

John F Atkins

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

198
papers

10,790
citations

59
h-index

96
g-index

209
ext. papers

12,074
ext. citations

13.4
avg, IF

6.11
L-index

#	Paper	IF	Citations
198	Evaluating ribosomal frameshifting in CCR5 mRNA decoding.. <i>Nature</i> , 2022 , 604, E16-E23	50.4	0
197	Structural basis of ribosomal frameshifting during translation of the SARS-CoV-2 RNA genome. <i>Science</i> , 2021 , 372, 1306-1313	33.3	49
196	Tissue-specific dynamic codon redefinition in. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021 , 118,	11.5	3
195	Polysomes Bypass a 50-Nucleotide Coding Gap Less Efficiently Than Monosomes Due to Attenuation of a 5' mRNA Stem-Loop and Enhanced Drop-off. <i>Journal of Molecular Biology</i> , 2020 , 432, 4369-4387	6.5	3
194	The energy landscape of -1 ribosomal frameshifting. <i>Science Advances</i> , 2020 , 6, eaax6969	14.3	31
193	Stop codon readthrough contexts influence reporter expression differentially depending on the presence of an IRES.. <i>Wellcome Open Research</i> , 2020 , 5, 221	4.8	0
192	Unusually efficient CUG initiation of an overlapping reading frame in mRNA yields novel protein POLGARF. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020 , 117, 24936-24946	11.5	14
191	Processive Recoding and Metazoan Evolution of Selenoprotein P: Up to 132 UGAs in Molluscs. <i>Journal of Molecular Biology</i> , 2019 , 431, 4381-4407	6.5	12
190	Polyamine Control of Translation Elongation Regulates Start Site Selection on Antizyme Inhibitor mRNA via Ribosome Queuing. <i>Molecular Cell</i> , 2018 , 70, 254-264.e6	17.6	69
189	Stop codon readthrough generates a C-terminally extended variant of the human vitamin D receptor with reduced calcitriol response. <i>Journal of Biological Chemistry</i> , 2018 , 293, 4434-4444	5.4	30
188	AMD1 mRNA employs ribosome stalling as a mechanism for molecular memory formation. <i>Nature</i> , 2018 , 553, 356-360	50.4	45
187	Translational autoregulation of BZW1 and BZW2 expression by modulating the stringency of start codon selection. <i>PLoS ONE</i> , 2018 , 13, e0192648	3.7	11
186	Pyrrolysine in archaea: a 22nd amino acid encoded through a genetic code expansion. <i>Emerging Topics in Life Sciences</i> , 2018 , 2, 607-618	3.5	8
185	Culmination of a half-century quest reveals insight into mutant tRNA-mediated frameshifting after tRNA departure from the decoding site. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018 , 115, 11121-11123	11.5	2
184	A [Cu]rious Ribosomal Profiling Pattern Leads to the Discovery of Ribosomal Frameshifting in the Synthesis of a Copper Chaperone. <i>Molecular Cell</i> , 2017 , 65, 203-204	17.6	3
183	Avoidance of reporter assay distortions from fused dual reporters. <i>Rna</i> , 2017 , 23, 1285-1289	5.8	34
182	Stimulation of reverse transcriptase generated cDNAs with specific indels by template RNA structure: retrotransposon, dNTP balance, RT-reagent usage. <i>Nucleic Acids Research</i> , 2017 , 45, 10143-10155	20.1	5

