

# Silke Szymczak

## List of Publications by Year in descending order

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Version: 2024-02-01

69  
papers

7,145  
citations

159585

30  
h-index

91884

69  
g-index

71  
all docs

71  
docs citations

71  
times ranked

15284  
citing authors

#	ARTICLE	IF	CITATIONS
1	Genomewide Association Analysis of Coronary Artery Disease. <i>New England Journal of Medicine</i> , 2007, 357, 443-453.	27.0	1,865
2	A catalog of genetic loci associated with kidney function from analyses of a million individuals. <i>Nature Genetics</i> , 2019, 51, 957-972.	21.4	549
3	Genetics and Beyond – The Transcriptome of Human Monocytes and Disease Susceptibility. <i>PLoS ONE</i> , 2010, 5, e10693.	2.5	539
4	Genome-wide association analysis identifies variation in vitamin D receptor and other host factors influencing the gut microbiota. <i>Nature Genetics</i> , 2016, 48, 1396-1406.	21.4	533
5	Evaluation of variable selection methods for random forests and omics data sets. <i>Briefings in Bioinformatics</i> , 2019, 20, 492-503.	6.5	342
6	Increased Tryptophan Metabolism Is Associated With Activity of Inflammatory Bowel Diseases. <i>Gastroenterology</i> , 2017, 153, 1504-1516.e2.	1.3	338
7	Trans-ancestry genome-wide association study identifies 12 genetic loci influencing blood pressure and implicates a role for DNA methylation. <i>Nature Genetics</i> , 2015, 47, 1282-1293.	21.4	294
8	Atopic Dermatitis Is an IL-13–Dominant Disease with Greater Molecular Heterogeneity Compared to Psoriasis. <i>Journal of Investigative Dermatology</i> , 2019, 139, 1480-1489.	0.7	283
9	A trans-acting locus regulates an anti-viral expression network and type 1 diabetes risk. <i>Nature</i> , 2010, 467, 460-464.	27.8	271
10	Metabolic Functions of Gut Microbes Associate With Efficacy of Tumor Necrosis Factor Antagonists in Patients With Inflammatory Bowel Diseases. <i>Gastroenterology</i> , 2019, 157, 1279-1292.e11.	1.3	180
11	Genome-wide association meta-analyses and fine-mapping elucidate pathways influencing albuminuria. <i>Nature Communications</i> , 2019, 10, 4130.	12.8	133
12	A Genome-Wide Association Study Identifies <i>LIPA</i> as a Susceptibility Gene for Coronary Artery Disease. <i>Circulation: Cardiovascular Genetics</i> , 2011, 4, 403-412.	5.1	130
13	Integrating Genome-Wide Genetic Variations and Monocyte Expression Data Reveals Trans-Regulated Gene Modules in Humans. <i>PLoS Genetics</i> , 2011, 7, e1002367.	3.5	126
14	A Hereditary Form of Small Intestinal Carcinoid Associated With a Germline Mutation in Inositol Polyphosphate Multikinase. <i>Gastroenterology</i> , 2015, 149, 67-78.	1.3	96
15	A fungal pathogen induces systemic susceptibility and systemic shifts in wheat metabolome and microbiome composition. <i>Nature Communications</i> , 2020, 11, 1910.	12.8	85
16	Construction of a Large Signature-Tagged Mini-Tn5 Transposon Library and Its Application to Mutagenesis of <i>Sinorhizobium meliloti</i> . <i>Applied and Environmental Microbiology</i> , 2006, 72, 4329-4337.	3.1	84
17	Individual Radiosensitivity Measured With Lymphocytes May Predict the Risk of Acute Reaction After Radiotherapy. <i>International Journal of Radiation Oncology Biology Physics</i> , 2008, 71, 256-264.	0.8	79
18	Whole Exome Sequencing of Distant Relatives in Multiplex Families Implicates Rare Variants in Candidate Genes for Oral Clefts. <i>Genetics</i> , 2014, 197, 1039-1044.	2.9	79

