

# Joseph F Ryan

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/228498/publications.pdf>

Version: 2024-02-01

61  
papers

4,217  
citations

147786

31  
h-index

128286

60  
g-index

84  
all docs

84  
docs citations

84  
times ranked

5244  
citing authors

#	ARTICLE	IF	CITATIONS
1	The Genome of the Ctenophore <i>Mnemiopsis leidyi</i> and Its Implications for Cell Type Evolution. <i>Science</i> , 2013, 342, 1242592.	12.6	570
2	Genomic evidence for ameiotic evolution in the bdelloid rotifer <i>Adineta vaga</i> . <i>Nature</i> , 2013, 500, 453-457.	27.8	352
3	The mid-developmental transition and the evolution of animal body plans. <i>Nature</i> , 2016, 531, 637-641.	27.8	231
4	Pre-Bilaterian Origins of the Hox Cluster and the Hox Code: Evidence from the Sea Anemone, <i>Nematostella vectensis</i> . <i>PLoS ONE</i> , 2007, 2, e153.	2.5	198
5	Rising starlet: the starlet sea anemone, <i>Nematostella vectensis</i> . <i>BioEssays</i> , 2005, 27, 211-221.	2.5	189
6	Phylogenomics provides a robust topology of the major cnidarian lineages and insights on the origins of key organismal traits. <i>BMC Evolutionary Biology</i> , 2018, 18, .	3.2	182
7	The Breast Cancer Information Core: Database design, structure, and scope. <i>Human Mutation</i> , 2000, 16, 123-131.	2.5	174
8	The cnidarian-bilaterian ancestor possessed at least 56 homeoboxes: evidence from the starlet sea anemone, <i>Nematostella vectensis</i> . <i>Genome Biology</i> , 2006, 7, R64.	9.6	162
9	The homeodomain complement of the ctenophore <i>Mnemiopsis leidyi</i> suggests that Ctenophora and Porifera diverged prior to the ParaHoxozoa. <i>EvoDevo</i> , 2010, 1, 9.	3.2	133
10	Genomic organization, evolution, and expression of photoprotein and opsin genes in <i>Mnemiopsis leidyi</i> : a new view of ctenophore photocytes. <i>BMC Biology</i> , 2012, 10, 107.	3.8	107
11	StellaBase: The <i>Nematostella vectensis</i> Genomics Database. <i>Nucleic Acids Research</i> , 2006, 34, D495-D499.	14.5	101
12	Genomic insights into Wnt signaling in an early diverging metazoan, the ctenophore <i>Mnemiopsis leidyi</i> . <i>EvoDevo</i> , 2010, 1, 10.	3.2	100
13	The Global Invertebrate Genomics Alliance (GIGA): Developing Community Resources to Study Diverse Invertebrate Genomes. <i>Journal of Heredity</i> , 2014, 105, 1-18.	2.4	96
14	Evolution of the TGF- $\beta$ Signaling Pathway and Its Potential Role in the Ctenophore, <i>Mnemiopsis leidyi</i> . <i>PLoS ONE</i> , 2011, 6, e24152.	2.5	85
15	Extreme mitochondrial evolution in the ctenophore <i>Mnemiopsis leidyi</i> : Insight from mtDNA and the nuclear genome. <i>Mitochondrial DNA</i> , 2011, 22, 130-142.	0.6	81
16	Genetic Analysis of Hematological Parameters in Incipient Lines of the Collaborative Cross. <i>G3: Genes, Genomes, Genetics</i> , 2012, 2, 157-165.	1.8	80
17	Tracing animal genomic evolution with the chromosomal-level assembly of the freshwater sponge <i>Ephydatia muelleri</i> . <i>Nature Communications</i> , 2020, 11, 3676.	12.8	72
18	Parallel Construction of Orthologous Sequence-Ready Clone Contig Maps in Multiple Species. <i>Genome Research</i> , 2002, 12, 1277-1285.	5.5	62

