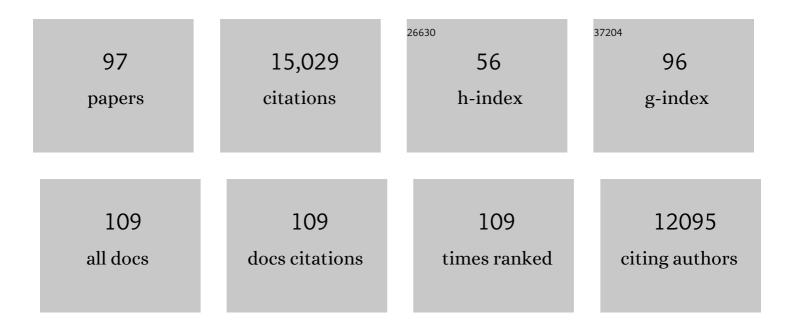
Hugh M Robertson

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/1481916/publications.pdf Version: 2024-02-01



#	Article	IF	CITATIONS
1	Genome size evolution in the beetle genus <i>Diabrotica</i> . G3: Genes, Genomes, Genetics, 2022, 12, .	1.8	5
2	Genus-Wide Characterization of Bumblebee Genomes Provides Insights into Their Evolution and Variation in Ecological and Behavioral Traits. Molecular Biology and Evolution, 2021, 38, 486-501.	8.9	58
3	The genome of the stable fly, Stomoxys calcitrans, reveals potential mechanisms underlying reproduction, host interactions, and novel targets for pest control. BMC Biology, 2021, 19, 41.	3.8	19
4	The genomic basis of evolutionary differentiation among honey bees. Genome Research, 2021, 31, 1203-1215.	5.5	17
5	Selective Sweeps in a Nutshell: The Genomic Footprint of Rapid Insecticide Resistance Evolution in the Almond Agroecosystem. Genome Biology and Evolution, 2021, 13, .	2.5	19
6	The Genome of the Blind Soil-Dwelling and Ancestrally Wingless Dipluran Campodea augens: A Key Reference Hexapod for Studying the Emergence of Insect Innovations. Genome Biology and Evolution, 2020, 12, 3534-3549.	2.5	3
7	Genome-enabled insights into the biology of thrips as crop pests. BMC Biology, 2020, 18, 142.	3.8	54
8	Brown marmorated stink bug, Halyomorpha halys (Stål), genome: putative underpinnings of polyphagy, insecticide resistance potential and biology of a top worldwide pest. BMC Genomics, 2020, 21, 227.	2.8	60
9	Genome of the Parasitoid Wasp Diachasma alloeum, an Emerging Model for Ecological Speciation and Transitions to Asexual Reproduction. Genome Biology and Evolution, 2019, 11, 2767-2773.	2.5	34
10	A hybrid de novo genome assembly of the honeybee, Apis mellifera, with chromosome-length scaffolds. BMC Genomics, 2019, 20, 275.	2.8	171
11	Molecular evolutionary trends and feeding ecology diversification in the Hemiptera, anchored by the milkweed bug genome. Genome Biology, 2019, 20, 64.	8.8	114
12	The chemoreceptors and odorant binding proteins of the soybean and pea aphids. Insect Biochemistry and Molecular Biology, 2019, 105, 69-78.	2.7	26
13	Molecular Evolution of the Major Arthropod Chemoreceptor Gene Families. Annual Review of Entomology, 2019, 64, 227-242.	11.8	156
14	The Toxicogenome of <i>Hyalella azteca</i> : A Model for Sediment Ecotoxicology and Evolutionary Toxicology. Environmental Science & Technology, 2018, 52, 6009-6022.	10.0	79
15	Enormous expansion of the chemosensory gene repertoire in the omnivorous German cockroach <i>Blattella germanica</i> . Journal of Experimental Zoology Part B: Molecular and Developmental Evolution, 2018, 330, 265-278.	1.3	71
16	Hemimetabolous genomes reveal molecular basis of termite eusociality. Nature Ecology and Evolution, 2018, 2, 557-566.	7.8	223
17	A model species for agricultural pest genomics: the genome of the Colorado potato beetle, Leptinotarsa decemlineata (Coleoptera: Chrysomelidae). Scientific Reports, 2018, 8, 1931.	3.3	215
18	Improved reference genome of Aedes aegypti informs arbovirus vector control. Nature, 2018, 563, 501-507.	27.8	426

