Roger A Garrett

List of Publications by Year
in descending order

218 papers	14,860 citations	20759 60 h-index	23472 111 g-index
226 all docs	226 docs citations	226 times ranked	7849 citing authors

#	Article	IF	Citations
1	CRISPR-Cas systems are widespread accessory elements across bacterial and archaeal plasmids. Nucleic Acids Research, 2022, 50, 4315-4328.	6.5	44
2	Type IV CRISPRâ€“Cas systems are highly diverse and involved in competition between plasmids. Nucleic Acids Research, 2020, 48, 2000-2012.	6.5	128
3	Evolutionary classification of CRISPRâ€“Cas systems: a burst of class 2 and derived variants. Nature Reviews Microbiology, 2020, 18, 67-83.	13.6	1,427
4	Archaeal Viruses and Their Interactions with CRISPR-Cas Systems. , 2020, , 199-220.		0
5	Comprehensive search for accessory proteins encoded with archaeal and bacterial type III CRISPR-<i>cas</i> gene cassettes reveals 39 new <i>cas</i> gene families. RNA Biology, 2019, 16, 530-542.	1.5	97
6	Stable maintenance of the rudivirus SIRV3 in a carrier state in <i>Sulfolobus islandicus</i> despite activation of the CRISPR-Cas immune response by a second virus SMV1. RNA Biology, 2019, 16, 557-565.	1.5	12
7	Predicted highly derived class 1 CRISPR-Cas system in Haloarchaea containing diverged Cas5 and Cas7 homologs but no CRISPR array. FEMS Microbiology Letters, 2019, 366, .	0.7	10
8	Repression of RNA polymerase by the archaeo-viral regulator ORF145/RIP. Nature Communications, 2016, 7, 13595.	5.8	20
9	Characterizing leader sequences of CRISPR loci. Bioinformatics, 2016, 32, i576-i585.	1.8	81
10	Major and minor crRNA annealing sites facilitate low stringency DNA protospacer binding prior to Type I-A CRISPR-Cas interference in <i>Sulfolobus</i>. RNA Biology, 2016, 13, 1166-1173.	1.5	15
11	Archaeal physiology: The secrets of termination. Nature Microbiology, 2016, 1, 16159.	5.9	2
12	Diverse CRISPR-Cas responses and dramatic cellular DNA changes and cell death in pKEF9-conjugated<i>Sulfolobus</i>species. Nucleic Acids Research, 2016, 44, 4233-4242.	6.5	18
13	Transcriptome changes in STSV2â€infected <i>Sulfolobus islandicus</i>â€…REY15A undergoing continuous CRISPR spacer acquisition. Molecular Microbiology, 2016, 99, 719-728.	1.2	34
14	CRISPR-Cas Adaptive Immune Systems of the Sulfolobales: Unravelling Their Complexity and Diversity. Life, 2015, 5, 783-817.	1.1	39
15	Genomic context drives transcription of insertion sequences in the bacterial endosymbiont Wolbachia wVulC. Gene, 2015, 564, 81-86.	1.0	1
16	An updated evolutionary classification of CRISPRâ€“Cas systems. Nature Reviews Microbiology, 2015, 13, 722-736.	13.6	2,081
17	Archaeal Viruses of the Sulfolobales: Isolation, Infection, and CRISPR Spacer Acquisition. Methods in Molecular Biology, 2015, 1311, 223-232.	0.4	2
18	Structure of the Yeast Ribosomal Stalk. , 2014, , 115-125.		10

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19	CRISPR adaptive immune systems of Archaea. RNA Biology, 2014, 11, 156-167.	1.5	129
20	A backward view from 16S rRNA to archaea to the universal tree of life to progenotes. RNA Biology, 2014, 11, 232-235.	1.5	5
21	Interâ€viral conflicts that exploit host <scp>CRISPR</scp> immune systems of <scp><i>S</i></scp><i>ulfolobus</i>. Molecular Microbiology, 2014, 91, 900-917.	1.2	68
22	CRISPRstrand: predicting repeat orientations to determine the crRNA-encoding strand at CRISPR loci. Bioinformatics, 2014, 30, i489-i496.	1.8	57
23	A novel single-tailed fusiform Sulfolobus virus STSV2 infecting model Sulfolobus species. Extremophiles, 2014, 18, 51-60.	0.9	38
24	Adenosine triphosphatases of thermophilic archaeal double-stranded DNA viruses. Cell and Bioscience, 2014, 4, 37.	2.1	7
