

Friedhelm Pfeiffer

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.

99 papers	4,890 citations	37 h-index	69 g-index
104 ext. papers	5,417 ext. citations	7 avg, IF	4.94 L-index

#	Paper	IF	Citations
99	Adaptation to Varying Salinity in : Much More Than Ectoine Accumulation.. <i>Frontiers in Microbiology</i> , 2022 , 13, 846677	5.7	0
98	Genome Sequence of Micromonospora aurantiaca Strain G9, a Member of a Bacterial Consortium Capable of Polyethylene Degradation.. <i>Microbiology Resource Announcements</i> , 2022 , e0114821	1.3	0
97	Comprehensive glycoproteomics shines new light on the complexity and extent of glycosylation in archaea. <i>PLoS Biology</i> , 2021 , 19, e3001277	9.7	3
96	Open Issues for Protein Function Assignment in and Other Halophilic Archaea. <i>Genes</i> , 2021 , 12,	4.2	3
95	The Novel Halovirus Hardycor1, and the Presence of Active (Induced) Proviruses in Four Haloarchaea. <i>Genes</i> , 2021 , 12,	4.2	3
94	Cellular and Genomic Properties of LR2-5, the Host of Euryarchaeal Virus HFTV1. <i>Frontiers in Microbiology</i> , 2021 , 12, 625599	5.7	2
93	Lipid Anchoring of Archaeosortase Substrates and Midcell Growth in Haloarchaea. <i>MBio</i> , 2020 , 11,	7.8	20
92	The Archaeal Proteome Project advances knowledge about archaeal cell biology through comprehensive proteomics. <i>Nature Communications</i> , 2020 , 11, 3145	17.4	24
91	Identification of RNA 3' ends and termination sites in. <i>RNA Biology</i> , 2020 , 17, 663-676	4.8	8
90	Comparative Genomics of Two New HF1-like Haloviruses. <i>Genes</i> , 2020 , 11,	4.2	4
89	Contribution of mechanosensitive channels to osmoadaptation and ectoine excretion in Halomonas elongata. <i>Extremophiles</i> , 2020 , 24, 421-432	3	8
88	Mutations Affecting HVO_1357 or HVO_2248 Cause Hypermotility in , Suggesting Roles in Motility Regulation. <i>Genes</i> , 2020 , 12,	4.2	3
87	Whole-genome comparison between the type strain of Halobacterium salinarum (DSM 3754) and the laboratory strains R1 and NRC-1. <i>MicrobiologyOpen</i> , 2020 , 9, e974	3.4	10
86	Characterization of the transcriptome of Haloferax volcanii, grown under four different conditions, with mixed RNA-Seq. <i>PLoS ONE</i> , 2019 , 14, e0215986	3.7	16
85	virus , a Novel Halovirus Related to PhiH1 and PhiCh1. <i>Genes</i> , 2019 , 10,	4.2	7
84	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
83	The Response of Haloferax volcanii to Salt and Temperature Stress: A Proteome Study by Label-Free Mass Spectrometry. <i>Proteomics</i> , 2019 , 19, e1800491	4.8	18

