

# Colin N Dewey

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/7898475/publications.pdf>

Version: 2024-02-01

33  
papers

19,200  
citations

394390  
19  
h-index

477281  
29  
g-index

37  
all docs

37  
docs citations

37  
times ranked

38357  
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.	4.8	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.	4.1	14
3	CellO: comprehensive and hierarchical cell type classification of human cells with the Cell Ontology. <i>IScience</i> , 2021, 24, 101913.	4.1	26
4	RNA-regulatory exosome complex confers cellular survival to promote erythropoiesis. <i>Nucleic Acids Research</i> , 2021, 49, 9007-9025.	14.5	8
5	Annotating cell types in human single-cell RNA-seq data with Cello. <i>STAR Protocols</i> , 2021, 2, 100705.	1.2	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.	3.3	16
7	Giant Island Mice Exhibit Widespread Gene Expression Changes in Key Metabolic Organs. <i>Genome Biology and Evolution</i> , 2020, 12, 1277-1301.	2.5	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.	5.5	2
9	Whole-Genome Alignment. <i>Methods in Molecular Biology</i> , 2019, 1910, 121-147.	0.9	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.	7.1	189
11	MetaSRA: normalized human sample-specific metadata for the Sequence Read Archive. <i>Bioinformatics</i> , 2017, 33, 2914-2923.	4.1	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.	7.0	29
13	Zebrafish <i>zic2</i> controls formation of periocular neural crest and choroid fissure morphogenesis. <i>Developmental Biology</i> , 2017, 429, 92-104.	2.0	32
14	Analysis of embryonic development in the unsequenced axolotl: Waves of transcriptomic upheaval and stability. <i>Developmental Biology</i> , 2017, 426, 143-154.	2.0	34
15	Integrative analysis with ChIP-seq advances the limits of transcript quantification from RNA-seq. <i>Genome Research</i> , 2016, 26, 1124-1133.	5.5	19
16	Mechanism governing heme synthesis reveals a GATA factor/heme circuit that controls differentiation. <i>EMBO Reports</i> , 2016, 17, 249-265.	4.5	55
17	EBSeq-HMM: a Bayesian approach for identifying gene-expression changes in ordered RNA-seq experiments. <i>Bioinformatics</i> , 2015, 31, 2614-2622.	4.1	93
18	Hematopoietic Signaling Mechanism Revealed from a Stem/Progenitor Cell Cistrome. <i>Molecular Cell</i> , 2015, 59, 62-74.	9.7	40

#	ARTICLE	IF	CITATIONS
19	Cis-regulatory mechanisms governing stem and progenitor cell transitions. Science Advances, 2015, 1, e1500503.	10.3	57
20	Perm-seq: Mapping Protein-DNA Interactions in Segmental Duplication and Highly Repetitive Regions of Genomes with Prior-Enhanced Read Mapping. PLoS Computational Biology, 2015, 11, e1004491.	3.2	11
21	Cistrome Control of Hematopoietic Stem/Progenitor Cell Function. Blood, 2015, 126, 43-43.	1.4	0
22	Mechanism Governing Heme Synthesis Reveals a GATA Factor-Heme Circuit That Controls Differentiation. Blood, 2015, 126, 161-161.	1.4	0
23	<i>Gata2</i> cis-element is required for hematopoietic stem cell generation in the mammalian embryo. Journal of Experimental Medicine, 2013, 210, 2833-2842.	8.5	127
24	Whole-Genome Alignment. Methods in Molecular Biology, 2012, 855, 237-257.	0.9	27
25	RSEM: accurate transcript quantification from RNA-Seq data with or without a reference genome. BMC Bioinformatics, 2011, 12, 323.	2.6	16,042
26	Positional orthology: putting genomic evolutionary relationships into context. Briefings in Bioinformatics, 2011, 12, 401-412.	6.5	78
27	RNA-Seq gene expression estimation with read mapping uncertainty. Bioinformatics, 2010, 26, 493-500.	4.1	1,012
28	Fast Statistical Alignment. PLoS Computational Biology, 2009, 5, e1000392.	3.2	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. Genome Research, 2007, 17, 760-774.	5.5	184
31	Aligning Multiple Whole Genomes with Mercator and MAVID. Methods in Molecular Biology, 2007, 395, 221-235.	0.9	83
32	Discovery of functional elements in 12 Drosophila genomes using evolutionary signatures. Nature, 2007, 450, 219-232.	27.8	573
33	Evolution at the nucleotide level: the problem of multiple whole-genome alignment. Human Molecular Genetics, 2006, 15, R51-R56.	2.9	51