

Sven Bergmann

List of Publications by Year in descending order

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Version: 2024-02-01

139
papers

34,164
citations

12330

69
h-index

9103

144
g-index

156
all docs

156
docs citations

156
times ranked

43514
citing authors

#	ARTICLE	IF	CITATIONS
1	Association analyses of 249,796 individuals reveal 18 new loci associated with body mass index. <i>Nature Genetics</i> , 2010, 42, 937-948.	21.4	2,634
2	New genetic loci implicated in fasting glucose homeostasis and their impact on type 2 diabetes risk. <i>Nature Genetics</i> , 2010, 42, 105-116.	21.4	1,982
3	Genetic variants in novel pathways influence blood pressure and cardiovascular disease risk. <i>Nature</i> , 2011, 478, 103-109.	27.8	1,855
4	Defining the role of common variation in the genomic and biological architecture of adult human height. <i>Nature Genetics</i> , 2014, 46, 1173-1186.	21.4	1,818
5	Hundreds of variants clustered in genomic loci and biological pathways affect human height. <i>Nature</i> , 2010, 467, 832-838.	27.8	1,789
6	Genes mirror geography within Europe. <i>Nature</i> , 2008, 456, 98-101.	27.8	1,287
7	Common variants near MC4R are associated with fat mass, weight and risk of obesity. <i>Nature Genetics</i> , 2008, 40, 768-775.	21.4	1,179
8	Genome-wide association study identifies eight loci associated with blood pressure. <i>Nature Genetics</i> , 2009, 41, 666-676.	21.4	1,104
9	The evolution of gene expression levels in mammalian organs. <i>Nature</i> , 2011, 478, 343-348.	27.8	1,080
10	Genetic variants associated with subjective well-being, depressive symptoms, and neuroticism identified through genome-wide analyses. <i>Nature Genetics</i> , 2016, 48, 624-633.	21.4	870
11	Meta-analysis identifies 13 new loci associated with waist-hip ratio and reveals sexual dimorphism in the genetic basis of fat distribution. <i>Nature Genetics</i> , 2010, 42, 949-960.	21.4	836
12	Genome-wide association analysis identifies 20 loci that influence adult height. <i>Nature Genetics</i> , 2008, 40, 575-583.	21.4	742
13	Revealing modular organization in the yeast transcriptional network. <i>Nature Genetics</i> , 2002, 31, 370-377.	21.4	664
14	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
15	Meta-Analysis of 28,141 Individuals Identifies Common Variants within Five New Loci That Influence Uric Acid Concentrations. <i>PLoS Genetics</i> , 2009, 5, e1000504.	3.5	572
16	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
17	Parent-of-origin-specific allelic associations among 106 genomic loci for age at menarche. <i>Nature</i> , 2014, 514, 92-97.	27.8	548
18	Rare and low-frequency coding variants alter human adult height. <i>Nature</i> , 2017, 542, 186-190.	27.8	544

