

Joseph D Puglisi

List of Publications by Year in descending order

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138
papers

12,437
citations

26630

56
h-index

26613

107
g-index

150
all docs

150
docs citations

150
times ranked

9866
citing authors

#	ARTICLE	IF	CITATIONS
1	Direct tracking of eukaryotic translation termination dynamics. <i>Biophysical Journal</i> , 2022, 121, 202a.	0.5	0
2	eIF5B and eIF1A reorient initiator tRNA to allow ribosomal subunit joining. <i>Nature</i> , 2022, 607, 185-190.	27.8	25
3	6-Methyladenosines in mRNAs reduce the accuracy of codon reading by transfer RNAs and peptide release factors. <i>Nucleic Acids Research</i> , 2021, 49, 2684-2699.	14.5	10
4	Mechanisms that ensure speed and fidelity in eukaryotic translation termination. <i>Science</i> , 2021, 373, 876-882.	12.6	33
5	Dynamic competition between SARS-CoV-2 NSP1 and mRNA on the human ribosome inhibits translation initiation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	7.1	145
6	Dynamics of the context-specific translation arrest by chloramphenicol and linezolid. <i>Nature Chemical Biology</i> , 2020, 16, 310-317.	8.0	43
7	Structural basis for the transition from translation initiation to elongation by an 80S-eIF5B complex. <i>Nature Communications</i> , 2020, 11, 5003.	12.8	26
8	A memory of eS25 loss drives resistance phenotypes. <i>Nucleic Acids Research</i> , 2020, 48, 7279-7297.	14.5	4
9	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.	4.2	5
10	The energy landscape of ~ 1 ribosomal frameshifting. <i>Science Advances</i> , 2020, 6, eaax6969.	10.3	51
11	Single-Molecule Fluorescence Applied to Translation. <i>Cold Spring Harbor Perspectives in Biology</i> , 2019, 11, a032714.	5.5	26
12	RPS25 is required for efficient RAN translation of C9orf72 and other neurodegenerative disease-associated nucleotide repeats. <i>Nature Neuroscience</i> , 2019, 22, 1383-1388.	14.8	87
13	Relating Structure and Dynamics in RNA Biology. <i>Cold Spring Harbor Perspectives in Biology</i> , 2019, 11, a032474.	5.5	21
14	eIF5B gates the transition from translation initiation to elongation. <i>Nature</i> , 2019, 573, 605-608.	27.8	60
15	Expanding single-molecule fluorescence spectroscopy to capture complexity in biology. <i>Current Opinion in Structural Biology</i> , 2019, 58, 233-240.	5.7	6
16	RACK1 on and off the ribosome. <i>Rna</i> , 2019, 25, 881-895.	3.5	38
17	Transient Protein-RNA Interactions Guide Nascent Ribosomal RNA Folding. <i>Cell</i> , 2019, 179, 1357-1369.e16.	28.9	61
18	Mechanism of ribosome stalling during translation of a poly(A) tail. <i>Nature Structural and Molecular Biology</i> , 2019, 26, 1132-1140.	8.2	114

