Peter A 't Hoen

List of Publications by Year
in descending order

214 papers	26,535 citations	25034 57 h-index	7950 149 g-index
234 all docs	234 docs citations	234 times ranked	53781 citing authors

#	Article	IF	Citations
1	The FAIR Guiding Principles for scientific data management and stewardship. Scientific Data, 2016, 3, 160018.	5.3	8,670
2	Transcriptome and genome sequencing uncovers functional variation in humans. Nature, 2013, 501, 506-511.	27.8	1,857
3	A promoter-level mammalian expression atlas. Nature, 2014, 507, 462-470.	27.8	1,838
4	Systematic identification of trans eQTLs as putative drivers of known disease associations. Nature Genetics, 2013, 45, 1238-1243.	21.4	1,544
5	Gateways to the FANTOM5 promoter level mammalian expression atlas. Genome Biology, 2015, 16, 22.	8.8	687
6	Deep sequencing-based expression analysis shows major advances in robustness, resolution and inter-lab portability over five microarray platforms. Nucleic Acids Research, 2008, 36, e141-e141.	14.5	653
7	Deep sequencing of RNA from immune cell-derived vesicles uncovers the selective incorporation of small non-coding RNA biotypes with potential regulatory functions. Nucleic Acids Research, 2012, 40, 9272-9285.	14.5	595
8	Large-scale cis- and trans-eQTL analyses identify thousands of genetic loci and polygenic scores that regulate blood gene expression. Nature Genetics, 2021, 53, 1300-1310.	21.4	590
9	Genome-wide association study identifies six new loci influencing pulse pressure and mean arterial pressure. Nature Genetics, 2011, 43, 1005-1011.	21.4	403
10	Disease variants alter transcription factor levels and methylation of their binding sites. Nature Genetics, 2017, 49, 131-138.	21.4	390
11	Identification of context-dependent expression quantitative trait loci in whole blood. Nature Genetics, 2017, 49, 139-145.	21.4	363
12	Alternative mRNA transcription, processing, and translation: insights from RNA sequencing. Trends in Genetics, 2015, 31, 128-139.	6.7	283
13	Effect of predicted protein-truncating genetic variants on the human transcriptome. Science, 2015, 348, 666-669.	12.6	252
14	Reproducibility of high-throughput mRNA and small RNA sequencing across laboratories. Nature Biotechnology, 2013, 31, 1015-1022.	17.5	251
15	Prorenin Induces Intracellular Signaling in Cardiomyocytes Independently of Angiotensin II. Hypertension, 2006, 48, 564-571.	2.7	228
16	Genome-wide association study identifies novel genetic variants contributing to variation in blood metabolite levels. Nature Communications, 2015, 6, 7208.	12.8	178
17	Genetic variation in T-box binding element functionally affects SCN5A/SCN10A enhancer. Journal of Clinical Investigation, 2012, 122, 2519-2530.	8.2	167
18	Blood lipids influence DNA methylation in circulating cells. Genome Biology, 2016, 17, 138.	8.8	154

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19	DNA Methylation Analysis Identifies Loci for Blood Pressure Regulation. American Journal of Human Genetics, 2017, 101, 888-902.	6.2	154
20	Phage display screening without repetitious selection rounds. Analytical Biochemistry, 2012, 421, 622-631.	2.4	149
21	Poly(A) binding protein nuclear 1 levels affect alternative polyadenylation. Nucleic Acids Research, 2012, 40, 9089-9101.	14.5	148
22	T-box transcription factor TBX3 reprogrammes mature cardiac myocytes into pacemaker-like cells. Cardiovascular Research, 2012, 94, 439-449.	3.8	136
23	Genome-wide assessment of differential roles for p300 and CBP in transcription regulation. Nucleic Acids Research, 2010, 38, 5396-5408.	14.5	133
