Klaudia Walter

List of Publications by Year
in descending order

25 papers	9,086 citations	394421 19 h-index	552781 26 g-index
34 all docs	34 docs citations	34 times ranked	21811 citing authors

#	Article	IF	Citations
1	Genetic associations at regulatory phenotypes improve fine-mapping of causal variants for 12 immune-mediated diseases. Nature Genetics, 2022, 54, 251-262.	21.4	23
2	Whole-exome sequencing identifies rare genetic variants associated with human plasma metabolites. American Journal of Human Genetics, 2022, 109, 1038-1054.	6.2	17
3	Genetic perturbation of PU.1 binding and chromatin looping at neutrophil enhancers associates with autoimmune disease. Nature Communications, 2021, 12, 2298.	12.8	32
4	Effects of adiposity on the human plasma proteome: observational and Mendelian randomisation estimates. International Journal of Obesity, 2021, 45, 2221-2229.	3.4	31
5	Mitochondrial DNA variants modulate N-formylmethionine, proteostasis and risk of late-onset human diseases. Nature Medicine, 2021, 27, 1564-1575.	30.7	40
6	Whole-genome sequencing in diverse subjects identifies genetic correlates of leukocyte traits: The NHLBI TOPMed program. American Journal of Human Genetics, 2021, 108, 1836-1851.	6.2	14
7	The Polygenic and Monogenic Basis of Blood Traits and Diseases. Cell, 2020, 182, 1214-1231.e11.	28.9	388
8	The influence of rare variants in circulating metabolic biomarkers. PLoS Genetics, 2020, 16, e1008605.	3.5	9
9	GARFIELD classifies disease-relevant genomic features through integration of functional annotations with association signals. Nature Genetics, 2019, 51, 343-353.	21.4	147
10	Cohort-wide deep whole genome sequencing and the allelic architecture of complex traits. Nature Communications, 2018, 9, 4674.	12.8	33
11	Whole-genome view of the consequences of a population bottleneck using 2926 genome sequences from Finland and United Kingdom. European Journal of Human Genetics, 2017, 25, 477-484.	2.8	60
12	Whole-Genome Sequencing Coupled to Imputation Discovers Genetic Signals for Anthropometric Traits. American Journal of Human Genetics, 2017, 100, 865-884.	6.2	131
13	The impact of rare and low-frequency genetic variants in common disease. Genome Biology, 2017, 18, 77.	8.8	277
14	Discovery and refinement of genetic loci associated with cardiometabolic risk using dense imputation maps. Nature Genetics, 2016, 48, 1303-1312.	21.4	66
15	Whole-Exome Sequencing Identifies Loci Associated with Blood Cell Traits and Reveals a Role for Alternative GFI1B Splice Variants in Human Hematopoiesis. American Journal of Human Genetics, 2016, 99, 481-488.	6.2	45
16	A reference panel of 64,976 haplotypes for genotype imputation. Nature Genetics, 2016, 48, 1279-1283.	21.4	2,421
17	The Allelic Landscape of Human Blood Cell Trait Variation and Links to Common Complex Disease. Cell, 2016, 167, 1415-1429.e19.	28.9	1,052
18	Genetic Drivers of Epigenetic and Transcriptional Variation in Human Immune Cells. Cell, 2016, 167, 1398-1414.e24.	28.9	573

#	Article	IF	Citations
19	Whole-genome sequence-based analysis of thyroid function. Nature Communications, 2015, 6, 5681.	12.8	75
20	The UK10K project identifies rare variants in health and disease. Nature, 2015, 526, 82-90.	27.8	1,014
21	Improved imputation of low-frequency and rare variants using the UK10K haplotype reference panel. Nature Communications, 2015, 6, 8111.	12.8	300
22	An atlas of genetic influences on human blood metabolites. Nature Genetics, 2014, 46, 543-550.	21.4	1,084
23	Estimating Genomeâ€Wide Significance for Wholeâ€Genome Sequencing Studies. Genetic Epidemiology, 2014, 38, 281-290.	1.3	72
24	A rare variant in APOC3 is associated with plasma triglyceride and VLDL levels in Europeans. Nature Communications, 2014, 5, 4871.	12.8	62
25	A Systematic Survey of Loss-of-Function Variants in Human Protein-Coding Genes. Science, 2012, 335, 823-828.	12.6	1,095