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19	A new highly penetrant form of obesity due to deletions on chromosome 16p11.2. <i>Nature</i> , 2010, 463, 671-675.	27.8	476
20	A Higher Mutational Burden in Females Supports a "Female Protective Model" in Neurodevelopmental Disorders. <i>American Journal of Human Genetics</i> , 2014, 94, 415-425.	6.2	457
21	Physical Activity Attenuates the Influence of FTO Variants on Obesity Risk: A Meta-Analysis of 218,166 Adults and 19,268 Children. <i>PLoS Medicine</i> , 2011, 8, e1001116.	8.4	446
22	Thirty new loci for age at menarche identified by a meta-analysis of genome-wide association studies. <i>Nature Genetics</i> , 2010, 42, 1077-1085.	21.4	445
23	Genomic analyses identify hundreds of variants associated with age at menarche and support a role for puberty timing in cancer risk. <i>Nature Genetics</i> , 2017, 49, 834-841.	21.4	426
24	Genome-wide association study identifies six new loci influencing pulse pressure and mean arterial pressure. <i>Nature Genetics</i> , 2011, 43, 1005-1011.	21.4	403
25	Population-Based Genome-wide Association Studies Reveal Six Loci Influencing Plasma Levels of Liver Enzymes. <i>American Journal of Human Genetics</i> , 2008, 83, 520-528.	6.2	402
26	Mirror extreme BMI phenotypes associated with gene dosage at the chromosome 16p11.2 locus. <i>Nature</i> , 2011, 478, 97-102.	27.8	394
27	Large-scale genomic analyses link reproductive aging to hypothalamic signaling, breast cancer susceptibility and BRCA1-mediated DNA repair. <i>Nature Genetics</i> , 2015, 47, 1294-1303.	21.4	357
28	The trans-ancestral genomic architecture of glycemic traits. <i>Nature Genetics</i> , 2021, 53, 840-860.	21.4	341
29	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> , 2015, 11, e1005378.	3.5	331
30	Fast and Rigorous Computation of Gene and Pathway Scores from SNP-Based Summary Statistics. <i>PLoS Computational Biology</i> , 2016, 12, e1004714.	3.2	330
31	Iterative signature algorithm for the analysis of large-scale gene expression data. <i>Physical Review E</i> , 2003, 67, 031902.	2.1	322
32	Tissue-specific regulatory circuits reveal variable modular perturbations across complex diseases. <i>Nature Methods</i> , 2016, 13, 366-370.	19.0	306
33	Defining transcription modules using large-scale gene expression data. <i>Bioinformatics</i> , 2004, 20, 1993-2003.	4.1	301
34	Similarities and Differences in Genome-Wide Expression Data of Six Organisms. <i>PLoS Biology</i> , 2003, 2, e9.	5.6	294
35	Protein-altering variants associated with body mass index implicate pathways that control energy intake and expenditure in obesity. <i>Nature Genetics</i> , 2018, 50, 26-41.	21.4	286
36	Genome-wide analysis identifies 12 loci influencing human reproductive behavior. <i>Nature Genetics</i> , 2016, 48, 1462-1472.	21.4	284

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37	Rewiring of the Yeast Transcriptional Network Through the Evolution of Motif Usage. <i>Science</i> , 2005, 309, 938-940.	12.6	268
38	Target genes, variants, tissues and transcriptional pathways influencing human serum urate levels. <i>Nature Genetics</i> , 2019, 51, 1459-1474.	21.4	251
39	Assessment of network module identification across complex diseases. <i>Nature Methods</i> , 2019, 16, 843-852.	19.0	213
40	CUBN Is a Gene Locus for Albuminuria. <i>Journal of the American Society of Nephrology: JASN</i> , 2011, 22, 555-570.	6.1	208
41	SIRT1 Activates MAO-A in the Brain to Mediate Anxiety and Exploratory Drive. <i>Cell</i> , 2011, 147, 1459-1472.	28.9	202
42	Pre-Steady-State Decoding of the Bicoid Morphogen Gradient. <i>PLoS Biology</i> , 2007, 5, e46.	5.6	183
43	Genetic insights into biological mechanisms governing human ovarian ageing. <i>Nature</i> , 2021, 596, 393-397.	27.8	183
44	Comparative genome hybridization reveals widespread aneuploidy in <i>Candida albicans</i> laboratory strains. <i>Molecular Microbiology</i> , 2005, 55, 1553-1565.	2.5	175
45	Directional dominance on stature and cognition in diverse human populations. <i>Nature</i> , 2015, 523, 459-462.	27.8	173
46	Genome-wide association study identifies new HLA class II haplotypes strongly protective against narcolepsy. <i>Nature Genetics</i> , 2010, 42, 786-789.	21.4	170
47	Genome-wide meta-analysis of 241,258 adults accounting for smoking behaviour identifies novel loci for obesity traits. <i>Nature Communications</i> , 2017, 8, 14977.	12.8	169
48	Association of genetic variation with systolic and diastolic blood pressure among African Americans: the Candidate Gene Association Resource study. <i>Human Molecular Genetics</i> , 2011, 20, 2273-2284.	2.9	168
49	Genome-Wide Association and Functional Follow-Up Reveals New Loci for Kidney Function. <i>PLoS Genetics</i> , 2012, 8, e1002584.	3.5	166
50	Chromatin three-dimensional interactions mediate genetic effects on gene expression. <i>Science</i> , 2019, 364, .	12.6	163
51	Genome-wide physical activity interactions in adiposity â€• A meta-analysis of 200,452 adults. <i>PLoS Genetics</i> , 2017, 13, e1006528.	3.5	158
52	Meta-Analysis of Genome-Wide Association Studies Identifies Six New Loci for Serum Calcium Concentrations. <i>PLoS Genetics</i> , 2013, 9, e1003796.	3.5	142
53	Genome-wide Association Studies Identify Genetic Loci Associated With Albuminuria in Diabetes. <i>Diabetes</i> , 2016, 65, 803-817.	0.6	131
54	Comparative Gene Expression Analysis by a Differential Clustering Approach: Application to the <i>Candida albicans</i> Transcription Program. <i>PLoS Genetics</i> , 2005, 1, e39.	3.5	124

