

# Elisabeth Anne Herniou

## List of Publications by Year in descending order

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73  
papers

5,958  
citations

94433

37  
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85541

71  
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79  
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79  
docs citations

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times ranked

4281  
citing authors

#	ARTICLE	IF	CITATIONS
1	Virulence and genetic characterization of six baculovirus strains isolated from different populations of <i>Spodoptera frugiperda</i> (Lepidoptera: Noctuidae). <i>Archives of Microbiology</i> , 2022, 204, 108.	2.2	5
2	Transposable element repression using piRNAs, and its relevance to endogenous viral elements (EVEs) and immunity in insects. <i>Current Opinion in Insect Science</i> , 2022, 50, 100876.	4.4	3
3	First Evidence of Past and Present Interactions between Viruses and the Black Soldier Fly, <i>Hermetia illucens</i> . <i>Viruses</i> , 2022, 14, 1274.	3.3	5
4	Monitoring Insect Transposable Elements in Large Double-Stranded DNA Viruses Reveals Host-to-Virus and Virus-to-Virus Transposition. <i>Molecular Biology and Evolution</i> , 2021, 38, 3512-3530.	8.9	8
5	Chromosomal scale assembly of parasitic wasp genome reveals symbiotic virus colonization. <i>Communications Biology</i> , 2021, 4, 104.	4.4	27
6	Occurrence and Molecular Phylogeny of Honey Bee Viruses in Vespids. <i>Viruses</i> , 2020, 12, 6.	3.3	27
7	Wide spectrum and high frequency of genomic structural variation, including transposable elements, in large double-stranded DNA viruses. <i>Virus Evolution</i> , 2020, 6, vez060.	4.9	24
8	ICTV Virus Taxonomy Profile: Nudiviridae. <i>Journal of General Virology</i> , 2020, 101, 3-4.	2.9	19
9	Viruses in the Invasive Hornet <i>Vespa velutina</i> . <i>Viruses</i> , 2019, 11, 1041.	3.3	39
10	Relative Influence of Host, <i>Wolbachia</i> , Geography and Climate on the Genetic Structure of the Sub-saharan Parasitic Wasp <i>Cotesia sesamiae</i> . <i>Frontiers in Ecology and Evolution</i> , 2019, 7, .	2.2	7
11	Genetic footprints of adaptive divergence in the bracovirus of <i>Cotesia sesamiae</i> identified by targeted resequencing. <i>Molecular Ecology</i> , 2018, 27, 2109-2123.	3.9	23
12	The recurrent domestication of viruses: major evolutionary transitions in parasitic wasps. <i>Parasitology</i> , 2018, 145, 713-723.	1.5	45
13	The Domestication of a Large DNA Virus by the Wasp <i>Venturia canescens</i> Involves Targeted Genome Reduction through Pseudogenization. <i>Genome Biology and Evolution</i> , 2018, 10, 1745-1764.	2.5	28
14	Biodiversity, Evolution and Ecological Specialization of Baculoviruses: A Treasure Trove for Future Applied Research. <i>Viruses</i> , 2018, 10, 366.	3.3	33
15	Discovery of <i>Culex pipiens</i> associated tunisia virus: a new ssRNA(+) virus representing a new insect associated virus family. <i>Virus Evolution</i> , 2018, 4, vex040.	4.9	17
16	ICTV Virus Taxonomy Profile: Baculoviridae. <i>Journal of General Virology</i> , 2018, 99, 1185-1186.	2.9	101
17	The <i>Cotesia sesamiae</i> story: insight into host-range evolution in a Hymenoptera parasitoid and implication for its use in biological control programs. <i>Genetica</i> , 2017, 145, 455-468.	1.1	28
18	Endogenous viruses of parasitic wasps: variations on a common theme. <i>Current Opinion in Virology</i> , 2017, 25, 41-48.	5.4	70

