Anna M Pyle

List of Publications by Year
in descending order

94 papers	6,347 citations	76031 42 h-index	84171 75 g-index
101 all docs	101 docs citations	101 times ranked	7515 citing authors

#	ARTICLE	IF	CITATIONS
1	A stem-loop RNA RIG-I agonist protects against acute and chronic SARS-CoV-2 infection in mice. Journal of Experimental Medicine, 2022, 219, .	4.2	46
2	<i>CSSR</i>: assignment of secondary structure to coarse-grained RNA tertiary structures. Acta Crystallographica Section D: Structural Biology, 2022, 78, 466-471.	1.1	7
3	The <i>In Vivo</i> and <i>In Vitro</i> Architecture of the Hepatitis C Virus RNA Genome Uncovers Functional RNA Secondary and Tertiary Structures. Journal of Virology, 2022, 96, e0194621.	1.5	7
4	De novo emergence of a remdesivir resistance mutation during treatment of persistent SARS-CoV-2 infection in an immunocompromised patient: a case report. Nature Communications, 2022, 13, 1547.	5.8	159
5	AMIGOS III: pseudo-torsion angle visualization and motif-based structure comparison of nucleic acids. Bioinformatics, 2022, 38, 2937-2939.	1.8	1
6	A molecular beacon assay for monitoring RNA splicing. Nucleic Acids Research, 2022, 50, e74-e74.	6.5	1
7	Direct tracking of reverse-transcriptase speed and template sensitivity: implications for sequencing and analysis of long RNA molecules. Nucleic Acids Research, 2022, 50, 6980-6989.	6.5	8
8	The Global and Local Distribution of RNA Structure throughout the SARS-CoV-2 Genome. Journal of Virology, 2021, 95, .	1.5	67
9	Comprehensive inÂvivo secondary structure of the SARS-CoV-2 genome reveals novel regulatory motifs and mechanisms. Molecular Cell, 2021, 81, 584-598.e5.	4.5	198
10	Insights into the structure and RNA-binding specificity of <i>Caenorhabditis elegans</i> Dicer-related helicase 3 (DRH-3). Nucleic Acids Research, 2021, 49, 9978-9991.	6.5	4
11	The molecular mechanism of RIGâ€ł activation and signaling. Immunological Reviews, 2021, 304, 154-168.	2.8	93
12	Evolving A RIG-I Antagonist: A Modified DNA Aptamer Mimics Viral RNA. Journal of Molecular Biology, 2021, 433, 167227.	2.0	10
13	Discovery of highly reactive self-splicing group II introns within the mitochondrial genomes of human pathogenic fungi. Nucleic Acids Research, 2021, 49, 12422-12432.	6.5	6
14	Structural Optimization of Polymeric Carriers to Enhance the Immunostimulatory Activity of Molecularly Defined RIG-I Agonists. ACS Central Science, 2020, 6, 2008-2022.	5.3	20
15	Small-Molecule Antagonists of the RIG-I Innate Immune Receptor. ACS Chemical Biology, 2020, 15, 311-317.	1.6	8
16	Sequencing and Structure Probing of Long RNAs Using MarathonRT: A Next-Generation Reverse Transcriptase. Journal of Molecular Biology, 2020, 432, 3338-3352.	2.0	46
17	Discovery of <i>N</i>-Substituted 3-Amino-4-(3-boronopropyl)pyrrolidine-3-carboxylic Acids as Highly Potent Third-Generation Inhibitors of Human Arginase I and II. Journal of Medicinal Chemistry, 2019, 62, 8164-8177.	2.9	21
18	RNA binding activates RIG-I by releasing an autorepressed signaling domain. Science Advances, 2019, 5, eaax3641.	4.7	13

