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	A comprehensive atlas of fetal splicing patterns in the brain of adult myotonic dystrophy type 1 patients. NAR Genomics and Bioinformatics, 2022, 4, lqac016.	3.2	2
2	The RDâ€Connect Genomeâ€Phenome Analysis Platform: Accelerating diagnosis, research, and gene discovery for rare diseases. Human Mutation, 2022, , .	2.5	18
3	FAIR Genomes metadata schema promoting Next Generation Sequencing data reuse in Dutch healthcare and research. Scientific Data, 2022, 9, 169.	5.3	8
4	Comprehensive diagnostics of acute myeloid leukemia by whole transcriptome RNA sequencing. Leukemia, 2021, 35, 47-61.	7.2	47
5	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
6	Benchmarking deep learning splice prediction tools using functional splice assays. Human Mutation, 2021, 42, 799-810.	2.5	59
7	Discovery of widespread transcription initiation at microsatellites predictable by sequence-based deep neural network. Nature Communications, 2021, 12, 3297.	12.8	11
8	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
9	Solving patients with rare diseases through programmatic reanalysis of genome-phenome data. European Journal of Human Genetics, 2021, 29, 1337-1347.	2.8	34
10	Clinical Outcome Evaluations and CBT Response Prediction in Myotonic Dystrophy. Journal of Neuromuscular Diseases, 2021, 8, 1031-1046.	2.6	4
11	How Patient Organizations Can Drive FAIR Data Efforts to Facilitate Research and Health Care: A Report of the Virtual Second International Meeting on Duchenne Data Sharing, March 3, 2021. Journal of Neuromuscular Diseases, 2021, 8, 1097-1108.	2.6	5
12	The de novo FAIRification process of a registry for vascular anomalies. Orphanet Journal of Rare Diseases, 2021, 16, 376.	2.7	8
13	Federated Networks for Distributed Analysis of Health Data. Frontiers in Public Health, 2021, 9, 712569.	2.7	20
14	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
15	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
16	Prioritization of novel ADPKD drug candidates from disease-stage specific gene expression profiles. EBioMedicine, 2020, 51, 102585.	6.1	16
17	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
18	TCTEX1D1 is a genetic modifier of disease progression in Duchenne muscular dystrophy. European Journal of Human Genetics, 2020, 28, 815-825.	2.8	36

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19	Genome-wide identification of genes regulating DNA methylation using genetic anchors for causal inference. Genome Biology, 2020, 21, 220.	8.8	27
20	Optimized Whole Genome Association Scanning for Discovery of HLA Class I-Restricted Minor Histocompatibility Antigens. Frontiers in Immunology, 2020, 11, 659.	4.8	8
21	Recommendations for the analysis of gene expression data to identify intrinsic differences between similar tissues. Genomics, 2020, 112, 3157-3165.	2.9	10
22	RNA-Seq in 296 phased trios provides a high-resolution map of genomic imprinting. BMC Biology, 2019, 17, 50.	3.8	23
23	Increasing phenotypic annotation improves the diagnostic rate of exome sequencing in a rare neuromuscular disorder. Human Mutation, 2019, 40, 1797-1812.	2.5	22
24	Search for Early Pancreatic Cancer Blood Biomarkers in Five European Prospective Population Biobanks Using Metabolomics. Endocrinology, 2019, 160, 1731-1742.	2.8	19
25	Drug prioritization using the semantic properties of a knowledge graph. Scientific Reports, 2019, 9, 6281.	3.3	33
26	Large-scale plasma metabolome analysis reveals alterations in HDL metabolism in migraine. Neurology, 2019, 92, e1899-e1911.	1.1	42
27	Meeting on data sharing for Duchenne 21â€“22 March 2019 Amsterdam, the Netherlands. Neuromuscular Disorders, 2019, 29, 800-810.	0.6	3
28	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
29	Insulin Signaling as a Key Moderator in Myotonic Dystrophy Type 1. Frontiers in Neurology, 2019, 10, 1229.	2.4	17
30	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
31	Skewed X-inactivation is common in the general female population. European Journal of Human Genetics, 2019, 27, 455-465.	2.8	119
32	Computational approaches for the analysis of RNAâ€“protein interactions: A primer for biologists. Journal of Biological Chemistry, 2019, 294, 1-9.	3.4	9
33	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
34	Csde1 binds transcripts involved in protein homeostasis and controls their expression in an erythroid cell line. Scientific Reports, 2018, 8, 2628.	3.3	20
35	Full-length mRNA sequencing uncovers a widespread coupling between transcription initiation and mRNA processing. Genome Biology, 2018, 19, 46.	8.8	106
36	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