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55	The protective effect of the obesity-associated rs9939609 A variant in fat mass- and obesity-associated gene on depression. <i>Molecular Psychiatry</i> , 2013, 18, 1281-1286.	7.9	115
56	A genome-wide association meta-analysis on lipoprotein (a) concentrations adjusted for apolipoprotein (a) isoforms. <i>Journal of Lipid Research</i> , 2017, 58, 1834-1844.	4.2	114
57	A modular approach for integrative analysis of large-scale gene-expression and drug-response data. <i>Nature Biotechnology</i> , 2008, 26, 531-539.	17.5	111
58	Light intensity modulates the regulatory network of the shade avoidance response in <i>Arabidopsis</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 6515-6520.	7.1	111
59	Cell-mediated cytotoxicity in rainbow trout, <i>Oncorhynchus mykiss</i> , infected with viral haemorrhagic septicaemia virus. <i>Fish and Shellfish Immunology</i> , 2007, 22, 182-196.	3.6	108
60	Dpp Signaling Activity Requires Pentagone to Scale with Tissue Size in the Growing <i>Drosophila</i> Wing Imaginal Disc. <i>PLoS Biology</i> , 2011, 9, e1001182.	5.6	107
61	A genome-wide association study of early menopause and the combined impact of identified variants. <i>Human Molecular Genetics</i> , 2013, 22, 1465-1472.	2.9	104
62	Protein-coding variants implicate novel genes related to lipid homeostasis contributing to body-fat distribution. <i>Nature Genetics</i> , 2019, 51, 452-469.	21.4	89
63	Genome-Wide Association Study of Metabolic Traits Reveals Novel Gene-Metabolite-Disease Links. <i>PLoS Genetics</i> , 2014, 10, e1004132.	3.5	86
64	Common Variants in UMOD Associate with Urinary Uromodulin Levels. <i>Journal of the American Society of Nephrology: JASN</i> , 2014, 25, 1869-1882.	6.1	85
65	Genome-Wide Meta-Analysis for Serum Calcium Identifies Significantly Associated SNPs near the Calcium-Sensing Receptor (CASR) Gene. <i>PLoS Genetics</i> , 2010, 6, e1001035.	3.5	84
66	Genome-Wide Association Study with Targeted and Non-targeted NMR Metabolomics Identifies 15 Novel Loci of Urinary Human Metabolic Individuality. <i>PLoS Genetics</i> , 2015, 11, e1005487.	3.5	83
67	Phytochrome Kinase Substrate 4 is phosphorylated by the phototropin 1 photoreceptor. <i>EMBO Journal</i> , 2012, 31, 3457-3467.	7.8	82
68	Novel Approach Identifies SNPs in SLC2A10 and KCNK9 with Evidence for Parent-of-Origin Effect on Body Mass Index. <i>PLoS Genetics</i> , 2014, 10, e1004508.	3.5	80
69	Formation of the Long Range Dpp Morphogen Gradient. <i>PLoS Biology</i> , 2011, 9, e1001111.	5.6	75
70	A principal component meta-analysis on multiple anthropometric traits identifies novel loci for body shape. <i>Nature Communications</i> , 2016, 7, 13357.	12.8	74
71	The Hourglass and the Early Conservation Models—Co-Existing Patterns of Developmental Constraints in Vertebrates. <i>PLoS Genetics</i> , 2013, 9, e1003476.	3.5	73
72	Effects of Long-Term Averaging of Quantitative Blood Pressure Traits on the Detection of Genetic Associations. <i>American Journal of Human Genetics</i> , 2014, 95, 49-65.	6.2	73

