Monika Stoll

List of Publications by Year
in descending order

64 papers	4,202 citations	257450 24 h-index	118850 62 g-index
74 all docs	74 docs citations	74 times ranked	9637 citing authors

#	Article	IF	Citations
1	Large-scale association analysis identifies 13 new susceptibility loci for coronary artery disease. Nature Genetics, 2011, 43, 333-338.	21.4	1,685
2	Genetic variation in DLG5 is associated with inflammatory bowel disease. Nature Genetics, 2004, 36, 476-480.	21.4	443
3	Autoinhibitory regulation of S100A8/S100A9 alarmin activity locally restricts sterile inflammation. Journal of Clinical Investigation, 2018, 128, 1852-1866.	8.2	166
4	IBD5 is a General Risk Factor for Inflammatory Bowel Disease: Replication of Association with Crohn Disease and Identification of a Novel Association with Ulcerative Colitis. American Journal of Human Genetics, 2003, 73, 205-211.	6.2	147
5	A genome-wide association study identifies 6p21 as novel risk locus for dilated cardiomyopathy. European Heart Journal, 2014, 35, 1069-1077.	2.2	137
6	Systematic Association Mapping Identifies NELL1 as a Novel IBD Disease Gene. PLoS ONE, 2007, 2, e691.	2.5	123
7	A roadmap to improve the quality of atrial fibrillation management: proceedings from the fifth Atrial Fibrillation Network/European Heart Rhythm Association consensus conference. Europace, 2016, 18, 37-50.	1.7	121
8	Nur77 serves as a molecular brake of the metabolic switch during T cell activation to restrict autoimmunity. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E8017-E8026.	7.1	93
9	Teriflunomide treatment for multiple sclerosis modulates T cell mitochondrial respiration with affinity-dependent effects. Science Translational Medicine, 2019, 11, .	12.4	92
10	HBEGF, SRA1, and IK: Three cosegregating genes as determinants of cardiomyopathy. Genome Research, 2009, 19, 395-403.	5.5	80
11	Natural genetic variation of the cardiac transcriptome in non-diseased donors and patients with dilated cardiomyopathy. Genome Biology, 2017, 18, 170.	8.8	70
12	Transcriptome Assessment Reveals a Dominant Role for TLR4 in the Activation of Human Monocytes by the Alarmin MRP8. Journal of Immunology, 2015, 194, 575-583.	0.8	68
13	Deep Sequencing in Conjunction with Expression and Functional Analyses Reveals Activation of FGFR1 in Ewing Sarcoma. Clinical Cancer Research, 2015, 21, 4935-4946.	7.0	68
14	A genome-wide association study identifies a gene network of ADAMTS genes in the predisposition to pediatric stroke. Blood, 2012, 120, 5231-5236.	1.4	62
15	Evidence of transmission ratio distortion of DLG5 R30Q variant in general and implication of an association with Crohn disease in men. Human Genetics, 2006, 119, 305-311.	3.8	61
16	Role of reduced ADAMTS13 in arterial ischemic stroke: A Pediatric Cohort Study. Annals of Neurology, 2013, 73, 58-64.	5.3	48
17	Ablation of biglycan attenuates cardiac hypertrophy and fibrosis after left ventricular pressure overload. Journal of Molecular and Cellular Cardiology, 2016, 101, 145-155.	1.9	42
18	DLG5 R30Q Variant Is a Female-Specific Protective Factor in Pediatric Onset Crohn's Disease. American Journal of Gastroenterology, 2007, 102, 391-398.	0.4	41

