

Bianca H Habermann

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

124
papers

9,349
citations

54
h-index

96
g-index

144
ext. papers

10,956
ext. citations

10.9
avg, IF

5.74
L-index

#	Paper	IF	Citations
124	Complete Genome Assembly of <i>Myxococcus xanthus</i> Strain DZ2 Using Long High-Fidelity (HiFi) Reads Generated with PacBio Technology. <i>Microbiology Resource Announcements</i> , 2021 , 10, e0053021	1.3	3
123	RNfuzzyApp: an R shiny RNA-seq data analysis app for visualisation, differential expression analysis, time-series clustering and enrichment analysis.. <i>F1000Research</i> , 2021 , 10, 654	3.6	1
122	AnnoMiner is a new web-tool to integrate epigenetics, transcription factor occupancy and transcriptomics data to predict transcriptional regulators. <i>Scientific Reports</i> , 2021 , 11, 15463	4.9	0
121	Prednisolone rescues Duchenne muscular dystrophy phenotypes in human pluripotent stem cell-derived skeletal muscle in vitro. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021 , 118,	11.5	8
120	The Hippo pathway controls myofibril assembly and muscle fiber growth by regulating sarcomeric gene expression. <i>ELife</i> , 2021 , 10,	8.9	8
119	and Expression in Mouse Striatal Cholinergic Interneurons: Implications for Autism Spectrum Disorder. <i>Frontiers in Genetics</i> , 2021 , 12, 683959	4.5	2
118	Introducing the novel Cytoscape app TimeNexus to analyze time-series data using temporal MultiLayer Networks (tMLNs). <i>Scientific Reports</i> , 2021 , 11, 13691	4.9	0
117	Evolution of mechanisms controlling epithelial morphogenesis across animals: new insights from dissociation-reaggregation experiments in the sponge <i>Oscarella lobularis</i> . <i>Bmc Ecology and Evolution</i> , 2021 , 21, 160	21	0
116	A Tad-like apparatus is required for contact-dependent prey killing in predatory social bacteria. <i>ELife</i> , 2021 , 10,	8.9	5
115	BCL-XL blockage in TNBC models confers vulnerability to inhibition of specific cell cycle regulators. <i>Theranostics</i> , 2021 , 11, 9180-9197	12.1	0
114	Transcriptomic analysis of <i>Chlorella</i> sp. HS2 suggests the overflow of acetyl-CoA and NADPH cofactor induces high lipid accumulation and halotolerance. <i>Food and Energy Security</i> , 2021 , 10, e267	4.1	2
113	The Integrated RNA Landscape of Renal Preconditioning against Ischemia-Reperfusion Injury. <i>Journal of the American Society of Nephrology: JASN</i> , 2020 , 31, 716-730	12.7	11
112	Whole-genome comparison between the type strain of <i>Halobacterium salinarum</i> (DSM 3754) and the laboratory strains R1 and NRC-1. <i>MicrobiologyOpen</i> , 2020 , 9, e974	3.4	10
111	mitoXplorer, a visual data mining platform to systematically analyze and visualize mitochondrial expression dynamics and mutations. <i>Nucleic Acids Research</i> , 2020 , 48, 605-632	20.1	15
110	Mitochondrial fusion is required for regulation of mitochondrial DNA replication. <i>PLoS Genetics</i> , 2019 , 15, e1008085	6	62
109	Slx5/Slx8-dependent ubiquitin hotspots on chromatin contribute to stress tolerance. <i>EMBO Journal</i> , 2019 , 38,	13	5
108	Postnatal Tshz3 Deletion Drives Altered Corticostriatal Function and Autism Spectrum Disorder-like Behavior. <i>Biological Psychiatry</i> , 2019 , 86, 274-285	7.9	9

