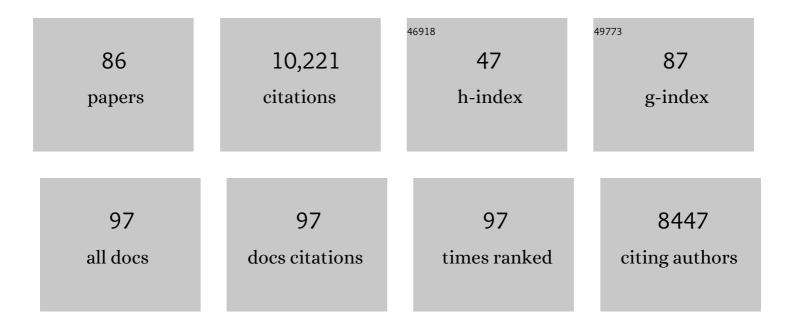
## Stephen Anthony Cusack

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	A second class of synthetase structure revealed by X-ray analysis of Escherichia coli seryl-tRNA synthetase at 2.5 A Nature, 1990, 347, 249-255.	13.7	667
2	The cap-snatching endonuclease of influenza virus polymerase resides in the PA subunit. Nature, 2009, 458, 914-918.	13.7	630
3	An Antifungal Agent Inhibits an Aminoacyl-tRNA Synthetase by Trapping tRNA in the Editing Site. Science, 2007, 316, 1759-1761.	6.0	556
4	Structural Basis for the Activation of Innate Immune Pattern-Recognition Receptor RIG-I by Viral RNA. Cell, 2011, 147, 423-435.	13.5	543
5	The structural basis for cap binding by influenza virus polymerase subunit PB2. Nature Structural and Molecular Biology, 2008, 15, 500-506.	3.6	436
6	Structure of influenza A polymerase bound to the viral RNA promoter. Nature, 2014, 516, 355-360.	13.7	404
7	Structural insight into cap-snatching and RNA synthesis by influenza polymerase. Nature, 2014, 516, 361-366.	13.7	376
8	A triple β-spiral in the adenovirus fibreÂshaft reveals a new structural motif for a fibrous protein. Nature, 1999, 401, 935-938.	13.7	310
9	The structure of the Escherichia coli EF-Tu· EF-Ts complex at 2.5 à resolution. Nature, 1996, 379, 511-518.	13.7	307
10	Characterization of influenza virus variants induced by treatment with the endonuclease inhibitor baloxavir marboxil. Scientific Reports, 2018, 8, 9633.	1.6	306
11	Structure and nuclear import function of the C-terminal domain of influenza virus polymerase PB2 subunit. Nature Structural and Molecular Biology, 2007, 14, 229-233.	3.6	275
12	Sequence, structural and evolutionary relationships between class 2 aminoacyl-tRNA synthetases. Nucleic Acids Research, 1991, 19, 3489-3498.	6.5	270
13	The 2 Ã crystal structure of leucyl-tRNA synthetase and its complex with a leucyl-adenylate analogue. EMBO Journal, 2000, 19, 2351-2361.	3.5	244
14	Bunyaviridae RNA Polymerases (L-Protein) Have an N-Terminal, Influenza-Like Endonuclease Domain, Essential for Viral Cap-Dependent Transcription. PLoS Pathogens, 2010, 6, e1001101.	2.1	215
15	RNA Clamping by Vasa Assembles a piRNA Amplifier Complex on Transposon Transcripts. Cell, 2014, 157, 1698-1711.	13.5	208
16	Eleven down and nine to go. Nature Structural Biology, 1995, 2, 824-831.	9.7	192
17	Large-scale induced fit recognition of an m7GpppG cap analogue by the human nuclear cap-binding complex. EMBO Journal, 2002, 21, 5548-5557.	3.5	171
18	Host Determinant Residue Lysine 627 Lies on the Surface of a Discrete, Folded Domain of Influenza Virus Polymerase PB2 Subunit. PLoS Pathogens, 2008, 4, e1000136.	2.1	165