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73	Depressive disorder moderates the effect of the FTO gene on body mass index. <i>Molecular Psychiatry</i> , 2012, 17, 604-611.	7.9	72
74	Discovery and Fine Mapping of Serum Protein Loci through Transethnic Meta-analysis. <i>American Journal of Human Genetics</i> , 2012, 91, 744-753.	6.2	69
75	cis -Acting Complex-Trait-Associated lincRNA Expression Correlates with Modulation of Chromosomal Architecture. <i>Cell Reports</i> , 2017, 18, 2280-2288.	6.4	67
76	Integration of genome-wide association studies with biological knowledge identifies six novel genes related to kidney function. <i>Human Molecular Genetics</i> , 2012, 21, 5329-5343.	2.9	64
77	The DCX Superfamily 1: Common and Divergent Roles for Members of the Mouse DCX Superfamily. <i>Cell Cycle</i> , 2006, 5, 976-983.	2.6	62
78	Multi-Omics and Genome-Scale Modeling Reveal a Metabolic Shift During <i>C. elegans</i> Aging. <i>Frontiers in Molecular Biosciences</i> , 2019, 6, 2.	3.5	61
79	PhenoMeNal: processing and analysis of metabolomics data in the cloud. <i>GigaScience</i> , 2019, 8, .	6.4	60
80	DNA mismatch repair gene MSH6 implicated in determining age at natural menopause. <i>Human Molecular Genetics</i> , 2014, 23, 2490-2497.	2.9	56
81	A genetic risk score combining 32 SNPs is associated with body mass index and improves obesity prediction in people with major depressive disorder. <i>BMC Medicine</i> , 2015, 13, 86.	5.5	56
82	Caffeine intake and CYP1A2 variants associated with high caffeine intake protect non-smokers from hypertension. <i>Human Molecular Genetics</i> , 2012, 21, 3283-3292.	2.9	55
83	Genome-Wide Analysis Reveals Novel Regulators of Growth in <i>Drosophila melanogaster</i> . <i>PLoS Genetics</i> , 2016, 12, e1005616.	3.5	55
84	Nuclear Phytochrome A Signaling Promotes Phototropism in <i>Arabidopsis</i> . <i>Plant Cell</i> , 2012, 24, 566-576.	6.6	54
85	Plasma membrane H ⁺ ATPase regulation is required for auxin gradient formation preceding phototropic growth. <i>Molecular Systems Biology</i> , 2014, 10, 751.	7.2	54
86	Distinct levels in Pom1 gradients limit Cdr2 activity and localization to time and position division. <i>Cell Cycle</i> , 2014, 13, 538-552.	2.6	54
87	A Potential Contributory Role for Ciliary Dysfunction in the 16p11.2 600 kb BP4-BP5 Pathology. <i>American Journal of Human Genetics</i> , 2015, 96, 784-796.	6.2	53
88	GWAS of human bitter taste perception identifies new loci and reveals additional complexity of bitter taste genetics. <i>Human Molecular Genetics</i> , 2014, 23, 259-267.	2.9	51
89	Interaction between the <i>FTO</i> gene, body mass index and depression: meta-analysis of 13701 individuals. <i>British Journal of Psychiatry</i> , 2017, 211, 70-76.	2.8	49
90	Defining the Site of Light Perception and Initiation of Phototropism in <i>Arabidopsis</i> . <i>Current Biology</i> , 2013, 23, 1934-1938.	3.9	47

