

List of Publications by Citations

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

152 papers	5,691 citations	35 h-index	72 g-index
173 ext. papers	8,651 ext. citations	8.8 avg, IF	5.94 L-index

#	Paper	IF	Citations
152	Phosphorylation of innate immune adaptor proteins MAVS, STING, and TRIF induces IRF3 activation. <i>Science</i> , 2015 , 347, aaa2630	33.3	805
151	Accurate prediction of protein structures and interactions using a three-track neural network. <i>Science</i> , 2021 , 373, 871-876	33.3	522
150	Modeling of the spatial structure of eukaryotic ornithine decarboxylases. <i>Protein Science</i> , 1995 , 4, 1291-304	30.4	332
149	Spectrum of diverse genomic alterations define non-clear cell renal carcinoma subtypes. <i>Nature Genetics</i> , 2015 , 47, 13-21	36.3	247
148	Insights into the evolution of longevity from the bowhead whale genome. <i>Cell Reports</i> , 2015 , 10, 112-22	10.6	203
147	The WAVE regulatory complex links diverse receptors to the actin cytoskeleton. <i>Cell</i> , 2014 , 156, 195-207	56.2	189
146	ECOD: an evolutionary classification of protein domains. <i>PLoS Computational Biology</i> , 2014 , 10, e1003925	5	184
145	Large-scale determination of previously unsolved protein structures using evolutionary information. <i>ELife</i> , 2015 , 4, e09248	8.9	173
144	GGDEF domain is homologous to adenylyl cyclase. <i>Proteins: Structure, Function and Bioinformatics</i> , 2001 , 42, 210-6	4.2	128
143	CARF and WYL domains: ligand-binding regulators of prokaryotic defense systems. <i>Frontiers in Genetics</i> , 2014 , 5, 102	4.5	118
142	Beclin 2 functions in autophagy, degradation of G protein-coupled receptors, and metabolism. <i>Cell</i> , 2013 , 154, 1085-1099	56.2	115
141	Protein interaction networks revealed by proteome coevolution. <i>Science</i> , 2019 , 365, 185-189	33.3	112
140	The Ancient Gamete Fusogen HAP2 Is a Eukaryotic Class II Fusion Protein. <i>Cell</i> , 2017 , 168, 904-915.	e10 56.2	109
139	Marker for type VI secretion system effectors. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014 , 111, 9271-6	11.5	98
138	Protein AMPylation by an Evolutionarily Conserved Pseudokinase. <i>Cell</i> , 2018 , 175, 809-821.	e19 56.2	87
137	LocNES: a computational tool for locating classical NESs in CRM1 cargo proteins. <i>Bioinformatics</i> , 2015 , 31, 1357-65	7.2	80
136	A tethered delivery mechanism explains the catalytic action of a microtubule polymerase. <i>ELife</i> , 2014 , 3, e03069	8.9	74