181	ASXL gain-of-function truncation mutants: defective and dysregulated forms of a natural ribosomal frameshifting product?. <i>Biology Direct</i> , 2017 , 12, 24	7.2	7
180	Specific reverse transcriptase slippage at the HIV ribosomal frameshift sequence: potential implications for modulation of GagPol synthesis. <i>Nucleic Acids Research</i> , 2017 , 45, 10156-10167	20.1	7
179	Translation Initiation from Conserved Non-AUG Codons Provides Additional Layers of Regulation and Coding Capacity. <i>MBio</i> , 2017 , 8,	7.8	13
178	Position-dependent termination and widespread obligatory frameshifting in Euplotes translation. <i>Nature Structural and Molecular Biology</i> , 2017 , 24, 61-68	17.6	38
177	Multiple RNA structures affect translation initiation and UGA redefinition efficiency during synthesis of selenoprotein P. <i>Nucleic Acids Research</i> , 2017 , 45, 13004-13015	20.1	14
176	An Expanded CAG Repeat in Huntingtin Causes +1 Frameshifting. <i>Journal of Biological Chemistry</i> , 2016 , 291, 18505-13	5.4	14
175	Novel Ciliate Genetic Code Variants Including the Reassignment of All Three Stop Codons to Sense Codons in <i>Condylostoma magnum</i> . <i>Molecular Biology and Evolution</i> , 2016 , 33, 2885-2889	8.3	69
174	Human selenoprotein P and S variant mRNAs with different numbers of SECIS elements and inferences from mutant mice of the roles of multiple SECIS elements. <i>Open Biology</i> , 2016 , 6,	7	10
173	Systematic analysis of the PTEN 5Qleader identifies a major AUU initiated proteoform. <i>Open Biology</i> , 2016 , 6,	7	25
172	Ribosomal frameshifting and transcriptional slippage: From genetic steganography and cryptography to adventitious use. <i>Nucleic Acids Research</i> , 2016 , 44, 7007-78	20.1	157
171	Productive mRNA stem loop-mediated transcriptional slippage: Crucial features in common with intrinsic terminators. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015 , 112, E1984-93	11.5	13
170	Augmented genetic decoding: global, local and temporal alterations of decoding processes and codon meaning. <i>Nature Reviews Genetics</i> , 2015 , 16, 517-29	30.1	47
169	Coupling of mRNA Structure Rearrangement to Ribosome Movement during Bypassing of Non-coding Regions. <i>Cell</i> , 2015 , 163, 1267-1280	56.2	28
168	A Nascent Peptide Signal Responsive to Endogenous Levels of Polyamines Acts to Stimulate Regulatory Frameshifting on Antizyme mRNA. <i>Journal of Biological Chemistry</i> , 2015 , 290, 17863-17878	5.4	15
167	Transcriptional slippage in the positive-sense RNA virus family Potyviridae. <i>EMBO Reports</i> , 2015 , 16, 995-1004	10.4	125
166	Human DNA tumor viruses generate alternative reading frame proteins through repeat sequence recoding. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014 , 111, E4342-9	11.5	14
165	High-efficiency translational bypassing of non-coding nucleotides specified by mRNA structure and nascent peptide. <i>Nature Communications</i> , 2014 , 5, 4459	17.4	24
164	Sepp1(UF) forms are N-terminal selenoprotein P truncations that have peroxidase activity when coupled with thioredoxin reductase-1. <i>Free Radical Biology and Medicine</i> , 2014 , 69, 67-76	7.8	33

