

# Stefan Enroth

## List of Publications by Citations

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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.

89 papers	10,551 citations	37 h-index	102 g-index
105 ext. papers	12,846 ext. citations	10.5 avg, IF	5.17 L-index

#	Paper	IF	Citations
89	Identification and analysis of functional elements in 1% of the human genome by the ENCODE pilot project. <i>Nature</i> , <b>2007</b> , 447, 799-816	50.4	4121
88	Kcnq1ot1 antisense noncoding RNA mediates lineage-specific transcriptional silencing through chromatin-level regulation. <i>Molecular Cell</i> , <b>2008</b> , 32, 232-46	17.6	961
87	MEG3 long noncoding RNA regulates the TGF- $\beta$ pathway genes through formation of RNA-DNA triplex structures. <i>Nature Communications</i> , <b>2015</b> , 6, 7743	17.4	414
86	Genetic analysis of over 1 million people identifies 535 new loci associated with blood pressure traits. <i>Nature Genetics</i> , <b>2018</b> , 50, 1412-1425	36.3	386
85	Genome-wide association analysis identifies novel blood pressure loci and offers biological insights into cardiovascular risk. <i>Nature Genetics</i> , <b>2017</b> , 49, 403-415	36.3	313
84	Genetic associations at 53 loci highlight cell types and biological pathways relevant for kidney function. <i>Nature Communications</i> , <b>2016</b> , 7, 10023	17.4	295
83	The genetics of blood pressure regulation and its target organs from association studies in 342,415 individuals. <i>Nature Genetics</i> , <b>2016</b> , 48, 1171-1184	36.3	251
82	Nucleosomes are well positioned in exons and carry characteristic histone modifications. <i>Genome Research</i> , <b>2009</b> , 19, 1732-41	9.7	242
81	The Influence of Age and Sex on Genetic Associations with Adult Body Size and Shape: A Large-Scale Genome-Wide Interaction Study. <i>PLoS Genetics</i> , <b>2015</b> , 11, e1005378	6	220
80	Continuous Aging of the Human DNA Methylome Throughout the Human Lifespan. <i>PLoS ONE</i> , <b>2013</b> , 8, e67378	3.7	220
79	Genome-wide association analyses for lung function and chronic obstructive pulmonary disease identify new loci and potential druggable targets. <i>Nature Genetics</i> , <b>2017</b> , 49, 416-425	36.3	170
78	New genetic signals for lung function highlight pathways and chronic obstructive pulmonary disease associations across multiple ancestries. <i>Nature Genetics</i> , <b>2019</b> , 51, 481-493	36.3	156
77	Monte Carlo feature selection for supervised classification. <i>Bioinformatics</i> , <b>2008</b> , 24, 110-7	7.2	155
76	KLB is associated with alcohol drinking, and its gene product $\beta$ klotho is necessary for FGF21 regulation of alcohol preference. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2016</b> , 113, 14372-14377	11.5	150
75	Genetic adaptation of fatty-acid metabolism: a human-specific haplotype increasing the biosynthesis of long-chain omega-3 and omega-6 fatty acids. <i>American Journal of Human Genetics</i> , <b>2012</b> , 90, 809-20	11	148
74	Directional dominance on stature and cognition in diverse human populations. <i>Nature</i> , <b>2015</b> , 523, 459-463	50.4	119
73	Genome-wide association study of susceptibility loci for cervical cancer. <i>Journal of the National Cancer Institute</i> , <b>2013</b> , 105, 624-33	9.7	113

