Edwin Cuppen

List of Publications by Year
in descending order

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307 papers	36,675 citations	4388 86 h-index	4015 176 g-index
348 all docs	348 docs citations	348 times ranked	53787 citing authors

#	Article	IF	Citations
1	Organoid Models of Human and Mouse Ductal Pancreatic Cancer. Cell, 2015, 160, 324-338.	28.9	1,584
2	Sambamba: fast processing of NGS alignment formats. Bioinformatics, 2015, 31, 2032-2034.	4.1	1,487
3	SARS-CoV-2 productively infects human gut enterocytes. Science, 2020, 369, 50-54.	12.6	1,347
4	A Living Biobank of Breast Cancer Organoids Captures Disease Heterogeneity. Cell, 2018, 172, 373-386.e10.	28.9	1,201
5	Phylogenetic Shadowing and Computational Identification of Human microRNA Genes. Cell, 2005, 120, 21-24.	28.9	1,194
6	Long-Term Culture of Genome-Stable Bipotent Stem Cells from Adult Human Liver. Cell, 2015, 160, 299-312.	28.9	1,166
7	Functional Repair of CFTR by CRISPR/Cas9 in Intestinal Stem Cell Organoids of Cystic Fibrosis Patients. Cell Stem Cell, 2013, 13, 653-658.	11.1	1,149
8	Sequential cancer mutations in cultured human intestinal stem cells. Nature, 2015, 521, 43-47.	27.8	853
9	Tissue-specific mutation accumulation in human adult stem cells during life. Nature, 2016, 538, 260-264.	27.8	759
10	Pan-cancer whole-genome analyses of metastatic solid tumours. Nature, 2019, 575, 210-216.	27.8	722
11	Mammalian Mirtron Genes. Molecular Cell, 2007, 28, 328-336.	9.7	675
12	Longâ€term expanding human airway organoids for disease modeling. EMBO Journal, 2019, 38, .	7.8	619
13	Identification of Multipotent Luminal Progenitor Cells in Human Prostate Organoid Cultures. Cell, 2014, 159, 163-175.	28.9	609
14	Mutational signature in colorectal cancer caused by genotoxic pks+ E. coli. Nature, 2020, 580, 269-273.	27.8	587
15	A systematic genome-wide analysis of zebrafish protein-coding gene function. Nature, 2013, 496, 494-497.	27.8	579
16	MutationalPatterns: comprehensive genome-wide analysis of mutational processes. Genome Medicine, 2018, 10, 33.	8.2	482
17	Diversity of microRNAs in human and chimpanzee brain. Nature Genetics, 2006, 38, 1375-1377.	21.4	457
18	Approaches to microRNA discovery. Nature Genetics, 2006, 38, S2-S7.	21.4	453

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19	Patient-derived organoids can predict response to chemotherapy in metastatic colorectal cancer patients. Science Translational Medicine, 2019, 11, .	12.4	451
20	The microRNA-producing enzyme Dicer1 is essential for zebrafish development. Nature Genetics, 2003, 35, 217-218.	21.4	429
21	Efficient Target-Selected Mutagenesis in Zebrafish. Genome Research, 2003, 13, 2700-2707.	5.5	409
22	The Wnt/Î²-catenin pathway regulates cardiac valve formation. Nature, 2003, 425, 633-637.	27.8	367
23	Preserved genetic diversity in organoids cultured from biopsies of human colorectal cancer metastases. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 13308-13311.	7.1	356
24	Use of CRISPR-modified human stem cell organoids to study the origin of mutational signatures in cancer. Science, 2017, 358, 234-238.	12.6	337
25	Genome sequencing of normal cells reveals developmental lineages and mutational processes. Nature, 2014, 513, 422-425.	27.8	315
26	Mapping and phasing of structural variation in patient genomes using nanopore sequencing. Nature Communications, 2017, 8, 1326.	12.8	315
27	Extensive localization of long noncoding RNAs to the cytosol and mono- and polyribosomal complexes. Genome Biology, 2014, 15, R6.	9.6	305