24	Serum matrix metalloproteinase-9 (MMP-9) as a biomarker for monitoring disease progression in Duchenne muscular dystrophy (DMD). Neuromuscular Disorders, 2011, 21, 569-578.	0.6	132
25	Formation of S-Nitrosothiols via Direct Nucleophilic Nitrosation of Thiols by Peroxynitrite with Elimination of Hydrogen Peroxide. Journal of Biological Chemistry, 1998, 273, 30255-30262.	3.4	131
26	The value of data. Nature Genetics, 2011, 43, 281-283.	21.4	126
27	Guidelines for Antisense Oligonucleotide Design and Insight Into Splice-modulating Mechanisms. Molecular Therapy, 2009, 17, 548-553.	8.2	125
28	Timing and localization of human dystrophin isoform expression provide insights into the cognitive phenotype of Duchenne muscular dystrophy. Scientific Reports, 2017, 7, 12575.	3.3	123
29	Age-related accrual of methylomic variability is linked to fundamental ageing mechanisms. Genome Biology, 2016, 17, 191.	8.8	120
30	Skewed X-inactivation is common in the general female population. European Journal of Human Genetics, 2019, 27, 455-465.	2.8	119
31	Aorta of ApoE-Deficient Mice Responds to Atherogenic Stimuli by a Prelesional Increase and Subsequent Decrease in the Expression of Antioxidant Enzymes. Circulation Research, 2003, 93, 262-269.	4.5	110
32	Tbx2 and Tbx3 induce atrioventricular myocardial development and endocardial cushion formation. Cellular and Molecular Life Sciences, 2012, 69, 1377-1389.	5.4	110
33	Tumor cell migration screen identifies SRPK1 as breast cancer metastasis determinant. Journal of Clinical Investigation, 2015, 125, 1648-1664.	8.2	110
34	Full-length mRNA sequencing uncovers a widespread coupling between transcription initiation and mRNA processing. Genome Biology, 2018, 19, 46.	8.8	106
35	Affinity proteomics within rare diseases: a <scp>BIO</scp>â€<scp>NMD</scp> study for blood biomarkers of muscular dystrophies. EMBO Molecular Medicine, 2014, 6, 918-936.	6.9	105
36	The Effects of Low Levels of Dystrophin on Mouse Muscle Function and Pathology. PLoS ONE, 2012, 7, e31937.	2.5	96

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37	Muscle regeneration in dystrophin-deficient mdx mice studied by gene expression profiling. BMC Genomics, 2005, 6, 98.	2.8	95
38	mRNA degradation controls differentiation state-dependent differences in transcript and splice variant abundance. Nucleic Acids Research, 2011, 39, 556-566.	14.5	95
39	Low dystrophin levels increase survival and improve muscle pathology and function in dystrophin/utrophin doubleâ€knockout mice. FASEB Journal, 2013, 27, 2484-2495.	0.5	94
40	Fluorescent labelling of cRNA for microarray applications. Nucleic Acids Research, 2003, 31, 20e-20.	14.5	92
41	Validation of genetic modifiers for Duchenne muscular dystrophy: a multicentre study assessingSPP1andLTBP4variants. Journal of Neurology, Neurosurgery and Psychiatry, 2015, 86, 1060-1065.	1.9	86
42	New methods for next generation sequencing based microRNA expression profiling. BMC Genomics, 2010, 11, 716.	2.8	85
43	Coexpression Network Analysis Identifies Transcriptional Modules Related to Proastrocytic Differentiation and Sprouty Signaling in Glioma. Cancer Research, 2010, 70, 10060-10070.	0.9	82
44	Gene Expression Profiling of the Forming Atrioventricular Node Using a Novel Tbx3 -Based Node-Specific Transgenic Reporter. Circulation Research, 2009, 105, 61-69.	4.5	80
45	Roux-en-Y Gastric Bypass Surgery, but Not Calorie Restriction, Reduces Plasma Branched-Chain Amino Acids in Obese Women Independent of Weight Loss or the Presence of Type 2 Diabetes. Diabetes Care, 2014, 37, 3150-3156.	8.6	80
