

George E Fox

List of Publications by Year in descending order

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82
papers

3,579
citations

212478

28
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162838

57
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92
all docs

92
docs citations

92
times ranked

3388
citing authors

#	ARTICLE	IF	CITATIONS
1	Nonstandard RNA/RNA interactions likely enhance folding and stability of segmented ribosomes. <i>Rna</i> , 2022, 28, 340-352.	1.6	3
2	In Vivo Production of Small Embedded in 5S rRNA-Derived Protective Scaffold. <i>Methods in Molecular Biology</i> , 2021, 2323, 75-97.	0.4	1
3	Expansion segments in bacterial and archaeal 5S ribosomal RNAs. <i>Rna</i> , 2021, 27, 133-150.	1.6	9
4	The Peptidyl Transferase Center: a Window to the Past. <i>Microbiology and Molecular Biology Reviews</i> , 2021, 85, e0010421.	2.9	22
5	Net Charges of the Ribosomal Proteins of the <i>S10</i> and <i>Spc</i> Clusters of Halophiles Are Inversely Related to the Degree of Halotolerance. <i>Microbiology Spectrum</i> , 2021, 9, e0178221.	1.2	3
6	Further Characterization of the Pseudo-Symmetrical Ribosomal Region. <i>Life</i> , 2020, 10, 201.	1.1	10
7	Cryo-electron microscopy visualization of a large insertion in the 5S ribosomal RNA of the extremely halophilic archaeon <i>Halococcus morrhuae</i> . <i>FEBS Open Bio</i> , 2020, 10, 1938-1946.	1.0	9
8	Evaluation of Acquired Antibiotic Resistance in <i>Escherichia coli</i> Exposed to Long-Term Low-Shear Modeled Microgravity and Background Antibiotic Exposure. <i>MBio</i> , 2019, 10, .	1.8	46
9	Characterization of the total and viable bacterial and fungal communities associated with the International Space Station surfaces. <i>Microbiome</i> , 2019, 7, 50.	4.9	158
10	Reply to Mortazavi, "Acquired Antibiotic Resistance in <i>Escherichia coli</i> Exposed to Simulated Microgravity: Possible Role of Other Space Stressors and Adaptive Responses" <i>MBio</i> , 2019, 10, .	1.8	1
11	Exploration of RNA Sequence Space in the Absence of a Replicase. <i>Journal of Molecular Evolution</i> , 2018, 86, 264-276.	0.8	3
12	<i>Bacillus safensis</i> FO-36b and <i>Bacillus pumilus</i> SAFR-032: a whole genome comparison of two spacecraft assembly facility isolates. <i>BMC Microbiology</i> , 2018, 18, 57.	1.3	16
13	Draft Genome Sequences from a Novel Clade of <i>Bacillus cereus</i> <i>Sensu Lato</i> Strains, Isolated from the International Space Station. <i>Genome Announcements</i> , 2017, 5, .	0.8	14
14	The adaptation of <i>Escherichia coli</i> cells grown in simulated microgravity for an extended period is both phenotypic and genomic. <i>Npj Microgravity</i> , 2017, 3, 15.	1.9	48
15	Draft Genome Sequence of <i>Marinobacter vinifirmus</i> Type Strain FB1. <i>Genome Announcements</i> , 2017, 5, .	0.8	0
16	Origins and Early Evolution of the Ribosome. , 2016, , 31-60.		9
17	Draft Genome Sequence of <i>Marinobacter</i> sp. Strain P4B1, an Electrogenic Perchlorate-Reducing Strain Isolated from a Long-Term Mixed Enrichment Culture of Marine Bacteria. <i>Genome Announcements</i> , 2016, 4, .	0.8	13
18	Centers of motion associated with EF-Tu binding to the ribosome. <i>RNA Biology</i> , 2016, 13, 524-530.	1.5	14