107	Compromised Mitochondrial Protein Import Acts as a Signal for UPR. <i>Cell Reports</i> , 2019 , 28, 1659-1669.e50.6	50.6	59
106	The Genome Sequence of the Halobacterium salinarum Type Strain Is Closely Related to That of Laboratory Strains NRC-1 and R1. <i>Microbiology Resource Announcements</i> , 2019 , 8,	1.3	5
105	Evaluating the landscape of gene cooperativity with receptor tyrosine kinases in liver tumorigenesis using transposon-mediated mutagenesis. <i>Journal of Hepatology</i> , 2019 , 70, 470-482	13.4	6
104	High-resolution TADs reveal DNA sequences underlying genome organization in flies. <i>Nature Communications</i> , 2018 , 9, 189	17.4	292
103	The axolotl genome and the evolution of key tissue formation regulators. <i>Nature</i> , 2018 , 554, 50-55	50.4	279
102	Integrative analysis and machine learning on cancer genomics data using the Cancer Systems Biology Database (CancerSysDB). <i>BMC Bioinformatics</i> , 2018 , 19, 156	3.6	20
101	The deregulated microRNAome contributes to the cellular response to aneuploidy. <i>BMC Genomics</i> , 2018 , 19, 197	4.5	8
100	Regulation and function of H3K36 di-methylation by the trithorax-group protein complex AMC. <i>Development (Cambridge)</i> , 2018 , 145,	6.6	20
99	The complete and fully assembled genome sequence of <i>Aeromonas salmonicida</i> subsp. <i>pectinolytica</i> and its comparative analysis with other <i>Aeromonas</i> species: investigation of the mobilome in environmental and pathogenic strains. <i>BMC Genomics</i> , 2018 , 19, 20	4.5	15
98	SLALOM, a flexible method for the identification and statistical analysis of overlapping continuous sequence elements in sequence- and time-series data. <i>BMC Bioinformatics</i> , 2018 , 19, 24	3.6	1
97	Hypermethylation of gene body CpG islands predicts high dosage of functional oncogenes in liver cancer. <i>Nature Communications</i> , 2018 , 9, 3164	17.4	80
96	Atf3 links loss of epithelial polarity to defects in cell differentiation and cytoarchitecture. <i>PLoS Genetics</i> , 2018 , 14, e1007241	6	11
95	Phenotypic and genomic comparison of <i>Photobacterium luminescens</i> subsp. <i>laumondii</i> TT01 and a widely used rifampicin-resistant <i>Photobacterium luminescens</i> laboratory strain. <i>BMC Genomics</i> , 2018 , 19, 854	4.5	11
94	A transcriptomics resource reveals a transcriptional transition during ordered sarcomere morphogenesis in flight muscle. <i>ELife</i> , 2018 , 7,	8.9	37
93	The enigmatic meiotic dense body and its newly discovered component, SCML1, are dispensable for fertility and gametogenesis in mice. <i>Chromosoma</i> , 2017 , 126, 399-415	2.8	0
92	A Guide to Computational Methods for Predicting Mitochondrial Localization. <i>Methods in Molecular Biology</i> , 2017 , 1567, 1-14	1.4	2
91	HH-MOTiF: de novo detection of short linear motifs in proteins by Hidden Markov Model comparisons. <i>Nucleic Acids Research</i> , 2017 , 45, W470-W477	20.1	7
90	Revision and reannotation of the <i>Halomonas elongata</i> DSM 2581 genome. <i>MicrobiologyOpen</i> , 2017 , 6, e00465	3.4	8

