Patrick O'Donoghue

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	RNA-dependent conversion of phosphoserine forms selenocysteine in eukaryotes and archaea. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 18923-18927.	3.3	428
2	Evolutionary Profiles Derived from the QR Factorization of Multiple Structural Alignments Gives an Economy of Information. Journal of Molecular Biology, 2005, 346, 875-894.	2.0	293
3	UGA is an additional glycine codon in uncultured SR1 bacteria from the human microbiota. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 5540-5545.	3.3	290
4	On the Evolution of Structure in Aminoacyl-tRNA Synthetases. Microbiology and Molecular Biology Reviews, 2003, 67, 550-573.	2.9	228
5	Structure of pyrrolysyl-tRNA synthetase, an archaeal enzyme for genetic code innovation. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 11268-11273.	3.3	194
6	Pyrrolysyl-tRNA synthetase–tRNAPyl structure reveals the molecular basis of orthogonality. Nature, 2009, 457, 1163-1167.	13.7	161
7	Upgrading protein synthesis for synthetic biology. Nature Chemical Biology, 2013, 9, 594-598.	3.9	143
8	Genetic code flexibility in microorganisms: novel mechanisms and impact on physiology. Nature Reviews Microbiology, 2015, 13, 707-721.	13.6	104
9	Polyspecific pyrrolysyl-tRNA synthetases from directed evolution. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 16724-16729.	3.3	101
10	Recoding the Genetic Code with Selenocysteine. Angewandte Chemie - International Edition, 2014, 53, 319-323.	7.2	72
11	The evolutionary history of Cys-tRNACys formation. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 19003-19008.	3.3	71
12	Near ognate suppression of amber, opal and quadruplet codons competes with aminoacylâ€ŧRNA ^{Pyl} for genetic code expansion. FEBS Letters, 2012, 586, 3931-3937.	1.3	70
13	Distinct genetic code expansion strategies for selenocysteine and pyrrolysine are reflected in different aminoacylâ€ŧRNA formation systems. FEBS Letters, 2010, 584, 342-349.	1.3	69
14	Revealing the amino acid composition of proteins within an expanded genetic code. Nucleic Acids Research, 2015, 43, e8-e8.	6.5	68
15	Carbon source-dependent expansion of the genetic code in bacteria. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 21070-21075.	3.3	59
16	Pathways to disease from natural variations in human cytoplasmic tRNAs. Journal of Biological Chemistry, 2019, 294, 5294-5308.	1.6	59
17	Emergence of the universal genetic code imprinted in an RNA record. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 18095-18100.	3.3	55
18	The amino-terminal domain of pyrrolysyl-tRNA synthetase is dispensable in vitro but required for in vivo activity. FFBS Letters, 2007, 581, 3197-3203.	1.3	54

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19	Structural insights into RNA-dependent eukaryal and archaeal selenocysteine formation. Nucleic Acids Research, 2007, 36, 1187-1199.	6.5	48
20	The appearance of pyrrolysine in tRNA ^{His} guanylyltransferase by neutral evolution. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 21103-21108.	3.3	48
21	Genetic selection for mistranslation rescues a defective co-chaperone in yeast. Nucleic Acids Research, 2017, 45, 3407-3421.	6.5	38
22	Evolutionary profiles from the QR factorization of multiple sequence alignments. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 4045-4050.	3.3	36
23	tRNAHis-guanylyltransferase establishes tRNAHis identity. Nucleic Acids Research, 2012, 40, 333-344.	6.5	35
24	Visualizing tRNA-dependent mistranslation in human cells. RNA Biology, 2018, 15, 567-575.	1.5	35
25	Phosphorylation-dependent substrate selectivity of protein kinase B (AKT1). Journal of Biological Chemistry, 2020, 295, 8120-8134.	1.6	35
26	Structure of an archaeal non-discriminating glutamyl-tRNA synthetase: a missing link in the evolution of Gln-tRNAGIn formation. Nucleic Acids Research, 2010, 38, 7286-7297.	6.5	34
27	Phosphorylation-Dependent Inhibition of Akt1. Genes, 2018, 9, 450.	1.0	33
28	Characterization and evolutionary history of an archaeal kinase involved in selenocysteinyl-tRNA formation. Nucleic Acids Research, 2008, 36, 1247-1259.	6.5	32
29	Generation of phosphoâ€ubiquitin variants by orthogonal translation reveals codon skipping. FEBS Letters, 2016, 590, 1530-1542.	1.3	32
30	Genetic code expansion and live cell imaging reveal that Thr-308 phosphorylation is irreplaceable and sufficient for Akt1 activity. Journal of Biological Chemistry, 2018, 293, 10744-10756.	1.6	31
31	Dual Targeting of a tRNAAsp Requires Two Different Aspartyl-tRNA Synthetases in Trypanosoma brucei. Journal of Biological Chemistry, 2009, 284, 16210-16217.	1.6	30
32	Evolving Mistranslating tRNAs Through a Phenotypically Ambivalent Intermediate in Saccharomyces cerevisiae. Genetics, 2017, 206, 1865-1879.	1.2	24
33	Acetylation Regulates Thioredoxin Reductase Oligomerization and Activity. Antioxidants and Redox Signaling, 2018, 29, 377-388.	2.5	21
34	How an obscure archaeal gene inspired the discovery of selenocysteine biosynthesis in humans. IUBMB Life, 2009, 61, 35-39.	1.5	20
35	Rational design of an evolutionary precursor of glutaminyl-tRNA synthetase. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 20485-20490.	3.3	19
36	Targeted sequencing reveals expanded genetic diversity of human transfer RNAs. RNA Biology, 2019, 16, 1574-1585.	1.5	19