25	Discovery and Seminal Developments in the CRISPR Field. , 2013, , 1-31.		9
26	Archaeal Type II Toxin-Antitoxins. , 2013, , 225-238.		4
27	Genome Sequence of a Novel Archaeal Rudivirus Recovered from a Mexican Hot Spring. Genome Announcements, 2013, 1, .	0.8	13
28	Genome Sequence of a Novel Archaeal Fusellovirus Assembled from the Metagenome of a Mexican Hot Spring. Genome Announcements, 2013, 1, e0016413.	0.8	11
29	Solution properties of the archaeal CRISPR DNA repeat-binding homeodomain protein Cbp2. Nucleic Acids Research, 2013, 41, 3424-3435.	6.5	10
30	SMV1 virus-induced CRISPR spacer acquisition from the conjugative plasmid pMGB1 in <i>Sulfolobus solfataricus</i> P2. Biochemical Society Transactions, 2013, 41, 1449-1458.	1.6	22
31	A novel interference mechanism by a type <scp>IIIB CRISPR</scp>â€<scp>Cmr</scp> module in <i><scp>S</scp>ulfolobus</i>. Molecular Microbiology, 2013, 87, 1088-1099.	1.2	224
32	Protospacer recognition motifs. RNA Biology, 2013, 10, 891-899.	1.5	309
33	Novel insights into gene regulation of the rudivirus SIRV2 infecting<i>Sulfolobus</i>cells. RNA Biology, 2013, 10, 875-885.	1.5	43
34	Genome Sequence of the Acidophilic Bacterium <i>Acidocella</i> sp. Strain MX-AZ02. Genome Announcements, 2013, 1, .	0.8	8
35	Discovery and Seminal Developments in the CRISPR Field. , 2013, , 1-31.		8
36	Selective and hyperactive uptake of foreign DNA by adaptive immune systems of an archaeon via two distinct mechanisms. Molecular Microbiology, 2012, 85, 1044-1056.	1.2	134

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37	Modulation of CRISPR locus transcription by the repeat-binding protein Cbp1 in Sulfolobus. Nucleic Acids Research, 2012, 40, 2470-2480.	6.5	70
38	The expression of one ankyrin pk2 allele of the WO prophage is correlated with the Wolbachia feminizing effect in isopods. BMC Microbiology, 2012, 12, 55.	1.3	23
39	Selective and hyperactive uptake of foreign DNA by adaptive immune systems of an archaeon via two distinct mechanisms. Molecular Microbiology, 2012, 86, 757-757.	1.2	3
40	Archaeal virusesâ€"novel, diverse and enigmatic. Science China Life Sciences, 2012, 55, 422-433.	2.3	23
41	CRISPR/Cas and CRISPR/Cmr Immune Systems of Archaea. , 2012, , 163-181.		2
42	Crystal Structure of ATVORF273, a New Fold for a Thermo- and Acido-Stable Protein from the Acidianus Two-Tailed Virus. PLoS ONE, 2012, 7, e45847.	1.1	7
43	Archaeal CRISPR-based immune systems: exchangeable functional modules. Trends in Microbiology, 2011, 19, 549-556.	3.5	96
44	CRISPR/Cas and Cmr modules, mobility and evolution of adaptive immune systems. Research in Microbiology, 2011, 162, 27-38.	1.0	92
45	CRISPR-based immune systems of the Sulfolobales: complexity and diversity. Biochemical Society Transactions, 2011, 39, 51-57.	1.6	64
46	Dynamic properties of the <i>Sulfolobus</i> CRISPR/Cas and CRISPR/Cmr systems when challenged with vectorâ€borne viral and plasmid genes and protospacers. Molecular Microbiology, 2011, 79, 35-49.	1.2	205
47	AAA ATPase p529 of Acidianus two-tailed virus ATV and host receptor recognition. Virology, 2011, 421, 61-66.	1.1	15
48	Genomic analysis of Acidianus hospitalis W1 a host for studying crenarchaeal virus and plasmid life cycles. Extremophiles, 2011, 15, 487-497.	0.9	35
49	Chaperone Role for Proteins p618 and p892 in the Extracellular Tail Development of Acidianus Two-Tailed Virus. Journal of Virology, 2011, 85, 4812-4821.	1.5	26
50	A Dimeric Rep Protein Initiates Replication of a Linear Archaeal Virus Genome: Implications for the Rep Mechanism and Viral Replication. Journal of Virology, 2011, 85, 925-931.	1.5	36
51	Genome Analyses of Icelandic Strains of<i>Sulfolobus islandicus</i>, Model Organisms for Genetic and Virus-Host Interaction Studies. Journal of Bacteriology, 2011, 193, 1672-1680.	1.0	139
