

Joseph D Puglisi

List of Publications by Year in descending order

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138
papers

12,437
citations

26630

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107
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150
all docs

150
docs citations

150
times ranked

9866
citing authors

#	ARTICLE	IF	CITATIONS
1	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
2	Conformation of the TAR RNA-arginine complex by NMR spectroscopy. <i>Science</i> , 1992, 257, 76-80.	12.6	607
3	[22] absorbance melting curves of RNA. <i>Methods in Enzymology</i> , 1989, 180, 304-325.	1.0	591
4	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
5	Ligand-specific regulation of the extracellular surface of a G-protein-coupled receptor. <i>Nature</i> , 2010, 463, 108-112.	27.8	432
6	tRNA selection and kinetic proofreading in translation. <i>Nature Structural and Molecular Biology</i> , 2004, 11, 1008-1014.	8.2	426
7	Real-time tRNA transit on single translating ribosomes at codon resolution. <i>Nature</i> , 2010, 464, 1012-1017.	27.8	329
8	Preparation of isotopically labeled ribonucleotides for multidimensional NMR spectroscopy of RNA. <i>Nucleic Acids Research</i> , 1992, 20, 4515-4523.	14.5	288
9	Paromomycin binding induces a local conformational change in the A-site of 16 s rRNA. <i>Journal of Molecular Biology</i> , 1998, 277, 333-345.	4.2	288
10	Structure of HCV IRES domain II determined by NMR. <i>Nature Structural and Molecular Biology</i> , 2003, 10, 1033-1038.	8.2	260
11	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
12	Binding of neomycin-class aminoglycoside antibiotics to the A-site of 16 s rRNA. <i>Journal of Molecular Biology</i> , 1998, 277, 347-362.	4.2	241
13	The Pathway of HCV IRES-Mediated Translation Initiation. <i>Cell</i> , 2004, 119, 369-380.	28.9	241
14	Cotranslational Protein Folding inside the Ribosome Exit Tunnel. <i>Cell Reports</i> , 2015, 12, 1533-1540.	6.4	234
15	Recognition of the Codon-Anticodon Helix by Ribosomal RNA. <i>Science</i> , 1999, 285, 1722-1725.	12.6	221
16	tRNA Structure and Aminoacylation Efficiency. <i>Progress in Molecular Biology and Translational Science</i> , 1993, 45, 129-206.	1.9	218
17	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
18	Structures of two RNA domains essential for hepatitis C virus internal ribosome entry site function. <i>Nature Structural Biology</i> , 2000, 7, 1105-1110.	9.7	185

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19	Dynamic pathways of ± 1 translational frameshifting. <i>Nature</i> , 2014, 512, 328-332.	27.8	147
20	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
21	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
22	RNA pseudoknots. <i>Journal of Molecular Biology</i> , 1990, 214, 455-470.	4.2	141
23	Conformation of an RNA pseudoknot. <i>Journal of Molecular Biology</i> , 1990, 214, 437-453.	4.2	134
24	Structural origins of aminoglycoside specificity for prokaryotic ribosomes. <i>Journal of Molecular Biology</i> , 2001, 306, 1037-1058.	4.2	132
25	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
26	Translation at the Single-Molecule Level. <i>Annual Review of Biochemistry</i> , 2008, 77, 177-203.	11.1	117
27	Coordinated conformational and compositional dynamics drive ribosome translocation. <i>Nature Structural and Molecular Biology</i> , 2013, 20, 718-727.	8.2	117
28	Large-scale preparation and purification of polyacrylamide-free RNA oligonucleotides. <i>Rna</i> , 2004, 10, 889-893.	3.5	115
29	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
30	Quantitative polysome analysis identifies limitations in bacterial cell-free protein synthesis. <i>Biotechnology and Bioengineering</i> , 2005, 91, 425-435.	3.3	113
31	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
32	Site-specific labeling of the ribosome for single-molecule spectroscopy. <i>Nucleic Acids Research</i> , 2005, 33, 182-189.	14.5	111
33	A short translational ramp determines the efficiency of protein synthesis. <i>Nature Communications</i> , 2019, 10, 5774.	12.8	109
34	Peptide bond formation destabilizes Shine-Dalgarno interaction on the ribosome. <i>Nature</i> , 2007, 446, 454-457.	27.8	107
35	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
36	A pseudoknotted RNA oligonucleotide. <i>Nature</i> , 1988, 331, 283-286.	27.8	106