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19	A short translational ramp determines the efficiency of protein synthesis. <i>Nature Communications</i> , 2019, 10, 5774.	12.8	109
20	Architecture of an HIV-1 reverse transcriptase initiation complex. <i>Nature</i> , 2018, 557, 118-122.	27.8	44
21	2â€²-O-methylation in mRNA disrupts tRNA decoding during translation elongation. <i>Nature Structural and Molecular Biology</i> , 2018, 25, 208-216.	8.2	92
22	Fluorescently-tagged human eIF3 for single-molecule spectroscopy. <i>Nucleic Acids Research</i> , 2018, 46, e8-e8.	14.5	12
23	Real-time assembly of ribonucleoprotein complexes on nascent RNA transcripts. <i>Nature Communications</i> , 2018, 9, 5087.	12.8	43
24	De novo computational RNA modeling into cryo-EM maps of large ribonucleoprotein complexes. <i>Nature Methods</i> , 2018, 15, 947-954.	19.0	45
25	Dynamic Interplay of RNA and Protein in the Human Immunodeficiency Virus-1 Reverse Transcription Initiation Complex. <i>Journal of Molecular Biology</i> , 2018, 430, 5137-5150.	4.2	11
26	Ribosomal Protein Dynamics on the Human Ribosome. <i>Biophysical Journal</i> , 2018, 114, 595a.	0.5	1
27	How Messenger RNA and Nascent Chain Sequences Regulate Translation Elongation. <i>Annual Review of Biochemistry</i> , 2018, 87, 421-449.	11.1	62
28	Dynamics of IRES-mediated translation. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2017, 372, 20160177.	4.0	80
29	Dynamic basis of fidelity and speed in translation: Coordinated multistep mechanisms of elongation and termination. <i>Protein Science</i> , 2017, 26, 1352-1362.	7.6	30
30	Three tRNAs on the ribosome slow translation elongation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 13691-13696.	7.1	38
31	Post-termination Ribosome Intermediate Acts as the Gateway to Ribosome Recycling. <i>Cell Reports</i> , 2017, 20, 161-172.	6.4	39
32	The molecular choreography of protein synthesis: translational control, regulation, and pathways. <i>Quarterly Reviews of Biophysics</i> , 2016, 49, e11.	5.7	14
33	Multiple Parallel Pathways of Translation Initiation on the CrPV IRES. <i>Molecular Cell</i> , 2016, 62, 92-103.	9.7	59
34	Heterogeneous structures formed by conserved RNA sequences within the HIV reverse transcription initiation site. <i>Rna</i> , 2016, 22, 1689-1698.	3.5	13
35	Amino acid sequence repertoire of the bacterial proteome and the occurrence of untranslatable sequences. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 7166-7170.	7.1	15
36	N6-methyladenosine in mRNA disrupts tRNA selection and translation-elongation dynamics. <i>Nature Structural and Molecular Biology</i> , 2016, 23, 110-115.	8.2	202

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37	Concentric-flow electrokinetic injector enables serial crystallography of ribosome and photosystem II. <i>Nature Methods</i> , 2016, 13, 59-62.	19.0	103
38	The noncoding RNAs SNORD50A and SNORD50B bind K-Ras and are recurrently deleted in human cancer. <i>Nature Genetics</i> , 2016, 48, 53-58.	21.4	143
39	Probing the Translation Dynamics of Ribosomes Using Zero-Mode Waveguides. <i>Progress in Molecular Biology and Translational Science</i> , 2016, 139, 1-43.	1.7	13
40	RNA dances to center stage. <i>Rna</i> , 2015, 21, 712-713.	3.5	2
41	Ribosomal ties that bind. <i>Nature</i> , 2015, 524, 45-46.	27.8	1
42	The delicate dance of translation and folding. <i>Science</i> , 2015, 348, 399-400.	12.6	8
43	Cotranslational Protein Folding inside the Ribosome Exit Tunnel. <i>Cell Reports</i> , 2015, 12, 1533-1540.	6.4	234
44	A simple real-time assay for in vitro translation. <i>Rna</i> , 2015, 21, 296-305.	3.5	20
45	Coupling of mRNA Structure Rearrangement to Ribosome Movement during Bypassing of Non-coding Regions. <i>Cell</i> , 2015, 163, 1267-1280.	28.9	42
46	Kinetic pathway of 40S ribosomal subunit recruitment to hepatitis C virus internal ribosome entry site. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 319-325.	7.1	46
47	Aminoglycoside Antibiotics and Decoding. , 2014, , 419-429.		10
48	Signal Recognition Particle-ribosome Binding Is Sensitive to Nascent Chain Length. <i>Journal of Biological Chemistry</i> , 2014, 289, 19294-19305.	3.4	39
49	Sequence-Dependent Elongation Dynamics on Macrolide-Bound Ribosomes. <i>Cell Reports</i> , 2014, 7, 1534-1546.	6.4	36
50	High-throughput platform for real-time monitoring of biological processes by multicolor single-molecule fluorescence. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 664-669.	7.1	123
51	The Dynamics of SecM-Induced Translational Stalling. <i>Cell Reports</i> , 2014, 7, 1521-1533.	6.4	48
52	Single-Molecule Profiling of Ribosome Translational Phenomena. <i>Biophysical Journal</i> , 2014, 106, 239a.	0.5	0
53	Dynamic pathways of ~ 1 translational frameshifting. <i>Nature</i> , 2014, 512, 328-332.	27.8	147
54	Real-time observation of signal recognition particle binding to actively translating ribosomes. <i>ELife</i> , 2014, 3, .	6.0	41