28	Tubuloids derived from human adult kidney and urine for personalized disease modeling. Nature Biotechnology, 2019, 37, 303-313.	17.5	301
29	Limitations and possibilities of small RNA digital gene expression profiling. Nature Methods, 2009, 6, 474-476.	19.0	280
30	Pancreatic cancer organoids recapitulate disease and allow personalized drug screening. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 26580-26590.	7.1	279
31	Chromothripsis as a mechanism driving complex de novo structural rearrangements in the germlineâ€. Human Molecular Genetics, 2011, 20, 1916-1924.	2.9	268
32	Progress and prospects in rat genetics: a community view. Nature Genetics, 2008, 40, 516-522.	21.4	265
33	Pan-cancer landscape of homologous recombination deficiency. Nature Communications, 2020, 11, 5584.	12.8	262
34	The genomic landscape of balanced cytogenetic abnormalities associated with human congenital anomalies. Nature Genetics, 2017, 49, 36-45.	21.4	251
35	The genomic landscape of metastatic breast cancer highlights changes in mutation and signature frequencies. Nature Genetics, 2019, 51, 1450-1458.	21.4	250
36	Many novel mammalian microRNA candidates identified by extensive cloning and RAKE analysis. Genome Research, 2006, 16, 1289-1298.	5.5	242

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37	Characterization of the serotonin transporter knockout rat: A selective change in the functioning of the serotonergic system. Neuroscience, 2007, 146, 1662-1676.	2.3	226
38	Zebrafish as a Cancer Model. Molecular Cancer Research, 2008, 6, 685-694.	3.4	225
39	Ascl2 Acts as an R-spondin/Wnt-Responsive Switch to Control Stemness in Intestinal Crypts. Cell Stem Cell, 2015, 16, 158-170.	11.1	217
40	Genome-Wide Pattern of TCF7L2/TCF4 Chromatin Occupancy in Colorectal Cancer Cells. Molecular and Cellular Biology, 2008, 28, 2732-2744.	2.3	208
41	A study in male and female 5-HT transporter knockout rats: An animal model for anxiety and depression disorders. Neuroscience, 2008, 152, 573-584.	2.3	206
42	Disclosure of individual genetic data to research participants: the debate reconsidered. Trends in Genetics, 2011, 27, 41-47.	6.7	204
43	Diabetes Risk Gene and Wnt Effector Tcf7l2/TCF4 Controls Hepatic Response to Perinatal and Adult Metabolic Demand. Cell, 2012, 151, 1595-1607.	28.9	202
44	Genetic dissection of colorectal cancer progression by orthotopic transplantation of engineered cancer organoids. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, E2357-E2364.	7.1	198
45	Q methodology to select participants for a stakeholder dialogue on energy options from biomass in the Netherlands. Ecological Economics, 2010, 69, 579-591.	5.7	195
46	Constitutional Chromothripsis Rearrangements Involve Clustered Double-Stranded DNA Breaks and Nonhomologous Repair Mechanisms. Cell Reports, 2012, 1, 648-655.	6.4	193
47	Distribution and functional impact of DNA copy number variation in the rat. Nature Genetics, 2008, 40, 538-545.	21.4	186
48	Mutagenic Capacity of Endogenous G4 DNA Underlies Genome Instability in FANCJ-Defective C. elegans. Current Biology, 2008, 18, 900-905.	3.9	186
49	Dominant missense mutations in ABCC9 cause CantÃº syndrome. Nature Genetics, 2012, 44, 793-796.	21.4	184
50	Chromothripsis is a common mechanism driving genomic rearrangements in primary and metastatic colorectal cancer. Genome Biology, 2011, 12, R103.	9.6	177
51	Combined sequence-based and genetic mapping analysis of complex traits in outbred rats. Nature Genetics, 2013, 45, 767-775.	21.4	176