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19	Bacillus pumilus SAFR-032 Genome Revisited: Sequence Update and Re-Annotation. PLoS ONE, 2016, 11, e0157331.	1.1	21
20	Microbiomes of the dust particles collected from the International Space Station and Spacecraft Assembly Facilities. Microbiome, 2015, 3, 50.	4.9	175
21	Clues to unraveling the coral species problem: distinguishing species from geographic variation in <i>Porites</i> across the Pacific with molecular markers and microskeletal traits. PeerJ, 2015, 3, e751.	0.9	43
22	Major centers of motion in the large ribosomal RNAs. Nucleic Acids Research, 2015, 43, 4640-4649.	6.5	12
23	Extreme Sensory Complexity Encoded in the 10-Megabase Draft Genome Sequence of the Chromatically Acclimating Cyanobacterium <i>Tolypothrix</i> sp. PCC 7601. Genome Announcements, 2015, 3, .	0.8	25
24	Ribosome dynamics and the evolutionary history of ribosomes. Proceedings of SPIE, 2015, , .	0.8	1
25	History of the ribosome and the origin of translation. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 15396-15401.	3.3	224
26	In Vivo Production of Small Recombinant RNAs Embedded in a 5S rRNA-Derived Protective Scaffold. Methods in Molecular Biology, 2015, 1316, 45-65.	0.4	3
27	Secondary Structures of rRNAs from All Three Domains of Life. PLoS ONE, 2014, 9, e88222.	1.1	122
28	The presence of nitrate dramatically changed the predominant microbial community in perchlorate degrading cultures under saline conditions. BMC Microbiology, 2014, 14, 225.	1.3	23
29	Structure determination of noncanonical RNA motifs guided by 1H NMR chemical shifts. Nature Methods, 2014, 11, 413-416.	9.0	72
30	Evolution of the ribosome at atomic resolution. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 10251-10256.	3.3	172
31	An ICEBs1-like element may be associated with the extreme radiation and desiccation resistance of Bacillus pumilus SAFR-032 spores. Extremophiles, 2013, 17, 767-774.	0.9	15
32	Carl R. Woese, 1928–2012. Astrobiology, 2013, 13, 1201-1202.	1.5	1
33	Nanometer scale pores similar in size to the entrance of the ribosomal exit cavity are a common feature of large RNAs. Rna, 2013, 19, 1349-1354.	1.6	6
34	Secondary structure and domain architecture of the 23S and 5S rRNAs. Nucleic Acids Research, 2013, 41, 7522-7535.	6.5	78
35	Candidate Genes That May Be Responsible for the Unusual Resistances Exhibited by Bacillus pumilus SAFR-032 Spores. PLoS ONE, 2013, 8, e66012.	1.1	37
36	An Exit Cavity Was Crucial to the Polymerase Activity of the Early Ribosome. Astrobiology, 2012, 12, 57-60.	1.5	35

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37	UNAC tetraloops: to what extent do they mimic GNRA tetraloops?. <i>Biopolymers</i> , 2012, 97, 617-628.	1.2	18
38	Structural properties of DNA oligomers containing (GACX) _n and (GAXC) _n tandem repeats. <i>Biopolymers</i> , 2012, 97, 155-164.	1.2	1
39	Defining 5S rRNA Structure Space: Point Mutation Data Can Be Used to Predict the Phenotype of Multichange Variants. <i>Molecular Biology and Evolution</i> , 2011, 28, 2629-2636.	3.5	1
40	Resurrection of an ancestral 5S rRNA. <i>BMC Evolutionary Biology</i> , 2011, 11, 218.	3.2	3
41	DNAzyme-mediated recovery of small recombinant RNAs from a 5S rRNA-derived chimera expressed in <i>Escherichia coli</i> . <i>BMC Biotechnology</i> , 2010, 10, 85.	1.7	27
42	Origin and Evolution of the Ribosome. <i>Cold Spring Harbor Perspectives in Biology</i> , 2010, 2, a003483-a003483.	2.3	196
43	Many nonuniversal archaeal ribosomal proteins are found in conserved gene clusters. <i>Archaea</i> , 2009, 2, 241-251.	2.3	22
44	Engineered 5S ribosomal RNAs displaying aptamers recognizing vascular endothelial growth factor and malachite green. <i>Journal of Molecular Recognition</i> , 2009, 22, 154-161.	1.1	40
45	Rapid in vivo exploration of a 5S rRNA neutral network. <i>Journal of Microbiological Methods</i> , 2009, 76, 181-187.	0.7	6
46	Horizontal Gene Transfer in Cyanobacterial Signature Genes. <i>Methods in Molecular Biology</i> , 2009, 532, 339-366.	0.4	16
47	Genome display tool: visualizing features in complex data sets. <i>Source Code for Biology and Medicine</i> , 2007, 2, 1.	1.7	6
48	Characterization of <i>Escherichia coli</i> MG1655 grown in a low-shear modeled microgravity environment. <i>BMC Microbiology</i> , 2007, 7, 15.	1.3	69
49	Paradoxical DNA Repair and Peroxide Resistance Gene Conservation in <i>Bacillus pumilus</i> SAFR-032. <i>PLoS ONE</i> , 2007, 2, e928.	1.1	118
50	Regions of Unusual Statistical Properties as Tools in the Search for Horizontally Transferred Genes in <i>Escherichia coli</i> . <i>AIP Conference Proceedings</i> , 2006, , .	0.3	0
51	Statistical Properties of Short Subsequences in Microbial Genomes and Their Link to Pathogen Identification and Evolution. <i>AIP Conference Proceedings</i> , 2006, , .	0.3	2
52	Ribosome origins: The relative age of 23S rRNA Domains. <i>Origins of Life and Evolution of Biospheres</i> , 2006, 36, 421-429.	0.8	38
53	A parallel computing algorithm for 16S rRNA probe design. <i>Journal of Parallel and Distributed Computing</i> , 2006, 66, 1546-1551.	2.7	3
54	The application of cluster analysis in the intercomparison of loop structures in RNA. <i>Rna</i> , 2005, 11, 412-423.	1.6	34