46	Huntingtonâ€™s disease biomarker progression profile identified by transcriptome sequencing in peripheral blood. European Journal of Human Genetics, 2015, 23, 1349-1356.	2.8	79
47	Molecular and phenotypic characterization of a mouse model of oculopharyngeal muscular dystrophy reveals severe muscular atrophy restricted to fast glycolytic fibres. Human Molecular Genetics, 2010, 19, 2191-2207.	2.9	78
48	Exploring the Transcriptome of Ciliated Cells Using In Silico Dissection of Human Tissues. PLoS ONE, 2012, 7, e35618.	2.5	73
49	Fibronectin is a serum biomarker for <scp>D</scp>uchenne muscular dystrophy. Proteomics - Clinical Applications, 2014, 8, 269-278.	1.6	73
50	Insight in Genome-Wide Association of Metabolite Quantitative Traits by Exome Sequence Analyses. PLoS Genetics, 2015, 11, e1004835.	3.5	70
51	Generation and Characterization of Transgenic Mice with the Full-length Human DMD Gene. Journal of Biological Chemistry, 2008, 283, 5899-5907.	3.4	69
52	Common pathological mechanisms in mouse models for muscular dystrophies. FASEB Journal, 2006, 20, 127-129.	0.5	67
53	Mutant huntingtin activates Nrf2-responsive genes and impairs dopamine synthesis in a PC12 model of Huntington's disease. BMC Molecular Biology, 2008, 9, 84.	3.0	66
54	Comparison of skeletal muscle pathology and motor function of dystrophin and utrophin deficient mouse strains. Neuromuscular Disorders, 2012, 22, 406-417.	0.6	65

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55	Refined mapping of autoimmune disease associated genetic variants with gene expression suggests an important role for non-coding RNAs. Journal of Autoimmunity, 2016, 68, 62-74.	6.5	64
56	Relative power and sample size analysis on gene expression profiling data. BMC Genomics, 2009, 10, 439.	2.8	62
57	Increased sensitivity of next generation sequencing-based expression profiling after globin reduction in human blood RNA. BMC Genomics, 2012, 13, 28.	2.8	62
58	Proteomic Analysis of the Dysferlin Protein Complex Unveils Its Importance for Sarcolemmal Maintenance and Integrity. PLoS ONE, 2010, 5, e13854.	2.5	62
59	Benchmarking deep learning splice prediction tools using functional splice assays. Human Mutation, 2021, 42, 799-810.	2.5	59
60	Integrated analysis of microRNA and mRNA expression: adding biological significance to microRNA target predictions. Nucleic Acids Research, 2013, 41, e146-e146.	14.5	58
61	Cellâ€type specific regulation of myostatin signaling. FASEB Journal, 2012, 26, 1462-1472.	0.5	57
62	Immune stimuli shape the small non-coding transcriptome of extracellular vesicles released by dendritic cells. Cellular and Molecular Life Sciences, 2018, 75, 3857-3875.	5.4	57
63	FcÎ³ Receptor IIb Strongly Regulates FcÎ³ Receptor-Facilitated T Cell Activation by Dendritic Cells. Journal of Immunology, 2012, 189, 92-101.	0.8	56
64	Serum protein profiling in mice: Identification of Factor XIIIa as a potential biomarker for muscular dystrophy. Proteomics, 2008, 8, 1552-1563.	2.2	52
65	Peptide Conjugation of 2â€²-O-methyl Phosphorothioate Antisense Oligonucleotides Enhances Cardiac Uptake and Exon Skipping in mdx Mice. Nucleic Acid Therapeutics, 2014, 24, 25-36.	3.6	52
66	Non-sequential and multi-step splicing of the dystrophin transcript. RNA Biology, 2016, 13, 290-305.	3.1	52
67	Different roles for Abf1p and a T-rich promoter element in nucleosome organization of the yeast RPS28A gene. Nucleic Acids Research, 2000, 28, 1390-1396.	14.5	49
68	Solve-RD: systematic pan-European data sharing and collaborative analysis to solve rare diseases. European Journal of Human Genetics, 2021, 29, 1325-1331.	2.8	49
