

John F Atkins

List of Publications by Year in descending order

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203
papers

13,209
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19608

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104
g-index

209
all docs

209
docs citations

209
times ranked

8996
citing authors

#	ARTICLE	IF	CITATIONS
1	An overlapping essential gene in the Potyviridae. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 5897-5902.	3.3	718
2	Autoregulatory frameshifting in decoding mammalian ornithine decarboxylase antizyme. Cell, 1995, 80, 51-60.	13.5	486
3	Deletion of Selenoprotein P Alters Distribution of Selenium in the Mouse. Journal of Biological Chemistry, 2003, 278, 13640-13646.	1.6	401
4	Recoding: Dynamic Reprogramming of Translation. Annual Review of Biochemistry, 1996, 65, 741-768.	5.0	335
5	Location and identification of the genes for adenovirus type 2 early polypeptides. Cell, 1976, 7, 141-151.	13.5	295
6	Ribosome gymnastics—Degree of difficulty 9.5, style 10.0. Cell, 1990, 62, 413-423.	13.5	252
7	Slippery Runs, Shifty Stops, Backward Steps, and Forward Hops: -2, -1, +1, +2, +5, and +6 Ribosomal Frameshifting. Cold Spring Harbor Symposia on Quantitative Biology, 1987, 52, 687-693.	2.0	251
8	Discovery of a small arterivirus gene that overlaps the GP5 coding sequence and is important for virus production. Journal of General Virology, 2011, 92, 1097-1106.	1.3	247
9	Ribosomal frameshifting and transcriptional slippage: From genetic steganography and cryptography to adventitious use. Nucleic Acids Research, 2016, 44, gkw530.	6.5	238
10	Sequence specificity of aminoglycoside-induced stop codon readthrough: Potential implications for treatment of Duchenne muscular dystrophy. Annals of Neurology, 2000, 48, 164-169.	2.8	233
11	Efficient ~ 2 frameshifting by mammalian ribosomes to synthesize an additional arterivirus protein. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, E2920-8.	3.3	231
12	The signal for a leaky UAG stop codon in several plant viruses includes the two downstream codons. Journal of Molecular Biology, 1991, 218, 365-373.	2.0	226
13	Programmed ribosomal frameshifting in decoding the SARS-CoV genome. Virology, 2005, 332, 498-510.	1.1	201
14	Identification of evolutionarily conserved non-AUG-initiated N-terminal extensions in human coding sequences. Nucleic Acids Research, 2011, 39, 4220-4234.	6.5	195
15	Recoding: translational bifurcations in gene expression. Gene, 2002, 286, 187-201.	1.0	193
16	Transcriptional slippage in the positive-sense <i>scp</i> RNA virus family <i>Potyviridae</i> . EMBO Reports, 2015, 16, 995-1004.	2.0	192
17	Evidence of efficient stop codon readthrough in four mammalian genes. Nucleic Acids Research, 2014, 42, 8928-8938.	6.5	184
18	Observation of dually decoded regions of the human genome using ribosome profiling data. Genome Research, 2012, 22, 2219-2229.	2.4	169

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19	Structural basis of ribosomal frameshifting during translation of the SARS-CoV-2 RNA genome. <i>Science</i> , 2021, 372, 1306-1313.	6.0	165
20	Normal tRNAs promote ribosomal frameshifting. <i>Cell</i> , 1979, 18, 1119-1131.	13.5	158
21	NS1 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, 1641-1647.	1.5	150
22	Binding of mammalian ribosomes to ms2 phage rna reveals an overlapping gene encoding a lysis function. <i>Cell</i> , 1979, 18, 247-256.	13.5	138
23	Stimulation of stop codon readthrough: frequent presence of an extended 3' RNA structural element. <i>Nucleic Acids Research</i> , 2011, 39, 6679-6691.	6.5	134
24	Comparison of approaches for rational siRNA design leading to a new efficient and transparent method. <i>Nucleic Acids Research</i> , 2007, 35, e63-e63.	6.5	129
25	Further mapping of late adenovirus genes by cell-free translation of RNA selected by hybridization to specific DNA fragments. <i>Cell</i> , 1977, 12, 37-44.	13.5	126
26	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, 18056-18060.	3.3	125
27	Production of Selenoprotein P (Sepp1) by Hepatocytes Is Central to Selenium Homeostasis. <i>Journal of Biological Chemistry</i> , 2012, 287, 40414-40424.	1.6	124
28	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.	2.9	122
29	A conserved predicted pseudoknot in the NS2A-encoding sequence of West Nile and Japanese encephalitis flaviviruses suggests NS1' may derive from ribosomal frameshifting. <i>Virology Journal</i> , 2009, 6, 14.	1.4	120
30	Discovery of frameshifting in Alphavirus 6K resolves a 20-year enigma. <i>Virology Journal</i> , 2008, 5, 108.	1.4	118
31	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, 1842-1858.	6.5	114
32	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.	4.5	112
33	Predominance of six different hexanucleotide recoding signals 3' of read-through stop codons. <i>Nucleic Acids Research</i> , 2002, 30, 2011-2017.	6.5	110
34	A Second Mammalian Antizyme: Conservation of Programmed Ribosomal Frameshifting. <i>Genomics</i> , 1998, 52, 119-129.	1.3	108
35	The twenty-first amino acid. <i>Nature</i> , 2000, 407, 463-464.	13.7	106
36	Pyrolysine and Selenocysteine Use Dissimilar Decoding Strategies. <i>Journal of Biological Chemistry</i> , 2005, 280, 20740-20751.	1.6	104

