

Markus Scholz

List of Publications by Year in descending order

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Version: 2024-02-01

160
papers

10,585
citations

87888

38
h-index

42399

92
g-index

166
all docs

166
docs citations

166
times ranked

18577
citing authors

#	ARTICLE	IF	CITATIONS
1	Associations of carotid intima media thickness with gene expression in whole blood and genetically predicted gene expression across 48 tissues. <i>Human Molecular Genetics</i> , 2022, 31, 1171-1182.	2.9	4
2	Verification of immunology-related genetic associations in BPD supports ABCA3 and five other genes. <i>Pediatric Research</i> , 2022, 92, 190-198.	2.3	4
3	Perioperative Two-Dimensional Left Ventricular Global Longitudinal Strain in Coronary Artery Bypass Surgery: A Prospective Observational Pilot Study. <i>Journal of Cardiothoracic and Vascular Anesthesia</i> , 2022, 36, 166-174.	1.3	4
4	Meta-GWAS of PCSK9 levels detects two novel loci at <i>APOB</i> and <i>TM6SF2</i> . <i>Human Molecular Genetics</i> , 2022, 31, 999-1011.	2.9	9
5	Peripheral blood RNA biomarkers for cardiovascular disease from bench to bedside: a position paper from the EU-CardioRNA COST action CA17129. <i>Cardiovascular Research</i> , 2022, 118, 3183-3197.	3.8	18
6	Interplay between adipose tissue secreted proteins, eating behavior and obesity. <i>European Journal of Nutrition</i> , 2022, 61, 885-899.	3.9	8
7	Genetic Regulation of Cytokine Response in Patients with Acute Community-Acquired Pneumonia. <i>Genes</i> , 2022, 13, 111.	2.4	1
8	Genome-wide meta-analysis of phytosterols reveals five novel loci and a detrimental effect on coronary atherosclerosis. <i>Nature Communications</i> , 2022, 13, 143.	12.8	17
9	Whole Blood Metabolite Profiles Reflect Changes in Energy Metabolism in Heart Failure. <i>Metabolites</i> , 2022, 12, 216.	2.9	5
10	Colocalization analysis of pancreas eQTLs with risk loci from alcoholic and novel non-alcoholic chronic pancreatitis GWAS suggests potential disease causing mechanisms. <i>Pancreatology</i> , 2022, 22, 449-456.	1.1	3
11	Genetically Determined Reproductive Aging and Coronary Heart Disease: A Bidirectional 2-sample Mendelian Randomization. <i>Journal of Clinical Endocrinology and Metabolism</i> , 2022, 107, e2952-e2961.	3.6	13
12	Transcriptome Analyses of Adipose Tissue Samples Identify EGFL6 as a Candidate Gene Involved in Obesity-Related Adipose Tissue Dysfunction in Children. <i>International Journal of Molecular Sciences</i> , 2022, 23, 4349.	4.1	4
13	Impact of medication on blood transcriptome reveals off-target regulations of beta-blockers. <i>PLoS ONE</i> , 2022, 17, e0266897.	2.5	1
14	Genetically regulated gene expression and proteins revealed discordant effects. <i>PLoS ONE</i> , 2022, 17, e0268815.	2.5	1
15	Simultaneous Mass Spectrometry-Based Apolipoprotein Profiling and Apolipoprotein E Phenotyping in Patients with ASCVD and Mild Cognitive Impairment. <i>Nutrients</i> , 2022, 14, 2474.	4.1	5
16	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
17	Differential and shared genetic effects on kidney function between diabetic and non-diabetic individuals. <i>Communications Biology</i> , 2022, 5, .	4.4	17
18	DNA methylation patterns reflect individual's lifestyle independent of obesity. <i>Clinical and Translational Medicine</i> , 2022, 12, .	4.0	13