69	A decline in PABPN1 induces progressive muscle weakness in Oculopharyngeal muscle dystrophy and in muscle aging. Aging, 2013, 5, 412-426.	3.1	49
70	A SNP panel for identification of DNA and RNA specimens. BMC Genomics, 2018, 19, 90.	2.8	47
71	Transcriptional profiling and biomarker identification reveal tissue specific effects of expanded ataxin-3 in a spinocerebellar ataxia type 3 mouse model. Molecular Neurodegeneration, 2018, 13, 31.	10.8	47
72	Comprehensive diagnostics of acute myeloid leukemia by whole transcriptome RNA sequencing. Leukemia, 2021, 35, 47-61.	7.2	47

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73	Can subtle changes in gene expression be consistently detected with different microarray platforms?. BMC Genomics, 2008, 9, 124.	2.8	45
74	DeepSAGE Reveals Genetic Variants Associated with Alternative Polyadenylation and Expression of Coding and Non-coding Transcripts. PLoS Genetics, 2013, 9, e1003594.	3.5	45
75	Huntingtonâ€™s disease blood and brain show a common gene expression pattern and share an immune signature with Alzheimerâ€™s disease. Scientific Reports, 2017, 7, 44849.	3.3	45
76	Assessing the translational landscape of myogenic differentiation by ribosome profiling. Nucleic Acids Research, 2015, 43, 4408-4428.	14.5	43
77	Integration of targeted metabolomics and transcriptomics identifies deregulation of phosphatidylcholine metabolism in Huntingtonâ€™s disease peripheral blood samples. Metabolomics, 2016, 12, 137.	3.0	43
78	Large-scale plasma metabolome analysis reveals alterations in HDL metabolism in migraine. Neurology, 2019, 92, e1899-e1911.	1.1	42
79	Novel Protein-Protein Interactions Inferred from Literature Context. PLoS ONE, 2009, 4, e7894.	2.5	41
80	Deregulation of the ubiquitin-proteasome system is the predominant molecular pathology in OPMD animal models and patients. Skeletal Muscle, 2011, 1, 15.	4.2	40
81	Dual exon skipping in myostatin and dystrophin for Duchenne muscular dystrophy. BMC Medical Genomics, 2011, 4, 36.	1.5	40
82	Aging as Accelerated Accumulation of Somatic Variants: Whole-Genome Sequencing of Centenarian and Middle-Aged Monozygotic Twin Pairs. Twin Research and Human Genetics, 2013, 16, 1026-1032.	0.6	40
83	A 3 months mild functional test regime does not affect disease parameters in young mdx mice. Neuromuscular Disorders, 2010, 20, 273-280.	0.6	38
84	Downregulation of the acetyl-CoA metabolic network in adipose tissue of obese diabetic individuals and recovery after weight loss. Diabetologia, 2014, 57, 2384-2392.	6.3	38
85	Accurate quantification of dystrophin mRNA and exon skipping levels in Duchenne Muscular Dystrophy. Laboratory Investigation, 2010, 90, 1396-1402.	3.7	37
86	Exonic Sequences Provide Better Targets for Antisense Oligonucleotides Than Splice Site Sequences in the Modulation of Duchenne Muscular Dystrophy Splicing. Oligonucleotides, 2010, 20, 69-77.	2.7	37
87	Cortical Spreading Depression Causes Unique Dysregulation of Inflammatory Pathways in a Transgenic Mouse Model of Migraine. Molecular Neurobiology, 2017, 54, 2986-2996.	4.0	37
88	Large-scale gene expression analysis of human skeletal myoblast differentiation. Neuromuscular Disorders, 2004, 14, 507-518.	0.6	36
89	Literature-based priors for gene regulatory networks. Bioinformatics, 2009, 25, 1768-1774.	4.1	36
90	Overactive bone morphogenetic protein signaling in heterotopic ossification and Duchenne muscular dystrophy. Cellular and Molecular Life Sciences, 2013, 70, 407-423.	5.4	36