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19	Association of single nucleotide polymorphisms in ATM, GSTP1, SOD2, TGFB1, XPD and XRCC1 with clinical and cellular radiosensitivity. <i>Radiotherapy and Oncology</i> , 2010, 97, 26-32.	0.6	69
20	Identification of Genes Relevant to Symbiosis and Competitiveness in <i>Sinorhizobium meliloti</i> Using Signature-Tagged Mutants. <i>Molecular Plant-Microbe Interactions</i> , 2008, 21, 219-231.	2.6	63
21	Histologic improvement of NAFLD in patients with obesity after bariatric surgery based on standardized NAS (NAFLD activity score). <i>Surgery for Obesity and Related Diseases</i> , 2018, 14, 1607-1616.	1.2	56
22	r2VIM: A new variable selection method for random forests in genome-wide association studies. <i>BioData Mining</i> , 2016, 9, 7.	4.0	53
23	Deregulation of a distinct set of microRNAs is associated with transformation of gastritis into MALT lymphoma. <i>Virchows Archiv Fur Pathologische Anatomie Und Physiologie Und Fur Klinische Medizin</i> , 2012, 460, 371-377.	2.8	46
24	Increased cathepsin D protein expression is a biomarker for osteosarcomas, pulmonary metastases and other bone malignancies. <i>Oncotarget</i> , 2015, 6, 16517-16526.	1.8	44
25	Vy-PER: eliminating false positive detection of virus integration events in next generation sequencing data. <i>Scientific Reports</i> , 2015, 5, 11534.	3.3	42
26	Meta-analysis uncovers genome-wide significant variants for rapid kidney function decline. <i>Kidney International</i> , 2021, 99, 926-939.	5.2	42
27	Rare Variants in Specific Lysosomal Genes Are Associated With Parkinson's Disease. <i>Movement Disorders</i> , 2020, 35, 1245-1248.	3.9	37
28	Evaluation of interleukin-6 and its soluble receptor components sIL-6R and sgp130 as markers of inflammation in inflammatory bowel diseases. <i>International Journal of Colorectal Disease</i> , 2018, 33, 927-936.	2.2	34
29	Association of single nucleotide polymorphisms in the genes ATM, GSTP1, SOD2, TGFB1, XPD and XRCC1 with risk of severe erythema after breast conserving radiotherapy. <i>Radiation Oncology</i> , 2012, 7, 65.	2.7	33
30	Sparse Modeling Reveals miRNA Signatures for Diagnostics of Inflammatory Bowel Disease. <i>PLoS ONE</i> , 2015, 10, e0140155.	2.5	31
31	Topography of essential tremor. <i>Parkinsonism and Related Disorders</i> , 2017, 40, 58-63.	2.2	30
32	Picking single-nucleotide polymorphisms in forests. <i>BMC Proceedings</i> , 2007, 1, S59.	1.6	28
33	Surrogate minimal depth as an importance measure for variables in random forests. <i>Bioinformatics</i> , 2019, 35, 3663-3671.	4.1	26
34	Serologic Anti-GP2 Antibodies Are Associated with Genetic Polymorphisms, Fibrostenosis, and Need for Surgical Resection in Crohn's Disease. <i>Inflammatory Bowel Diseases</i> , 2016, 22, 2648-2657.	1.9	25
35	Influence of sex and genetic variability on expression of X-linked genes in human monocytes. <i>Genomics</i> , 2011, 98, 320-326.	2.9	23
36	Stress sensitivity is increased in transgenic rats with low brain angiotensinogen. <i>Journal of Endocrinology</i> , 2010, 204, 85-92.	2.6	18