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19	Integrational approaches for cross-species analysis of lung pathologies at single-cell resolution. <i>Pneumologie</i> , 2022, , .	0.1	0
20	On the Parametrization of Epidemiologic Modelsâ€™ Lessons from Modelling COVID-19 Epidemic. <i>Viruses</i> , 2022, 14, 1468.	3.3	7
21	Metabolite-Investigator: an integrated user-friendly workflow for metabolomics multi-study analysis. <i>Bioinformatics</i> , 2021, 37, 2218-2220.	4.1	12
22	Different DOACs Control Inflammation in Cardiac Ischemia-Reperfusion Differently. <i>Circulation Research</i> , 2021, 128, 513-529.	4.5	26
23	Meta-analysis uncovers genome-wide significant variants for rapid kidney function decline. <i>Kidney International</i> , 2021, 99, 926-939.	5.2	42
24	Higher BMI, but not obesity-related genetic polymorphisms, correlates with lower structural connectivity of the reward network in a population-based study. <i>International Journal of Obesity</i> , 2021, 45, 491-501.	3.4	16
25	The novel cystatin C, lactate, interleukin-6, and N-terminal pro-B-type natriuretic peptide (CLIP)-based mortality risk score in cardiogenic shock after acute myocardial infarction. <i>European Heart Journal</i> , 2021, 42, 2344-2352.	2.2	68
26	Genome-wide analysis identifies novel susceptibility loci for myocardial infarction. <i>European Heart Journal</i> , 2021, 42, 919-933.	2.2	113
27	Monocyte subtype counts are associated with 10-year cardiovascular disease risk as determined by the Framingham Risk Score among subjects of the LIFE-Adult study. <i>PLoS ONE</i> , 2021, 16, e0247480.	2.5	12
28	Evaluation of phosphodiesterase 9A as a novel biomarker in heart failure with preserved ejection fraction. <i>ESC Heart Failure</i> , 2021, 8, 1861-1872.	3.1	4
29	Genetically determined NLRP3 inflammasome activation associates with systemic inflammation and cardiovascular mortality. <i>European Heart Journal</i> , 2021, 42, 1742-1756.	2.2	63
30	The Effect of FGF21 and Its Genetic Variants on Food and Drug Cravings, Adipokines and Metabolic Traits. <i>Biomedicines</i> , 2021, 9, 345.	3.2	9
31	Proteomic profiling of low muscle and high fat mass: a machine learning approach in the KORA S4/FF4 study. <i>Journal of Cachexia, Sarcopenia and Muscle</i> , 2021, 12, 1011-1023.	7.3	7
32	Proteomics to improve phenotyping in obese patients with heart failure with preserved ejection fraction. <i>European Journal of Heart Failure</i> , 2021, 23, 1633-1644.	7.1	26
33	A pre-registered short-term forecasting study of COVID-19 in Germany and Poland during the second wave. <i>Nature Communications</i> , 2021, 12, 5173.	12.8	47
34	Deep learning detects heart failure with preserved ejection fraction using a baseline electrocardiogram. <i>European Heart Journal Digital Health</i> , 2021, 2, 699-703.	1.7	8
35	Large-scale cis- and trans-eQTL analyses identify thousands of genetic loci and polygenic scores that regulate blood gene expression. <i>Nature Genetics</i> , 2021, 53, 1300-1310.	21.4	590
36	Association of plasma trimethylamine N-oxide levels with atherosclerotic cardiovascular disease and factors of the metabolic syndrome. <i>Atherosclerosis</i> , 2021, 335, 62-67.	0.8	17