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91	PhD7FASTER: PREDICTING CLONES PROPAGATING FASTER FROM THE Ph.D.-7 PHAGE DISPLAY PEPTIDE LIBRARY. Journal of Bioinformatics and Computational Biology, 2014, 12, 1450005.	0.8	36
92	TCTEX1D1 is a genetic modifier of disease progression in Duchenne muscular dystrophy. European Journal of Human Genetics, 2020, 28, 815-825.	2.8	36
93	Induction of glutathione-S-transferase mRNA levels by chemopreventive selenocysteine Se-conjugates. Biochemical Pharmacology, 2002, 63, 1843-1849.	4.4	35
94	Solving patients with rare diseases through programmatic reanalysis of genome-phenome data. European Journal of Human Genetics, 2021, 29, 1337-1347.	2.8	34
95	Systematic genomic and translational efficiency studies of uveal melanoma. PLoS ONE, 2017, 12, e0178189.	2.5	34
96	CORE_TF: a user-friendly interface to identify evolutionary conserved transcription factor binding sites in sets of co-regulated genes. BMC Bioinformatics, 2008, 9, 495.	2.6	33
97	BMP antagonists enhance myogenic differentiation and ameliorate the dystrophic phenotype in a DMD mouse model. Neurobiology of Disease, 2011, 41, 353-360.	4.4	33
98	RNA sequencing: from tag-based profiling to resolving complete transcript structure. Cellular and Molecular Life Sciences, 2014, 71, 3537-3551.	5.4	33
99	Drug prioritization using the semantic properties of a knowledge graph. Scientific Reports, 2019, 9, 6281.	3.3	33
100	Intensity-based analysis of two-colour microarrays enables efficient and flexible hybridization designs. Nucleic Acids Research, 2004, 32, 41e-41.	14.5	32
101	Tissue-specific transcript annotation and expression profiling with complementary next-generation sequencing technologies. Nucleic Acids Research, 2010, 38, e165-e165.	14.5	32
102	Common disease signatures from gene expression analysis in Huntingtonâ€™s disease human blood and brain. Orphanet Journal of Rare Diseases, 2016, 11, 97.	2.7	32
103	Combined Effect of AAV-U7-Induced Dystrophin Exon Skipping and Soluble Activin Type IIB Receptor in mdx Mice. Human Gene Therapy, 2012, 23, 1269-1279.	2.7	31
104	DMD transcript imbalance determines dystrophin levels. FASEB Journal, 2013, 27, 4909-4916.	0.5	30
105	Antisense-Oligonucleotide Mediated Exon Skipping in Activin-Receptor-Like Kinase 2: Inhibiting the Receptor That Is Overactive in Fibrodysplasia Ossificans Progressiva. PLoS ONE, 2013, 8, e69096.	2.5	30
106	Determining the quality and complexity of next-generation sequencing data without a reference genome. Genome Biology, 2014, 15, 555.	8.8	30
107	204th ENMC International Workshop on Biomarkers in Duchenne Muscular Dystrophy 24â€“26 January 2014, Naarden, The Netherlands. Neuromuscular Disorders, 2015, 25, 184-198.	0.6	30
108	Induced pluripotency with endogenous and inducible genes. Experimental Cell Research, 2008, 314, 3255-3263.	2.6	29

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109	A characterization of cis- and trans-heritability of RNA-Seq-based gene expression. European Journal of Human Genetics, 2020, 28, 253-263.	2.8	29
110	Genetics of the human metabolome, what is next?. Biochimica Et Biophysica Acta - Molecular Basis of Disease, 2014, 1842, 1923-1931.	3.8	28
111	Comparative mass spectrometric and immunoassayâ€based proteome analysis in serum of Duchenne muscular dystrophy patients. Proteomics - Clinical Applications, 2016, 10, 290-299.	1.6	27
112	Selective glucocorticoid receptor modulation prevents and reverses non-alcoholic fatty liver disease in male mice. Endocrinology, 2018, 159, 3925-3936.	2.8	27
113	Annotating Transcriptional Effects of Genetic Variants in Diseaseâ€Relevant Tissue: Transcriptomeâ€Wide Allelic Imbalance in Osteoarthritic Cartilage. Arthritis and Rheumatology, 2019, 71, 561-570.	5.6	27