72	Butyrate mediates decrease of histone acetylation centered on transcription start sites and down-regulation of associated genes. <i>Genome Research</i> , <b>2007</b> , 17, 708-19	9.7	106
71	Genome-wide association analysis identifies six new loci associated with forced vital capacity. <i>Nature Genetics</i> , <b>2014</b> , 46, 669-77	36.3	104
70	Mapping of 79 loci for 83 plasma protein biomarkers in cardiovascular disease. <i>PLoS Genetics</i> , <b>2017</b> , 13, e1006706	6	102
69	Strong effects of genetic and lifestyle factors on biomarker variation and use of personalized cutoffs. <i>Nature Communications</i> , <b>2014</b> , 5, 4684	17.4	98
68	Novel Blood Pressure Locus and Gene Discovery Using Genome-Wide Association Study and Expression Data Sets From Blood and the Kidney. <i>Hypertension</i> , <b>2017</b> ,	8.5	85
67	Long noncoding RNA-mediated maintenance of DNA methylation and transcriptional gene silencing. <i>Development (Cambridge)</i> , <b>2012</b> , 139, 2792-803	6.6	85
66	Sixteen new lung function signals identified through 1000 Genomes Project reference panel imputation. <i>Nature Communications</i> , <b>2015</b> , 6, 8658	17.4	79
65	Whole-genome maps of USF1 and USF2 binding and histone H3 acetylation reveal new aspects of promoter structure and candidate genes for common human disorders. <i>Genome Research</i> , <b>2008</b> , 18, 380-92	9.7	72
64	1000 Genomes-based meta-analysis identifies 10 novel loci for kidney function. <i>Scientific Reports</i> , <b>2017</b> , 7, 45040	4.9	70
63	Epigenome-wide association study reveals differential DNA methylation in individuals with a history of myocardial infarction. <i>Human Molecular Genetics</i> , <b>2016</b> , 25, 4739-4748	5.6	67
62	Identification of genetic variants influencing the human plasma proteome. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2013</b> , 110, 4673-8	11.5	67
61	Binding sites for metabolic disease related transcription factors inferred at base pair resolution by chromatin immunoprecipitation and genomic microarrays. <i>Human Molecular Genetics</i> , <b>2005</b> , 14, 3435-47	5.6	66
60	Genomic and drug target evaluation of 90 cardiovascular proteins in 30,931 individuals. <i>Nature Metabolism</i> , <b>2020</b> , 2, 1135-1148	14.6	61
59	Molecular interactions between HNF4a, FOXA2 and GABP identified at regulatory DNA elements through ChIP-sequencing. <i>Nucleic Acids Research</i> , <b>2009</b> , 37, 7498-508	20.1	51
58	Stability of Proteins in Dried Blood Spot Biobanks. <i>Molecular and Cellular Proteomics</i> , <b>2017</b> , 16, 1286-1296	6.6	47
57	Genome-wide profiling of histone H3 lysine 27 and lysine 4 trimethylation in multiple myeloma reveals the importance of Polycomb gene targeting and highlights EZH2 as a potential therapeutic target. <i>Oncotarget</i> , <b>2016</b> , 7, 6809-23	3.3	47
56	Effects of Long-Term Storage Time and Original Sampling Month on Biobank Plasma Protein Concentrations. <i>EBioMedicine</i> , <b>2016</b> , 12, 309-314	8.8	45
55	High throughput proteomics identifies a high-accuracy 11 plasma protein biomarker signature for ovarian cancer. <i>Communications Biology</i> , <b>2019</b> , 2, 221	6.7	44

