

Nick V Grishin

List of Publications by Year in descending order

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Version: 2024-02-01

77
papers

7,131
citations

346980

22
h-index

120465

65
g-index

112
all docs

112
docs citations

112
times ranked

10579
citing authors

#	ARTICLE	IF	CITATIONS
1	Molecular analysis of primary testicular germ cell tumor and matched metastatic teratomas.. Journal of Clinical Oncology, 2022, 40, 425-425.	0.8	0
2	Genomics-based higher classification of the species-rich hairstreaks (Lepidoptera: Lycaenidae: Eumaeini). Systematic Entomology, 2022, 47, 445-469.	1.7	5
3	Gauging ages of tiger swallowtail butterflies using alternate SNP analyses. Molecular Phylogenetics and Evolution, 2022, 171, 107465.	1.2	2
4	Taxonomic changes suggested by the genomic analysis of Hesperiiidae (Lepidoptera).. , 2022, 2022, .		1
5	Genomic DNA sequencing reveals two new North American species of (Hesperiiidae: Pyrginae:) Tj ETQq1 1 0.784314 rgBT /Overlock 107	2.0	0
6	Checking the checked taxonomy of Plötz's checkered skippers (Hesperiiidae: Pyrgini).. The Taxonomic Report of the International Lepidoptera Survey, 2022, 10, .	2.0	0
7	Overlooked cryptic diversity in <i>Muschampia</i> (Lepidoptera: Hesperiiidae) adds two species to the European butterfly fauna. Zoological Journal of the Linnean Society, 2021, 193, 847-859.	1.0	9
8	A Fifth of the Protein World: Rossmann-like Proteins as an Evolutionarily Successful Structural unit. Journal of Molecular Biology, 2021, 433, 166788.	2.0	26
9	A switch to feeding on cycads generates parallel accelerated evolution of toxin tolerance in two clades of <i>Eumaeus</i> caterpillars (Lepidoptera: Lycaenidae). Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	3.3	7
10	A DNA barcode library for the butterflies of North America. PeerJ, 2021, 9, e11157.	0.9	14
11	The DBSAV Database: Predicting Deleteriousness of Single Amino Acid Variations in the Human Proteome. Journal of Molecular Biology, 2021, 433, 166915.	2.0	15
12	Accurate prediction of protein structures and interactions using a three-track neural network. Science, 2021, 373, 871-876.	6.0	2,843
13	Influence of the large-effect during contact between butterfly sister species. Ecology and Evolution, 2021, 11, 11615-11626.	0.8	0
14	Comment (Case 3709) – Additional comments on the proposed conservation of names for western North American <i>Hesperia</i> comma-group subspecies through designation of neotypes. Bulletin of Zoological Nomenclature, 2021, 78, .	0.2	1
15	Genomics Reveals the Origins of Historical Specimens. Molecular Biology and Evolution, 2021, 38, 2166-2176.	3.5	24
16	Orange fringes, crenulate hindwings and genomic DNA identify a new species of from Honduras (Hesperiiidae: Pyrrhopyginae). Tropical Lepidoptera Research, 2021, 31, 48-52.	0.0	0
17	A uniquely patterned new species of from Honduras (Riodinidae). Tropical Lepidoptera Research, 2021, 31, 53-59.	0.0	0
18	Two new species of from North America and three neotype designations (Nymphalidae: Satyrinae). The Taxonomic Report of the International Lepidoptera Survey, 2021, 9, .	2.0	1