135	Structure, lipid scrambling activity and role in autophagosome formation of ATG9A. <i>Nature Structural and Molecular Biology</i> , 2020 , 27, 1194-1201	17.6	73
134	Tiger Swallowtail Genome Reveals Mechanisms for Speciation and Caterpillar Chemical Defense. <i>Cell Reports</i> , 2015 , 10, 910-919	10.6	66
133	Nuclear genomes distinguish cryptic species suggested by their DNA barcodes and ecology. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017 , 114, 8313-8318	11.5	64
132	The subunit interfaces of oligomeric enzymes are conserved to a similar extent to the overall protein sequences. <i>Protein Science</i> , 1994 , 3, 2455-8	6.3	62
131	Pet10p is a yeast perilipin that stabilizes lipid droplets and promotes their assembly. <i>Journal of Cell Biology</i> , 2017 , 216, 3199-3217	7.3	61
130	Evaluation of free modeling targets in CASP11 and ROLL. <i>Proteins: Structure, Function and Bioinformatics</i> , 2016 , 84 Suppl 1, 51-66	4.2	60
129	Acute Hepatopancreatic Necrosis Disease-Causing <i>Vibrio parahaemolyticus</i> Strains Maintain an Antibacterial Type VI Secretion System with Versatile Effector Repertoires. <i>Applied and Environmental Microbiology</i> , 2017 , 83,	4.8	51
128	Computed structures of core eukaryotic protein complexes. <i>Science</i> , 2021 , 374, eabm4805	33.3	51
127	Type VI Secretion System Toxins Horizontally Shared between Marine Bacteria. <i>PLoS Pathogens</i> , 2015 , 11, e1005128	7.6	48
126	Effectors of animal and plant pathogens use a common domain to bind host phosphoinositides. <i>Nature Communications</i> , 2013 , 4, 2973	17.4	46
125	Genomes of skipper butterflies reveal extensive convergence of wing patterns. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019 , 116, 6232-6237	11.5	44
124	Targeting the Conserved Fusion Loop of HAP2 Inhibits the Transmission of <i>Plasmodium berghei</i> and <i>falciparum</i> . <i>Cell Reports</i> , 2017 , 21, 2868-2878	10.6	43
123	ECOD: new developments in the evolutionary classification of domains. <i>Nucleic Acids Research</i> , 2017 , 45, D296-D302	20.1	38
122	Estimation of evolutionary distances from protein spatial structures. <i>Journal of Molecular Evolution</i> , 1997 , 45, 359-69	3.1	38
121	Flatworm-specific transcriptional regulators promote the specification of tegumental progenitors in. <i>ELife</i> , 2018 , 7,	8.9	36
120	Requirement of the fusogenic micropeptide myomixer for muscle formation in zebrafish. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017 , 114, 11950-11955	11.5	35
119	Complete genome of , a resilient alien, a cabbage pest, and a source of anti-cancer proteins. <i>F1000Research</i> , 2016 , 5, 2631	3.6	35
118	Complete genomes of Hairstreak butterflies, their speciation, and nucleo-mitochondrial incongruence. <i>Scientific Reports</i> , 2016 , 6, 24863	4.9	35

117	Combined Blockade of Activating Mutations and ER Results in Synthetic Lethality of ER+/HER2 Mutant Breast Cancer. <i>Clinical Cancer Research</i> , 2019 , 25, 277-289	12.9	35
116	Bile salt receptor complex activates a pathogenic type III secretion system. <i>ELife</i> , 2016 , 5,	8.9	34
115	Speciation in Cloudless Sulphurs Gleaned from Complete Genomes. <i>Genome Biology and Evolution</i> , 2016 , 8, 915-31	3.9	33
114	Manual classification strategies in the ECOD database. <i>Proteins: Structure, Function and Bioinformatics</i> , 2015 , 83, 1238-51	4.2	33
113	MESSA: MEta-Server for protein Sequence Analysis. <i>BMC Biology</i> , 2012 , 10, 82	7.3	33
112	ChSeq: A database of chameleon sequences. <i>Protein Science</i> , 2015 , 24, 1075-86	6.3	32
111	Skipper genome sheds light on unique phenotypic traits and phylogeny. <i>BMC Genomics</i> , 2015 , 16, 639	4.5	32
110	A lytic polysaccharide monooxygenase-like protein functions in fungal copper import and meningitis. <i>Nature Chemical Biology</i> , 2020 , 16, 337-344	11.7	32
109	The C-terminal domain of HPIL catalase is a member of the type I glutamine amidotransferase superfamily. <i>Proteins: Structure, Function and Bioinformatics</i> , 2001 , 42, 230-236	4.2	30
108	When COI barcodes deceive: complete genomes reveal introgression in hairstreaks. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2017 , 284,	4.4	29
107	CASP13 target classification into tertiary structure prediction categories. <i>Proteins: Structure, Function and Bioinformatics</i> , 2019 , 87, 1021-1036	4.2	29
106	CASP 11 target classification. <i>Proteins: Structure, Function and Bioinformatics</i> , 2016 , 84 Suppl 1, 20-33	4.2	28
105	High-accuracy refinement using Rosetta in CASP13. <i>Proteins: Structure, Function and Bioinformatics</i> , 2019 , 87, 1276-1282	4.2	26
104	Structure of protein O-mannose kinase reveals a unique active site architecture. <i>ELife</i> , 2016 , 5,	8.9	23
103	An automatic method for CASP9 free modeling structure prediction assessment. <i>Bioinformatics</i> , 2011 , 27, 3371-8	7.2	22
102	The synthetase domains of cobalamin biosynthesis amidotransferases cobB and cobQ belong to a new family of ATP-dependent amidoligases, related to dethiobiotin synthetase. <i>Proteins: Structure, Function and Bioinformatics</i> , 2000 , 41, 238-47	4.2	22
101	Phylogeny Reconstruction with Alignment-Free Method That Corrects for Horizontal Gene Transfer. <i>PLoS Computational Biology</i> , 2016 , 12, e1004985	5	21
100	Functional Assessment of Lipoyltransferase-1 Deficiency in Cells, Mice, and Humans. <i>Cell Reports</i> , 2019 , 27, 1376-1386.e6	10.6	19

