

David J Fredman

List of Publications by Year in descending order

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31
papers

2,647
citations

304743

22
h-index

434195

31
g-index

33
all docs

33
docs citations

33
times ranked

4433
citing authors

#	ARTICLE	IF	CITATIONS
1	Transcriptome-wide mapping of signaling pathways and early immune responses in lumpfish leukocytes upon in vitro bacterial exposure. <i>Scientific Reports</i> , 2018, 8, 5261.	3.3	31
2	Two-miRNA classifiers differentiate mutation-negative follicular thyroid carcinomas and follicular thyroid adenomas in fine needle aspirations with high specificity. <i>Endocrine</i> , 2016, 54, 440-447.	2.3	27
3	Adoption of conserved developmental genes in development and origin of the medusa body plan. <i>EvoDevo</i> , 2015, 6, 23.	3.2	36
4	Axis Patterning by BMPs: Cnidarian Network Reveals Evolutionary Constraints. <i>Cell Reports</i> , 2015, 10, 1646-1654.	6.4	90
5	Cnidarian microRNAs frequently regulate targets by cleavage. <i>Genome Research</i> , 2014, 24, 651-663.	5.5	104
6	Evolutionary conservation of the eumetazoan gene regulatory landscape. <i>Genome Research</i> , 2014, 24, 639-650.	5.5	143
7	Spectral sensitivity of the ctenid spider <i>Cupiennius salei</i> Keys. <i>Journal of Experimental Biology</i> , 2013, 216, 4103-8.	1.7	14
8	The Evolution of MicroRNA Pathway Protein Components in Cnidaria. <i>Molecular Biology and Evolution</i> , 2013, 30, 2541-2552.	8.9	57
9	Employing BAC-reporter constructs in the sea anemone <i>Nematostella vectensis</i> . <i>Integrative and Comparative Biology</i> , 2013, 53, 832-846.	2.0	2
10	Characterisation and localisation of the opsin protein repertoire in the brain and retinas of a spider and an onychophoran. <i>BMC Evolutionary Biology</i> , 2013, 13, 186.	3.2	47
11	Recurrent Horizontal Transfer of Bacterial Toxin Genes to Eukaryotes. <i>Molecular Biology and Evolution</i> , 2012, 29, 2223-2230.	8.9	91
12	Making enhancers from spare parts of the genome. <i>Genome Biology</i> , 2011, 12, 138.	9.6	1
13	Regulatory divergence of the duplicated chromosomal loci <i>sox11a/b</i> by subpartitioning and sequence evolution of enhancers in zebrafish. <i>Molecular Genetics and Genomics</i> , 2010, 283, 171-184.	2.1	24
14	Exonic remnants of whole-genome duplication reveal cis-regulatory function of coding exons. <i>Nucleic Acids Research</i> , 2010, 38, 1071-1085.	14.5	46
15	Long-range gene regulation links genomic type 2 diabetes and obesity risk regions to <i>HHEX</i> , <i>SOX4</i> , and <i>IRX3</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 775-780.	7.1	189
16	Web-based tools and approaches to study long-range gene regulation in Metazoa. <i>Briefings in Functional Genomics & Proteomics</i> , 2009, 8, 231-242.	3.8	6
17	The phenotype and genotype experiment object model (PaGE-OM): a robust data structure for information related to DNA variation. <i>Human Mutation</i> , 2009, 30, 968-977.	2.5	18
18	The transcriptional network that controls growth arrest and differentiation in a human myeloid leukemia cell line. <i>Nature Genetics</i> , 2009, 41, 553-562.	21.4	408

#	ARTICLE	IF	CITATIONS
19	Systematic human/zebrafish comparative identification of cis-regulatory activity around vertebrate developmental transcription factor genes. <i>Developmental Biology</i> , 2009, 327, 526-540.	2.0	108
20	Synorth: exploring the evolution of synteny and long-range regulatory interactions in vertebrate genomes. <i>Genome Biology</i> , 2009, 10, R86.	9.6	25
21	Transcriptional features of genomic regulatory blocks. <i>Genome Biology</i> , 2009, 10, R38.	9.6	90
22	Genetic Structures of Copy Number Variants Revealed by Genotyping Single Sperm. <i>PLoS ONE</i> , 2009, 4, e5236.	2.5	3
23	Ancora: a web resource for exploring highly conserved noncoding elements and their association with developmental regulatory genes. <i>Genome Biology</i> , 2008, 9, R34.	9.6	84
24	Retroviral enhancer detection insertions in zebrafish combined with comparative genomics reveal genomic regulatory blocks - a fundamental feature of vertebrate genomes. <i>Genome Biology</i> , 2007, 8, S4.	9.6	43
25	Genomic regulatory blocks encompass multiple neighboring genes and maintain conserved synteny in vertebrates. <i>Genome Research</i> , 2007, 17, 545-555.	5.5	312
26	Nonsynonymous SNPs: validation characteristics, derived allele frequency patterns, and suggestive evidence for natural selection. <i>Human Mutation</i> , 2006, 27, 173-186.	2.5	9
27	Evolutionary turnover of mammalian transcription start sites. <i>Genome Research</i> , 2006, 16, 713-722.	5.5	68
28	Complex SNP-related sequence variation in segmental genome duplications. <i>Nature Genetics</i> , 2004, 36, 861-866.	21.4	220
29	DFold: PCR design that minimizes secondary structure and optimizes downstream genotyping applications. <i>Human Mutation</i> , 2004, 24, 1-8.	2.5	17
30	HGVbase: a human sequence variation database emphasizing data quality and a broad spectrum of data sources. <i>Nucleic Acids Research</i> , 2002, 30, 387-391.	14.5	129
31	SNP association studies in Alzheimer's disease highlight problems for complex disease analysis. <i>Trends in Genetics</i> , 2001, 17, 407-413.	6.7	169