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37	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, 803-810.	1.6	104
38	Identification and mapping of the transcriptional and translational products of the yeast plasmid, 2¼ circle. <i>Cell</i> , 1979, 16, 827-839.	13.5	102
39	BIOCHEMISTRY: The 22nd Amino Acid. <i>Science</i> , 2002, 296, 1409-1410.	6.0	100
40	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.	3.5	100
41	Ribosomal Frameshifting from -2 to +50 Nucleotides. <i>Progress in Molecular Biology and Translational Science</i> , 1990, 39, 159-183.	1.9	99
42	Stringency of start codon selection modulates autoregulation of translation initiation factor eIF5. <i>Nucleic Acids Research</i> , 2012, 40, 2898-2906.	6.5	99
43	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, 10972-10980.	1.6	94
44	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, 10079-10084.	3.3	90
45	Deficiency of 1-Methylguanosine in tRNA from <i>Salmonella typhimurium</i> Induces Frameshifting by Quadruplet Translocation. <i>Journal of Molecular Biology</i> , 1993, 232, 756-765.	2.0	88
46	Structural probing and mutagenic analysis of the stem-loop required for <i>Escherichia coli</i> dnaX ribosomal frameshifting: programmed efficiency of 50%. <i>Journal of Molecular Biology</i> , 1997, 271, 47-60.	2.0	85
47	SURVEY AND SUMMARY: 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, 3185-3196.	6.5	85
48	Recoding elements located adjacent to a subset of eukaryal selenocysteine-specifying UGA codons. <i>EMBO Journal</i> , 2005, 24, 1596-1607.	3.5	84
49	P-site tRNA is a crucial initiator of ribosomal frameshifting. <i>Rna</i> , 2004, 10, 221-230.	1.6	82
50	Translational recoding signals between gag and pol in diverse LTR retrotransposons. <i>Rna</i> , 2003, 9, 1422-1430.	1.6	80
51	Release factor 2 frameshifting sites in different bacteria. <i>EMBO Reports</i> , 2002, 3, 373-377.	2.0	79
52	Recoding in bacteriophages and bacterial IS elements. <i>Trends in Genetics</i> , 2006, 22, 174-181.	2.9	79
53	A profusion of upstream open reading frame mechanisms in polyamine-responsive translational regulation. <i>Nucleic Acids Research</i> , 2010, 38, 353-359.	6.5	78
54	Augmented genetic decoding: global, local and temporal alterations of decoding processes and codon meaning. <i>Nature Reviews Genetics</i> , 2015, 16, 517-529.	7.7	75