52	Genetic variation in the zebrafish. Genome Research, 2006, 16, 491-497.	5.5	173
53	SNP and haplotype mapping for genetic analysis in the rat. Nature Genetics, 2008, 40, 560-566.	21.4	172
54	Cloning and expression of new microRNAs from zebrafish. Nucleic Acids Research, 2006, 34, 2558-2569.	14.5	169

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55	Angiogenin variants in Parkinson disease and amyotrophic lateral sclerosis. Annals of Neurology, 2011, 70, 964-973.	5.3	168
56	Generation of gene knockouts and mutant models in the laboratory rat by ENU-driven target-selected mutagenesis. Pharmacogenetics and Genomics, 2006, 16, 159-169.	1.5	161
57	Wnt-induced transcriptional activation is exclusively mediated by TCF/LEF. EMBO Journal, 2014, 33, 146-156.	7.8	157
58	Mechanisms of Therapy Resistance in Patient-Derived Xenograft Models of BRCA1-Deficient Breast Cancer. Journal of the National Cancer Institute, 2016, 108, djw148.	6.3	157
59	Patient-Derived Ovarian Cancer Organoids Mimic Clinical Response and Exhibit Heterogeneous Inter- and Intrapatient Drug Responses. Cell Reports, 2020, 31, 107762.	6.4	155
60	Genome Sequencing Reveals Loci under Artificial Selection that Underlie Disease Phenotypes in the Laboratory Rat. Cell, 2013, 154, 691-703.	28.9	154
61	The Drug Rediscovery protocol facilitates the expanded use of existing anticancer drugs. Nature, 2019, 574, 127-131.	27.8	152
62	Zebrafish development and regeneration: new tools for biomedical research. International Journal of Developmental Biology, 2009, 53, 835-850.	0.6	143
63	Targeted next-generation sequencing: AÂnovel diagnostic tool for primary immunodeficiencies. Journal of Allergy and Clinical Immunology, 2014, 133, 529-534.e1.	2.9	143
64	5-Fluorouracil treatment induces characteristic T>G mutations in human cancer. Nature Communications, 2019, 10, 4571.	12.8	143
65	Nucleosomal DNA binding drives the recognition of H3K36-methylated nucleosomes by the PSIP1-PWWP domain. Epigenetics and Chromatin, 2013, 6, 12.	3.9	141
66	A deep learning system accurately classifies primary and metastatic cancers using passenger mutation patterns. Nature Communications, 2020, 11, 728.	12.8	140
67	Serotonin transporter deficiency in rats improves inhibitory control but not behavioural flexibility. European Journal of Neuroscience, 2007, 26, 2066-2073.	2.6	139
68	Generation of medaka gene knockout models by target-selected mutagenesis. Genome Biology, 2006, 7, R116.	9.6	137
69	Primary Colorectal Cancers and Their Subsequent Hepatic Metastases Are Genetically Different: Implications for Selection of Patients for Targeted Treatment. Clinical Cancer Research, 2012, 18, 688-699.	7.0	136
70	PDZ Motifs in PTP-BL and RIL Bind to Internal Protein Segments in the LIM Domain Protein RIL. Molecular Biology of the Cell, 1998, 9, 671-683.	2.1	131
71	The genomic landscape of metastatic castration-resistant prostate cancers reveals multiple distinct genotypes with potential clinical impact. Nature Communications, 2019, 10, 5251.	12.8	130
72	The PLETHORA Gene Regulatory Network Guides Growth and Cell Differentiation in Arabidopsis Roots. Plant Cell, 2016, 28, 2937-2951.	6.6	127

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73	Challenges in Establishing Pure Lung Cancer Organoids Limit Their Utility for Personalized Medicine. Cell Reports, 2020, 31, 107588.	6.4	125
