

Friedhelm Pfeiffer

List of Publications by Year in descending order

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97
papers

5,940
citations

76326

40
h-index

76900

74
g-index

104
all docs

104
docs citations

104
times ranked

4554
citing authors

#	ARTICLE	IF	CITATIONS
1	Complete DNA sequence of yeast chromosome XI. <i>Nature</i> , 1994, 369, 371-378.	27.8	382
2	Distribution of glycine receptors at central synapses: an immunoelectron microscopy study.. <i>Journal of Cell Biology</i> , 1985, 101, 683-688.	5.2	357
3	The genome of the square archaeon <i>Haloquadratum walsbyi</i> : life at the limits of water activity. <i>BMC Genomics</i> , 2006, 7, 169.	2.8	247
4	The Complete Genome Sequence of <i>Haloferax volcanii</i> DS2, a Model Archaeon. <i>PLoS ONE</i> , 2010, 5, e9605.	2.5	234
5	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, 1973-1994.	3.8	224
6	MIPS: a database for protein sequences, homology data and yeast genome information. <i>Nucleic Acids Research</i> , 1997, 25, 28-30.	14.5	217
7	Metabolism of halophilic archaea. <i>Extremophiles</i> , 2008, 12, 177-196.	2.3	214
8	Living with two extremes: Conclusions from the genome sequence of <i>Natronomonas pharaonis</i> . <i>Genome Research</i> , 2005, 15, 1336-1343.	5.5	183
9	The Protein Information Resource (PIR). <i>Nucleic Acids Research</i> , 2000, 28, 41-44.	14.5	165
10	Purification and characterization of the glycine receptor of pig spinal cord. <i>Biochemistry</i> , 1985, 24, 990-994.	2.5	153
11	The PIR-International Protein Sequence Database. <i>Nucleic Acids Research</i> , 1999, 27, 39-43.	14.5	149
12	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, 335-346.	2.9	127
13	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.	2.8	125
14	An Archaeal Immune System Can Detect Multiple Protospacer Adjacent Motifs (PAMs) to Target Invader DNA. <i>Journal of Biological Chemistry</i> , 2012, 287, 33351-33363.	3.4	110
15	Large-Scale Identification of N-Terminal Peptides in the Halophilic Archaea <i>Halobacterium salinarum</i> and <i>Natronomonas pharaonis</i> . <i>Journal of Proteome Research</i> , 2007, 6, 2195-2204.	3.7	109
16	The membrane proteome of <i>Halobacterium salinarum</i> . <i>Proteomics</i> , 2005, 5, 180-197.	2.2	101
17	<i>Haloquadratum walsbyi</i> : Limited Diversity in a Global Pond. <i>PLoS ONE</i> , 2011, 6, e20968.	2.5	97
18	Photoaffinity-Labeling of the Glycine Receptor of Rat Spinal Cord. <i>FEBS Journal</i> , 1983, 131, 519-525.	0.2	95