89	Structural basis for the antagonistic roles of RNP-8 and GLD-3 in GLD-2 poly(A)-polymerase activity. <i>Rna</i> , 2016 , 22, 1139-45	5.8	7
88	Structure of a Cytoplasmic 11-Subunit RNA Exosome Complex. <i>Molecular Cell</i> , 2016 , 63, 125-34	17.6	53
87	Altered lipid metabolism in the aging kidney identified by three layered omic analysis. <i>Aging</i> , 2016 , 8, 441-57	5.6	33
86	Mechanical regulation of transcription controls Polycomb-mediated gene silencing during lineage commitment. <i>Nature Cell Biology</i> , 2016 , 18, 864-75	23.4	241
85	Vav Proteins Are Key Regulators of Card9 Signaling for Innate Antifungal Immunity. <i>Cell Reports</i> , 2016 , 17, 2572-2583	10.6	47
84	Secretory cargo sorting by Ca ²⁺ -dependent Cab45 oligomerization at the trans-Golgi network. <i>Journal of Cell Biology</i> , 2016 , 213, 305-14	7.3	30
83	mRNA export through an additional cap-binding complex consisting of NCBP1 and NCBP3. <i>Nature Communications</i> , 2015 , 6, 8192	17.4	47
82	The RNA-binding protein Arrest (Bruno) regulates alternative splicing to enable myofibril maturation in Drosophila flight muscle. <i>EMBO Reports</i> , 2015 , 16, 178-91	6.5	39
81	Virtual pathway explorer (viPER) and pathway enrichment analysis tool (PEANuT): creating and analyzing focus networks to identify cross-talk between molecules and pathways. <i>BMC Genomics</i> , 2015 , 16, 790	4.5	4
80	Tools for visualization and analysis of molecular networks, pathways, and -omics data. <i>Advances and Applications in Bioinformatics and Chemistry</i> , 2015 , 8, 11-22	1.5	29
79	Merging and scoring molecular interactions utilising existing community standards: tools, use-cases and a case study. <i>Database: the Journal of Biological Databases and Curation</i> , 2015 , 2015,	5	36
78	DNA-protein crosslink repair: proteases as DNA repair enzymes. <i>Trends in Biochemical Sciences</i> , 2015 , 40, 67-71	10.3	70
77	Human Holliday junction resolvase GEN1 uses a chromodomain for efficient DNA recognition and cleavage. <i>ELife</i> , 2015 , 4,	8.9	21
76	A cell cycle-regulated Slx4-Dpb11 complex promotes the resolution of DNA repair intermediates linked to stalled replication. <i>Genes and Development</i> , 2014 , 28, 1604-19	12.6	70
75	morFeus: a web-based program to detect remotely conserved orthologs using symmetrical best hits and orthology network scoring. <i>BMC Bioinformatics</i> , 2014 , 15, 263	3.6	5
74	Cofilin recruits F-actin to SPCA1 and promotes Ca ²⁺ -mediated secretory cargo sorting. <i>Journal of Cell Biology</i> , 2014 , 206, 635-54	7.3	27
73	Characterization of the sea urchin mitochondrial transcription factor A reveals unusual features. <i>Mitochondrion</i> , 2014 , 14, 34-41	4.9	2
72	NSUN4 is a dual function mitochondrial protein required for both methylation of 12S rRNA and coordination of mitoribosomal assembly. <i>PLoS Genetics</i> , 2014 , 10, e1004110	6	179