99	Deoxyhypusine Modification of Eukaryotic Translation Initiation Factor 5A (eIF5A) Is Essential for Trypanosoma brucei Growth and for Expression of Polyprolyl-containing Proteins. <i>Journal of Biological Chemistry</i> , 2015 , 290, 19987-98	5.4	19
98	Predictive sequence analysis of the Candidatus Liberibacter asiaticus proteome. <i>PLoS ONE</i> , 2012 , 7, e41037	3.7	19
97	Assessment of CASP11 contact-assisted predictions. <i>Proteins: Structure, Function and Bioinformatics</i> , 2016 , 84 Suppl 1, 164-80	4.2	19
96	Vibrio type III effector VPA1380 is related to the cysteine protease domain of large bacterial toxins. <i>PLoS ONE</i> , 2014 , 9, e104387	3.7	18
95	Pyrimidine Salvage Enzymes Are Essential for De Novo Biosynthesis of Deoxypyrimidine Nucleotides in Trypanosoma brucei. <i>PLoS Pathogens</i> , 2016 , 12, e1006010	7.6	18
94	Genomes reveal drastic and recurrent phenotypic divergence in firetip skipper butterflies (Hesperiidae: Pyrrhopyginae). <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2019 , 286, 20190609	4.4	17
93	The complete mitochondrial genome of Papilio glaucus and its phylogenetic implications. <i>Meta Gene</i> , 2015 , 5, 68-83	0.7	17
92	Classification of proteins with shared motifs and internal repeats in the ECOD database. <i>Protein Science</i> , 2016 , 25, 1188-203	6.3	17
91	Complete Genome of , The First Representative of the Eudaminae Subfamily of Skippers. <i>Current Genomics</i> , 2017 , 18, 366-374	2.6	17
90	Expanding clinical phenotype in CACNA1C related disorders: From neonatal onset severe epileptic encephalopathy to late-onset epilepsy. <i>American Journal of Medical Genetics, Part A</i> , 2018 , 176, 2733-2739	3.5	16
89	Functional expression and characterization of the envelope glycoprotein E1E2 heterodimer of hepatitis C virus. <i>PLoS Pathogens</i> , 2019 , 15, e1007759	7.6	15
88	Absence of TLR11 in Mice Does Not Confer Susceptibility to Salmonella Typhi. <i>Cell</i> , 2016 , 164, 827-8	56.2	15
87	The first complete genomes of Metalmarks and the classification of butterfly families. <i>Genomics</i> , 2017 , 109, 485-493	4.3	15
86	Long-Range Epistasis Mediated by Structural Change in a Model of Ligand Binding Proteins. <i>PLoS ONE</i> , 2016 , 11, e0166739	3.7	15
85	The complete mitochondrial genome of Lerema accius and its phylogenetic implications. <i>PeerJ</i> , 2016 , 4, e1546	3.1	15
84	Gypsy moth genome provides insights into flight capability and virus-host interactions. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019 , 116, 1669-1678	11.5	15
83	C2H2 zinc finger proteins of the SP/KLF, Wilms tumor, EGR, Hucklebein, and Klumpfuss families in metazoans and beyond. <i>Gene</i> , 2015 , 573, 91-9	3.8	14
82	The complete mitogenome of (Lepidoptera: Hesperiidae). <i>Mitochondrial DNA Part B: Resources</i> , 2017 , 2, 136-138	0.5	14