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55	Involvement of protein IF2 N domain in ribosomal subunit joining revealed from architecture and function of the full-length initiation factor. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 15656-15661.	7.1	48
56	Dynamic Recognition of the mRNA Cap by <i>Saccharomyces cerevisiae</i> eIF4E. Structure, 2013, 21, 2197-2207.	3.3	36
57	Coordinated conformational and compositional dynamics drive ribosome translocation. Nature Structural and Molecular Biology, 2013, 20, 718-727.	8.2	117
58	The Impact of Aminoglycosides on the Dynamics of Translation Elongation. Cell Reports, 2013, 3, 497-508.	6.4	72
59	1SBP-03 Dynamics of translation elongation in real time(1SBP Advanced Single Molecule Sequencing) Tj ETQq1 1 0.784314 rgBT /Over 53, S87.	0.1	0
60	Unraveling the dynamics of ribosome translocation. Current Opinion in Structural Biology, 2012, 22, 804-814.	5.7	58
61	Nonfluorescent Quenchers To Correlate Single-Molecule Conformational and Compositional Dynamics. Journal of the American Chemical Society, 2012, 134, 5734-5737.	13.7	39
62	Precursor Directed Biosynthesis of an Orthogonally Functional Erythromycin Analogue: Selectivity in the Ribosome Macrolide Binding Pocket. Journal of the American Chemical Society, 2012, 134, 12259-12265.	13.7	53
63	Initiation factor 2, tRNA, and 50S subunits cooperatively stabilize mRNAs on the ribosome during initiation. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 4881-4885.	7.1	10
64	Single-Molecule Analysis of Translational Dynamics. Cold Spring Harbor Perspectives in Biology, 2012, 4, a011551-a011551.	5.5	31
65	Heterogeneous pathways and timing of factor departure during translation initiation. Nature, 2012, 487, 390-393.	27.8	83
66	Secondary Structure of the HIV Reverse Transcription Initiation Complex by NMR. Journal of Molecular Biology, 2011, 410, 863-874.	4.2	23
67	Following the intersubunit conformation of the ribosome during translation in real time. Nature Structural and Molecular Biology, 2010, 17, 793-800.	8.2	97
68	Ligand-specific regulation of the extracellular surface of a G-protein-coupled receptor. Nature, 2010, 463, 108-112.	27.8	432
69	Real-time tRNA transit on single translating ribosomes at codon resolution. Nature, 2010, 464, 1012-1017.	27.8	329
70	Site-specific labeling of <i>Saccharomyces cerevisiae</i> ribosomes for single-molecule manipulations. Nucleic Acids Research, 2010, 38, e143-e143.	14.5	22
71	Single Ribosome Dynamics and the Mechanism of Translation. Annual Review of Biophysics, 2010, 39, 491-513.	10.0	84
72	Realtime Observation of tRNA Dynamics at High Concentrations in Single Molecule Translation. Biophysical Journal, 2010, 98, 260a-261a.	0.5	0

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73	Translational insensitivity to potent activation of PKR by HCV IRES RNA. <i>Antiviral Research</i> , 2009, 83, 228-237.	4.1	56
74	GTP Hydrolysis by IF2 Guides Progression of the Ribosome into Elongation. <i>Molecular Cell</i> , 2009, 35, 37-47.	9.7	87
75	Resolving the Elegant Architecture of the Ribosome. <i>Molecular Cell</i> , 2009, 36, 720-723.	9.7	6
76	Translation at the Single-Molecule Level. <i>Annual Review of Biochemistry</i> , 2008, 77, 177-203.	11.1	117
77	An Oxygen Scavenging System for Improvement of Dye Stability in Single-Molecule Fluorescence Experiments. <i>Biophysical Journal</i> , 2008, 94, 1826-1835.	0.5	716
78	Single-molecule imaging of full protein synthesis by immobilized ribosomes. <i>Nucleic Acids Research</i> , 2008, 36, e70-e70.	14.5	41
79	Irreversible chemical steps control intersubunit dynamics during translation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 15364-15369.	7.1	112
80	2P-126 Real time imaging of tRNA dynamics with a zero-mode waveguides during translation(The 46th Tj ETQq0 0.0 rgBT /Oyerlock 10 0.1)	0.1	0
81	Molecular Framework for the Activation of RNA-dependent Protein Kinase. <i>Journal of Biological Chemistry</i> , 2007, 282, 11474-11486.	3.4	56
82	The role of fluctuations in tRNA selection by the ribosome. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 13661-13665.	7.1	96
83	Thiostrepton inhibition of tRNA delivery to the ribosome. <i>Rna</i> , 2007, 13, 2091-2097.	3.5	50
84	Biophysical and Biochemical Investigations of dsRNA-Activated Kinase PKR. <i>Methods in Enzymology</i> , 2007, 430, 373-396.	1.0	15
85	Solution mapping of T cell receptor docking footprints on peptide-MHC. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 13080-13085.	7.1	45
86	Viral dsRNA Inhibitors Prevent Self-association and Autophosphorylation of PKR. <i>Journal of Molecular Biology</i> , 2007, 372, 103-113.	4.2	46
87	Probing the conformation of human tRNA ₃ ^{Lys} in solution by NMR. <i>FEBS Letters</i> , 2007, 581, 5307-5314.	2.8	12
88	Fluctuations of Transfer RNAs between Classical and Hybrid States. <i>Biophysical Journal</i> , 2007, 93, 3575-3582.	0.5	91
89	PKR: A NMR perspective. <i>Progress in Nuclear Magnetic Resonance Spectroscopy</i> , 2007, 51, 199-215.	7.5	4
90	The dance of domains. <i>Nature</i> , 2007, 450, 1171-1172.	27.8	3

