

# Kim M Rutherford

## List of Publications by Year in descending order

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Version: 2024-02-01

67  
papers

39,018  
citations

53794

45  
h-index

95266

68  
g-index

76  
all docs

76  
docs citations

76  
times ranked

51988  
citing authors

#	ARTICLE	IF	CITATIONS
1	Genome sequence of the human malaria parasite <i>Plasmodium falciparum</i> . <i>Nature</i> , 2002, 419, 498-511.	27.8	3,881
2	The Gene Ontology Resource: 20 years and still GOing strong. <i>Nucleic Acids Research</i> , 2019, 47, D330-D338.	14.5	3,474
3	Complete genome sequence of the model actinomycete <i>Streptomyces coelicolor</i> A3(2). <i>Nature</i> , 2002, 417, 141-147.	27.8	2,940
4	Artemis: sequence visualization and annotation. <i>Bioinformatics</i> , 2000, 16, 944-945.	4.1	2,912
5	Gene Ontology Consortium: going forward. <i>Nucleic Acids Research</i> , 2015, 43, D1049-D1056.	14.5	2,743
6	The Gene Ontology resource: enriching a GOLD mine. <i>Nucleic Acids Research</i> , 2021, 49, D325-D334.	14.5	2,416
7	The genome sequence of the food-borne pathogen <i>Campylobacter jejuni</i> reveals hypervariable sequences. <i>Nature</i> , 2000, 403, 665-668.	27.8	1,869
8	Expansion of the Gene Ontology knowledgebase and resources. <i>Nucleic Acids Research</i> , 2017, 45, D331-D338.	14.5	1,838
9	Massive gene decay in the leprosy bacillus. <i>Nature</i> , 2001, 409, 1007-1011.	27.8	1,607
10	ACT: the Artemis comparison tool. <i>Bioinformatics</i> , 2005, 21, 3422-3423.	4.1	1,536
11	The genome sequence of <i>Schizosaccharomyces pombe</i> . <i>Nature</i> , 2002, 415, 871-880.	27.8	1,508
12	Complete genome sequence of a multiple drug resistant <i>Salmonella enterica</i> serovar Typhi CT18. <i>Nature</i> , 2001, 413, 848-852.	27.8	1,192
13	Genome sequence of <i>Yersinia pestis</i> , the causative agent of plague. <i>Nature</i> , 2001, 413, 523-527.	27.8	1,144
14	Identification of Functional Elements and Regulatory Circuits by <i>Drosophila</i> modENCODE. <i>Science</i> , 2010, 330, 1787-1797.	12.6	1,124
15	Integrative Analysis of the <i>Caenorhabditis elegans</i> Genome by the modENCODE Project. <i>Science</i> , 2010, 330, 1775-1787.	12.6	912
16	Complete genomes of two clinical <i>Staphylococcus aureus</i> strains: Evidence for the rapid evolution of virulence and drug resistance. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 9786-9791.	7.1	830
17	A Comprehensive Survey of the <i>Plasmodium</i> Life Cycle by Genomic, Transcriptomic, and Proteomic Analyses. <i>Science</i> , 2005, 307, 82-86.	12.6	743
18	Complete DNA sequence of a serogroup A strain of <i>Neisseria meningitidis</i> Z2491. <i>Nature</i> , 2000, 404, 502-506.	27.8	687

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19	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.	7.1	675
20	Gene Ontology Annotations and Resources. Nucleic Acids Research, 2012, 41, D530-D535.	14.5	456
21	FlyMine: an integrated database for <i>Drosophila</i> and <i>Anopheles</i> genomics. Genome Biology, 2007, 8, R129.	9.6	345
22	A Human-Curated Annotation of the <i>Candida albicans</i> Genome. PLoS Genetics, 2005, 1, e1.	3.5	293
23	PomBase: a comprehensive online resource for fission yeast. Nucleic Acids Research, 2012, 40, D695-D699.	14.5	288
24	The complete genome sequence and analysis of <i>Corynebacterium diphtheriae</i> NCTC13129. Nucleic Acids Research, 2003, 31, 6516-6523.	14.5	285
25	Dense sampling of bird diversity increases power of comparative genomics. Nature, 2020, 587, 252-257.	27.8	251
26	PHI-base: a new interface and further additions for the multi-species pathogen-host interactions database. Nucleic Acids Research, 2017, 45, D604-D610.	14.5	231
27	InterMine: a flexible data warehouse system for the integration and analysis of heterogeneous biological data. Bioinformatics, 2012, 28, 3163-3165.	4.1	229
28	GeneDB: a resource for prokaryotic and eukaryotic organisms. Nucleic Acids Research, 2004, 32, 339D-343.	14.5	199
29	The Gene Ontology: enhancements for 2011. Nucleic Acids Research, 2012, 40, D559-D564.	14.5	191
30	PomBase 2018: user-driven reimplemention of the fission yeast database provides rapid and intuitive access to diverse, interconnected information. Nucleic Acids Research, 2019, 47, D821-D827.	14.5	157
31	Sequence of <i>Plasmodium falciparum</i> chromosomes 1, 3 and 13. Nature, 2002, 419, 527-531.	27.8	156
32	RNAcentral: a hub of information for non-coding RNA sequences. Nucleic Acids Research, 2019, 47, D221-D229.	14.5	153
33	PHI-base: the pathogen-host interactions database. Nucleic Acids Research, 2020, 48, D613-D620.	14.5	145
34	Viewing and annotating sequence data with Artemis. Briefings in Bioinformatics, 2003, 4, 124-132.	6.5	136
35	modMine: flexible access to modENCODE data. Nucleic Acids Research, 2012, 40, D1082-D1088.	14.5	126
36	The tuatara genome reveals ancient features of amniote evolution. Nature, 2020, 584, 403-409.	27.8	105