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19	Long non-coding RNA Databases in Cardiovascular Research. Genomics, Proteomics and Bioinformatics, 2016, 14, 191-199.	6.9	38
20	Revised roles of ISL1 in a hES cell-based model of human heart chamber specification. ELife, 2018, 7, .	6.0	38
21	Role of discs large homolog 5. World Journal of Gastroenterology, 2006, 12, 3651.	3.3	31
22	Fibrinogen Î± and Î³ genes and factor VLeiden in children with thromboembolism: results from 2 family-based association studies. Blood, 2009, 114, 1947-1953.	1.4	29
23	Recurrent stroke: the role of thrombophilia in a large international pediatric stroke population. Haematologica, 2019, 104, 1676-1681.	3.5	28
24	DNA methylation in an engineered heart tissue model of cardiac hypertrophy: common signatures and effects of DNA methylation inhibitors. Basic Research in Cardiology, 2016, 111, 9.	5.9	27
25	CD163 expression defines specific, IRF8-dependent, immune-modulatory macrophages in the bone marrow. Journal of Allergy and Clinical Immunology, 2020, 146, 1137-1151.	2.9	27
26	Postgwas: Advanced GWAS Interpretation in R. PLoS ONE, 2013, 8, e71775.	2.5	24
27	Heritability in a SCN5A -mutation founder population with increased female susceptibility to non-nocturnal ventricular tachyarrhythmia and sudden cardiac death. Heart Rhythm, 2017, 14, 1873-1881.	0.7	23
28	ADAMTS genes and the risk of cerebral aneurysm. Journal of Neurosurgery, 2016, 125, 269-274.	1.6	22
29	LncRNA secondary structure in the cardiovascular system. Non-coding RNA Research, 2017, 2, 137-142.	4.6	21
30	The Crohnâ€™s disease susceptibility gene DLG5 as a member of the CARD interaction network. Journal of Molecular Medicine, 2008, 86, 423-432.	3.9	20
31	Promotor polymorphisms of plasminogen activator inhibitor-1 and other thrombophilic genotypes in cerebral venous thrombosis: a case-control study in adults. Journal of Neurology, 2012, 259, 2287-2292.	3.6	20
32	Rare Variants in the ADAMTS13 Von Willebrand Factorâ€“Binding Domain Contribute to Pediatric Stroke. Circulation: Cardiovascular Genetics, 2016, 9, 357-367.	5.1	19
33	Rare genetic variants in SMAP1, B3GAT2, and RIMS1 contribute to pediatric venous thromboembolism. Blood, 2017, 129, 783-790.	1.4	19
34	Characterization of the Genetic Program Linked to the Development of Atrial Fibrillation in CREM-IbÎ”C-X Mice. Circulation: Arrhythmia and Electrophysiology, 2017, 10, .	4.8	19
35	Advances in predicting venous thromboembolism risk in children. British Journal of Haematology, 2018, 180, 654-665.	2.5	19
36	Evolutionary Patterns of Non-Coding RNA in Cardiovascular Biology. Non-coding RNA, 2019, 5, 15.	2.6	16