54	The relative contribution of DNA methylation and genetic variants on protein biomarkers for human diseases. <i>PLoS Genetics</i> , <b>2017</b> , 13, e1007005	6	39
53	Causal and synthetic associations of variants in the SERPINA gene cluster with alpha1-antitrypsin serum levels. <i>PLoS Genetics</i> , <b>2013</b> , 9, e1003585	6	37
52	The LCB Data Warehouse. <i>Bioinformatics</i> , <b>2006</b> , 22, 1024-6	7.2	34
51	Combinations of histone modifications mark exon inclusion levels. <i>PLoS ONE</i> , <b>2012</b> , 7, e29911	3.7	29
50	Integrative epigenomic and genomic analysis of malignant pheochromocytoma. <i>Experimental and Molecular Medicine</i> , <b>2010</b> , 42, 484-502	12.8	29
49	Chronic obstructive pulmonary disease and related phenotypes: polygenic risk scores in population-based and case-control cohorts. <i>Lancet Respiratory Medicine</i> , <b>2020</b> , 8, 696-708	35.1	29
48	Protein profiling reveals consequences of lifestyle choices on predicted biological aging. <i>Scientific Reports</i> , <b>2015</b> , 5, 17282	4.9	28
47	Cancer associated epigenetic transitions identified by genome-wide histone methylation binding profiles in human colorectal cancer samples and paired normal mucosa. <i>BMC Cancer</i> , <b>2011</b> , 11, 450	4.8	27
46	Evidence for large-scale gene-by-smoking interaction effects on pulmonary function. <i>International Journal of Epidemiology</i> , <b>2017</b> , 46, 894-904	7.8	25
45	Randomised study shows that repeated self-sampling and HPV test has more than two-fold higher detection rate of women with CIN2+ histology than Pap smear cytology. <i>British Journal of Cancer</i> , <b>2018</b> , 118, 896-904	8.7	25
44	Genome-wide binding of transcription factor ZEB1 in triple-negative breast cancer cells. <i>Journal of Cellular Physiology</i> , <b>2018</b> , 233, 7113-7127	7	25
43	Histone H3 lysine 27 trimethylation in adult differentiated colon associated to cancer DNA hypermethylation. <i>Epigenetics</i> , <b>2009</b> , 4, 107-13	5.7	24
42	Genome-wide DNA methylation study identifies genes associated with the cardiovascular biomarker GDF-15. <i>Human Molecular Genetics</i> , <b>2016</b> , 25, 817-27	5.6	23
41	Genomewide binding of transcription factor Snail1 in triple-negative breast cancer cells. <i>Molecular Oncology</i> , <b>2018</b> , 12, 1153-1174	7.9	20
40	Improved power and precision with whole genome sequencing data in genome-wide association studies of inflammatory biomarkers. <i>Scientific Reports</i> , <b>2019</b> , 9, 16844	4.9	20
39	A Meta-Analysis of Genome-Wide Association Studies of Growth Differentiation Factor-15 Concentration in Blood. <i>Frontiers in Genetics</i> , <b>2018</b> , 9, 97	4.5	19
38	Prevalence and sensitization of atopic allergy and coeliac disease in the Northern Sweden Population Health Study. <i>International Journal of Circumpolar Health</i> , <b>2013</b> , 72,	1.7	19
37	PATZ1 down-regulates FADS1 by binding to rs174557 and is opposed by SP1/SREBP1c. <i>Nucleic Acids Research</i> , <b>2017</b> , 45, 2408-2422	20.1	18

36	Systemic and specific effects of antihypertensive and lipid-lowering medication on plasma protein biomarkers for cardiovascular diseases. <i>Scientific Reports</i> , <b>2018</b> , 8, 5531	4.9	18
35	Genetic variants influencing phenotypic variance heterogeneity. <i>Human Molecular Genetics</i> , <b>2018</b> , 27, 799-810	5.6	18
34	Systematic validation of hypothesis-driven candidate genes for cervical cancer in a genome-wide association study. <i>Carcinogenesis</i> , <b>2014</b> , 35, 2084-8	4.6	18
33	Homozygous loss-of-function variants in European cosmopolitan and isolate populations. <i>Human Molecular Genetics</i> , <b>2015</b> , 24, 5464-74	5.6	18
32	Pathway analysis of cervical cancer genome-wide association study highlights the MHC region and pathways involved in response to infection. <i>Human Molecular Genetics</i> , <b>2014</b> , 23, 6047-60	5.6	17
31	Meta-analysis of exome array data identifies six novel genetic loci for lung function. <i>Wellcome Open Research</i> , <b>2018</b> , 3, 4	4.8	16
30	Pooled analysis of genome-wide association studies of cervical intraepithelial neoplasia 3 (CIN3) identifies a new susceptibility locus. <i>Oncotarget</i> , <b>2016</b> , 7, 42216-42224	3.3	16
29	Identification of Candidate Plasma Protein Biomarkers for Cervical Cancer Using the Multiplex Proximity Extension Assay. <i>Molecular and Cellular Proteomics</i> , <b>2019</b> , 18, 735-743	7.6	15
28	CanvasDB: a local database infrastructure for analysis of targeted- and whole genome re-sequencing projects. <i>Database: the Journal of Biological Databases and Curation</i> , <b>2014</b> , 2014,	5	14
27	Novel genes in cell cycle control and lipid metabolism with dynamically regulated binding sites for sterol regulatory element-binding protein 1 and RNA polymerase II in HepG2 cells detected by chromatin immunoprecipitation with microarray detection. <i>FEBS Journal</i> , <b>2009</b> , 276, 1878-90	5.7	14
26	Growth signals employ CGGBP1 to suppress transcription of Alu-SINEs. <i>Cell Cycle</i> , <b>2016</b> , 15, 1558-71	4.7	13
25	Immune cells lacking Y chromosome show dysregulation of autosomal gene expression. <i>Cellular and Molecular Life Sciences</i> , <b>2021</b> , 78, 4019-4033	10.3	13
24	Clinical validation of the HPVIR high-risk HPV test on cervical samples according to the international guidelines for human papillomavirus DNA test requirements for cervical cancer screening. <i>Virology Journal</i> , <b>2019</b> , 16, 107	6.1	12
23	Effect of genetic and environmental factors on protein biomarkers for common non-communicable disease and use of personally normalized plasma protein profiles (PNPPP). <i>Biomarkers</i> , <b>2015</b> , 20, 355-64	2.6	12
22	A two-step strategy for identification of plasma protein biomarkers for endometrial and ovarian cancer. <i>Clinical Proteomics</i> , <b>2018</b> , 15, 38	5	11
21	Randomised study of HPV prevalence and detection of CIN2+ in vaginal self-sampling compared to cervical specimens collected by medical personnel. <i>International Journal of Cancer</i> , <b>2019</b> , 144, 89-97	7.5	10
20	Peak Finder Metaserver - a novel application for finding peaks in ChIP-seq data. <i>BMC Bioinformatics</i> , <b>2013</b> , 14, 280	3.6	10
19	SICTIN: Rapid footprinting of massively parallel sequencing data. <i>BioData Mining</i> , <b>2010</b> , 3, 4	4.3	9