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37	Prognostic impact of rapid reduction of involved free light chains in multiple myeloma patients under first-line treatment with Bendamustine, Prednisone, and Bortezomib (BPV). <i>Journal of Cancer Research and Clinical Oncology</i> , 2021, 147, 2349-2359.	2.5	3
38	Individual prediction of thrombocytopenia at next chemotherapy cycle: Evaluation of dynamic model performances. <i>British Journal of Clinical Pharmacology</i> , 2021, 87, 3127-3138.	2.4	5
39	Proteomics-Enabled Deep Learning Machine Algorithms Can Enhance Prediction of Mortality. <i>Journal of the American College of Cardiology</i> , 2021, 78, 1621-1631.	2.8	25
40	Sex-Specific Causal Relations between Steroid Hormones and Obesityâ€”A Mendelian Randomization Study. <i>Metabolites</i> , 2021, 11, 738.	2.9	7
41	The power of genetic diversity in genome-wide association studies of lipids. <i>Nature</i> , 2021, 600, 675-679.	27.8	353
42	Genetic correlations and genome-wide associations of cortical structure in general population samples of 22,824 adults. <i>Nature Communications</i> , 2020, 11, 4796.	12.8	61
43	The Obesity-Susceptibility Gene TMEM18 Promotes Adipogenesis through Activation of PPAR γ . <i>Cell Reports</i> , 2020, 33, 108295.	6.4	28
44	Analysis of GPRC6A variants in different pancreatitis etiologies. <i>Pancreatology</i> , 2020, 20, 1262-1267.	1.1	1
45	Novel loci for childhood body mass index and shared heritability with adult cardiometabolic traits. <i>PLoS Genetics</i> , 2020, 16, e1008718.	3.5	95
46	Cohort Profile: The Leipzig Research Center for Civilization Diseasesâ€”Heart Study (LIFE-Heart). <i>International Journal of Epidemiology</i> , 2020, 49, 1439-1440h.	1.9	19
47	Genome-wide association analysis of pulse wave velocity traits provide new insights into the causal relationship between arterial stiffness and blood pressure. <i>PLoS ONE</i> , 2020, 15, e0237237.	2.5	18
48	Dynamics of cytokines, immune cell counts and disease severity in patients with community-acquired pneumonia â€” Unravelling potential causal relationships. <i>Cytokine</i> , 2020, 136, 155263.	3.2	6
49	Mendelian randomization analysis does not support causal associations of birth weight with hypertension risk and blood pressure in adulthood. <i>European Journal of Epidemiology</i> , 2020, 35, 685-697.	5.7	9
50	A biomathematical model of human erythropoiesis and iron metabolism. <i>Scientific Reports</i> , 2020, 10, 8602.	3.3	5
51	Genome-wide analysis of carotid plaque burden suggests a role of IL5 in men. <i>PLoS ONE</i> , 2020, 15, e0233728.	2.5	7
52	Propionic Acid Shapes the Multiple Sclerosis Disease Course by an Immunomodulatory Mechanism. <i>Cell</i> , 2020, 180, 1067-1080.e16.	28.9	367
53	Global and Regional Development of the Human Cerebral Cortex: Molecular Architecture and Occupational Aptitudes. <i>Cerebral Cortex</i> , 2020, 30, 4121-4139.	2.9	16
54	Genetically programmed changes in transcription of the novel progranulin regulator. <i>Journal of Molecular Medicine</i> , 2020, 98, 1139-1148.	3.9	4

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55	Markov State Modelling of Disease Courses and Mortality Risks of Patients with Community-Acquired Pneumonia. <i>Journal of Clinical Medicine</i> , 2020, 9, 393.	2.4	3
56	Sepsis-associated acute respiratory distress syndrome in individuals of European ancestry: a genome-wide association study. <i>Lancet Respiratory Medicine</i> , 2020, 8, 258-266.	10.7	38
57	Integration of mathematical model predictions into routine workflows to support clinical decision making in haematology. <i>BMC Medical Informatics and Decision Making</i> , 2020, 20, 28.	3.0	12
58	HLA Class II Allele Analyses Implicate Common Genetic Components in Type 1 and Non-Insulin-Treated Type 2 Diabetes. <i>Journal of Clinical Endocrinology and Metabolism</i> , 2020, 105, e245-e254.	3.6	15
59	Adipocytokines are not associated with gestational diabetes mellitus but with pregnancy status. <i>Cytokine</i> , 2020, 131, 155088.	3.2	7
60	Neutralizing Complement C5a Protects Mice with Pneumococcal Pulmonary Sepsis. <i>Anesthesiology</i> , 2020, 132, 795-807.	2.5	17
61	A biomathematical model of immune response and barrier function in mice with pneumococcal lung infection. <i>PLoS ONE</i> , 2020, 15, e0243147.	2.5	4
62	Transcriptomic Research in Heart Failure with Preserved Ejection Fraction: Current State and Future Perspectives. <i>Cardiac Failure Review</i> , 2020, 6, e24.	3.0	3
63	Cyclin dependent kinase inhibitor 1 C is a female-specific marker of left ventricular function after acute myocardial infarction. <i>International Journal of Cardiology</i> , 2019, 274, 319-325.	1.7	10
64	Genetic Association Study of Eight Steroid Hormones and Implications for Sexual Dimorphism of Coronary Artery Disease. <i>Journal of Clinical Endocrinology and Metabolism</i> , 2019, 104, 5008-5023.	3.6	37
65	Circulating Oxytocin Is Genetically Determined and Associated With Obesity and Impaired Glucose Tolerance. <i>Journal of Clinical Endocrinology and Metabolism</i> , 2019, 104, 5621-5632.	3.6	14
66	Common variants in glyoxalase I do not increase chronic pancreatitis risk. <i>PLoS ONE</i> , 2019, 14, e0222927.	2.5	0
67	Clinical and lifestyle related factors influencing whole blood metabolite levels – A comparative analysis of three large cohorts. <i>Molecular Metabolism</i> , 2019, 29, 76-85.	6.5	26
68	Genome-wide association meta-analyses and fine-mapping elucidate pathways influencing albuminuria. <i>Nature Communications</i> , 2019, 10, 4130.	12.8	133
69	Target genes, variants, tissues and transcriptional pathways influencing human serum urate levels. <i>Nature Genetics</i> , 2019, 51, 1459-1474.	21.4	251
70	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
71	Subsequent Event Risk in Individuals With Established Coronary Heart Disease. <i>Circulation Genomic and Precision Medicine</i> , 2019, 12, e002470.	3.6	17
72	Circulating Adipokine VASPIN Is Associated with Serum Lipid Profiles in Humans. <i>Lipids</i> , 2019, 54, 203-210.	1.7	8