52	The Scottish Structural Proteomics Facility: targets, methods and outputs. Journal of Structural and Functional Genomics, 2010, 11, 167-180.	1.2	107
53	Getting the best out of long-wavelength X-rays:<i>de novo</i>chlorine/sulfur SAD phasing of a structural protein from ATV. Acta Crystallographica Section D: Biological Crystallography, 2010, 66, 304-308.	2.5	37
54	Metagenomic analyses of novel viruses and plasmids from a cultured environmental sample of hyperthermophilic neutrophiles. Environmental Microbiology, 2010, 12, 2918-2930.	1.8	39

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55	The mosaic genome structure of the <i>Wolbachia w</i> Ri strain infecting <i>Drosophila simulans</i>. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 5725-5730.	3.3	236
56	CRISPR families of the crenarchaeal genus <i>Sulfolobus:</i> bidirectional transcription and dynamic properties. Molecular Microbiology, 2009, 72, 259-272.	1.2	214
57	Four newly isolated fuselloviruses from extreme geothermal environments reveal unusual morphologies and a possible interviral recombination mechanism. Environmental Microbiology, 2009, 11, 2849-2862.	1.8	85
58	Conservation of the Type IV Secretion System throughout Wolbachia evolution. Biochemical and Biophysical Research Communications, 2009, 385, 557-562.	1.0	49
59	Distribution of CRISPR spacer matches in viruses and plasmids of crenarchaeal acidothermophiles and implications for their inhibitory mechanism. Biochemical Society Transactions, 2009, 37, 23-28.	1.6	93
60	Viruses in acidic geothermal environments of the Kamchatka Peninsula. Research in Microbiology, 2008, 159, 358-366.	1.0	41
61	Characterization and transcriptional analysis of two gene clusters for typeÂIVÂsecretion machinery in Wolbachia of Armadillidium vulgare. Research in Microbiology, 2008, 159, 481-485.	1.0	20
62	Stygiolobus Rod-Shaped Virus and the Interplay of Crenarchaeal Rudiviruses with the CRISPR Antiviral System. Journal of Bacteriology, 2008, 190, 6837-6845.	1.0	58
63	Structure of the <i>Acidianus</i> Filamentous Virus 3 and Comparative Genomics of Related Archaeal Lipothrixviruses. Journal of Virology, 2008, 82, 371-381.	1.5	49
64	The genome of<i>Hyperthermus butylicus</i>: a sulfur-reducing, peptide fermenting, neutrophilic Crenarchaeote growing up to 108 Â°C. Archaea, 2007, 2, 127-135.	2.3	41
65	Genome of the Acidianus bottle-shaped virus and insights into the replication and packaging mechanisms. Virology, 2007, 364, 237-243.	1.1	49
66	Structural and Genomic Properties of the Hyperthermophilic Archaeal Virus ATV with an Extracellular Stage of the Reproductive Cycle. Journal of Molecular Biology, 2006, 359, 1203-1216.	2.0	110
67	Evolutionary genomics of archaeal viruses: Unique viral genomes in the third domain of life. Virus Research, 2006, 117, 52-67.	1.1	198
68	A putative viral defence mechanism in archaeal cells. Archaea, 2006, 2, 59-72.	2.3	235
69	Crystallization and preliminary X-ray diffraction analysis of protein 14 fromSulfolobus islandicusfilamentous virus (SIFV). Acta Crystallographica Section F: Structural Biology Communications, 2006, 62, 884-886.	0.7	4
70	Viruses of the Archaea: a unifying view. Nature Reviews Microbiology, 2006, 4, 837-848.	13.6	344
71	Mutations and Rearrangements in the Genome of Sulfolobus solfataricus P2. Journal of Bacteriology, 2006, 188, 4198-4206.	1.0	59
72	Divergent transcriptional and translational signals in Archaea. Environmental Microbiology, 2005, 7, 47-54.	1.8	113

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73	Independent virus development outside a host. Nature, 2005, 436, 1101-1102.	13.7	169