82	Structure of the archaeal chemotaxis protein CheY in a domain-swapped dimeric conformation. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2019 , 75, 576-585	1.1	7
81	Bioinformatic and genetic characterization of three genes localized adjacent to the major replication origin of <i>Haloferax volcanii</i> . <i>FEMS Microbiology Letters</i> , 2019 , 366,	2.9	5
80	The PL6-Family Plasmids of Are Virus-Related. <i>Frontiers in Microbiology</i> , 2018 , 9, 1070	5.7	3
79	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
78	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
77	Archaeal cell surface biogenesis. <i>FEMS Microbiology Reviews</i> , 2018 , 42, 694-717	15.1	38
76	Taxis in archaea. <i>Emerging Topics in Life Sciences</i> , 2018 , 2, 535-546	3.5	10
75	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
74	Complete Genome Sequence of the Model Halovirus PhiH1 (H1). <i>Genes</i> , 2018 , 9,	4.2	5
73	ThiN as a Versatile Domain of Transcriptional Repressors and Catalytic Enzymes of Thiamine Biosynthesis. <i>Journal of Bacteriology</i> , 2017 , 199,	3.5	7
72	Osmoregulation in the Halophilic Bacterium <i>Halomonas elongata</i> : A Case Study for Integrative Systems Biology. <i>PLoS ONE</i> , 2017 , 12, e0168818	3.7	29
71	Revision and reannotation of the <i>Halomonas elongata</i> DSM 2581 genome. <i>MicrobiologyOpen</i> , 2017 , 6, e00465	3.4	8
70	Model Construction and Analysis of Respiration in <i>Halobacterium salinarum</i> . <i>PLoS ONE</i> , 2016 , 11, e0151839	3.7	2
69	The complete genome of a viable archaeum isolated from 123-million-year-old rock salt. <i>Environmental Microbiology</i> , 2016 , 18, 565-79	5.2	24
68	Genome-wide identification of transcriptional start sites in the haloarchaeon <i>Haloferax volcanii</i> based on differential RNA-Seq (dRNA-Seq). <i>BMC Genomics</i> , 2016 , 17, 629	4.5	78
67	Fluorescence microscopy visualization of halomucin, a secreted 927 kDa protein surrounding <i>Haloquadratum walsbyi</i> cells. <i>Frontiers in Microbiology</i> , 2015 , 6, 249	5.7	11
66	A manual curation strategy to improve genome annotation: application to a set of haloarchaeal genomes. <i>Life</i> , 2015 , 5, 1427-44	3	29
65	<i>Haloferax volcanii</i> , a prokaryotic species that does not use the Shine Dalgarno mechanism for translation initiation at 5'-UTRs. <i>PLoS ONE</i> , 2014 , 9, e94979	3.7	26

64	Conserved active site cysteine residue of archaeal THI4 homolog is essential for thiamine biosynthesis in <i>Haloferax volcanii</i> . <i>BMC Microbiology</i> , 2014 , 14, 260	4.5	9
63	Chloride and organic osmolytes: a hybrid strategy to cope with elevated salinities by the moderately halophilic, chloride-dependent bacterium <i>Halobacillus halophilus</i> . <i>Environmental Microbiology</i> , 2013 , 15, 1619-33	5.2	33
62	The ring of confidence: a haloarchaeal CRISPR/Cas system. <i>Biochemical Society Transactions</i> , 2013 , 41, 374-8	5.1	13
61	<i>Haloferax volcanii</i> archaeosortase is required for motility, mating, and C-terminal processing of the S-layer glycoprotein. <i>Molecular Microbiology</i> , 2013 , 88, 1164-75	4.1	41
60	Genome of the haloarchaeon <i>Natronomonas moolapensis</i> , a neutrophilic member of a previously haloalkaliphilic genus. <i>Genome Announcements</i> , 2013 , 1, e0009513		10
59	A comparative genomics perspective on the genetic content of the alkaliphilic haloarchaeon <i>Natrialba magadii</i> ATCC 43099T. <i>BMC Genomics</i> , 2012 , 13, 165	4.5	33
58	The immune system of halophilic archaea. <i>Mobile Genetic Elements</i> , 2012 , 2, 228-232		17
57	An archaeal immune system can detect multiple protospacer adjacent motifs (PAMs) to target invader DNA. <i>Journal of Biological Chemistry</i> , 2012 , 287, 33351-63	5.4	95
56	<i>Haloquadratum walsbyi</i> : limited diversity in a global pond. <i>PLoS ONE</i> , 2011 , 6, e20968	3.7	87
55	A blueprint of ectoine metabolism from the genome of the industrial producer <i>Halomonas elongata</i> DSM 2581 T. <i>Environmental Microbiology</i> , 2011 , 13, 1973-94	5.2	170
54	Mutational and bioinformatic analysis of haloarchaeal lipobox-containing proteins. <i>Archaea</i> , 2010 , 2010,	2	28
53	The complete genome sequence of <i>Haloferax volcanii</i> DS2, a model archaeon. <i>PLoS ONE</i> , 2010 , 5, e96053.7	3.7	197
52	Characterization of growth and metabolism of the haloalkaliphile <i>Natronomonas pharaonis</i> . <i>PLoS Computational Biology</i> , 2010 , 6, e1000799	5	19
51	Systems analysis of bioenergetics and growth of the extreme halophile <i>Halobacterium salinarum</i> . <i>PLoS Computational Biology</i> , 2009 , 5, e1000332	5	34
50	Life-style changes of a halophilic archaeon analyzed by quantitative proteomics. <i>Proteomics</i> , 2009 , 9, 3843-55	4.8	18
49	A small protein from the bop-brp intergenic region of <i>Halobacterium salinarum</i> contains a zinc finger motif and regulates bop and crtB1 transcription. <i>Molecular Microbiology</i> , 2008 , 67, 772-80	4.1	25
48	Evolution in the laboratory: the genome of <i>Halobacterium salinarum</i> strain R1 compared to that of strain NRC-1. <i>Genomics</i> , 2008 , 91, 335-46	4.3	109
47	Genome sequences of <i>Halobacterium salinarum</i> : A reply. <i>Genomics</i> , 2008 , 91, 553-554	4.3	8