163	Evidence of efficient stop codon readthrough in four mammalian genes. <i>Nucleic Acids Research</i> , 2014 , 42, 8928-38	20.1	130
162	Transcriptional frameshifting rescues <i>Citrobacter rodentium</i> type VI secretion by the production of two length variants from the prematurely interrupted <i>tssM</i> gene. <i>PLoS Genetics</i> , 2014 , 10, e1004869	6	9
161	Analysis of tetra- and hepta-nucleotides motifs promoting -1 ribosomal frameshifting in <i>Escherichia coli</i> . <i>Nucleic Acids Research</i> , 2014 , 42, 7210-25	20.1	19
160	Cryptic MHC class I-binding peptides are revealed by aminoglycoside-induced stop codon read-through into the 3'UTR. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014 , 111, 5670-5	11.5	29
159	rRNA:mRNA pairing alters the length and the symmetry of mRNA-protected fragments in ribosome profiling experiments. <i>Bioinformatics</i> , 2013 , 29, 1488-91	7.2	44
158	Identification of the nature of reading frame transitions observed in prokaryotic genomes. <i>Nucleic Acids Research</i> , 2013 , 41, 6514-30	20.1	22
157	Alternative reading frame selection mediated by a tRNA-like domain of an internal ribosome entry site. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012 , 109, E630-9	11.5	47
156	Observation of dually decoded regions of the human genome using ribosome profiling data. <i>Genome Research</i> , 2012 , 22, 2219-29	9.7	137
155	Efficient -2 frameshifting by mammalian ribosomes to synthesize an additional arterivirus protein. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012 , 109, E2920-8	11.5	187
154	Production of selenoprotein P (Sepp1) by hepatocytes is central to selenium homeostasis. <i>Journal of Biological Chemistry</i> , 2012 , 287, 40414-24	5.4	98
153	Stringency of start codon selection modulates autoregulation of translation initiation factor eIF5. <i>Nucleic Acids Research</i> , 2012 , 40, 2898-906	20.1	74
152	Selenoprotein P (Sepp1) Synthesis by the Liver Protects against Selenium Deficiency. <i>FASEB Journal</i> , 2012 , 26, 241.3	0.9	
151	Molecular biology. Translation goes global. <i>Science</i> , 2011 , 334, 1509-10	33.3	12
150	Stimulation of stop codon readthrough: frequent presence of an extended 3'RNA structural element. <i>Nucleic Acids Research</i> , 2011 , 39, 6679-91	20.1	100
149	Programmed ribosomal frameshifting in the expression of the regulator of intestinal stem cell proliferation, adenomatous polyposis coli (APC). <i>RNA Biology</i> , 2011 , 8, 637-47	4.8	13
148	A pilot study of bacterial genes with disrupted ORFs reveals a surprising profusion of protein sequence recoding mediated by ribosomal frameshifting and transcriptional realignment. <i>Molecular Biology and Evolution</i> , 2011 , 28, 3195-211	8.3	38
147	The interplay of mRNA stimulatory signals required for AUU-mediated initiation and programmed -1 ribosomal frameshifting in decoding of transposable element IS911. <i>Journal of Bacteriology</i> , 2011 , 193, 2735-44	3.5	10
146	Two groups of phenylalanine biosynthetic operon leader peptides genes: a high level of apparently incidental frameshifting in decoding <i>Escherichia coli</i> pheL. <i>Nucleic Acids Research</i> , 2011 , 39, 3079-92	20.1	7

145	Ribosomal frameshifting into an overlapping gene in the 2B-encoding region of the cardiovirus genome. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011 , 108, E1111-9	11.5	54
144	Identification of evolutionarily conserved non-AUG-initiated N-terminal extensions in human coding sequences. <i>Nucleic Acids Research</i> , 2011 , 39, 4220-34	20.1	147
143	Discovery of a small arterivirus gene that overlaps the GP5 coding sequence and is important for virus production. <i>Journal of General Virology</i> , 2011 , 92, 1097-1106	4.9	222
142	The distinction between recoding and codon reassignment. <i>Genetics</i> , 2010 , 185, 1535-6	4	16
141	A profusion of upstream open reading frame mechanisms in polyamine-responsive translational regulation. <i>Nucleic Acids Research</i> , 2010 , 38, 353-9	20.1	66
140	Initiation context modulates autoregulation of eukaryotic translation initiation factor 1 (eIF1). <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010 , 107, 18056-60	11.5	92
139	NS1Q of flaviviruses in the Japanese encephalitis virus serogroup is a product of ribosomal frameshifting and plays a role in viral neuroinvasiveness. <i>Journal of Virology</i> , 2010 , 84, 1641-7	6.6	134
138	Candidates in Astroviruses, Seadornaviruses, Cytorhabdoviruses and Coronaviruses for +1 frame overlapping genes accessed by leaky scanning. <i>Virology Journal</i> , 2010 , 7, 17	6.1	22
137	Recode-2: new design, new search tools, and many more genes. <i>Nucleic Acids Research</i> , 2010 , 38, D69-74	20.1	42
136	Frameshifting in alphaviruses: a diversity of 3Q stimulatory structures. <i>Journal of Molecular Biology</i> , 2010 , 397, 448-56	6.5	36
135	Recurrent emergence of catalytically inactive ornithine decarboxylase homologous forms that likely have regulatory function. <i>Journal of Molecular Evolution</i> , 2010 , 70, 289-302	3.1	19
134	Evidence for ribosomal frameshifting and a novel overlapping gene in the genomes of insect-specific flaviviruses. <i>Virology</i> , 2010 , 399, 153-166	3.6	54
133	Versatile dual reporter gene systems for investigating stop codon readthrough in plants. <i>PLoS ONE</i> , 2009 , 4, e7354	3.7	7
132	A gripping tale of ribosomal frameshifting: extragenic suppressors of frameshift mutations spotlight P-site realignment. <i>Microbiology and Molecular Biology Reviews</i> , 2009 , 73, 178-210	13.2	103
131	A case for a CUG-initiated coding sequence overlapping torovirus ORF1a and encoding a novel 30 kDa product. <i>Virology Journal</i> , 2009 , 6, 136	6.1	7
130	A conserved predicted pseudoknot in the NS2A-encoding sequence of West Nile and Japanese encephalitis flaviviruses suggests NS1Q may derive from ribosomal frameshifting. <i>Virology Journal</i> , 2009 , 6, 14	6.1	107
129	Bioinformatic evidence for a stem-loop structure 5Q adjacent to the IGR-IRES and for an overlapping gene in the bee paralysis dicistroviruses. <i>Virology Journal</i> , 2009 , 6, 193	6.1	26
128	Analysis of the coding potential of the partially overlapping 3QORF in segment 5 of the plant fijiviruses. <i>Virology Journal</i> , 2009 , 6, 32	6.1	26