74	Adaptations in pre- and postsynaptic 5-HT1A receptor function and cocaine supersensitivity in serotonin transporter knockout rats. Psychopharmacology, 2008, 200, 367-380.	3.1	117
75	Characteristics of de novo structural changes in the human genome. Genome Research, 2015, 25, 792-801.	5.5	115
76	Quantitative and Qualitative Proteome Characteristics Extracted from In-Depth Integrated Genomics and Proteomics Analysis. Cell Reports, 2013, 5, 1469-1478.	6.4	113
77	Epigenomic annotation of gene regulatory alterations during evolution of the primate brain. Nature Neuroscience, 2016, 19, 494-503.	14.8	113
78	Molecular Tumor Boards: current practice and future needs. Annals of Oncology, 2017, 28, 3070-3075.	1.2	112
79	Repertoire and evolution of miRNA genes in four divergent nematode species. Genome Research, 2009, 19, 2064-2074.	5.5	107
80	Systemic miRNA-7 delivery inhibits tumor angiogenesis and growth in murine xenograft glioblastoma. Oncotarget, 2014, 5, 6687-6700.	1.8	105
81	Genomeâ€wide analysis of FOXO3 mediated transcription regulation through RNA polymerase II profiling. Molecular Systems Biology, 2013, 9, 638.	7.2	104
82	MEFVmutations affecting pyrin amino acid 577 cause autosomal dominant autoinflammatory disease. Annals of the Rheumatic Diseases, 2014, 73, 455-461.	0.9	101
83	Dominant-Negative ALK2 Allele Associates With Congenital Heart Defects. Circulation, 2009, 119, 3062-3069.	1.6	97
84	Mouse microRNA profiles determined with a new and sensitive cloning method. Nucleic Acids Research, 2006, 34, e115-e115.	14.5	96
85	Tracing the History of Goat Pastoralism: New Clues from Mitochondrial and Y Chromosome DNA in North Africa. Molecular Biology and Evolution, 2009, 26, 2765-2773.	8.9	96
86	Acute and constitutive increases in central serotonin levels reduce social play behaviour in peri-adolescent rats. Psychopharmacology, 2007, 195, 175-82.	3.1	92
87	Many Inflammatory Bowel Disease Risk Loci Include Regions ThatÂRegulate Gene Expression in Immune Cells and the IntestinalÂEpithelium. Gastroenterology, 2014, 146, 1040-1047.	1.3	92
88	E2F7 represses a network of oscillating cell cycle genes to control S-phase progression. Nucleic Acids Research, 2012, 40, 3511-3523.	14.5	91
89	A Deep Sequencing Approach to Uncover the miRNOME in the Human Heart. PLoS ONE, 2013, 8, e57800.	2.5	88
90	Ethical, Legal, and Counseling Challenges Surrounding the Return of Genetic Results in Oncology. Journal of Clinical Oncology, 2013, 31, 1842-1848.	1.6	85

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91	Serotonin transporter dosage modulates long-term decision-making in rat and human. Neuropharmacology, 2008, 55, 80-84.	4.1	84
92	The genome sequence of the spontaneously hypertensive rat: Analysis and functional significance. Genome Research, 2010, 20, 791-803.	5.5	84
93	Genomic landscape of rat strain and substrain variation. BMC Genomics, 2015, 16, 357.	2.8	84
94	Portrait of a cancer: mutational signature analyses for cancer diagnostics. BMC Cancer, 2019, 19, 457.	2.6	84
95	Planar cell polarity defects and defective Vangl2 trafficking in mutants for the COPII gene Sec24b. Development (Cambridge), 2010, 137, 1067-1073.	2.5	83
96	Chromothripsis in congenital disorders and cancer: similarities and differences. Current Opinion in Cell Biology, 2013, 25, 341-348.	5.4	83
97	Accurate SNP and mutation detection by targeted custom microarray-based genomic enrichment of short-fragment sequencing libraries. Nucleic Acids Research, 2010, 38, e116-e116.	14.5	79
98	Dual Origins of Dairy Cattle Farming â€“ Evidence from a Comprehensive Survey of European Y-Chromosomal Variation. PLoS ONE, 2011, 6, e15922.	2.5	79