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19	MIPS: a database for protein sequences and complete genomes. <i>Nucleic Acids Research</i> , 1998, 26, 33-37.	14.5	85
20	Genome information management and integrated data analysis with HaloLex. <i>Archives of Microbiology</i> , 2008, 190, 281-299.	2.2	83
21	Archaeal N-terminal Protein Maturation Commonly Involves N-terminal Acetylation: A Large-scale Proteomics Survey. <i>Journal of Molecular Biology</i> , 2006, 362, 915-924.	4.2	80
22	The PIR-International Protein Sequence Database. <i>Nucleic Acids Research</i> , 1998, 26, 27-32.	14.5	79
23	Solubilization of the glycine receptor from rat spinal cord. <i>Brain Research</i> , 1981, 226, 273-279.	2.2	75
24	The PIR-International databases. <i>Nucleic Acids Research</i> , 1993, 21, 3089-3092.	14.5	72
25	Protein Information Resource: a community resource for expert annotation of protein data. <i>Nucleic Acids Research</i> , 2001, 29, 29-32.	14.5	72
26	Analysis of the cytosolic proteome of <i>Halobacterium salinarum</i> and its implication for genome annotation. <i>Proteomics</i> , 2005, 5, 168-179.	2.2	69
27	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, 1330-1335.	2.1	63
28	The Low Molecular Weight Proteome of <i>Halobacterium salinarum</i> . <i>Journal of Proteome Research</i> , 2007, 6, 1510-1518.	3.7	63
29	<i>Halobacterium salinarum</i> archaeosortase is required for motility, mating, and C-terminal processing of the S-layer glycoprotein. <i>Molecular Microbiology</i> , 2013, 88, 1164-1175.	2.5	61
30	The PIR-International Protein Sequence Database. <i>Nucleic Acids Research</i> , 1996, 24, 17-20.	14.5	59
31	Reconstruction, modeling & analysis of <i>Halobacterium salinarum</i> R-1 metabolism. <i>Molecular BioSystems</i> , 2008, 4, 148-159.	2.9	58
32	Quantitative Profiling of the Membrane Proteome in a Halophilic Archaeon. <i>Molecular and Cellular Proteomics</i> , 2006, 5, 1543-1558.	3.8	57
33	Biochemical and Molecular Characterization of the Biosynthesis of Glutamine and Glutamate, Two Major Compatible Solutes in the Moderately Halophilic Bacterium <i>Halobacillus halophilus</i> . <i>Journal of Bacteriology</i> , 2006, 188, 6808-6815.	2.2	57
34	Archaeal cell surface biogenesis. <i>FEMS Microbiology Reviews</i> , 2018, 42, 694-717.	8.6	55
35	Osmoregulation in the Halophilic Bacterium <i>Halomonas elongata</i> : A Case Study for Integrative Systems Biology. <i>PLoS ONE</i> , 2017, 12, e0168818.	2.5	49
36	Superfamily classification in PIR-international protein sequence database. <i>Methods in Enzymology</i> , 1996, 266, 59-71.	1.0	47

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37	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, 1619-1633.	3.8	45
38	Systems Analysis of Bioenergetics and Growth of the Extreme Halophile <i>Halobacterium salinarum</i> . <i>PLoS Computational Biology</i> , 2009, 5, e1000332.	3.2	42
39	Avermectin B1a inhibits the binding of strychnine to the glycine receptor of rat spinal cord. <i>Neuroscience Letters</i> , 1982, 29, 173-176.	2.1	41
40	Autoinducer-2-Producing Protein LuxS, a Novel Salt- and Chloride-Induced Protein in the Moderately Halophilic Bacterium <i>Halobacillus halophilus</i> . <i>Applied and Environmental Microbiology</i> , 2007, 73, 371-379.	3.1	41
41	The Archaeal Proteome Project advances knowledge about archaeal cell biology through comprehensive proteomics. <i>Nature Communications</i> , 2020, 11, 3145.	12.8	40
42	Characterization of the transcriptome of <i>Haloferax volcanii</i> , grown under four different conditions, with mixed RNA-Seq. <i>PLoS ONE</i> , 2019, 14, e0215986.	2.5	39
43	A Manual Curation Strategy to Improve Genome Annotation: Application to a Set of Haloarchaeal Genomes. <i>Life</i> , 2015, 5, 1427-1444.	2.4	38
44	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.	2.8	36
45	Mutational and Bioinformatic Analysis of Haloarchaeal Lipobox-Containing Proteins. <i>Archaea</i> , 2010, 2010, 1-11.	2.3	35
46	Lipid Anchoring of Archaeosortase Substrates and Midcell Growth in Haloarchaea. <i>MBio</i> , 2020, 11, .	4.1	35
47	A small protein from the <i>bop</i> intergenic region of <i>Halobacterium salinarum</i> contains a zinc finger motif and regulates <i>bop</i> and <i>crtB1</i> transcription. <i>Molecular Microbiology</i> , 2008, 67, 772-780.	2.5	33
48	BACCardI—a tool for the validation of genomic assemblies, assisting genome finishing and intergenome comparison. <i>Bioinformatics</i> , 2005, 21, 853-859.	4.1	32
49	The complete genome of a viable archaeum isolated from 123-million-year-old rock salt. <i>Environmental Microbiology</i> , 2016, 18, 565-579.	3.8	31
50	<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.	2.5	30
51	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.	2.8	28
52	The Response of <i>Haloferax volcanii</i> to Salt and Temperature Stress: A Proteome Study by Label-Free Mass Spectrometry. <i>Proteomics</i> , 2019, 19, 1800491.	2.2	28
53	Whole-genome comparison between the type strain of <i>Halobacterium salinarum</i> (DSM Tj ETQq1 1 0.784314 rgBT /Overlock 3.0 26	3.0	26
54	Genome-Wide Proteomics of <i>Natronomonas pharaonis</i> . <i>Journal of Proteome Research</i> , 2007, 6, 185-193.	3.7	25

