# Silke Szymczak

List of Publications by Year
in descending order



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|---|---|---|---|
| 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 | Linkage analysis identifies novel genetic modifiers of microbiome traits in families with inflammatory bowel disease. Gut Microbes, 2022, 14, 2024415. | 9.8 | 5 |
| 2 | Blood transcriptome profiling identifies 2 candidate endotypes of atopic dermatitis. Journal of Allergy and Clinical Immunology, 2022, 150, 385-395. | 2.9 | 17 |
| 3 | Genetic loci and prioritization of genes for kidney function decline derived from a meta-analysis of 62 longitudinal genome-wide association studies. Kidney International, 2022, 102, 624-639. | 5.2 | 18 |
| 4 | 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 |
| 5 | Meta-analysis uncovers genome-wide significant variants for rapid kidney function decline. Kidney International, 2021, 99, 926-939. | 5.2 | 42 |
| 6 | Genotype imputation in case-only studies of gene-environment interaction: validity and power. Human Genetics, 2021, 140, 1217-1228. | 3.8 | 3 |
| 7 | Host traits, lifestyle and environment are associated with human skin bacteria. British Journal of Dermatology, 2021, 185, 573-584. | 1.5 | 14 |
| 8 | The BIOMarkers in Atopic Dermatitis and Psoriasis (BIOMAP) glossary: developing a lingua franca to facilitate data harmonization and crossâ€cohort analyses. British Journal of Dermatology, 2021, 185, 1066-1069. | 1.5 | 10 |
| 9 | Integrating biological knowledge and gene expression data using pathway-guided random forests: a benchmarking study. Bioinformatics, 2020, 36, 4301-4308. | 4.1 | 8 |
| 10 | DNA methylation QTL analysis identifies new regulators of human longevity. Human Molecular Genetics, 2020, 29, 1154-1167. | 2.9 | 15 |
| 11 | Rare Variants in Specific Lysosomal Genes Are Associated With Parkinson's Disease. Movement Disorders, 2020, 35, 1245-1248. | 3.9 | 37 |
| 12 | A fungal pathogen induces systemic susceptibility and systemic shifts in wheat metabolome and microbiome composition. Nature Communications, 2020, 11, 1910. | 12.8 | 85 |
| 13 | Private variants in PRKN are associated with late-onset Parkinson's disease. Parkinsonism and Related Disorders, 2020, 75, 24-26. | 2.2 | 4 |
| 14 | Genome-wide association meta-analyses and fine-mapping elucidate pathways influencing albuminuria. Nature Communications, 2019, 10, 4130. | 12.8 | 133 |
| 15 | Metabolic Functions of Gut Microbes Associate With Efficacy ofÂTumor Necrosis Factor Antagonists in Patients With Inflammatory Bowel Diseases. Gastroenterology, 2019, 157, 1279-1292.e11. | 1.3 | 180 |
| 16 | A catalog of genetic loci associated with kidney function from analyses of a million individuals. Nature Genetics, 2019, 51, 957-972. | 21.4 | 549 |
| 17 | Heterogeneous intracellular TRAIL-receptor distribution predicts poor outcome in breast cancer patients. Journal of Molecular Medicine, 2019, 97, 1155-1167. | 3.9 | 9 |
| 18 | Atopic Dermatitis Is an IL-13â€“Dominant Disease with Greater Molecular Heterogeneity Compared to Psoriasis. Journal of Investigative Dermatology, 2019, 139, 1480-1489. | 0.7 | 283 |