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19	Genome sequence of the wheat stem sawfly, Cephus cinctus, representing an early-branching lineage of the Hymenoptera, illuminates evolution of hymenopteran chemoreceptors. Genome Biology and Evolution, 2018, 10, 2997-3011.	2.5	24
20	Changes in the Peripheral Chemosensory System Drive Adaptive Shifts in Food Preferences in Insects. Frontiers in Cellular Neuroscience, 2018, 12, 281.	3.7	18
21	Whole Genome Sequence of the Parasitoid Wasp <i>Microplitis demolitor</i> That Harbors an Endogenous Virus Mutualist. G3: Genes, Genomes, Genetics, 2018, 8, 2875-2880.	1.8	33
22	A foreleg transcriptome for Ixodes scapularis ticks: Candidates for chemoreceptors and binding proteins that might be expressed in the sensory Haller's organ. Ticks and Tick-borne Diseases, 2018, 9, 1317-1327.	2.7	39
23	The origin of the odorant receptor gene family in insects. ELife, 2018, 7, .	6.0	103
24	Genomic features of the damselfly <i>Calopteryx splendens</i> representing a sister clade to most insect orders. Genome Biology and Evolution, 2017, 9, evx006.	2.5	53
25	Cytochrome P450 diversification and hostplant utilization patterns in specialist and generalist moths: Birth, death and adaptation. Molecular Ecology, 2017, 26, 6021-6035.	3.9	68
26	Comment on Que et al. 2016. Journal of Medical Entomology, 2017, 54, 1-2.	1.8	5
27	Noncanonical GA and GG 5′ Intron Donor Splice Sites Are Common in the Copepod Eurytemora affinis. G3: Genes, Genomes, Genetics, 2017, 7, 3967-3969.	1.8	8
28	Genome Sequencing of the Phytoseiid Predatory Mite <i>Metaseiulus occidentalis</i> Reveals Completely Atomized <i>Hox</i> Genes and Superdynamic Intron Evolution. Genome Biology and Evolution, 2016, 8, 1762-1775.	2.5	102
29	The whole genome sequence of the Mediterranean fruit fly, Ceratitis capitata (Wiedemann), reveals insights into the biology and adaptive evolution of a highly invasive pest species. Genome Biology, 2016, 17, 192.	8.8	130
30	Genome of the Asian longhorned beetle (Anoplophora glabripennis), a globally significant invasive species, reveals key functional and evolutionary innovations at the beetle–plant interface. Genome Biology, 2016, 17, 227.	8.8	244
31	Unique features of a global human ectoparasite identified through sequencing of the bed bug genome. Nature Communications, 2016, 7, 10165.	12.8	184
32	Genomic insights into the Ixodes scapularis tick vector of Lyme disease. Nature Communications, 2016, 7, 10507.	12.8	450
33	Positive selection in extra cellular domains in the diversification of Strigamia maritima chemoreceptors. Frontiers in Ecology and Evolution, 2015, 3, .	2.2	3
34	Genome of <i>Rhodnius prolixus</i> , an insect vector of Chagas disease, reveals unique adaptations to hematophagy and parasite infection. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 14936-14941.	7.1	329
35	A Massive Expansion of Effector Genes Underlies Gall-Formation in the Wheat Pest Mayetiola destructor. Current Biology, 2015, 25, 613-620.	3.9	171
36	The genomes of two key bumblebee species with primitive eusocial organization. Genome Biology, 2015, 16, 76.	8.8	330