99	Translational regulation shapes the molecular landscape of complex disease phenotypes. Nature Communications, 2015, 6, 7200.	12.8	79
100	Targeted Next Generation Sequencing as a Reliable Diagnostic Assay for the Detection of Somatic Mutations in Tumours Using Minimal DNA Amounts from Formalin Fixed Paraffin Embedded Material. PLoS ONE, 2016, 11, e0149405.	2.5	79
101	CONREAL: Conserved Regulatory Elements Anchored Alignment Algorithm for Identification of Transcription Factor Binding Sites by Phylogenetic Footprinting. Genome Research, 2003, 14, 170-178.	5.5	78
102	CONREAL web server: identification and visualization of conserved transcription factor binding sites. Nucleic Acids Research, 2005, 33, W447-W450.	14.5	78
103	Large-Scale Identification of Coregulated Enhancer Networks in the Adult Human Brain. Cell Reports, 2014, 9, 767-779.	6.4	78
104	Prioritization and burden analysis of rare variants in 208 candidate genes suggest they do not play a major role in CAKUT. Kidney International, 2016, 89, 476-486.	5.2	78
105	The Serotonin Transporter Plays an Important Role in Male Sexual Behavior: A Study in Serotonin Transporter Knockout Rats. Journal of Sexual Medicine, 2011, 8, 97-108.	0.6	77
106	Melanocortin Receptor 4 Deficiency Affects Body Weight Regulation, Grooming Behavior, and Substrate Preference in the Rat. Obesity, 2012, 20, 612-621.	3.0	77
107	Target-selected mutagenesis of the rat. Genomics, 2004, 83, 332-334.	2.9	76
108	Chromothripsis in Healthy Individuals Affects Multiple Protein-Coding Genes and Can Result in Severe Congenital Abnormalities in Offspring. American Journal of Human Genetics, 2015, 96, 651-656.	6.2	76

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109	RAS pathway mutations as a predictive biomarker for treatment adaptation in pediatric B-cell precursor acute lymphoblastic leukemia. Leukemia, 2018, 32, 931-940.	7.2	75
110	Genotyping by Allele-Specific Amplification (KASPar). Cold Spring Harbor Protocols, 2007, 2007, pdb.prot4841.	0.3	74
111	GRIDSS2: comprehensive characterisation of somatic structural variation using single breakend variants and structural variant phasing. Genome Biology, 2021, 22, 202.	8.8	73
112	Genomic and transcriptomic plasticity in treatment-naÃ¯ve ovarian cancer. Genome Research, 2014, 24, 200-211.	5.5	72
113	Small RNA expression and strain specificity in the rat. BMC Genomics, 2010, 11, 249.	2.8	71
114	Reduced Rates of Gene Loss, Gene Silencing, and Gene Mutation in Dnmt1 -Deficient Embryonic Stem Cells. Molecular and Cellular Biology, 2001, 21, 7587-7600.	2.3	66
115	Haplotype Block Structure Is Conserved across Mammals. PLoS Genetics, 2006, 2, e121.	3.5	66
116	FUS Mutations in Familial Amyotrophic Lateral Sclerosis in the Netherlands. Archives of Neurology, 2010, 67, 224-30.	4.5	66
117	Deficiency of nucleotide excision repair is associated with mutational signature observed in cancer. Genome Research, 2019, 29, 1067-1077.	5.5	66
118	MutationalPatterns: the one stop shop for the analysis of mutational processes. BMC Genomics, 2022, 23, 134.	2.8	66
119	The zyxin-related protein TRIP6 interacts with PDZ motifs in the adaptor protein RIL and the protein tyrosine phosphatase PTP-BL. European Journal of Cell Biology, 2000, 79, 283-293.	3.6	65
120	Mlh1 Deficiency in Zebrafish Results in Male Sterility and Aneuploid as Well as Triploid Progeny in Females. Genetics, 2007, 175, 1561-1569.	2.9	65