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|---|---|---|---|
| 19 | Surrogate minimal depth as an importance measure for variables in random forests. Bioinformatics, 2019, 35, 3663-3671. | 4.1 | 26 |
| 20 | 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 |
| 21 | Evaluation of variable selection methods for random forests and omics data sets. Briefings in Bioinformatics, 2019, 20, 492-503. | 6.5 | 342 |
| 22 | Heterogeneous intracellular TRAIL-receptor distribution predicts poor outcome in breast cancer patients. Senologie - Zeitschrift FÃ¼r Mammadiagnostik Und -therapie, 2019, 16, . | 0.0 | 0 |
| 23 | NGS-based methylation profiling differentiates TCF3-HLF and TCF3-PBX1 positive B-cell acute lymphoblastic leukemia. Epigenomics, 2018, 10, 133-147. | 2.1 | 10 |
| 24 | Histologic improvement of NAFLD in patients with obesity after bariatric surgery based on standardized NAS (NAFLD activity score). Surgery for Obesity and Related Diseases, 2018, 14, 1607-1616. | 1.2 | 56 |
| 25 | Evaluation of interleukin-6 and its soluble receptor components sIL-6R and sgp130 as markers of inflammation in inflammatory bowel diseases. International Journal of Colorectal Disease, 2018, 33, 927-936. | 2.2 | 34 |
| 26 | Topography of essential tremor. Parkinsonism and Related Disorders, 2017, 40, 58-63. | 2.2 | 30 |
| 27 | Increased Tryptophan Metabolism Is Associated With Activity of Inflammatory Bowel Diseases. Gastroenterology, 2017, 153, 1504-1516.e2. | 1.3 | 338 |
| 28 | Serologic Anti-GP2 Antibodies Are Associated with Genetic Polymorphisms, Fibrostenosis, and Need for Surgical Resection in CrohnÊ¼s Disease. Inflammatory Bowel Diseases, 2016, 22, 2648-2657. | 1.9 | 25 |
| 29 | Genome-wide association study of serum coenzyme Q<sub>10</sub>levels identifies susceptibility loci linked to neuronal diseases. Human Molecular Genetics, 2016, 25, ddw134. | 2.9 | 15 |
| 30 | Genome-wide association analysis identifies variation in vitamin D receptor and other host factors influencing the gut microbiota. Nature Genetics, 2016, 48, 1396-1406. | 21.4 | 533 |
| 31 | Paternal chronic colitis causes epigenetic inheritance of susceptibility to colitis. Scientific Reports, 2016, 6, 31640. | 3.3 | 15 |
| 32 | 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 |
| 33 | r2VIM: A new variable selection method for random forests in genome-wide association studies. BioData Mining, 2016, 9, 7. | 4.0 | 53 |
| 34 | Association between SNPs in defined functional pathways and risk of early or late toxicity as well as individual radiosensitivity. Strahlentherapie Und Onkologie, 2015, 191, 59-66. | 2.0 | 12 |
| 35 | A Hereditary Form of Small Intestinal Carcinoid Associated With a Germline Mutation in Inositol Polyphosphate Multikinase. Gastroenterology, 2015, 149, 67-78. | 1.3 | 96 |
| 36 | Vy-PER: eliminating false positive detection of virus integration events in next generation sequencing data. Scientific Reports, 2015, 5, 11534. | 3.3 | 42 |

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|---|---|---|---|
| 37 | Trans-ancestry genome-wide association study identifies 12 genetic loci influencing blood pressure and implicates a role for DNA methylation. Nature Genetics, 2015, 47, 1282-1293. | 21.4 | 294 |
| 38 | Sparse Modeling Reveals miRNA Signatures for Diagnostics of Inflammatory Bowel Disease. PLoS ONE, 2015, 10, e0140155. | 2.5 | 31 |
| 39 | Increased cathepsin D protein expression is a biomarker for osteosarcomas, pulmonary metastases and other bone malignancies. Oncotarget, 2015, 6, 16517-16526. | 1.8 | 44 |
| 40 | Variable selection method for the identification of epistatic models. Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing, 2015, , 195-206. | 0.7 | 6 |
| 41 | Genomewide <scp>RNA</scp>i screen identifies protein kinase <scp>C</scp>Î² and new members of mitogenâ€activated protein kinase pathway as regulators of melanoma cell growth and metastasis. Pigment Cell and Melanoma Research, 2014, 27, 418-430. | 3.3 | 12 |
| 42 | False-positive rates in two-point parametric linkage analysis. BMC Proceedings, 2014, 8, S110. | 1.6 | 1 |
| 43 | Whole Exome Sequencing of Distant Relatives in Multiplex Families Implicates Rare Variants in Candidate Genes for Oral Clefts. Genetics, 2014, 197, 1039-1044. | 2.9 | 79 |
| 44 | Risk estimation using probability machines. BioData Mining, 2014, 7, 2. | 4.0 | 14 |
| 45 | Adaptive linear rank tests for eQTL studies. Statistics in Medicine, 2013, 32, 524-537. | 1.6 | 4 |
| 46 | Chromosomal Aneuploidy Affects the Global Proteome Equilibrium of Colorectal Cancer Cells. Analytical Cellular Pathology, 2013, 36, 149-161. | 1.4 | 17 |
| 47 | Chromosomal aneuploidy affects the global proteome equilibrium of colorectal cancer cells. Analytical Cellular Pathology, 2013, 36, 149-61. | 1.4 | 10 |
| 48 | Association of single nucleotide polymorphisms in the genes ATM, GSTP1, SOD2, TGFB1, XPD and XRCC1 with risk of severe erythema after breast conserving radiotherapy. Radiation Oncology, 2012, 7, 65. | 2.7 | 33 |
| 49 | Deregulation of a distinct set of microRNAs is associated with transformation of gastritis into MALT lymphoma. Virchows Archiv Fur Pathologische Anatomie Und Physiologie Und Fur Klinische Medizin, 2012, 460, 371-377. | 2.8 | 46 |
| 50 | Protein profiling of genomic instability in endometrial cancer. Cellular and Molecular Life Sciences, 2012, 69, 325-333. | 5.4 | 8 |
| 51 | Influence of sex and genetic variability on expression of X-linked genes in human monocytes. Genomics, 2011, 98, 320-326. | 2.9 | 23 |
| 52 | A Genome-Wide Association Study Identifies LIPA as a Susceptibility Gene for Coronary Artery Disease. Circulation: Cardiovascular Genetics, 2011, 4, 403-412. | 5.1 | 130 |
| 53 | HDAC2 and TXNL1 distinguish aneuploid from diploid colorectal cancers. Cellular and Molecular Life Sciences, 2011, 68, 3261-3274. | 5.4 | 17 |
| 54 | Integrating Genome-Wide Genetic Variations and Monocyte Expression Data Reveals Trans-Regulated Gene Modules in Humans. PLoS Genetics, 2011, 7, e1002367. | 3.5 | 126 |