71	<i>Drosophila melanogaster</i> LRPPRC2 is involved in coordination of mitochondrial translation. <i>Nucleic Acids Research</i> , 2014 , 42, 13920-38	20.1	18
70	The cytoplasmic poly(A) polymerases GLD-2 and GLD-4 promote general gene expression via distinct mechanisms. <i>Nucleic Acids Research</i> , 2014 , 42, 11622-33	20.1	27
69	KEGGViewer, a BioJS component to visualize KEGG Pathways. <i>F1000Research</i> , 2014 , 3, 43	3.6	7
68	PsicquicGraph, a BioJS component to visualize molecular interactions from PSICQUIC servers. <i>F1000Research</i> , 2014 , 3, 44	3.6	4
67	Transcriptional profiling reveals progeroid Ercc1(-/-) mice as a model system for glomerular aging. <i>BMC Genomics</i> , 2013 , 14, 559	4.5	11
66	MTERF1 binds mtDNA to prevent transcriptional interference at the light-strand promoter but is dispensable for rRNA gene transcription regulation. <i>Cell Metabolism</i> , 2013 , 17, 618-26	24.6	78
65	Designing efficient and specific endoribonuclease-prepared siRNAs. <i>Methods in Molecular Biology</i> , 2013 , 942, 193-204	1.4	15
64	MTERF3 regulates mitochondrial ribosome biogenesis in invertebrates and mammals. <i>PLoS Genetics</i> , 2013 , 9, e1003178	6	70
63	Dietary restriction induced longevity is mediated by nuclear receptor NHR-62 in <i>Caenorhabditis elegans</i> . <i>PLoS Genetics</i> , 2013 , 9, e1003651	6	58
62	Human intellectual disability genes form conserved functional modules in <i>Drosophila</i> . <i>PLoS Genetics</i> , 2013 , 9, e1003911	6	32
61	Molecular strategies of the <i>Caenorhabditis elegans</i> dauer larva to survive extreme desiccation. <i>PLoS ONE</i> , 2013 , 8, e82473	3.7	67
60	Comparative RNA-seq analysis in the unsequenced axolotl: the oncogene burst highlights early gene expression in the blastema. <i>PLoS Computational Biology</i> , 2013 , 9, e1002936	5	92
59	Comparative transcriptional profiling of the axolotl limb identifies a tripartite regeneration-specific gene program. <i>PLoS ONE</i> , 2013 , 8, e61352	3.7	82
58	<i>Caenorhabditis elegans</i> screen reveals role of PAR-5 in RAB-11-recycling endosome positioning and apicobasal cell polarity. <i>Nature Cell Biology</i> , 2012 , 14, 666-76	23.4	73
57	The interaction properties of the human Rab GTPase family--comparative analysis reveals determinants of molecular binding selectivity. <i>PLoS ONE</i> , 2012 , 7, e34870	3.7	32
56	A novel 3-hydroxysteroid dehydrogenase that regulates reproductive development and longevity. <i>PLoS Biology</i> , 2012 , 10, e1001305	9.7	54
55	Structure of the human MTERF4-NSUN4 protein complex that regulates mitochondrial ribosome biogenesis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012 , 109, 15253-8	11.5	87
54	Correction for Zayas et al., The planarian <i>Schmidtea mediterranea</i> as a model for epigenetic germ cell specification: Analysis of ESTs from the hermaphroditic strain. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012 , 109, 19033-19033	11.5	78

