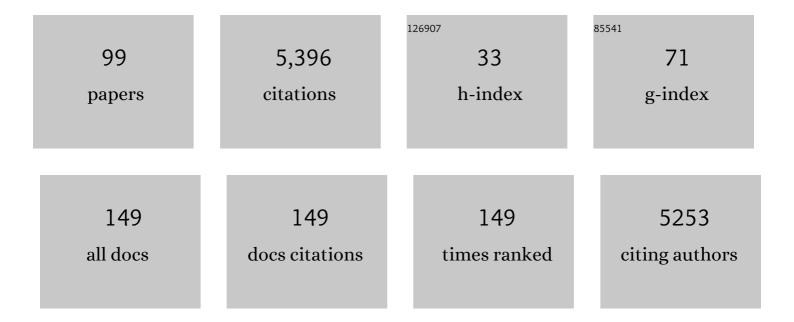
List of Publications by Year in descending order

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FDANK T ROBB

#	Article	IF	CITATIONS
1	The genomic basis of trophic strategy in marine bacteria. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 15527-15533.	7.1	685
2	Complete Sequence and Gene Organization of the Genome of a Hyper-thermophilic Archaebacterium, Pyrococcus horikoshii OT3. DNA Research, 1998, 5, 55-76.	3.4	605
3	Protein thermostability above 100ÂC: A key role for ionic interactions. Proceedings of the National Academy of Sciences of the United States of America, 1998, 95, 12300-12305.	7.1	266
4	Pyrococcus horikoshii sp. nov., a hyperthermophilic archaeon isolated from a hydrothermal vent at the Okinawa Trough. Extremophiles, 1998, 2, 123-130.	2.3	239
5	Life in Hot Carbon Monoxide: The Complete Genome Sequence of Carboxydothermus hydrogenoformans Z-2901. PLoS Genetics, 2005, 1, e65.	3.5	226
6	Genomic sequence of hyperthermophile, Pyrococcus furiosus: Implications for physiology and enzymology. Methods in Enzymology, 2001, 330, 134-157.	1.0	201
7	Evolutionary relationships of bacterial and archaeal glutamine synthetase genes. Journal of Molecular Evolution, 1994, 38, 566-76.	1.8	174
8	Identification and characterization of a multidomain hyperthermophilic cellulase from an archaeal enrichment. Nature Communications, 2011, 2, 375.	12.8	163
9	Detection of circular polarization in light scattered from photosynthetic microbes. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 7816-7821.	7.1	123
10	Characterization of an extremely thermostable glutamate dehydrogenase: a key enzyme in the primary metabolism of the hyperthermophilic archaebacterium, Pyrococcus furiosus. BBA - Proteins and Proteomics, 1992, 1120, 267-272.	2.1	121
11	Enzymes of hydrogen metabolism in <i>Pyrococcus furiosus</i> . FEBS Journal, 2000, 267, 6541-6551.	0.2	118
12	Divergence of the Hyperthermophilic Archaea Pyrococcus furiosus and P. horikoshii Inferred From Complete Genomic Sequences. Genetics, 1999, 152, 1299-1305.	2.9	115
13	Thermosinus carboxydivorans gen. nov., sp. nov., a new anaerobic, thermophilic, carbon-monoxide-oxidizing, hydrogenogenic bacterium from a hot pool of Yellowstone National Park. International Journal of Systematic and Evolutionary Microbiology, 2004, 54, 2353-2359.	1.7	114
14	Complete Genome Sequence of the Aerobic CO-Oxidizing Thermophile Thermomicrobium roseum. PLoS ONE, 2009, 4, e4207.	2.5	113
15	Evidence of recent lateral gene transfer among hyperthermophilic Archaea. Molecular Microbiology, 2000, 38, 684-693.	2.5	107
16	Insights into the molecular basis of thermal stability from the analysis of ion-pair networks in the Glutamate Dehydrogenase family. FEBS Journal, 1998, 255, 336-346.	0.2	103
17	Insights into Thermal Stability from a Comparison of the Glutamate Dehydrogenases from Pyrococcus furiosus and Thermococcus litoralis. FEBS Journal, 1995, 229, 688-695.	0.2	89
18	Small heat shock proteins from extremophiles: a review. Extremophiles, 2004, 8, 1-11.	2.3	87

