

John F Atkins

List of Publications by Year in descending order

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203
papers

13,209
citations

19608

61
h-index

29081

104
g-index

209
all docs

209
docs citations

209
times ranked

8996
citing authors

#	ARTICLE	IF	CITATIONS
1	Immune cells alter genetic decoding in cancer. <i>Nature</i> , 2022, 603, 582-583.	13.7	2
2	Evaluating ribosomal frameshifting in CCR5 mRNA decoding. <i>Nature</i> , 2022, 604, E16-E23.	13.7	18
3	Maximum depth sequencing reveals an ON/OFF replication slippage switch and apparent in vivo selection for bifidobacterial pilus expression. <i>Scientific Reports</i> , 2022, 12, .	1.6	2
4	Structural basis of ribosomal frameshifting during translation of the SARS-CoV-2 RNA genome. <i>Science</i> , 2021, 372, 1306-1313.	6.0	165
5	From Recoding to Peptides for MHC Class I Immune Display: Enriching Viral Expression, Virus Vulnerability and Virus Evasion. <i>Viruses</i> , 2021, 13, 1251.	1.5	3
6	Tissue-specific dynamic codon redefinition in <i>Drosophila</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	10
7	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
8	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.	2.0	5
9	The energy landscape of ~ 1 ribosomal frameshifting. <i>Science Advances</i> , 2020, 6, eaax6969.	4.7	51
10	Stop codon readthrough contexts influence reporter expression differentially depending on the presence of an IRES. <i>Wellcome Open Research</i> , 2020, 5, 221.	0.9	1
11	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
12	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
13	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
14	AMD1 mRNA employs ribosome stalling as a mechanism for molecular memory formation. <i>Nature</i> , 2018, 553, 356-360.	13.7	63
15	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
16	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.	3.3	2
17	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
18	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.	4.5	4

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19	Avoidance of reporter assay distortions from fused dual reporters. <i>Rna</i> , 2017, 23, 1285-1289.	1.6	63
20	Translation Initiation from Conserved Non-AUG Codons Provides Additional Layers of Regulation and Coding Capacity. <i>MBio</i> , 2017, 8, .	1.8	25
21	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
22	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
23	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.	6.5	7
24	ASXL gain-of-function truncation mutants: defective and dysregulated forms of a natural ribosomal frameshifting product?. <i>Biology Direct</i> , 2017, 12, 24.	1.9	12
25	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.	6.5	9
26	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, 160241.	1.5	12
27	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
28	Ribosomal frameshifting and transcriptional slippage: From genetic steganography and cryptography to adventitious use. <i>Nucleic Acids Research</i> , 2016, 44, gkw530.	6.5	238
29	An Expanded CAG Repeat in Huntingtin Causes +1 Frameshifting. <i>Journal of Biological Chemistry</i> , 2016, 291, 18505-18513.	1.6	19
30	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
31	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
32	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
33	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
34	Coupling of mRNA Structure Rearrangement to Ribosome Movement during Bypassing of Non-coding Regions. <i>Cell</i> , 2015, 163, 1267-1280.	13.5	42
35	Transcriptional slippage in the positive-sense RNA virus family <i>Potyviridae</i> . <i>EMBO Reports</i> , 2015, 16, 995-1004.	2.0	192
36	Evidence of efficient stop codon readthrough in four mammalian genes. <i>Nucleic Acids Research</i> , 2014, 42, 8928-8938.	6.5	184

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37	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.	1.5	14
38	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
39	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
40	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
41	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
42	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
43	Antibiotic re-frames decoding. <i>Nature</i> , 2013, 503, 478-479.	13.7	3
44	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
45	Identification of the nature of reading frame transitions observed in prokaryotic genomes. <i>Nucleic Acids Research</i> , 2013, 41, 6514-6530.	6.5	26
46	Observation of dually decoded regions of the human genome using ribosome profiling data. <i>Genome Research</i> , 2012, 22, 2219-2229.	2.4	169
47	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.	3.3	231
48	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
49	Stringency of start codon selection modulates autoregulation of translation initiation factor eIF5. <i>Nucleic Acids Research</i> , 2012, 40, 2898-2906.	6.5	99
50	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
51	Selenoprotein P (Sepp1) Synthesis by the Liver Protects against Selenium Deficiency. <i>FASEB Journal</i> , 2012, 26, 241.3.	0.2	0
52	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
53	Translation Goes Global. <i>Science</i> , 2011, 334, 1509-1510.	6.0	14
54	Programmed ribosomal frameshifting in the expression of the regulator of intestinal stem cell proliferation, adenomatous polyposis coli (APC). <i>RNA Biology</i> , 2011, 8, 637-647.	1.5	16