46	Genome information management and integrated data analysis with HaloLex. <i>Archives of Microbiology</i> , 2008 , 190, 281-99	3	74
45	Metabolism of halophilic archaea. <i>Extremophiles</i> , 2008 , 12, 177-96	3	174
44	Reconstruction, modeling & analysis of Halobacterium salinarum R-1 metabolism. <i>Molecular BioSystems</i> , 2008 , 4, 148-59		52
43	Large-scale identification of N-terminal peptides in the halophilic archaea Halobacterium salinarum and Natronomonas pharaonis. <i>Journal of Proteome Research</i> , 2007 , 6, 2195-204	5.6	100
42	Genome-wide proteomics of Natronomonas pharaonis. <i>Journal of Proteome Research</i> , 2007 , 6, 185-93	5.6	24
41	Microarray analysis in the archaeon Halobacterium salinarum strain R1. <i>PLoS ONE</i> , 2007 , 2, e1064	3.7	24
40	Autoinducer-2-producing protein LuxS, a novel salt- and chloride-induced protein in the moderately halophilic bacterium Halobacillus halophilus. <i>Applied and Environmental Microbiology</i> , 2007 , 73, 371-9	4.8	23
39	An Integrated Services Approach to Biological Sequence Databases 2007 , 3-16		
38	Modelling the CheY(D10K,Y100W) Halobacterium salinarum mutant: sensitivity analysis allows choice of parameter to be modified in the phototaxis model. <i>IET Systems Biology</i> , 2007 , 1, 207-21	1.4	11
37	The low molecular weight proteome of Halobacterium salinarum. <i>Journal of Proteome Research</i> , 2007 , 6, 1510-8	5.6	60
36	The genome of the square archaeon Haloquadratum walsbyi : life at the limits of water activity. <i>BMC Genomics</i> , 2006 , 7, 169	4.5	218
35	Biochemical and molecular characterization of the biosynthesis of glutamine and glutamate, two major compatible solutes in the moderately halophilic bacterium Halobacillus halophilus. <i>Journal of Bacteriology</i> , 2006 , 188, 6808-15	3.5	47
34	Quantitative profiling of the membrane proteome in a halophilic archaeon. <i>Molecular and Cellular Proteomics</i> , 2006 , 5, 1543-58	7.6	54
33	Archaeal N-terminal protein maturation commonly involves N-terminal acetylation: a large-scale proteomics survey. <i>Journal of Molecular Biology</i> , 2006 , 362, 915-24	6.5	74
32	Living with two extremes: conclusions from the genome sequence of Natronomonas pharaonis. <i>Genome Research</i> , 2005 , 15, 1336-43	9.7	172
31	Analysis of the cytosolic proteome of Halobacterium salinarum and its implication for genome annotation. <i>Proteomics</i> , 2005 , 5, 168-79	4.8	65
30	The membrane proteome of Halobacterium salinarum. <i>Proteomics</i> , 2005 , 5, 180-97	4.8	94
29	BACCardI--a tool for the validation of genomic assemblies, assisting genome finishing and intergenome comparison. <i>Bioinformatics</i> , 2005 , 21, 853-9	7.2	32