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37	Genomic signatures of evolutionary transitions from solitary to group living. Science, 2015, 348, 1139-1143.	12.6	357
38	The Insect Chemoreceptor Superfamily Is Ancient in Animals. Chemical Senses, 2015, 40, 609-614.	2.0	75
39	Genome of the house fly, Musca domestica L., a global vector of diseases with adaptations to a septic environment. Genome Biology, 2014, 15, 466.	8.8	252
40	Odorant and Gustatory Receptors in the Tsetse Fly Glossina morsitans morsitans. PLoS Neglected Tropical Diseases, 2014, 8, e2663.	3.0	51
41	The First Myriapod Genome Sequence Reveals Conservative Arthropod Gene Content and Genome Organisation in the Centipede Strigamia maritima. PLoS Biology, 2014, 12, e1002005.	5.6	221
42	Sex- and tissue-specific profiles of chemosensory gene expression in a herbivorous gall-inducing fly (Diptera: Cecidomyiidae). BMC Genomics, 2014, 15, 501.	2.8	81
43	Finding the missing honey bee genes: lessons learned from a genome upgrade. BMC Genomics, 2014, 15, 86.	2.8	375
44	Molecular traces of alternative social organization in a termite genome. Nature Communications, 2014, 5, 3636.	12.8	371
45	Premetazoan genome evolution and the regulation of cell differentiation in the choanoflagellate Salpingoeca rosetta. Genome Biology, 2013, 14, R15.	9.6	219
46	Distribution of Genes and Repetitive Elements in the <i>Diabrotica virgifera virgifera</i> Genome Estimated Using BAC Sequencing. Journal of Biomedicine and Biotechnology, 2012, 2012, 1-9.	3.0	20
47	Sequencing and characterizing odorant receptors of the cerambycid beetle Megacyllene caryae. Insect Biochemistry and Molecular Biology, 2012, 42, 499-505.	2.7	124
48	Creating a Buzz About Insect Genomes. Science, 2011, 331, 1386-1386.	12.6	185
49	Odorant Binding Proteins of the Red Imported Fire Ant, Solenopsis invicta: An Example of the Problems Facing the Analysis of Widely Divergent Proteins. PLoS ONE, 2011, 6, e16289.	2.5	42
50	The Ecoresponsive Genome of <i>Daphnia pulex</i> . Science, 2011, 331, 555-561.	12.6	1,086
51	Draft genome of the globally widespread and invasive Argentine ant (<i>Linepithema humile</i>). Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 5673-5678.	7.1	257
52	Draft genome of the red harvester ant <i>Pogonomyrmex barbatus</i> . Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 5667-5672.	7.1	222
53	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
54	Functional and Evolutionary Insights from the Genomes of Three Parasitoid <i>Nasonia</i> Species. Science, 2010, 327, 343-348.	12.6	808

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55	Expressed Sequence Tags from Cephalic Chemosensory Organs of the Northern Walnut Husk Fly,Rhagoletis suavis, Including a Putative Canonical Odorant Receptor. Journal of Insect Science, 2010, 10, 1-11.	1.5	13
56	The Insect Chemoreceptor Superfamily in <i>Drosophila pseudoobscura</i> : Molecular Evolution of Ecologically-Relevant Genes Over 25 Million Years. Journal of Insect Science, 2009, 9, 1-14.	1.5	19
57	Simple Telomeres in a Simple Animal: Absence of Subtelomeric Repeat Regions in the Placozoan <i>Trichoplax adhaerens</i> . Genetics, 2009, 181, 323-325.	2.9	3
58	A Candidate Pheromone Receptor and Two Odorant Receptors of the Hawkmoth Manduca sexta. Chemical Senses, 2009, 34, 305-316.	2.0	53
59	Large Gene Family Expansions and Adaptive Evolution for Odorant and Gustatory Receptors in the Pea Aphid, Acyrthosiphon pisum. Molecular Biology and Evolution, 2009, 26, 2073-2086.	8.9	176
60	Evolution of the sugar receptors in insects. BMC Evolutionary Biology, 2009, 9, 41.	3.2	90
61	The chemoreceptor genes of the waterflea Daphnia pulex: many Grs but no Ors. BMC Evolutionary Biology, 2009, 9, 79.	3.2	107
62	The choanoflagellate Monosiga brevicollis karyotype revealed by the genome sequence: Telomere-linked helicase genes resemble those of some fungi. Chromosome Research, 2009, 17, 873-882.	2.2	4
63	Evolution of the Gene Lineage Encoding the Carbon Dioxide Receptor in Insects. Journal of Insect Science, 2009, 9, 1-14.	1.5	144
64	The Caenorhabditis chemoreceptor gene families. BMC Biology, 2008, 6, 42.	3.8	106
65	The red flour beetle's large nose: An expanded odorant receptor gene family in Tribolium castaneum. Insect Biochemistry and Molecular Biology, 2008, 38, 387-397.	2.7	225
66	The Gr Family of Candidate Gustatory and Olfactory Receptors in the Yellow-Fever Mosquito Aedes aegypti. Chemical Senses, 2008, 33, 79-93.	2.0	105
67	A honey bee odorant receptor for the queen substance 9-oxo-2-decenoic acid. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 14383-14388.	7.1	198
68	The Bursicon Gene in Mosquitoes: An Unusual Example of mRNA Trans-splicing. Genetics, 2007, 176, 1351-1353.	2.9	40
69	Manual superscaffolding of honey bee (Apis mellifera) chromosomes 12?16: implications for the draft genome assembly version 4, gene annotation, and chromosome structure. Insect Molecular Biology, 2007, 16, 401-410.	2.0	10
70	Molecular and phylogenetic analyses reveal mammalian-like clockwork in the honey bee (Apis) Tj ETQq0 0 0 rgl 2006, 16, 1352-1365.	3T /Overlocl 5.5	k 10 Tf 50 14 223
71	Canonical TTAGG-repeat telomeres and telomerase in the honey bee, Apis mellifera. Genome Research, 2006, 16, 1345-1351.	5.5	47
	The chemoreceptor superfamily in the honey bee. <i>Apis mellifera</i> : Expansion of the odorant, but		