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73	Modeling individual time courses of thrombopoiesis during multi-cyclic chemotherapy. PLoS Computational Biology, 2019, 15, e1006775.	3.2	15
74	Catalyzing Transcriptomics Research in Cardiovascular Disease: The CardioRNA COST Action CA17129. Non-coding RNA, 2019, 5, 31.	2.6	14
75	Sequential organ failure assessment score is an excellent operationalization of disease severity of adult patients with hospitalized community acquired pneumonia – results from the prospective observational PROGRESS study. Critical Care, 2019, 23, 110.	5.8	43
76	Genetic architecture of subcortical brain structures in 38,851 individuals. Nature Genetics, 2019, 51, 1624-1636.	21.4	192
77	Plasma levels of apolipoproteins C-III, A-IV, and E are independently associated with stable atherosclerotic cardiovascular disease. Atherosclerosis, 2019, 281, 17-24.	0.8	28
78	Genome-wide association study identifies an acute myeloid leukemia susceptibility locus near BICRA. Leukemia, 2019, 33, 771-775.	7.2	15
79	Prognostic and Pathogenic Role of Angiotensin-1 and -2 in Pneumonia. American Journal of Respiratory and Critical Care Medicine, 2018, 198, 220-231.	5.6	58
80	Genome-wide meta-analysis identifies novel determinants of circulating serum progranulin. Human Molecular Genetics, 2018, 27, 546-558.	2.9	15
81	Relationship Between 12 Adipocytokines and Distinct Components of the Metabolic Syndrome. Journal of Clinical Endocrinology and Metabolism, 2018, 103, 1015-1023.	3.6	55
82	Genome-wide association study identifies inversion in the <i>CTRB1-CTRB2</i> locus to modify risk for alcoholic and non-alcoholic chronic pancreatitis. Gut, 2018, 67, 1855-1863.	12.1	97
83	Increased Level of Interleukin 6 Associates With Increased 90-Day and 1-Year Mortality in Patients With End-Stage Liver Disease. Clinical Gastroenterology and Hepatology, 2018, 16, 730-737.	4.4	38
84	Model-based optimization of G-CSF treatment during cytotoxic chemotherapy. Journal of Cancer Research and Clinical Oncology, 2018, 144, 343-358.	2.5	8
85	GWAS and colocalization analyses implicate carotid intima-media thickness and carotid plaque loci in cardiovascular outcomes. Nature Communications, 2018, 9, 5141.	12.8	119
86	Genome-wide association study of 23,500 individuals identifies 7 loci associated with brain ventricular volume. Nature Communications, 2018, 9, 3945.	12.8	31
87	Study of 300,486 individuals identifies 148 independent genetic loci influencing general cognitive function. Nature Communications, 2018, 9, 2098.	12.8	484
88	Parameters of pulse wave velocity: determinants and reference values assessed in the population-based study LIFE-Adult. Clinical Research in Cardiology, 2018, 107, 1050-1061.	3.3	52
89	Genetic Regulation of PCSK9 (Proprotein Convertase Subtilisin/Kexin Type 9) Plasma Levels and Its Impact on Atherosclerotic Vascular Disease Phenotypes. Circulation Genomic and Precision Medicine, 2018, 11, e001992.	3.6	37
90	Common variants in the CLDN2-MORC4 and PRSS1-PRSS2 loci confer susceptibility to acute pancreatitis. Pancreatology, 2018, 18, 477-481.	1.1	14