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37	The distinct transcriptomes of slow and fast adult muscles are delineated by noncoding RNAs. FASEB Journal, 2018, 32, 1579-1590.	0.5	25
38	Selective glucocorticoid receptor modulation prevents and reverses non-alcoholic fatty liver disease in male mice. Endocrinology, 2018, 159, 3925-3936.	2.8	27
39	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
40	Ribosome profiling uncovers selective mRNA translation associated with eIF2 phosphorylation in erythroid progenitors. PLoS ONE, 2018, 13, e0193790.	2.5	12
41	Autosomal genetic variation is associated with DNA methylation in regions variably escaping X-chromosome inactivation. Nature Communications, 2018, 9, 3738.	12.8	24
42	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
43	A SNP panel for identification of DNA and RNA specimens. BMC Genomics, 2018, 19, 90.	2.8	47
44	Brain Transcriptomic Analysis of Hereditary Cerebral Hemorrhage With Amyloidosis-Dutch Type. Frontiers in Aging Neuroscience, 2018, 10, 102.	3.4	13
45	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
46	Strap associates with Csde1 and affects expression of select Csde1-bound transcripts. PLoS ONE, 2018, 13, e0201690.	2.5	5
47	Genome-wide identification of directed gene networks using large-scale population genomics data. Nature Communications, 2018, 9, 3097.	12.8	18
48	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
49	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
50	Identifying a gene expression signature of cluster headache in blood. Scientific Reports, 2017, 7, 40218.	3.3	20
51	Disease variants alter transcription factor levels and methylation of their binding sites. Nature Genetics, 2017, 49, 131-138.	21.4	390
52	Identification of context-dependent expression quantitative trait loci in whole blood. Nature Genetics, 2017, 49, 139-145.	21.4	363
53	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
54	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

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55	DNA Methylation Analysis Identifies Loci for Blood Pressure Regulation. American Journal of Human Genetics, 2017, 101, 888-902.	6.2	154
56	An alanine expanded PABPN1 causes increased utilization of intronic polyadenylation sites. Npj Aging and Mechanisms of Disease, 2017, 3, 6.	4.5	15
57	Evaluation of serum MMP-9 as predictive biomarker for antisense therapy in Duchenne. Scientific Reports, 2017, 7, 17888.	3.3	20
58	Systematic genomic and translational efficiency studies of uveal melanoma. PLoS ONE, 2017, 12, e0178189.	2.5	34
59	Dysfunctional transcripts are formed by alternative polyadenylation in OPMD. Oncotarget, 2017, 8, 73516-73528.	1.8	12
60	Consistency of biological networks inferred from microarray and sequencing data. BMC Bioinformatics, 2016, 17, 254.	2.6	4
61	B16â€...Common disease signatures from gene expression analysis in huntingtonâ€™s disease human blood and brain. Journal of Neurology, Neurosurgery and Psychiatry, 2016, 87, A14.2-A15.	1.9	0
62	Drug Repositioning through Systematic Mining of Gene Coexpression Networks in Cancer. PLoS ONE, 2016, 11, e0165059.	2.5	25
63	The Implicitome: A Resource for Rationalizing Gene-Disease Associations. PLoS ONE, 2016, 11, e0149621.	2.5	22
64	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
65	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
66	B17â€...Blood transcriptome replicates dysregulation found in human huntingtonâ€™s disease brain and shares an immune signature with alzheimerâ€™s disease. Journal of Neurology, Neurosurgery and Psychiatry, 2016, 87, A15.1-A15.	1.9	0
67	The FAIR Guiding Principles for scientific data management and stewardship. Scientific Data, 2016, 3, 160018.	5.3	8,670
68	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
69	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
70	Age-related accrual of methylomic variability is linked to fundamental ageing mechanisms. Genome Biology, 2016, 17, 191.	8.8	120
71	Blood lipids influence DNA methylation in circulating cells. Genome Biology, 2016, 17, 138.	8.8	154
72	Non-sequential and multi-step splicing of the dystrophin transcript. RNA Biology, 2016, 13, 290-305.	3.1	52