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55	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, 1029-1048.	2.0	74
56	Sequences that direct significant levels of frameshifting are frequent in coding regions of <i>Escherichia coli</i> . <i>EMBO Journal</i> , 2003, 22, 5941-5950.	3.5	74
57	External suppression of a frameshift mutant in <i>Salmonella</i> . <i>Journal of Molecular Biology</i> , 1968, 34, 541-557.	2.0	73
58	Computational identification of putative programmed translational frameshift sites. <i>Bioinformatics</i> , 2002, 18, 1046-1053.	1.8	72
59	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, 1416-1422.	0.5	70
60	tRNA hopping: enhancement by an expanded anticodon.. <i>EMBO Journal</i> , 1989, 8, 4315-4323.	3.5	68
61	A Functional ϵ 1 Ribosomal Frameshift Signal in the Human Paraneoplastic Ma3 Gene. <i>Journal of Biological Chemistry</i> , 2006, 281, 7082-7088.	1.6	67
62	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.	3.3	67
63	Coupling of Open Reading Frames by Translational Bypassing. <i>Annual Review of Biochemistry</i> , 2000, 69, 343-372.	5.0	65
64	Pseudoknot-dependent read-through of retroviral gag termination codons: importance of sequences in the spacer and loop 2.. <i>EMBO Journal</i> , 1994, 13, 4137-4144.	3.5	64
65	A case for trans translation. <i>Nature</i> , 1996, 379, 769-771.	13.7	64
66	RECODE 2003. <i>Nucleic Acids Research</i> , 2003, 31, 87-89.	6.5	64
67	Functional and structural analysis of a pseudoknot upstream of the tag-encoded sequence in <i>E. coli</i> tmRNA 1 Edited by D. E. Draper. <i>Journal of Molecular Biology</i> , 1999, 286, 733-744.	2.0	63
68	Avoidance of reporter assay distortions from fused dual reporters. <i>Rna</i> , 2017, 23, 1285-1289.	1.6	63
69	AMD1 mRNA employs ribosome stalling as a mechanism for molecular memory formation. <i>Nature</i> , 2018, 553, 356-360.	13.7	63
70	Transcriptional slippage in bacteria: distribution in sequenced genomes and utilization in IS element gene expression. <i>Genome Biology</i> , 2005, 6, R25.	13.9	59
71	Evidence for ribosomal frameshifting and a novel overlapping gene in the genomes of insect-specific flaviviruses. <i>Virology</i> , 2010, 399, 153-166.	1.1	59
72	Recode-2: new design, new search tools, and many more genes. <i>Nucleic Acids Research</i> , 2010, 38, D69-D74.	6.5	59

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73	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.	1.6	59
74	Quadruplet codons: implications for code expansion and the specification of translation step size. <i>Journal of Molecular Biology</i> , 2000, 298, 195-209.	2.0	58
75	The nucleotide sequence of the first externally suppressible -1 frameshift mutant, and of some nearby leaky frameshift mutants.. <i>EMBO Journal</i> , 1983, 2, 1345-1350.	3.5	56
76	Position-dependent termination and widespread obligatory frameshifting in <i>Euplotes</i> translation. <i>Nature Structural and Molecular Biology</i> , 2017, 24, 61-68.	3.6	56
77	Functional tRNAs with altered 3' ends.. <i>EMBO Journal</i> , 1993, 12, 2559-2566.	3.5	55
78	Programmed translational -1 frameshifting on hexanucleotide motifs and the wobble properties of tRNAs. <i>EMBO Journal</i> , 2003, 22, 4770-4778.	3.5	55
79	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, 577-587.	2.0	54
80	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.	3.3	54
81	Nucleotide sequence of a single-stranded RNA phage from <i>Pseudomonas aeruginosa</i> : Kinship to coliphages and conservation of regulatory RNA structures. <i>Virology</i> , 1995, 206, 611-625.	1.1	52
82	Frameshifting in Alphaviruses: A Diversity of 3' Stimulatory Structures. <i>Journal of Molecular Biology</i> , 2010, 397, 448-456.	2.0	52
83	The energy landscape of +1 ribosomal frameshifting. <i>Science Advances</i> , 2020, 6, eaax6969.	4.7	51
84	Seven, eight and nine-membered anticodon loop mutants of tRNA ^{2Arg} which cause +1 frameshifting. <i>Journal of Molecular Biology</i> , 1992, 228, 1042-1054.	2.0	50
85	rRNA:mRNA pairing alters the length and the symmetry of mRNA-protected fragments in ribosome profiling experiments. <i>Bioinformatics</i> , 2013, 29, 1488-1491.	1.8	50
86	Is UAA or UGA part of the recognition signal for ribosomal initiation?. <i>Nucleic Acids Research</i> , 1979, 7, 1035-1042.	6.5	49
87	An analysis of sequences stimulating frameshifting in the decoding of gene 10 of bacteriophage T7. <i>Nucleic Acids Research</i> , 1991, 19, 5607-5612.	6.5	49
88	A map of the restriction targets in yeast 2 micron plasmid DNA cloned on bacteriophage lambda. <i>Molecular Genetics and Genomics</i> , 1976, 148, 287-294.	2.4	47
89	Efficient stimulation of site-specific ribosome frameshifting by antisense oligonucleotides. <i>Rna</i> , 2004, 10, 1653-1661.	1.6	47
90	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, 837-852.	2.0	46