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19	Intratumoral delivery of RIG-I agonist SLR14 induces robust antitumor responses. Journal of Experimental Medicine, 2019, 216, 2854-2868.	4.2	49
20	Sensitive detection of structural features and rearrangements in long, structured RNA molecules. Methods in Enzymology, 2019, 623, 249-289.	0.4	6
21	Phylogenetic Analysis with Improved Parameters Reveals Conservation in lncRNA Structures. Journal of Molecular Biology, 2019, 431, 1592-1603.	2.0	46
22	RIG-I Selectively Discriminates against 5â€²-Monophosphate RNA. Cell Reports, 2019, 26, 2019-2027.e4.	2.9	43
23	RIG-I Recognition of RNA Targets: The Influence of Terminal Base Pair Sequence and Overhangs on Affinity and Signaling. Cell Reports, 2019, 29, 3807-3815.e3.	2.9	15
24	A minimal RNA ligand for potent RIG-I activation in living mice. Science Advances, 2018, 4, e1701854.	4.7	79
25	NS3 from Hepatitis C Virus Strain JFH-1 Is an Unusually Robust Helicase That Is Primed To Bind and Unwind Viral RNA. Journal of Virology, 2018, 92, .	1.5	12
26	An ultraprocessive, accurate reverse transcriptase encoded by a metazoan group II intron. Rna, 2018, 24, 183-195.	1.6	69
27	Small molecules that target group II introns are potent antifungal agents. Nature Chemical Biology, 2018, 14, 1073-1078.	3.9	61
28	Therapeutically Active RIG-I Agonist Induces Immunogenic Tumor Cell Killing in Breast Cancers. Cancer Research, 2018, 78, 6183-6195.	0.4	130
29	Regional Differences in Airway Epithelial Cells Reveal Tradeoff between Defense against Oxidative Stress and Defense against Rhinovirus. Cell Reports, 2018, 24, 3000-3007.e3.	2.9	46
30	microRNA-122 amplifies hepatitis C virus translation by shaping the structure of the internal ribosomal entry site. Nature Communications, 2018, 9, 2613.	5.8	90
31	Visualizing the secondary and tertiary architectural domains of lncRNA RepA. Nature Chemical Biology, 2017, 13, 282-289.	3.9	121
32	Functional RNA structures throughout the Hepatitis C Virus genome. Current Opinion in Virology, 2017, 24, 79-86.	2.6	29
33	Structural Insights into the Mechanism of Group II Intron Splicing. Trends in Biochemical Sciences, 2017, 42, 470-482.	3.7	50
34	The group II intron maturase: a reverse transcriptase and splicing factor go hand in hand. Current Opinion in Structural Biology, 2017, 47, 30-39.	2.6	19
35	Structural basis for IL-1Î± recognition by a modified DNA aptamer that specifically inhibits IL-1Î± signaling. Nature Communications, 2017, 8, 810.	5.8	49
36	The SMAD3 transcription factor binds complex RNA structures with high affinity. Nucleic Acids Research, 2017, 45, 11980-11988.	6.5	10

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37	Group II Intron Self-Splicing. Annual Review of Biophysics, 2016, 45, 183-205.	4.5	87
38	Crystal structures of a group II intron maturase reveal a missing link in spliceosome evolution. Nature Structural and Molecular Biology, 2016, 23, 558-565.	3.6	79
39	Selective RNA targeting and regulated signaling by RIG-I is controlled by coordination of RNA and ATP binding. Nucleic Acids Research, 2016, 45, gkw816.	6.5	15
40	Inverted repeatAluelements in the human lincRNA-p21 adopt a conserved secondary structure that regulates RNA function. Nucleic Acids Research, 2016, 44, gkw599.	6.5	64
41	Transcriptome analysis of human cumulus cells reveals hypoxia as the main determinant of follicular senescence. Molecular Human Reproduction, 2016, 22, 866-876.	1.3	37
42	Challenges in RNA Structural Modeling and Design. Journal of Molecular Biology, 2016, 428, 733-735.	2.0	17
43	The Coding Region of the HCV Genome Contains a Network of Regulatory RNA Structures. Molecular Cell, 2016, 62, 111-120.	4.5	101
44	Editorial overview: Nucleic acids and their protein complexes. Current Opinion in Structural Biology, 2016, 36, vii-viii.	2.6	1
45	Rediscovering RNA. Rna, 2015, 21, 714-715.	1.6	2
46	Temperature-dependent innate defense against the common cold virus limits viral replication at warm temperature in mouse airway cells. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 827-832.	3.3	199
47	Native Purification and Analysis of Long RNAs. Methods in Enzymology, 2015, 558, 3-37.	0.4	49
48	HOTAIR Forms an Intricate and Modular Secondary Structure. Molecular Cell, 2015, 58, 353-361.	4.5	299
49	Crystal structure of group II intron domain 1 reveals a template for RNA assembly. Nature Chemical Biology, 2015, 11, 967-972.	3.9	23
50	Establishing the role of ATP for the function of the RIG-I innate immune sensor. ELife, 2015, 4, .	2.8	52
51	The RIG-I ATPase core has evolved a functional requirement for allosteric stabilization by the Pincer domain. Nucleic Acids Research, 2014, 42, 11601-11611.	6.5	23
52	Dicer-related helicase 3 forms an obligate dimer for recognizing 22G-RNA. Nucleic Acids Research, 2014, 42, 3919-3930.	6.5	14
53	Visualizing the ai5Î³ group IIB intron. Nucleic Acids Research, 2014, 42, 1947-1958.	6.5	15
54	Parts, assembly and operation of the RIG-I family of motors. Current Opinion in Structural Biology, 2014, 25, 25-33.	2.6	43