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19	Structural Insights into Bunyavirus Replication and Its Regulation by the vRNA Promoter. Cell, 2015, 161, 1267-1279.	13.5	164
20	Capped RNA primer binding to influenza polymerase and implications for the mechanism of cap-binding inhibitors. Nucleic Acids Research, 2018, 46, 956-971.	6.5	154
21	Structural Analysis of Specific Metal Chelating Inhibitor Binding to the Endonuclease Domain of Influenza pH1N1 (2009) Polymerase. PLoS Pathogens, 2012, 8, e1002831.	2.1	149
22	Crystal structure of the RNA-dependent RNA polymerase from influenza C virus. Nature, 2015, 527, 114-117.	13.7	145
23	CBC–ARS2 stimulates 3′-end maturation of multiple RNA families and favors cap-proximal processing. Nature Structural and Molecular Biology, 2013, 20, 1358-1366.	3.6	143
24	Structural insights into RNA synthesis by the influenza virus transcription-replication machine. Virus Research, 2017, 234, 103-117.	1.1	143
25	Structural dynamics of the aminoacylation and proofreading functional cycle of bacterial leucyl-tRNA synthetase. Nature Structural and Molecular Biology, 2012, 19, 677-684.	3.6	131
26	Crystal Structure of the Human Nuclear Cap Binding Complex. Molecular Cell, 2001, 8, 383-396.	4.5	126
27	Molecular mechanism of influenza A NS1-mediated TRIM25 recognition and inhibition. Nature Communications, 2018, 9, 1820.	5.8	124
28	Influenza Polymerase Can Adopt an Alternative Configuration Involving a Radical Repacking of PB2 Domains. Molecular Cell, 2016, 61, 125-137.	4.5	123
29	Structural Analysis of dsRNA Binding to Anti-viral Pattern Recognition Receptors LGP2 and MDA5. Molecular Cell, 2016, 62, 586-602.	4.5	113
30	Structural basis of an essential interaction between influenza polymerase and Pol II CTD. Nature, 2017, 541, 117-121.	13.7	98
31	Towards an atomic resolution understanding of the influenza virus replication machinery. Current Opinion in Structural Biology, 2010, 20, 104-113.	2.6	95
32	A Structure-Based Model for the Complete Transcription Cycle of Influenza Polymerase. Cell, 2020, 181, 877-893.e21.	13.5	90
33	Crystal Structures of the Human and Fungal Cytosolic Leucyl-tRNA Synthetase Editing Domains: A Structural Basis for the Rational Design of Antifungal Benzoxaboroles. Journal of Molecular Biology, 2009, 390, 196-207.	2.0	89
34	Discovery of Novel Oral Protein Synthesis Inhibitors of Mycobacterium tuberculosis That Target Leucyl-tRNA Synthetase. Antimicrobial Agents and Chemotherapy, 2016, 60, 6271-6280.	1.4	88
35	Comparative Structural and Functional Analysis of Bunyavirus and Arenavirus Cap-Snatching Endonucleases. PLoS Pathogens, 2016, 12, e1005636.	2.1	84
36	Mutational and Metal Binding Analysis of the Endonuclease Domain of the Influenza Virus Polymerase PA Subunit. Journal of Virology, 2010, 84, 9096-9104.	1.5	81