PATRICK O'DONOGHUE

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37	A bacterial ortholog of class II lysylâ€ŧRNA synthetase activates lysine. FEBS Letters, 2010, 584, 3055-3060.	1.3	17
38	Aminoacylation of tRNA 2′―or 3′â€hydroxyl by phosphoseryl―and pyrrolysylâ€ŧRNA synthetases. FEBS I 2013, 587, 3360-3364.	etters, 1.3	16
39	Phospho-Form Specific Substrates of Protein Kinase B (AKT1). Frontiers in Bioengineering and Biotechnology, 2020, 8, 619252.	2.0	16
40	Ubiquitin phosphorylated at Ser57 hyper-activates parkin. Biochimica Et Biophysica Acta - General Subjects, 2017, 1861, 3038-3046.	1.1	15
41	Transfer RNA function and evolution. RNA Biology, 2018, 15, 423-426.	1.5	15
42	Mistranslation: from adaptations to applications. Biochimica Et Biophysica Acta - General Subjects, 2017, 1861, 3070-3080.	1.1	14
43	Formation and persistence of polyglutamine aggregates in mistranslating cells. Nucleic Acids Research, 2021, 49, 11883-11899.	6.5	14
44	Reducing the genetic code induces massive rearrangement of the proteome. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 17206-17211.	3.3	13
45	Programmed ubiquitin acetylation using genetic code expansion reveals altered ubiquitination patterns. FEBS Letters, 2020, 594, 1226-1234.	1.3	10
46	miRNA-Dependent Regulation of AKT1 Phosphorylation. Cells, 2022, 11, 821.	1.8	8
47	Gld2 activity is regulated by phosphorylation in the N-terminal domain. RNA Biology, 2019, 16, 1022-1033.	1.5	7
48	Acetylated Thioredoxin Reductase 1 Resists Oxidative Inactivation. Frontiers in Chemistry, 2021, 9, 747236.	1.8	6
49	A novel fluorescent reporter sensitive to serine mis-incorporation. RNA Biology, 2022, 19, 220-232.	1.5	6
50	The Molecular Architecture of Unnatural Amino Acid Translation Systems. Structure, 2019, 27, 1192-1194.	1.6	1
51	Synthetic DNA and RNA Programming. Genes, 2019, 10, 523.	1.0	1
52	Editorial: Synthetic Nucleic Acids for Expanding Genetic Codes and Probing Living Cells. Frontiers in Bioengineering and Biotechnology, 2021, 9, 720534.	2.0	1
53	1P-036 X-ray crystallographic analysis of pyrrolysyl-tRNA synthetase from the eubacteria(The 46th) Tj ETQq1 1 0	.784314 r	gBT /Overloc
54	Biochemistry of Synthetic Biology - Recent Developments. Biochimica Et Biophysica Acta - General Subjects, 2017, 1861, 2945-2947.	1.1	0

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55	Expanding codon size. ELife, 2022, 11, .	2.8	Ο