127	Evidence for a novel coding sequence overlapping the 5' terminal approximately 90 codons of the gill-associated and yellow head okavirus envelope glycoprotein gene. <i>Virology Journal</i> , 2009 , 6, 222	6.1	4
126	Translational bypassing without peptidyl-tRNA anticodon scanning of coding gap mRNA. <i>EMBO Journal</i> , 2008 , 27, 2533-44	13	22
125	Foot and Mouth @ Achilles' Heel?. <i>Nature Biotechnology</i> , 2008 , 26, 1335-6	44.5	1
124	Ornithine decarboxylase antizyme finder (OAF): fast and reliable detection of antizymes with frameshifts in mRNAs. <i>BMC Bioinformatics</i> , 2008 , 9, 178	3.6	12
123	Discovery of frameshifting in Alphavirus 6K resolves a 20-year enigma. <i>Virology Journal</i> , 2008 , 5, 108	6.1	91
122	Bioinformatic analysis suggests that the Cypovirus 1 major core protein cistron harbours an overlapping gene. <i>Virology Journal</i> , 2008 , 5, 62	6.1	6
121	An overlapping essential gene in the Potyviridae. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008 , 105, 5897-902	11.5	582
120	uORFs with unusual translational start codons autoregulate expression of eukaryotic ornithine decarboxylase homologs. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008 , 105, 10079-84	11.5	74
119	Bioinformatic analysis suggests that a conserved ORF in the waikaviruses encodes an overlapping gene. <i>Archives of Virology</i> , 2008 , 153, 1379-83	2.6	16
118	Ribosomal frameshifting in decoding antizyme mRNAs from yeast and protists to humans: close to 300 cases reveal remarkable diversity despite underlying conservation. <i>Nucleic Acids Research</i> , 2007 , 35, 1842-58	20.1	92
117	Comparison of approaches for rational siRNA design leading to a new efficient and transparent method. <i>Nucleic Acids Research</i> , 2007 , 35, e63	20.1	105
116	A case for "StopGo": reprogramming translation to augment codon meaning of GGN by promoting unconventional termination (Stop) after addition of glycine and then allowing continued translation (Go). <i>Rna</i> , 2007 , 13, 803-10	5.8	87
115	The selenium-rich C-terminal domain of mouse selenoprotein P is necessary for the supply of selenium to brain and testis but not for the maintenance of whole body selenium. <i>Journal of Biological Chemistry</i> , 2007 , 282, 10972-80	5.4	81
114	Novel antizyme gene in <i>Danio rerio</i> expressed in brain and retina. <i>Gene</i> , 2007 , 387, 87-92	3.8	11
113	Recoding in bacteriophages and bacterial IS elements. <i>Trends in Genetics</i> , 2006 , 22, 174-81	8.5	71
112	The potential role of ribosomal frameshifting in generating aberrant proteins implicated in neurodegenerative diseases. <i>Rna</i> , 2006 , 12, 1149-53	5.8	19
111	ARFA: a program for annotating bacterial release factor genes, including prediction of programmed ribosomal frameshifting. <i>Bioinformatics</i> , 2006 , 22, 2463-5	7.2	25
110	Sequencing and haplotype analysis of the activator of CREM in the testis (ACT) gene in populations of fertile and infertile males. <i>Molecular Human Reproduction</i> , 2006 , 12, 257-62	4.4	19

