Kim M Rutherford

List of Publications by Year
in descending order

67 papers	39,018 citations	53751 45 h-index	95218 68 g-index
76 all docs	76 docs citations	76 times ranked	51988 citing authors

#	Article	IF	Citations
1	PHI-base in 2022: a multi-species phenotype database for Pathogenâ€“Host Interactions. Nucleic Acids Research, 2022, 50, D837-D847.	6.5	53
2	JaponicusDB: rapid deployment of a model organism database for an emerging model species. Genetics, 2022, 220, .	1.2	21
3	Fission stories: using PomBase to understand Schizosaccharomyces pombe biology. Genetics, 2022, 220, .	1.2	60
4	A genomeâ€wide investigation of adaptive signatures in proteinâ€coding genes related to tool behaviour in New Caledonian and Hawaiian crows. Molecular Ecology, 2021, 30, 973-986.	2.0	2
5	The Gene Ontology resource: enriching a GOld mine. Nucleic Acids Research, 2021, 49, D325-D334.	6.5	2,416
6	PHI-base: the pathogenâ€“host interactions database. Nucleic Acids Research, 2020, 48, D613-D620.	6.5	145
7	Community curation in PomBase: enabling fission yeast experts to provide detailed, standardized, sharable annotation from research publications. Database: the Journal of Biological Databases and Curation, 2020, 2020, .	1.4	19
8	Dense sampling of bird diversity increases power of comparative genomics. Nature, 2020, 587, 252-257.	13.7	251
9	The tuatara genome reveals ancient features of amniote evolution. Nature, 2020, 584, 403-409.	13.7	105
10	Term Matrix: a novel Gene Ontology annotation quality control system based on ontology term co-annotation patterns. Open Biology, 2020, 10, 200149.	1.5	7
11	DNA from mollusc shell: a valuable and underutilised substrate for genetic analyses. PeerJ, 2020, 8, e9420.	0.9	14
12	Stress, novel sex genes, and epigenetic reprogramming orchestrate socially controlled sex change. Science Advances, 2019, 5, eaaw7006.	4.7	99
13	PomBase 2018: user-driven reimplementation of the fission yeast database provides rapid and intuitive access to diverse, interconnected information. Nucleic Acids Research, 2019, 47, D821-D827.	6.5	157
14	Hidden in plain sight: what remains to be discovered in the eukaryotic proteome?. Open Biology, 2019, 9, 180241.	1.5	80
15	Molecular structure of sauropsid Î²-keratins from tuatara (Sphenodon punctatus). Journal of Structural Biology, 2019, 207, 21-28.	1.3	13
16	RNAcentral: a hub of information for non-coding RNA sequences. Nucleic Acids Research, 2019, 47, D221-D229.	6.5	153
17	The Gene Ontology Resource: 20 years and still GOing strong. Nucleic Acids Research, 2019, 47, D330-D338.	6.5	3,474
18	De novo draft assembly of the Botrylloides leachii genome provides further insight into tunicate evolution. Scientific Reports, 2018, 8, 5518.	1.6	36

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19	Genetic sex assignment in wild populations using genotypingâ€byâ€sequencing data: A statistical threshold approach. Molecular Ecology Resources, 2018, 18, 179-190.	2.2	17
20	Identification of sex differences in zebrafish (Danio rerio) brains during early sexual differentiation and masculinization using 17Î±-methyltestoteroneâ€. Biology of Reproduction, 2018, 99, 446-460.	1.2	21
21	Female Mimicry by Sneaker Males Has a Transcriptomic Signature in Both the Brain and the Gonad in a Sex-Changing Fish. Molecular Biology and Evolution, 2018, 35, 225-241.	3.5	29
22	Reduced representation sequencing detects only subtle regional structure in a heavily exploited and rapidly recolonizing marine mammal species. Ecology and Evolution, 2018, 8, 8736-8749.	0.8	9
23	PomBase: The Scientific Resource for Fission Yeast. Methods in Molecular Biology, 2018, 1757, 49-68.	0.4	32
24	Evolutionary history of the podoplanin gene. Gene Reports, 2018, 13, 28-37.	0.4	3
25	Adipose transcriptome analysis provides novel insights into molecular regulation of prolonged fasting in northern elephant seal pups. Physiological Genomics, 2018, 50, 495-503.	1.0	15
26	PHI-base: a new interface and further additions for the multi-species pathogenâ€“host interactions database. Nucleic Acids Research, 2017, 45, D604-D610.	6.5	231
27	Expansion of the Gene Ontology knowledgebase and resources. Nucleic Acids Research, 2017, 45, D331-D338.	6.5	1,838
28	Maleâ€“female relatedness at specific SNP-linkage groups influences cryptic female choice in Chinook salmon (Oncorhynchus tshawytscha). Proceedings of the Royal Society B: Biological Sciences, 2017, 284, 20170853.	1.2	9
29	Histological and transcriptomic effects of 17Î±-methyltestosterone on zebrafish gonad development. BMC Genomics, 2017, 18, 557.	1.2	52
30	Analysis of the genome of the New Zealand giant collembolan (Holacanthella duospinosa) sheds light on hexapod evolution. BMC Genomics, 2017, 18, 795.	1.2	28
31	Uncovering the pathways underlying whole body regeneration in a chordate model, Botrylloides leachi using de novo transcriptome analysis. BMC Genomics, 2016, 17, 114.	1.2	34
32	Large-scale transcriptome sequencing reveals novel expression patterns for key sex-related genes in a sex-changing fish. Biology of Sex Differences, 2015, 6, 26.	1.8	100
33	PomBase 2015: updates to the fission yeast database. Nucleic Acids Research, 2015, 43, D656-D661.	6.5	95
34	Gene Ontology Consortium: going forward. Nucleic Acids Research, 2015, 43, D1049-D1056.	6.5	2,743
35	Molecular evolution of Dmrt1 accompanies change of sex-determining mechanisms in reptilia. Biology Letters, 2014, 10, 20140809.	1.0	20
36	Canto: an online tool for community literature curation. Bioinformatics, 2014, 30, 1791-1792.	1.8	41

