

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	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
2	Genome Sequence of <i>Micromonospora aurantiaca</i> Strain G9, a Member of a Bacterial Consortium Capable of Polyethylene Degradation. <i>Microbiology Resource Announcements</i> , 2022, , e0114821.	0.6	2
3	The Novel Halovirus HardyCor1, and the Presence of Active (Induced) Proviruses in Four Haloarchaea. <i>Genes</i> , 2021, 12, 149.	2.4	9
4	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
5	Genome Sequence of HardyHis2, a Gammaleolipovirus Infecting <i>Haloarcula hispanica</i> . <i>Microbiology Resource Announcements</i> , 2021, 10, .	0.6	2
6	Comprehensive glycoproteomics shines new light on the complexity and extent of glycosylation in archaea. <i>PLoS Biology</i> , 2021, 19, e3001277.	5.6	9
7	Open Issues for Protein Function Assignment in <i>Haloferax volcanii</i> and Other Halophilic Archaea. <i>Genes</i> , 2021, 12, 963.	2.4	4
8	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
9	Halovirus HF2 Intergenic Repeat Sequences Carry Promoters. <i>Viruses</i> , 2021, 13, 2388.	3.3	0
10	Whole-genome comparison between the type strain of <i>Halobacterium salinarum</i> (DSM Tj ETQq0 0 0 rgBT/Overlock_10 Tf 50 3	3.0	26
11	Lipid Anchoring of Archaeosortase Substrates and Midcell Growth in Haloarchaea. <i>MBio</i> , 2020, 11, .	4.1	35
12	The Archaeal Proteome Project advances knowledge about archaeal cell biology through comprehensive proteomics. <i>Nature Communications</i> , 2020, 11, 3145.	12.8	40
13	Identification of RNA 3' ends and termination sites in <i>Haloferax volcanii</i> . <i>RNA Biology</i> , 2020, 17, 663-676.	3.1	16
14	Comparative Genomics of Two New HF1-like Haloviruses. <i>Genes</i> , 2020, 11, 405.	2.4	9
15	Contribution of mechanosensitive channels to osmoadaptation and ectoine excretion in <i>Halomonas elongata</i> . <i>Extremophiles</i> , 2020, 24, 421-432.	2.3	16
16	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
17	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
18	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

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19	Halobacterium salinarum virus ChaoS9, a Novel Halovirus Related to PhiH1 and PhiCh1. <i>Genes</i> , 2019, 10, 194.	2.4	11
20	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
21	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
22	Taxis in archaea. <i>Emerging Topics in Life Sciences</i> , 2018, 2, 535-546.	2.6	19
23	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
24	Complete Genome Sequence of the Model Halovirus PhiH1 (ΦH1). <i>Genes</i> , 2018, 9, 493.	2.4	11
25	The PL6-Family Plasmids of <i>Haloquadratum</i> Are Virus-Related. <i>Frontiers in Microbiology</i> , 2018, 9, 1070.	3.5	3
26	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
27	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.	2.6	2
28	Archaeal cell surface biogenesis. <i>FEMS Microbiology Reviews</i> , 2018, 42, 694-717.	8.6	55
29	ThiN as a Versatile Domain of Transcriptional Repressors and Catalytic Enzymes of Thiamine Biosynthesis. <i>Journal of Bacteriology</i> , 2017, 199, .	2.2	11
30	Revision and reannotation of the <i>Halomonas elongata</i> DSM 2581 ^T genome. <i>MicrobiologyOpen</i> , 2017, 6, e00465.	3.0	13
31	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
32	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
33	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
34	Model Construction and Analysis of Respiration in <i>Halobacterium salinarum</i> . <i>PLoS ONE</i> , 2016, 11, e0151839.	2.5	4
35	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
36	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