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91	Relations between lipoprotein(a) concentrations, LPA genetic variants, and the risk of mortality in patients with established coronary heart disease: a molecular and genetic association study. <i>Lancet Diabetes and Endocrinology</i> , 2017, 5, 534-543.	11.4	84
92	Genome-wide meta-analysis identifies novel loci of plaque burden in carotid artery. <i>Atherosclerosis</i> , 2017, 259, 32-40.	0.8	33
93	Growth and Final Height Among Children With Phenylketonuria. <i>Pediatrics</i> , 2017, 140, e20170015.	2.1	12
94	Genetic correlations reveal the shared genetic architecture of transcription in human peripheral blood. <i>Nature Communications</i> , 2017, 8, 483.	12.8	22
95	Urine Biomarkers of Tubular Renal Cell Damage for the Prediction of Acute Kidney Injury After Cardiac Surgery—A Pilot Study. <i>Journal of Cardiothoracic and Vascular Anesthesia</i> , 2017, 31, 2072-2079.	1.3	38
96	Response to Sabour. <i>Pediatric Research</i> , 2017, 82, 177-177.	2.3	0
97	Genome-Wide Association Analysis for Severity of Coronary Artery Disease Using the Gensini Scoring System. <i>Frontiers in Cardiovascular Medicine</i> , 2017, 4, 57.	2.4	14
98	Low sphingosine-1-phosphate plasma levels are predictive for increased mortality in patients with liver cirrhosis. <i>PLoS ONE</i> , 2017, 12, e0174424.	2.5	29
99	On the impact of relatedness on SNP association analysis. <i>BMC Genetics</i> , 2017, 18, 104.	2.7	3
100	Association between lipoprotein(a) level and type 2 diabetes: no evidence for a causal role of lipoprotein(a) and insulin. <i>Acta Diabetologica</i> , 2017, 54, 1031-1038.	2.5	22
101	Relationship Between Determinants of Arterial Stiffness Assessed by Diastolic and Suprasystolic Pulse Oscillometry. <i>Medicine (United States)</i> , 2016, 95, e2963.	1.0	10
102	Comparing performance of modern genotype imputation methods in different ethnicities. <i>Scientific Reports</i> , 2016, 6, 34386.	3.3	49
103	P3-086: FTO is Not Related to Imaging Parameters of the Hippocampus: A Volumetric and Diffusion Tensor Imaging Study. , 2016, 12, P851-P851.		0
104	PROGRESS – prospective observational study on hospitalized community acquired pneumonia. <i>BMC Pulmonary Medicine</i> , 2016, 16, 108.	2.0	15
105	Genetic Factors of the Disease Course after Sepsis: A Genome-Wide Study for 28 Day Mortality. <i>EBioMedicine</i> , 2016, 12, 239-246.	6.1	52
106	Circular non-coding RNA ANRIL modulates ribosomal RNA maturation and atherosclerosis in humans. <i>Nature Communications</i> , 2016, 7, 12429.	12.8	859
107	No Association of Coronary Artery Disease with X-Chromosomal Variants in Comprehensive International Meta-Analysis. <i>Scientific Reports</i> , 2016, 6, 35278.	3.3	25
108	Modeling combined chemo- and immunotherapy of high-grade non-Hodgkin lymphoma. <i>Leukemia and Lymphoma</i> , 2016, 57, 1697-1708.	1.3	5