114	Genome-wide identification of genes regulating DNA methylation using genetic anchors for causal inference. Genome Biology, 2020, 21, 220.	8.8	27
115	Gene expression profiling to monitor therapeutic and adverse effects of antisense therapies for Duchenne muscular dystrophy. Pharmacogenomics, 2006, 7, 281-297.	1.3	26
116	Microarray retriever: a web-based tool for searching and large scale retrieval of public microarray data. Nucleic Acids Research, 2008, 36, W327-W331.	14.5	26
117	PASSion: a pattern growth algorithm-based pipeline for splice junction detection in paired-end RNA-Seq data. Bioinformatics, 2012, 28, 479-486.	4.1	26
118	Structuring research methods and data with the research object model: genomics workflows as a case study. Journal of Biomedical Semantics, 2014, 5, 41.	1.6	26
119	Targeting TGF-Î² Signaling by Antisense Oligonucleotide-mediated Knockdown of TGF-Î² Type I Receptor. Molecular Therapy - Nucleic Acids, 2014, 3, e156.	5.1	26
120	Regulation of skeletal muscle energy/nutrient-sensing pathways during metabolic adaptation to fasting in healthy humans. American Journal of Physiology - Endocrinology and Metabolism, 2014, 307, E885-E895.	3.5	26
121	Meta-analysis of polycystic kidney disease expression profiles defines strong involvement of injury repair processes. American Journal of Physiology - Renal Physiology, 2017, 312, F806-F817.	2.7	26
122	Evaluation of commonly used analysis strategies for epigenome- and transcriptome-wide association studies through replication of large-scale population studies. Genome Biology, 2019, 20, 235.	8.8	26
123	Drug Repositioning through Systematic Mining of Gene Coexpression Networks in Cancer. PLoS ONE, 2016, 11, e0165059.	2.5	25
124	The distinct transcriptomes of slow and fast adult muscles are delineated by noncoding RNAs. FASEB Journal, 2018, 32, 1579-1590.	0.5	25
125	Gene expression profiling highlights defective myogenesis in DMD patients and a possible role for bone morphogenetic protein 4. Neurobiology of Disease, 2006, 23, 228-236.	4.4	24
126	Novel Ex Vivo Culture Method for the Study of Dupuytren's Disease: Effects of TGFÎ² Type 1 Receptor Modulation by Antisense Oligonucleotides. Molecular Therapy - Nucleic Acids, 2014, 3, e142.	5.1	24

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127	Autosomal genetic variation is associated with DNA methylation in regions variably escaping X-chromosome inactivation. Nature Communications, 2018, 9, 3738.	12.8	24
128	Gene expression variation between mouse inbred strains. BMC Genomics, 2004, 5, 57.	2.8	23
129	Calpain 3 Is a Rapid-Action, Unidirectional Proteolytic Switch Central to Muscle Remodeling. PLoS ONE, 2010, 5, e11940.	2.5	23
130	RNA-Seq in 296 phased trios provides a high-resolution map of genomic imprinting. BMC Biology, 2019, 17, 50.	3.8	23
131	Sox4 mediates Tbx3 transcriptional regulation of the gap junction protein Cx43. Cellular and Molecular Life Sciences, 2011, 68, 3949-3961.	5.4	22
132	Accounting for immunoprecipitation efficiencies in the statistical analysis of ChIP-seq data. BMC Bioinformatics, 2013, 14, 169.	2.6	22
133	The Implicitome: A Resource for Rationalizing Gene-Disease Associations. PLoS ONE, 2016, 11, e0149621.	2.5	22
134	Increasing phenotypic annotation improves the diagnostic rate of exome sequencing in a rare neuromuscular disorder. Human Mutation, 2019, 40, 1797-1812.	2.5	22
135	Literature-aided meta-analysis of microarray data: a compendium study on muscle development and disease. BMC Bioinformatics, 2008, 9, 291.	2.6	21