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37	<i>Haloferax volcanii</i> , a Prokaryotic Species that Does Not Use the Shine Dalgarno Mechanism for Translation Initiation at 5'â€²-UTRs. PLoS ONE, 2014, 9, e94979.	2.5	30
38	Conserved active site cysteine residue of archaeal THI4 homolog is essential for thiamine biosynthesis in <i>Haloferax volcanii</i> . BMC Microbiology, 2014, 14, 260.	3.3	14
39	Chloride and organic osmolytes: a hybrid strategy to cope with elevated salinities by the moderately halophilic, chlorideâ€dependent bacterium <i>Halobacillus halophilus</i> . Environmental Microbiology, 2013, 15, 1619-1633.	3.8	45
40	The ring of confidence: a haloarchaeal CRISPR/Cas system. Biochemical Society Transactions, 2013, 41, 374-378.	3.4	13
41	<i>Haloferax volcanii</i> archaeosortase is required for motility, mating, and C-terminal processing of the S-layer glycoprotein. Molecular Microbiology, 2013, 88, 1164-1175.	2.5	61
42	Genome of the Haloarchaeon <i>Natronomonas moolapensis</i> , a Neutrophilic Member of a Previously Haloalkaliphilic Genus. Genome Announcements, 2013, 1, e0009513.	0.8	10
43	The immune system of halophilic archaea. Mobile Genetic Elements, 2012, 2, 228-232.	1.8	18
44	An Archaeal Immune System Can Detect Multiple Protospacer Adjacent Motifs (PAMs) to Target Invader DNA. Journal of Biological Chemistry, 2012, 287, 33351-33363.	3.4	110
45	A comparative genomics perspective on the genetic content of the alkaliphilic haloarchaeon <i>Natrialba magadii</i> ATCC 43099T. BMC Genomics, 2012, 13, 165.	2.8	36
46	<i>Haloquadratum walsbyi</i> : Limited Diversity in a Global Pond. PLoS ONE, 2011, 6, e20968.	2.5	97
47	A blueprint of ectoine metabolism from the genome of the industrial producer <i>Halomonas elongata</i> DSM 2581 ^T . Environmental Microbiology, 2011, 13, 1973-1994.	3.8	224
48	Mutational and Bioinformatic Analysis of Haloarchaeal Lipobox-Containing Proteins. Archaea, 2010, 2010, 1-11.	2.3	35
49	The Complete Genome Sequence of <i>Haloferax volcanii</i> DS2, a Model Archaeon. PLoS ONE, 2010, 5, e9605.	2.5	234
50	Characterization of Growth and Metabolism of the Haloalkaliphile <i>Natronomonas pharaonis</i> . PLoS Computational Biology, 2010, 6, e1000799.	3.2	24
51	Systems Analysis of Bioenergetics and Growth of the Extreme Halophile <i>Halobacterium salinarum</i> . PLoS Computational Biology, 2009, 5, e1000332.	3.2	42
52	Life-style changes of a halophilic archaeon analyzed by quantitative proteomics. Proteomics, 2009, 9, 3843-3855.	2.2	21
53	Genome information management and integrated data analysis with HaloLex. Archives of Microbiology, 2008, 190, 281-299.	2.2	83
54	Metabolism of halophilic archaea. Extremophiles, 2008, 12, 177-196.	2.3	214

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55	Reconstruction, modeling & analysis of Halobacterium salinarum R-1 metabolism. Molecular BioSystems, 2008, 4, 148-159.	2.9	58
56	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. Molecular Microbiology, 2008, 67, 772-780.	2.5	33
57	Evolution in the laboratory: The genome of Halobacterium salinarum strain R1 compared to that of strain NRC-1. Genomics, 2008, 91, 335-346.	2.9	127
58	Genome sequences of Halobacterium salinarum: A reply. Genomics, 2008, 91, 553-554.	2.9	8
59	Autoinducer-2-Producing Protein LuxS, a Novel Salt- and Chloride-Induced Protein in the Moderately Halophilic Bacterium Halobacillus halophilus. Applied and Environmental Microbiology, 2007, 73, 371-379.	3.1	41
60	Modelling the CheYD10K,Y100W Halobacterium salinarum mutant: sensitivity analysis allows choice of parameter to be modified in the phototaxis model. IET Systems Biology, 2007, 1, 207-221.	1.5	12
61	The Low Molecular Weight Proteome of Halobacterium salinarum. Journal of Proteome Research, 2007, 6, 1510-1518.	3.7	63
62	Large-Scale Identification of N-Terminal Peptides in the Halophilic Archaea Halobacterium salinarum and Natronomonas pharaonis. Journal of Proteome Research, 2007, 6, 2195-2204.	3.7	109
63	Genome-Wide Proteomics of Natronomonas pharaonis. Journal of Proteome Research, 2007, 6, 185-193.	3.7	25
64	Microarray Analysis in the Archaeon Halobacterium salinarum Strain R1. PLoS ONE, 2007, 2, e1064.	2.5	24
65	Quantitative Profiling of the Membrane Proteome in a Halophilic Archaeon. Molecular and Cellular Proteomics, 2006, 5, 1543-1558.	3.8	57
66	Archaeal N-terminal Protein Maturation Commonly Involves N-terminal Acetylation: A Large-scale Proteomics Survey. Journal of Molecular Biology, 2006, 362, 915-924.	4.2	80
67	The genome of the square archaeon Haloquadratum walsbyi : life at the limits of water activity. BMC Genomics, 2006, 7, 169.	2.8	247
68	Biochemical and Molecular Characterization of the Biosynthesis of Glutamine and Glutamate, Two Major Compatible Solutes in the Moderately Halophilic Bacterium Halobacillus halophilus. Journal of Bacteriology, 2006, 188, 6808-6815.	2.2	57
69	Analysis of the cytosolic proteome of <i>Halobacterium salinarum</i> and its implication for genome annotation. Proteomics, 2005, 5, 168-179.	2.2	69
70	The membrane proteome of <i>Halobacterium salinarum</i> . Proteomics, 2005, 5, 180-197.	2.2	101
71	BACCardl—a tool for the validation of genomic assemblies, assisting genome finishing and intergenome comparison. Bioinformatics, 2005, 21, 853-859.	4.1	32
72	Living with two extremes: Conclusions from the genome sequence of Natronomonas pharaonis. Genome Research, 2005, 15, 1336-1343.	5.5	183