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19	†That which does not kill us only makes us stronger': the role of carbon monoxide in thermophilic microbial consortia. Environmental Microbiology, 2009, 11, 1027-1037.	3.8	84
20	Evidence for Horizontal Gene Transfer of Anaerobic Carbon Monoxide Dehydrogenases. Frontiers in Microbiology, 2012, 3, 132.	3.5	82
21	Microbial survival of space vacuum and extreme ultraviolet irradiation: strain isolation and analysis during a rocket flight. FEMS Microbiology Letters, 2002, 215, 163-168.	1.8	72
22	Minimal protein-folding systems in hyperthermophilic archaea. Nature Reviews Microbiology, 2004, 2, 315-324.	28.6	68
23	Evidence for the early divergence of tryptophanyl- and tyrosyl-tRNA synthetases. Journal of Molecular Evolution, 1997, 45, 9-16.	1.8	67
24	Conformational Stability of PrP Amyloid Fibrils Controls Their Smallest Possible Fragment Size. Journal of Molecular Biology, 2008, 376, 1155-1167.	4.2	65
25	DNA Repair Systems in Archaea: Mementos from the Last Universal Common Ancestor?. Journal of Molecular Evolution, 1999, 49, 474-484.	1.8	59
26	Regulation and Mechanism of Action of the Small Heat Shock Protein from the Hyperthermophilic Archaeon Pyrococcus furiosus. Journal of Bacteriology, 2001, 183, 5198-5202.	2.2	58
27	The structure of the regulatory region of the rat L1 (L1Rn, long interspersed repeated) DNA family of transposable elements. Nucleic Acids Research, 1988, 16, 9215-9231.	14.5	57
28	Peptone Induction and Rifampin-Insensitive Collagenase Production by <i>Vibrio alginolyticus</i> . Journal of Bacteriology, 1980, 142, 447-454.	2.2	53
29	Nucleotide sequence of the Vibrio alginolyticus calcium-dependent, detergent-resistant alkaline serine exoprotease A. Gene, 1989, 76, 281-288.	2.2	48
30	Pressureâ€induced thermostabilization of glutamate dehydrogenase from the hyperthermophile pyrococcus furiosus. Protein Science, 1999, 8, 1056-1063.	7.6	44
31	Evolutionary divergence between sympatric species of southern African Hakes, Merluccius capensis and M. paradoxus. II. restriction enzyme analysis of mitochondrial DNA. Heredity, 1988, 61, 21-30.	2.6	38
32	Analysis of three genomes within the thermophilic bacterial species Caldanaerobacter subterraneus with a focus on carbon monoxide dehydrogenase evolution and hydrolase diversity. BMC Genomics, 2015, 16, 757.	2.8	38
33	Nucleotide sequence and analysis of the Vibrio alginolyticus sucrase gene (scrB). Gene, 1989, 80, 49-56.	2.2	35
34	Life on the fringe: microbial adaptation to growth on carbon monoxide. F1000Research, 2018, 7, 1981.	1.6	35
35	Anthranilate Synthetase. Journal of Biological Chemistry, 1971, 246, 6908-6912.	3.4	34
36	Stabilization ofTaq DNA Polymerase at High Temperature by Protein Folding Pathways From a Hyperthermophilic Archaeon,Pyrococcus furiosus. Biotechnology and Bioengineering, 2006, 93, 1-5.	3.3	33

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37	Archaeal-like chaperonins in bacteria. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 20269-20274.	7.1	32
38	Cloning and Sequence Analysis of the Mercury Resistance Operon of Streptomyces sp. Strain CHR28 Reveals a Novel Putative Second Regulatory Gene. Journal of Bacteriology, 2000, 182, 2345-2349.	2.2	30
39	A proposal to rename the hyperthermophile <i>Pyrococcus woesei</i> as <i>Pyrococcus furiosus</i> subsp. <i>woesei</i> . Archaea, 2004, 1, 277-283.	2.3	30
40	Regulation of exoprotease production by temperature and oxygen in Vibrio alginolyticus. Archives of Microbiology, 1981, 130, 276-280.	2.2	29
41	A gene from the hyperthermophile Pyrococcus furiosus whose deduced product is homologous to members of the prolyl oligopeptidase family of proteases. Gene, 1995, 152, 103-106.	2.2	28
42	Insights into Thermal Stability from a Comparison of the Glutamate Dehydrogenases from <i>Pyrococcus furiosus</i> and <i>Thermococcus litoralis</i> . FEBS Journal, 1995, 229, 688-695.	0.2	28
43	Genetic analysis ofCarboxydothermus hydrogenoformanscarbon monoxide dehydrogenase genescooFandcooS. FEMS Microbiology Letters, 2000, 191, 243-247.	1.8	25
44	Prokaryotic Chaperonins as Experimental Models for Elucidating Structure-Function Abnormalities of Human Pathogenic Mutant Counterparts. Frontiers in Molecular Biosciences, 2016, 3, 84.	3.5	24
45	Maintenance of Different Mannitol Uptake Systems during Starvation in Oxidative and Fermentative Marine Bacteria. Applied and Environmental Microbiology, 1985, 50, 743-748.	3.1	23
46	Isolation of maltose-regulated genes from the hyperthermophilic archaeum, Pyrococcus furiosus, by subtractive hybridization. Gene, 1994, 148, 137-141.	2.2	22
47	Novel evolutionary histories and adaptive features of proteins from hyperthermophiles. Current Opinion in Biotechnology, 1998, 9, 288-291.	6.6	22
48	Effects of a Novel Disulfide Bond and Engineered Electrostatic Interactions on the Thermostability of Azurinâ€. Biochemistry, 2004, 43, 12563-12574.	2.5	20
49	Regulation of Multiple Carbon Monoxide Consumption Pathways in Anaerobic Bacteria. Frontiers in Microbiology, 2011, 2, 147.	3.5	20
50	Remote sensing of chiral signatures on Mars. Planetary and Space Science, 2012, 72, 111-115.	1.7	20
51	Rapid degradation kinetics of amyloid fibrils under mild conditions by an archaeal chaperonin. Biochemical and Biophysical Research Communications, 2012, 422, 97-102.	2.1	20
52	Cellulolytic bacteria as primary colonizers ofPotamogeton pectinatus L. (Sago Pond Weed) from a Brackish South-Temperate Coastal Lake. Microbial Ecology, 1979, 5, 167-177.	2.8	19
53	Methylpurine DNA Glycosylase of the Hyperthermophilic ArchaeonArchaeoglobus fulgidusâ€. Biochemistry, 2002, 41, 12697-12705.	2.5	19
54	A human CCT5 gene mutation causing distal neuropathy impairs hexadecamer assembly in an archaeal model. Scientific Reports, 2014, 4, 6688.	3.3	19