136	Joint modeling of ChIP-seq data via a Markov random field model. Biostatistics, 2014, 15, 296-310.	1.5	21
137	Myostatin/activin blocking combined with exercise reconditions skeletal muscle expression profile of mdx mice. Molecular and Cellular Endocrinology, 2015, 399, 131-142.	3.2	21
138	Integrated Whole Genome and Transcriptome Analysis Identified a Therapeutic Minor Histocompatibility Antigen in a Splice Variant of ITGB2. Clinical Cancer Research, 2016, 22, 4185-4196.	7.0	21
139	In silico discovery and experimental validation of new proteinâ€“protein interactions. Proteomics, 2011, 11, 843-853.	2.2	20
140	LPAR1andITGA4regulate peripheral blood monocyte counts. Human Mutation, 2011, 32, 873-876.	2.5	20
141	Identifying a gene expression signature of cluster headache in blood. Scientific Reports, 2017, 7, 40218.	3.3	20
142	Evaluation of serum MMP-9 as predictive biomarker for antisense therapy in Duchenne. Scientific Reports, 2017, 7, 17888.	3.3	20
143	Csde1 binds transcripts involved in protein homeostasis and controls their expression in an erythroid cell line. Scientific Reports, 2018, 8, 2628.	3.3	20
144	Federated Networks for Distributed Analysis of Health Data. Frontiers in Public Health, 2021, 9, 712569.	2.7	20

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145	Literature-aided interpretation of gene expression data with the weighted global test. Briefings in Bioinformatics, 2011, 12, 518-529.	6.5	19
146	Repeated FcÎµRI triggering reveals modified mast cell function related to chronic allergic responses in tissue. Journal of Allergy and Clinical Immunology, 2016, 138, 869-880.	2.9	19
147	Cyclic Peptides to Improve Delivery and Exon Skipping of Antisense Oligonucleotides in a Mouse Model for Duchenne Muscular Dystrophy. Molecular Therapy, 2018, 26, 132-147.	8.2	19
148	Search for Early Pancreatic Cancer Blood Biomarkers in Five European Prospective Population Biobanks Using Metabolomics. Endocrinology, 2019, 160, 1731-1742.	2.8	19
149	Inhibition of IL-1 Signaling by Antisense Oligonucleotide-mediated Exon Skipping of IL-1 Receptor Accessory Protein (IL-1RAcP). Molecular Therapy - Nucleic Acids, 2013, 2, e66.	5.1	18
150	Genome-wide identification of directed gene networks using large-scale population genomics data. Nature Communications, 2018, 9, 3097.	12.8	18
151	Comprehensive Gene-Expression Survey Identifies Wif1 as a Modulator of Cardiomyocyte Differentiation. PLoS ONE, 2010, 5, e15504.	2.5	18
152	The RDâ€Connect Genomeâ€Phenome Analysis Platform: Accelerating diagnosis, research, and gene discovery for rare diseases. Human Mutation, 2022, , .	2.5	18
153	SlicePie: a novel analytical approach for the detection of alternative, non-sequential and recursive splicing. Nucleic Acids Research, 2015, 43, e80-e80.	14.5	17
154	Comparative transcriptomics of shear stress treated Pkd1â^'/â^' cells and pre-cystic kidneys reveals pathways involved in early polycystic kidney disease. Biomedicine and Pharmacotherapy, 2018, 108, 1123-1134.	5.6	17
155	Insulin Signaling as a Key Moderator in Myotonic Dystrophy Type 1. Frontiers in Neurology, 2019, 10, 1229.	2.4	17
156	Despite differential gene expression profiles pediatric MDS derived mesenchymal stromal cells display functionality in vitro. Stem Cell Research, 2015, 14, 198-210.	0.7	16
157	Prioritization of novel ADPKD drug candidates from disease-stage specific gene expression profiles. EBioMedicine, 2020, 51, 102585.	6.1	16
158	Interspecies Translation of Disease Networks Increases Robustness and Predictive Accuracy. PLoS Computational Biology, 2011, 7, e1002258.	3.2	15
