

# Falk Butter

## List of Publications by Year in descending order

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79  
papers

4,005  
citations

159585

30  
h-index

138484

58  
g-index

109  
all docs

109  
docs citations

109  
times ranked

7427  
citing authors

#	ARTICLE	IF	CITATIONS
1	Membrane-associated cytoplasmic granules carrying the Argonaute protein WAGO-3 enable paternal epigenetic inheritance in <i>Caenorhabditis elegans</i> . <i>Nature Cell Biology</i> , 2022, 24, 217-229.	10.3	11
2	Class I HDAC overexpression promotes temozolomide resistance in glioma cells by regulating RAD18 expression. <i>Cell Death and Disease</i> , 2022, 13, 293.	6.3	20
3	The <i>Caenorhabditis elegans</i> TDRD5/7-like protein, LOTR-1, interacts with the helicase ZNFX-1 to balance epigenetic signals in the germline. <i>PLoS Genetics</i> , 2022, 18, e1010245.	3.5	7
4	A novel SNF2 ATPase complex in <i>Trypanosoma brucei</i> with a role in H2A.Z-mediated chromatin remodelling. <i>PLoS Pathogens</i> , 2022, 18, e1010514.	4.7	7
5	Autophagy interferes with human cytomegalovirus genome replication, morphogenesis, and progeny release. <i>Autophagy</i> , 2021, 17, 779-795.	9.1	18
6	PAR-TERRA is the main contributor to telomeric repeat-containing RNA transcripts in normal and cancer mouse cells. <i>Rna</i> , 2021, 27, 106-121.	3.5	16
7	The RNA polymerase II subunit RPB9 recruits the integrator complex to terminate <i>Caenorhabditis elegans</i> piRNA transcription. <i>EMBO Journal</i> , 2021, 40, e105565.	7.8	19
8	TbSAP is a novel chromatin protein repressing metacyclic variant surface glycoprotein expression sites in bloodstream form <i>Trypanosoma brucei</i> . <i>Nucleic Acids Research</i> , 2021, 49, 3242-3262.	14.5	7
9	Characterization of the novel mitochondrial genome segregation factor TAP110 in <i>Trypanosoma brucei</i> . <i>Journal of Cell Science</i> , 2021, 134, .	2.0	26
10	The double-stranded DNA-binding proteins TEBP-1 and TEBP-2 form a telomeric complex with POT-1. <i>Nature Communications</i> , 2021, 12, 2668.	12.8	12
11	Oncogenic Kinase Cascades Induce Molecular Mechanisms That Protect Leukemic Cell Models from Lethal Effects of De Novo dNTP Synthesis Inhibition. <i>Cancers</i> , 2021, 13, 3464.	3.7	5
12	Identification of the transcription factor MAZ as a regulator of erythropoiesis. <i>Blood Advances</i> , 2021, 5, 3002-3015.	5.2	8
13	The nucleolar DEXD/H protein Hel66 is involved in ribosome biogenesis in <i>Trypanosoma brucei</i> . <i>Scientific Reports</i> , 2021, 11, 18325.	3.3	5
14	Ythdf is a N6-methyladenosine reader that modulates Fmr1 target mRNA selection and restricts axonal growth in <i>Drosophila</i> . <i>EMBO Journal</i> , 2021, 40, e104975.	7.8	56
15	Intrinsically disordered protein PID2 modulates Z granules and is required for heritable piRNA-induced silencing in the <i>Caenorhabditis elegans</i> embryo. <i>EMBO Journal</i> , 2021, 40, e105280.	7.8	14
16	A DOT1B/Ribonuclease H2 Protein Complex Is Involved in R-Loop Processing, Genomic Integrity, and Antigenic Variation in <i>Trypanosoma brucei</i> . <i>MBio</i> , 2021, 12, e0135221.	4.1	6
17	Transcriptional activity and epigenetic regulation of transposable elements in the symbiotic fungus <i>Rhizophagus irregularis</i> . <i>Genome Research</i> , 2021, 31, 2290-2302.	5.5	19
18	3136 IDENTIFICATION OF THE TRANSCRIPTION FACTOR MAZ AS A REGULATOR OF ERYTHROPOIESIS. <i>Experimental Hematology</i> , 2021, 100, S108.	0.4	0