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55	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
56	The Interplay of mRNA Stimulatory Signals Required for AUU-Mediated Initiation and Programmed +1 Ribosomal Frameshifting in Decoding of Transposable Element IS <i>911</i> . <i>Journal of Bacteriology</i> , 2011, 193, 2735-2744.	1.0	12
57	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, 3079-3092.	6.5	9
58	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
59	Identification of evolutionarily conserved non-AUG-initiated N-terminal extensions in human coding sequences. <i>Nucleic Acids Research</i> , 2011, 39, 4220-4234.	6.5	195
60	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.	1.3	247
61	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
62	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
63	The Distinction Between Recoding and Codon Reassignment. <i>Genetics</i> , 2010, 185, 1535-1536.	1.2	19
64	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
65	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
66	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
67	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
68	Recode-2: new design, new search tools, and many more genes. <i>Nucleic Acids Research</i> , 2010, 38, D69-D74.	6.5	59
69	Frameshifting in Alphaviruses: A Diversity of Stimulatory Structures. <i>Journal of Molecular Biology</i> , 2010, 397, 448-456.	2.0	52
70	Versatile Dual Reporter Gene Systems for Investigating Stop Codon Readthrough in Plants. <i>PLoS ONE</i> , 2009, 4, e7354.	1.1	8
71	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
72	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.	1.4	8

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73	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
74	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
75	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
76	Evidence for a novel coding sequence overlapping the 5'-terminal ~90 codons of the Gill-associated and Yellow head okavirus envelope glycoprotein gene. <i>Virology Journal</i> , 2009, 6, 222.	1.4	4
77	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
78	Translational bypassing without peptidyl-tRNA anticodon scanning of coding gap mRNA. <i>EMBO Journal</i> , 2008, 27, 2533-2544.	3.5	25
79	Foot and Mouth's Achilles' heel?. <i>Nature Biotechnology</i> , 2008, 26, 1335-1336.	9.4	2
80	Ornithine decarboxylase antizyme finder (OAF): Fast and reliable detection of antizymes with frameshifts in mRNAs. <i>BMC Bioinformatics</i> , 2008, 9, 178.	1.2	16
81	Discovery of frameshifting in Alphavirus 6K resolves a 20-year enigma. <i>Virology Journal</i> , 2008, 5, 108.	1.4	118
82	Bioinformatic analysis suggests that the Cypovirus 1 major core protein cistron harbours an overlapping gene. <i>Virology Journal</i> , 2008, 5, 62.	1.4	6
83	An overlapping essential gene in the Potyviridae. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 5897-5902.	3.3	718
84	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
85	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
86	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
87	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
88	Novel antizyme gene in <i>Danio rerio</i> expressed in brain and retina. <i>Gene</i> , 2007, 387, 87-92.	1.0	11
89	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
90	Duality in the genetic code. <i>Nature</i> , 2007, 448, 1004-1005.	13.7	9

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91	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
92	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
93	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
94	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	13
95	Recoding in bacteriophages and bacterial IS elements. <i>Trends in Genetics</i> , 2006, 22, 174-181.	2.9	79
96	The potential role of ribosomal frameshifting in generating aberrant proteins implicated in neurodegenerative diseases. <i>Rna</i> , 2006, 12, 1149-1153.	1.6	20
97	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
98	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
99	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
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	Polyamine Analogs with Xylene Rings Induce Antizyme Frameshifting, Reduce ODC Activity, and Deplete Cellular Polyamines. <i>Journal of Biochemistry</i> , 2006, 140, 657-666.	0.9	12
102	A Functional +1 Ribosomal Frameshift Signal in the Human Paraneoplastic Ma3 Gene. <i>Journal of Biological Chemistry</i> , 2006, 281, 7082-7088.	1.6	67
103	Recoding elements located adjacent to a subset of eukaryal selenocysteine-specifying UGA codons. <i>EMBO Journal</i> , 2005, 24, 1596-1607.	3.5	84
104	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
105	Pyrrolysine and Selenocysteine Use Dissimilar Decoding Strategies. <i>Journal of Biological Chemistry</i> , 2005, 280, 20740-20751.	1.6	104
106	Screening the SPO11 and EIF5A2 genes in a population of infertile men. <i>Fertility and Sterility</i> , 2005, 84, 758-760.	0.5	31
107	Programmed ribosomal frameshifting in decoding the SARS-CoV genome. <i>Virology</i> , 2005, 332, 498-510.	1.1	201
108	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.	2.0	16

