William Schierding

List of Publications by Year
in descending order

52	10,822	304368	205818
papers	citations	22 h-index	48 g-index

67	67	67	19545
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Integrated genomic analyses of ovarian carcinoma. Nature, 2011, 474, 609-615.	13.7	6,541
2	Genome remodelling in a basal-like breast cancer metastasis and xenograft. Nature, 2010, 464, 999-1005.	13.7	1,077
3	Whole-genome analysis informs breast cancer response to aromatase inhibition. Nature, 2012, 486, 353-360.	13.7	922
4	MuSiC: Identifying mutational significance in cancer genomes. Genome Research, 2012, 22, 1589-1598.	2.4	586
5	SciClone: Inferring Clonal Architecture and Tracking the Spatial and Temporal Patterns of Tumor Evolution. PLoS Computational Biology, 2014, 10, e1003665.	1.5	400
6	Machine Learning SNP Based Prediction for Precision Medicine. Frontiers in Genetics, 2019, 10, 267.	1.1	142
7	GWAS on longitudinal growth traits reveals different genetic factors influencing infant, child, and adult BMI. Science Advances, 2019, 5, eaaw3095.	4.7	86
8	Physical Interactions and Expression Quantitative Traits Loci Identify Regulatory Connections for Obesity and Type 2 Diabetes Associated SNPs. Frontiers in Genetics, 2017, 8, 150.	1.1	84
9	Genome Modeling System: A Knowledge Management Platform for Genomics. PLoS Computational Biology, 2015, 11, e1004274.	1.5	83
10	Effects of Fecal Microbiome Transfer in Adolescents With Obesity. JAMA Network Open, 2020, 3, e2030415.	2.8	76
11	Plasticity of the Systemic Inflammatory Response to Acute Infection during Critical Illness: Development of the Riboleukogram. PLoS ONE, 2008, 3, e1564.	1.1	68
12	Chromatin interactions and expression quantitative trait loci reveal genetic drivers of multimorbidities. Nature Communications, 2018, 9, 5198.	5.8	64
13	Differences in outcome between obese and nonobese patients following severe blunt trauma are not consistent with an early inflammatory genomic response. Critical Care Medicine, 2010, 38, 51-58.	0.4	55
14	Strain engraftment competition and functional augmentation in a multi-donor fecal microbiota transplantation trial for obesity. Microbiome, 2021, 9, 107.	4.9	55
15	The missing story behind Genome Wide Association Studies: single nucleotide polymorphisms in gene deserts have a story to tell. Frontiers in Genetics, 2014, 5, 39.	1.1	51
16	Smooth muscle cells from abdominal aortic aneurysms are unique and can independently and synergistically degrade insoluble elastin. Journal of Vascular Surgery, 2014, 60, 1033-1042.e5.	0.6	48
17	TARGETED DELIVERY OF siRNA TO CELL DEATH PROTEINS IN SEPSIS. Shock, 2009, 32, 131-139.	1.0	40
18	The role of DNA methylation in human trophoblast differentiation. Epigenetics, 2018, 13, 1154-1173.	1.3	38