74	A novel rudivirus, ARV1, of the hyperthermophilic archaeal genus Acidianus. Virology, 2005, 336, 83-92.	1.1	61
75	Novel RepA-MCM proteins encoded in plasmids pTAU4, pORA1 and pTIK4 from<i>Sulfolobus neozealandicus</i>. Archaea, 2005, 1, 319-325.	2.3	23
76	The Genome of Sulfolobus acidocaldarius , a Model Organism of the Crenarchaeota. Journal of Bacteriology, 2005, 187, 4992-4999.	1.0	262
77	Viral Diversity in Hot Springs of Pozzuoli, Italy, and Characterization of a Unique Archaeal Virus, Acidianus Bottle-Shaped Virus, from a New Family, the Ampullaviridae. Journal of Virology, 2005, 79, 9904-9911.	1.5	101
78	Structure and Genome Organization of AFV2, a Novel Archaeal Lipothrixvirus with Unusual Terminal and Core Structures. Journal of Bacteriology, 2005, 187, 3855-3858.	1.0	51
79	Viruses of hyperthermophilic Crenarchaea. Trends in Microbiology, 2005, 13, 535-542.	3.5	74
80	Genomic comparison of archaeal conjugative plasmids from<i>Sulfolobus</i>. Archaea, 2004, 1, 231-239.	2.3	85
81	Multiple variants of the archaeal DNA rudivirus SIRV1 in a single host and a novel mechanism of genomic variation. Molecular Microbiology, 2004, 54, 366-375.	1.2	35
82	Identification of novel non-coding RNAs as potential antisense regulators in the archaeon Sulfolobus solfataricus. Molecular Microbiology, 2004, 55, 469-481.	1.2	189
83	Morphology and genome organization of the virus PSV of the hyperthermophilic archaeal genera Pyrobaculum and Thermoproteus: a novel virus family, the Globuloviridae. Virology, 2004, 323, 233-242.	1.1	112
84	AFV1, a novel virus infecting hyperthermophilic archaea of the genus acidianus. Virology, 2003, 315, 68-79.	1.1	124
85	Relationships between fuselloviruses infecting the extremely thermophilic archaeon Sulfolobus: SSV1 and SSV2. Research in Microbiology, 2003, 154, 295-302.	1.0	104
86	Genus-Specific Protein Binding to the Large Clusters of DNA Repeats (Short Regularly Spaced Repeats) Present in Sulfolobus Genomes. Journal of Bacteriology, 2003, 185, 2410-2417.	1.0	67
87	Mobile elements in archaeal genomes. FEMS Microbiology Letters, 2002, 206, 131-141.	0.7	89
88	Non-autonomous mobile elements in the crenarchaeon Sulfolobus solfataricus11Edited by J. Karn. Journal of Molecular Biology, 2001, 306, 1-6.	2.0	40
89	Sequences and Replication of Genomes of the Archaeal Rudiviruses SIRV1 and SIRV2: Relationships to the Archaeal Lipothrixvirus SIFV and Some Eukaryal Viruses. Virology, 2001, 291, 226-234.	1.1	112
90	Gene capture in archaeal chromosomes. Nature, 2001, 409, 478-478.	13.7	52

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91	Puromycinâ€"rRNA interaction sites at the peptidyl transferase center. Rna, 2000, 6, 744-754.	1.6	26
92	Gene content and organization of a 281-kbp contig from the genome of the extremely thermophilic archaeon,Sulfolobus solfataricusP2. Genome, 2000, 43, 116-136.	0.9	11
93	pING Family of Conjugative Plasmids from the Extremely Thermophilic Archaeon Sulfolobus islandicus: Insights into Recombination and Conjugation in Crenarchaeota. Journal of Bacteriology, 2000, 182, 7014-7020.	1.0	74
94	A Bac Library and Paired-PCR Approach to Mapping and Completing the Genome Sequence of<i>Sulfolobus Solfataricus</i>P2. DNA Sequence, 2000, 11, 183-192.	0.7	10
95	Evolution of the family of pRN plasmids and their integrase-mediated insertion into the chromosome of the crenarchaeon Sulfolobus solfataricus 1 1Edited by J. Karn. Journal of Molecular Biology, 2000, 303, 449-454.	2.0	67
96	Gene content and organization of a 281-kbp contig from the genome of the extremely thermophilic archaeon, <i>Sulfolobus solfataricus</i> P2. Genome, 2000, 43, 116-136.	0.9	2