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73	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
74	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
75	Whole Transcriptome Sequencing (RNAseq) As a Comprehensive, Cost-Efficient Diagnostic Tool for Acute Myeloid Leukemia. Blood, 2016, 128, 1701-1701.	1.4	4
76	Molecular signatures of age-associated chronic degeneration of shoulder muscles. Oncotarget, 2016, 7, 8513-8523.	1.8	7
77	Gene-expression and in vitro function of mesenchymal stromal cells are affected in juvenile myelomonocytic leukemia. Haematologica, 2015, 100, 1434-1441.	3.5	5
78	Genome-wide association study identifies novel genetic variants contributing to variation in blood metabolite levels. Nature Communications, 2015, 6, 7208.	12.8	178
79	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
80	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
81	Alternative mRNA transcription, processing, and translation: insights from RNA sequencing. Trends in Genetics, 2015, 31, 128-139.	6.7	283
82	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
83	Gateways to the FANTOM5 promoter level mammalian expression atlas. Genome Biology, 2015, 16, 22.	8.8	687
84	Response to: Evaluation of the serum matrix metalloproteinase-9 as a biomarker for monitoring disease progression in Duchenne muscular dystrophy. Neuromuscular Disorders, 2015, 25, 446-447.	0.6	3
85	Insight in Genome-Wide Association of Metabolite Quantitative Traits by Exome Sequence Analyses. PLoS Genetics, 2015, 11, e1004835.	3.5	70
86	SplicePie: a novel analytical approach for the detection of alternative, non-sequential and recursive splicing. Nucleic Acids Research, 2015, 43, e80-e80.	14.5	17
87	Effect of predicted protein-truncating genetic variants on the human transcriptome. Science, 2015, 348, 666-669.	12.6	252
88	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
89	Assessing the translational landscape of myogenic differentiation by ribosome profiling. Nucleic Acids Research, 2015, 43, 4408-4428.	14.5	43
90	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

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91	Tumor cell migration screen identifies SRPK1 as breast cancer metastasis determinant. Journal of Clinical Investigation, 2015, 125, 1648-1664.	8.2	110
92	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
93	Determining the quality and complexity of next-generation sequencing data without a reference genome. Genome Biology, 2014, 15, 555.	8.8	30
94	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
95	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
96	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
97	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
98	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
99	EHMTI-0262. Dysregulation of inflammatory pathways in a familial hemiplegic migraine 1 mouse model after the induction of cortical spreading depression. Journal of Headache and Pain, 2014, 15, .	6.0	0
100	RNA expression profiling in brains of familial hemiplegic migraine type 1 knock-in mice. Cephalalgia, 2014, 34, 174-182.	3.9	9
101	Joint modeling of ChIP-seq data via a Markov random field model. Biostatistics, 2014, 15, 296-310.	1.5	21
102	A promoter-level mammalian expression atlas. Nature, 2014, 507, 462-470.	27.8	1,838
103	Fibronectin is a serum biomarker for <scp>D</scp>uchenne muscular dystrophy. Proteomics - Clinical Applications, 2014, 8, 269-278.	1.6	73
104	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
105	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
106	RNA sequencing: from tag-based profiling to resolving complete transcript structure. Cellular and Molecular Life Sciences, 2014, 71, 3537-3551.	5.4	33
107	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
108	Genetics of the human metabolome, what is next?. Biochimica Et Biophysica Acta - Molecular Basis of Disease, 2014, 1842, 1923-1931.	3.8	28