#	ARTICLE	IF	CITATIONS
19	Do novel genes drive morphological novelty? An investigation of the nematosomes in the sea anemone <i>Nematostella vectensis</i> . <i>BMC Evolutionary Biology</i> , 2016, 16, 114.	3.2	56
20	Box, stalked, and upside-down? Draft genomes from diverse jellyfish (Cnidaria, Acraspeda) lineages: <i>Alatina alata</i> (Cubozoa), <i>Calvadosia cruxmelitensis</i> (Staurozoa), and <i>Cassiopea xamachana</i> (Scyphozoa). <i>GigaScience</i> , 2019, 8, .	6.4	53
21	Did the ctenophore nervous system evolve independently?. <i>Zoology</i> , 2014, 117, 225-226.	1.2	52
22	Where is my mind? How sponges and placozoans may have lost neural cell types. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2015, 370, 20150059.	4.0	52
23	The Diversification of the LIM Superclass at the Base of the Metazoa Increased Subcellular Complexity and Promoted Multicellular Specialization. <i>PLoS ONE</i> , 2012, 7, e33261.	2.5	50
24	Opsin Repertoire and Expression Patterns in Horseshoe Crabs: Evidence from the Genome of <i>Limulus polyphemus</i> (Arthropoda: Chelicerata). <i>Genome Biology and Evolution</i> , 2016, 8, 1571-1589.	2.5	50
25	Hox, Wnt, and the evolution of the primary body axis: insights from the early-divergent phyla. <i>Biology Direct</i> , 2007, 2, 37.	4.6	48
26	The evolution of animal genomes. <i>Current Opinion in Genetics and Development</i> , 2015, 35, 25-32.	3.3	48
27	Timing and Scope of Genomic Expansion within Annelida: Evidence from Homeoboxes in the Genome of the Earthworm <i>Eisenia fetida</i> . <i>Genome Biology and Evolution</i> , 2016, 8, 271-281.	2.5	45
28	MicroRNAs and essential components of the microRNA processing machinery are not encoded in the genome of the ctenophore <i>Mnemiopsis leidyi</i> . <i>BMC Genomics</i> , 2012, 13, 714.	2.8	43
29	Coral Comparative Genomics Reveal Expanded Hox Cluster in the Cnidarian-Bilaterian Ancestor. <i>Integrative and Comparative Biology</i> , 2012, 52, 835-841.	2.0	40
30	Automation and Evaluation of the SOWH Test with SOWHAT. <i>Systematic Biology</i> , 2015, 64, 1048-1058.	5.6	40
31	Increased taxon sampling reveals thousands of hidden orthologs in flatworms. <i>Genome Research</i> , 2017, 27, 1263-1272.	5.5	39
32	Low coverage sequencing of three echinoderm genomes: the brittle star <i>Ophionereis fasciata</i> , the sea star <i>Patiriella regularis</i> , and the sea cucumber <i>Australostichopus mollis</i> . <i>GigaScience</i> , 2016, 5, 20.	6.4	33
33	Nuclear receptors from the ctenophore <i>Mnemiopsis leidyi</i> lack a zinc-finger DNA-binding domain: lineage-specific loss or ancestral condition in the emergence of the nuclear receptor superfamily?. <i>EvoDevo</i> , 2011, 2, 3.	3.2	32
34	A new transcriptome and transcriptome profiling of adult and larval tissue in the box jellyfish <i>Alatina alata</i> : an emerging model for studying venom, vision and sex. <i>BMC Genomics</i> , 2016, 17, 650.	2.8	31
35	Six-State Amino Acid Recoding is not an Effective Strategy to Offset Compositional Heterogeneity and Saturation in Phylogenetic Analyses. <i>Systematic Biology</i> , 2021, 70, 1200-1212.	5.6	31
36	ANISEED 2019: 4D exploration of genetic data for an extended range of tunicates. <i>Nucleic Acids Research</i> , 2020, 48, D668-D675.	14.5	30