72The chemoreceptor superfamily in the honey bee, <i>Apis mellifera</i>Expansion of the odorant, but5.551272not gustatory, receptor family. Genome Research, 2006, 16, 1395-1403.5.5512

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73	The putative chemoreceptor families of C. elegans. WormBook, 2006, , 1-12.	5.3	100
74	Insect Genomes. American Entomologist, 2005, 51, 166-173.	0.2	12
75	Pteropsin: A vertebrate-like non-visual opsin expressed in the honey bee brain. Insect Biochemistry and Molecular Biology, 2005, 35, 1367-1377.	2.7	138
76	Adaptive evolution in the SRZ chemoreceptor families of Caenorhabditis elegans and Caenorhabditis briggsae. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 4476-4481.	7.1	76
77	Genes Encoding Vitamin-K Epoxide Reductase Are Present in Drosophila and Trypanosomatid Protists. Genetics, 2004, 168, 1077-1080.	2.9	29
78	Neutral Evolution of Ten Types of mariner Transposons in the Genomes of Caenorhabditis elegans and Caenorhabditis briggsae. Journal of Molecular Evolution, 2003, 56, 751-769.	1.8	44
79	Recent Horizontal Transfer of Mellifera Subfamily Mariner Transposons into Insect Lineages Representing Four Different Orders Shows that Selection Acts Only During Horizontal Transfer. Molecular Biology and Evolution, 2003, 20, 554-562.	8.9	95
80	Molecular evolution of the insect chemoreceptor gene superfamily in Drosophila melanogaster. Proceedings of the National Academy of Sciences of the United States of America, 2003, 100, 14537-14542.	7.1	703
81	Annotated Expressed Sequence Tags and cDNA Microarrays for Studies of Brain and Behavior in the Honey Bee. Genome Research, 2002, 12, 555-566.	5.5	253
82	G Protein-Coupled Receptors inAnopheles gambiae. Science, 2002, 298, 176-178.	12.6	630
83	The mariner Transposons of Animals. , 2002, , 173-185.		11
84	Loss of Transposase-DNA Interaction May Underlie the Divergence of mariner Family Transposable Elements and the Ability of More than One mariner to Occupy the Same Genome. Molecular Biology and Evolution, 2001, 18, 954-961.	8.9	67
85	Taste: Independent origins of chemoreception coding systems?. Current Biology, 2001, 11, R560-R562.	3.9	12
86	Localization of mariner DNA Transposons in the Human Genome by PRINS. Genome Research, 1999, 9, 839-843.	5.5	29
87	Two Large Families of Chemoreceptor Genes in the Nematodes <i>Caenorhabditis elegans</i> and <i>Caenorhabditis briggsae</i> Reveal Extensive Gene Duplication, Diversification, Movement, and Intron Loss. Genome Research, 1998, 8, 449-463.	5.5	164
88	Factors Affecting Transposition of the Himar1 mariner Transposon in Vitro. Genetics, 1998, 149, 179-187.	2.9	207
89	Molecular evolution of the second ancient human mariner transposon, Hsmar2, illustrates patterns of neutral evolution in the human genome lineage. Gene, 1997, 205, 219-228.	2.2	70
90	Molecular evolution of an ancient mariner transposon, Hsmarl, in the human genome. Gene, 1997, 205, 203-217.	2.2	114

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91	Bmmarl: a basal lineage of the mariner family of transposable elements in the silkworm moth, Bombyx mori. Insect Biochemistry and Molecular Biology, 1996, 26, 945-954.	2.7	98
92	The genomes of most animals have multiple members of the Tc1 family of transposable elements. Genetica, 1996, 98, 131-140.	1.1	41
93	Reconstructing the ancient mariners of humans. Nature Genetics, 1996, 12, 360-361.	21.4	38
94	The Tcl-mariner superfamily of transposons in animals. Journal of Insect Physiology, 1995, 41, 99-105.	2.0	166
95	The mariner transposable element is widespread in insects. Nature, 1993, 362, 241-245.	27.8	402
96	Infiltration of mariner elements. Nature, 1993, 364, 109-110.	27.8	35
97	Amarinertransposable element from a lacewing. Nucleic Acids Research, 1992, 20, 6409-6409.	14.5	27