

Kevin J Peterson

List of Publications by Year in descending order

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Version: 2024-02-01

71
papers

11,465
citations

38742

50
h-index

88630

70
g-index

76
all docs

76
docs citations

76
times ranked

9805
citing authors

#	ARTICLE	IF	CITATIONS
1	MirGeneDB 2.1: toward a complete sampling of all major animal phyla. <i>Nucleic Acids Research</i> , 2022, 50, D204-D210.	14.5	63
2	MicroRNAs as Indicators into the Causes and Consequences of Whole-Genome Duplication Events. <i>Molecular Biology and Evolution</i> , 2022, 39, .	8.9	17
3	RNAcentral 2021: secondary structure integration, improved sequence search and new member databases. <i>Nucleic Acids Research</i> , 2021, 49, D212-D220.	14.5	160
4	MirGeneDB 2.0: the metazoan microRNA complement. <i>Nucleic Acids Research</i> , 2020, 48, D132-D141.	14.5	194
5	Quo vadis microRNAs?. <i>Trends in Genetics</i> , 2020, 36, 461-463.	6.7	24
6	Response to: Xâ€linked miRâ€506 family miRNAs promote FMRP expression in mouse spermatogonia. <i>EMBO Reports</i> , 2020, 21, e49354.	4.5	1
7	A micro <scp>RNA</scp> cluster in the Fragileâ€X region expressed during spermatogenesis targets <scp>FMR</scp>. <i>EMBO Reports</i> , 2019, 20, .	4.5	25
8	Big Strides in Cellular MicroRNA Expression. <i>Trends in Genetics</i> , 2018, 34, 165-167.	6.7	32
9	Large scale changes in the transcriptome of <i>Eisenia fetida</i> during regeneration. <i>PLoS ONE</i> , 2018, 13, e0204234.	2.5	31
10	Unicellular Origin of the Animal MicroRNA Machinery. <i>Current Biology</i> , 2018, 28, 3288-3295.e5.	3.9	42
11	Evolution of metazoan morphological disparity. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E8909-E8918.	7.1	78
12	Well-Annotated microRNAomes Do Not Evidence Pervasive miRNA Loss. <i>Genome Biology and Evolution</i> , 2018, 10, 1457-1470.	2.5	41
13	The Antagonistic Gene Paralogs Upf3a and Upf3b Govern Nonsense-Mediated RNA Decay. <i>Cell</i> , 2016, 165, 382-395.	28.9	132
14	The Interrelationships of Placental Mammals and the Limits of Phylogenetic Inference. <i>Genome Biology and Evolution</i> , 2016, 8, 330-344.	2.5	195
15	The phylogeny, evolutionary developmental biology, and paleobiology of the Deuterostomia: 25Âyears of new techniques, new discoveries, and new ideas. <i>Organisms Diversity and Evolution</i> , 2016, 16, 401-418.	1.6	30
16	A Uniform System for the Annotation of Vertebrate microRNA Genes and the Evolution of the Human microRNAome. <i>Annual Review of Genetics</i> , 2015, 49, 213-242.	7.6	467
17	Toward consilience in reptile phylogeny: miRNAs support an archosaur, not lepidosaur, affinity for turtles. <i>Evolution & Development</i> , 2014, 16, 189-196.	2.0	106
18	The end of the Ediacara biota: Extinction, biotic replacement, or Cheshire Cat?. <i>Gondwana Research</i> , 2013, 23, 558-573.	6.0	220