28	Protein Information Resource: a community resource for expert annotation of protein data. <i>Nucleic Acids Research</i> , 2001 , 29, 29-32	20.1	53
27	The protein information resource (PIR). <i>Nucleic Acids Research</i> , 2000 , 28, 41-4	20.1	128
26	The PIR-International Protein Sequence Database. <i>Nucleic Acids Research</i> , 1999 , 27, 39-43	20.1	97
25	The domain-server: direct prediction of protein domain-homologies from BLAST search. <i>Bioinformatics</i> , 1999 , 15, 343-4	7.2	8
24	Database of protein sequence alignments: PIR-ALN. <i>Nucleic Acids Research</i> , 1999 , 27, 284-5	20.1	11
23	The PIR-International Protein Sequence Database. <i>Nucleic Acids Research</i> , 1998 , 26, 27-32	20.1	74
22	MIPS: a database for protein sequences and complete genomes. <i>Nucleic Acids Research</i> , 1998 , 26, 33-7	20.1	60
21	MIPS: a database for protein sequences, homology data and yeast genome information. <i>Nucleic Acids Research</i> , 1997 , 25, 28-30	20.1	201
20	Overview of the yeast genome. <i>Nature</i> , 1997 , 387, 7-65	50.4	304
19	The PIR-International Protein Sequence Database. <i>Nucleic Acids Research</i> , 1996 , 24, 17-20	20.1	55
18	Superfamily classification in PIR-International Protein Sequence Database. <i>Methods in Enzymology</i> , 1996 , 266, 59-71	1.7	38
17	Superfamily and Domain 1995 , 473-481		
16	Complete DNA sequence of yeast chromosome XI. <i>Nature</i> , 1994 , 369, 371-8	50.4	336
15	The PIR-International databases. <i>Nucleic Acids Research</i> , 1993 , 21, 3089-92	20.1	62
14	Isolation and characterization of a cDNA clone encoding a novel short-chain alcohol dehydrogenase from Norway spruce (<i>Picea abies</i> L. Karst). <i>Plant Physiology</i> , 1993 , 103, 1479-80	6.6	8
13	Phytochrome regulation of mRNA levels of ribulose-1,5-bisphosphate carboxylase in etiolated rye seedlings (<i>Secale cereale</i>). <i>Plant Molecular Biology</i> , 1987 , 10, 21-33	4.6	21
12	Synapses on the mauthner cell of the goldfish: Thin section, freeze-fracture, and immunocytochemical studies. <i>Journal of Electron Microscopy Technique</i> , 1987 , 6, 143-153		6
11	Distribution of glycine receptors at central synapses: an immunoelectron microscopy study. <i>Journal of Cell Biology</i> , 1985 , 101, 683-8	7.3	342

10	Purification and characterization of the glycine receptor of pig spinal cord. <i>Biochemistry</i> , 1985 , 24, 990-4	3.2	139
9	Characterization and Purification of the Glycine Receptor of Rat Spinal Cord 1984 , 509-511		
8	Photoaffinity-labelling of the glycine receptor of rat spinal cord. <i>FEBS Journal</i> , 1983 , 131, 519-25		82
7	α-Bungarotoxin and Strychnine as Tools to Characterize Neurotransmitter Receptors of the Central Nervous System 1983 , 245-256		4
6	Avermectin B1a inhibits the binding of strychnine to the glycine receptor of rat spinal cord. <i>Neuroscience Letters</i> , 1982 , 29, 173-6	3.3	40
5	UV light-induced cross-linking of strychnine to the glycine receptor of rat spinal cord membranes. <i>Biochemical and Biophysical Research Communications</i> , 1981 , 102, 1330-5	3.4	58
4	Solubilization of the glycine receptor from rat spinal cord. <i>Brain Research</i> , 1981 , 226, 273-9	3.7	70
3	Identification of RNA 3' ends and termination sites in <i>Haloferax volcanii</i>		1
2	Cellular and genomic properties of <i>Haloferax gibbonsii</i> LR2-5, the host of euryarchaeal virus HFTV1		2
1	Glycoproteomics of <i>Haloferax volcanii</i> reveals an extensive glycoproteome and concurrence of different N-glycosylation pathways		2