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91	Ribosomal Protein L9 Interactions with 23 S rRNA: The Use of a Translational Bypass Assay to Study the Effect of Amino Acid Substitutions. <i>Journal of Molecular Biology</i> , 1996, 261, 357-371.	2.0	45
92	A three-way junction and constituent stem-loops as the stimulator for programmed +1 frameshifting in bacterial insertion sequence IS 911 1 1 Edited by D. E. Draper. <i>Journal of Molecular Biology</i> , 1999, 286, 1365-1378.	2.0	45
93	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, 4023-4032.	1.0	45
94	Ribosomal +1 Frameshifting during Decoding of <i>Bacillus subtilis</i> cdd Occurs at the Sequence CGA AAG. <i>Journal of Bacteriology</i> , 1999, 181, 2930-2937.	1.0	45
95	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, 3195-3211.	3.5	43
96	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, 5670-5675.	3.3	43
97	The 23 S rRNA environment of ribosomal protein L9 in the 50 S ribosomal subunit 1 Edited by D. E. Draper. <i>Journal of Molecular Biology</i> , 2000, 297, 1129-1143.	2.0	42
98	Coupling of mRNA Structure Rearrangement to Ribosome Movement during Bypassing of Non-coding Regions. <i>Cell</i> , 2015, 163, 1267-1280.	13.5	42
99	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, 217-232.	2.0	42
100	Epitopes Derived by Incidental Translational Frameshifting Give Rise to a Protective CTL Response. <i>Journal of Immunology</i> , 2006, 176, 6928-6934.	0.4	41
101	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, 1553-1561.	1.1	40
102	Influence of the stacking potential of the base 3' of tandem shift codons on +1 ribosomal frameshifting used for gene expression. <i>Rna</i> , 2002, 8, 16-28.	1.6	40
103	Polyamine sensing during antizyme mRNA programmed frameshifting. <i>Biochemical and Biophysical Research Communications</i> , 2005, 338, 1478-1489.	1.0	39
104	Systematic analysis of the <i>PTEN</i> 5' leader identifies a major AUU initiated proteoform. <i>Open Biology</i> , 2016, 6, 150203.	1.5	39
105	Maintenance of the correct open reading frame by the ribosome. <i>EMBO Reports</i> , 2003, 4, 499-504.	2.0	38
106	Structural organization of <i>Escherichia coli</i> tmRNA. <i>Biochimie</i> , 1996, 78, 979-983.	1.3	37
107	Sepp1UF 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.	1.3	37
108	Prediction of antisense oligonucleotide efficacy by in vitro methods. <i>Nature Biotechnology</i> , 1998, 16, 1374-1375.	9.4	36

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109	Programmed frameshifting in the synthesis of mammalian antizyme is +1 in mammals, predominantly +1 in fission yeast, but $\hat{\alpha}^2$ in budding yeast. <i>Rna</i> , 1998, 4, 1230-1238.	1.6	35
110	Mutations which alter the elbow region of tRNA ^{2Gly} reduce T4 gene 60 translational bypassing efficiency. <i>EMBO Journal</i> , 1999, 18, 2886-2896.	3.5	32
111	Drop-off during ribosome hopping 1 Edited by M. Gottesman. <i>Journal of Molecular Biology</i> , 2001, 311, 445-452.	2.0	32
112	Cell culture analysis of the regulatory frameshift event required for the expression of mammalian antizymes. <i>Genes To Cells</i> , 2001, 6, 931-941.	0.5	32
113	Analysis of the coding potential of the partially overlapping 3' ORF in segment 5 of the plant fijiviruses. <i>Virology Journal</i> , 2009, 6, 32.	1.4	32
114	The role of EF-Tu and other translation components in determining translocation step size. <i>Biochimica Et Biophysica Acta Gene Regulatory Mechanisms</i> , 1990, 1050, 274-278.	2.4	31
115	Screening the SPO11 and EIF5A2 genes in a population of infertile men. <i>Fertility and Sterility</i> , 2005, 84, 758-760.	0.5	31
116	ARFA: a program for annotating bacterial release factor genes, including prediction of programmed ribosomal frameshifting. <i>Bioinformatics</i> , 2006, 22, 2463-2465.	1.8	31
117	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, 409-413.	0.2	30
118	Factors That Influence Selection of Coding Resumption Sites in Translational Bypassing. <i>Journal of Biological Chemistry</i> , 2004, 279, 11081-11087.	1.6	30
119	Unusually efficient CUG initiation of an overlapping reading frame in <i>POLG</i> mRNA yields novel protein POLGARF. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 24936-24946.	3.3	30
120	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, 981-996.	1.6	29
121	Bioinformatic evidence for a stem-loop structure 5'-adjacent to the IGR-IRES and for an overlapping gene in the bee paralysis dicistroviruses. <i>Virology Journal</i> , 2009, 6, 193.	1.4	29
122	Candidates in Astroviruses, Seadornaviruses, Cytorhabdoviruses and Coronaviruses for +1 frame overlapping genes accessed by leaky scanning. <i>Virology Journal</i> , 2010, 7, 17.	1.4	28
123	High-efficiency translational bypassing of non-coding nucleotides specified by mRNA structure and nascent peptide. <i>Nature Communications</i> , 2014, 5, 4459.	5.8	28
124	Identification of the nature of reading frame transitions observed in prokaryotic genomes. <i>Nucleic Acids Research</i> , 2013, 41, 6514-6530.	6.5	26
125	Eubacterial tmRNAs: everywhere except the alpha-Proteobacteria?. <i>Biochimica Et Biophysica Acta Gene Regulatory Mechanisms</i> , 1999, 1446, 145-148.	2.4	25
126	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.	2.0	25

