Nadia A Ayoub

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Impacts of the Cretaceous Terrestrial Revolution and KPg Extinction on Mammal Diversification. Science, 2011, 334, 521-524.	6.0	1,264
2	Blueprint for a High-Performance Biomaterial: Full-Length Spider Dragline Silk Genes. PLoS ONE, 2007, 2, e514.	1.1	336
3	The house spider genome reveals an ancient whole-genome duplication during arachnid evolution. BMC Biology, 2017, 15, 62.	1.7	286
4	Insight into the routes of <i>Wolbachia</i> invasion: high levels of horizontal transfer in the spider genus <i>Agelenopsis</i> revealed by <i>Wolbachia</i> strain and mitochondrial DNA diversity. Molecular Ecology, 2008, 17, 557-569.	2.0	154
5	Gene content evolution in the arthropods. Genome Biology, 2020, 21, 15.	3.8	150
6	Untangling spider silk evolution with spidroin terminal domains. BMC Evolutionary Biology, 2010, 10, 243.	3.2	135
7	Dramatic expansion of the black widow toxin arsenal uncovered by multi-tissue transcriptomics and venom proteomics. BMC Genomics, 2014, 15, 366.	1.2	93
8	Utility of the nuclear protein-coding gene, elongation factor-1 gamma (EF-1γ), for spider systematics, emphasizing family level relationships of tarantulas and their kin (Araneae: Mygalomorphae). Molecular Phylogenetics and Evolution, 2007, 42, 394-409.	1.2	76
9	Ancient Properties of Spider Silks Revealed by the Complete Gene Sequence of the Prey-Wrapping Silk Protein (AcSp1). Molecular Biology and Evolution, 2013, 30, 589-601.	3.5	76
10	Spider Transcriptomes Identify Ancient Large-Scale Gene Duplication Event Potentially Important in Silk Gland Evolution. Genome Biology and Evolution, 2015, 7, 1856-1870.	1.1	74
11	Multi-tissue transcriptomics of the black widow spider reveals expansions, co-options, and functional processes of the silk gland gene toolkit. BMC Genomics, 2014, 15, 365.	1.2	70
12	Molecular evidence for Pleistocene glacial cycles driving diversification of a North American desert spider, Agelenopsis aperta. Molecular Ecology, 2004, 13, 3453-3465.	2.0	62
13	Multiple Recombining Loci Encode MaSp1, the Primary Constituent of Dragline Silk, in Widow Spiders (Latrodectus: Theridiidae). Molecular Biology and Evolution, 2008, 25, 277-286.	3.5	60
14	Genomic perspectives of spider silk genes through target capture sequencing: Conservation of stabilization mechanisms and homology-based structural models of spidroin terminal regions. International Journal of Biological Macromolecules, 2018, 113, 829-840.	3.6	57
15	Evidence from Multiple Species that Spider Silk Glue Component ASG2 is a Spidroin. Scientific Reports, 2016, 6, 21589.	1.6	54
16	Effects of Gene Duplication, Positive Selection, and Shifts in Gene Expression on the Evolution of the Venom Gland Transcriptome in Widow Spiders. Genome Biology and Evolution, 2016, 8, 228-242.	1.1	54
17	Proteomic Evidence for Components of Spider Silk Synthesis from Black Widow Silk Glands and Fibers. Journal of Proteome Research, 2015, 14, 4223-4231.	1.8	53
18	Intragenic homogenization and multiple copies of prey-wrapping silk genes in Argiope garden spiders. BMC Evolutionary Biology, 2014, 14, 31.	3.2	46

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19	Recent progress and prospects for advancing arachnid genomics. Current Opinion in Insect Science, 2018, 25, 51-57.	2.2	44
20	Duplication and concerted evolution of MiSp-encoding genes underlie the material properties of minor ampullate silks of cobweb weaving spiders. BMC Evolutionary Biology, 2017, 17, 78.	3.2	33
21	Evolutionary shifts in gene expression decoupled from gene duplication across functionally distinct spider silk glands. Scientific Reports, 2017, 7, 8393.	1.6	26
22	Complex gene expression in the dragline silk producing glands of the Western black widow (Latrodectus hesperus). BMC Genomics, 2013, 14, 846.	1.2	25
23	Speciation history of the North American funnel web spiders, Agelenopsis (Araneae: Agelenidae): Phylogenetic inferences at the population–species interface. Molecular Phylogenetics and Evolution, 2005, 36, 42-57.	1.2	22
24	Silk gene transcripts in the developing tubuliform glands of the Western black widow, Latrodectus hesperus. Journal of Arachnology, 2010, 38, 99-103.	0.3	22
25	Silk gene expression of theridiid spiders: implications for male-specific silk use. Zoology, 2017, 122, 107-114.	0.6	20
26	Evolution and phylogenetic utility of the melanocortin-1 receptor gene (MC1R) in Cetartiodactyla. Molecular Phylogenetics and Evolution, 2009, 52, 550-557.	1.2	18
27	Chromosome Mapping of Dragline Silk Genes in the Genomes of Widow Spiders (Araneae, Theridiidae). PLoS ONE, 2010, 5, e12804.	1.1	17
28	Gene structure, regulatory control, and evolution of black widow venom latrotoxins. FEBS Letters, 2014, 588, 3891-3897.	1.3	16
29	Hemocyanin gene family evolution in spiders (Araneae), with implications for phylogenetic relationships and divergence times in the infraorder Mygalomorphae. Gene, 2013, 524, 175-186.	1.0	14
30	Protein composition and associated material properties of cobweb spiders' gumfoot glue droplets. Integrative and Comparative Biology, 2021, 61, 1459-1480.	0.9	10
31	Gene expression profiling reveals candidate genes for defining spider silk gland types. Insect Biochemistry and Molecular Biology, 2021, 135, 103594.	1.2	9
32	The evolutionary history of cribellate orb-weaver capture thread spidroins. Bmc Ecology and Evolution, 2022, 22, .	0.7	6
33	Locomotor activity patterns in three spider species suggest relaxed selection on endogenous circadian period and novel features of chronotype. Journal of Comparative Physiology A: Neuroethology, Sensory, Neural, and Behavioral Physiology, 2020, 206, 499-515.	0.7	3
34	The common house spider, Parasteatoda tepidariorum, maintains silk gene expression on sub-optimal diet. PLoS ONE, 2020, 15, e0237286.	1.1	2
35	Ovarian Transcriptomic Analyses in the Urban Human Health Pest, the Western Black Widow Spider. Genes, 2020, 11, 87.	1.0	1

#	Article	IF	CITATIONS
37	Title is missing!. , 2020, 15, e0237286.		0
38	Title is missing!. , 2020, 15, e0237286.		0
39	Title is missing!. , 2020, 15, e0237286.		0