109	Evolutionary specialization of recoding: frameshifting in the expression of <i>S. cerevisiae</i> antizyme mRNA is via an atypical antizyme shift site but is still +1. <i>Rna</i> , 2006 , 12, 332-7	5.8	14
108	Epitopes derived by incidental translational frameshifting give rise to a protective CTL response. <i>Journal of Immunology</i> , 2006 , 176, 6928-34	5.3	32
107	Polyamine analogs with xylene rings induce antizyme frameshifting, reduce ODC activity, and deplete cellular polyamines. <i>Journal of Biochemistry</i> , 2006 , 140, 657-66	3.1	10
106	A functional -1 ribosomal frameshift signal in the human paraneoplastic Ma3 gene. <i>Journal of Biological Chemistry</i> , 2006 , 281, 7082-8	5.4	56
105	Diverse bacterial genomes encode an operon of two genes, one of which is an unusual class-I release factor that potentially recognizes atypical mRNA signals other than normal stop codons. <i>Biology Direct</i> , 2006 , 1, 28	7.2	22
104	Identification of polymorphisms in the Hrb, GOPC, and Csnk2a2 genes in two men with globozoospermia. <i>Journal of Andrology</i> , 2006 , 27, 11-5		22
103	Identification of novel polymorphisms in the nuclear protein genes and their relationship with human sperm protamine deficiency and severe male infertility. <i>Fertility and Sterility</i> , 2006 , 86, 1416-22	4.8	62
102	Identification of polymorphisms and balancing selection in the male infertility candidate gene, ornithine decarboxylase antizyme 3. <i>BMC Medical Genetics</i> , 2006 , 7, 27	2.1	10
101	Screening the SPO11 and EIF5A2 genes in a population of infertile men. <i>Fertility and Sterility</i> , 2005 , 84, 758-60	4.8	27
100	Programmed ribosomal frameshifting in decoding the SARS-CoV genome. <i>Virology</i> , 2005 , 332, 498-510	3.6	155
99	P-site pairing subtleties revealed by the effects of different tRNAs on programmed translational bypassing where anticodon re-pairing to mRNA is separated from dissociation. <i>Journal of Molecular Biology</i> , 2005 , 345, 39-49	6.5	15
98	Polyamine sensing during antizyme mRNA programmed frameshifting. <i>Biochemical and Biophysical Research Communications</i> , 2005 , 338, 1478-89	3.4	33
97	Transcriptional slippage in bacteria: distribution in sequenced genomes and utilization in IS element gene expression. <i>Genome Biology</i> , 2005 , 6, R25	18.3	56
96	Recoding elements located adjacent to a subset of eukaryal selenocysteine-specifying UGA codons. <i>EMBO Journal</i> , 2005 , 24, 1596-607	13	79
95	Expression levels influence ribosomal frameshifting at the tandem rare arginine codons AGG_AGG and AGA_AGA in <i>Escherichia coli</i> . <i>Journal of Bacteriology</i> , 2005 , 187, 4023-32	3.5	38
94	Pyrrolysine and selenocysteine use dissimilar decoding strategies. <i>Journal of Biological Chemistry</i> , 2005 , 280, 20740-51	5.4	87
93	Efficient stimulation of site-specific ribosome frameshifting by antisense oligonucleotides. <i>Rna</i> , 2004 , 10, 1653-61	5.8	42
92	P-site tRNA is a crucial initiator of ribosomal frameshifting. <i>Rna</i> , 2004 , 10, 221-30	5.8	73