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19	The Identification of MicroRNAs in Calcisponges: Independent Evolution of MicroRNAs in Basal Metazoans. <i>Journal of Experimental Zoology Part B: Molecular and Developmental Evolution</i> , 2013, 320, 84-93.	1.3	18
20	MicroRNAs support the monophyly of enteropneust hemichordates. <i>Journal of Experimental Zoology Part B: Molecular and Developmental Evolution</i> , 2013, 320, 368-374.	1.3	24
21	miRNAs: Small Genes with Big Potential in Metazoan Phylogenetics. <i>Molecular Biology and Evolution</i> , 2013, 30, 2369-2382.	8.9	118
22	Reconstruction of Family-Level Phylogenetic Relationships within Demospongiae (Porifera) Using Nuclear Encoded Housekeeping Genes. <i>PLoS ONE</i> , 2013, 8, e50437.	2.5	47
23	CD2AP Regulates SUMOylation of CIN85 in Podocytes. <i>Molecular and Cellular Biology</i> , 2012, 32, 1068-1079.	2.3	18
24	Do miRNAs have a deep evolutionary history?. <i>BioEssays</i> , 2012, 34, 857-866.	2.5	96
25	A molecular palaeobiological hypothesis for the origin of aplacophoran molluscs and their derivation from chiton-like ancestors. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2012, 279, 1259-1268.	2.6	86
26	Resolving phylogenetic signal from noise when divergence is rapid: A new look at the old problem of echinoderm class relationships. <i>Molecular Phylogenetics and Evolution</i> , 2012, 62, 27-34.	2.7	70
27	MicroRNAs support a turtle + lizard clade. <i>Biology Letters</i> , 2012, 8, 104-107.	2.3	96
28	Episodic radiations in the fly tree of life. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 5690-5695.	7.1	739
29	A congruent solution to arthropod phylogeny: phylogenomics, microRNAs and morphology support monophyletic Mandibulata. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2011, 278, 298-306.	2.6	227
30	MicroRNAs and phylogenomics resolve the relationships of Tardigrada and suggest that velvet worms are the sister group of Arthropoda. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 15920-15924.	7.1	212
31	The Cambrian Conundrum: Early Divergence and Later Ecological Success in the Early History of Animals. <i>Science</i> , 2011, 334, 1091-1097.	12.6	1,055
32	microRNA complements in deuterostomes: origin and evolution of microRNAs. <i>Evolution & Development</i> , 2011, 13, 15-27.	2.0	113
33	Molecular paleobiological insights into the origin of the Brachiopoda. <i>Evolution & Development</i> , 2011, 13, 290-303.	2.0	55
34	Acoelomorph flatworms are deuterostomes related to Xenoturbella. <i>Nature</i> , 2011, 470, 255-258.	27.8	400
35	Developmental expression of COE across the Metazoa supports a conserved role in neuronal cell-type specification and mesodermal development. <i>Development Genes and Evolution</i> , 2010, 220, 221-234.	0.9	28
36	The dynamic genome of Hydra. <i>Nature</i> , 2010, 464, 592-596.	27.8	743

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37	microRNAs reveal the interrelationships of hagfish, lampreys, and gnathostomes and the nature of the ancestral vertebrate. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 19379-19383.	7.1	257
38	MicroRNAs resolve an apparent conflict between annelid systematics and their fossil record. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2009, 276, 4315-4322.	2.6	54
39	MicroRNAs and metazoan macroevolution: insights into canalization, complexity, and the Cambrian explosion. <i>BioEssays</i> , 2009, 31, 736-747.	2.5	225
40	The deep evolution of metazoan microRNAs. <i>Evolution & Development</i> , 2009, 11, 50-68.	2.0	491
41	Phylogenetic-Signal Dissection of Nuclear Housekeeping Genes Supports the Paraphyly of Sponges and the Monophyly of Eumetazoa. <i>Molecular Biology and Evolution</i> , 2009, 26, 2261-2274.	8.9	158
42	MicroRNAs and metazoan phylogeny: big trees from little genes. , 2009, , 157-170.		29
43	The Ediacaran emergence of bilaterians: congruence between the genetic and the geological fossil records. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2008, 363, 1435-1443.	4.0	286
44	MicroRNAs and the advent of vertebrate morphological complexity. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 2946-2950.	7.1	373
45	Molecular Paleobiology and the Cambrian Explosion: 21 st Century Answers to 19 th Century Problems. <i>The Paleontological Society Papers</i> , 2008, 14, 105-116.	0.6	0
46	Molecular paleoecology: using gene regulatory analysis to address the origins of complex life cycles in the late Precambrian. <i>Evolution & Development</i> , 2007, 9, 10-24.	2.0	80
47	Poriferan ANTP genes: primitively simple or secondarily reduced?. <i>Evolution & Development</i> , 2007, 9, 405-408.	2.0	31
48	Phylogenetic distribution of microRNAs supports the basal position of acoel flatworms and the polyphyly of Platyhelminthes. <i>Evolution & Development</i> , 2007, 9, 409-415.	2.0	98
49	MOLECULAR PALAEOBIOLOGY. <i>Palaeontology</i> , 2007, 50, 775-809.	2.2	83
50	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.	2.0	64
51	Paleogenomics of Echinoderms. <i>Science</i> , 2006, 314, 956-960.	12.6	117
52	Unusual gene order and organization of the sea urchin hox cluster. <i>Journal of Experimental Zoology Part B: Molecular and Developmental Evolution</i> , 2006, 306B, 45-58.	1.3	145
53	The phylogenetic distribution of metazoan microRNAs: insights into evolutionary complexity and constraint. <i>Journal of Experimental Zoology Part B: Molecular and Developmental Evolution</i> , 2006, 306B, 575-588.	1.3	272
54	Origin of the Eumetazoa: Testing ecological predictions of molecular clocks against the Proterozoic fossil record. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 9547-9552.	7.1	327