121	Multiplexed array-based and in-solution genomic enrichment for flexible and cost-effective targeted next-generation sequencing. Nature Protocols, 2011, 6, 1870-1886.	12.0	65
122	Integrated genome-wide analysis of transcription factor occupancy, RNA polymerase II binding and steady-state RNA levels identify differentially regulated functional gene classes. Nucleic Acids Research, 2012, 40, 148-158.	14.5	65
123	X-exome sequencing identifies aHDAC8variant in a large pedigree with X-linked intellectual disability, truncal obesity, gynaecomastia, hypogonadism and unusual face. Journal of Medical Genetics, 2012, 49, 539-543.	3.2	65
124	Mutation discovery by targeted genomic enrichment of multiplexed barcoded samples. Nature Methods, 2010, 7, 913-915.	19.0	64
125	Rb and FZR1/Cdh1 determine CDK4/6-cyclin D requirement in C. elegans and human cancer cells. Nature Communications, 2015, 6, 5906.	12.8	62
126	Prospective experimental treatment of colorectal cancer patients based on organoid drug responses. ESMO Open, 2021, 6, 100103.	4.5	62

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127	The mutational impact of culturing human pluripotent and adult stem cells. Nature Communications, 2020, 11, 2493.	12.8	61
128	miR-127 Protects Proximal Tubule Cells against Ischemia/Reperfusion: Identification of Kinesin Family Member 3B as miR-127 Target. PLoS ONE, 2012, 7, e44305.	2.5	59
129	Next generation sequencing of triple negative breast cancer to find predictors for chemotherapy response. Breast Cancer Research, 2015, 17, 134.	5.0	58
130	Cancer cells copy migratory behavior and exchange signaling networks via extracellular vesicles. EMBO Journal, 2018, 37, .	7.8	58
131	Stress-induced hyperthermia and basal body temperature are mediated by different 5-HT1A receptor populations: A study in SERT knockout rats. European Journal of Pharmacology, 2008, 590, 190-197.	3.5	57
132	Next-generation sequencing-based genome diagnostics across clinical genetics centers: implementation choices and their effects. European Journal of Human Genetics, 2015, 23, 1142-1150.	2.8	56
133	The G-Protein Î²-Subunit GPB-2 in Caenorhabditis elegans Regulates the GoÎ±-GqÎ± Signaling Network Through Interactions With the Regulator of G-Protein Signaling Proteins EGL-10 and EAT-16. Genetics, 2001, 158, 221-235.	2.9	56
134	Zebrafish with Mutations in Mismatch Repair Genes Develop Neurofibromas and Other Tumors. Cancer Research, 2008, 68, 5059-5066.	0.9	55
135	The genomic landscape of 85 advanced neuroendocrine neoplasms reveals subtype-heterogeneity and potential therapeutic targets. Nature Communications, 2021, 12, 4612.	12.8	55
136	SMN1 gene duplications are associated with sporadic ALS. Neurology, 2012, 78, 776-780.	1.1	54
137	No Evidence for Involvement of Mouse Protein-tyrosine Phosphatase-BAS-like Fas-associated Phosphatase-1 in Fas-mediated Apoptosis. Journal of Biological Chemistry, 1997, 272, 30215-30220.	3.4	53
138	Natural variation of histone modification and its impact on gene expression in the rat genome. Genome Research, 2014, 24, 942-953.	5.5	53
139	Effector identification in the lettuce downy mildew Bremia lactucae by massively parallel transcriptome sequencing. Molecular Plant Pathology, 2012, 13, 719-731.	4.2	52
140	Measuring mutation accumulation in single human adult stem cells by whole-genome sequencing of organoid cultures. Nature Protocols, 2018, 13, 59-78.	12.0	52
141	A Functional Screen Identifies Specific MicroRNAs Capable of Inhibiting Human Melanoma Cell Viability. PLoS ONE, 2012, 7, e43569.	2.5	52