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19	The PHIST protein GEXP02 targets the host cytoskeleton during sexual development of <i>Plasmodium falciparum</i> . <i>Cellular Microbiology</i> , 2020, 22, e13123.	2.1	9
20	Proteotranscriptomics assisted gene annotation and spatial proteomics of <i>Bombyx mori</i> BmN4 cell line. <i>BMC Genomics</i> , 2020, 21, 690.	2.8	7
21	Fertility Relevance Probability Analysis Shortlists Genetic Markers for Male Fertility Impairment. <i>Cytogenetic and Genome Research</i> , 2020, 160, 506-522.	1.1	14
22	Genome maintenance functions of a putative <i>Trypanosoma brucei</i> translesion DNA polymerase include telomere association and a role in antigenic variation. <i>Nucleic Acids Research</i> , 2020, 48, 9660-9680.	14.5	12
23	Misactivation of multiple starvation responses in yeast by loss of tRNA modifications. <i>Nucleic Acids Research</i> , 2020, 48, 7307-7320.	14.5	12
24	The RNA fold interactome of evolutionary conserved RNA structures in <i>S. cerevisiae</i> . <i>Nature Communications</i> , 2020, 11, 2789.	12.8	11
25	Cell-based and multi-omics profiling reveals dynamic metabolic repurposing of mitochondria to drive developmental progression of <i>Trypanosoma brucei</i> . <i>PLoS Biology</i> , 2020, 18, e3000741.	5.6	32
26	Quantitative Proteomics to Identify Nuclear RNA-Binding Proteins of Malat1. <i>International Journal of Molecular Sciences</i> , 2020, 21, 1166.	4.1	17
27	Histone deacetylase inhibitors dysregulate DNA repair proteins and antagonize metastasis-associated processes. <i>Journal of Cancer Research and Clinical Oncology</i> , 2020, 146, 343-356.	2.5	37
28	Npl3 stabilizes R-loops at telomeres to prevent accelerated replicative senescence. <i>EMBO Reports</i> , 2020, 21, e49087.	4.5	13
29	Chromatin modifiers and recombination factors promote a telomere fold-back structure, that is lost during replicative senescence. <i>PLoS Genetics</i> , 2020, 16, e1008603.	3.5	6
30	PU.1 controls fibroblast polarization and tissue fibrosis. <i>Nature</i> , 2019, 566, 344-349.	27.8	121
31	PETISCO is a novel protein complex required for 21U RNA biogenesis and embryonic viability. <i>Genes and Development</i> , 2019, 33, 857-870.	5.9	34
32	ZBTB10 binds the telomeric variant repeat TTGGGG and interacts with TRF2. <i>Nucleic Acids Research</i> , 2019, 47, 1896-1907.	14.5	28
33	Trypanosomes can initiate nuclear export co-transcriptionally. <i>Nucleic Acids Research</i> , 2019, 47, 266-282.	14.5	25
34	Human platelet lysate as validated replacement for animal serum to assess chemosensitivity. <i>ALTEX: Alternatives To Animal Experimentation</i> , 2019, 36, 277-288.	1.5	12
35	A Vastly Increased Chemical Variety of RNA Modifications Containing a Thioacetal Structure. <i>Angewandte Chemie - International Edition</i> , 2018, 57, 7893-7897.	13.8	44
36	The Linker Histone GH1-HMGA1 Is Involved in Telomere Stability and DNA Damage Repair. <i>Plant Physiology</i> , 2018, 177, 311-327.	4.8	14