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55	The Linker Region of NS3 Plays a Critical Role in the Replication and Infectivity of Hepatitis C Virus. Journal of Virology, 2014, 88, 10970-10974.	1.5	19
56	Looking at LncRNAs with the Ribozyme Toolkit. Molecular Cell, 2014, 56, 13-17.	4.5	13
57	An evolving arsenal: viral RNA detection by RIG-I-like receptors. Current Opinion in Microbiology, 2014, 20, 76-81.	2.3	38
58	Coordinating the Party: Assembly Factors and Ribogenesis. Molecular Cell, 2013, 52, 469-470.	4.5	0
59	Duplex RNA activated ATPases (DRAs). RNA Biology, 2013, 10, 111-120.	1.5	59
60	Defining the functional determinants for RNA surveillance by RIGâ€I. EMBO Reports, 2013, 14, 772-779.	2.0	97
61	ATPase coupling in the processive RNA helicase NS3 from hepatitis C virus. FASEB Journal, 2013, 27, 999.2.	0.2	0
62	Visualizing Group II Intron Catalysis through the Stages of Splicing. Cell, 2012, 151, 497-507.	13.5	155
63	The Thermodynamic Basis for Viral RNA Detection by the RIG-I Innate Immune Sensor. Journal of Biological Chemistry, 2012, 287, 42564-42573.	1.6	52
64	Visualizing the Determinants of Viral RNA Recognition by Innate Immune Sensor RIG-I. Structure, 2012, 20, 1983-1988.	1.6	73
65	Group II intron architecture and its implications for the development of eukaryotic splicing systems. FASEB Journal, 2012, 26, 217.3.	0.2	0
66	Structural Insights into RNA Recognition by RIG-I. Cell, 2011, 147, 409-422.	13.5	337
67	Mechanism of Mss116 ATPase Reveals Functional Diversity of DEAD-Box Proteins. Journal of Molecular Biology, 2011, 409, 399-414.	2.0	63
68	The ever-growing complexity of nucleic acids: from small DNA and RNA motifs to large molecular assemblies and machines. Current Opinion in Structural Biology, 2011, 21, 293-295.	2.6	2
69	RNA helicases and remodeling proteins. Current Opinion in Chemical Biology, 2011, 15, 636-642.	2.8	35
70	The Acidic Domain of Hepatitis C Virus NS4A Contributes to RNA Replication and Virus Particle Assembly. Journal of Virology, 2011, 85, 1193-1204.	1.5	43
71	Dual roles for the Mss116 cofactor during splicing of the ai5Î³ group II intron. Nucleic Acids Research, 2010, 38, 6602-6609.	6.5	30
72	Double-stranded RNA-dependent ATPase DRH-3. Journal of Biological Chemistry, 2010, 285, 25363-25371.	1.6	20