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55	Tempo and mode of early animal evolution: inferences from rocks, Hox, and molecular clocks. <i>Paleobiology</i> , 2005, 31, 36-55.	2.0	158
56	Macroevolutionary interplay between planktic larvae and benthic predators. <i>Geology</i> , 2005, 33, 929.	4.4	105
57	Isolation of Hox and Parahox genes in the hemichordate <i>Ptychodera flava</i> and the evolution of deuterostome Hox genes. <i>Molecular Phylogenetics and Evolution</i> , 2004, 31, 1208-1215.	2.7	103
58	Estimating metazoan divergence times with a molecular clock. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 6536-6541.	7.1	403
59	Expression of an NK2 homeodomain gene in the apical ectoderm defines a new territory in the early sea urchin embryo. <i>Developmental Biology</i> , 2004, 269, 152-164.	2.0	71
60	Spdeadringer, a sea urchin embryo gene required separately in skeletogenic and oral ectoderm gene regulatory networks. <i>Developmental Biology</i> , 2003, 261, 55-81.	2.0	67
61	A Fungal Analog for Newfoundland Ediacaran Fossils?. <i>Integrative and Comparative Biology</i> , 2003, 43, 127-136.	2.0	113
62	Dating the Time of Origin of Major Clades: Molecular Clocks and the Fossil Record. <i>Annual Review of Earth and Planetary Sciences</i> , 2002, 30, 65-88.	11.0	170
63	Testing putative hemichordate homologues of the chordate dorsal nervous system and endostyle: expression of NK2.1 (TTF-1) in the acorn worm <i>Ptychodera flava</i> (Hemichordata, Ptychoderidae). <i>Evolution & Development</i> , 2002, 4, 405-417.	2.0	54
64	Animal phylogeny and the ancestry of bilaterians: inferences from morphology and 18S rDNA gene sequences. <i>Evolution & Development</i> , 2001, 3, 170-205.	2.0	490
65	The A/P axis in echinoderm ontogeny and evolution: evidence from fossils and molecules. <i>Evolution & Development</i> , 2000, 2, 93-101.	2.0	109
66	Bilaterian Origins: Significance of New Experimental Observations. <i>Developmental Biology</i> , 2000, 219, 1-17.	2.0	122
67	Expression Pattern of Brachyury and Not in the Sea Urchin: Comparative Implications for the Origins of Mesoderm in the Basal Deuterostomes. <i>Developmental Biology</i> , 1999, 207, 419-431.	2.0	79
68	Developmental Gene Regulation and the Evolution of Large Animal Body Plans. <i>American Zoologist</i> , 1998, 38, 609-620.	0.7	33
69	Set-aside cells in maximal indirect development: Evolutionary and developmental significance. <i>BioEssays</i> , 1997, 19, 623-631.	2.5	152
70	Spatial expression of a forkhead homologue in the sea urchin embryo. <i>Mechanisms of Development</i> , 1996, 60, 163-173.	1.7	37
71	A phylogenetic test of the calcichordate scenario. <i>Lethaia</i> , 1995, 28, 25-38.	1.4	65