STEPHEN ANTHONY CUSACK

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37	Structural snapshots of actively transcribing influenza polymerase. Nature Structural and Molecular Biology, 2019, 26, 460-470.	3.6	78
38	The Cap-Snatching Mechanism of Bunyaviruses. Trends in Microbiology, 2020, 28, 293-303.	3.5	74
39	Solution Structure of NOD1 CARD and Mutational Analysis of its Interaction with the CARD of Downstream Kinase RICK. Journal of Molecular Biology, 2007, 365, 160-174.	2.0	69
40	New 7-Methylguanine Derivatives Targeting the Influenza Polymerase PB2 Cap-Binding Domain. Journal of Medicinal Chemistry, 2013, 56, 8915-8930.	2.9	64
41	Towards a structural understanding of RNA synthesis by negative strand RNA viral polymerases. Current Opinion in Structural Biology, 2016, 36, 75-84.	2.6	63
42	Targeting <i>Toxoplasma gondii</i> <scp>CPSF</scp> 3 as a new approach to control toxoplasmosis. EMBO Molecular Medicine, 2017, 9, 385-394.	3.3	61
43	Specificity of recognition of mRNA 5' cap by human nuclear cap-binding complex. Rna, 2005, 11, 1355-1363.	1.6	59
44	The physiological target for Leu <scp>RS</scp> translational quality control is norvaline. EMBO Journal, 2014, 33, 1639-1653.	3.5	58
45	Antimalarial Benzoxaboroles Target Plasmodium falciparum Leucyl-tRNA Synthetase. Antimicrobial Agents and Chemotherapy, 2016, 60, 4886-4895.	1.4	58
46	Inelastic neutron scattering analysis of hexokinase dynamics and its modification on binding of glucose. Nature, 1982, 300, 84-86.	13.7	56
47	Cryptosporidium and Toxoplasma Parasites Are Inhibited by a Benzoxaborole Targeting Leucyl-tRNA Synthetase. Antimicrobial Agents and Chemotherapy, 2016, 60, 5817-5827.	1.4	55
48	RIP2 filament formation is required for NOD2 dependent NF-κB signalling. Nature Communications, 2018, 9, 4043.	5.8	55
49	Structural analysis of human ARS2 asÂa platform for co-transcriptional RNA sorting. Nature Communications, 2018, 9, 1701.	5.8	53
50	Anin vitrofluorescence based study of initiation of RNA synthesis by influenza B polymerase. Nucleic Acids Research, 2017, 45, gkx043.	6.5	49
51	Structure and Function of Influenza Polymerase. Cold Spring Harbor Perspectives in Medicine, 2021, 11, a038372.	2.9	48
52	Kinetic discrimination of self/non-self RNA by the ATPase activity of RIG-I and MDA5. BMC Biology, 2015, 13, 54.	1.7	47
53	Escherichia coliSecA shape and dimensions. FEBS Letters, 1998, 436, 277-282.	1.3	46
54	Structural and functional characterization of the severe fever with thrombocytopenia syndrome virus L protein. Nucleic Acids Research, 2020, 48, 5749-5765.	6.5	44

STEPHEN ANTHONY CUSACK

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55	Influenza A virus progeny vRNP trafficking in live infected cells studied with the virus-encoded fluorescently tagged PB2 protein. Vaccine, 2012, 30, 7411-7417.	1.7	43
56	Molecular basis of host-adaptation interactions between influenza virus polymerase PB2 subunit and ANP32A. Nature Communications, 2020, 11, 3656.	5.8	43
57	Crystal Structure of Vaccinia Virus mRNA Capping Enzyme Provides Insights into the Mechanism and Evolution of the Capping Apparatus. Structure, 2014, 22, 452-465.	1.6	41
58	Variation of longitudinal acoustic velocity at gigahertz frequencies with water content in rat-tail tendon fibers. Biopolymers, 1984, 23, 337-351.	1.2	39
59	Crystallization of the seryl-tRNA synthetase: tRNAsercomplex ofEscherichia coli. FEBS Letters, 1993, 324, 167-170.	1.3	36
60	Pre-initiation and elongation structures of full-length La Crosse virus polymerase reveal functionally important conformational changes. Nature Communications, 2020, 11, 3590.	5.8	36
61	Segmented negative strand RNA virus nucleoprotein structure. Current Opinion in Virology, 2014, 5, 7-15.	2.6	35
62	Structures of the inactive and active states of RIP2 kinase inform on the mechanism of activation. PLoS ONE, 2017, 12, e0177161.	1.1	35
63	Direct Measurement of Hydration-Related Dynamic Changes in Lysozyme using Inelastic Neutron Scattering Spectroscopy. Journal of Biomolecular Structure and Dynamics, 1987, 4, 583-588.	2.0	34
64	Systems To Establish Bunyavirus Genome Replication in the Absence of Transcription. Journal of Virology, 2013, 87, 8205-8212.	1.5	32
65	Structural insights into reptarenavirus cap-snatching machinery. PLoS Pathogens, 2017, 13, e1006400.	2.1	32
66	Hierarchical assembly of the Alu domain of the mammalian signal recognition particle. Rna, 2001, 7, 731-740.	1.6	31
67	Structural basis for mutually exclusive co-transcriptional nuclear cap-binding complexes with either NELF-E or ARS2. Nature Communications, 2017, 8, 1302.	5.8	31
68	Atomic Structure and Biochemical Characterization of an RNA Endonuclease in the N Terminus of Andes Virus L Protein. PLoS Pathogens, 2016, 12, e1005635.	2.1	31
69	NCBP3 positively impacts mRNA biogenesis. Nucleic Acids Research, 2020, 48, 10413-10427.	6.5	27
70	Conformational changes in Lassa virus L protein associated with promoter binding and RNA synthesis activity. Nature Communications, 2021, 12, 7018.	5.8	26
71	Structural snapshots of La Crosse virus polymerase reveal the mechanisms underlying Peribunyaviridae replication and transcription. Nature Communications, 2022, 13, 902.	5.8	23
72	Analysis of the Resistance Mechanism of a Benzoxaborole Inhibitor Reveals Insight into the Leucyl-tRNA Synthetase Editing Mechanism. ACS Chemical Biology, 2015, 10, 2277-2285.	1.6	22