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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	Effect of mutations in the A site of 16 S rRNA on aminoglycoside antibiotic-ribosome interaction. <i>Journal of Molecular Biology</i> , 1999, 286, 33-43.	4.2	99
39	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
40	Following the intersubunit conformation of the ribosome during translation in real time. <i>Nature Structural and Molecular Biology</i> , 2010, 17, 793-800.	8.2	97
41	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
42	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
43	Fluctuations of Transfer RNAs between Classical and Hybrid States. <i>Biophysical Journal</i> , 2007, 93, 3575-3582.	0.5	91
44	NMR Study of 100 kDa HCV IRES RNA Using Segmental Isotope Labeling. <i>Journal of the American Chemical Society</i> , 2002, 124, 9338-9339.	13.7	90
45	Rapid purification of RNAs using fast performance liquid chromatography (FPLC). <i>Rna</i> , 2006, 13, 289-294.	3.5	90
46	Purification and characterization of transcribed RNAs using gel filtration chromatography. <i>Nature Protocols</i> , 2007, 2, 3270-3277.	12.0	88
47	Ribosomal proteins mediate the hepatitis C virus IRES???HeLa 40S interaction. <i>Rna</i> , 2002, 8, 913-923.	3.5	88
48	GTP Hydrolysis by IF2 Guides Progression of the Ribosome into Elongation. <i>Molecular Cell</i> , 2009, 35, 37-47.	9.7	87
49	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
50	Single Ribosome Dynamics and the Mechanism of Translation. <i>Annual Review of Biophysics</i> , 2010, 39, 491-513.	10.0	84
51	Heterogeneous pathways and timing of factor departure during translation initiation. <i>Nature</i> , 2012, 487, 390-393.	27.8	83
52	Dynamics of IRES-mediated translation. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2017, 372, 20160177.	4.0	80
53	The Impact of Aminoglycosides on the Dynamics of Translation Elongation. <i>Cell Reports</i> , 2013, 3, 497-508.	6.4	72
54	Interaction of translation initiation factor IF1 with the E. coli ribosomal A site 1 1Edited by D. E. Draper. <i>Journal of Molecular Biology</i> , 2000, 299, 1-15.	4.2	63

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55	HIV-1 A-rich RNA loop mimics the tRNA anticodon structure. <i>Nature Structural Biology</i> , 1998, 5, 1033-1036.	9.7	62
56	How Messenger RNA and Nascent Chain Sequences Regulate Translation Elongation. <i>Annual Review of Biochemistry</i> , 2018, 87, 421-449.	11.1	62
57	Transient Protein-RNA Interactions Guide Nascent Ribosomal RNA Folding. <i>Cell</i> , 2019, 179, 1357-1369.e16.	28.9	61
58	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
59	eIF5B gates the transition from translation initiation to elongation. <i>Nature</i> , 2019, 573, 605-608.	27.8	60
60	Multiple Parallel Pathways of Translation Initiation on the CrPV IRES. <i>Molecular Cell</i> , 2016, 62, 92-103.	9.7	59
61	Unraveling the dynamics of ribosome translocation. <i>Current Opinion in Structural Biology</i> , 2012, 22, 804-814.	5.7	58
62	RNA folding: Pseudoknots, loops and bulges. <i>BioEssays</i> , 1989, 11, 100-106.	2.5	57
63	Aminoglycoside Resistance with Homogeneous and Heterogeneous Populations of Antibiotic-Resistant Ribosomes. <i>Antimicrobial Agents and Chemotherapy</i> , 2001, 45, 2414-2419.	3.2	57
64	Molecular Framework for the Activation of RNA-dependent Protein Kinase. <i>Journal of Biological Chemistry</i> , 2007, 282, 11474-11486.	3.4	56
65	Translational insensitivity to potent activation of PKR by HCV IRES RNA. <i>Antiviral Research</i> , 2009, 83, 228-237.	4.1	56
66	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
67	Structure Determination of Large Biological RNAs. <i>Methods in Enzymology</i> , 2005, 394, 399-416.	1.0	53
68	Precursor Directed Biosynthesis of an Orthogonally Functional Erythromycin Analogue: Selectivity in the Ribosome Macrolide Binding Pocket. <i>Journal of the American Chemical Society</i> , 2012, 134, 12259-12265.	13.7	53
69	Structure of a eukaryotic decoding region A-site RNA. <i>Journal of Molecular Biology</i> , 2001, 306, 1023-1035.	4.2	52
70	The energy landscape of $\hat{\sim}1$ ribosomal frameshifting. <i>Science Advances</i> , 2020, 6, eaax6969.	10.3	51
71	Specific Recognition of HIV TAR RNA by the dsRNA Binding Domains (dsRBD1 and dsRBD2) of PKR. <i>Journal of Molecular Biology</i> , 2006, 358, 430-442.	4.2	50
72	Thiostrepton inhibition of tRNA delivery to the ribosome. <i>Rna</i> , 2007, 13, 2091-2097.	3.5	50