142	The neuronal nitric oxide synthase PDZ motif binds to -G(D,E)XV*carboxyterminal sequences. FEBS Letters, 1997, 409, 53-56.	2.8	51
143	Single Nucleotide Polymorphisms Associated With Rat Expressed Sequences. Genome Research, 2004, 14, 1438-1443.	5.5	50
144	A novel Caenorhabditis elegans allele, smn-1(cb131), mimicking a mild form of spinal muscular atrophy, provides a convenient drug screening platform highlighting new and pre-approved compounds. Human Molecular Genetics, 2011, 20, 245-260.	2.9	50

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145	Generation and characterization of rat liver stem cell lines and their engraftment in a rat model of liver failure. Scientific Reports, 2016, 6, 22154.	3.3	50
146	RAP-1 and the RAL-1/exocyst pathway coordinate hypodermal cell organization in Caenorhabditis elegans. EMBO Journal, 2007, 26, 5083-5092.	7.8	49
147	NIPA1 polyalanine repeat expansions are associated with amyotrophic lateral sclerosis. Human Molecular Genetics, 2012, 21, 2497-2502.	2.9	49
148	Clinical Validation of Whole Genome Sequencing for Cancer Diagnostics. Journal of Molecular Diagnostics, 2021, 23, 816-833.	2.8	47
149	A genome-wide SNP panel for mapping and association studies in the rat. BMC Genomics, 2008, 9, 95.	2.8	46
150	Toward effective software solutions for big biology. Nature Biotechnology, 2015, 33, 686-687.	17.5	46
151	Identification of factors required for meristem function in Arabidopsis using a novel next generation sequencing fast forward genetics approach. BMC Genomics, 2011, 12, 256.	2.8	45
152	Highly Efficient ENU Mutagenesis in Zebrafish. Methods in Molecular Biology, 2009, 546, 3-12.	0.9	43
153	Human extrahepatic and intrahepatic cholangiocyte organoids show region-specific differentiation potential and model cystic fibrosis-related bile duct disease. Scientific Reports, 2020, 10, 21900.	3.3	43
154	Chronic Loss of Melanin-Concentrating Hormone Affects Motivational Aspects of Feeding in the Rat. PLoS ONE, 2011, 6, e19600.	2.5	43
155	Deletion of the serotonin transporter in rats disturbs serotonin homeostasis without impairing liver regeneration. American Journal of Physiology - Renal Physiology, 2009, 296, G963-G968.	3.4	42
156	Phylogeny of Y chromosomes from bovine species. Cladistics, 2008, 24, 723-726.	3.3	41
157	The effect of COMT Val158 Met genotype on decision-making and preliminary findings on its interaction with the 5-HTTLPR in healthy females. Neuropharmacology, 2009, 56, 493-498.	4.1	41
158	Effect of vertical sleeve gastrectomy in melanocortin receptor 4-deficient rats. American Journal of Physiology - Endocrinology and Metabolism, 2012, 303, E103-E110.	3.5	41
159	Single-cell derived tumor organoids display diversity in HLA class I peptide presentation. Nature Communications, 2020, 11, 5338.	12.8	41
160	Limited evolution of the actionable metastatic cancer genome under therapeutic pressure. Nature Medicine, 2021, 27, 1553-1563.	30.7	41
161	High-Throughput Target-Selected Gene Inactivation in Zebrafish. Methods in Cell Biology, 2011, 104, 121-127.	1.1	40
162	Cell Autonomous Lipin 1 Function Is Essential for Development and Maintenance of White and Brown Adipose Tissue. Molecular and Cellular Biology, 2012, 32, 4794-4810.	2.3	40

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163	High-throughput semiquantitative analysis of insertional mutations in heterogeneous tumors. Genome Research, 2011, 21, 2181-2189.	5.5	39