#	ARTICLE	IF	CITATIONS
37	Integrating embryonic development and evolutionary history to characterize tentacle-specific cell types in a ctenophore. <i>Molecular Biology and Evolution</i> , 2018, 35, 2940-2956.	8.9	29
38	Conserved and novel Wnt clusters in the basal eumetazoan <i>Nematostella vectensis</i> . <i>Development Genes and Evolution</i> , 2007, 217, 235-239.	0.9	28
39	A customized Web portal for the genome of the ctenophore <i>Mnemiopsis leidyi</i> . <i>BMC Genomics</i> , 2014, 15, 316.	2.8	28
40	Comparative Genome Mapping in the Sequence-based Era: Early Experience with Human Chromosome 7. <i>Genome Research</i> , 2000, 10, 624-633.	5.5	27
41	A hybrid <i>de novo</i> assembly of the sea pansy ( <i>Renilla muelleri</i> ) genome. <i>GigaScience</i> , 2019, 8, .	6.4	27
42	“Dorsal-Ventral” Genes Are Part of an Ancient Axial Patterning System: Evidence from <i>Trichoplax adhaerens</i> (Placozoa). <i>Molecular Biology and Evolution</i> , 2019, 36, 966-973.	8.9	26
43	Genomic analysis of the tryptome reveals molecular mechanisms of gland cell evolution. <i>EvoDevo</i> , 2019, 10, 23.	3.2	21
44	A reconstruction of sexual modes throughout animal evolution. <i>BMC Evolutionary Biology</i> , 2017, 17, 242.	3.2	20
45	Phylotocol: Promoting Transparency and Overcoming Bias in Phylogenetics. <i>Systematic Biology</i> , 2019, 68, 672-678.	5.6	20
46	CnidBase: The Cnidarian Evolutionary Genomics Database. <i>Nucleic Acids Research</i> , 2003, 31, 159-163.	14.5	19
47	Insights into the Biodiversity, Behavior, and Bioluminescence of Deep-Sea Organisms Using Molecular and Maritime Technology. <i>Oceanography</i> , 2017, 30, 38-47.	1.0	19
48	The <i>Mnemiopsis</i> Genome Project Portal: integrating new gene expression resources and improving data visualization. <i>Database: the Journal of Biological Databases and Curation</i> , 2020, 2020, .	3.0	18
49	Lineage-specific evolution of the vertebrate Otopetringene family revealed by comparative genomic analyses. <i>BMC Evolutionary Biology</i> , 2011, 11, 23.	3.2	16
50	The Homeodomain Resource: a comprehensive collection of sequence, structure, interaction, genomic and functional information on the homeodomain protein family. <i>Database: the Journal of Biological Databases and Curation</i> , 2009, 2009, bap004-bap004.	3.0	15
51	The Homeodomain Resource: sequences, structures and genomic information. <i>Nucleic Acids Research</i> , 1999, 27, 336-337.	14.5	14
52	Draft Genome of the Sea Cucumber <i>Holothuria glaberrima</i> , a Model for the Study of Regeneration. <i>Frontiers in Marine Science</i> , 2021, 8, .	2.5	14
53	The sex lives of ctenophores: the influence of light, body size, and self-fertilization on the reproductive output of the sea walnut, <i>Mnemiopsis leidyi</i> . <i>PeerJ</i> , 2016, 4, e1846.	2.0	14
54	Inferring Tunicate Relationships and the Evolution of the Tunicate Hox Cluster with the Genome of <i>Corella inflata</i> . <i>Genome Biology and Evolution</i> , 2020, 12, 948-964.	2.5	12

#	ARTICLE	IF	CITATIONS
55	A novel regulatory gene promotes novel cell fate by suppressing ancestral fate in the sea anemone <i>Nematostella vectensis</i> . Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, e2113701119.	7.1	12
56	Sponges Lack ParaHox Genes. Genome Biology and Evolution, 2019, 11, 1250-1257.	2.5	11
57	The state of Medusozoa genomics: current evidence and future challenges. GigaScience, 2022, 11, .	6.4	8
58	The ctenophore <i>Mnemiopsis leidyi</i> regulates egg production via conspecific communication. BMC Ecology, 2018, 18, 12.	3.0	7
59	Horizontally transferred genes in the ctenophore <i>Mnemiopsis leidyi</i> . PeerJ, 2018, 6, e5067.	2.0	7
60	Meeting report of Ctenopalooza: the first international meeting of ctenophorologists. EvoDevo, 2016, 7, .	3.2	1
61	Regeneration of Planarian Auricles and Reestablishment of Chemotactic Ability. Frontiers in Cell and Developmental Biology, 2021, 9, 777951.	3.7	1