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19	Genomics-guided refinement of butterfly taxonomy.. The Taxonomic Report of the International Lepidoptera Survey, 2021, 9, .	2.0	8
20	Recognition of nuclear export signals by CRM1 carrying the oncogenic E571K mutation. Molecular Biology of the Cell, 2020, 31, 1879-1891.	0.9	22
21	Mutation severity spectrum of rare alleles in the human genome is predictive of disease type. PLoS Computational Biology, 2020, 16, e1007775.	1.5	11
22	The mitogenome of a Malagasy butterfly <i>Malaza fastuosus</i> (Mabille, 1884) recovered from the holotype collected over 140 years ago adds support for a new subfamily of HesperIIDae (Lepidoptera). Genome, 2020, 63, 195-202.	0.9	11
23	Speciation in North American <i>Junonia</i> from a genomic perspective. Systematic Entomology, 2020, 45, 803-837.	1.7	11
24	Genomic evidence suggests further changes of butterfly names.. The Taxonomic Report of the International Lepidoptera Survey, 2020, 8, .	2.0	2
25	Assessing predictions on fitness effects of missense variants in calmodulin. Human Mutation, 2019, 40, 1463-1473.	1.1	8
26	Genomic analysis of the tribe Emesidini (Lepidoptera: Riodinidae). Zootaxa, 2019, 4668, zootaxa.4668.4.2.	0.2	10
27	ECOD: identification of distant homology among multidomain and transmembrane domain proteins. BMC Molecular and Cell Biology, 2019, 20, 18.	1.0	12
28	Genomes reveal drastic and recurrent phenotypic divergence in firetip skipper butterflies (HesperIIDae: <i>Tj ETQq0 0 0 rgBT /Overlock 10</i>)	1.25	31
29	Genomes of skipper butterflies reveal extensive convergence of wing patterns. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 6232-6237.	3.3	86
30	Identification of residues critical for topology inversion of the transmembrane protein TM4SF20 through regulated alternative translocation. Journal of Biological Chemistry, 2019, 294, 6054-6061.	1.6	5
31	Gypsy moth genome provides insights into flight capability and virus-host interactions. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 1669-1678.	3.3	30
32	The Bear Giant-Skipper genome suggests genetic adaptations to living inside yucca roots. Molecular Genetics and Genomics, 2019, 294, 211-226.	1.0	10
33	NK cell defects in X-linked pigmentary reticulate disorder. JCI Insight, 2019, 4, .	2.3	17
34	Three new subfamilies of skipper butterflies (Lepidoptera, HesperIIDae). ZooKeys, 2019, 861, 91-105.	0.5	29
35	Comment (Case 3709) – More comments on the proposed conservation of names for western North American <i>Hesperia comma</i> -group subspecies through designation of neotypes. Bulletin of Zoological Nomenclature, 2019, 76, 57.	0.2	2
36	Monotypy Justified: Genitalia and DNA Move <i>Ephyriades eugramma</i> (Mabille) to New Genus <i>Neomorphuncus</i> Burns (Lepidoptera: HesperIIDae: Pyrginae). Proceedings of the Entomological Society of Washington, 2019, 121, 557.	0.0	0

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37	Changes to North American butterfly names. The Taxonomic Report of the International Lepidoptera Survey, 2019, 8, 1-12.	2.0	4
38	Fifty new genera of HesperIIDae (Lepidoptera).. , 2019, 2019, .		5
39	Comparative analysis of swallowtail transcriptomes suggests molecular determinants for speciation and adaptation. Genome, 2018, 61, 843-855.	0.9	2
40	When COI barcodes deceive: complete genomes reveal introgression in hairstreaks. Proceedings of the Royal Society B: Biological Sciences, 2017, 284, 20161735.	1.2	39
41	Acute Hepatopancreatic Necrosis Disease-Causing <i>Vibrio parahaemolyticus</i> Strains Maintain an Antibacterial Type VI Secretion System with Versatile Effector Repertoires. Applied and Environmental Microbiology, 2017, 83, .	1.4	88
42	Assessing predictions of fitness effects of missense mutations in SUMOâ€conjugating enzyme UBE2I. Human Mutation, 2017, 38, 1051-1063.	1.1	12
43	Nuclear genomes distinguish cryptic species suggested by their DNA barcodes and ecology. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, 8313-8318.	3.3	89
44	The complete mitogenome of <i>Euschemon rafflesia</i> (Lepidoptera: HesperIIDae). Mitochondrial DNA Part B: Resources, 2017, 2, 136-138.	0.2	17
45	The first complete genomes of Metalmarks and the classification of butterfly families. Genomics, 2017, 109, 485-493.	1.3	20
46	The complete mitochondrial genome of a skipper <i>Burara striata</i> (Lepidoptera: HesperIIDae). Mitochondrial DNA Part B: Resources, 2017, 2, 145-147.	0.2	8
47	Mitogenomes of the four <i>Agathymus</i> holotypes collected 55 years ago. Mitochondrial DNA Part B: Resources, 2017, 2, 598-600.	0.2	1
48	Mitogenomes of Giant-Skipper Butterflies reveal an ancient split between deep and shallow root feeders. F1000Research, 2017, 6, 222.	0.8	14
49	Complete Genome of <i>Achalarus lyciades</i> , The First Representative of the Eudaminae Subfamily of Skippers. Current Genomics, 2017, 18, 366-374.	0.7	22
50	Relief of autoinhibition by conformational switch explains enzyme activation by a catalytically dead paralog. ELife, 2016, 5, .	2.8	19
51	Complete genomes of Hairstreak butterflies, their speciation and nucleo-mitochondrial incongruence. Scientific Reports, 2016, 6, 24863.	1.6	44
52	The complete mitogenome of <i>Achalarus lyciades</i> (Lepidoptera: HesperIIDae). Mitochondrial DNA Part B: Resources, 2016, 1, 581-583.	0.2	14
53	The <i>Penaincisalia amatista</i> species-group (Lepidoptera: Lycaenidae, Eumaeini) in Colombia, insights from mtDNA barcodes and the description of a new species. Systematics and Biodiversity, 2016, 14, 171-183.	0.5	6
54	Speciation in Cloudless Sulphurs Gleaned from Complete Genomes. Genome Biology and Evolution, 2016, 8, 915-931.	1.1	40