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37	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.	4.1	100
38	Stress, novel sex genes, and epigenetic reprogramming orchestrate socially controlled sex change. <i>Science Advances</i> , 2019, 5, eaaw7006.	10.3	99
39	PomBase 2015: updates to the fission yeast database. <i>Nucleic Acids Research</i> , 2015, 43, D656-D661.	14.5	95
40	WebACT—an online companion for the Artemis Comparison Tool. <i>Bioinformatics</i> , 2005, 21, 3665-3666.	4.1	84
41	Hidden in plain sight: what remains to be discovered in the eukaryotic proteome?. <i>Open Biology</i> , 2019, 9, 180241.	3.6	80
42	A Re-Annotation of the <i>Saccharomyces cerevisiae</i> Genome. <i>Comparative and Functional Genomics</i> , 2001, 2, 143-154.	2.0	72
43	Fission stories: using PomBase to understand <i>Schizosaccharomyces pombe</i> biology. <i>Genetics</i> , 2022, 220, .	2.9	60
44	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.	14.5	56
45	PHI-base in 2022: a multi-species phenotype database for Pathogen-Host Interactions. <i>Nucleic Acids Research</i> , 2022, 50, D837-D847.	14.5	53
46	Histological and transcriptomic effects of 17 $\beta$ -methyltestosterone on zebrafish gonad development. <i>BMC Genomics</i> , 2017, 18, 557.	2.8	52
47	Canto: an online tool for community literature curation. <i>Bioinformatics</i> , 2014, 30, 1791-1792.	4.1	41
48	De novo draft assembly of the <i>Botrylloides leachii</i> genome provides further insight into tunicate evolution. <i>Scientific Reports</i> , 2018, 8, 5518.	3.3	36
49	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.	2.8	34
50	PomBase: The Scientific Resource for Fission Yeast. <i>Methods in Molecular Biology</i> , 2018, 1757, 49-68.	0.9	32
51	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.	8.9	29
52	Analysis of the genome of the New Zealand giant collembolan ( <i>Holocanthella duospinosa</i> ) sheds light on hexapod evolution. <i>BMC Genomics</i> , 2017, 18, 795.	2.8	28
53	Improving functional annotation for industrial microbes: a case study with <i>Pichia pastoris</i> . <i>Trends in Biotechnology</i> , 2014, 32, 396-399.	9.3	23
54	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.	2.7	21

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55	JaponicusDB: rapid deployment of a model organism database for an emerging model species. <i>Genetics</i> , 2022, 220, .	2.9	21
56	Molecular evolution of <i>Dmrt1</i> accompanies change of sex-determining mechanisms in reptilia. <i>Biology Letters</i> , 2014, 10, 20140809.	2.3	20
57	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, .	3.0	19
58	Genetic sex assignment in wild populations using genotyping-by-sequencing data: A statistical threshold approach. <i>Molecular Ecology Resources</i> , 2018, 18, 179-190.	4.8	17
59	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.	2.3	15
60	DNA from mollusc shell: a valuable and underutilised substrate for genetic analyses. <i>PeerJ</i> , 2020, 8, e9420.	2.0	14
61	Molecular structure of sauropsid $\beta^2$ -keratins from tuatara ( <i>Sphenodon punctatus</i> ). <i>Journal of Structural Biology</i> , 2019, 207, 21-28.	2.8	13
62	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.	2.6	9
63	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.	1.9	9
64	Term Matrix: a novel Gene Ontology annotation quality control system based on ontology term co-annotation patterns. <i>Open Biology</i> , 2020, 10, 200149.	3.6	7
65	Analysis of 114 kb of DNA sequence from fission yeast chromosome 2 immediately centromere-distal to his5. <i>Yeast</i> , 2000, 16, 1405-1411.	1.7	6
66	Evolutionary history of the podoplanin gene. <i>Gene Reports</i> , 2018, 13, 28-37.	0.8	3
67	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.	3.9	2