91	-1 frameshifting at a CGA AAG hexanucleotide site is required for transposition of insertion sequence IS1222. <i>Journal of Bacteriology</i> , 2004 , 186, 3274-7	3.5	9
90	Factors that influence selection of coding resumption sites in translational bypassing: minimal conventional peptidyl-tRNA:mRNA pairing can suffice. <i>Journal of Biological Chemistry</i> , 2004 , 279, 11081-7	5.4	27
89	A cryptic lysis gene near the start of the Qbeta replicase gene in the +1 frame. <i>Genes To Cells</i> , 2004 , 9, 877-89	2.3	3
88	Identification of regions in multiple sequence alignments thermodynamically suitable for targeting by consensus oligonucleotides: application to HIV genome. <i>BMC Bioinformatics</i> , 2004 , 5, 44	3.6	3
87	Identification of a new antizyme mRNA +1 frameshifting stimulatory pseudoknot in a subset of diverse invertebrates and its apparent absence in intermediate species. <i>Journal of Molecular Biology</i> , 2004 , 339, 495-504	6.5	24
86	Deletion of selenoprotein P alters distribution of selenium in the mouse. <i>Journal of Biological Chemistry</i> , 2003 , 278, 13640-6	5.4	348
85	Sequences that direct significant levels of frameshifting are frequent in coding regions of Escherichia coli. <i>EMBO Journal</i> , 2003 , 22, 5941-50	13	61
84	Maintenance of the correct open reading frame by the ribosome. <i>EMBO Reports</i> , 2003 , 4, 499-504	6.5	36
83	Programmed translational -1 frameshifting on hexanucleotide motifs and the wobble properties of tRNAs. <i>EMBO Journal</i> , 2003 , 22, 4770-8	13	48
82	Translational recoding signals between gag and pol in diverse LTR retrotransposons. <i>Rna</i> , 2003 , 9, 1422-30	3.8	68
81	RECODE 2003. <i>Nucleic Acids Research</i> , 2003 , 31, 87-9	20.1	59
80	Comparative studies of frameshifting and nonframeshifting RNA pseudoknots: a mutational and NMR investigation of pseudoknots derived from the bacteriophage T2 gene 32 mRNA and the retroviral gag-pro frameshift site. <i>Rna</i> , 2002 , 8, 981-96	5.8	26
79	Release factor 2 frameshifting sites in different bacteria. <i>EMBO Reports</i> , 2002 , 3, 373-7	6.5	61
78	Predominance of six different hexanucleotide recoding signals 3Qf read-through stop codons. <i>Nucleic Acids Research</i> , 2002 , 30, 2011-7	20.1	89
77	Computational identification of putative programmed translational frameshift sites. <i>Bioinformatics</i> , 2002 , 18, 1046-53	7.2	64
76	Artificial neural network prediction of antisense oligodeoxynucleotide activity. <i>Nucleic Acids Research</i> , 2002 , 30, 4295-304	20.1	21
75	Recoding: translational bifurcations in gene expression. <i>Gene</i> , 2002 , 286, 187-201	3.8	181
74	Biochemistry. The 22nd amino acid. <i>Science</i> , 2002 , 296, 1409-10	33.3	86