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73	The tertiary structure of group II introns: implications for biological function and evolution. Critical Reviews in Biochemistry and Molecular Biology, 2010, 45, 215-232.	2.3	108
74	Structural insights into RNA splicing. Current Opinion in Structural Biology, 2009, 19, 260-266.	2.6	60
75	How to Drive Your Helicase in a Straight Line. Cell, 2009, 139, 458-459.	13.5	4
76	Translocation and Unwinding Mechanisms of RNA and DNA Helicases. Annual Review of Biophysics, 2008, 37, 317-336.	4.5	444
77	The GANC Tetraloop: A Novel Motif in the Group IIC Intron Structure. Journal of Molecular Biology, 2008, 383, 475-481.	2.0	31
78	Evaluating and Learning from RNA Pseudotorsional Space: Quantitative Validation of a Reduced Representation for RNA Structure. Journal of Molecular Biology, 2007, 372, 942-957.	2.0	72
79	Folding of group II introns: a model system for large, multidomain RNAs?. Trends in Biochemical Sciences, 2007, 32, 138-145.	3.7	98
80	Robust Translocation Along a Molecular Monorail: the NS3 Helicase from Hepatitis C Virus Traverses Unusually Large Disruptions in its Track. Journal of Molecular Biology, 2006, 358, 974-982.	2.0	45
81	Prediction of functional tertiary interactions and intermolecular interfaces from primary sequence data. Journal of Experimental Zoology Part B: Molecular and Developmental Evolution, 2005, 304B, 50-63.	0.6	11
82	Capping by Branching: A New Ribozyme Makes Tiny Lariats. Science, 2005, 309, 1530-1531.	6.0	7
83	Choosing between DNA and RNA: the polymer specificity of RNA helicase NPH-II. Nucleic Acids Research, 2005, 33, 644-649.	6.5	25
84	The identification of novel RNA structural motifs using COMPADRES: an automated approach to structural discovery. Nucleic Acids Research, 2004, 32, 6650-6659.	6.5	65
85	A Group II Intron Inserted into a Bacterial Heat-Shock Operon Shows Autocatalytic Activity and Unusual Thermostability. Biochemistry, 2003, 42, 3409-3418.	1.2	42
86	An Alternative Route for the Folding of Large RNAs: Apparent Two-state Folding by a Group II Intron Ribozyme. Journal of Molecular Biology, 2003, 334, 639-652.	2.0	67
87	Domains 2 and 3 Interact to Form Critical Elements of the Group II Intron Active Site. Journal of Molecular Biology, 2003, 330, 197-209.	2.0	36
88	mda-5: An interferon-inducible putative RNA helicase with double-stranded RNA-dependent ATPase activity and melanoma growth-suppressive properties. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 637-642.	3.3	577
89	Active Disruption of an RNA-Protein Interaction by a DExH/D RNA Helicase. Science, 2001, 291, 121-125.	6.0	280
90	Analysis of putative RNase sensitivity and protease insensitivity of demethylation activity in extracts from rat myoblasts. Nucleic Acids Research, 1998, 26, 5573-5580.	6.5	37

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91	Stopped-Flow Fluorescence Spectroscopy of a Group II Intron Ribozyme Reveals that Domain 1 Is an Independent Folding Unit with a Requirement for Specific Mg2+Ions in the Tertiary Structureâ€. Biochemistry, 1997, 36, 4718-4730.	1.2	69
92	Two Competing Pathways for Self-splicing by Group II Introns: A Quantitative Analysis ofin VitroReaction Rates and Products. Journal of Molecular Biology, 1996, 256, 31-49.	2.0	121
93	Building a Kinetic Framework for Group II Intron Ribozyme Activity: Quantitation of Interdomain Binding and Reaction Rate. Biochemistry, 1994, 33, 2716-2725.	1.2	109
94	Direct measurement of oligonucleotide substrate binding to wild-type and mutant ribozymes from Tetrahymena.. Proceedings of the National Academy of Sciences of the United States of America, 1990, 87, 8187-8191.	3.3	138