

# A Maxwell Burroughs

## List of Publications by Year in descending order

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Version: 2024-02-01

54  
papers

8,881  
citations

147801

31  
h-index

161849

54  
g-index

57  
all docs

57  
docs citations

57  
times ranked

17051  
citing authors

#	ARTICLE	IF	CITATIONS
1	Ribosome collisions induce mRNA cleavage and ribosome rescue in bacteria. <i>Nature</i> , 2022, 603, 503-508.	27.8	50
2	Discovering Biological Conflict Systems Through Genome Analysis: Evolutionary Principles and Biochemical Novelty. <i>Annual Review of Biomedical Data Science</i> , 2022, 5, 367-391.	6.5	15
3	Jumbo Phages: A Comparative Genomic Overview of Core Functions and Adaptions for Biological Conflicts. <i>Viruses</i> , 2021, 13, 63.	3.3	54
4	Bacterial death and TRADD-N domains help define novel apoptosis and immunity mechanisms shared by prokaryotes and metazoans. <i>ELife</i> , 2021, 10, .	6.0	17
5	Spliceostatin A interaction with SF3B limits U1 snRNP availability and causes premature cleavage and polyadenylation. <i>Cell Chemical Biology</i> , 2021, 28, 1356-1365.e4.	5.2	8
6	NONU-1 Encodes a Conserved Endonuclease Required for mRNA Translation Surveillance. <i>Cell Reports</i> , 2020, 30, 4321-4331.e4.	6.4	60
7	Identification of Uncharacterized Components of Prokaryotic Immune Systems and Their Diverse Eukaryotic Reformulations. <i>Journal of Bacteriology</i> , 2020, 202, .	2.2	49
8	Comprehensive classification of ABC ATPases and their functional radiation in nucleoprotein dynamics and biological conflict systems. <i>Nucleic Acids Research</i> , 2020, 48, 10045-10075.	14.5	39
9	Functional Innovation in the Evolution of the Calcium-Dependent System of the Eukaryotic Endoplasmic Reticulum. <i>Frontiers in Genetics</i> , 2020, 11, 34.	2.3	9
10	An RNA Repair Operon Regulated by Damaged tRNAs. <i>Cell Reports</i> , 2020, 33, 108527.	6.4	33
11	Highly regulated, diversifying NTP-dependent biological conflict systems with implications for the emergence of multicellularity. <i>ELife</i> , 2020, 9, .	6.0	30
12	Identifying and characterizing functional 3' nucleotide addition in the miRNA pathway. <i>Methods</i> , 2019, 152, 23-30.	3.8	12
13	Oxidative opening of the aromatic ring: Tracing the natural history of a large superfamily of dioxygenase domains and their relatives. <i>Journal of Biological Chemistry</i> , 2019, 294, 10211-10235.	3.4	24
14	The Origin and Evolution of Release Factors: Implications for Translation Termination, Ribosome Rescue, and Quality Control Pathways. <i>International Journal of Molecular Sciences</i> , 2019, 20, 1981.	4.1	38
15	Deciphering the Role of a SLOG Superfamily Protein YpsA in Gram-Positive Bacteria. <i>Frontiers in Microbiology</i> , 2019, 10, 623.	3.5	15
16	Vms1 and ANKZF1 peptidyl-tRNA hydrolases release nascent chains from stalled ribosomes. <i>Nature</i> , 2018, 557, 446-451.	27.8	122
17	Unexpected Evolution of Lesion-Recognition Modules in Eukaryotic NER and Kinetoplast DNA Dynamics Proteins from Bacterial Mobile Elements. <i>iScience</i> , 2018, 9, 192-208.	4.1	8
18	An atlas of human long non-coding RNAs with accurate 5' ends. <i>Nature</i> , 2017, 543, 199-204.	27.8	898

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19	Novel clades of the HU/IHF superfamily point to unexpected roles in the eukaryotic centrosome, chromosome partitioning, and biologic conflicts. <i>Cell Cycle</i> , 2017, 16, 1093-1103.	2.6	14
20	Polyvalent Proteins, a Pervasive Theme in the Intergenomic Biological Conflicts of Bacteriophages and Conjugative Elements. <i>Journal of Bacteriology</i> , 2017, 199, .	2.2	33
21	An integrated expression atlas of miRNAs and their promoters in human and mouse. <i>Nature Biotechnology</i> , 2017, 35, 872-878.	17.5	456
22	Global analysis of pre-mRNA subcellular localization following splicing inhibition by spliceostatin A. <i>Rna</i> , 2017, 23, 47-57.	3.5	61
23	Transposons to toxins: the provenance, architecture and diversification of a widespread class of eukaryotic effectors. <i>Nucleic Acids Research</i> , 2016, 44, 3513-3533.	14.5	54
24	RNA damage in biological conflicts and the diversity of responding RNA repair systems. <i>Nucleic Acids Research</i> , 2016, 44, 8525-8555.	14.5	64
25	Exploring allosteric activation of LigAB from <i>Sphingobium</i> sp. strain SYK-6 through kinetics, mutagenesis and computational studies. <i>Archives of Biochemistry and Biophysics</i> , 2015, 567, 35-45.	3.0	11
26	The eukaryotic translation initiation regulator CDC123 defines a divergent clade of ATP-grasp enzymes with a predicted role in novel protein modifications. <i>Biology Direct</i> , 2015, 10, 21.	4.6	9
27	Comparative genomic analyses reveal a vast, novel network of nucleotide-centric systems in biological conflicts, immunity and signaling. <i>Nucleic Acids Research</i> , 2015, 43, 10633-10654.	14.5	200
28	A highly conserved family of domains related to the DNA-glycosylase fold helps predict multiple novel pathways for RNA modifications. <i>RNA Biology</i> , 2014, 11, 360-372.	3.1	35
29	Analysis of two domains with novel RNA-processing activities throws light on the complex evolution of ribosomal RNA biogenesis. <i>Frontiers in Genetics</i> , 2014, 5, 424.	2.3	21
30	PAPD5-mediated 3' adenylation and subsequent degradation of miR-21 is disrupted in proliferative disease. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 11467-11472.	7.1	130
31	A promoter-level mammalian expression atlas. <i>Nature</i> , 2014, 507, 462-470.	27.8	1,838
32	An atlas of active enhancers across human cell types and tissues. <i>Nature</i> , 2014, 507, 455-461.	27.8	2,269
33	Resilience of biochemical activity in protein domains in the face of structural divergence. <i>Current Opinion in Structural Biology</i> , 2014, 26, 92-103.	5.7	39
34	Protein and DNA Modifications: Evolutionary Imprints of Bacterial Biochemical Diversification and Geochemistry on the Provenance of Eukaryotic Epigenetics. <i>Cold Spring Harbor Perspectives in Biology</i> , 2014, 6, a016063-a016063.	5.5	26
35	Comprehensive analysis of the HEPN superfamily: identification of novel roles in intra-genomic conflicts, defense, pathogenesis and RNA processing. <i>Biology Direct</i> , 2013, 8, 15.	4.6	221
36	Two novel PIWI families: roles in inter-genomic conflicts in bacteria and Mediator-dependent modulation of transcription in eukaryotes. <i>Biology Direct</i> , 2013, 8, 13.	4.6	45