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109	The value of noncoronary atherosclerosis for identifying coronary artery disease: results of the Leipzig LIFE Heart Study. <i>Clinical Research in Cardiology</i> , 2016, 105, 172-181.	3.3	15
110	Association of metabolic parameters and rs726344 in FNDC5 with serum irisin concentrations. <i>International Journal of Obesity</i> , 2016, 40, 260-265.	3.4	28
111	Genetic variants of lipase activity in chronic pancreatitis: Table A1. <i>Gut</i> , 2016, 65, 184-185.	12.1	10
112	A Biomathematical Model of Pneumococcal Lung Infection and Antibiotic Treatment in Mice. <i>PLoS ONE</i> , 2016, 11, e0156047.	2.5	18
113	FTO Obesity Risk Variants Are Linked to Adipocyte IRX3 Expression and BMI of Children - Relevance of FTO Variants to Defend Body Weight in Lean Children?. <i>PLoS ONE</i> , 2016, 11, e0161739.	2.5	31
114	Monitoring Disease Progression and Therapeutic Response in a Disseminated Tumor Model for Non-Hodgkin Lymphoma by Bioluminescence Imaging. <i>Molecular Imaging</i> , 2015, 14, 7290.2015.00010.	1.4	6
115	Low-Dose Irradiation Affects Expression of Inflammatory Markers in the Heart of ApoE ^{-/-} Mice. <i>PLoS ONE</i> , 2015, 10, e0119661.	2.5	36
116	Integration of Genome-Wide SNP Data and Gene-Expression Profiles Reveals Six Novel Loci and Regulatory Mechanisms for Amino Acids and Acylcarnitines in Whole Blood. <i>PLoS Genetics</i> , 2015, 11, e1005510.	3.5	41
117	Associations between DNA methylation and schizophrenia-related intermediate phenotypes – A gene set enrichment analysis. <i>Progress in Neuro-Psychopharmacology and Biological Psychiatry</i> , 2015, 59, 31-39.	4.8	29
118	Dissecting the genetics of the human transcriptome identifies novel trait-related <i>trans</i> -eQTLs and corroborates the regulatory relevance of non-protein coding loci. <i>Human Molecular Genetics</i> , 2015, 24, 4746-4763.	2.9	94
119	Impact of genetic similarity on imputation accuracy. <i>BMC Genetics</i> , 2015, 16, 90.	2.7	24
120	The LIFE-Adult-Study: objectives and design of a population-based cohort study with 10,000 deeply phenotyped adults in Germany. <i>BMC Public Health</i> , 2015, 15, 691.	2.9	287
121	A comprehensive 1000 Genomes-based genome-wide association meta-analysis of coronary artery disease. <i>Nature Genetics</i> , 2015, 47, 1121-1130.	21.4	2,054
122	Polymorphisms at <i>PRSS1</i> and <i>PRSS2</i> and <i>CLDN2</i> and <i>MORC4</i> loci associate with alcoholic and non-alcoholic chronic pancreatitis in a European replication study. <i>Gut</i> , 2015, 64, 1426-1433.	12.1	105
123	Indications for Potential Parent-of-Origin Effects within the FTO Gene. <i>PLoS ONE</i> , 2015, 10, e0119206.	2.5	7
124	Lineage-Specific Changes in Biomarkers in Great Apes and Humans. <i>PLoS ONE</i> , 2015, 10, e0134548.	2.5	7
125	Genetic Contribution of Variants near SORT1 and APOE on LDL Cholesterol Independent of Obesity in Children. <i>PLoS ONE</i> , 2015, 10, e0138064.	2.5	20
126	Association of head and neck cancer (HNSCC) subgroups defined by HPV RNA status, gene expression patterns, and TP53 mutations with lymph node metastasis and survival.. <i>Journal of Clinical Oncology</i> , 2015, 33, 6046-6046.	1.6	1

