cell Structure for Biological and Pharmacological Inference		3
3	Elucidating mechanisms of genetic cross-disease associations: an integrative approach implicates protein C as a causal pathway in arterial and venous diseases		2
2	Actionable druggable genome-wide Mendelian randomization identifies repurposing opportunities for COVID-19		1
1	Genetically distinct clinical subsets, and associations with asthma and eosinophil abundance, within Eosinophilic Granulomatosis with Polyangiitis		3