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109	Overactive bone morphogenetic protein signaling in heterotopic ossification and Duchenne muscular dystrophy. Cellular and Molecular Life Sciences, 2013, 70, 407-423.	5.4	36
110	Accounting for immunoprecipitation efficiencies in the statistical analysis of ChIP-seq data. BMC Bioinformatics, 2013, 14, 169.	2.6	22
111	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
112	Automated workflow-based exploitation of pathway databases provides new insights into genetic associations of metabolite profiles. BMC Genomics, 2013, 14, 865.	2.8	14
113	Reproducibility of high-throughput mRNA and small RNA sequencing across laboratories. Nature Biotechnology, 2013, 31, 1015-1022.	17.5	251
114	Transcriptome and genome sequencing uncovers functional variation in humans. Nature, 2013, 501, 506-511.	27.8	1,857
115	Systematic identification of trans eQTLs as putative drivers of known disease associations. Nature Genetics, 2013, 45, 1238-1243.	21.4	1,544
116	Integrated analysis of microRNA and mRNA expression: adding biological significance to microRNA target predictions. Nucleic Acids Research, 2013, 41, e146-e146.	14.5	58
117	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
118	DeepSAGE Reveals Genetic Variants Associated with Alternative Polyadenylation and Expression of Coding and Non-coding Transcripts. PLoS Genetics, 2013, 9, e1003594.	3.5	45
119	DMD transcript imbalance determines dystrophin levels. FASEB Journal, 2013, 27, 4909-4916.	0.5	30
120	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
121	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
122	Generic Information Can Retrieve Known Biological Associations: Implications for Biomedical Knowledge Discovery. PLoS ONE, 2013, 8, e78665.	2.5	10
123	A decline in PABPN1 induces progressive muscle weakness in Oculopharyngeal muscle dystrophy and in muscle aging. Aging, 2013, 5, 412-426.	3.1	49
124	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
125	Poly(A) binding protein nuclear 1 levels affect alternative polyadenylation. Nucleic Acids Research, 2012, 40, 9089-9101.	14.5	148
126	F03â€…Whole blood SAGE digital gene expression profiling from Huntington's disease patients. Journal of Neurology, Neurosurgery and Psychiatry, 2012, 83, A22.1-A22.	1.9	0

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127	T-box transcription factor TBX3 reprogrammes mature cardiac myocytes into pacemaker-like cells. Cardiovascular Research, 2012, 94, 439-449.	3.8	136
128	FcÎ³ Receptor IIb Strongly Regulates FcÎ³ Receptor-Facilitated T Cell Activation by Dendritic Cells. Journal of Immunology, 2012, 189, 92-101.	0.8	56
129	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
130	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
131	B15â€...CTCF in Huntington's disease. Journal of Neurology, Neurosurgery and Psychiatry, 2012, 83, A10.2-A10.	1.9	0
132	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
133	Cellâ€type specific regulation of myostatin signaling. FASEB Journal, 2012, 26, 1462-1472.	0.5	57
134	Comparison of skeletal muscle pathology and motor function of dystrophin and utrophin deficient mouse strains. Neuromuscular Disorders, 2012, 22, 406-417.	0.6	65
135	Increased sensitivity of next generation sequencing-based expression profiling after globin reduction in human blood RNA. BMC Genomics, 2012, 13, 28.	2.8	62
136	T.P.26 Low dystrophin levels increase survival and improve pathology and motor function in dystrophin/utrophin double knockout mice. Neuromuscular Disorders, 2012, 22, 860.	0.6	0
137	The Effects of Low Levels of Dystrophin on Mouse Muscle Function and Pathology. PLoS ONE, 2012, 7, e31937.	2.5	96
138	Exploring the Transcriptome of Ciliated Cells Using In Silico Dissection of Human Tissues. PLoS ONE, 2012, 7, e35618.	2.5	73
139	Tbx2 and Tbx3 induce atrioventricular myocardial development and endocardial cushion formation. Cellular and Molecular Life Sciences, 2012, 69, 1377-1389.	5.4	110
140	Phage display screening without repetitious selection rounds. Analytical Biochemistry, 2012, 421, 622-631.	2.4	149
141	Genetic variation in T-box binding element functionally affects SCN5A/SCN10A enhancer. Journal of Clinical Investigation, 2012, 122, 2519-2530.	8.2	167
142	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
143	P1.22 Low dystrophin levels improve life expectancy, phenotype and functional performance in the mdx/utrn -/- mouse. Neuromuscular Disorders, 2011, 21, 648.	0.6	0
144	P1.23 The effects of low dystrophin levels on muscle function and pathology. Neuromuscular Disorders, 2011, 21, 648.	0.6	0

