

Colin N Dewey

List of Publications by Year in descending order

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33
papers

19,200
citations

448610

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536525

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all docs

37
docs citations

37
times ranked

42133
citing authors

#	ARTICLE	IF	CITATIONS
1	Cell Type-Specific Transcriptome Profiling Reveals a Role for Thioredoxin During Tumor Initiation. <i>Frontiers in Immunology</i> , 2022, 13, 818893.	2.2	1
2	PLK1 and NOTCH Positively Correlate in Melanoma and Their Combined Inhibition Results in Synergistic Modulations of Key Melanoma Pathways. <i>Molecular Cancer Therapeutics</i> , 2021, 20, 161-172.	1.9	14
3	CellO: comprehensive and hierarchical cell type classification of human cells with the Cell Ontology. <i>IScience</i> , 2021, 24, 101913.	1.9	26
4	RNA-regulatory exosome complex confers cellular survival to promote erythropoiesis. <i>Nucleic Acids Research</i> , 2021, 49, 9007-9025.	6.5	8
5	Annotating cell types in human single-cell RNA-seq data with Cello. <i>STAR Protocols</i> , 2021, 2, 100705.	0.5	1
6	Cell type specific gene expression profiling reveals a role for complement component C3 in neutrophil responses to tissue damage. <i>Scientific Reports</i> , 2020, 10, 15716.	1.6	16
7	Giant Island Mice Exhibit Widespread Gene Expression Changes in Key Metabolic Organs. <i>Genome Biology and Evolution</i> , 2020, 12, 1277-1301.	1.1	1
8	PRAM: a novel pooling approach for discovering intergenic transcripts from large-scale RNA sequencing experiments. <i>Genome Research</i> , 2020, 30, 1655-1666.	2.4	2
9	Whole-Genome Alignment. <i>Methods in Molecular Biology</i> , 2019, 1910, 121-147.	0.4	5
10	Genome-wide effects on <i>Escherichia coli</i> transcription from ppGpp binding to its two sites on RNA polymerase. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 8310-8319.	3.3	189
11	MetaSRA: normalized human sample-specific metadata for the Sequence Read Archive. <i>Bioinformatics</i> , 2017, 33, 2914-2923.	1.8	84
12	GATA Factor-Regulated Samd14 Enhancer Confers Red Blood Cell Regeneration and Survival in Severe Anemia. <i>Developmental Cell</i> , 2017, 42, 213-225.e4.	3.1	29
13	Zebrafish <i>zic2</i> controls formation of periocular neural crest and choroid fissure morphogenesis. <i>Developmental Biology</i> , 2017, 429, 92-104.	0.9	32
14	Analysis of embryonic development in the unsequenced axolotl: Waves of transcriptomic upheaval and stability. <i>Developmental Biology</i> , 2017, 426, 143-154.	0.9	34
15	Integrative analysis with ChIP-seq advances the limits of transcript quantification from RNA-seq. <i>Genome Research</i> , 2016, 26, 1124-1133.	2.4	19
16	Mechanism governing heme synthesis reveals a GATA factor/heme circuit that controls differentiation. <i>EMBO Reports</i> , 2016, 17, 249-265.	2.0	55
17	EBSeq-HMM: a Bayesian approach for identifying gene-expression changes in ordered RNA-seq experiments. <i>Bioinformatics</i> , 2015, 31, 2614-2622.	1.8	93
18	Hematopoietic Signaling Mechanism Revealed from a Stem/Progenitor Cell Cistrome. <i>Molecular Cell</i> , 2015, 59, 62-74.	4.5	40

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19	Cis-regulatory mechanisms governing stem and progenitor cell transitions. <i>Science Advances</i> , 2015, 1, e1500503.	4.7	57
20	Perm-seq: Mapping Protein-DNA Interactions in Segmental Duplication and Highly Repetitive Regions of Genomes with Prior-Enhanced Read Mapping. <i>PLoS Computational Biology</i> , 2015, 11, e1004491.	1.5	11
21	Cistrome Control of Hematopoietic Stem/Progenitor Cell Function. <i>Blood</i> , 2015, 126, 43-43.	0.6	0
22	Mechanism Governing Heme Synthesis Reveals a GATA Factor-Heme Circuit That Controls Differentiation. <i>Blood</i> , 2015, 126, 161-161.	0.6	0
23	<i>Gata2</i> cis-element is required for hematopoietic stem cell generation in the mammalian embryo. <i>Journal of Experimental Medicine</i> , 2013, 210, 2833-2842.	4.2	127
24	Whole-Genome Alignment. <i>Methods in Molecular Biology</i> , 2012, 855, 237-257.	0.4	27
25	RSEM: accurate transcript quantification from RNA-Seq data with or without a reference genome. <i>BMC Bioinformatics</i> , 2011, 12, 323.	1.2	16,042
26	Positional orthology: putting genomic evolutionary relationships into context. <i>Briefings in Bioinformatics</i> , 2011, 12, 401-412.	3.2	78
27	RNA-Seq gene expression estimation with read mapping uncertainty. <i>Bioinformatics</i> , 2010, 26, 493-500.	1.8	1,012
28	Fast Statistical Alignment. <i>PLoS Computational Biology</i> , 2009, 5, e1000392.	1.5	302
29	Reconstructing latent periods in genome sequences with insertions and deletions. , 2009, , .		0
30	Analyses of deep mammalian sequence alignments and constraint predictions for 1% of the human genome. <i>Genome Research</i> , 2007, 17, 760-774.	2.4	184
31	Aligning Multiple Whole Genomes with Mercator and MAVID. <i>Methods in Molecular Biology</i> , 2007, 395, 221-235.	0.4	83
32	Discovery of functional elements in 12 <i>Drosophila</i> genomes using evolutionary signatures. <i>Nature</i> , 2007, 450, 219-232.	13.7	573
33	Evolution at the nucleotide level: the problem of multiple whole-genome alignment. <i>Human Molecular Genetics</i> , 2006, 15, R51-R56.	1.4	51