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37	Structural and Functional Characterization of MppR, an Enduracididine Biosynthetic Enzyme from <i>Streptomyces hygroscopicus</i> : Functional Diversity in the Acetoacetate Decarboxylase-like Superfamily. <i>Biochemistry</i> , 2013, 52, 4492-4506.	2.5	31
38	Computational identification of novel biochemical systems involved in oxidation, glycosylation and other complex modifications of bases in DNA. <i>Nucleic Acids Research</i> , 2013, 41, 7635-7655.	14.5	115
39	RNA-Interference Components Are Dispensable for Transcriptional Silencing of the Drosophila Bithorax-Complex. <i>PLoS ONE</i> , 2013, 8, e65740.	2.5	7
40	pre-miRNA profiles obtained through application of locked nucleic acids and deep sequencing reveals complex 5' arm variation including concomitant cleavage and polyuridylation patterns. <i>Nucleic Acids Research</i> , 2012, 40, 1424-1437.	14.5	30
41	Nonimmunoglobulin target loci of activation-induced cytidine deaminase (AID) share unique features with immunoglobulin genes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 2479-2484.	7.1	64
42	Structure and Evolution of Ubiquitin and Ubiquitin-Related Domains. <i>Methods in Molecular Biology</i> , 2012, 832, 15-63.	0.9	37
43	Functional diversification of the RING finger and other binuclear treble clef domains in prokaryotes and the early evolution of the ubiquitin system. <i>Molecular BioSystems</i> , 2011, 7, 2261.	2.9	55
44	Chromatin-associated RNA interference components contribute to transcriptional regulation in <i>Drosophila</i> . <i>Nature</i> , 2011, 480, 391-395.	27.8	203
45	A comprehensive survey of animal miRNA modification events and a possible role for adenylation in modulating miRNA targeting effectiveness. <i>Genome Research</i> , 2010, 20, 1398-1410.	5.5	309
46	Natural history of the E1-like superfamily: Implication for adenylation, sulfur transfer, and ubiquitin conjugation. <i>Proteins: Structure, Function and Bioinformatics</i> , 2009, 75, 895-910.	2.6	86
47	Amidoligases with ATP-grasp, glutamine synthetase-like and acetyltransferase-like domains: synthesis of novel metabolites and peptide modifications of proteins. <i>Molecular BioSystems</i> , 2009, 5, 1636.	2.9	95
48	The X-ray crystallographic structure and activity analysis of a <i>Pseudomonas</i> -specific subfamily of the HAD enzyme superfamily evidences a novel biochemical function. <i>Proteins: Structure, Function and Bioinformatics</i> , 2008, 70, 197-207.	2.6	5
49	Anatomy of the E2 ligase fold: Implications for enzymology and evolution of ubiquitin/Ub-like protein conjugation. <i>Journal of Structural Biology</i> , 2008, 162, 205-218.	2.8	93
50	Small but versatile: the extraordinary functional and structural diversity of the Î²-grasp fold. <i>Biology Direct</i> , 2007, 2, 18.	4.6	127
51	A novel superfamily containing the beta-grasp fold involved in binding diverse soluble ligands. <i>Biology Direct</i> , 2007, 2, 4.	4.6	46
52	The prokaryotic antecedents of the ubiquitin-signaling system and the early evolution of ubiquitin-like beta-grasp domains. <i>Genome Biology</i> , 2006, 7, R60.	9.6	148
53	Evolutionary Genomics of the HAD Superfamily: Understanding the Structural Adaptations and Catalytic Diversity in a Superfamily of Phosphoesterases and Allied Enzymes. <i>Journal of Molecular Biology</i> , 2006, 361, 1003-1034.	4.2	376
54	The ASCH superfamily: novel domains with a fold related to the PUA domain and a potential role in RNA metabolism. <i>Bioinformatics</i> , 2006, 22, 257-263.	4.1	47