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37	Improving functional annotation for industrial microbes: a case study with Pichia pastoris. Trends in Biotechnology, 2014, 32, 396-399.	4.9	23
38	The Gene Ontology: enhancements for 2011. Nucleic Acids Research, 2012, 40, D559-D564.	6.5	191
39	Gene Ontology Annotations and Resources. Nucleic Acids Research, 2012, 41, D530-D535.	6.5	456
40	PomBase: a comprehensive online resource for fission yeast. Nucleic Acids Research, 2012, 40, D695-D699.	6.5	288
41	modMine: flexible access to modENCODE data. Nucleic Acids Research, 2012, 40, D1082-D1088.	6.5	126
42	InterMine: a flexible data warehouse system for the integration and analysis of heterogeneous biological data. Bioinformatics, 2012, 28, 3163-3165.	1.8	229
43	Integrative Analysis of the Caenorhabditis elegans Genome by the modENCODE Project. Science, 2010, 330, 1775-1787.	6.0	912
44	Identification of Functional Elements and Regulatory Circuits by Drosophila modENCODE. Science, 2010, 330, 1787-1797.	6.0	1,124
45	FlyMine: an integrated database for Drosophila and Anopheles genomics. Genome Biology, 2007, 8, R129.	13.9	345
46	ACT: the Artemis comparison tool. Bioinformatics, 2005, 21, 3422-3423.	1.8	1,536
47	A Human-Curated Annotation of the Candida albicans Genome. PLoS Genetics, 2005, 1, e1.	1.5	293
48	WebACT--an online companion for the Artemis Comparison Tool. Bioinformatics, 2005, 21, 3665-3666.	1.8	84
49	A Comprehensive Survey of the Plasmodium Life Cycle by Genomic, Transcriptomic, and Proteomic Analyses. Science, 2005, 307, 82-86.	6.0	743
50	Complete genomes of two clinical Staphylococcus aureus strains: Evidence for the rapid evolution of virulence and drug resistance. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 9786-9791.	3.3	830
51	Genomic plasticity of the causative agent of melioidosis, Burkholderia pseudomallei. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 14240-14245.	3.3	675
52	GeneDB: a resource for prokaryotic and eukaryotic organisms. Nucleic Acids Research, 2004, 32, 339D-343.	6.5	199
53	The complete genome sequence and analysis of Corynebacterium diphtheriae NCTC13129. Nucleic Acids Research, 2003, 31, 6516-6523.	6.5	285
54	Viewing and annotating sequence data with Artemis. Briefings in Bioinformatics, 2003, 4, 124-132.	3.2	136

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55	The DNA sequence of chromosome I of an African trypanosome: gene content, chromosome organisation, recombination and polymorphism. Nucleic Acids Research, 2003, 31, 4864-4873.	6.5	56
56	Sequence of Plasmodium falciparum chromosomes 1, 3â€"9 and 13. Nature, 2002, 419, 527-531.	13.7	156
57	Genome sequence of the human malaria parasite Plasmodium falciparum. Nature, 2002, 419, 498-511.	13.7	3,881
58	The genome sequence of Schizosaccharomyces pombe. Nature, 2002, 415, 871-880.	13.7	1,508
59	Complete genome sequence of the model actinomycete Streptomyces coelicolor A3(2). Nature, 2002, 417, 141-147.	13.7	2,940
60	A Re-Annotation of theSaccharomyces cerevisiaeGenome. Comparative and Functional Genomics, 2001, 2, 143-154.	2.0	72
61	Massive gene decay in the leprosy bacillus. Nature, 2001, 409, 1007-1011.	13.7	1,607
62	Genome sequence of Yersinia pestis, the causative agent of plague. Nature, 2001, 413, 523-527.	13.7	1,144
63	Complete genome sequence of a multiple drug resistant Salmonella enterica serovar Typhi CT18. Nature, 2001, 413, 848-852.	13.7	1,192
64	Analysis of 114 kb of DNA sequence from fission yeast chromosome 2 immediately centromere-distal tohis5. Yeast, 2000, 16, 1405-1411.	0.8	6
65	The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hypervariable sequences. Nature, 2000, 403, 665-668.	13.7	1,869
66	Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z2491. Nature, 2000, 404, 502-506.	13.7	687
67	Artemis: sequence visualization and annotation. Bioinformatics, 2000, 16, 944-945.	1.8	2,912