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91	A genome-wide association meta-analysis on apolipoprotein A-IV concentrations. <i>Human Molecular Genetics</i> , 2016, 25, 3635-3646.	2.9	46
92	Precision and scaling in morphogen gradient readout. <i>Molecular Systems Biology</i> , 2010, 6, 351.	7.2	41
93	Sensitivity of Genome-Wide-Association Signals to Phenotyping Strategy: The PROP-TAS2R38 Taste Association as a Benchmark. <i>PLoS ONE</i> , 2011, 6, e27745.	2.5	41
94	High capacity in G protein-coupled receptor signaling. <i>Nature Communications</i> , 2018, 9, 876.	12.8	40
95	Mechanical forces drive ordered patterning of hair cells in the mammalian inner ear. <i>Nature Communications</i> , 2020, 11, 5137.	12.8	38
96	Pathology and mass mortality of Pacific oysters, <i>Crassostrea gigas</i> (Thunberg), in 2005 at the East Frisian coast, Germany. <i>Journal of Fish Diseases</i> , 2008, 31, 621-630.	1.9	37
97	Using Transcription Modules to Identify Expression Clusters Perturbed in Williams-Beuren Syndrome. <i>PLoS Computational Biology</i> , 2011, 7, e1001054.	3.2	36
98	Methods for testing association between uncertain genotypes and quantitative traits. <i>Biostatistics</i> , 2011, 12, 1-17.	1.5	35
99	Genome-Wide Meta-Analysis Unravels Interactions between Magnesium Homeostasis and Metabolic Phenotypes. <i>Journal of the American Society of Nephrology: JASN</i> , 2018, 29, 335-348.	6.1	34
100	Common Variants in Mendelian Kidney Disease Genes and Their Association with Renal Function. <i>Journal of the American Society of Nephrology: JASN</i> , 2013, 24, 2105-2117.	6.1	33
101	Cardiovascular Response to Beta-Adrenergic Blockade or Activation in 23 Inbred Mouse Strains. <i>PLoS ONE</i> , 2009, 4, e6610.	2.5	32
102	Genome-wide association study identifies two loci strongly affecting transferrin glycosylation. <i>Human Molecular Genetics</i> , 2011, 20, 3710-3717.	2.9	31
103	Re-examining the Stability of the Bicoid Morphogen Gradient. <i>Cell</i> , 2008, 132, 15-17.	28.9	29
104	Aging of myelinating glial cells predominantly affects lipid metabolism and immune response pathways. <i>Glia</i> , 2012, 60, 751-760.	4.9	27
105	Modeling morphogen gradient formation from arbitrary realistically shaped sources. <i>Journal of Theoretical Biology</i> , 2012, 294, 130-138.	1.7	24
106	NFAT5 and SLC4A10 Loci Associate with Plasma Osmolality. <i>Journal of the American Society of Nephrology: JASN</i> , 2017, 28, 2311-2321.	6.1	24
107	Novel method to estimate the phenotypic variation explained by genome-wide association studies reveals large fraction of the missing heritability. <i>Genetic Epidemiology</i> , 2011, 35, 341-349.	1.3	23
108	No Interactions Between Previously Associated 2-Hour Glucose Gene Variants and Physical Activity or BMI on 2-Hour Glucose Levels. <i>Diabetes</i> , 2012, 61, 1291-1296.	0.6	23

