

Steven Kelly

List of Publications by Year in descending order

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Version: 2024-02-01

83
papers

10,723
citations

101543

36
h-index

51608

86
g-index

111
all docs

111
docs citations

111
times ranked

14404
citing authors

#	ARTICLE	IF	CITATIONS
1	SHOOT: phylogenetic gene search and ortholog inference. <i>Genome Biology</i> , 2022, 23, 85.	8.8	28
2	Ten years (and counting) of <i>Biology Open</i> . <i>Biology Open</i> , 2022, 11, .	1.2	1
3	A single <scp>promoterâ€ALE</scp> system for tissueâ€specific and tuneable expression of multiple genes in rice. <i>Plant Biotechnology Journal</i> , 2022, 20, 1786-1806.	8.3	6
4	The continuing challenge of paper-mills to publishing in the biological sciences. <i>Biology Open</i> , 2022, 11, .	1.2	3
5	Limited domestic introgression in a final refuge of the wild pigeon. <i>IScience</i> , 2022, 25, 104620.	4.1	11
6	Installation of C₄ photosynthetic pathway enzymes in rice using a single construct. <i>Plant Biotechnology Journal</i> , 2021, 19, 575-588.	8.3	78
7	NO GAMETOPHORES 2 Is a Novel Regulator of the 2D to 3D Growth Transition in the Moss <i>Physcomitrella patens</i> . <i>Current Biology</i> , 2021, 31, 555-563.e4.	3.9	27
8	Rubisco Adaptation Is More Limited by Phylogenetic Constraint Than by Catalytic Trade-off. <i>Molecular Biology and Evolution</i> , 2021, 38, 2880-2896.	8.9	33
9	Finding the C4 sweet spot: cellular compartmentation of carbohydrate metabolism in C4 photosynthesis. <i>Journal of Experimental Botany</i> , 2021, 72, 6018-6026.	4.8	14
10	Conditional stomatal closure in a fern shares molecular features with flowering plant active stomatal responses. <i>Current Biology</i> , 2021, 31, 4560-4570.e5.	3.9	12
11	Early-career researchers: answering the most important scientific questions of our time. <i>Biology Open</i> , 2021, 10, .	1.2	2
12	The economics of organellar gene loss and endosymbiotic gene transfer. <i>Genome Biology</i> , 2021, 22, 345.	8.8	28
13	Metabolic quirks and the colourful history of the <i>Euglena gracilis</i> secondary plastid. <i>New Phytologist</i> , 2020, 225, 1578-1592.	7.3	65
14	Gene Duplication Accelerates the Pace of Protein Gain and Loss from Plant Organelles. <i>Molecular Biology and Evolution</i> , 2020, 37, 969-981.	8.9	6
15	Subdivision of Light Signaling Networks Contributes to Partitioning of C₄ Photosynthesis. <i>Plant Physiology</i> , 2020, 182, 1297-1309.	4.8	8
16	Gene expression data support the hypothesis that Isoetes rootlets are true roots and not modified leaves. <i>Scientific Reports</i> , 2020, 10, 21547.	3.3	9
17	Benchmarking Orthogroup Inference Accuracy: Revisiting Orthobench. <i>Genome Biology and Evolution</i> , 2020, 12, 2258-2266.	2.5	23
18	The Quest for Orthologs benchmark service and consensus calls in 2020. <i>Nucleic Acids Research</i> , 2020, 48, W538-W545.	14.5	41