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|---|---|---|---|
| 55 | A trans-acting locus regulates an anti-viral expression network and type 1 diabetes risk. Nature, 2010, 467, 460-464. | 27.8 | 271 |
| 56 | Genetics and Beyond â€“ The Transcriptome of Human Monocytes and Disease Susceptibility. PLoS ONE, 2010, 5, e10693. | 2.5 | 539 |
| 57 | Stress sensitivity is increased in transgenic rats with low brain angiotensinogen. Journal of Endocrinology, 2010, 204, 85-92. | 2.6 | 18 |
| 58 | Association of single nucleotide polymorphisms in ATM, GSTP1, SOD2, TGFB1, XPD and XRCC1 with clinical and cellular radiosensitivity. Radiotherapy and Oncology, 2010, 97, 26-32. | 0.6 | 69 |
| 59 | The potential role of G2- but not of G0-radiosensitivity for predisposition of prostate cancer. Radiotherapy and Oncology, 2010, 96, 19-24. | 0.6 | 15 |
| 60 | ACPA: automated cluster plot analysis of genotype data. BMC Proceedings, 2009, 3, S58. | 1.6 | 9 |
| 61 | Genetic Analysis Workshop 16: Strategies for genome-wide association study analyses. BMC Proceedings, 2009, 3, S1. | 1.6 | 8 |
| 62 | Evaluation of single-nucleotide polymorphism imputation using random forests. BMC Proceedings, 2009, 3, S65. | 1.6 | 7 |
| 63 | Detecting SNPâ€expression associations: A comparison of mutual information and median test with standard statistical approaches. Statistics in Medicine, 2009, 28, 3581-3596. | 1.6 | 17 |
| 64 | Individual Radiosensitivity Measured With Lymphocytes May Predict the Risk of Acute Reaction After Radiotherapy. International Journal of Radiation Oncology Biology Physics, 2008, 71, 256-264. | 0.8 | 79 |
| 65 | Identification of Genes Relevant to Symbiosis and Competitiveness in Sinorhizobium meliloti Using Signature-Tagged Mutants. Molecular Plant-Microbe Interactions, 2008, 21, 219-231. | 2.6 | 63 |
| 66 | Genomewide Association Analysis of Coronary Artery Disease. New England Journal of Medicine, 2007, 357, 443-453. | 27.0 | 1,865 |
| 67 | 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 |
| 68 | Picking single-nucleotide polymorphisms in forests. BMC Proceedings, 2007, 1, S59. | 1.6 | 28 |
| 69 | Construction of a Large Signature-Tagged Mini-Tn5 Transposon Library and Its Application to Mutagenesis of Sinorhizobium meliloti. Applied and Environmental Microbiology, 2006, 72, 4329-4337. | 3.1 | 84 |