164	Systematic biases in DNA copy number originate from isolation procedures. Genome Biology, 2013, 14, R33.	9.6	39
165	Systematic analysis of chromatin interactions at disease associated loci links novel candidate genes to inflammatory bowel disease. Genome Biology, 2016, 17, 247.	8.8	39
166	Whole genome sequencing of metastatic colorectal cancer reveals prior treatment effects and specific metastasis features. Nature Communications, 2021, 12, 574.	12.8	39
167	Efficient Double Fragmentation ChIP-seq Provides Nucleotide Resolution Protein-DNA Binding Profiles. PLoS ONE, 2010, 5, e15092.	2.5	39
168	Proteins Interacting withCaenorhabditis elegansâ€‰Î±Subunits. Comparative and Functional Genomics, 2003, 4, 479-491.	2.0	37
169	Genetic Variation in Coding Regions Between and Within Commonly Used Inbred Rat Strains. Genome Research, 2004, 14, 1285-1290.	5.5	37
170	Expanding the spectrum of phenotypes associated with germline PIGA mutations: A child with developmental delay, accelerated linear growth, facial dysmorphisms, elevated alkaline phosphatase, and progressive CNS abnormalities. American Journal of Medical Genetics, Part A, 2014, 164, 29-35.	1.2	37
171	Sperm DNA damage causes genomic instability in early embryonic development. Science Advances, 2020, 6, eaaz7602.	10.3	37
172	Reconstructing single-cell karyotype alterations in colorectal cancer identifies punctuated and gradual diversification patterns. Nature Genetics, 2021, 53, 1187-1195.	21.4	37
173	Incomplete segregation of MYH11 variants with thoracic aortic aneurysms and dissections and patent ductus arteriosus. European Journal of Human Genetics, 2013, 21, 487-493.	2.8	36
174	Improving mammalian genome scaffolding using large insert mate-pair next-generation sequencing. BMC Genomics, 2013, 14, 257.	2.8	35
175	Simultaneous Detection of Clinically Relevant Mutations and Amplifications for Routine Cancer Pathology. Journal of Molecular Diagnostics, 2015, 17, 10-18.	2.8	35
176	The role of the dopamine D1 receptor in social cognition: studies using a novel genetic rat model. DMM Disease Models and Mechanisms, 2016, 9, 1147-1158.	2.4	35
177	Clinical utility of whole-genome sequencing in precision oncology. Seminars in Cancer Biology, 2022, 84, 32-39.	9.6	35
178	An ENU-Mutagenesis Screen in the Mouse: Identification of Novel Developmental Gene Functions. PLoS ONE, 2011, 6, e19357.	2.5	35
179	Haplotype-based genetics in mice and rats. Trends in Genetics, 2005, 21, 318-322.	6.7	34
180	Complete knockout of the nociceptin/orphanin FQ receptor in the rat does not induce compensatory changes in Î¼, Î´ and Îº opioid receptors. Neuroscience, 2009, 163, 308-315.	2.3	34

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181	Unscrambling cancer genomes via integrated analysis of structural variation and copy number. Cell Genomics, 2022, 2, 100112.	6.5	34
182	Pmchexpression during early development is critical for normal energy homeostasis. American Journal of Physiology - Endocrinology and Metabolism, 2010, 298, E477-E488.	3.5	33
183	Homozygous and Heterozygous p53 Knockout Rats Develop Metastasizing Sarcomas with High Frequency. American Journal of Pathology, 2011, 179, 1616-1622.	3.8	33
184	ALK2 mutation in a patient with Down's syndrome and a congenital heart defect. European Journal of Human Genetics, 2011, 19, 389-393.	2.8	33
185	Genome-wide analysis of somatic noncoding mutation patterns in cancer. Science, 2022, 376, eabg5601.	12.6	33
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