

Patrick O Donoghue

List of Publications by Citations

Source: <https://exaly.com/author-pdf/6941501/patrick-odonoghue-publications-by-citations.pdf>

Version: 2024-04-26

This document has been generated based on the publications and citations recorded by exaly.com. For the latest version of this publication list, visit the link given above.

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

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	RNA-dependent conversion of phosphoserine forms selenocysteine in eukaryotes and archaea. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006 , 103, 18923-7	11.5	359
51	Evolutionary profiles derived from the QR factorization of multiple structural alignments gives an economy of information. <i>Journal of Molecular Biology</i> , 2005 , 346, 875-94	6.5	246
50	UGA is an additional glycine codon in uncultured SR1 bacteria from the human microbiota. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013 , 110, 5540-5	11.5	199
49	On the evolution of structure in aminoacyl-tRNA synthetases. <i>Microbiology and Molecular Biology Reviews</i> , 2003 , 67, 550-73	13.2	193
48	Structure of pyrrolysyl-tRNA synthetase, an archaeal enzyme for genetic code innovation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007 , 104, 11268-73	11.5	156
47	Pyrrolysyl-tRNA synthetase-tRNA(Pyl) structure reveals the molecular basis of orthogonality. <i>Nature</i> , 2009 , 457, 1163-7	50.4	133
46	Titelbild: Umkodierung des genetischen Codes mit Selenocystein (Angew. Chem. 1/2014). <i>Angewandte Chemie</i> , 2014 , 126, 1-1	3.6	124
45	Upgrading protein synthesis for synthetic biology. <i>Nature Chemical Biology</i> , 2013 , 9, 594-8	11.7	114
44	Genetic code flexibility in microorganisms: novel mechanisms and impact on physiology. <i>Nature Reviews Microbiology</i> , 2015 , 13, 707-721	22.2	77
43	Polyspecific pyrrolysyl-tRNA synthetases from directed evolution. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014 , 111, 16724-9	11.5	75
42	The evolutionary history of Cys-tRNA ^{Cys} formation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005 , 102, 19003-8	11.5	70
41	Recoding the genetic code with selenocysteine. <i>Angewandte Chemie - International Edition</i> , 2014 , 53, 319-23	16.4	60
40	Distinct genetic code expansion strategies for selenocysteine and pyrrolysine are reflected in different aminoacyl-tRNA formation systems. <i>FEBS Letters</i> , 2010 , 584, 342-9	3.8	59
39	Near-cognate suppression of amber, opal and quadruplet codons competes with aminoacyl-tRNA ^{Pyl} for genetic code expansion. <i>FEBS Letters</i> , 2012 , 586, 3931-7	3.8	58
38	Revealing the amino acid composition of proteins within an expanded genetic code. <i>Nucleic Acids Research</i> , 2015 , 43, e8	20.1	52
37	Emergence of the universal genetic code imprinted in an RNA record. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006 , 103, 18095-100	11.5	50
36	The appearance of pyrrolysine in tRNA ^{His} guanylyltransferase by neutral evolution. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009 , 106, 21103-8	11.5	43