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73	[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
74	Involvement of protein IF2 N domain in ribosomal subunit joining revealed from architecture and function of the full-length initiation factor. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 15656-15661.	7.1	48
75	The Dynamics of SecM-Induced Translational Stalling. <i>Cell Reports</i> , 2014, 7, 1521-1533.	6.4	48
76	Viral dsRNA Inhibitors Prevent Self-association and Autophosphorylation of PKR. <i>Journal of Molecular Biology</i> , 2007, 372, 103-113.	4.2	46
77	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
78	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
79	De novo computational RNA modeling into cryo-EM maps of large ribonucleoprotein complexes. <i>Nature Methods</i> , 2018, 15, 947-954.	19.0	45
80	Architecture of an HIV-1 reverse transcriptase initiation complex. <i>Nature</i> , 2018, 557, 118-122.	27.8	44
81	Real-time assembly of ribonucleoprotein complexes on nascent RNA transcripts. <i>Nature Communications</i> , 2018, 9, 5087.	12.8	43
82	Dynamics of the context-specific translation arrest by chloramphenicol and linezolid. <i>Nature Chemical Biology</i> , 2020, 16, 310-317.	8.0	43
83	Approaching translation at atomic resolution. <i>Nature Structural Biology</i> , 2000, 7, 855-861.	9.7	42
84	Coupling of mRNA Structure Rearrangement to Ribosome Movement during Bypassing of Non-coding Regions. <i>Cell</i> , 2015, 163, 1267-1280.	28.9	42
85	Single-molecule imaging of full protein synthesis by immobilized ribosomes. <i>Nucleic Acids Research</i> , 2008, 36, e70-e70.	14.5	41
86	Real-time observation of signal recognition particle binding to actively translating ribosomes. <i>ELife</i> , 2014, 3, .	6.0	41
87	Nonfluorescent Quenchers To Correlate Single-Molecule Conformational and Compositional Dynamics. <i>Journal of the American Chemical Society</i> , 2012, 134, 5734-5737.	13.7	39
88	Signal Recognition Particle-ribosome Binding Is Sensitive to Nascent Chain Length. <i>Journal of Biological Chemistry</i> , 2014, 289, 19294-19305.	3.4	39
89	Post-termination Ribosome Intermediate Acts as the Gateway to Ribosome Recycling. <i>Cell Reports</i> , 2017, 20, 161-172.	6.4	39
90	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

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91	RACK1 on and off the ribosome. <i>Rna</i> , 2019, 25, 881-895.	3.5	38
92	Dynamic Recognition of the mRNA Cap by <i>Saccharomyces cerevisiae</i> eIF4E. <i>Structure</i> , 2013, 21, 2197-2207.	3.3	36
93	Sequence-Dependent Elongation Dynamics on Macrolide-Bound Ribosomes. <i>Cell Reports</i> , 2014, 7, 1534-1546.	6.4	36
94	Structure of a conserved RNA component of the peptidyl transferase centre. <i>Nature Structural Biology</i> , 1997, 4, 775-778.	9.7	35
95	Mechanisms that ensure speed and fidelity in eukaryotic translation termination. <i>Science</i> , 2021, 373, 876-882.	12.6	33
96	RNA pseudoknots. <i>Accounts of Chemical Research</i> , 1991, 24, 152-158.	15.6	31
97	Single-Molecule Analysis of Translational Dynamics. <i>Cold Spring Harbor Perspectives in Biology</i> , 2012, 4, a011551-a011551.	5.5	31
98	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
99	Single-Molecule Fluorescence Applied to Translation. <i>Cold Spring Harbor Perspectives in Biology</i> , 2019, 11, a032714.	5.5	26
100	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
101	eIF5B and eIF1A reorient initiator tRNA to allow ribosomal subunit joining. <i>Nature</i> , 2022, 607, 185-190.	27.8	25
102	[16] Biochemical and nuclear magnetic resonance studies of aminoglycoside-RNA complexes. <i>Methods in Enzymology</i> , 2000, 317, 240-261.	1.0	24
103	Secondary Structure of the HIV Reverse Transcription Initiation Complex by NMR. <i>Journal of Molecular Biology</i> , 2011, 410, 863-874.	4.2	23
104	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
105	Site-specific labeling of <i>Saccharomyces cerevisiae</i> ribosomes for single-molecule manipulations. <i>Nucleic Acids Research</i> , 2010, 38, e143-e143.	14.5	22
106	Relating Structure and Dynamics in RNA Biology. <i>Cold Spring Harbor Perspectives in Biology</i> , 2019, 11, a032474.	5.5	21
107	A simple real-time assay for in vitro translation. <i>Rna</i> , 2015, 21, 296-305.	3.5	20
108	Application of Residual Dipolar Coupling Measurements To Identify Conformational Changes in RNA Induced by Antibiotics. <i>Journal of the American Chemical Society</i> , 2000, 122, 7853-7854.	13.7	16