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55	Microarray Analysis in the Archaeon <i>Halobacterium salinarum</i> Strain R1. <i>PLoS ONE</i> , 2007, 2, e1064.	2.5	24
56	Characterization of Growth and Metabolism of the Haloalkaliphile <i>Natronomonas pharaonis</i> . <i>PLoS Computational Biology</i> , 2010, 6, e1000799.	3.2	24
57	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.	3.9	23
58	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.	2.8	22
59	Life-style changes of a halophilic archaeon analyzed by quantitative proteomics. <i>Proteomics</i> , 2009, 9, 3843-3855.	2.2	21
60	Taxis in archaea. <i>Emerging Topics in Life Sciences</i> , 2018, 2, 535-546.	2.6	19
61	The immune system of halophilic archaea. <i>Mobile Genetic Elements</i> , 2012, 2, 228-232.	1.8	18
62	Fluorescence microscopy visualization of halomucin, a secreted 927 kDa protein surrounding <i>Haloquadratum walsbyi</i> cells. <i>Frontiers in Microbiology</i> , 2015, 6, 249.	3.5	17
63	Identification of RNA 3' ends and termination sites in <i>Haloferax volcanii</i> . <i>RNA Biology</i> , 2020, 17, 663-676.	3.1	16
64	Contribution of mechanosensitive channels to osmoadaptation and ectoine excretion in <i>Halomonas elongata</i> . <i>Extremophiles</i> , 2020, 24, 421-432.	2.3	16
65	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.	3.3	14
66	The ring of confidence: a haloarchaeal CRISPR/Cas system. <i>Biochemical Society Transactions</i> , 2013, 41, 374-378.	3.4	13
67	Revision and reannotation of the <i>Halomonas elongata</i> DSM 2581 ^T genome. <i>MicrobiologyOpen</i> , 2017, 6, e00465.	3.0	13
68	Database of protein sequence alignments: PIR-ALN. <i>Nucleic Acids Research</i> , 1999, 27, 284-285.	14.5	12
69	Modelling the CheYD10K,Y100W <i>Halobacterium salinarum</i> mutant: sensitivity analysis allows choice of parameter to be modified in the phototaxis model. <i>IET Systems Biology</i> , 2007, 1, 207-221.	1.5	12
70	ThiN as a Versatile Domain of Transcriptional Repressors and Catalytic Enzymes of Thiamine Biosynthesis. <i>Journal of Bacteriology</i> , 2017, 199, .	2.2	11
71	Complete Genome Sequence of the Model Halovirus PhiH1 (Î H1). <i>Genes</i> , 2018, 9, 493.	2.4	11
72	<i>Halobacterium salinarum</i> virus ChaoS9, a Novel Halovirus Related to PhiH1 and PhiCh1. <i>Genes</i> , 2019, 10, 194.	2.4	11

