J Spencer Johnston

List of Publications by Year
in descending order

63	7,789	36	63
papers	citations	h-index	g-index
		101543	114465

68	68	68	10209
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	The Genome of Rhyzopertha dominica (Fab.) (Coleoptera: Bostrichidae): Adaptation for Success. Genes, 2022, 13, 446.	2.4	10
2	Comparison of long-read sequencing technologies in interrogating bacteria and fly genomes. G3: Genes, Genomes, Genetics, 2021, 11, .	1.8	26
3	Rapid genomic expansion and purging associated with habitat transitions in a clade of beach crustaceans (Amphipoda: Haustoriidae). Journal of Crustacean Biology, 2021, 41, .	0.8	3
4	Whole genome sequence of the soybean aphid, Aphis glycines. Insect Biochemistry and Molecular Biology, 2020, 123, 102917.	2.7	91
5	Lineage-specific patterns of chromosome evolution are the rule not the exception in Polyneoptera insects. Proceedings of the Royal Society B: Biological Sciences, 2020, 287, 20201388.	2.6	19
6	Improved reference genome of the arboviral vector Aedes albopictus. Genome Biology, 2020, 21, 215.	8.8	65
7	Brown marmorated stink bug, Halyomorpha halys (StÃ¥l), genome: putative underpinnings of polyphagy, insecticide resistance potential and biology of a top worldwide pest. BMC Genomics, 2020, 21, 227.	2.8	60
8	Measuring Genome Sizes Using Read-Depth, k-mers, and Flow Cytometry: Methodological Comparisons in Beetles (Coleoptera). G3: Genes, Genomes, Genetics, 2020, 10, 3047-3060.	1.8	78
9	The genome of pest Rhynchophorus ferrugineus reveals gene families important at the plant-beetle interface. Communications Biology, 2020, 3, 323.	4.4	44
10	Effect of Phenotype Selection on Genome Size Variation in Two Species of Diptera. Genes, 2020, 11, 218.	2.4	6
11	Flying Highâ€"Muscle-Specific Underreplication in Drosophila. Genes, 2020, 11, 246.	2.4	4
12	Molecular evolutionary trends and feeding ecology diversification in the Hemiptera, anchored by the milkweed bug genome. Genome Biology, 2019, 20, 64.	8.8	114
13	Genome Size Evolution Differs Between<i>Drosophila</i>Subgenera with Striking Differences in Male and Female Genome Size in<i>Sophophora</i>. G3: Genes, Genomes, Genetics, 2019, 9, 3167-3179.	1.8	8
14	Genome Size Evolution within and between the Sexes. Journal of Heredity, 2019, 110, 219-228.	2.4	4
15	Genome Size Estimation and Quantitative Cytogenetics in Insects. Methods in Molecular Biology, 2019, 1858, 15-26.	0.9	36
16	Inheritance, distribution and genetic differentiation of a color polymorphism in Panamanian populations of the tortoise beetle, Chelymorpha alternans (Coleoptera: Chrysomelidae). Heredity, 2019, 122, 558-569.	2.6	7
17	Improved reference genome of Aedes aegypti informs arbovirus vector control. Nature, 2018, 563, 501-507.	27.8	426
18	Genome Size in North American Fireflies: Substantial Variation Likely Driven by Neutral Processes. Genome Biology and Evolution, 2017, 9, 1499-1512.	2.5	41