53	MTERF4 regulates translation by targeting the methyltransferase NSUN4 to the mammalian mitochondrial ribosome. <i>Cell Metabolism</i> , 2011 , 13, 527-39	24.6	190
52	HMMerThread: detecting remote, functional conserved domains in entire genomes by combining relaxed sequence-database searches with fold recognition. <i>PLoS ONE</i> , 2011 , 6, e17568	3.7	2
51	The bicoid stability factor controls polyadenylation and expression of specific mitochondrial mRNAs in <i>Drosophila melanogaster</i> . <i>PLoS Genetics</i> , 2011 , 7, e1002324	6	46
50	Systems survey of endocytosis by multiparametric image analysis. <i>Nature</i> , 2010 , 464, 243-9	50.4	340
49	Mutations in mouse <i>Aspm</i> (abnormal spindle-like microcephaly associated) cause not only microcephaly but also major defects in the germline. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010 , 107, 16595-600	11.5	143
48	SeLOX--a locus of recombination site search tool for the detection and directed evolution of site-specific recombination systems. <i>Nucleic Acids Research</i> , 2010 , 38, W293-8	20.1	16
47	The MMS22L-TONSL complex mediates recovery from replication stress and homologous recombination. <i>Molecular Cell</i> , 2010 , 40, 619-31	17.6	85
46	Rec8 phosphorylation by casein kinase 1 and Cdc7-Dbf4 kinase regulates cohesin cleavage by separase during meiosis. <i>Developmental Cell</i> , 2010 , 18, 397-409	10.2	158
45	Interaction between Sec7p and Pik1p: the first clue for the regulation of a coincidence detection signal. <i>European Journal of Cell Biology</i> , 2010 , 89, 575-83	6.1	15
44	A user-centred evaluation framework for the Sealife semantic web browsers. <i>BMC Bioinformatics</i> , 2009 , 10 Suppl 10, S14	3.6	4
43	HAUS, the 8-subunit human Augmin complex, regulates centrosome and spindle integrity. <i>Current Biology</i> , 2009 , 19, 816-26	6.3	186
42	Conformational adaptability of Redbeta during DNA annealing and implications for its structural relationship with Rad52. <i>Journal of Molecular Biology</i> , 2009 , 391, 586-98	6.5	50
41	Chromatin Central: towards the comparative proteome by accurate mapping of the yeast proteomic environment. <i>Genome Biology</i> , 2008 , 9, R167	18.3	96
40	The endosomal protein App11 mediates Akt substrate specificity and cell survival in vertebrate development. <i>Cell</i> , 2008 , 133, 486-97	56.2	260
39	LET-767 is required for the production of branched chain and long chain fatty acids in <i>Caenorhabditis elegans</i> . <i>Journal of Biological Chemistry</i> , 2008 , 283, 17550-60	5.4	64
38	The clathrin adaptor Gga2p is a phosphatidylinositol 4-phosphate effector at the Golgi exit. <i>Molecular Biology of the Cell</i> , 2008 , 19, 1991-2002	3.5	63
37	Identification of the <i>C. elegans</i> anaphase promoting complex subunit Cdc26 by phenotypic profiling and functional rescue in yeast. <i>BMC Developmental Biology</i> , 2007 , 7, 19	3.1	11
36	Genome-scale RNAi profiling of cell division in human tissue culture cells. <i>Nature Cell Biology</i> , 2007 , 9, 1401-12	23.4	254

35	Genome-wide resources of endoribonuclease-prepared short interfering RNAs for specific loss-of-function studies. <i>Nature Methods</i> , 2007 , 4, 337-44	21.6	151
34	Protein Domains of GTPases on Membranes: Do They Rely on Turing Mechanism? 2007 , 33-46		
33	ProFAT: a web-based tool for the functional annotation of protein sequences. <i>BMC Bioinformatics</i> , 2006 , 7, 466	3.6	6
32	Erythroid progenitor renewal versus differentiation: genetic evidence for cell autonomous, essential functions of EpoR, Stat5 and the GR. <i>Oncogene</i> , 2006 , 25, 2890-900	9.2	46
31	PDZ-domain-binding sites are common among cadherins. <i>Development Genes and Evolution</i> , 2006 , 216, 737-41	1.8	8
30	Modulation of receptor recycling and degradation by the endosomal kinesin KIF16B. <i>Cell</i> , 2005 , 121, 437-50	56.2	257
29	An essential function of the <i>C. elegans</i> ortholog of TPX2 is to localize activated aurora A kinase to mitotic spindles. <i>Developmental Cell</i> , 2005 , 9, 237-48	10.2	94
28	Dynamin and the actin cytoskeleton cooperatively regulate plasma membrane invagination by BAR and F-BAR proteins. <i>Developmental Cell</i> , 2005 , 9, 791-804	10.2	484
27	Production of endoribonuclease-prepared short interfering RNAs for gene silencing in mammalian cells. <i>Nature Methods</i> , 2005 , 2, 779-84	21.6	69
26	Genome-wide analysis of human kinases in clathrin- and caveolae/raft-mediated endocytosis. <i>Nature</i> , 2005 , 436, 78-86	50.4	523
25	Distinct roles for two <i>C. elegans</i> anillins in the gonad and early embryo. <i>Development (Cambridge)</i> , 2005 , 132, 2837-48	6.6	127
24	The planarian <i>Schmidtea mediterranea</i> as a model for epigenetic germ cell specification: analysis of ESTs from the hermaphroditic strain. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005 , 102, 18491-6	11.5	128
23	Swm1/Apc13 is an evolutionarily conserved subunit of the anaphase-promoting complex stabilizing the association of Cdc16 and Cdc27. <i>Molecular and Cellular Biology</i> , 2004 , 24, 3562-76	4.8	55
22	The power and the limitations of cross-species protein identification by mass spectrometry-driven sequence similarity searches. <i>Molecular and Cellular Proteomics</i> , 2004 , 3, 238-49	7.6	133
21	DEQOR: a web-based tool for the design and quality control of siRNAs. <i>Nucleic Acids Research</i> , 2004 , 32, W113-20	20.1	120
20	Translational control of putative protooncogene Nm23-M2 by cytokines via phosphoinositide 3-kinase signaling. <i>Journal of Biological Chemistry</i> , 2004 , 279, 38169-76	5.4	20
19	The BAR-domain family of proteins: a case of bending and binding?. <i>EMBO Reports</i> , 2004 , 5, 250-5	6.5	237
18	An endoribonuclease-prepared siRNA screen in human cells identifies genes essential for cell division. <i>Nature</i> , 2004 , 432, 1036-40	50.4	339