81	RUVBL1/RUVBL2 ATPase Activity Drives PAQosome Maturation, DNA Replication and Radioresistance in Lung Cancer. <i>Cell Chemical Biology</i> , 2020 , 27, 105-121.e14	8.2	14
80	Functional analysis of Rossmann-like domains reveals convergent evolution of topology and reaction pathways. <i>PLoS Computational Biology</i> , 2019 , 15, e1007569	5	14
79	Topology evaluation of models for difficult targets in the 14th round of the critical assessment of protein structure prediction (CASP14). <i>Proteins: Structure, Function and Bioinformatics</i> , 2021 , 89, 1673-1686	4.2	14
78	Expansion of divergent SEA domains in cell surface proteins and nucleoporin 54. <i>Protein Science</i> , 2017 , 26, 617-630	6.3	13
77	Direct Demonstration That Loop1 of Scap Binds to Loop7: A CRUCIAL EVENT IN CHOLESTEROL HOMEOSTASIS. <i>Journal of Biological Chemistry</i> , 2016 , 291, 12888-12896	5.4	12
76	A new <i>Hermeuptychia</i> (Lepidoptera, Nymphalidae, Satyrinae) is sympatric and synchronic with <i>H. sosybius</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 , 43-91	1.2	12
75	Three new subfamilies of skipper butterflies (Lepidoptera, HesperIIDae). <i>ZooKeys</i> , 2019 , 861, 91-105	1.2	12
74	Mitogenomes of Giant-Skipper Butterflies reveal an ancient split between deep and shallow root feeders. <i>F1000Research</i> , 2017 , 6, 222	3.6	11
73	Genomics of a complete butterfly continent		11
72	The complete mitogenome of (Lepidoptera: HesperIIDae). <i>Mitochondrial DNA Part B: Resources</i> , 2016 , 1, 581-583	0.5	11
71	Predictive and comparative analysis of Ebolavirus proteins. <i>Cell Cycle</i> , 2015 , 14, 2785-97	4.7	10
70	Proteomics Analysis Reveals Previously Uncharacterized Virulence Factors in <i>Vibrio proteolyticus</i> . <i>MBio</i> , 2016 , 7,	7.8	10
69	Compact Structure Patterns in Proteins. <i>Journal of Molecular Biology</i> , 2016 , 428, 4392-4412	6.5	10
68	Target classification in the 14th round of the critical assessment of protein structure prediction (CASP14). <i>Proteins: Structure, Function and Bioinformatics</i> , 2021 , 89, 1618-1632	4.2	10
67	Functional and evolutionary analysis of viral proteins containing a Rossmann-like fold. <i>Protein Science</i> , 2018 , 27, 1450-1463	6.3	9
66	Assessing predictions of fitness effects of missense mutations in SUMO-conjugating enzyme UBE2I. <i>Human Mutation</i> , 2017 , 38, 1051-1063	4.7	9
65	A new <i>Heraclides</i> swallowtail (Lepidoptera, Papilionidae) from North America is recognized by the pattern on its neck. <i>ZooKeys</i> , 2014 , 85-135	1.2	9
64	Accurate prediction of protein structures and interactions using a 3-track network		9

63	Structural prerequisites for CRM1-dependent nuclear export signaling peptides: accessibility, adapting conformation, and the stability at the binding site. <i>Scientific Reports</i> , 2019 , 9, 6627	4.9	8
62	An ancient autoproteolytic domain found in GAIN, ZU5 and Nucleoporin98. <i>Journal of Molecular Biology</i> , 2014 , 426, 3935-3945	6.5	8
61	Genomics reveals the origins of ancient specimens		8
60	The Bear Giant-Skipper genome suggests genetic adaptations to living inside yucca roots. <i>Molecular Genetics and Genomics</i> , 2019 , 294, 211-226	3.1	8
59	Recent advances suggest increased influence of selective pressure in allostery. <i>Current Opinion in Structural Biology</i> , 2020 , 62, 183-188	8.1	8
58	Template-based modeling by ClusPro in CASP13 and the potential for using co-evolutionary information in docking. <i>Proteins: Structure, Function and Bioinformatics</i> , 2019 , 87, 1241-1248	4.2	7
57	Crystallization and preliminary X-ray studies of ornithine decarboxylase from <i>Trypanosoma brucei</i> . <i>Proteins: Structure, Function and Bioinformatics</i> , 1996 , 24, 272-3	4.2	7
56	NK cell defects in X-linked pigmentary reticulate disorder. <i>JCI Insight</i> , 2019 , 4,	9.9	7
55	Estimation of Uncertainties in the Global Distance Test (GDT_TS) for CASP Models. <i>PLoS ONE</i> , 2016 , 11, e0154786	3.7	7
54	Structures of core eukaryotic protein complexes		7
53	Truncated Adenomatous Polyposis Coli Mutation Induces Asef-Activated Golgi Fragmentation. <i>Molecular and Cellular Biology</i> , 2018 , 38,	4.8	6
52	The complete mitochondrial genome of a skipper (Lepidoptera: Hesperidae). <i>Mitochondrial DNA Part B: Resources</i> , 2017 , 2, 145-147	0.5	6
51	Crystal Structure of the CLOCK Transactivation Domain Exon19 in Complex with a Repressor. <i>Structure</i> , 2017 , 25, 1187-1194.e3	5.2	6
50	Using homology relations within a database markedly boosts protein sequence similarity search. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015 , 112, 7003-8	11.5	6
49	A novel approach to phylogeny reconstruction from protein sequences. <i>Journal of Molecular Evolution</i> , 1999 , 48, 264-73	3.1	6
48	Evolution of off-lattice model proteins under ligand binding constraints. <i>Physical Review E</i> , 2016 , 94, 022410	2.4	6
47	TMEM120A is a coenzyme A-binding membrane protein with structural similarities to ELOVL fatty acid elongase. <i>ELife</i> , 2021 , 10,	8.9	6
46	Mutation severity spectrum of rare alleles in the human genome is predictive of disease type. <i>PLoS Computational Biology</i> , 2020 , 16, e1007775	5	5