159	An alanine expanded PABPN1 causes increased utilization of intronic polyadenylation sites. Npj Aging and Mechanisms of Disease, 2017, 3, 6.	4.5	15
160	Automated workflow-based exploitation of pathway databases provides new insights into genetic associations of metabolite profiles. BMC Genomics, 2013, 14, 865.	2.8	14
161	Brain Transcriptomic Analysis of Hereditary Cerebral Hemorrhage With Amyloidosis-Dutch Type. Frontiers in Aging Neuroscience, 2018, 10, 102.	3.4	13
162	Ribosome profiling uncovers selective mRNA translation associated with eIF2 phosphorylation in erythroid progenitors. PLoS ONE, 2018, 13, e0193790.	2.5	12

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163	De-novo FAIRification via an Electronic Data Capture system by automated transformation of filled electronic Case Report Forms into machine-readable data. Journal of Biomedical Informatics, 2021, 122, 103897.	4.3	12
164	Dysfunctional transcripts are formed by alternative polyadenylation in OPMD. Oncotarget, 2017, 8, 73516-73528.	1.8	12
165	Discovery of widespread transcription initiation at microsatellites predictable by sequence-based deep neural network. Nature Communications, 2021, 12, 3297.	12.8	11
166	Selection of effective antisense oligodeoxynucleotides with a green fluorescent protein-based assay. FEBS Journal, 2002, 269, 2574-2583.	0.2	10
167	Exploiting the full power of temporal gene expression profiling through a new statistical test: application to the analysis of muscular dystrophy data. BMC Bioinformatics, 2006, 7, 183.	2.6	10
168	Generic Information Can Retrieve Known Biological Associations: Implications for Biomedical Knowledge Discovery. PLoS ONE, 2013, 8, e78665.	2.5	10
169	Recommendations for the analysis of gene expression data to identify intrinsic differences between similar tissues. Genomics, 2020, 112, 3157-3165.	2.9	10
170	Personalized Proteome: Comparing Proteogenomics and Open Variant Search Approaches for Single Amino Acid Variant Detection. Journal of Proteome Research, 2021, 20, 3353-3364.	3.7	10
171	RNA expression profiling in brains of familial hemiplegic migraine type 1 knock-in mice. Cephalalgia, 2014, 34, 174-182.	3.9	9
172	Characterisation of transcription factor profiles in polycystic kidney disease (PKD): identification and validation of STAT3 and RUNX1 in the injury/repair response and PKD progression. Journal of Molecular Medicine, 2019, 97, 1643-1656.	3.9	9
173	Computational approaches for the analysis of RNAâ€“protein interactions: A primer for biologists. Journal of Biological Chemistry, 2019, 294, 1-9.	3.4	9
174	Optimized Whole Genome Association Scanning for Discovery of HLA Class I-Restricted Minor Histocompatibility Antigens. Frontiers in Immunology, 2020, 11, 659.	4.8	8
175	The de novo FAIRification process of a registry for vascular anomalies. Orphanet Journal of Rare Diseases, 2021, 16, 376.	2.7	8
176	FAIR Genomes metadata schema promoting Next Generation Sequencing data reuse in Dutch healthcare and research. Scientific Data, 2022, 9, 169.	5.3	8
177	Antisense oligonucleotide mediated exon skipping as a potential strategy for the treatment of a variety of inflammatory diseases such as rheumatoid arthritis. Annals of the Rheumatic Diseases, 2012, 71, i75-i77.	0.9	7
178	Molecular signatures of age-associated chronic degeneration of shoulder muscles. Oncotarget, 2016, 7, 8513-8523.	1.8	7
179	The identification of informative genes from multiple datasets with increasing complexity. BMC Bioinformatics, 2010, 11, 32.	2.6	6
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