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55	Complete genome of <i>Pieris rapae</i> , a resilient alien, a cabbage pest, and a source of anti-cancer proteins. <i>F1000Research</i> , 2016, 5, 2631.	0.8	47
56	The complete mitochondrial genome of <i>Lerema accius</i> and its phylogenetic implications. <i>PeerJ</i> , 2016, 4, e1546.	0.9	20
57	A new species of <i>Oeneis</i> from Alaska, United States, with notes on the <i>Oeneis chryxus</i> complex (Lepidoptera: Nymphalidae: Satyrinae). <i>The Journal of Research on the Lepidoptera</i> , 2016, 49, 1-20.	0.1	1
58	Review of the West Indian <i>Astraptus xagua</i> (Lucas) complex (Hesperiidae: Eudaminae) with the description of a new subspecies from the Bahamas. <i>The Journal of Research on the Lepidoptera</i> , 2016, 49, 81-90.	0.1	1
59	Tiger Swallowtail Genome Reveals Mechanisms for Speciation and Caterpillar Chemical Defense. <i>Cell Reports</i> , 2015, 10, 910-919.	2.9	77
60	The cytoplasmic domain of the gamete membrane fusion protein HAP2 targets the protein to the fusion site in <i>Chlamydomonas</i> and regulates the fusion reaction. <i>Development (Cambridge)</i> , 2015, 142, 962-71.	1.2	35
61	Phosphorylation of innate immune adaptor proteins MAVS, STING, and TRIF induces IRF3 activation. <i>Science</i> , 2015, 347, aaa2630.	6.0	1,280
62	A Single Kinase Generates the Majority of the Secreted Phosphoproteome. <i>Cell</i> , 2015, 161, 1619-1632.	13.5	264
63	The complete mitochondrial genome of <i>Papilio glaucus</i> and its phylogenetic implications. <i>Meta Gene</i> , 2015, 5, 68-83.	0.3	20
64	Skipper genome sheds light on unique phenotypic traits and phylogeny. <i>BMC Genomics</i> , 2015, 16, 639.	1.2	38
65	A cryptic new <i>Potamanaxas</i> (Hesperiidae: Pyrginae: Erynnini) stands out by terminally elongated genitalic valvae. <i>The Journal of Research on the Lepidoptera</i> , 2015, 48, 13-20.	0.1	1
66	ECOD: An Evolutionary Classification of Protein Domains. <i>PLoS Computational Biology</i> , 2014, 10, e1003926.	1.5	321
67	A new <i>Hermeuptychia</i> (Lepidoptera, Nymphalidae, Satyrinae) is sympatric and synchronic with <i>H. asosybius</i> in southeast US coastal plains, while another new <i>Hermeuptychia</i> species "not hermes" inhabits south Texas and northeast Mexico. <i>ZooKeys</i> , 2014, 379, 43-91.	0.5	19
68	A new <i>Heraclides</i> swallowtail (Lepidoptera, Papilionidae) from North America is recognized by the pattern on its neck. <i>ZooKeys</i> , 2014, 468, 85-135.	0.5	12
69	PROMALS3D: Multiple Protein Sequence Alignment Enhanced with Evolutionary and Three-Dimensional Structural Information. <i>Methods in Molecular Biology</i> , 2014, 1079, 263-271.	0.4	206
70	A Novel Germline Mutation in <i>BAP1</i> Predisposes to Familial Clear-Cell Renal Cell Carcinoma. <i>Molecular Cancer Research</i> , 2013, 11, 1061-1071.	1.5	135
71	Hiding Behind Gaudy Looks, a New Central American Species of <i>Phareas</i> (Hesperiidae: Eudaminae). <i>Journal of the Lepidopterists' Society</i> , 2013, 67, 161-174.	0.0	10
72	A new <i>Entheus</i> (Hesperiidae: Eudaminae) from Colombia and Panama is most distinctive in the <i>E. gentius</i> group. <i>The Journal of Research on the Lepidoptera</i> , 2013, 46, 91-103.	0.1	1

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73	MESSA: MEta-Server for protein Sequence Analysis. BMC Biology, 2012, 10, 82.	1.7	43
74	Uncus shaped akin to elephant tusks defines a new genus for two very different-in-appearance Neotropical skippers (Hesperiidae: Pyrginae). The Journal of Research on the Lepidoptera, 2012, 45, 101-112.	0.1	0
75	PROMALS: towards accurate multiple sequence alignments of distantly related proteins. Bioinformatics, 2007, 23, 802-808.	1.8	315
76	Investigation of the folding profiles of evolutionarily selected model proteins. Journal of Chemical Physics, 2003, 118, 3342-3349.	1.2	4
77	Autosomal Recessive Hypercholesterolemia Caused by Mutations in a Putative LDL Receptor Adaptor Protein. Science, 2001, 292, 1394-1398.	6.0	539