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127	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.	1.9	25
128	Bioinformatic analysis suggests that a conserved ORF in the waikaviruses encodes an overlapping gene. <i>Archives of Virology</i> , 2008, 153, 1379-1383.	0.9	25
129	Translational bypassing without peptidyl-tRNA anticodon scanning of coding gap mRNA. <i>EMBO Journal</i> , 2008, 27, 2533-2544.	3.5	25
130	Analysis of tetra- and hepta-nucleotides motifs promoting -1 ribosomal frameshifting in <i>Escherichia coli</i> . <i>Nucleic Acids Research</i> , 2014, 42, 7210-7225.	6.5	25
131	Translation Initiation from Conserved Non-AUG Codons Provides Additional Layers of Regulation and Coding Capacity. <i>MBio</i> , 2017, 8, .	1.8	25
132	Artificial neural network prediction of antisense oligodeoxynucleotide activity. <i>Nucleic Acids Research</i> , 2002, 30, 4295-4304.	6.5	24
133	Identification of Polymorphisms in the Hrb, GOPC, and Csnk2a2 Genes in Two Men With Globozoospermia. <i>Journal of Andrology</i> , 2006, 27, 11-15.	2.0	23
134	Recurrent Emergence of Catalytically Inactive Ornithine Decarboxylase Homologous Forms That Likely Have Regulatory Function. <i>Journal of Molecular Evolution</i> , 2010, 70, 289-302.	0.8	23
135	Pyrrolysine in archaea: a 22nd amino acid encoded through a genetic code expansion. <i>Emerging Topics in Life Sciences</i> , 2018, 2, 607-618.	1.1	22
136	ODNBase—a web database for antisense oligonucleotide effectiveness studies. <i>Bioinformatics</i> , 2000, 16, 843-844.	1.8	21
137	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, 257-262.	1.3	21
138	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.	1.6	21
139	The potential role of ribosomal frameshifting in generating aberrant proteins implicated in neurodegenerative diseases. <i>Rna</i> , 2006, 12, 1149-1153.	1.6	20
140	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.	3.3	20
141	Translational autoregulation of BZW1 and BZW2 expression by modulating the stringency of start codon selection. <i>PLoS ONE</i> , 2018, 13, e0192648.	1.1	20
142	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, 332-337.	1.6	19
143	The Distinction Between Recoding and Codon Reassignment. <i>Genetics</i> , 2010, 185, 1535-1536.	1.2	19
144	An Expanded CAG Repeat in Huntingtin Causes +1 Frameshifting. <i>Journal of Biological Chemistry</i> , 2016, 291, 18505-18513.	1.6	19

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145	The synthetase gene of the RNA phages R17, MS2 and f2 has a single UAG terminator codon. <i>Molecular Genetics and Genomics</i> , 1975, 139, 19-31.	2.4	18
146	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-E4349.	3.3	18
147	Multiple RNA structures affect translation initiation and UGA redefinition efficiency during synthesis of selenoprotein P. <i>Nucleic Acids Research</i> , 2017, 45, 13004-13015.	6.5	18
148	Processive Recoding and Metazoan Evolution of Selenoprotein P: Up to 132 UGAs in Molluscs. <i>Journal of Molecular Biology</i> , 2019, 431, 4381-4407.	2.0	18
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