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37	TelAP1 links telomere complexes with developmental expression site silencing in African trypanosomes. <i>Nucleic Acids Research</i> , 2018, 46, 2820-2833.	14.5	24
38	Loss of Wilms tumor 1 protein is a marker for apoptosis in response to replicative stress in leukemic cells. <i>Archives of Toxicology</i> , 2018, 92, 2119-2135.	4.2	9
39	Quantifying post-transcriptional regulation in the development of <i>Drosophila melanogaster</i> . <i>Nature Communications</i> , 2018, 9, 4970.	12.8	63
40	A DNA methylation reader complex that enhances gene transcription. <i>Science</i> , 2018, 362, 1182-1186.	12.6	181
41	Genome-wide Rules of Nucleosome Phasing in <i>Drosophila</i> . <i>Molecular Cell</i> , 2018, 72, 661-672.e4.	9.7	31
42	<i>GTSF1</i> is required for formation of a functional RNA-dependent RNA Polymerase complex in <i>Caenorhabditis elegans</i> . <i>EMBO Journal</i> , 2018, 37, .	7.8	23
43	The histone deacetylases HDAC1 and HDAC2 are required for the growth and survival of renal carcinoma cells. <i>Archives of Toxicology</i> , 2018, 92, 2227-2243.	4.2	57
44	<i>Tdrd6a</i> Regulates the Aggregation of <i>Buc</i> into Functional Subcellular Compartments that Drive Germ Cell Specification. <i>Developmental Cell</i> , 2018, 46, 285-301.e9.	7.0	68
45	The long noncoding RNA <i>lncR492</i> inhibits neural differentiation of murine embryonic stem cells. <i>PLoS ONE</i> , 2018, 13, e0191682.	2.5	16
46	Phylointeractomics reconstructs functional evolution of protein binding. <i>Nature Communications</i> , 2017, 8, 14334.	12.8	26
47	<i>ZBTB48</i> is both a vertebrate telomere-binding protein and a transcriptional activator. <i>EMBO Reports</i> , 2017, 18, 929-946.	4.5	50
48	Characterization of genetic loss-of-function of <i>Fus</i> in zebrafish. <i>RNA Biology</i> , 2017, 14, 29-35.	3.1	16
49	The developmental proteome of <i>Drosophila melanogaster</i> . <i>Genome Research</i> , 2017, 27, 1273-1285.	5.5	135
50	Dynamic RNA-protein interactions underlie the zebrafish maternal-to-zygotic transition. <i>Genome Research</i> , 2017, 27, 1184-1194.	5.5	58
51	Analysis of RNA-protein interactions in vertebrate embryos using UV crosslinking approaches. <i>Methods</i> , 2017, 126, 44-53.	3.8	2
52	The FOXP2-Driven Network in Developmental Disorders and Neurodegeneration. <i>Frontiers in Cellular Neuroscience</i> , 2017, 11, 212.	3.7	38
53	The nuclear proteome of <i>Trypanosoma brucei</i> . <i>PLoS ONE</i> , 2017, 12, e0181884.	2.5	51
54	Quantitative Proteomics Uncovers Novel Factors Involved in Developmental Differentiation of <i>Trypanosoma brucei</i> . <i>PLoS Pathogens</i> , 2016, 12, e1005439.	4.7	85