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37	Genetic loci and prioritization of genes for kidney function decline derived from a meta-analysis of 62 longitudinal genome-wide association studies. <i>Kidney International</i> , 2022, 102, 624-639.	5.2	18
38	Detecting SNP-expression associations: A comparison of mutual information and median test with standard statistical approaches. <i>Statistics in Medicine</i> , 2009, 28, 3581-3596.	1.6	17
39	HDAC2 and TXNL1 distinguish aneuploid from diploid colorectal cancers. <i>Cellular and Molecular Life Sciences</i> , 2011, 68, 3261-3274.	5.4	17
40	Chromosomal Aneuploidy Affects the Global Proteome Equilibrium of Colorectal Cancer Cells. <i>Analytical Cellular Pathology</i> , 2013, 36, 149-161.	1.4	17
41	Blood transcriptome profiling identifies 2 candidate endotypes of atopic dermatitis. <i>Journal of Allergy and Clinical Immunology</i> , 2022, 150, 385-395.	2.9	17
42	The potential role of G2- but not of G0-radiosensitivity for predisposition of prostate cancer. <i>Radiotherapy and Oncology</i> , 2010, 96, 19-24.	0.6	15
43	Genome-wide association study of serum coenzyme Q <sub>10</sub> levels identifies susceptibility loci linked to neuronal diseases. <i>Human Molecular Genetics</i> , 2016, 25, ddw134.	2.9	15
44	Paternal chronic colitis causes epigenetic inheritance of susceptibility to colitis. <i>Scientific Reports</i> , 2016, 6, 31640.	3.3	15
45	DNA methylation QTL analysis identifies new regulators of human longevity. <i>Human Molecular Genetics</i> , 2020, 29, 1154-1167.	2.9	15
46	Risk estimation using probability machines. <i>BioData Mining</i> , 2014, 7, 2.	4.0	14
47	Host traits, lifestyle and environment are associated with human skin bacteria. <i>British Journal of Dermatology</i> , 2021, 185, 573-584.	1.5	14
48	Genomewide RNAi screen identifies protein kinase C <sup>Î²</sup> and new members of mitogen-activated protein kinase pathway as regulators of melanoma cell growth and metastasis. <i>Pigment Cell and Melanoma Research</i> , 2014, 27, 418-430.	3.3	12
49	Association between SNPs in defined functional pathways and risk of early or late toxicity as well as individual radiosensitivity. <i>Strahlentherapie Und Onkologie</i> , 2015, 191, 59-66.	2.0	12
50	NGS-based methylation profiling differentiates TCF3-HLF and TCF3-PBX1 positive B-cell acute lymphoblastic leukemia. <i>Epigenomics</i> , 2018, 10, 133-147.	2.1	10
51	The BIOMarkers in Atopic Dermatitis and Psoriasis (BIOMAP) glossary: developing a lingua franca to facilitate data harmonization and cross-cohort analyses. <i>British Journal of Dermatology</i> , 2021, 185, 1066-1069.	1.5	10
52	Chromosomal aneuploidy affects the global proteome equilibrium of colorectal cancer cells. <i>Analytical Cellular Pathology</i> , 2013, 36, 149-61.	1.4	10
53	ACPA: automated cluster plot analysis of genotype data. <i>BMC Proceedings</i> , 2009, 3, S58.	1.6	9
54	Heterogeneous intracellular TRAIL-receptor distribution predicts poor outcome in breast cancer patients. <i>Journal of Molecular Medicine</i> , 2019, 97, 1155-1167.	3.9	9

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55	Genetic Analysis Workshop 16: Strategies for genome-wide association study analyses. BMC Proceedings, 2009, 3, S1.	1.6	8
56	Protein profiling of genomic instability in endometrial cancer. Cellular and Molecular Life Sciences, 2012, 69, 325-333.	5.4	8
57	Integrating biological knowledge and gene expression data using pathway-guided random forests: a benchmarking study. Bioinformatics, 2020, 36, 4301-4308.	4.1	8
58	Evaluation of single-nucleotide polymorphism imputation using random forests. BMC Proceedings, 2009, 3, S65.	1.6	7
59	Genetic association studies for gene expressions: permutation-based mutual information in a comparison with standard ANOVA and as a novel approach for feature selection. BMC Proceedings, 2007, 1, S9.	1.6	6
60	The metabolic network coherence of human transcriptomes is associated with genetic variation at the cadherin 18 locus. Human Genetics, 2019, 138, 375-388.	3.8	6
61	Variable selection method for the identification of epistatic models. Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing, 2015, , 195-206.	0.7	6
62	Linkage analysis identifies novel genetic modifiers of microbiome traits in families with inflammatory bowel disease. Gut Microbes, 2022, 14, 2024415.	9.8	5
63	Adaptive linear rank tests for eQTL studies. Statistics in Medicine, 2013, 32, 524-537.	1.6	4
64	Early prediction of final infarct volume with material decomposition images of dual-energy CT after mechanical thrombectomy. Neuroradiology, 2021, 63, 695-704.	2.2	4
65	Private variants in PRKN are associated with late-onset Parkinson's disease. Parkinsonism and Related Disorders, 2020, 75, 24-26.	2.2	4
66	Genotype imputation in case-only studies of gene-environment interaction: validity and power. Human Genetics, 2021, 140, 1217-1228.	3.8	3
67	False-positive rates in two-point parametric linkage analysis. BMC Proceedings, 2014, 8, S110.	1.6	1
68	Comparison of parametric and machine methods for variable selection in simulated Genetic Analysis Workshop 19 data. BMC Proceedings, 2016, 10, 147-152.	1.6	1
69	Heterogeneous intracellular TRAIL-receptor distribution predicts poor outcome in breast cancer patients. Senologie - Zeitschrift für Mammadiagnostik Und -therapie, 2019, 16, .	0.0	0