17	From biomedicine to natural history research: EST resources for ambystomatid salamanders. <i>BMC Genomics</i> , 2004 , 5, 54	4.5	75
16	The <i>Caenorhabditis elegans</i> centrosomal protein SPD-2 is required for both pericentriolar material recruitment and centriole duplication. <i>Current Biology</i> , 2004 , 14, 863-73	6.3	186
15	Homology-based functional proteomics by mass spectrometry: application to the <i>Xenopus</i> microtubule-associated proteome. <i>Proteomics</i> , 2004 , 4, 2707-21	4.8	64
14	An <i>Ambystoma mexicanum</i> EST sequencing project: analysis of 17,352 expressed sequence tags from embryonic and regenerating blastema cDNA libraries. <i>Genome Biology</i> , 2004 , 5, R67	18.3	64
13	Centriole assembly requires both centriolar and pericentriolar material proteins. <i>Developmental Cell</i> , 2004 , 7, 815-29	10.2	239
12	APPL proteins link Rab5 to nuclear signal transduction via an endosomal compartment. <i>Cell</i> , 2004 , 116, 445-56	56.2	453
11	Islet cell autoantigen of 69 kDa is an arfaptin-related protein associated with the Golgi complex of insulinoma INS-1 cells. <i>Journal of Biological Chemistry</i> , 2003 , 278, 26166-73	5.4	27
10	Apoptosis protection by the Epo target Bcl-X(L) allows factor-independent differentiation of primary erythroblasts. <i>Current Biology</i> , 2002 , 12, 1076-85	6.3	119
9	XMAP215: a key component of the dynamic microtubule cytoskeleton. <i>Trends in Cell Biology</i> , 2002 , 12, 267-73	18.3	117
8	The kinetically dominant assembly pathway for centrosomal asters in <i>Caenorhabditis elegans</i> is gamma-tubulin dependent. <i>Journal of Cell Biology</i> , 2002 , 157, 591-602	7.3	178
7	Stu2 promotes mitotic spindle elongation in anaphase. <i>Journal of Cell Biology</i> , 2001 , 153, 435-42	7.3	104
6	Isolation of translationally controlled mRNAs by differential screening. <i>FASEB Journal</i> , 2000 , 14, 1641-52	6.9	69
5	Structure of leech derived trypsin inhibitor (LDTI-C) in solution. <i>FEBS Letters</i> , 1994 , 355, 290-6	3.8	33
4	RNfuzzyApp: an R shiny RNA-seq data analysis app for visualisation, differential expression analysis, time-series clustering and enrichment analysis. <i>F1000Research</i> , 10 , 654	3.6	
3	Systematic transcriptomics reveals a biphasic mode of sarcomere morphogenesis in flight muscles regulated by Spalt		1
2	mitoXplorer, a visual data mining platform to systematically analyze and visualize mitochondrial expression dynamics and mutations		1
1	A Tad-like apparatus is required for contact-dependent prey killing in predatory social bacteria		1