18	Nucleosome regulatory dynamics in response to TGF $\beta$ <i>Nucleic Acids Research</i> , <b>2014</b> , 42, 6921-34	20.1	6
17	Meta-analysis of exome array data identifies six novel genetic loci for lung function. <i>Wellcome Open Research</i> , <b>2018</b> , 3, 4	4.8	6
16	Targeted plasma proteomics identifies a novel, robust association between cornulin and Swedish moist snuff. <i>Scientific Reports</i> , <b>2018</b> , 8, 2320	4.9	5
15	Genomic evaluation of circulating proteins for drug target characterisation and precision medicine		5
14	New genetic signals for lung function highlight pathways and pleiotropy, and chronic obstructive pulmonary disease associations across multiple ancestries		5
13	Protein Detection Using the Multiplexed Proximity Extension Assay (PEA) From Plasma and Vaginal Fluid Applied to the Indicating FTA Elute Micro Card <i>Journal of Circulating Biomarkers</i> , <b>2016</b> , 5, 9	3.3	4
12	A strand specific high resolution normalization method for chip-sequencing data employing multiple experimental control measurements. <i>Algorithms for Molecular Biology</i> , <b>2012</b> , 7, 2	1.8	4
11	Genetic analysis of over one million people identifies 535 novel loci for blood pressure		4
10	Temporal changes in the vaginal microbiota in self-samples and its association with persistent HPV16 infection and CIN2. <i>Virology Journal</i> , <b>2020</b> , 17, 147	6.1	4
9	HPV viral load in self-collected vaginal fluid samples as predictor for presence of cervical intraepithelial neoplasia. <i>Virology Journal</i> , <b>2019</b> , 16, 146	6.1	4
8	Invasive cervical tumors with high and low HPV titer represent molecular subgroups with different disease etiology. <i>Carcinogenesis</i> , <b>2019</b> , 40, 269-278	4.6	3
7	Identification of Candidate Protein Biomarkers for CIN2+ Lesions from Self-Sampled, Dried Cervico-Vaginal Fluid Using LC-MS/MS. <i>Cancers</i> , <b>2021</b> , 13,	6.6	2
6	Distinct genetic regions are associated with differential population susceptibility to chemical exposures. <i>Environment International</i> , <b>2021</b> , 152, 106488	12.9	2
5	Meta-analysis of exome array data identifies six novel genetic loci for lung function. <i>Wellcome Open Research</i> , <b>2018</b> , 3, 4	4.8	1
4	Visualization of Rules in Rule-Based Classifiers. <i>Smart Innovation, Systems and Technologies</i> , <b>2012</b> , 329-338	3.5	1
3	Evaluation of 92 cardiovascular proteins in dried blood spots collected under field-conditions: Off-the-shelf affinity-based multiplexed assays work well, allowing for simplified sample collection. <i>BioEssays</i> , <b>2021</b> , 43, e2000299	4.1	1
2	Contribution of rare whole-genome sequencing variants to plasma protein levels and the missing heritability.. <i>Nature Communications</i> , <b>2022</b> , 13, 2532	17.4	0
1	Long noncoding RNA-mediated maintenance of DNA methylation and transcriptional gene silencing. <i>Journal of Cell Science</i> , <b>2012</b> , 125, e1-e1	5.3	

