Patrick O Donoghue

List of Publications by Year in Descending Order

52 papers	3,251 citations	27 h-index	57 g-index
59 ext. papers	3,796 ext. citations	9.3 avg, IF	5.22 L-index

#	Paper	IF	Citations
52	A novel fluorescent reporter sensitive to serine mis-incorporation.. *RNA Biology*, **2022**, 19, 221-233	4.8	2
51	Formation and persistence of polyglutamine aggregates in mistranslating cells. *Nucleic Acids Research*, **2021**, 49, 11883-11899	20.1	4
50	Acetylated Thioredoxin Reductase 1 Resists Oxidative Inactivation. *Frontiers in Chemistry*, **2021**, 9, 747236	5	0
49	Phosphorylation-dependent substrate selectivity of protein kinase B (AKT1). *Journal of Biological Chemistry*, **2020**, 295, 8120-8134	5.4	16
48	Programmed ubiquitin acetylation using genetic code expansion reveals altered ubiquitination patterns. *FEBS Letters*, **2020**, 594, 1226-1234	3.8	5
47	Phospho-Form Specific Substrates of Protein Kinase B (AKT1). *Frontiers in Bioengineering and Biotechnology*, **2020**, 8, 619252	5.8	4
46	Gld2 activity is regulated by phosphorylation in the N-terminal domain. *RNA Biology*, **2019**, 16, 1022-1033	4.8	5
45	The Molecular Architecture of Unnatural Amino Acid Translation Systems. *Structure*, **2019**, 27, 1192-1194	5.2	
44	Targeted sequencing reveals expanded genetic diversity of human transfer RNAs. *RNA Biology*, **2019**, 16, 1574-1585	4.8	9
43	Pathways to disease from natural variations in human cytoplasmic tRNAs. *Journal of Biological Chemistry*, **2019**, 294, 5294-5308	5.4	31
42	Visualizing tRNA-dependent mistranslation in human cells. *RNA Biology*, **2018**, 15, 567-575	4.8	20
41	Transfer RNA function and evolution. *RNA Biology*, **2018**, 15, 423-426	4.8	10
40	Acetylation Regulates Thioredoxin Reductase Oligomerization and Activity. *Antioxidants and Redox Signaling*, **2018**, 29, 377-388	8.4	9
39	Phosphorylation-Dependent Inhibition of Akt1. *Genes*, **2018**, 9,	4.2	19
38	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	5.4	17
37	Mistranslation: from adaptations to applications. *Biochimica Et Biophysica Acta - General Subjects*, **2017**, 1861, 3070-3080	4	5
36	Genetic selection for mistranslation rescues a defective co-chaperone in yeast. *Nucleic Acids Research*, **2017**, 45, 3407-3421	20.1	26