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109	Polyamine sensing during antizyme mRNA programmed frameshifting. <i>Biochemical and Biophysical Research Communications</i> , 2005, 338, 1478-1489.	1.0	39
110	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
111	Efficient stimulation of site-specific ribosome frameshifting by antisense oligonucleotides. <i>Rna</i> , 2004, 10, 1653-1661.	1.6	47
112	P-site tRNA is a crucial initiator of ribosomal frameshifting. <i>Rna</i> , 2004, 10, 221-230.	1.6	82
113	$\hat{\alpha}^1$ Frameshifting at a CGA AAG Hexanucleotide Site Is Required for Transposition of Insertion Sequence IS1222. <i>Journal of Bacteriology</i> , 2004, 186, 3274-3277.	1.0	12
114	Factors That Influence Selection of Coding Resumption Sites in Translational Bypassing. <i>Journal of Biological Chemistry</i> , 2004, 279, 11081-11087.	1.6	30
115	A cryptic lysis gene near the start of the $Q\hat{1}^2$ replicase gene in the +1 frame. <i>Genes To Cells</i> , 2004, 9, 877-889.	0.5	3
116	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.	1.2	3
117	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
118	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
119	Maintenance of the correct open reading frame by the ribosome. <i>EMBO Reports</i> , 2003, 4, 499-504.	2.0	38
120	Programmed translational -1 frameshifting on hexanucleotide motifs and the wobble properties of tRNAs. <i>EMBO Journal</i> , 2003, 22, 4770-4778.	3.5	55
121	Translational recoding signals between gag and pol in diverse LTR retrotransposons. <i>Rna</i> , 2003, 9, 1422-1430.	1.6	80
122	RECODE 2003. <i>Nucleic Acids Research</i> , 2003, 31, 87-89.	6.5	64
123	Deletion of Selenoprotein P Alters Distribution of Selenium in the Mouse. <i>Journal of Biological Chemistry</i> , 2003, 278, 13640-13646.	1.6	401
124	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
125	Computational identification of putative programmed translational frameshift sites. <i>Bioinformatics</i> , 2002, 18, 1046-1053.	1.8	72
126	Artificial neural network prediction of antisense oligodeoxynucleotide activity. <i>Nucleic Acids Research</i> , 2002, 30, 4295-4304.	6.5	24

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127	Recoding: translational bifurcations in gene expression. <i>Gene</i> , 2002, 286, 187-201.	1.0	193
128	BIOCHEMISTRY: The 22nd Amino Acid. <i>Science</i> , 2002, 296, 1409-1410.	6.0	100
129	Influence of the stacking potential of the base 3' of tandem shift codons on 5' ribosomal frameshifting used for gene expression. <i>Rna</i> , 2002, 8, 16-28.	1.6	40
130	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
131	Release factor 2 frameshifting sites in different bacteria. <i>EMBO Reports</i> , 2002, 3, 373-377.	2.0	79
132	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
133	Drop-off during ribosome hopping 1 Edited by M. Gottesman. <i>Journal of Molecular Biology</i> , 2001, 311, 445-452.	2.0	32
134	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
135	mRNA readout at 40. <i>Nature</i> , 2001, 414, 693-693.	13.7	3
136	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
137	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.	2.8	233
138	The twenty-first amino acid. <i>Nature</i> , 2000, 407, 463-464.	13.7	106
139	Coupling of Open Reading Frames by Translational Bypassing. <i>Annual Review of Biochemistry</i> , 2000, 69, 343-372.	5.0	65
140	ODNBase--a web database for antisense oligonucleotide effectiveness studies. <i>Bioinformatics</i> , 2000, 16, 843-844.	1.8	21
141	Decoding of tandem quadruplets by adjacent tRNAs with eight-base anticodon loops. <i>Nucleic Acids Research</i> , 2000, 28, 3615-3624.	6.5	11
142	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
143	The 23 S rRNA environment of ribosomal protein L9 in the 50 S ribosomal subunit Edited by D. E. Draper. <i>Journal of Molecular Biology</i> , 2000, 297, 1129-1143.	2.0	42
144	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

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145	Intricacies of ribosomal frameshifting. , 1999, 6, 206-207.		9
146	Mutations which alter the elbow region of tRNA ² Gly reduce T4 gene 60 translational bypassing efficiency. EMBO Journal, 1999, 18, 2886-2896.	3.5	32
147	Structure of human ornithine decarboxylase antizyme 2 gene. Gene, 1999, 232, 165-171.	1.0	8
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