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55	A modulator domain controlling thermal stability in the Group II chaperonins of Archaea. Archives of Biochemistry and Biophysics, 2011, 512, 111-118.	3.0	18
56	Pawnobiome: manipulation of the hologenome within one host generation and beyond. Frontiers in Microbiology, 2015, 6, 697.	3.5	17
57	Genome Sequence of the Sulfate-Reducing Thermophilic Bacterium Thermodesulfovibrio yellowstonii Strain DSM 11347 ^T (Phylum <i>Nitrospirae</i>). Genome Announcements, 2015, 3, .	0.8	17
58	Purification and regulation of glutamine synthetase in a collagenolytic Vibrio alginolyticus strain. Archives of Microbiology, 1985, 140, 369-374.	2.2	16
59	Extremely thermostable glutamate dehydrogenase (GDH) from the freshwater archaeon Thermococcus waiotapuensis : cloning and comparison with two marine hyperthermophilic GDHs. Extremophiles, 2002, 6, 151-159.	2.3	16
60	Regulation of ribosomal RNA transcription by growth rate of the hyperthermophilic Archaeon,Pyrococcus furiosus. FEMS Microbiology Letters, 1993, 111, 159-164.	1.8	15
61	A Survey of the Genome of the Hyperthermophilic Archaeon, Pyrococcus furiosus. Genome Science & Technology, 1996, 1, 37-46.	0.7	15
62	Bacterial degradation of dichloromethane in cultures and natural environments. Journal of Microbiological Methods, 2003, 54, 419-422.	1.6	15
63	Mechanism of pressure-induced thermostabilization of proteins: Studies of glutamate dehydrogenases from the hyperthermophileThermococcus litoralis. Protein Science, 2001, 10, 1750-1757.	7.6	14
64	Biodegradation of Dichloromethane in an Estuarine Environment. Hydrobiologia, 2006, 559, 77-83.	2.0	14
65	The Complete Genome Sequence of Hyperthermophile Dictyoglomus turgidum DSM 6724â,,¢ Reveals a Specialized Carbohydrate Fermentor. Frontiers in Microbiology, 2016, 7, 1979.	3.5	14
66	Novel Extracellular Electron Transfer Channels in a Gram-Positive Thermophilic Bacterium. Frontiers in Microbiology, 2020, 11, 597818.	3.5	14
67	An exceptionally stable Group II chaperonin from the hyperthermophile Pyrococcus furiosus. Archives of Biochemistry and Biophysics, 2009, 486, 12-18.	3.0	13
68	Chaperone action of a versatile small heat shock protein from <i>Methanococcoides burtonii</i> , a cold adapted archaeon. Proteins: Structure, Function and Bioinformatics, 2009, 75, 275-281.	2.6	11
69	Structural and mechanistic characterization of an archaeal-like chaperonin from a thermophilic bacterium. Nature Communications, 2017, 8, 827.	12.8	11
70	Enzymes of Central Nitrogen Metabolism from Hyperthermophiles: Characterization, Thermostability, and Genetics. Advances in Protein Chemistry, 1996, 48, 311-339.	4.4	10
71	Characterization of technetium(vII) reduction by cell suspensions of thermophilic bacteria and archaea. Applied Microbiology and Biotechnology, 2007, 76, 467-472.	3.6	9
72	Deconstruction of Stable Cross-Beta Fibrillar Structures into Toxic and Nontoxic Products Using a Mutated Archaeal Chaperonin. ACS Chemical Biology, 2013, 8, 2095-2101.	3.4	9