97	Peptidyl transferase antibiotics perturb the relative positioning of the 3â€²-terminal adenosine of P/Pâ€²-site-bound tRNA and 23S rRNA in the ribosome. Rna, 1999, 5, 1003-1013.	1.6	31
98	UV-induced modifications in the peptidyl transferase loop of 23S rRNA dependent on binding of the streptogramin B antibiotic, pristinamycin IA. Rna, 1999, 5, 585-595.	1.6	18
99	The genetic element pSSVx of the extremely thermophilic crenarchaeon Sulfolobus is a hybrid between a plasmid and a virus. Molecular Microbiology, 1999, 34, 217-226.	1.2	107
100	Mechanics of the ribosome. Nature, 1999, 400, 811-812.	13.7	28
101	Ribosomal Mechanics, Antibiotics, and GTP Hydrolysis. Cell, 1999, 97, 423-426.	13.5	45
102	Sites of interaction of streptogramin A and B antibiotics in the peptidyl transferase loop of 23 S rRNA and the synergism of their inhibitory mechanisms 1 1Edited by D. E. Draper. Journal of Molecular Biology, 1999, 286, 375-387.	2.0	74
103	The antibiotic micrococcin acts on protein L11 at the ribosomal GTPase centre 1 1Edited by D. E. Draper. Journal of Molecular Biology, 1999, 287, 33-45.	2.0	56
104	Genetic elements in the extremely thermophilic archaeon Sulfolobus. Extremophiles, 1998, 2, 131-140.	0.9	148
105	Completing the sequence of the Sulfolobus solfataricus P2 genome. Extremophiles, 1998, 2, 305-312.	0.9	58
106	Archaea and the new age of microorganisms. Trends in Ecology and Evolution, 1998, 13, 190-194.	4.2	21
107	Sulfolobus genome: from genomics to biology. Current Opinion in Microbiology, 1998, 1, 584-588.	2.3	23
108	The antibiotic thiostrepton inhibits a functional transition within protein L11 at the ribosomal GTPase centre 1 1Edited by D. E. Draper. Journal of Molecular Biology, 1998, 276, 391-404.	2.0	114

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109	Assembly of proteins and 5 S rRNA to transcripts of the major structural domains of 23 S rRNA 1 1Edited by D. E. Draper. Journal of Molecular Biology, 1998, 284, 227-240.	2.0	36
110	Movement of the 3â€²-end of tRNA through the peptidyl transferase centre and its inhibition by antibiotics. FEBS Letters, 1997, 406, 223-233.	1.3	54
111	A Sparsomycin-resistant Mutant ofHalobacterium salinariumLacks a Modification at Nucleotide U2603 in the Peptidyl Transferase Centre of 23 S rRNA. Journal of Molecular Biology, 1996, 261, 231-238.	2.0	42
112	The Donor Substrate Site within the Peptidyl Transferase Loop of 23 S rRNA and its Putative Interactions with the CCA-end of N-blocked Aminoacyl-tRNAPhe. Journal of Molecular Biology, 1996, 264, 472-483.	2.0	37
113	Genomes: Methanococcus jannaschii and the golden fleece. Current Biology, 1996, 6, 1377-1380.	1.8	12
114	Phylogenetic Analysis of the Archaeal Order of Sulfolobales Based on Sequences of 23S rRNA Genes and 16S/23S rDNA Spacers. Systematic and Applied Microbiology, 1996, 19, 61-65.	1.2	11
115	General vectors for archaeal hyperthermophiles: Strategies based on a mobile intron and a plasmid. FEMS Microbiology Reviews, 1996, 18, 93-104.	3.9	65
116	General vectors for archaeal hyperthermophiles: Strategies based on a mobile intron and a plasmid. FEMS Microbiology Reviews, 1996, 18, 93-104.	3.9	2
117	Role for the highly conserved region of domain IV of 23 S-1 ike rRNA in subunit-subunit interactions at the peptidyl transferase centre. Nucleic Acids Research, 1995, 23, 1512-1517.	6.5	33
118	Fine Structure of the Peptidyl Transferase Centre on 23 S-like rRNAs Deduced from Chemical Probing of Antibiotic-Ribosome Complexes. Journal of Molecular Biology, 1995, 247, 224-235.	2.0	153
119	Mapping Important Nucleotides in the Peptidyl Transferase Centre of 23 S rRNA using a Random Mutagenesis Approach. Journal of Molecular Biology, 1995, 249, 1-10.	2.0	76