35	Structural insights into RNA-dependent eukaryal and archaeal selenocysteine formation. <i>Nucleic Acids Research</i> , 2008 , 36, 1187-99	20.1	43
34	Carbon source-dependent expansion of the genetic code in bacteria. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012 , 109, 21070-5	11.5	40
33	The amino-terminal domain of pyrrolysyl-tRNA synthetase is dispensable in vitro but required for in vivo activity. <i>FEBS Letters</i> , 2007 , 581, 3197-203	3.8	39
32	Evolutionary profiles from the QR factorization of multiple sequence alignments. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005 , 102, 4045-50	11.5	34
31	Pathways to disease from natural variations in human cytoplasmic tRNAs. <i>Journal of Biological Chemistry</i> , 2019 , 294, 5294-5308	5.4	31
30	Structure of an archaeal non-discriminating glutamyl-tRNA synthetase: a missing link in the evolution of Gln-tRNA ^{Gln} formation. <i>Nucleic Acids Research</i> , 2010 , 38, 7286-97	20.1	29
29	tRNA ^{His} -guanylyltransferase establishes tRNA ^{His} identity. <i>Nucleic Acids Research</i> , 2012 , 40, 333-44	20.1	29
28	Dual targeting of a tRNA ^{Asp} requires two different aspartyl-tRNA synthetases in <i>Trypanosoma brucei</i> . <i>Journal of Biological Chemistry</i> , 2009 , 284, 16210-16217	5.4	28
27	Characterization and evolutionary history of an archaeal kinase involved in selenocysteinyl-tRNA formation. <i>Nucleic Acids Research</i> , 2008 , 36, 1247-59	20.1	28
26	Genetic selection for mistranslation rescues a defective co-chaperone in yeast. <i>Nucleic Acids Research</i> , 2017 , 45, 3407-3421	20.1	26
25	Generation of phospho-ubiquitin variants by orthogonal translation reveals codon skipping. <i>FEBS Letters</i> , 2016 , 590, 1530-42	3.8	23
24	Visualizing tRNA-dependent mistranslation in human cells. <i>RNA Biology</i> , 2018 , 15, 567-575	4.8	20
23	How an obscure archaeal gene inspired the discovery of selenocysteine biosynthesis in humans. <i>IUBMB Life</i> , 2009 , 61, 35-9	4.7	19
22	Phosphorylation-Dependent Inhibition of Akt1. <i>Genes</i> , 2018 , 9,	4.2	19
21	Rational design of an evolutionary precursor of glutamyl-tRNA synthetase. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011 , 108, 20485-90	11.5	17
20	Genetic code expansion and live cell imaging reveal that Thr-308 phosphorylation is irreplaceable and sufficient for Akt1 activity. <i>Journal of Biological Chemistry</i> , 2018 , 293, 10744-10756	5.4	17
19	Phosphorylation-dependent substrate selectivity of protein kinase B (AKT1). <i>Journal of Biological Chemistry</i> , 2020 , 295, 8120-8134	5.4	16
18	A bacterial ortholog of class II lysyl-tRNA synthetase activates lysine. <i>FEBS Letters</i> , 2010 , 584, 3055-60	3.8	15

17	Evolving Mistranslating tRNAs Through a Phenotypically Ambivalent Intermediate in. <i>Genetics</i> , 2017 , 206, 1865-1879	4	14
16	Aminoacylation of tRNA 2U or 3Uhydroxyl by phosphoseryl- and pyrrolysyl-tRNA synthetases. <i>FEBS Letters</i> , 2013 , 587, 3360-4	3.8	11
15	Transfer RNA function and evolution. <i>RNA Biology</i> , 2018 , 15, 423-426	4.8	10
14	Targeted sequencing reveals expanded genetic diversity of human transfer RNAs. <i>RNA Biology</i> , 2019 , 16, 1574-1585	4.8	9
13	Reducing the genetic code induces massive rearrangement of the proteome. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014 , 111, 17206-11	11.5	9
12	Ubiquitin phosphorylated at Ser57 hyper-activates parkin. <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2017 , 1861, 3038-3046	4	9
11	Acetylation Regulates Thioredoxin Reductase Oligomerization and Activity. <i>Antioxidants and Redox Signaling</i> , 2018 , 29, 377-388	8.4	9
10	Umkodierung des genetischen Codes mit Selenocystein. <i>Angewandte Chemie</i> , 2014 , 126, 325-330	3.6	8
9	Mistranslation: from adaptations to applications. <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2017 , 1861, 3070-3080	4	5
8	Gld2 activity is regulated by phosphorylation in the N-terminal domain. <i>RNA Biology</i> , 2019 , 16, 1022-1033	4.8	5
7	Programmed ubiquitin acetylation using genetic code expansion reveals altered ubiquitination patterns. <i>FEBS Letters</i> , 2020 , 594, 1226-1234	3.8	5
6	Formation and persistence of polyglutamine aggregates in mistranslating cells. <i>Nucleic Acids Research</i> , 2021 , 49, 11883-11899	20.1	4
5	Phospho-Form Specific Substrates of Protein Kinase B (AKT1). <i>Frontiers in Bioengineering and Biotechnology</i> , 2020 , 8, 619252	5.8	4
4	A novel fluorescent reporter sensitive to serine mis-incorporation.. <i>RNA Biology</i> , 2022 , 19, 221-233	4.8	2
3	Acetylated Thioredoxin Reductase 1 Resists Oxidative Inactivation. <i>Frontiers in Chemistry</i> , 2021 , 9, 747236	3.6	0
2	The Molecular Architecture of Unnatural Amino Acid Translation Systems. <i>Structure</i> , 2019 , 27, 1192-1194	5.2	0
1	1P-036 X-ray crystallographic analysis of pyrrolysyl-tRNA synthetase from the eubacteria(The 46th Annual Meeting of the Biophysical Society of Japan). <i>Seibutsu Butsuri</i> , 2008 , 48, S26	0	0