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109	Genome-Wide Association between Transcription Factor Expression and Chromatin Accessibility Reveals Regulators of Chromatin Accessibility. <i>PLoS Computational Biology</i> , 2017, 13, e1005311.	3.2	23
110	Pom1 gradient buffering through intermolecular auto-phosphorylation. <i>Molecular Systems Biology</i> , 2015, 11, 818.	7.2	22
111	Interoperable and scalable data analysis with microservices: applications in metabolomics. <i>Bioinformatics</i> , 2019, 35, 3752-3760.	4.1	22
112	No interaction between alcohol consumption and HDL-related genes on HDL cholesterol levels. <i>Atherosclerosis</i> , 2010, 211, 551-557.	0.8	21
113	Challenges and prospects in the analysis of large-scale gene expression data. <i>Briefings in Bioinformatics</i> , 2004, 5, 313-327.	6.5	19
114	Metabomatching: Using genetic association to identify metabolites in proton NMR spectroscopy. <i>PLoS Computational Biology</i> , 2017, 13, e1005839.	3.2	17
115	Gene-educational attainment interactions in a multi-ancestry genome-wide meta-analysis identify novel blood pressure loci. <i>Molecular Psychiatry</i> , 2020, 26, 2111-2125.	7.9	17
116	<i>MONET</i> : a toolbox integrating top-performing methods for network modularization. <i>Bioinformatics</i> , 2020, 36, 3920-3921.	4.1	15
117	Association of ABCB1 genetic variants with renal function in Africans and in Caucasians. <i>BMC Medical Genomics</i> , 2008, 1, 21.	1.5	14
118	Meta-GWAS Reveals Novel Genetic Variants Associated with Urinary Excretion of Uromodulin. <i>Journal of the American Society of Nephrology: JASN</i> , 2022, 33, 511-529.	6.1	14
119	Fifteen years SIB Swiss Institute of Bioinformatics: life science databases, tools and support. <i>Nucleic Acids Research</i> , 2014, 42, W436-W441.	14.5	13
120	Global Transcriptional Programs in Peripheral Nerve Endoneurium and DRG Are Resistant to the Onset of Type 1 Diabetic Neuropathy in <i>Ins2Akita/+</i> Mice. <i>PLoS ONE</i> , 2010, 5, e10832.	2.5	12
121	Inosine Substitutions in RNA Activate Latent G-Quadruplexes. <i>Journal of the American Chemical Society</i> , 2021, 143, 15120-15130.	13.7	12
122	Variant Within the Promoter Region of the <i>CHRNA3</i> Gene Associated With FTN Dependence Is Not Related to Self-Reported Willingness to Quit Smoking. <i>Nicotine and Tobacco Research</i> , 2011, 13, 833-839.	2.6	9
123	Comparative modular analysis of gene expression in vertebrate organs. <i>BMC Genomics</i> , 2012, 13, 124.	2.8	9
124	<i>Sox4</i> participates in the modulation of Schwann cell myelination. <i>European Journal of Neuroscience</i> , 2015, 42, 1788-1796.	2.6	9
125	RNAseq analysis of heart tissue from mice treated with atenolol and isoproterenol reveals a reciprocal transcriptional response. <i>BMC Genomics</i> , 2016, 17, 717.	2.8	9
126	Pre-steady and stable morphogen gradients: can they coexist?. <i>Molecular Systems Biology</i> , 2010, 6, .	7.2	8

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127	Mapping Genetic Variants Associated with Beta-Adrenergic Responses in Inbred Mice. PLoS ONE, 2012, 7, e41032.	2.5	8
128	Comparison of Strategies to Detect Epistasis from eQTL Data. PLoS ONE, 2011, 6, e28415.	2.5	8
129	Genetic Polymorphisms of the Main Transcription Factors for Adiponectin Gene Promoter in Regulation of Adiponectin Levels: Association Analysis in Three European Cohorts. PLoS ONE, 2012, 7, e52497.	2.5	7
130	Manipulating the Sensitivity of Signal-Induced Repression: Quantification and Consequences of Altered Brinker Gradients. PLoS ONE, 2013, 8, e71224.	2.5	7
131	Iterative Estimation of Rigid-Body Transformations. Journal of Mathematical Imaging and Vision, 2012, 43, 1-9.	1.3	6
132	Validation of a serum neutralization test for detection of antibodies specific to cyprinid herpesvirus 3 in infected common and koi carp (<i>Cyprinus carpio</i>). Journal of Fish Diseases, 2017, 40, 687-701.	1.9	6
133	Untargeted Metabolome- and Transcriptome-Wide Association Study Suggests Causal Genes Modulating Metabolite Concentrations in Urine. Journal of Proteome Research, 2021, 20, 5103-5114.	3.7	6
134	Automated Analysis of Large-Scale NMR Data Generates Metabolomic Signatures and Links Them to Candidate Metabolites. Journal of Proteome Research, 2019, 18, 3360-3368.	3.7	5
135	Genome-wide Association Study of Change in Fasting Glucose over time in 13,807 non-diabetic European Ancestry Individuals. Scientific Reports, 2019, 9, 9439.	3.3	5
136	Estimating RNA dynamics using one time point for one sample in a single-pulse metabolic labeling experiment. BMC Bioinformatics, 2022, 23, 147.	2.6	3
137	Statistical mediation of the relationships between chronological age and lipoproteins by nonessential amino acids in healthy men. Computational and Structural Biotechnology Journal, 2021, 19, 6169-6178.	4.1	1
138	From Modules to Models: Advanced Analysis Methods for Large-Scale Data. , 2009, , 59-83.		0
139	Analysis of Eukaryotic lincRNA Sequences Indicates Signatures of Hindered Translation Linked to Selection Pressure. Molecular Biology and Evolution, 2022, 39, .	8.9	0