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73	Protein Information Resource: a community resource for expert annotation of protein data. <i>Nucleic Acids Research</i> , 2001, 29, 29-32.	14.5	72
74	The Protein Information Resource (PIR). <i>Nucleic Acids Research</i> , 2000, 28, 41-44.	14.5	165
75	The PIR-International Protein Sequence Database. <i>Nucleic Acids Research</i> , 1999, 27, 39-43.	14.5	149
76	The domain-server: direct prediction of protein domain-homologies from BLAST search. <i>Bioinformatics</i> , 1999, 15, 343-344.	4.1	8
77	Database of protein sequence alignments: PIR-ALN. <i>Nucleic Acids Research</i> , 1999, 27, 284-285.	14.5	12
78	The PIR-International Protein Sequence Database. <i>Nucleic Acids Research</i> , 1998, 26, 27-32.	14.5	79
79	MIPS: a database for protein sequences and complete genomes. <i>Nucleic Acids Research</i> , 1998, 26, 33-37.	14.5	85
80	MIPS: a database for protein sequences, homology data and yeast genome information. <i>Nucleic Acids Research</i> , 1997, 25, 28-30.	14.5	217
81	The PIR-International Protein Sequence Database. <i>Nucleic Acids Research</i> , 1996, 24, 17-20.	14.5	59
82	Superfamily classification in PIR-international protein sequence database. <i>Methods in Enzymology</i> , 1996, 266, 59-71.	1.0	47
83	Superfamily and Domain. , 1995, , 473-481.		0
84	Complete DNA sequence of yeast chromosome XI. <i>Nature</i> , 1994, 369, 371-378.	27.8	382
85	The PIR-International databases. <i>Nucleic Acids Research</i> , 1993, 21, 3089-3092.	14.5	72
86	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
87	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
88	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
89	Distribution of glycine receptors at central synapses: an immunoelectron microscopy study.. <i>Journal of Cell Biology</i> , 1985, 101, 683-688.	5.2	357
90	Purification and characterization of the glycine receptor of pig spinal cord. <i>Biochemistry</i> , 1985, 24, 990-994.	2.5	153

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91	Characterization and Purification of the Glycine Receptor of Rat Spinal Cord. , 1984, , 509-511.		0
92	Photoaffinity-Labeling of the Glycine Receptor of Rat Spinal Cord. FEBS Journal, 1983, 131, 519-525.	0.2	95
93	Î±-Bungarotoxin and Strychnine as Tools to Characterize Neurotransmitter Receptors of the Central Nervous System. , 1983, , 245-256.		5
94	Avermectin B1a inhibits the binding of strychnine to the glycine receptor of rat spinal cord. Neuroscience Letters, 1982, 29, 173-176.	2.1	41
95	UV light-induced cross-linking of strychnine to the glycine receptor of rat spinal cord membranes. Biochemical and Biophysical Research Communications, 1981, 102, 1330-1335.	2.1	63
96	Solubilization of the glycine receptor from rat spinal cord. Brain Research, 1981, 226, 273-279.	2.2	75
97	Genome Sequence of Pseudomonas veronii Strain G2, a Member of a Bacterial Consortium Capable of Polyethylene Degradation. Microbiology Resource Announcements, 0, , .	0.6	1