Frank T Robb

List of Publications by Year
in descending order

98 papers	5,396 citations	126858 33 h-index	85498 71 g-index
149 all docs	149 docs citations	149 times ranked	5253 citing authors

#	Article	IF	Citations
1	Aspartic acid racemization and repair in the survival and recovery of hyperthermophiles after prolonged starvation at high temperature. FEMS Microbiology Ecology, 2021, 97, .	1.3	5
2	Improved folding of recombinant protein via co-expression of exogenous chaperones. Methods in Enzymology, 2021, 659, 145-170.	0.4	3
3	Novel Extracellular Electron Transfer Channels in a Gram-Positive Thermophilic Bacterium. Frontiers in Microbiology, 2020, 11, 597818.	1.5	14
4	Aspartic acid racemization constrains long-term viability and longevity of endospores. FEMS Microbiology Ecology, 2019, 95, .	1.3	7
5	Bridging human chaperonopathies and microbial chaperonins. Communications Biology, 2019, 2, 103.	2.0	5
6	A Multipronged Method for Unveiling Subtle Structuralâ€“Functional Defects of Mutant Chaperone Molecules Causing Human Chaperonopathies. Methods in Molecular Biology, 2019, 1873, 69-92.	0.4	1
7	Life on the fringe: microbial adaptation to growth on carbon monoxide. F1000Research, 2018, 7, 1981.	0.8	35
8	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.	0.7	5
9	Structural and mechanistic characterization of an archaeal-like chaperonin from a thermophilic bacterium. Nature Communications, 2017, 8, 827.	5.8	11
10	Structure, Function and Evolution of theÂHsp60 Chaperonins. Heat Shock Proteins, 2017, , 3-20.	0.2	3
11	The Complete Genome Sequence of Hyperthermophile Dictyoglomus turgidum DSM 6724â„¢ Reveals a Specialized Carbohydrate Fermentor. Frontiers in Microbiology, 2016, 7, 1979.	1.5	14
12	Purification, crystallization, and preliminary X-ray crystallographic analysis of the Group III chaperonin from Carboxydothermus hydrogenoformans. Journal of Microbiology, 2016, 54, 440-444.	1.3	4
13	Prokaryotic Chaperonins as Experimental Models for Elucidating Structure-Function Abnormalities of Human Pathogenic Mutant Counterparts. Frontiers in Molecular Biosciences, 2016, 3, 84.	1.6	24
14	Pawnobiome: manipulation of the hologenome within one host generation and beyond. Frontiers in Microbiology, 2015, 6, 697.	1.5	17
15	Genome Sequence of the Sulfate-Reducing Thermophilic Bacterium Thermodesulfovibrio yellowstonii Strain DSM 11347 ^T (Phylum Nitrospirae). Genome Announcements, 2015, 3, .	0.8	17
16	Genome Sequence of a Sulfate-Reducing Thermophilic Bacterium, Thermodesulfobacterium commune DSM 2178 T (Phylum Thermodesulfobacteria). Genome Announcements, 2015, 3, .	0.8	4
17	Isolation, characterization, and survival strategies of Thermotoga sp. strain PD524, a hyperthermophile from a hot spring in Northern Thailand. Extremophiles, 2015, 19, 853-861.	0.9	8
18	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.	1.2	38

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19	Draft Genome Sequence of the Pyridinediol-Fermenting Bacterium Synergistes jonesii 78-1. Genome Announcements, 2014, 2, .	0.8	1
20	Complete Genome Sequence of Coprothermobacter proteolyticus DSM 5265. Genome Announcements, 2014, 2, .	0.8	8
21	A human CCT5 gene mutation causing distal neuropathy impairs hexadecamer assembly in an archaeal model. Scientific Reports, 2014, 4, 6688.	1.6	19
22	Deconstruction of Stable Cross-Beta Fibrillar Structures into Toxic and Nontoxic Products Using a Mutated Archaeal Chaperonin. ACS Chemical Biology, 2013, 8, 2095-2101.	1.6	9
23	Remote sensing of chiral signatures on Mars. Planetary and Space Science, 2012, 72, 111-115.	0.9	20
24	Rapid degradation kinetics of amyloid fibrils under mild conditions by an archaeal chaperonin. Biochemical and Biophysical Research Communications, 2012, 422, 97-102.	1.0	20
25	Evidence for Horizontal Gene Transfer of Anaerobic Carbon Monoxide Dehydrogenases. Frontiers in Microbiology, 2012, 3, 132.	1.5	82
26	The modern â€œ3Gâ€•age of archaeal molecular biology. Frontiers in Microbiology, 2012, 3, 430.	1.5	0
27	Identification and characterization of a multidomain hyperthermophilic cellulase from an archaeal enrichment. Nature Communications, 2011, 2, 375.	5.8	163
28	Thermophilic Protein Folding Systems. , 2011, , 583-599.		5
29	A modulator domain controlling thermal stability in the Group II chaperonins of Archaea. Archives of Biochemistry and Biophysics, 2011, 512, 111-118.	1.4	18
30	Oligomerization of an archaeal group II chaperonin is mediated by N-terminal salt bridges. Biochemical and Biophysical Research Communications, 2011, 413, 389-394.	1.0	4
31	Regulation of Multiple Carbon Monoxide Consumption Pathways in Anaerobic Bacteria. Frontiers in Microbiology, 2011, 2, 147.	1.5	20
32	Archaeal-like chaperonins in bacteria. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 20269-20274.	3.3	32
33	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.	3.3	685
34	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.	3.3	123
35	Chaperone action of a versatile small heat shock protein from Methanococcoides burtonii, a cold adapted archaeon. Proteins: Structure, Function and Bioinformatics, 2009, 75, 275-281.	1.5	11
36	â€˜That which does not kill us only makes us strongerâ€™: the role of carbon monoxide in thermophilic microbial consortia. Environmental Microbiology, 2009, 11, 1027-1037.	1.8	84