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127	Genetic Association of Objective Sleep Phenotypes with a Functional Polymorphism in the Neuropeptide S Receptor Gene. PLoS ONE, 2014, 9, e98789.	2.5	27
128	Modelling chemotherapy effects on granulopoiesis. BMC Systems Biology, 2014, 8, 138.	3.0	14
129	<i>MB-COMT</i> promoter DNA methylation is associated with working-memory processing in schizophrenia patients and healthy controls. Epigenetics, 2014, 9, 1101-1107.	2.7	65
130	Genome Wide Meta-analysis Highlights the Role of Genetic Variation in RARRES2 in the Regulation of Circulating Serum Chemerin. PLoS Genetics, 2014, 10, e1004854.	3.5	31
131	Modelling Lymphoma Therapy and Outcome. Bulletin of Mathematical Biology, 2014, 76, 401-430.	1.9	29
132	Ycascâ€“ a tool for capturing and scaling data from graphical representations. BMC Bioinformatics, 2014, 15, 219.	2.6	35
133	A combined model of human erythropoiesis and granulopoiesis under growth factor and chemotherapy treatment. Theoretical Biology and Medical Modelling, 2014, 11, 24.	2.1	14
134	fcGENE: A Versatile Tool for Processing and Transforming SNP Datasets. PLoS ONE, 2014, 9, e97589.	2.5	52
135	Identification of Adipokine Clusters Related to Parameters of Fat Mass, Insulin Sensitivity and Inflammation. PLoS ONE, 2014, 9, e99785.	2.5	107
136	Comparison and modelling of pegylated or unpegylated G-CSF schedules in CHOP-14 regimen of elderly patients with aggressive B-cell lymphoma. Annals of Hematology, 2013, 92, 1641-1652.	1.8	8
137	Secretory Phospholipase A2-IIA and Cardiovascular Disease. Journal of the American College of Cardiology, 2013, 62, 1966-1976.	2.8	115
138	Validity, intra- and inter-observer reliability of automated devices for the assessment of ankle brachial index using photo-plethysmography. BMC Cardiovascular Disorders, 2013, 13, 81.	1.7	10
139	Alu Elements in ANRIL Non-Coding RNA at Chromosome 9p21 Modulate Atherogenic Cell Functions through Trans-Regulation of Gene Networks. PLoS Genetics, 2013, 9, e1003588.	3.5	323
140	The role of rs2237781 within <i>GRM8</i> in eating behavior. Brain and Behavior, 2013, 3, 495-502.	2.2	14
141	A Biomathematical Model of Human Erythropoiesis under Erythropoietin and Chemotherapy Administration. PLoS ONE, 2013, 8, e65630.	2.5	21
142	Pharmacokinetic and -dynamic modelling of G-CSF derivatives in humans. Theoretical Biology and Medical Modelling, 2012, 9, 32.	2.1	32
143	Rationale and Design of the Leipzig (LIFE) Heart Study: Phenotyping and Cardiovascular Characteristics of Patients with Coronary Artery Disease. PLoS ONE, 2011, 6, e29070.	2.5	45
144	Genetic variation in the Sorbs of eastern Germany in the context of broader European genetic diversity. European Journal of Human Genetics, 2011, 19, 995-1001.	2.8	59

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145	Comparison of scoring methods for the detection of causal genes with or without rare variants. BMC Proceedings, 2011, 5, S49.	1.6	4
146	Population-genetic comparison of the Sorbian isolate population in Germany with the German KORA population using genome-wide SNP arrays. BMC Genetics, 2011, 12, 67.	2.7	26
147	Impact of first- and second-line treatment for Hodgkin's lymphoma on the incidence of AML/MDS and NHL: experience of the German Hodgkin's Lymphoma Study Group analyzed by a parametric model of carcinogenesis. Annals of Oncology, 2011, 22, 681-688.	1.2	16
148	A biomathematical model of human thrombopoiesis under chemotherapy. Journal of Theoretical Biology, 2010, 264, 287-300.	1.7	25
149	<i>ANRIL</i> Expression Is Associated With Atherosclerosis Risk at Chromosome 9p21. Arteriosclerosis, Thrombosis, and Vascular Biology, 2010, 30, 620-627.	2.4	402
150	Genetic Regulation of Serum Phytosterol Levels and Risk of Coronary Artery Disease. Circulation: Cardiovascular Genetics, 2010, 3, 331-339.	5.1	141
151	A pharmacokinetic model of filgrastim and pegfilgrastim application in normal mice and those with cyclophosphamide-induced granulocytopenia. Cell Proliferation, 2009, 42, 813-822.	5.3	17
152	Pharmacokinetic and pharmacodynamic modelling of the novel human granulocyte colony-stimulating factor derivative Maxy-G34 and pegfilgrastim in rats. Cell Proliferation, 2009, 42, 823-837.	5.3	15
153	Effectiveness of cytopenia prophylaxis for different filgrastim and pegfilgrastim schedules in a chemotherapy mouse model. Biologics: Targets and Therapy, 2009, 3, 27-37.	3.2	7
154	Neuronal hypoxia: protective effects of mononuclear cord blood cells after direct and indirect application. Journal of Stem Cells and Regenerative Medicine, 2007, 2, 16.	2.2	0
155	Model-based design of chemotherapeutic regimens that account for heterogeneity in leucopenia. British Journal of Haematology, 2006, 132, 723-735.	2.5	22
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