

# Kim M Rutherford

## List of Publications by Year in descending order

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Version: 2024-02-01

67  
papers

39,018  
citations

53660

45  
h-index

95083

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

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19	Genetic sex assignment in wild populations using genotyping-by-sequencing data: A statistical threshold approach. <i>Molecular Ecology Resources</i> , 2018, 18, 179-190.	2.2	17
20	Identification of sex differences in zebrafish ( <i>Danio rerio</i> ) brains during early sexual differentiation and masculinization using 17 $\beta$ -methyltestosterone. <i>Biology of Reproduction</i> , 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. <i>Molecular Biology and Evolution</i> , 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. <i>Ecology and Evolution</i> , 2018, 8, 8736-8749.	0.8	9
23	PomBase: The Scientific Resource for Fission Yeast. <i>Methods in Molecular Biology</i> , 2018, 1757, 49-68.	0.4	32
24	Evolutionary history of the podoplanin gene. <i>Gene Reports</i> , 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. <i>Physiological Genomics</i> , 2018, 50, 495-503.	1.0	15
26	PHI-base: a new interface and further additions for the multi-species pathogen-host interactions database. <i>Nucleic Acids Research</i> , 2017, 45, D604-D610.	6.5	231
27	Expansion of the Gene Ontology knowledgebase and resources. <i>Nucleic Acids Research</i> , 2017, 45, D331-D338.	6.5	1,838
28	Male-female relatedness at specific SNP-linkage groups influences cryptic female choice in Chinook salmon ( <i>Oncorhynchus tshawytscha</i> ). <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2017, 284, 20170853.	1.2	9
29	Histological and transcriptomic effects of 17 $\beta$ -methyltestosterone on zebrafish gonad development. <i>BMC Genomics</i> , 2017, 18, 557.	1.2	52
30	Analysis of the genome of the New Zealand giant collembolan ( <i>Holacanthella duospinosa</i> ) sheds light on hexapod evolution. <i>BMC Genomics</i> , 2017, 18, 795.	1.2	28
31	Uncovering the pathways underlying whole body regeneration in a chordate model, <i>Botrylloides leachi</i> using de novo transcriptome analysis. <i>BMC Genomics</i> , 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. <i>Biology of Sex Differences</i> , 2015, 6, 26.	1.8	100
33	PomBase 2015: updates to the fission yeast database. <i>Nucleic Acids Research</i> , 2015, 43, D656-D661.	6.5	95
34	Gene Ontology Consortium: going forward. <i>Nucleic Acids Research</i> , 2015, 43, D1049-D1056.	6.5	2,743
35	Molecular evolution of <i>Dmrt1</i> accompanies change of sex-determining mechanisms in reptilia. <i>Biology Letters</i> , 2014, 10, 20140809.	1.0	20
36	Canto: an online tool for community literature curation. <i>Bioinformatics</i> , 2014, 30, 1791-1792.	1.8	41

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37	Improving functional annotation for industrial microbes: a case study with <i>Pichia pastoris</i> . 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 <i>Caenorhabditis elegans</i> Genome by the modENCODE Project. Science, 2010, 330, 1775-1787.	6.0	912
44	Identification of Functional Elements and Regulatory Circuits by <i>Drosophila</i> modENCODE. Science, 2010, 330, 1787-1797.	6.0	1,124
45	FlyMine: an integrated database for <i>Drosophila</i> and <i>Anopheles</i> 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 <i>Candida albicans</i> 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 <i>Staphylococcus aureus</i> 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, <i>Burkholderia pseudomallei</i> . 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 <i>Corynebacterium diphtheriae</i> 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. <i>Nucleic Acids Research</i> , 2003, 31, 4864-4873.	6.5	56
56	Sequence of <i>Plasmodium falciparum</i> chromosomes 1, 3 and 13. <i>Nature</i> , 2002, 419, 527-531.	13.7	156
57	Genome sequence of the human malaria parasite <i>Plasmodium falciparum</i> . <i>Nature</i> , 2002, 419, 498-511.	13.7	3,881
58	The genome sequence of <i>Schizosaccharomyces pombe</i> . <i>Nature</i> , 2002, 415, 871-880.	13.7	1,508
59	Complete genome sequence of the model actinomycete <i>Streptomyces coelicolor</i> A3(2). <i>Nature</i> , 2002, 417, 141-147.	13.7	2,940
60	A Re-Annotation of the <i>Saccharomyces cerevisiae</i> Genome. <i>Comparative and Functional Genomics</i> , 2001, 2, 143-154.	2.0	72
61	Massive gene decay in the leprosy bacillus. <i>Nature</i> , 2001, 409, 1007-1011.	13.7	1,607
62	Genome sequence of <i>Yersinia pestis</i> , the causative agent of plague. <i>Nature</i> , 2001, 413, 523-527.	13.7	1,144
63	Complete genome sequence of a multiple drug resistant <i>Salmonella enterica</i> serovar Typhi CT18. <i>Nature</i> , 2001, 413, 848-852.	13.7	1,192
64	Analysis of 114 kb of DNA sequence from fission yeast chromosome 2 immediately centromere-distal to his5. <i>Yeast</i> , 2000, 16, 1405-1411.	0.8	6
65	The genome sequence of the food-borne pathogen <i>Campylobacter jejuni</i> reveals hypervariable sequences. <i>Nature</i> , 2000, 403, 665-668.	13.7	1,869
66	Complete DNA sequence of a serogroup A strain of <i>Neisseria meningitidis</i> Z2491. <i>Nature</i> , 2000, 404, 502-506.	13.7	687
67	Artemis: sequence visualization and annotation. <i>Bioinformatics</i> , 2000, 16, 944-945.	1.8	2,912