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37	An exceptionally stable Group II chaperonin from the hyperthermophile Pyrococcus furiosus. Archives of Biochemistry and Biophysics, 2009, 486, 12-18.	1.4	13
38	Complete Genome Sequence of the Aerobic CO-Oxidizing Thermophile Thermomicrobium roseum. PLoS ONE, 2009, 4, e4207.	1.1	113
39	Conformational Stability of PrP Amyloid Fibrils Controls Their Smallest Possible Fragment Size. Journal of Molecular Biology, 2008, 376, 1155-1167.	2.0	65
40	Characterization of technetium(vII) reduction by cell suspensions of thermophilic bacteria and archaea. Applied Microbiology and Biotechnology, 2007, 76, 467-472.	1.7	9
41	10 Heat Shock Proteins in Hyperthermophiles. Methods in Microbiology, 2006, 35, 233-252.	0.4	1
42	Biodegradation of Dichloromethane in an Estuarine Environment. Hydrobiologia, 2006, 559, 77-83.	1.0	14
43	Stabilization ofTaq DNA Polymerase at High Temperature by Protein Folding Pathways From a Hyperthermophilic Archaeon,Pyrococcus furiosus. Biotechnology and Bioengineering, 2006, 93, 1-5.	1.7	33
44	Life in Hot Carbon Monoxide: The Complete Genome Sequence of Carboxydothermus hydrogenoformans Z-2901. PLoS Genetics, 2005, 1, e65.	1.5	226
45	Life in Hot Carbon Monoxide: the Complete Genome Sequence of Carboxydothermus hydrogenoformans Z-2901. PLoS Genetics, 2005, preprint, e65.	1.5	1
46	A proposal to rename the hyperthermophilePyrococcus woeseiasPyrococcus furiosussubsp.woesei. Archaea, 2004, 1, 277-283.	2.3	30
47	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.	0.8	114
48	Early Evolution of DNA Repair Mechanisms. , 2004, , 169-182.		5
49	Minimal protein-folding systems in hyperthermophilic archaea. Nature Reviews Microbiology, 2004, 2, 315-324.	13.6	68
50	Small heat shock proteins from extremophiles: a review. Extremophiles, 2004, 8, 1-11.	0.9	87
51	Effects of a Novel Disulfide Bond and Engineered Electrostatic Interactions on the Thermostability of Azurinâ€. Biochemistry, 2004, 43, 12563-12574.	1.2	20
52	Bacterial degradation of dichloromethane in cultures and natural environments. Journal of Microbiological Methods, 2003, 54, 419-422.	0.7	15
53	Methylpurine DNA Glycosylase of the Hyperthermophilic ArchaeonArchaeoglobus fulgidusâ€. Biochemistry, 2002, 41, 12697-12705.	1.2	19
54	Extremely thermostable glutamate dehydrogenase (GDH) from the freshwater archaeon Thermococcus waiotapuensis : cloning and comparison with two marine hyperthermophilic GDHs. Extremophiles, 2002, 6, 151-159.	0.9	16