45	The mitogenome of a Malagasy butterfly (Mabille, 1884) recovered from the holotype collected over 140 years ago adds support for a new subfamily of Hesperidae (Lepidoptera). <i>Genome</i> , 2020 , 63, 195-202	2.4	5
44	The <i>Penaincisalia amatista</i> species-group (Lepidoptera: Lycaenidae, Eumaeini) in Colombia, insights from mtDNA barcodes and the description of a new species. <i>Systematics and Biodiversity</i> , 2016 , 14, 171-183	1.7	5
43	Role of Two Metacaspases in Development and Pathogenicity of the Rice Blast Fungus <i>Magnaporthe oryzae</i> . <i>MBio</i> , 2021 , 12,	7.8	5
42	Genomic analysis of the tribe Emesidini (Lepidoptera: Riodinidae). <i>Zootaxa</i> , 2019 , 4668, zootaxa.4668.4.2.5	2.5	4
41	A sequence family database built on ECOD structural domains. <i>Bioinformatics</i> , 2018 , 34, 2997-3003	7.2	4
40	The DBSAV Database: Predicting Deleteriousness of Single Amino Acid Variations in the Human Proteome. <i>Journal of Molecular Biology</i> , 2021 , 433, 166915	6.5	4
39	Searching ECOD for Homologous Domains by Sequence and Structure. <i>Current Protocols in Bioinformatics</i> , 2018 , 61, e45	24.2	4
38	Assessment of domain interactions in the fourteenth round of the Critical Assessment of Structure Prediction (CASP14). <i>Proteins: Structure, Function and Bioinformatics</i> , 2021 , 89, 1700-1710	4.2	4
37	Schnyder corneal dystrophy-associated UBIAD1 is defective in MK-4 synthesis and resists autophagy-mediated degradation. <i>Journal of Lipid Research</i> , 2020 , 61, 746-757	6.3	3
36	A genomic perspective on the taxonomy of the subtribe Carcharodina (Lepidoptera: Hesperidae: Carcharodini). <i>Zootaxa</i> , 2020 , 4748, zootaxa.4748.1.10	0.5	3
35	Inference of epistatic effects in a key mitochondrial protein. <i>Physical Review E</i> , 2018 , 97, 062404	2.4	3
34	FlyXCDB-A Resource for Drosophila Cell Surface and Secreted Proteins and Their Extracellular Domains. <i>Journal of Molecular Biology</i> , 2018 , 430, 3353-3411	6.5	3
33	Assessing predictions on fitness effects of missense variants in calmodulin. <i>Human Mutation</i> , 2019 , 40, 1463-1473	4.7	3
32	Unveiling one of the rarest butterflies Sever (Lepidoptera: Hesperidae, Noctuidae). <i>Systematic Entomology</i> , 2019 , 44, 384-395	3.4	3
31	A switch to feeding on cycads generates parallel accelerated evolution of toxin tolerance in two clades of caterpillars (Lepidoptera: Lycaenidae). <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021 , 118,	11.5	3
30	Evolution of a chordate-specific mechanism for myoblast fusion		3
29	Genomics Reveals the Origins of Historical Specimens. <i>Molecular Biology and Evolution</i> , 2021 , 38, 2166-2176	2.7	3
28	Anomalous diffusion in neutral evolution of model proteins. <i>Physical Review E</i> , 2015 , 91, 060701	2.4	2