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73	[3] Glutamate dehydrogenases from hyperthermophiles. Methods in Enzymology, 2001, 331, 26-41.	1.0	8
74	Complete Genome Sequence of Coprothermobacter proteolyticus DSM 5265. Genome Announcements, 2014, 2, .	0.8	8
75	Isolation, characterization, and survival strategies of Thermotoga sp. strain PD524, a hyperthermophile from a hot spring in Northern Thailand. Extremophiles, 2015, 19, 853-861.	2.3	8
76	Aspartic acid racemization constrains long-term viability and longevity of endospores. FEMS Microbiology Ecology, 2019, 95, .	2.7	7
77	Regulation of nitrogen catabolic enzymes inVibrio alginolyticus. FEMS Microbiology Letters, 1983, 19, 175-177.	1.8	5
78	Temperature activation of foot muscle d-(â^')-lactate dehydrogenase in the whelk Bullia digitalis. BBA - Proteins and Proteomics, 1986, 872, 286-293.	2.1	5
79	Early Evolution of DNA Repair Mechanisms. , 2004, , 169-182.		5
80	Thermophilic Protein Folding Systems. , 2011, , 583-599.		5
81	Quantitative analysis of the impact of a human pathogenic mutation on the CCT5 chaperonin subunit using a proxy archaeal ortholog. Biochemistry and Biophysics Reports, 2017, 12, 66-71.	1.3	5
82	Bridging human chaperonopathies and microbial chaperonins. Communications Biology, 2019, 2, 103.	4.4	5
83	Aspartic acid racemization and repair in the survival and recovery of hyperthermophiles after prolonged starvation at high temperature. FEMS Microbiology Ecology, 2021, 97, .	2.7	5
84	Oligomerization of an archaeal group II chaperonin is mediated by N-terminal salt bridges. Biochemical and Biophysical Research Communications, 2011, 413, 389-394.	2.1	4
85	Genome Sequence of a Sulfate-Reducing Thermophilic Bacterium, Thermodesulfobacterium commune DSM 2178 T (Phylum Thermodesulfobacteria). Genome Announcements, 2015, 3, .	0.8	4
86	Purification, crystallization, and preliminary X-ray crystallographic analysis of the Group III chaperonin from Carboxydothermus hydrogenoformans. Journal of Microbiology, 2016, 54, 440-444.	2.8	4
87	Temperature and oxygen regulated expression of a glutamine synthetase gene fromVibrio alginolyticus cloned inEscherichia coli. Archives of Microbiology, 1986, 146, 30-34.	2.2	3
88	Structure, Function and Evolution of theÂHsp60 Chaperonins. Heat Shock Proteins, 2017, , 3-20.	0.2	3
89	Geochemistry and microbial diversity of a trichloroethene-contaminated Superfund site undergoing intrinsic in situ reductive dechlorination. FEMS Microbiology Ecology, 2002, 40, 123-134.	2.7	3
90	Improved folding of recombinant protein via co-expression of exogenous chaperones. Methods in Enzymology, 2021, 659, 145-170.	1.0	3

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91	Key Enzymes in the Primary Nitrogen Metabolism of a Hyperthermophile. ACS Symposium Series, 1992, , 74-85.	0.5	1
92	10 Heat Shock Proteins in Hyperthermophiles. Methods in Microbiology, 2006, 35, 233-252.	0.8	1
93	Draft Genome Sequence of the Pyridinediol-Fermenting Bacterium Synergistes jonesii 78-1. Genome Announcements, 2014, 2, .	0.8	1
94	A Multipronged Method for Unveiling Subtle Structural–Functional Defects of Mutant Chaperone Molecules Causing Human Chaperonopathies. Methods in Molecular Biology, 2019, 1873, 69-92.	0.9	1
95	Life in Hot Carbon Monoxide: the Complete Genome Sequence of Carboxydothermus hydrogenoformans Z-2901. PLoS Genetics, 2005, preprint, e65.	3.5	1
96	Rapid extraction of plasmid pGT5 from the hyperthermophilic archaeonPyrococcus abyssi. Molecular Biotechnology, 1999, 11, 221-224.	2.4	0
97	The modern "3G―age of archaeal molecular biology. Frontiers in Microbiology, 2012, 3, 430.	3.5	0
98	Protein-Folding Systems. , 0, , 209-223.		0
99	Functional Genomics in Thermophilic Microorganisms. , 0, , 30-38.		0