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37	Catalyzing Transcriptomics Research in Cardiovascular Disease: The CardioRNA COST Action CA17129. Non-coding RNA, 2019, 5, 31.	2.6	14
38	Single- and Multimarker Genome-Wide Scans Evidence Novel Genetic Risk Modifiers for Venous Thromboembolism. Thrombosis and Haemostasis, 2021, 121, 1169-1180.	3.4	14
39	Genomic instability in the naturally and prematurely aged myocardium. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	7.1	14
40	The Beaverâ€™s Phylogenetic Lineage Illuminated by Retroposon Reads. Scientific Reports, 2017, 7, 43562.	3.3	13
41	Climate change facilitates a parasiteâ€™s host exploitation via temperatureâ€mediated immunometabolic processes. Global Change Biology, 2021, 27, 94-107.	9.5	13
42	Insights into evolution and coexistence of the colibactin- and yersiniabactin secondary metabolite determinants in enterobacterial populations. Microbial Genomics, 2021, 7, .	2.0	13
43	Immunity comes first: The effect of parasite genotypes on adaptive immunity and immunization in three-spined sticklebacks. Developmental and Comparative Immunology, 2016, 54, 137-144.	2.3	12
44	A systematic SNP selection approach to identify mechanisms underlying disease aetiology: linking height to post-menopausal breast and colorectal cancer risk. Scientific Reports, 2017, 7, 41034.	3.3	10
45	Targeted resequencing of a locus for heparin-induced thrombocytopenia on chromosome 5 identified in a genome-wide association study. Journal of Molecular Medicine, 2018, 96, 765-775.	3.9	10
46	Non-Coding RNA Databases in Cardiovascular Research. Non-coding RNA, 2020, 6, 35.	2.6	10
47	A genome-wide association study in autoimmune neurological syndromes with anti-GAD65 autoantibodies. Brain, 2023, 146, 977-990.	7.6	10
48	ADAMTS12, a new candidate gene for pediatric stroke. PLoS ONE, 2020, 15, e0237928.	2.5	9
49	A genetic variant alters the secondary structure of the lncRNA H19 and is associated with dilated cardiomyopathy. RNA Biology, 2021, 18, 409-415.	3.1	9
50	Pathway-based variant enrichment analysis on the example of dilated cardiomyopathy. Human Genetics, 2016, 135, 31-40.	3.8	8
51	C/EBPÎ´-induced epigenetic changes control the dynamic gene transcription of S100a8 and S100a9. ELife, 2022, 11, .	6.0	8
52	Monocyte subpopulation profiling indicates CDK6-derived cell differentiation and identifies subpopulation-specific miRNA expression sets in acute and stable coronary artery disease. Scientific Reports, 2022, 12, 5589.	3.3	7
53	Advances in understanding stroke risk in children â€“ a geneticist's view. British Journal of Haematology, 2014, 164, 636-645.	2.5	5
54	Suppressor of Cytokine Signaling 1 is Involved in Gene Regulation Which Controls the Survival of Ly6Clow Monocytes in Mice. Cellular Physiology and Biochemistry, 2019, 52, 336-353.	1.6	5

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55	Fetal-Adult Cardiac Transcriptome Analysis in Rats with Contrasting Left Ventricular Mass Reveals New Candidates for Cardiac Hypertrophy. PLoS ONE, 2015, 10, e0116807.	2.5	4
56	Inherited Risk Factors for Thrombotic Diseases in Children: The Genome-Wide Perspective. Seminars in Thrombosis and Hemostasis, 2011, 37, 848-855.	2.7	3
57	Induction of ICER is superseded by smICER, challenging the impact of ICER under chronic betaâ€adrenergic stimulation. FASEB Journal, 2020, 34, 11272-11291.	0.5	2
58	Polymorphisms in the mTOR-PI3K-Akt pathway, energy balance-related exposures and colorectal cancer risk in the Netherlands Cohort Study. BioData Mining, 2022, 15, 2.	4.0	2
59	Genetic factors in pediatric venous thromboembolism. Thrombosis Research, 2017, 151, S97-S99.	1.7	1
60	Leukocyte gene expression in post-thrombotic syndrome. Thrombosis Research, 2021, 202, 40-42.	1.7	1
61	Evolutionarily conserved transcriptional landscape of the heart defining the chamber specific physiology. Genomics, 2021, 113, 3782-3792.	2.9	1
62	Validation of a predictive model for identifying an increased risk for recurrence in adolescents and young adults with a first provoked thromboembolism. Blood Cells, Molecules, and Diseases, 2022, 94, 102651.	1.4	1
63	Cardiac chamber-specific genetic alterations suggest candidate genes and pathways implicating the left ventricle in the pathogenesis of atrial fibrillation. Genomics, 2022, 114, 110320.	2.9	1
64	Low Density Lipoprotein Exposure of Plasmacytoid Dendritic Cells Blunts Toll-like Receptor 7/9 Signaling via NUR77. Biomedicines, 2022, 10, 1152.	3.2	1