#	Article	IF	Citations
19	<scp>SNP</scp>s selected by information content outperform randomly selected microsatellite loci for delineating genetic identification and introgression in the endangered dark European honeybee (<i>Apis mellifera mellifera</i>). Molecular Ecology Resources, 2017, 17, 783-795.	4.8	40
20	The mode and tempo of genome size evolution in the subgenus Sophophora. PLoS ONE, 2017, 12, e0173505.	2.5	13
21	Genome of the Asian longhorned beetle (Anoplophora glabripennis), a globally significant invasive species, reveals key functional and evolutionary innovations at the beetleâ€"plant interface. Genome Biology, 2016, 17, 227.	8.8	244
22	Unique features of a global human ectoparasite identified through sequencing of the bed bug genome. Nature Communications, 2016, 7, 10165.	12.8	184
23	Reduced SNP Panels for Genetic Identification and Introgression Analysis in the Dark Honey Bee (Apis) Tj ETQq1 1 0.784314 rgBT /Overl	2.5	46
24	Comparison of life history and genetic properties of cowpea bruchid strains and their response to hypoxia. Journal of Insect Physiology, 2015, 75, 5-11.	2.0	13
25	Revisiting the <scp>I</scp>berian honey bee (<i><scp>A</scp>pis mellifera iberiensis</i>) contact zone: maternal and genomeâ€wide nuclear variations provide support for secondary contact from historical refugia. Molecular Ecology, 2015, 24, 2973-2992.	3.9	31
26	Genome size correlates with reproductive fitness in seed beetles. Proceedings of the Royal Society B: Biological Sciences, 2015, 282, 20151421.	2.6	25
27	Endopolyploidy Changes with Age-Related Polyethism in the Honey Bee, Apis mellifera. PLoS ONE, 2015, 10, e0122208.	2.5	18
28	Natural variation in genome architecture among 205 <i>Drosophila melanogaster</i> Genetic Reference Panel lines. Genome Research, 2014, 24, 1193-1208.	5.5	565
29	Intrapopulation Genome Size Variation in D. melanogaster Reflects Life History Variation and Plasticity. PLoS Genetics, 2014, 10, e1004522.	3.5	64
30	Stick Insect Genomes Reveal Natural Selectionâ€™s Role in Parallel Speciation. Science, 2014, 344, 738-742.	12.6	386
31	Compact genome of the Antarctic midge is likely an adaptation to an extreme environment. Nature Communications, 2014, 5, 4611.	12.8	128
32	Increasing Precision in Development-Based Postmortem Interval Estimates: What's Sex Got to Do With It?. Journal of Medical Entomology, 2013, 50, 425-431.	1.8	23
33	Signatures of selection in the <scp>I</scp>berian honey bee (<i><scp>A</scp>pis mellifera) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf Ecology, 2013, 22, 5890-5907.	3.9	47
34	DNA Underreplication in the Majority of Nuclei in the Drosophila Melanogaster Thorax: Evidence from Suur and Flow Cytometry. Journal of Molecular Biology Research, 2013, 3, .	0.1	7
35	Genome Size Determination Using Flow Cytometry of Propidium Iodide-Stained Nuclei. Methods in Molecular Biology, 2012, 772, 3-12.	0.9	104
36	Genome size and phylogenetic analysis of the A and L races of Botryococcus braunii. Journal of Applied Phycology, 2011, 23, 833-839.	2.8	29

