

R Andrew Cameron

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

53
papers

5,570
citations

31
h-index

55
g-index

55
ext. papers

6,221
ext. citations

6.8
avg, IF

4.89
L-index

#	Paper	IF	Citations
53	Echinobase: leveraging an extant model organism database to build a knowledgebase supporting research on the genomics and biology of echinoderms. <i>Nucleic Acids Research</i> , 2021 ,	20.1	5
52	Genomic insights of body plan transitions from bilateral to pentamer symmetry in Echinoderms. <i>Communications Biology</i> , 2020 , 3, 371	6.7	5
51	A personal history of the echinoderm genome sequencing. <i>Methods in Cell Biology</i> , 2019 , 151, 55-61	1.8	
50	Genomic resources for the study of echinoderm development and evolution. <i>Methods in Cell Biology</i> , 2019 , 151, 65-88	1.8	3
49	Developmental effector gene regulation: Multiplexed strategies for functional analysis. <i>Developmental Biology</i> , 2019 , 445, 68-79	3.1	1
48	Bacterial artificial chromosomes as recombinant reporter constructs to investigate gene expression and regulation in echinoderms. <i>Briefings in Functional Genomics</i> , 2018 , 17, 362-371	4.9	8
47	EchinoBase: Tools for Echinoderm Genome Analyses. <i>Methods in Molecular Biology</i> , 2018 , 1757, 349-369	1.4	21
46	Echinobase: an expanding resource for echinoderm genomic information. <i>Database: the Journal of Biological Databases and Curation</i> , 2017 , 2017,	5	38
45	DNA Extraction Protocols for Whole-Genome Sequencing in Marine Organisms. <i>Methods in Molecular Biology</i> , 2016 , 1452, 13-44	1.4	29
44	Do echinoderm genomes measure up?. <i>Marine Genomics</i> , 2015 , 22, 1-9	1.9	19
43	Quantitative developmental transcriptomes of the sea urchin <i>Strongylocentrotus purpuratus</i> . <i>Developmental Biology</i> , 2014 , 385, 160-7	3.1	89
42	Tools for sea urchin genomic analysis. <i>Methods in Molecular Biology</i> , 2014 , 1128, 295-310	1.4	3
41	Gene structure in the sea urchin <i>Strongylocentrotus purpuratus</i> based on transcriptome analysis. <i>Genome Research</i> , 2012 , 22, 2079-87	9.7	113
40	microRNA complements in deuterostomes: origin and evolution of microRNAs. <i>Evolution & Development</i> , 2011 , 13, 15-27	2.6	93
39	SpBase: the sea urchin genome database and web site. <i>Nucleic Acids Research</i> , 2009 , 37, D750-4	20.1	161
38	Flexibility of transcription factor target site position in conserved cis-regulatory modules. <i>Developmental Biology</i> , 2009 , 336, 122-35	3.1	19
37	The sea urchin genome as a window on function. <i>Biological Bulletin</i> , 2008 , 214, 266-73	1.5	9