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55	Reader interactome of epigenetic histone marks in birds. <i>Proteomics</i> , 2016, 16, 427-436.	2.2	25
56	tRNA anticodon loop modifications ensure protein homeostasis and cell morphogenesis in yeast. <i>Nucleic Acids Research</i> , 2016, 44, 10946-10959.	14.5	56
57	Two flagellar BAR domain proteins in <i>Trypanosoma brucei</i> with stage-specific regulation. <i>Scientific Reports</i> , 2016, 6, 35826.	3.3	2
58	Identification of TTAGGG-binding proteins in <i>Neurospora crassa</i> , a fungus with vertebrate-like telomere repeats. <i>BMC Genomics</i> , 2015, 16, 965.	2.8	16
59	Piwi Proteins and piRNAs in Mammalian Oocytes and Early Embryos. <i>Cell Reports</i> , 2015, 10, 2069-2082.	6.4	183
60	Deep Proteomic Evaluation of Primary and Cell Line Motoneuron Disease Models Delineates Major Differences in Neuronal Characteristics. <i>Molecular and Cellular Proteomics</i> , 2014, 13, 3410-3420.	3.8	51
61	The ETS family member GABP $\pm$ modulates androgen receptor signalling and mediates an aggressive phenotype in prostate cancer. <i>Nucleic Acids Research</i> , 2014, 42, 6256-6269.	14.5	33
62	The Coilin Interactome Identifies Hundreds of Small Noncoding RNAs that Traffic through Cajal Bodies. <i>Molecular Cell</i> , 2014, 56, 389-399.	9.7	88
63	On the extent and role of the small proteome in the parasitic eukaryote <i>Trypanosoma brucei</i> . <i>BMC Biology</i> , 2014, 12, 14.	3.8	19
64	Alleles of a Polymorphic ETV6 Binding Site in DCDC2 Confer Risk of Reading and Language Impairment. <i>American Journal of Human Genetics</i> , 2014, 94, 798.	6.2	1
65	Quantitative interaction screen of telomeric repeat-containing RNA reveals novel TERRA regulators. <i>Genome Research</i> , 2013, 23, 2149-2157.	5.5	69
66	A DNA-Centric Protein Interaction Map of Ultraconserved Elements Reveals Contribution of Transcription Factor Binding Hubs to Conservation. <i>Cell Reports</i> , 2013, 5, 531-545.	6.4	26
67	Interrogating the relationship between transcription factor complex binding and transcriptional activation. <i>Experimental Hematology</i> , 2013, 41, S19.	0.4	0
68	Alleles of a Polymorphic ETV6 Binding Site in DCDC2 Confer Risk of Reading and Language Impairment. <i>American Journal of Human Genetics</i> , 2013, 93, 19-28.	6.2	60
69	HOT1 is a mammalian direct telomere repeat-binding protein contributing to telomerase recruitment. <i>EMBO Journal</i> , 2013, 32, 1681-1701.	7.8	74
70	Quantitative proteomic analysis reveals concurrent RNA-protein interactions and identifies new RNA-binding proteins in <i>Saccharomyces cerevisiae</i> . <i>Genome Research</i> , 2013, 23, 1028-1038.	5.5	56
71	Comparative Proteomics of Two Life Cycle Stages of Stable Isotope-labeled <i>Trypanosoma brucei</i> Reveals Novel Components of the Parasite's Host Adaptation Machinery. <i>Molecular and Cellular Proteomics</i> , 2013, 12, 172-179.	3.8	75
72	Proteome-Wide Analysis of Disease-Associated SNPs That Show Allele-Specific Transcription Factor Binding. <i>PLoS Genetics</i> , 2012, 8, e1002982.	3.5	92

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73	Quantitative mass spectrometry and PAR-CLIP to identify RNA-protein interactions. <i>Nucleic Acids Research</i> , 2012, 40, 9897-9902.	14.5	45
74	TNF receptor 1 genetic risk mirrors outcome of anti-TNF therapy in multiple sclerosis. <i>Nature</i> , 2012, 488, 508-511.	27.8	323
75	A domesticated transposon mediates the effects of a single nucleotide polymorphism responsible for enhanced muscle growth. <i>EMBO Reports</i> , 2010, 11, 305-311.	4.5	53
76	Quantitative Interaction Proteomics and Genome-wide Profiling of Epigenetic Histone Marks and Their Readers. <i>Cell</i> , 2010, 142, 967-980.	28.9	710
77	A SILAC-based DNA protein interaction screen that identifies candidate binding proteins to functional DNA elements. <i>Genome Research</i> , 2009, 19, 284-293.	5.5	144
78	Unbiased RNA-protein interaction screen by quantitative proteomics. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 10626-10631.	7.1	124
79	A comparative analysis of two conserved motifs in bacterial poly(A) polymerase and CCA-adding enzyme. <i>Nucleic Acids Research</i> , 2008, 36, 5212-5220.	14.5	25