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19	Intergenic GWAS SNPs are key components of the spatial and regulatory network for human growth. Human Molecular Genetics, 2016, 25, 3372-3382.	1.4	36
20	Validation of the Riboleukogram to Detect Ventilator-Associated Pneumonia After Severe Injury. Annals of Surgery, 2009, 250, 531-539.	2.1	32
21	Common Variants Coregulate Expression of <scp>GBA</scp> and Modifier Genes to Delay Parkinson's Disease Onset. Movement Disorders, 2020, 35, 1346-1356.	2.2	30
22	Identification of human skeletal muscle miRNA related to strength by high-throughput sequencing. Physiological Genomics, 2018, 50, 416-424.	1.0	27
23	GWAS on prolonged gestation (post-term birth): analysis of successive Finnish birth cohorts. Journal of Medical Genetics, 2018, 55, 55-63.	1.5	23
24	Myocardial transcriptional profiles in a murine model of sepsis: Evidence for the importance of age*. Pediatric Critical Care Medicine, 2008, 9, 530-535.	0.2	18
25	Connecting SNPs in Diabetes: A Spatial Analysis of Meta-GWAS Loci. Frontiers in Endocrinology, 2015, 6, 102.	1.5	18
26	Transcriptional profiling of the zebrafish proximal tubule. American Journal of Physiology - Renal Physiology, 2019, 317, F478-F488.	1.3	17
27	Protocol for the Gut Bugs Trial: a randomised double-blind placebo-controlled trial of gut microbiome transfer for the treatment of obesity in adolescents. BMJ Open, 2019, 9, e026174.	0.8	16
28	Estimating Sparse Gene Regulatory Networks Using a Bayesian Linear Regression. IEEE Transactions on Nanobioscience, 2010, 9, 121-131.	2.2	15
29	A diffusion model for the coordination of DNA replication in Schizosaccharomyces pombe. Scientific Reports, 2016, 6, 18757.	1.6	15
30	Unravelling the Shared Genetic Mechanisms Underlying 18 Autoimmune Diseases Using a Systems Approach. Frontiers in Immunology, 2021, 12, 693142.	2.2	14
31	Evidence for a Novel Blood RNA Diagnostic for Pediatric Appendicitis. Pediatric Emergency Care, 2010, 26, 333-338.	0.5	13
32	Assigning function to SNPs: Considerations when interpreting genetic variation. Seminars in Cell and Developmental Biology, 2022, 121, 135-142.	2.3	13
33	Genes and post-term birth: late for delivery. BMC Research Notes, 2014, 7, 720.	0.6	11
34	High prevalence of undiagnosed comorbidities among adolescents with obesity. Scientific Reports, 2020, 10, 20101.	1.6	10
35	Establishing gene regulatory networks from Parkinsonâ€™s disease risk loci. Brain, 2022, 145, 2422-2435.	3.7	10
36	Comprehensive Profiling of the Circulatory miRNAome Response to a High Protein Diet in Elderly Men: A Potential Role in Inflammatory Response Modulation. Molecular Nutrition and Food Research, 2019, 63, 1800811.	1.5	9

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37	Differences in Compositions of Gut Bacterial Populations and Bacteriophages in 5â€“11 Year-Olds Born Preterm Compared to Full Term. Frontiers in Cellular and Infection Microbiology, 2020, 10, 276.	1.8	9
38	Human trophoblasts are primarily distinguished from somatic cells by differences in the pattern rather than the degree of global CpG methylation. Biology Open, 2018, 7, .	0.6	6
39	Reconstructing the blood metabolome and genotype using long-range chromatin interactions. Metabolism Open, 2020, 6, 100035.	1.4	6
40	Preliminary Evidence for Leukocyte Transcriptional Signatures for Pediatric Ventilator-Associated Pneumonia. Journal of Intensive Care Medicine, 2012, 27, 362-369.	1.3	5
41	Shared Regulatory Pathways Reveal Novel Genetic Correlations Between Grip Strength and Neuromuscular Disorders. Frontiers in Genetics, 2020, 11, 393.	1.1	5
42	A systematic review of asthma case definitions in 67 birth cohort studies. Paediatric Respiratory Reviews, 2021, 37, 89-98.	1.2	5
43	Transcriptional Regulation of RUNX1: An Informatics Analysis. Genes, 2021, 12, 1175.	1.0	4
44	Machine Learning Identifies Six Genetic Variants and Alterations in the Heart Atrial Appendage as Key Contributors to PD Risk Predictivity. Frontiers in Genetics, 2021, 12, 785436.	1.1	4
45	Low tolerance for transcriptional variation at cohesin genes is accompanied by functional links to disease-relevant pathways. Journal of Medical Genetics, 2021, 58, 534-542.	1.5	3
46	Smooth Muscle Cells from Abdominal Aortic Aneurysms Are Unique and Can Independently and Synergistically Degrade Insoluble Elastin. Journal of Vascular Surgery, 2013, 57, 23S.	0.6	2
47	Identifying the lungs as a susceptible site for allele-specific regulatory changes associated with type 1 diabetes risk. Communications Biology, 2021, 4, 1072.	2.0	2
48	3D interactions with the growth hormone locus in cellular signalling and cancer-related pathways. Journal of Molecular Endocrinology, 2020, 64, 209-222.	1.1	2
49	Gene methylation regulates the acquisition of an invasive phenotype during extravillous trophoblast differentiation. Placenta, 2017, 57, 304.	0.7	0
50	PLASTICITY OF THE HUMAN INNATE IMMUNE RESPONSE TO ACUTE INFECTION DURING CRITICAL ILLNESS: DEVELOPMENT OF THE RIBOLEUKOGRAM.. Critical Care Medicine, 2006, 34, A47.	0.4	0
51	Whole Genome Sequencing Reveals Novel Recurring Somatic Mutations Affecting HUWE1 and DIAPH2 Genes in Multiple Myeloma. Blood, 2012, 120, 320-320.	0.6	0
52	Abstract LB-232: Tumor clonality detection using next generation sequencing data.. , 2013, , .		0