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91	Purification and characterization of transcribed RNAs using gel filtration chromatography. <i>Nature Protocols</i> , 2007, 2, 3270-3277.	12.0	88
92	Peptide bond formation destabilizes Shine-Dalgarno interaction on the ribosome. <i>Nature</i> , 2007, 446, 454-457.	27.8	107
93	Solution structure and proposed domain-domain recognition interface of an acyl carrier protein domain from a modular polyketide synthase. <i>Protein Science</i> , 2007, 16, 2093-2107.	7.6	107
94	Specific Recognition of HIV TAR RNA by the dsRNA Binding Domains (dsRBD1&dsRBD2) of PKR. <i>Journal of Molecular Biology</i> , 2006, 358, 430-442.	4.2	50
95	Uncoupling of RNA Binding and PKR Kinase Activation by Viral Inhibitor RNAs. <i>Journal of Molecular Biology</i> , 2006, 358, 1270-1285.	4.2	60
96	1P557 Peptide bond formation induces the breakage of Shine-Dalgarno interaction on the ribosome(26.) Tj ETQq0 0 0 rgBT /Overlock 10 Butsuri, 2006, 46, S286.	0.1	0
97	Rapid purification of RNAs using fast performance liquid chromatography (FPLC). <i>Rna</i> , 2006, 13, 289-294.	3.5	90
98	Dynamics of Translation. <i>FASEB Journal</i> , 2006, 20, A889.	0.5	0
99	Quantitative polysome analysis identifies limitations in bacterial cell-free protein synthesis. <i>Biotechnology and Bioengineering</i> , 2005, 91, 425-435.	3.3	113
100	Structure Determination of Large Biological RNAs. <i>Methods in Enzymology</i> , 2005, 394, 399-416.	1.0	53
101	Site-specific labeling of the ribosome for single-molecule spectroscopy. <i>Nucleic Acids Research</i> , 2005, 33, 182-189.	14.5	111
102	Large-scale preparation and purification of polyacrylamide-free RNA oligonucleotides. <i>Rna</i> , 2004, 10, 889-893.	3.5	115
103	tRNA dynamics on the ribosome during translation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 12893-12898.	7.1	435
104	tRNA selection and kinetic proofreading in translation. <i>Nature Structural and Molecular Biology</i> , 2004, 11, 1008-1014.	8.2	426
105	The Pathway of HCV IRES-Mediated Translation Initiation. <i>Cell</i> , 2004, 119, 369-380.	28.9	241
106	Comparison of X-Ray Crystal Structure of the 30S Subunit-Antibiotic Complex with NMR Structure of Decoding Site Oligonucleotide-Paromomycin Complex. <i>Structure</i> , 2003, 11, 43-53.	3.3	97
107	Structure of HCV IRES domain II determined by NMR. <i>Nature Structural and Molecular Biology</i> , 2003, 10, 1033-1038.	8.2	260
108	Design of a Cyclic Peptide that Targets a Viral RNA. <i>Journal of the American Chemical Society</i> , 2003, 125, 15704-15705.	13.7	22