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73	Genome of the Haloarchaeon <i>Natronomonas moolapensis</i> , a Neutrophilic Member of a Previously Haloalkaliphilic Genus. <i>Genome Announcements</i> , 2013, 1, e0009513.	0.8	10
74	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.	0.8	10
75	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, 1479-1480.	4.8	9
76	Comparative Genomics of Two New HF1-like Haloviruses. <i>Genes</i> , 2020, 11, 405.	2.4	9
77	The Novel Halovirus <i>Hardycor1</i> , and the Presence of Active (Induced) Proviruses in Four Haloarchaea. <i>Genes</i> , 2021, 12, 149.	2.4	9
78	Cellular and Genomic Properties of <i>Haloferax gibbonsii</i> LR2-5, the Host of Euryarchaeal Virus HFTV1. <i>Frontiers in Microbiology</i> , 2021, 12, 625599.	3.5	9
79	Comprehensive glycoproteomics shines new light on the complexity and extent of glycosylation in archaea. <i>PLoS Biology</i> , 2021, 19, e3001277.	5.6	9
80	Mutations Affecting HVO_1357 or HVO_2248 Cause Hypermotility in <i>Haloferax volcanii</i> , Suggesting Roles in Motility Regulation. <i>Genes</i> , 2021, 12, 58.	2.4	9
81	The domain-server: direct prediction of protein domain-homologies from BLAST search. <i>Bioinformatics</i> , 1999, 15, 343-344.	4.1	8
82	Genome sequences of <i>Halobacterium salinarum</i> : A reply. <i>Genomics</i> , 2008, 91, 553-554.	2.9	8
83	The Genome Sequence of the <i>Halobacterium salinarum</i> Type Strain Is Closely Related to That of Laboratory Strains NRC-1 and R1. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.6	8
84	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, .	1.8	8
85	Adaptation to Varying Salinity in <i>Halomonas elongata</i> : Much More Than Ectoine Accumulation. <i>Frontiers in Microbiology</i> , 2022, 13, 846677.	3.5	8
86	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.	1.1	6
87	Î±-Bungarotoxin and Strychnine as Tools to Characterize Neurotransmitter Receptors of the Central Nervous System. , 1983, , 245-256.		5
88	Open Issues for Protein Function Assignment in <i>Haloferax volcanii</i> and Other Halophilic Archaea. <i>Genes</i> , 2021, 12, 963.	2.4	4
89	Model Construction and Analysis of Respiration in <i>Halobacterium salinarum</i> . <i>PLoS ONE</i> , 2016, 11, e0151839.	2.5	4
90	The PL6-Family Plasmids of <i>Haloquadratum</i> Are Virus-Related. <i>Frontiers in Microbiology</i> , 2018, 9, 1070.	3.5	3

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91	SLALOM, a flexible method for the identification and statistical analysis of overlapping continuous sequence elements in sequence- and time-series data. BMC Bioinformatics, 2018, 19, 24.	2.6	2
92	Genome Sequence of Hardyhis2, a Gammaleolipovirus Infecting Haloarcula hispanica. Microbiology Resource Announcements, 2021, 10, .	0.6	2
93	Genome Sequence of Micromonospora aurantiaca Strain G9, a Member of a Bacterial Consortium Capable of Polyethylene Degradation. Microbiology Resource Announcements, 2022, , e0114821.	0.6	2
94	Genome Sequence of Pseudomonas veronii Strain G2, a Member of a Bacterial Consortium Capable of Polyethylene Degradation. Microbiology Resource Announcements, 0, , .	0.6	1
95	Characterization and Purification of the Glycine Receptor of Rat Spinal Cord. , 1984, , 509-511.		0
96	Superfamily and Domain. , 1995, , 473-481.		0
97	Halovirus HF2 Intergenic Repeat Sequences Carry Promoters. Viruses, 2021, 13, 2388.	3.3	0