#	Article	IF	Citations
37	New genome size estimates of 134 species of arthropods. Chromosome Research, 2011, 19, 809-823.	2.2	119
38	Linkage Mapping and Comparative Genomics Using Next-Generation RAD Sequencing of a Non-Model Organism. PLoS ONE, 2011, 6, e19315.	2.5	270
39	PHYLOGENETIC PLACEMENT, GENOME SIZE, AND GC CONTENT OF THE LIQUIDâ€HYDROCARBONâ€PRODUCING GREEN MICROALGA <i>BOTRYOCOCCUS BRAUNII</i> STRAIN BERKELEY (SHOWA) (CHLOROPHYTA)¹. Journal of Phycology, 2010, 46, 534-540.	2.3	37
40	Genome sequences of the human body louse and its primary endosymbiont provide insights into the permanent parasitic lifestyle. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 12168-12173.	7.1	482
41	Extremely small genomes in two unrelated dipteran insects with shared early developmental traits. Development Genes and Evolution, 2009, 219, 207-210.	0.9	22
42	The evolution of genome size in ants. BMC Evolutionary Biology, 2008, 8, 64.	3.2	70
43	The canine hookworm genome: Analysis and classification of Ancylostoma caninum survey sequences. Molecular and Biochemical Parasitology, 2008, 157, 187-192.	1.1	36
44	Anthocyanin Inhibits Propidium Iodide DNA Fluorescence in Euphorbia pulcherrima: Implications for Genome Size Variation and Flow Cytometry. Annals of Botany, 2008, 101, 777-790.	2.9	71
45	Body Lice and Head Lice (Anoplura: Pediculidae) Have the Smallest Genomes of Any Hemimetabolous Insect Reported to Date. Journal of Medical Entomology, 2007, 44, 1009-1012.	1.8	27
46	Variation in genome size of argasid and ixodid ticks. Insect Biochemistry and Molecular Biology, 2007, 37, 399-408.	2.7	66
47	Genome Sequence of Aedes aegypti, a Major Arbovirus Vector. Science, 2007, 316, 1718-1723.	12.6	1,025
48	Body Lice and Head Lice (Anoplura: Pediculidae) Have the Smallest Genomes of Any Hemimetabolous Insect Reported to Date. Journal of Medical Entomology, 2007, 44, 1009-1012.	1.8	22
49	Thrice Out of Africa: Ancient and Recent Expansions of the Honey Bee, Apis mellifera. Science, 2006, 314, 642-645.	12.6	333
50	A Genetic Linkage Map of the Mimetic Butterfly Heliconius melpomene. Genetics, 2005, 171, 557-570.	2.9	111
51	Genome Evolution in the Genus Sorghum (Poaceae). Annals of Botany, 2005, 95, 219-227.	2.9	167
52	Evolution of Genome Size in Brassicaceae. Annals of Botany, 2005, 95, 229-235.	2.9	383
53	Preparation of Samples for Comparative Studies of Arthropod Chromosomes: Visualization, In Situ Hybridization, and Genome Size Estimation. Methods in Enzymology, 2005, 395, 460-488.	1.0	39
54	Comparisons with Caenorhabditis (100 Mb) and Drosophila (175 Mb) Using Flow Cytometry Show Genome Size in Arabidopsis to be 157 Mb and thus 25 % Larger than the Arabidopsis Genome Initiative Estimate of 125 Mb. Annals of Botany, 2003, 91, 547-557.	2.9	363

#	Article	IF	Citations
55	Feast and famine in plant genomes. Genetica, 2002, 115, 37-47.	1.1	135
56	DNA content for Asian pines parallels New World relatives. Canadian Journal of Botany, 2001, 79, 192-196.	1.1	15
57	Evidence for DNA Loss as a Determinant of Genome Size. Science, 2000, 287, 1060-1062.	12.6	345
58	Reference standards for determination of DNA content of plant nuclei. American Journal of Botany, 1999, 86, 609-613.	1.7	247
59	DNA content of heterochromatin and euchromatin in tomato (Lycopersicon esculentum) pachytene chromosomes. Genome, 1996, 39, 77-82.	2.0	72
60	Environmentally induced nuclear 2C DNA content instability in <i>Helianthus annuus</i> (Asteraceae). American Journal of Botany, 1996, 83, 1113-1120.	1.7	19
61	Genome size and environmental factors in the genus <i>Pinus</i>. American Journal of Botany, 1993, 80, 1235-1241.	1.7	124
62	COMPARISON OF PLANT DNA CONTENTS DETERMINED BY FEULGEN MICROSPECTROPHOTOMETRY AND LASER FLOW CYTOMETRY. American Journal of Botany, 1991, 78, 183-188.	1.7	120
63	VARIATION OF NUCLEAR DNA CONTENT IN HELIANTHUS ANNUUS (ASTERACEAE). American Journal of Botany, 1991, 78, 1238-1243.	1.7	33