120	Antibiotic inhibition of the movement of tRNA substrates through a peptidyl transferase cavity. Biochemistry and Cell Biology, 1995, 73, 877-885.	0.9	21
121	Structural Characteristics of the Stable RNA Introns of Archaeal Hyperthermophiles and their Splicing Junctions. Journal of Molecular Biology, 1994, 243, 846-855.	2.0	41
122	Cross-hypersensitivity Effects of Mutations in 23 S rRNA Yield Insight into Aminoacyl-tRNA Binding. Journal of Molecular Biology, 1994, 244, 151-157.	2.0	34
123	DNA substrate specificity and cleavage kinetics of an archaeal homing-type endonuclease from Pyrobaculum organotrophum. Nucleic Acids Research, 1994, 22, 4583-4590.	6.5	34
124	Archaeal rRNA Operons, Intron Splicing and Homing Endonucleases, RNA Polymerase Operons and Phylogeny. Systematic and Applied Microbiology, 1993, 16, 680-691.	1.2	15
125	Stable Maintenance in Halobacteria of Plasmids Harboring rDNA. Systematic and Applied Microbiology, 1993, 16, 672-679.	1.2	1
126	Phylogenetic Relationships Amongst the Hyperthermophilic Archaea Determined from Partial 23S rRNA Gene Sequences. Systematic and Applied Microbiology, 1992, 15, 203-208.	1.2	27

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127	Protein-coding introns from the 23S rRNA-encoding gene form stable circles in the hyperthermophilic archaeon Pyrobaculum organotrophum. Gene, 1992, 121, 103-110.	1.0	50
128	Archaeal rRNA operons. Trends in Biochemical Sciences, 1991, 16, 22-26.	3.7	75
129	Attachment sites of primary binding proteins L1, L2 and L23 on 23 S ribosomal RNA of Escherichia coli. Journal of Molecular Biology, 1991, 222, 251-264.	2.0	49
130	Secondary structural elements exclusive to the sequences flanking ribosomal RNAs lend support to the monophyletic nature of the archaebacteria. Journal of Molecular Evolution, 1990, 31, 25-32.	0.8	20
131	Sequence, Organization and Transcription of the Ribosomal RNA Operon and the Downstream tRNA and Protein Genes in the Archaebacterium Thermofilum pendents. Systematic and Applied Microbiology, 1990, 13, 117-127.	1.2	21
132	Characterization of the binding sites of protein L11 and the L10.(L12)4 pentameric complex in the GTPase domain of 23 S ribosomal RNA from Escherichia coli. Journal of Molecular Biology, 1990, 213, 275-288.	2.0	134
133	The phylogenetic relations of DNA-dependent RNA polymerases of archaebacteria, eukaryotes, and eubacteria. Canadian Journal of Microbiology, 1989, 35, 73-80.	0.8	69
134	Comparison of transfer RNA and ribosomal RNA intron splicing in the extreme thermophile and archaebacterium <i>Desulfurococcus mobilis</i>. Canadian Journal of Microbiology, 1989, 35, 210-214.	0.8	44
135	Sequence, organization, transcription and evolution of RNA polymerase subunit genes from the archaebacterial extreme halophiles Halobacterium halobium and Halococcus morrhuae. Journal of Molecular Biology, 1989, 206, 1-17.	2.0	148
136	Protein L18 binds primarily at the junctions of helix II and internal loops A and B in Escherichia coli 5 S RNA. Journal of Molecular Biology, 1989, 206, 651-668.	2.0	32
137	Domain VI of Escherichia coli 23 S ribosomal RNA. Journal of Molecular Biology, 1988, 204, 507-522.	2.0	57
138	Novel splicing mechanism for the ribosomal RNA intron in the archaebacterium desulfurococcus mobilis. Cell, 1988, 54, 693-703.	13.5	136
139	[30] Enzymatic and chemical probing of ribosomal RNAâ€”Protein interactions. Methods in Enzymology, 1988, 164, 456-468.	0.4	21
140	[49] Primer-directed deletions in 5S ribosomal RNA. Methods in Enzymology, 1988, 164, 710-721.	0.4	3
141	Gene organization, transcription signals and processing of the single ribosomal RNA operon of the archaebacteriumThermoproteus tenax. Nucleic Acids Research, 1987, 15, 4821-4835.	6.5	53