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19	Foreign DNA acquisition by invertebrate genomes. <i>Journal of Invertebrate Pathology</i> , 2017, 147, 157-168.	3.2	32
20	Systematics and biology of <i>Cotesia typhae</i> sp. n. (Hymenoptera, Braconidae, Microgasterinae), a potential biological control agent against the noctuid Mediterranean corn borer, <i>Sesamia nonagrioides</i> . <i>ZooKeys</i> , 2017, 682, 105-136.	1.1	37
21	Impact of Lateral Transfers on the Genomes of Lepidoptera. <i>Genes</i> , 2017, 8, 315.	2.4	18
22	Qualitative proteomic analysis of <i>Tipula oleracea</i> nudivirus occlusion bodies. <i>Journal of General Virology</i> , 2017, 98, 284-295.	2.9	10
23	The discovery of Halictivirus resolves the Sinaivirus phylogeny. <i>Journal of General Virology</i> , 2017, 98, 2864-2875.	2.9	31
24	Continuous Influx of Genetic Material from Host to Virus Populations. <i>PLoS Genetics</i> , 2016, 12, e1005838.	3.5	63
25	Ultra Deep Sequencing of a Baculovirus Population Reveals Widespread Genomic Variations. <i>Viruses</i> , 2015, 7, 3625-3646.	3.3	57
26	Ongoing ecological speciation in <i>Cotesia sesamiae</i> , a biological control agent of cereal stem borers. <i>Evolutionary Applications</i> , 2015, 8, 807-820.	3.1	36
27	The Genome of the Nucleopolyhedrosis-Causing Virus from <i>Tipula oleracea</i> Sheds New Light on the Nudiviridae Family. <i>Journal of Virology</i> , 2015, 89, 3008-3025.	3.4	49
28	The systematics of <i>Echinorhynchus</i> Zoega in MÅller, 1776 (Acanthocephala, Echinorhynchidae) elucidated by nuclear and mitochondrial sequence data from eight European taxa. <i>ZooKeys</i> , 2015, 484, 25-52.	1.1	24
29	Gene Acquisition Convergence between Entomopoxviruses and Baculoviruses. <i>Viruses</i> , 2015, 7, 1960-1974.	3.3	41
30	Genomic and Proteomic Analyses Indicate that Banchine and Campoplegine Polydnviruses Have Similar, if Not Identical, Viral Ancestors. <i>Journal of Virology</i> , 2015, 89, 8909-8921.	3.4	49
31	Genomic diversity in European <i>Spodoptera exigua</i> multiple nucleopolyhedrovirus isolates. <i>Journal of General Virology</i> , 2014, 95, 2297-2309.	2.9	29
32	Population genomics supports baculoviruses as vectors of horizontal transfer of insect transposons. <i>Nature Communications</i> , 2014, 5, 3348.	12.8	97
33	When parasitic wasps hijacked viruses: genomic and functional evolution of polydnviruses. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2013, 368, 20130051.	4.0	150
34	Functional endogenous viral elements in the genome of the parasitoid wasp <i>Cotesia congregata</i> : insights into the evolutionary dynamics of bracoviruses. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2013, 368, 20130047.	4.0	68
35	New Insights into the Evolution of Entomopoxvirinae from the Complete Genome Sequences of Four Entomopoxviruses Infecting <i>Adoxophyes honmai</i> , <i>Choristoneura biennis</i> , <i>Choristoneura rosaceana</i> , and <i>Mythimna separata</i> . <i>Journal of Virology</i> , 2013, 87, 7992-8003.	3.4	43
36	Adaptive Selection on Bracovirus Genomes Drives the Specialization of <i>Cotesia</i> Parasitoid Wasps. <i>PLoS ONE</i> , 2013, 8, e64432.	2.5	54

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37	Multiple functionally divergent and conserved copies of alpha tubulin in bdelloid rotifers. <i>BMC Evolutionary Biology</i> , 2012, 12, 148.	3.2	13
38	Evolutionary Progenitors of Bracoviruses. , 2012, , 15-31.		13
39	Paleozoic origin of insect large dsDNA viruses. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 15931-15935.	7.1	136
40	Extreme levels of hidden diversity in microscopic animals (Rotifera) revealed by DNA taxonomy. <i>Molecular Phylogenetics and Evolution</i> , 2009, 53, 182-189.	2.7	160
41	A faunistic survey of bdelloid rotifers in Turkey. <i>Zoology in the Middle East</i> , 2009, 48, 114-116.	0.6	8
42	Inconsistent estimates of diversity between traditional and DNA taxonomy in bdelloid rotifers. <i>Organisms Diversity and Evolution</i> , 2009, 9, 3-12.	1.6	23
43	Molecular evidence for broad-scale distributions in bdelloid rotifers: everything is not everywhere but most things are very widespread. <i>Molecular Ecology</i> , 2008, 17, 3136-3146.	3.9	103
44	Independently Evolving Species in Asexual Bdelloid Rotifers. <i>PLoS Biology</i> , 2007, 5, e87.	5.6	311
45	Baculovirus Phylogeny and Evolution. <i>Current Drug Targets</i> , 2007, 8, 1043-1050.	2.1	110
46	Evidence for Inefficient Selection Against Deleterious Mutations in Cytochrome Oxidase I of Asexual Bdelloid Rotifers. <i>Molecular Biology and Evolution</i> , 2007, 24, 1952-1962.	8.9	64
47	On the reality and recognisability of asexual organisms: morphological analysis of the masticatory apparatus of bdelloid rotifers. <i>Zoologica Scripta</i> , 2007, 36, 361-370.	1.7	22
48	On the classification and nomenclature of baculoviruses: A proposal for revision. <i>Archives of Virology</i> , 2006, 151, 1257-1266.	2.1	481
49	Genomic comparison of <i>Neodiprion sertifer</i> and <i>Neodiprion lecontei</i> nucleopolyhedroviruses and identification of potential hymenopteran baculovirus-specific open reading frames. <i>Journal of General Virology</i> , 2006, 87, 1477-1489.	2.9	33
50	Genome sequence of <i>Chrysodeixis chalcites</i> nucleopolyhedrovirus, a baculovirus with two DNA photolyase genes. <i>Journal of General Virology</i> , 2005, 86, 2069-2080.	2.9	73
51	Identification and characterization of a DNA photolyase-containing baculovirus from <i>Chrysodeixis chalcites</i> . <i>Virology</i> , 2004, 330, 460-470.	2.4	39
52	Ancient Coevolution of Baculoviruses and Their Insect Hosts. <i>Journal of Virology</i> , 2004, 78, 3244-3251.	3.4	144
53	Why do species exist? Insights from sexuals and asexuals. <i>Zoology</i> , 2003, 106, 275-282.	1.2	14
54	Phylogenetic relationships of <i>Echinostoma Rudolphi</i> , 1809 (Digenea: Echinostomatidae) and related genera re-assessed via DNA and morphological analyses. <i>Systematic Parasitology</i> , 2003, 54, 159-176.	1.1	115