36	The larval stages of the sea urchin, <i>Strongylocentrotus purpuratus</i> . <i>Journal of Morphology</i> , 2008 , 269, 713-33	1.6	62
35	A basal deuterostome genome viewed as a natural experiment. <i>Gene</i> , 2007 , 406, 1-7	3.8	6
34	Unusual gene order and organization of the sea urchin hox cluster. <i>Journal of Experimental Zoology Part B: Molecular and Developmental Evolution</i> , 2006 , 306, 45-58	1.8	112
33	The transcriptome of the sea urchin embryo. <i>Science</i> , 2006 , 314, 960-2	33.3	77
32	An ancient evolutionary origin of the Rag1/2 gene locus. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006 , 103, 3728-33	11.5	140
31	The genome of the sea urchin <i>Strongylocentrotus purpuratus</i> . <i>Science</i> , 2006 , 314, 941-52	33.3	886
30	Genetic organization and embryonic expression of the ParaHox genes in the sea urchin <i>S. purpuratus</i> : insights into the relationship between clustering and colinearity. <i>Developmental Biology</i> , 2006 , 300, 63-73	3.1	53
29	Gene families encoding transcription factors expressed in early development of <i>Strongylocentrotus purpuratus</i> . <i>Developmental Biology</i> , 2006 , 300, 90-107	3.1	114
28	Identification and characterization of homeobox transcription factor genes in <i>Strongylocentrotus purpuratus</i> , and their expression in embryonic development. <i>Developmental Biology</i> , 2006 , 300, 74-89	3.1	108
27	The immune gene repertoire encoded in the purple sea urchin genome. <i>Developmental Biology</i> , 2006 , 300, 349-65	3.1	442
26	The <i>S. purpuratus</i> genome: a comparative perspective. <i>Developmental Biology</i> , 2006 , 300, 485-95	3.1	24
25	High regulatory gene use in sea urchin embryogenesis: Implications for bilaterian development and evolution. <i>Developmental Biology</i> , 2006 , 300, 27-34	3.1	47
24	Hindgut specification and cell-adhesion functions of Sphox11/13b in the endoderm of the sea urchin embryo. <i>Development Growth and Differentiation</i> , 2006 , 48, 463-72	3	31
23	Paleogenomics of echinoderms. <i>Science</i> , 2006 , 314, 956-60	33.3	88
22	Paircomp, FamilyRelationsII and Cartwheel: tools for interspecific sequence comparison. <i>BMC Bioinformatics</i> , 2005 , 6, 70	3.6	31
21	An evolutionary constraint: strongly disfavored class of change in DNA sequence during divergence of cis-regulatory modules. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005 , 102, 11769-74	11.5	34
20	cis-Regulatory activity of randomly chosen genomic fragments from the sea urchin. <i>Gene Expression Patterns</i> , 2004 , 4, 205-13	1.5	24
19	Genomic resources for the study of sea urchin development. <i>Methods in Cell Biology</i> , 2004 , 74, 733-57	1.8	10

18	Developmental gene regulatory network architecture across 500 million years of echinoderm evolution. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003 , 100, 13356-61	11.5	204
17	Majority of divergence between closely related DNA samples is due to indels. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003 , 100, 4661-5	11.5	156
16	A genomic regulatory network for development. <i>Science</i> , 2002 , 295, 1669-78	33.3	1180
15	New computational approaches for analysis of cis-regulatory networks. <i>Developmental Biology</i> , 2002 , 246, 86-102	3.1	95
14	A provisional regulatory gene network for specification of endomesoderm in the sea urchin embryo. <i>Developmental Biology</i> , 2002 , 246, 162-90	3.1	279
13	brachyury Target genes in the early sea urchin embryo isolated by differential macroarray screening. <i>Developmental Biology</i> , 2002 , 246, 191-208	3.1	70
12	A large-scale analysis of mRNAs expressed by primary mesenchyme cells of the sea urchin embryo. <i>Development (Cambridge)</i> , 2001 , 128, 2615-2627	6.6	91
11	Bilaterian origins: significance of new experimental observations. <i>Developmental Biology</i> , 2000 , 219, 1-17	3.1	109
10	Expression of the Hox gene complex in the indirect development of a sea urchin. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1998 , 95, 13062-7	11.5	103
9	Set-aside cells in maximal indirect development: evolutionary and developmental significance. <i>BioEssays</i> , 1997 , 19, 623-31	4.1	133
8	Development of sibling inbred sea urchins: normal embryogenesis, but frequent postembryonic malformation, arrest and lethality. <i>Mechanisms of Development</i> , 1994 , 45, 255-68	1.7	9
7	Cell type specification during sea urchin development. <i>Trends in Genetics</i> , 1991 , 7, 212-8	8.5	14
6	Expression of two actin genes during larval development in the sea urchin <i>Strongylocentrotus purpuratus</i> . <i>Molecular Reproduction and Development</i> , 1989 , 1, 149-55	2.6	24
5	The Control of Sea Urchin Metamorphosis: Ionic Effects. <i>Development Growth and Differentiation</i> , 1989 , 31, 589-594	3	27
4	Electrical activity at metamorphosis in larvae of the sea urchin <i>Lytechinus pictus</i> (Echinoidea: Echinodermata). <i>The Journal of Experimental Zoology</i> , 1985 , 235, 197-204		16
3	Early events in sea urchin metamorphosis, description and analysis. <i>Journal of Morphology</i> , 1978 , 157, 21-31	1.6	42
2	Initiation of metamorphosis in laboratory cultured sea urchins. <i>Biological Bulletin</i> , 1974 , 146, 335-42	1.5	112
1	Comparing the Human and Sea Urchin Genomes		1