27	Species richness of Eurasian Zephyrus hairstreaks (Lepidoptera: Lycaenidae: Theclini) with implications on historical biogeography: An NDM/VNDM approach. <i>PLoS ONE</i> , 2018 , 13, e0191049	3.7	2
26	SFESA: a web server for pairwise alignment refinement by secondary structure shifts. <i>BMC Bioinformatics</i> , 2015 , 16, 282	3.6	2
25	Structural evolution of proteinlike heteropolymers. <i>Physical Review E</i> , 2014 , 90, 062715	2.4	2
24	A New Species of Eracon (Hesperiidae: Pyrginae) Substantiated by a Number of Traits, Including Female Genitalia. <i>Journal of the Lepidopterists Society</i> , 2014 , 68, 149	0.4	2
23	A new species of from Mexico (Hesperiidae, Pyrginae, Pyrrhopygini). <i>ZooKeys</i> , 2017 , 155-164	1.2	2
22	Comment (Case 3709) [More comments on the proposed conservation of names for western North American Hesperia comma-group subspecies through designation of neotypes. <i>Bulletin of Zoological Nomenclature</i> , 2019 , 76, 57	0.2	2
21	Genomic determinants of speciation		2
20	A combined RAD-Seq and WGS approach reveals the genomic basis of yellow color variation in bumble bee <i>Bombus terrestris</i> . <i>Scientific Reports</i> , 2021 , 11, 7996	4.9	2
19	A pathogenic UFSP2 variant in an autosomal recessive form of pediatric neurodevelopmental anomalies and epilepsy. <i>Genetics in Medicine</i> , 2021 , 23, 900-908	8.1	2
18	Manipulation of IRE1-Dependent MAPK Signaling by a Vibrio Agonist-Antagonist Effector Pair. <i>MSystems</i> , 2021 , 6,	7.6	2
17	A Fifth of the Protein World: Rossmann-like Proteins as an Evolutionarily Successful Structural unit. <i>Journal of Molecular Biology</i> , 2021 , 433, 166788	6.5	2
16	Comparative analysis of swallowtail transcriptomes suggests molecular determinants for speciation and adaptation. <i>Genome</i> , 2018 , 61, 843-855	2.4	2
15	β-strand-mediated interactions of protein domains. <i>Proteins: Structure, Function and Bioinformatics</i> , 2020 , 88, 1513-1527	4.2	1
14	Speciation in North American from a genomic perspective. <i>Systematic Entomology</i> , 2020 , 45, 803-837	3.4	1
13	Mitogenomes of the four holotypes collected 55 years ago. <i>Mitochondrial DNA Part B: Resources</i> , 2017 , 2, 598-600	0.5	1
12	Membrane protein structure predictions for exploration. <i>Cell</i> , 2012 , 149, 1424-5	56.2	1
11	A putative RNA-interference-based immune system in prokaryotes: the epitome of prokaryotic genomic diversity39-64		1
10	Identification of Protein Homologs and Domain Boundaries by Iterative Sequence Alignment. <i>Methods in Molecular Biology</i> , 2019 , 1851, 277-286	1.4	1

- 9 Changes to North American butterfly names **2019**, 8, 1-12 1
- 8 Fifty new genera of HesperIIDae (Lepidoptera). **2019**, 2019, 1
- 7 Completeness and Consistency in Structural Domain Classifications. *ACS Omega*, **2021**, 6, 15698-15707 3.9 0
- 6 Predicting Sequence Features, Function, and Structure of Proteins Using MESSA. *Current Protocols in Bioinformatics*, **2019**, 67, e84 24.2
- 5 Two new species of Clito from South America and a revision of the Clito littera group (Lepidoptera: HesperIIDae: Pyrginae). *Zootaxa*, **2014**, 3861, 231-48 0.5
- 4 Monotypy Justified: Genitalia and DNA Move Ephyriades eugramma (Mabille) to New Genus Neomorphuncus Burns (Lepidoptera: HesperIIDae: Pyrginae). *Proceedings of the Entomological Society of Washington*, **2019**, 121, 557 0.2
- 3 Evolutionary origin and sequence signatures of the heterodimeric ABCG5/ABCG8 transporter.. *Protein Science*, **2022**, 31, e4297 6.3
- 2 Orange fringes, crenulate hindwings and genomic DNA identify a new species of from Honduras (HesperIIDae: Pyrrhopyginae) **2021**, 31, 48-52
- 1 A uniquely patterned new species of from Honduras (Riodinidae) **2021**, 31, 53-59