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55	The Interrelationships of the Gastrotricha Using Nuclear Small rRNA Subunit Sequence Data, with an Interpretation Based on Morphology. <i>Zoologischer Anzeiger</i> , 2003, 242, 145-156.	0.9	50
56	THE GENOME SEQUENCE AND EVOLUTION OF BACULOVIRUSES. <i>Annual Review of Entomology</i> , 2003, 48, 211-234.	11.8	402
57	Characterization and Complete Nucleotide Sequence of an Unusual Reptilian Retrovirus Recovered from the Order Crocodylia. <i>Journal of Virology</i> , 2002, 76, 4651-4654.	3.4	14
58	Whole genome analysis of the <i>Epiphyas postvittana</i> nucleopolyhedrovirus. <i>Journal of General Virology</i> , 2002, 83, 957-971.	2.9	88
59	The evolutionary nature of diversification in sexuals and asexuals. , 2001, , 29-45.		6
60	Elongation Factor 1-Alpha Sequences Alone Do Not Assist in Resolving the Position of the Acoela Within the Metazoa. <i>Molecular Biology and Evolution</i> , 2001, 18, 437-442.	8.9	56
61	Use of Whole Genome Sequence Data To Infer Baculovirus Phylogeny. <i>Journal of Virology</i> , 2001, 75, 8117-8126.	3.4	294
62	Phylogenies Inferred from Mitochondrial Gene Orders – A Cautionary Tale from the Parasitic Flatworms. <i>Molecular Biology and Evolution</i> , 2000, 17, 1123-1125.	8.9	187
63	The Interrelationships of Proseriata (Platyhelminthes: Seriata) Tested with Molecules and Morphology. <i>Molecular Phylogenetics and Evolution</i> , 2000, 16, 449-466.	2.7	346
64	Changes in mitochondrial genetic codes as phylogenetic characters: Two examples from the flatworms. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2000, 97, 11359-11364.	7.1	223
65	Phylogeny of the Platyhelminthes and the evolution of parasitism. <i>Biological Journal of the Linnean Society</i> , 1999, 68, 257-287.	1.6	95
66	Identification of Multiple Gypsy LTR-Retrotransposon Lineages in Vertebrate Genomes. <i>Journal of Molecular Evolution</i> , 1999, 49, 358-366.	1.8	48
67	Acoel Flatworms: Earliest Extant Bilaterian Metazoans, Not Members of Platyhelminthes. <i>Science</i> , 1999, 283, 1919-1923.	12.6	427
68	Interclass Transmission and Phyletic Host Tracking in Murine Leukemia Virus-Related Retroviruses. <i>Journal of Virology</i> , 1999, 73, 2442-2449.	3.4	106
69	Vintage Helminths Yield Valuable Molecules. <i>Parasitology Today</i> , 1998, 14, 289-292.	3.0	14
70	A phylogenetic reconstruction of the Ichneumonoidea (Hymenoptera) based on the D2 variable region of 28S ribosomal RNA. <i>Systematic Entomology</i> , 1998, 23, 109-123.	3.9	124
71	Retroviral Diversity and Distribution in Vertebrates. <i>Journal of Virology</i> , 1998, 72, 5955-5966.	3.4	172
72	Three retroviral sequences in amphibians are distinct from those in mammals and birds. <i>Journal of Virology</i> , 1996, 70, 4864-4870.	3.4	21

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73	Easel, a gypsy LTR-retrotransposon in the Salmonidae. <i>Molecular Genetics and Genomics</i> , 1995, 249, 229-236.	2.4	19