35	Ubiquitin phosphorylated at Ser57 hyper-activates parkin. *Biochimica Et Biophysica Acta - General Subjects*, **2017**, 1861, 3038-3046	4	9
34	Evolving Mistranslating tRNAs Through a Phenotypically Ambivalent Intermediate in. *Genetics*, **2017**, 206, 1865-1879	4	14
33	Generation of phospho-ubiquitin variants by orthogonal translation reveals codon skipping. *FEBS Letters*, **2016**, 590, 1530-42	3.8	23
32	Genetic code flexibility in microorganisms: novel mechanisms and impact on physiology. *Nature Reviews Microbiology*, **2015**, 13, 707-721	22.2	77
31	Revealing the amino acid composition of proteins within an expanded genetic code. *Nucleic Acids Research*, **2015**, 43, e8	20.1	52
30	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, 17206-11	11.5	9
29	Polyspecific pyrrolysyl-tRNA synthetases from directed evolution. *Proceedings of the National Academy of Sciences of the United States of America*, **2014**, 111, 16724-9	11.5	75
28	Recoding the genetic code with selenocysteine. *Angewandte Chemie - International Edition*, **2014**, 53, 319-23	16.4	60
27	Umkodierung des genetischen Codes mit Selenocystein. *Angewandte Chemie*, **2014**, 126, 325-330	3.6	8
26	Titelbild: Umkodierung des genetischen Codes mit Selenocystein (Angew. Chem. 1/2014). *Angewandte Chemie*, **2014**, 126, 1-1	3.6	124
25	Upgrading protein synthesis for synthetic biology. *Nature Chemical Biology*, **2013**, 9, 594-8	11.7	114
24	Aminoacylation of tRNA 2Ʉ or 3Ʉhydroxyl by phosphoseryl- and pyrrolysyl-tRNA synthetases. *FEBS Letters*, **2013**, 587, 3360-4	3.8	11
23	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, 5540-5	11.5	199
22	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, 21070-5	11.5	40
21	Near-cognate suppression of amber, opal and quadruplet codons competes with aminoacyl-tRNAPyl for genetic code expansion. *FEBS Letters*, **2012**, 586, 3931-7	3.8	58
20	tRNAHis-guanylyltransferase establishes tRNAHis identity. *Nucleic Acids Research*, **2012**, 40, 333-44	20.1	29
19	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, 20485-90	11.5	17
18	Structure of an archaeal non-discriminating glutamyl-tRNA synthetase: a missing link in the evolution of Gln-tRNAGln formation. *Nucleic Acids Research*, **2010**, 38, 7286-97	20.1	29

17	Distinct genetic code expansion strategies for selenocysteine and pyrrolysine are reflected in different aminoacyl-tRNA formation systems. *FEBS Letters*, **2010**, 584, 342-9	3.8	59
16	A bacterial ortholog of class II lysyl-tRNA synthetase activates lysine. *FEBS Letters*, **2010**, 584, 3055-60	3.8	15
15	The appearance of pyrrolysine in tRNAHis guanylyltransferase by neutral evolution. *Proceedings of the National Academy of Sciences of the United States of America*, **2009**, 106, 21103-8	11.5	43
14	Dual targeting of a tRNAAsp requires two different aspartyl-tRNA synthetases in Trypanosoma brucei. *Journal of Biological Chemistry*, **2009**, 284, 16210-16217	5.4	28
13	How an obscure archaeal gene inspired the discovery of selenocysteine biosynthesis in humans. *IUBMB Life*, **2009**, 61, 35-9	4.7	19
12	Pyrrolysyl-tRNA synthetase-tRNA(Pyl) structure reveals the molecular basis of orthogonality. *Nature*, **2009**, 457, 1163-7	50.4	133
11	Characterization and evolutionary history of an archaeal kinase involved in selenocysteinyl-tRNA formation. *Nucleic Acids Research*, **2008**, 36, 1247-59	20.1	28
10	1P-036 X-ray crystallographic analysis of pyrrolysyl-tRNA synthetase from the eubacteria(The 46th Annual Meeting of the Biophysical Society of Japan). *Seibutsu Butsuri*, **2008**, 48, S26	0	
9	Structural insights into RNA-dependent eukaryal and archaeal selenocysteine formation. *Nucleic Acids Research*, **2008**, 36, 1187-99	20.1	43
8	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, 11268-73	11.5	156
7	The amino-terminal domain of pyrrolysyl-tRNA synthetase is dispensable in vitro but required for in vivo activity. *FEBS Letters*, **2007**, 581, 3197-203	3.8	39
6	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, 18095-100	11.5	50
5	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, 18923-7	11.5	359
4	Evolutionary profiles derived from the QR factorization of multiple structural alignments gives an economy of information. *Journal of Molecular Biology*, **2005**, 346, 875-94	6.5	246
3	The evolutionary history of Cys-tRNACys formation. *Proceedings of the National Academy of Sciences of the United States of America*, **2005**, 102, 19003-8	11.5	70
2	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, 4045-50	11.5	34
1	On the evolution of structure in aminoacyl-tRNA synthetases. *Microbiology and Molecular Biology Reviews*, **2003**, 67, 550-73	13.2	193