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109	NMR Study of 100 kDa HCV IRES RNA Using Segmental Isotope Labeling. Journal of the American Chemical Society, 2002, 124, 9338-9339.	13.7	90
110	Ribosomal proteins mediate the hepatitis C virus IRES???HeLa 40S interaction. Rna, 2002, 8, 913-923.	3.5	88
111	Structure of a eukaryotic decoding region A-site RNA. Journal of Molecular Biology, 2001, 306, 1023-1035.	4.2	52
112	Structural origins of aminoglycoside specificity for prokaryotic ribosomes. Journal of Molecular Biology, 2001, 306, 1037-1058.	4.2	132
113	Aminoglycoside Resistance with Homogeneous and Heterogeneous Populations of Antibiotic-Resistant Ribosomes. Antimicrobial Agents and Chemotherapy, 2001, 45, 2414-2419.	3.2	57
114	[16] Biochemical and nuclear magnetic resonance studies of aminoglycoside-RNA complexes. Methods in Enzymology, 2000, 317, 240-261.	1.0	24
115	mRNA processing: the 3'-end justifies the means. , 2000, 7, 263-264.		3
116	Approaching translation at atomic resolution. Nature Structural Biology, 2000, 7, 855-861.	9.7	42
117	Structures of two RNA domains essential for hepatitis C virus internal ribosome entry site function. Nature Structural Biology, 2000, 7, 1105-1110.	9.7	185
118	Interaction of translation initiation factor IF1 with the E. coli ribosomal A site 1 Edited by D. E. Draper. Journal of Molecular Biology, 2000, 299, 1-15.	4.2	63
119	Application of Residual Dipolar Coupling Measurements To Identify Conformational Changes in RNA Induced by Antibiotics. Journal of the American Chemical Society, 2000, 122, 7853-7854.	13.7	16
120	The ribosome revealed. , 1999, 6, 999-1003.		10
121	Recognition of the Codon-Anticodon Helix by Ribosomal RNA. Science, 1999, 285, 1722-1725.	12.6	221
122	Effect of mutations in the A site of 16 S rRNA on aminoglycoside antibiotic-ribosome interaction. Journal of Molecular Biology, 1999, 286, 33-43.	4.2	99
123	HIV-1 A-rich RNA loop mimics the tRNA anticodon structure. Nature Structural Biology, 1998, 5, 1033-1036.	9.7	62
124	Paromomycin binding induces a local conformational change in the A-site of 16 s rRNA. Journal of Molecular Biology, 1998, 277, 333-345.	4.2	288
125	Binding of neomycin-class aminoglycoside antibiotics to the A-site of 16 s rRNA. Journal of Molecular Biology, 1998, 277, 347-362.	4.2	241
126	Structure of a conserved RNA component of the peptidyl transferase centre. Nature Structural Biology, 1997, 4, 775-778.	9.7	35

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127	RNA Sequence Determinants for Aminoglycoside Binding to an A-site rRNA Model Oligonucleotide. <i>Journal of Molecular Biology</i> , 1996, 262, 421-436.	4.2	252
128	[14] Biochemical and NMR studies of RNA conformation with an emphasis on RNA pseudoknots. <i>Methods in Enzymology</i> , 1995, 261, 323-350.	1.0	49
129	Influence of tRNA tertiary structure and stability on aminoacylation by yeast aspartyl-tRNA synthetase. <i>Nucleic Acids Research</i> , 1993, 21, 41-49.	14.5	54
130	tRNA Structure and Aminoacylation Efficiency. <i>Progress in Molecular Biology and Translational Science</i> , 1993, 45, 129-206.	1.9	218
131	Conformation of the TAR RNA-arginine complex by NMR spectroscopy. <i>Science</i> , 1992, 257, 76-80.	12.6	607
132	Preparation of isotopically labeled ribonucleotides for multidimensional NMR spectroscopy of RNA. <i>Nucleic Acids Research</i> , 1992, 20, 4515-4523.	14.5	288
133	RNA pseudoknots. <i>Accounts of Chemical Research</i> , 1991, 24, 152-158.	15.6	31
134	Conformation of an RNA pseudoknot. <i>Journal of Molecular Biology</i> , 1990, 214, 437-453.	4.2	134
135	RNA pseudoknots. <i>Journal of Molecular Biology</i> , 1990, 214, 455-470.	4.2	141
136	RNA folding: Pseudoknots, loops and bulges. <i>BioEssays</i> , 1989, 11, 100-106.	2.5	57
137	[22] absorbance melting curves of RNA. <i>Methods in Enzymology</i> , 1989, 180, 304-325.	1.0	591
138	A pseudoknotted RNA oligonucleotide. <i>Nature</i> , 1988, 331, 283-286.	27.8	106