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109	Biophysical and Biochemical Investigations of dsRNA-Activated Kinase PKR. <i>Methods in Enzymology</i> , 2007, 430, 373-396.	1.0	15
110	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
111	The molecular choreography of protein synthesis: translational control, regulation, and pathways. <i>Quarterly Reviews of Biophysics</i> , 2016, 49, e11.	5.7	14
112	Heterogeneous structures formed by conserved RNA sequences within the HIV reverse transcription initiation site. <i>Rna</i> , 2016, 22, 1689-1698.	3.5	13
113	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
114	Probing the conformation of human tRNA ³ Lys in solution by NMR. <i>FEBS Letters</i> , 2007, 581, 5307-5314.	2.8	12
115	Fluorescently-tagged human eIF3 for single-molecule spectroscopy. <i>Nucleic Acids Research</i> , 2018, 46, e8-e8.	14.5	12
116	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
117	The ribosome revealed. , 1999, 6, 999-1003.		10
118	Initiation factor 2, tRNA, and 50S subunits cooperatively stabilize mRNAs on the ribosome during initiation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 4881-4885.	7.1	10
119	Aminoglycoside Antibiotics and Decoding. , 2014, , 419-429.		10
120	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
121	The delicate dance of translation and folding. <i>Science</i> , 2015, 348, 399-400.	12.6	8
122	Resolving the Elegant Architecture of the Ribosome. <i>Molecular Cell</i> , 2009, 36, 720-723.	9.7	6
123	Expanding single-molecule fluorescence spectroscopy to capture complexity in biology. <i>Current Opinion in Structural Biology</i> , 2019, 58, 233-240.	5.7	6
124	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
125	PKR: A NMR perspective. <i>Progress in Nuclear Magnetic Resonance Spectroscopy</i> , 2007, 51, 199-215.	7.5	4
126	A memory of eS25 loss drives resistance phenotypes. <i>Nucleic Acids Research</i> , 2020, 48, 7279-7297.	14.5	4

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127	mRNA processing: the 3'-end justifies the means. , 2000, 7, 263-264.		3
128	The dance of domains. Nature, 2007, 450, 1171-1172.	27.8	3
129	RNA dances to center stage. Rna, 2015, 21, 712-713.	3.5	2
130	Ribosomal ties that bind. Nature, 2015, 524, 45-46.	27.8	1
131	Ribosomal Protein Dynamics on the Human Ribosome. Biophysical Journal, 2018, 114, 595a.	0.5	1
132	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
133	2P-126 Real time imaging of tRNA dynamics with a zero-mode waveguides during translation(The 46th) Tj ETQq1 1 0,784314 rgBT /Overlock 10	0.1	0
134	Realtime Observation of tRNA Dynamics at High Concentrations in Single Molecule Translation. Biophysical Journal, 2010, 98, 260a-261a.	0.5	0
135	1SBP-03 Dynamics of translation elongation in real time(1SBP Advanced Single Molecule Sequencing) Tj ETQq1 1 0.784314 rgBT /Overlock 10 53, S87.	0.1	0
136	Single-Molecule Profiling of Ribosome Translational Phenomena. Biophysical Journal, 2014, 106, 239a.	0.5	0
137	Dynamics of Translation. FASEB Journal, 2006, 20, A889.	0.5	0
138	Direct tracking of eukaryotic translation termination dynamics. Biophysical Journal, 2022, 121, 202a.	0.5	0