142	A plasmid-coded and site-directed mutation in Escherichia coli 23S RNA that confers resistance to erythromycin: implications for the mechanism of action of erythromycin. Biochimie, 1987, 69, 891-900.	1.3	94
143	A Ribosomal RNA Operon and its Flanking Region from the Archaebacterium Methanobacterium thermoautotrophicum, Marburg Strain: Transcription Signals, RNA Structure and Evolutionary Implications. Systematic and Applied Microbiology, 1987, 9, 199-209.	1.2	51
144	The sequence of the 16S RNA gene and its flanking region from the archaebacterium Desulfurococcus mobilis. Systematic and Applied Microbiology, 1987, 9, 22-28.	1.2	30

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145	Structure and accessibility of domain I of Escherichia coli 23 S RNA in free RNA, in the L24-RNA complex and in 50 S subunits. Journal of Molecular Biology, 1987, 196, 125-136.	2.0	56
146	Evolutionary relationships amongst archaebacteria. Journal of Molecular Biology, 1987, 195, 43-61.	2.0	198
147	Novel expression of the ribosomal RNA genes in the extreme thermophile and archaebacterium <i>Desulfurococcus mobilis</i>. EMBO Journal, 1987, 6, 3521-3530.	3.5	45
148	Evolutionary divergence between the ribosomal RNA operons of Halococcus morrhuae and Desulfurococcus mobilis. Systematic and Applied Microbiology, 1986, 7, 49-57.	1.2	39
149	A Domain of 23S Ribosomal RNA in Search of a Function. , 1986, , 221-237.		1
150	Molecular evolution: The uniqueness of Archaebacteria. Nature, 1985, 318, 233-234.	13.7	19
151	An intron in the 23S ribosomal RNA gene of the archaebacterium Desulfurococcus mobilis. Nature, 1985, 318, 675-677.	13.7	104
152	Comparison of eubacterial and eukaryotic 5S RNA structures: a chemical modification study. Biochemistry, 1985, 24, 241-250.	1.2	22
153	Alternative conformers of 5S ribosomal RNA and their biological relevance. Biochemistry, 1985, 24, 2284-2291.	1.2	23
154	Structure of a protein L23-RNA complex located at the A-site domain of the ribosomal peptidyl transferase centre. Journal of Molecular Biology, 1984, 179, 431-452.	2.0	50
155	Higher-order structure in the 3â€²-terminal domain VI of the 23 S ribosomal RNAs from Escherichia coli and Bacillus stearothermophilus. Journal of Molecular Biology, 1984, 179, 689-712.	2.0	18
156	Comparison of Escherichia coli tRNAPhe in the Free State, in the Ternary Complex and in the Ribosomal A and P Sites by Chemical Probing. FEBS Journal, 1983, 131, 261-269.	0.2	40
157	A consensus model of the Escherichia coli ribosome. Trends in Biochemical Sciences, 1983, 8, 359-363.	3.7	21
158	Higher order structure in the 3â€²-minor domain of small subunit ribosomal RNAs from a gram negative bacterium, a gram positive bacterium and a eukaryote. Journal of Molecular Biology, 1983, 169, 249-279.	2.0	64
159	Antibiotics and active ribosomal RNA sites. Trends in Biochemical Sciences, 1983, 8, 189-190.	3.7	7
160	Roles for ribosomal proteins. Trends in Biochemical Sciences, 1983, 8, 75-76.	3.7	6
161	The primary structures of two leghemoglobin genes from soybean. Nucleic Acids Research, 1982, 10, 689-701.	6.5	171
162	tRNA binding to ribosomes â€” two sites or more?. Trends in Biochemical Sciences, 1982, 7, 79.	3.7	4

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163	Structure of eukaryotic 5S ribonucleic acid: a study of Saccharomyces cerevisiae 5S RNA with ribonucleases. Biochemistry, 1982, 21, 4823-4830.	1.2	37
164	Binding sites of ribosomal proteins on prokaryotic 5S RNAs: a study with ribonucleases. Biochemistry, 1982, 21, 2313-2320.	1.2	51
165	Secondary structure of prokaryotic 5S ribosomal ribonucleic acids: a study with ribonucleases. Biochemistry, 1981, 20, 7301-7307.	1.2	54
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