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19	Multiple Metabolic Innovations and Losses Are Associated with Major Transitions in Land Plant Evolution. <i>Current Biology</i> , 2020, 30, 1783-1800.e11.	3.9	42
20	Neofunctionalisation of basic helix-loop-helix proteins occurred when embryophytes colonised the land. <i>New Phytologist</i> , 2019, 223, 993-1008.	7.3	18
21	Transcriptome, proteome and draft genome of <i>Euglena gracilis</i> . <i>BMC Biology</i> , 2019, 17, 11.	3.8	98
22	OrthoFinder: phylogenetic orthology inference for comparative genomics. <i>Genome Biology</i> , 2019, 20, 238.	8.8	3,367
23	A taxonomic monograph of <i>Ipomoea</i> integrated across phylogenetic scales. <i>Nature Plants</i> , 2019, 5, 1136-1144.	9.3	67
24	The molecular evolution of C4 photosynthesis: opportunities for understanding and improving the world's most productive plants. <i>Journal of Experimental Botany</i> , 2019, 70, 795-804.	4.8	32
25	Somatic hybridization provides segregating populations for the identification of causative mutations in sterile mutants of the moss <i>Physcomitrella patens</i> . <i>New Phytologist</i> , 2018, 218, 1270-1277.	7.3	12
26	Reconciling Conflicting Phylogenies in the Origin of Sweet Potato and Dispersal to Polynesia. <i>Current Biology</i> , 2018, 28, 1246-1256.e12.	3.9	133
27	Multiple mechanisms for enhanced plasmodesmata density in disparate subtypes of C4 grasses. <i>Journal of Experimental Botany</i> , 2018, 69, 1135-1145.	4.8	36
28	The Amount of Nitrogen Used for Photosynthesis Modulates Molecular Evolution in Plants. <i>Molecular Biology and Evolution</i> , 2018, 35, 1616-1625.	8.9	37
29	Genetic Regulation of the 2D to 3D Growth Transition in the Moss <i>Physcomitrella patens</i> . <i>Current Biology</i> , 2018, 28, 473-478.e5.	3.9	56
30	The continuing evolution of publishing in the biological sciences. <i>Biology Open</i> , 2018, 7, .	1.2	10
31	Clust: automatic extraction of optimal co-expressed gene clusters from gene expression data. <i>Genome Biology</i> , 2018, 19, 172.	8.8	141
32	Codon choice directs constitutive mRNA levels in trypanosomes. <i>ELife</i> , 2018, 7, .	6.0	52
33	OMGene: mutual improvement of gene models through optimisation of evolutionary conservation. <i>BMC Genomics</i> , 2018, 19, 307.	2.8	6
34	Selection-driven cost-efficiency optimization of transcripts modulates gene evolutionary rate in bacteria. <i>Genome Biology</i> , 2018, 19, 102.	8.8	31
35	Functional <i>PTB</i> phosphate transporters are present in streptophyte algae and early diverging land plants. <i>New Phytologist</i> , 2017, 214, 1158-1171.	7.3	25
36	Transcriptome Sequence of the Bloodstream Form of <i>Trypanoplasma borreli</i> , a Hematozoic Parasite of Fish Transmitted by Leeches. <i>Genome Announcements</i> , 2017, 5, .	0.8	5