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73	Kinetic Origin of Substrate Specificity in Post-Transfer Editing by Leucyl-tRNA Synthetase. Journal of Molecular Biology, 2018, 430, 1-16.	2.0	19
74	Influenza Virus RNA-Dependent RNA Polymerase and the Host Transcriptional Apparatus. Annual Review of Biochemistry, 2021, 90, 321-348.	5.0	19
75	Structure and RNA recognition by the snRNA and snoRNA transport factor PHAX. Rna, 2010, 16, 1205-1216.	1.6	18
76	Comparative Structural and Functional Analysis of Orthomyxovirus Polymerase Cap-Snatching Domains. PLoS ONE, 2014, 9, e84973.	1.1	18
77	Structural characterization of antibiotic self-immunity tRNA synthetase in plant tumour biocontrol agent. Nature Communications, 2016, 7, 12928.	5.8	15
78	Molecular basis of the multifaceted functions of human leucyl-tRNA synthetase in protein synthesis and beyond. Nucleic Acids Research, 2020, 48, 4946-4959.	6.5	11
79	Type B and type A influenza polymerases have evolved distinct binding interfaces to recruit the RNA polymerase II CTD. PLoS Pathogens, 2022, 18, e1010328.	2.1	11
80	RIG-I Self-Oligomerization Is Either Dispensable or Very Transient for Signal Transduction. PLoS ONE, 2014, 9, e108770.	1.1	10
81	Time-Resolved Visualisation of Nearly-Native Influenza A Virus Progeny Ribonucleoproteins and Their Individual Components in Live Infected Cells. PLoS ONE, 2016, 11, e0149986.	1.1	10
82	An RNA Hybridization Assay for Screening Influenza A Virus Polymerase Inhibitors Using the Entire Ribonucleoprotein Complex. Assay and Drug Development Technologies, 2015, 13, 488-506.	0.6	9
83	Crystal structure of a signal recognition particleAludomain in the elongation arrest conformation. Rna, 2014, 20, 1955-1962.	1.6	8
84	Errors in the deposited SFTSV L protein structure. Nature Microbiology, 2021, 6, 549-550.	5.9	7
85	Aminoacetylation Reaction Catalyzed by Leucyl-tRNA Synthetase Operates via a Self-Assisted Mechanism Using a Conserved Residue and the Aminoacyl Substrate. Journal of Physical Chemistry B, 2016, 120, 4388-4398.	1.2	6
86	Editorial overview: Protein–nucleic acid interactions: An expanding universe. Current Opinion in Structural Biology, 2017, 47, iv-v.	2.6	1