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145	P1.44 Development of heart failure in mice with low dystrophin levels. Neuromuscular Disorders, 2011, 21, 654-655.	0.6	0
146	P1.48 Serum matrix metalloproteinase-9 (MMP-9) as a biomarker for monitoring Duchenne muscular dystrophy (DMD) disease progression. Neuromuscular Disorders, 2011, 21, 656.	0.6	0
147	P1.49 Mass spectrometry based clinical proteomics for biomarker discovery in Duchenne muscular dystrophy. Neuromuscular Disorders, 2011, 21, 656.	0.6	0
148	P1.51 Serum protein profiling in mouse models with Dystrophin deficiency using bead-fractionation, MALDI-MS and linear regression. Neuromuscular Disorders, 2011, 21, 656-657.	0.6	0
149	P1.52 BIO-NMD: Discovery and validation of biomarkers for neuromuscular diseases (NMDs) â€“ An EU funded FP7 project. Neuromuscular Disorders, 2011, 21, 657.	0.6	0
150	P2.44 Accelerated skeletal muscle ageing is a molecular signature in OPMD. Neuromuscular Disorders, 2011, 21, 673.	0.6	0
151	O.10 Effect of combined treatment with soluble activin receptor IIB and AAV-U7-mediated dystrophin exon skipping on muscle function in mdx mice. Neuromuscular Disorders, 2011, 21, 703.	0.6	0
152	O.13 Interference of myostatin and TGF-beta signaling by antisense-mediated exon skipping in ALK4/5 receptors. Neuromuscular Disorders, 2011, 21, 704.	0.6	0
153	P4.29 Differential tissue expression and decay of dystrophin mRNA and protein. Neuromuscular Disorders, 2011, 21, 713.	0.6	0
154	The value of data. Nature Genetics, 2011, 43, 281-283.	21.4	126
155	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
156	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
157	Sox4 mediates Tbx3 transcriptional regulation of the gap junction protein Cx43. Cellular and Molecular Life Sciences, 2011, 68, 3949-3961.	5.4	22
158	Dual exon skipping in myostatin and dystrophin for Duchenne muscular dystrophy. BMC Medical Genomics, 2011, 4, 36.	1.5	40
159	In silico discovery and experimental validation of new proteinâ€“protein interactions. Proteomics, 2011, 11, 843-853.	2.2	20
160	LPAR1andITGA4regulate peripheral blood monocyte counts. Human Mutation, 2011, 32, 873-876.	2.5	20
161	Literature-aided interpretation of gene expression data with the weighted global test. Briefings in Bioinformatics, 2011, 12, 518-529.	6.5	19
162	Genome-wide association study identifies six new loci influencing pulse pressure and mean arterial pressure. Nature Genetics, 2011, 43, 1005-1011.	21.4	403

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163	Interspecies Translation of Disease Networks Increases Robustness and Predictive Accuracy. PLoS Computational Biology, 2011, 7, e1002258.	3.2	15
164	mRNA degradation controls differentiation state-dependent differences in transcript and splice variant abundance. Nucleic Acids Research, 2011, 39, 556-566.	14.5	95
165	The identification of informative genes from multiple datasets with increasing complexity. BMC Bioinformatics, 2010, 11, 32.	2.6	6
166	New methods for next generation sequencing based microRNA expression profiling. BMC Genomics, 2010, 11, 716.	2.8	85
167	Accurate quantification of dystrophin mRNA and exon skipping levels in Duchenne Muscular Dystrophy. Laboratory Investigation, 2010, 90, 1396-1402.	3.7	37
168	Calpain 3 Is a Rapid-Action, Unidirectional Proteolytic Switch Central to Muscle Remodeling. PLoS ONE, 2010, 5, e11940.	2.5	23
169	Genome-wide assessment of differential roles for p300 and CBP in transcription regulation. Nucleic Acids Research, 2010, 38, 5396-5408.	14.5	133
170	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
171	Tissue-specific transcript annotation and expression profiling with complementary next-generation sequencing technologies. Nucleic Acids Research, 2010, 38, e165-e165.	14.5	32
172	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
173	Coexpression Network Analysis Identifies Transcriptional Modules Related to Proastrocytic Differentiation and Sprouty Signaling in Glioma. Cancer Research, 2010, 70, 10060-10070.	0.9	82
174	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
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