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37	Evolution of the endomembrane systems of trypanosomatids: conservation and specialisation. <i>Journal of Cell Science</i> , 2017, 130, 1421-1434.	2.0	23
38	Description of <i>Phytomonas oxycareni</i> n. sp. from the Salivary Glands of <i>Oxycarenum lavaterae</i> . <i>Protist</i> , 2017, 168, 71-79.	1.5	25
39	Genome sequencing reveals metabolic and cellular interdependence in an amoeba-kinetoplastid symbiosis. <i>Scientific Reports</i> , 2017, 7, 11688.	3.3	44
40	Genome Sequence of <i>Phytomonas franseriai</i> , a Cassava (<i>Manihot esculenta</i>) Latex Parasite. <i>Genome Announcements</i> , 2017, 5, .	0.8	5
41	Transcriptional control of photosynthetic capacity: conservation and divergence from <i>Arabidopsis</i> to rice. <i>New Phytologist</i> , 2017, 216, 32-45.	7.3	45
42	Candidate regulators of Early Leaf Development in Maize Perturb Hormone Signalling and Secondary Cell Wall Formation When Constitutively Expressed in Rice. <i>Scientific Reports</i> , 2017, 7, 4535.	3.3	18
43	OrthoFiller: utilising data from multiple species to improve the completeness of genome annotations. <i>BMC Genomics</i> , 2017, 18, 390.	2.8	23
44	Engineering biosynthesis of high-value compounds in photosynthetic organisms. <i>Critical Reviews in Biotechnology</i> , 2017, 37, 779-802.	9.0	15
45	STRIDE: Species Tree Root Inference from Gene Duplication Events. <i>Molecular Biology and Evolution</i> , 2017, 34, 3267-3278.	8.9	192
46	An Alternative Strategy for Trypanosome Survival in the Mammalian Bloodstream Revealed through Genome and Transcriptome Analysis of the Ubiquitous Bovine Parasite <i>Trypanosoma (Megatrypanum) theileri</i> . <i>Genome Biology and Evolution</i> , 2017, 9, 2093-2109.	2.5	29
47	Combined Chlorophyll Fluorescence and Transcriptomic Analysis Identifies the P3/P4 Transition as a Key Stage in Rice Leaf Photosynthetic Development. <i>Plant Physiology</i> , 2016, 170, 1655-1674.	4.8	18
48	Independent and Parallel Evolution of New Genes by Gene Duplication in Two Origins of C4 Photosynthesis Provides New Insight into the Mechanism of Phloem Loading in C4 Species. <i>Molecular Biology and Evolution</i> , 2016, 33, 1796-1806.	8.9	66
49	The Stepwise Increase in the Number of Transcription Factor Families in the Precambrian Predated the Diversification of Plants On Land. <i>Molecular Biology and Evolution</i> , 2016, 33, 2815-2819.	8.9	86
50	Dietary nitrogen alters codon bias and genome composition in parasitic microorganisms. <i>Genome Biology</i> , 2016, 17, 226.	8.8	53
51	C ₄ Photosynthesis in the Rice Paddy: Insights from the Noxious Weed <i>Echinochloa glabrescens</i> . <i>Plant Physiology</i> , 2016, 170, 57-73.	4.8	28
52	Two forward genetic screens for vein density mutants in sorghum converge on a cytochrome P450 gene in the brassinosteroid pathway. <i>Plant Journal</i> , 2015, 84, 257-266.	5.7	36
53	OrthoFinder: solving fundamental biases in whole genome comparisons dramatically improves orthogroup inference accuracy. <i>Genome Biology</i> , 2015, 16, 157.	8.8	2,812
54	<i>Phytomonas</i> : Trypanosomatids Adapted to Plant Environments. <i>PLoS Pathogens</i> , 2015, 11, e1004484.	4.7	52