73	Influence of the stacking potential of the base 3Qf tandem shift codons on -1 ribosomal frameshifting used for gene expression. <i>Rna</i> , 2002 , 8, 16-28	5.8	36
72	Cell culture analysis of the regulatory frameshift event required for the expression of mammalian antizymes. <i>Genes To Cells</i> , 2001 , 6, 931-41	2.3	29
71	mRNA readout at 40. <i>Nature</i> , 2001 , 414, 693	50.4	2
70	Analysis of the roles of tRNA structure, ribosomal protein L9, and the bacteriophage T4 gene 60 bypassing signals during ribosome slippage on mRNA. <i>Journal of Molecular Biology</i> , 2001 , 309, 1029-48	6.5	63
69	Drop-off during ribosome hopping. <i>Journal of Molecular Biology</i> , 2001 , 311, 445-52	6.5	28
68	Overriding standard decoding: implications of recoding for ribosome function and enrichment of gene expression. <i>Cold Spring Harbor Symposia on Quantitative Biology</i> , 2001 , 66, 217-32	3.9	38
67	Sequence specificity of aminoglycoside-induced stop codon readthrough: Potential implications for treatment of Duchenne muscular dystrophy. <i>Annals of Neurology</i> , 2000 , 48, 164-169	9.4	204
66	Coupling of open reading frames by translational bypassing. <i>Annual Review of Biochemistry</i> , 2000 , 69, 343-72	29.1	56
65	ODNBase--a web database for antisense oligonucleotide effectiveness studies. Oligodeoxynucleotides. <i>Bioinformatics</i> , 2000 , 16, 843-4	7.2	19
64	Decoding of tandem quadruplets by adjacent tRNAs with eight-base anticodon loops. <i>Nucleic Acids Research</i> , 2000 , 28, 3615-24	20.1	8
63	Antizyme expression: a subversion of triplet decoding, which is remarkably conserved by evolution, is a sensor for an autoregulatory circuit. <i>Nucleic Acids Research</i> , 2000 , 28, 3185-96	20.1	69
62	The 23 S rRNA environment of ribosomal protein L9 in the 50 S ribosomal subunit. <i>Journal of Molecular Biology</i> , 2000 , 297, 1129-43	6.5	39
61	Quadruplet codons: implications for code expansion and the specification of translation step size. <i>Journal of Molecular Biology</i> , 2000 , 298, 195-209	6.5	54
60	Mutations which alter the elbow region of tRNA ^{2Gly} reduce T4 gene 60 translational bypassing efficiency. <i>EMBO Journal</i> , 1999 , 18, 2886-96	13	30
59	Structure of human ornithine decarboxylase antizyme 2 gene. <i>Gene</i> , 1999 , 232, 165-71	3.8	8
58	Eubacterial tmRNAs: everywhere except the alpha-proteobacteria?. <i>Biochimica Et Biophysica Acta Gene Regulatory Mechanisms</i> , 1999 , 1446, 145-8		22
57	Functional and structural analysis of a pseudoknot upstream of the tag-encoded sequence in E. coli tmRNA. <i>Journal of Molecular Biology</i> , 1999 , 286, 733-44	6.5	63
56	A three-way junction and constituent stem-loops as the stimulator for programmed -1 frameshifting in bacterial insertion sequence IS911. <i>Journal of Molecular Biology</i> , 1999 , 286, 1365-78	6.5	44

55	Structural studies of the RNA pseudoknot required for readthrough of the gag-termination codon of murine leukemia virus. <i>Journal of Molecular Biology</i> , 1999 , 288, 837-52	6.5	39
54	Ribosomal -1 frameshifting during decoding of <i>Bacillus subtilis</i> cdd occurs at the sequence CGA AAG. <i>Journal of Bacteriology</i> , 1999 , 181, 2930-7	3.5	39
53	Prediction of antisense oligonucleotide efficacy by in vitro methods. <i>Nature Biotechnology</i> , 1998 , 16, 1374-5	44.5	35
52	Flexibility of the nascent polypeptide chain within the ribosome--contacts from the peptide N-terminus to a specific region of the 30S subunit. <i>FEBS Journal</i> , 1998 , 255, 409-13		28
51	Does antizyme exist in <i>Escherichia coli</i> ?. <i>Molecular Microbiology</i> , 1998 , 29, 1521-2	4.1	13
50	A second mammalian antizyme: conservation of programmed ribosomal frameshifting. <i>Genomics</i> , 1998 , 52, 119-29	4.3	99
49	A nickel complex cleaves uridine in folded RNA structures: application to <i>E. coli</i> tmRNA and related engineered molecules. <i>Journal of Molecular Biology</i> , 1998 , 279, 577-87	6.5	50
48	The <i>Drosophila</i> gene for antizyme requires ribosomal frameshifting for expression and contains an intronic gene for snRNP Sm D3 on the opposite strand. <i>Molecular and Cellular Biology</i> , 1998 , 18, 1553-61 ^{4.8}		35
47	Effects of 3' terminal phosphates in RNA produced by ribozyme cleavage. <i>Rna</i> , 1998 , 4, 607-12	5.8	5
46	Programmed frameshifting in the synthesis of mammalian antizyme is +1 in mammals, predominantly +1 in fission yeast, but -2 in budding yeast. <i>Rna</i> , 1998 , 4, 1230-8	5.8	32
45	Does disparate occurrence of autoregulatory programmed frameshifting in decoding the release factor 2 gene reflect an ancient origin with loss in independent lineages?. <i>Journal of Bacteriology</i> , 1998 , 180, 3462-6	3.5	4
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