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55	Effect of an Artificial RNA Marker on Gene Expression in Escherichia coli. Applied and Environmental Microbiology, 2005, 71, 4156-4159.	1.4	5
56	NMR structure and Mg ²⁺ binding of an RNA segment that underlies the L7/L12 stalk in the E.coli 50S ribosomal subunit. Nucleic Acids Research, 2005, 33, 3145-3153.	6.5	7
57	The Evolutionary History of the Translation Machinery. , 2004, , 92-105.		28
58	Cyanobacterial signature genes. Photosynthesis Research, 2003, 75, 211-221.	1.6	19
59	RNA ligation and the origin of tRNA. Origins of Life and Evolution of Biospheres, 2003, 33, 199-209.	0.8	35
60	Common 5S rRNA Variants Are Likely To Be Accepted in Many Sequence Contexts. Journal of Molecular Evolution, 2003, 56, 69-76.	0.8	4
61	Small RNA Sequences Are Readily Stabilized by Inclusion in a Carrier rRNA. Biotechnology Progress, 2003, 19, 734-738.	1.3	12
62	Origins of the protein synthesis machinery: a genomics and structural perspective. , 2003, , .		0
63	Frequent occurrence of the T-loop RNA folding motif in ribosomal RNAs. Rna, 2002, 8, 1112-1119.	1.6	71
64	Ala-His mediated peptide bond formation revisited. Origins of Life and Evolution of Biospheres, 2001, 31, 511-526.	0.8	3
65	Phylogeny of Marine Bacillus Isolates from the Gulf of Mexico. Current Microbiology, 2000, 41, 84-88.	1.0	72
66	Expression of Marker RNAs in Pseudomonas putida. Current Microbiology, 2000, 40, 91-95.	1.0	5
67	A Genomically Modified Marker Strain of Escherichia coli. Current Microbiology, 1998, 37, 341-346.	1.0	8
68	A Low Molecular Weight Artificial RNA of Unique Size with Multiple Probe Target Regions. Systematic and Applied Microbiology, 1997, 20, 133-136.	1.2	15
69	Equally Parsimonious Pathways Through an RNA Sequence Space Are Not Equally Likely. Journal of Molecular Evolution, 1997, 45, 278-284.	0.8	25
70	Conserved Gene Clusters in Bacterial Genomes Provide Further Support for the Primacy of RNA. Journal of Molecular Evolution, 1997, 45, 467-472.	0.8	56
71	DNA CTC triplet repeats involved in dynamic mutations of neurologically related gene sequences form stable duplexes. Nucleic Acids Research, 1995, 23, 4303-4311.	6.5	63
72	Experimental investigation of an RNA sequence space. Origins of Life and Evolution of Biospheres, 1993, 23, 365-372.	0.8	14

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73	A Prototype Stable RNA Identification Cassette for Monitoring Plasmids of Genetically Engineered Microorganisms. Systematic and Applied Microbiology, 1993, 16, 280-286.	1.2	24
74	The Structure and Evolution of Archaeobacterial Ribosomal RNA. , 1985, , 257-310.		12
75	Molecular evidence for a close phylogenetic relationship among box-shaped halophilic bacteria, Halobacterium vallismortis, and Halobacterium marismortui. Canadian Journal of Microbiology, 1983, 29, 52-59.	0.8	19
76	An archaeobacterial 5S rRNA contains a long insertion sequence. Nature, 1981, 293, 755-756.	13.7	59
77	The concept of cellular evolution. Journal of Molecular Evolution, 1977, 10, 1-6.	0.8	345
78	Nucleotide sequence of Clostridium pasteurianum 5S rRNA. FEBS Letters, 1976, 64, 350-352.	1.3	29
79	Sequence characterization of 5S ribosomal RNA from eight gram positive procaryotes. Journal of Molecular Evolution, 1976, 8, 143-153.	0.8	27
80	The nucleotide sequence of the 5S ribosomal RNA from a photobacterium. Journal of Molecular Evolution, 1975, 5, 35-46.	0.8	42
81	5S RNA secondary structure. Nature, 1975, 256, 505-507.	13.7	507
82	Nucleotide sequence of Bacillus megaterium 5 S RNA. FEBS Letters, 1974, 44, 322-323.	1.3	25