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55	Splicing of many human genes involves sites embedded within introns. <i>Nucleic Acids Research</i> , 2015, 43, 4721-4732.	14.5	31
56	Exon Skipping Is Correlated with Exon Circularization. <i>Journal of Molecular Biology</i> , 2015, 427, 2414-2417.	4.2	308
57	An Ancestral Role for CONSTITUTIVE TRIPLE RESPONSE1 Proteins in Both Ethylene and Abscisic Acid Signaling. <i>Plant Physiology</i> , 2015, 169, 283-298.	4.8	41
58	Comparative Life Cycle Transcriptomics Revises <i>Leishmania mexicana</i> Genome Annotation and Links a Chromosome Duplication with Parasitism of Vertebrates. <i>PLoS Pathogens</i> , 2015, 11, e1005186.	4.7	85
59	Touching from a distance. <i>Nucleus</i> , 2014, 5, 304-310.	2.2	6
60	Deep Evolutionary Comparison of Gene Expression Identifies Parallel Recruitment of Trans-Factors in Two Independent Origins of C4 Photosynthesis. <i>PLoS Genetics</i> , 2014, 10, e1004365.	3.5	165
61	Phylogenetic trees do not reliably predict feature diversity. <i>Diversity and Distributions</i> , 2014, 20, 600-612.	4.1	83
62	The impact of widespread regulatory neofunctionalization on homeolog gene evolution following whole-genome duplication in maize. <i>Genome Research</i> , 2014, 24, 1348-1355.	5.5	94
63	Shared origins of a key enzyme during the evolution of C4 and CAM metabolism. <i>Journal of Experimental Botany</i> , 2014, 65, 3609-3621.	4.8	90
64	SLaP mapper: A webserver for identifying and quantifying spliced-leader addition and polyadenylation site usage in kinetoplastid genomes. <i>Molecular and Biochemical Parasitology</i> , 2014, 196, 71-74.	1.1	15
65	Horizontal transfer of an adaptive chimeric photoreceptor from bryophytes to ferns. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 6672-6677.	7.1	146
66	Nuclear pore complex evolution: a trypanosome Mlp analogue functions in chromosomal segregation but lacks transcriptional barrier activity. <i>Molecular Biology of the Cell</i> , 2014, 25, 1421-1436.	2.1	26
67	A draft genome for the African crocodylian trypanosome <i>Trypanosoma grayi</i> . <i>Scientific Data</i> , 2014, 1, 140024.	5.3	39
68	Genome-wide transcript analysis of early maize leaf development reveals gene cohorts associated with the differentiation of C ₄ Kranz anatomy. <i>Plant Journal</i> , 2013, 75, 656-670.	5.7	120
69	Evolution of GOLDEN2-LIKE gene function in C3 and C4 plants. <i>Planta</i> , 2013, 237, 481-495.	3.2	98
70	Adaptin evolution in kinetoplastids and emergence of the variant surface glycoprotein coat in African trypanosomatids. <i>Molecular Phylogenetics and Evolution</i> , 2013, 67, 123-128.	2.7	44
71	Nitric oxide generated by the rice blast fungus <i>Magnaporthe oryzae</i> drives plant infection. <i>New Phytologist</i> , 2013, 197, 207-222.	7.3	75
72	Differential Localization of the Two <i>T. brucei</i> Poly(A) Binding Proteins to the Nucleus and RNP Granules Suggests Binding to Distinct mRNA Pools. <i>PLoS ONE</i> , 2013, 8, e54004.	2.5	45

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73	DendroBLAST: Approximate Phylogenetic Trees in the Absence of Multiple Sequence Alignments. PLoS ONE, 2013, 8, e58537.	2.5	52
74	A modular and optimized single marker system for generating <i>Trypanosoma brucei</i> cell lines expressing T7 RNA polymerase and the tetracycline repressor. Open Biology, 2012, 2, 110037.	3.6	117
75	Genome organization is a major component of gene expression control in response to stress and during the cell division cycle in <i>trypanosomes</i> . Open Biology, 2012, 2, 120033.	3.6	38
76	Genome-wide Analysis Reveals Extensive Functional Interaction between DNA Replication Initiation and Transcription in the Genome of <i>Trypanosoma brucei</i> . Cell Reports, 2012, 2, 185-197.	6.4	93
77	MergeAlign: improving multiple sequence alignment performance by dynamic reconstruction of consensus multiple sequence alignments. BMC Bioinformatics, 2012, 13, 117.	2.6	64
78	Archaeal phylogenomics provides evidence in support of a methanogenic origin of the Archaea and a thaumarchaeal origin for the eukaryotes. Proceedings of the Royal Society B: Biological Sciences, 2011, 278, 1009-1018.	2.6	82
79	Ab Initio Identification of Novel Regulatory Elements in the Genome of <i>Trypanosoma brucei</i> by Bayesian Inference on Sequence Segmentation. PLoS ONE, 2011, 6, e25666.	2.5	8
80	Identification of a crenarchaeal orthologue of Elf1: implications for chromatin and transcription in Archaea. Biology Direct, 2009, 4, 24.	4.6	23
81	Diversification of Function by Different Isoforms of Conventionally Shared RNA Polymerase Subunits. Molecular Biology of the Cell, 2007, 18, 1293-1301.	2.1	37
82	Functional genomics in <i>Trypanosoma brucei</i> : A collection of vectors for the expression of tagged proteins from endogenous and ectopic gene loci. Molecular and Biochemical Parasitology, 2007, 154, 103-109.	1.1	189
83	Characterization and Differential Nuclear Localization of Nopp140 and a Novel Nopp140-Like Protein in Trypanosomes. Eukaryotic Cell, 2006, 5, 876-879.	3.4	18