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55	Microbial survival of space vacuum and extreme ultraviolet irradiation: strain isolation and analysis during a rocket flight. FEMS Microbiology Letters, 2002, 215, 163-168.	0.7	72
56	Genomic sequence of hyperthermophile, Pyrococcus furiosus: Implications for physiology and enzymology. Methods in Enzymology, 2001, 330, 134-157.	0.4	201
57	[3] Glutamate dehydrogenases from hyperthermophiles. Methods in Enzymology, 2001, 331, 26-41.	0.4	8
58	Mechanism of pressure-induced thermostabilization of proteins: Studies of glutamate dehydrogenases from the hyperthermophileThermococcus litoralis. Protein Science, 2001, 10, 1750-1757.	3.1	14
59	Regulation and Mechanism of Action of the Small Heat Shock Protein from the Hyperthermophilic Archaeon Pyrococcus furiosus. Journal of Bacteriology, 2001, 183, 5198-5202.	1.0	58
60	Evidence of recent lateral gene transfer among hyperthermophilic Archaea. Molecular Microbiology, 2000, 38, 684-693.	1.2	107
61	Enzymes of hydrogen metabolism in Pyrococcus furiosus. FEBS Journal, 2000, 267, 6541-6551.	0.2	118
62	Genetic analysis ofCarboxydothermus hydrogenoformanscarbon monoxide dehydrogenase genescooFandcooS. FEMS Microbiology Letters, 2000, 191, 243-247.	0.7	25
63	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.	1.0	30
64	DNA Repair Systems in Archaea: Mementos from the Last Universal Common Ancestor?. Journal of Molecular Evolution, 1999, 49, 474-484.	0.8	59
65	Pressureâ€induced thermostabilization of glutamate dehydrogenase from the hyperthermophile pyrococcus furiosus. Protein Science, 1999, 8, 1056-1063.	3.1	44
66	Rapid extraction of plasmid pGT5 from the hyperthermophilic archaeonPyrococcus abyssi. Molecular Biotechnology, 1999, 11, 221-224.	1.3	0
67	Divergence of the Hyperthermophilic Archaea Pyrococcus furiosus and P. horikoshii Inferred From Complete Genomic Sequences. Genetics, 1999, 152, 1299-1305.	1.2	115
68	Novel evolutionary histories and adaptive features of proteins from hyperthermophiles. Current Opinion in Biotechnology, 1998, 9, 288-291.	3.3	22
69	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
70	Pyrococcus horikoshii sp. nov., a hyperthermophilic archaeon isolated from a hydrothermal vent at the Okinawa Trough. Extremophiles, 1998, 2, 123-130.	0.9	239
71	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.	3.3	266
72	Complete Sequence and Gene Organization of the Genome of a Hyper-thermophilic Archaebacterium, Pyrococcus horikoshii OT3. DNA Research, 1998, 5, 55-76.	1.5	605

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73	Evidence for the early divergence of tryptophanyl- and tyrosyl-tRNA synthetases. Journal of Molecular Evolution, 1997, 45, 9-16.	0.8	67
74	A Survey of the Genome of the Hyperthermophilic Archaeon, Pyrococcus furiosus. Genome Science & Technology, 1996, 1, 37-46.	1.2	15
75	Enzymes of Central Nitrogen Metabolism from Hyperthermophiles: Characterization, Thermostability, and Genetics. Advances in Protein Chemistry, 1996, 48, 311-339.	4.4	10
76	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.	1.0	28
77	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	28
78	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
79	Evolutionary relationships of bacterial and archaeal glutamine synthetase genes. Journal of Molecular Evolution, 1994, 38, 566-76.	0.8	174
80	Isolation of maltose-regulated genes from the hyperthermophilic archaeum, Pyrococcus furiosus, by subtractive hybridization. Gene, 1994, 148, 137-141.	1.0	22
81	Regulation of ribosomal RNA transcription by growth rate of the hyperthermophilic Archaeon,Pyrococcus furiosus. FEMS Microbiology Letters, 1993, 111, 159-164.	0.7	15
82	Key Enzymes in the Primary Nitrogen Metabolism of a Hyperthermophile. ACS Symposium Series, 1992, , 74-85.	0.5	1
83	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
84	Nucleotide sequence and analysis of the Vibrio alginolyticus sucrase gene (scrB). Gene, 1989, 80, 49-56.	1.0	35
85	Nucleotide sequence of the Vibrio alginolyticus calcium-dependent, detergent-resistant alkaline serine exoprotease A. Gene, 1989, 76, 281-288.	1.0	48
86	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.	1.2	38
87	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.	6.5	57
88	Temperature and oxygen regulated expression of a glutamine synthetase gene fromVibrio alginolyticus cloned inEscherichia coli. Archives of Microbiology, 1986, 146, 30-34.	1.0	3
89	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
90	Purification and regulation of glutamine synthetase in a collagenolytic Vibrio alginolyticus strain. Archives of Microbiology, 1985, 140, 369-374.	1.0	16

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91	Maintenance of Different Mannitol Uptake Systems during Starvation in Oxidative and Fermentative Marine Bacteria. Applied and Environmental Microbiology, 1985, 50, 743-748.	1.4	23
92	Regulation of nitrogen catabolic enzymes inVibrio alginolyticus. FEMS Microbiology Letters, 1983, 19, 175-177.	0.7	5
93	Regulation of exoprotease production by temperature and oxygen in Vibrio alginolyticus. Archives of Microbiology, 1981, 130, 276-280.	1.0	29
94	Peptone Induction and Rifampin-Insensitive Collagenase Production by Vibrio alginolyticus. Journal of Bacteriology, 1980, 142, 447-454.	1.0	53
95	Cellulolytic bacteria as primary colonizers ofPotamogeton pectinatus L. (Sago Pond Weed) from a Brackish South-Temperate Coastal Lake. Microbial Ecology, 1979, 5, 167-177.	1.4	19
96	Anthranilate Synthetase. Journal of Biological Chemistry, 1971, 246, 6908-6912.	1.6	34
97	Protein-Folding Systems. , 0, , 209-223.		0
98	Functional Genomics in Thermophilic Microorganisms. , 0, , 30-38.		0