Stephen Anthony Cusack

List of Publications by Year
in descending order

86	10,221	46918 47	49773 87
papers	citations	h-index	g-index

97	97	97	8447
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Structural snapshots of La Crosse virus polymerase reveal the mechanisms underlying Peribunyaviridae replication and transcription. Nature Communications, 2022, 13, 902.	5.8	23
2	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
3	Structure and Function of Influenza Polymerase. Cold Spring Harbor Perspectives in Medicine, 2021, 11, a038372.	2.9	48
4	Errors in the deposited SFTSV L protein structure. Nature Microbiology, 2021, 6, 549-550.	5.9	7
5	Influenza Virus RNA-Dependent RNA Polymerase and the Host Transcriptional Apparatus. Annual Review of Biochemistry, 2021, 90, 321-348.	5.0	19
6	Conformational changes in Lassa virus L protein associated with promoter binding and RNA synthesis activity. Nature Communications, 2021, 12, 7018.	5.8	26
7	Molecular basis of host-adaptation interactions between influenza virus polymerase PB2 subunit and ANP32A. Nature Communications, 2020, 11, 3656.	5.8	43
8	NCBP3 positively impacts mRNA biogenesis. Nucleic Acids Research, 2020, 48, 10413-10427.	6.5	27
9	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
10	The Cap-Snatching Mechanism of Bunyaviruses. Trends in Microbiology, 2020, 28, 293-303.	3.5	74
11	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
12	A Structure-Based Model for the Complete Transcription Cycle of Influenza Polymerase. Cell, 2020, 181, 877-893.e21.	13.5	90
13	Structural and functional characterization of the severe fever with thrombocytopenia syndrome virus L protein. Nucleic Acids Research, 2020, 48, 5749-5765.	6.5	44
14	Structural snapshots of actively transcribing influenza polymerase. Nature Structural and Molecular Biology, 2019, 26, 460-470.	3.6	78
15	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
16	Structural analysis of human ARS2 asÂa platform for co-transcriptional RNA sorting. Nature Communications, 2018, 9, 1701.	5.8	53
17	Kinetic Origin of Substrate Specificity in Post-Transfer Editing by Leucyl-tRNA Synthetase. Journal of Molecular Biology, 2018, 430, 1-16.	2.0	19
18	RIP2 filament formation is required for NOD2 dependent NF-Î°B signalling. Nature Communications, 2018, 9, 4043.	5.8	55

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19	Characterization of influenza virus variants induced by treatment with the endonuclease inhibitor baloxavir marboxil. Scientific Reports, 2018, 8, 9633.	1.6	306
20	Molecular mechanism of influenza A NS1-mediated TRIM25 recognition and inhibition. Nature Communications, 2018, 9, 1820.	5.8	124
21	Structural insights into RNA synthesis by the influenza virus transcription-replication machine. Virus Research, 2017, 234, 103-117.	1.1	143
22	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
23	Anin vitrofluorescence based study of initiation of RNA synthesis by influenza B polymerase. Nucleic Acids Research, 2017, 45, gkx043.	6.5	49
24	Structural basis of an essential interaction between influenza polymerase and Pol II CTD. Nature, 2017, 541, 117-121.	13.7	98
25	Editorial overview: Proteinâ€“nucleic acid interactions: An expanding universe. Current Opinion in Structural Biology, 2017, 47, iv-v.	2.6	1
26	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
27	Structural insights into reptarenavirus cap-snatching machinery. PLoS Pathogens, 2017, 13, e1006400.	2.1	32
28	Structures of the inactive and active states of RIP2 kinase inform on the mechanism of activation. PLoS ONE, 2017, 12, e0177161.	1.1	35
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	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
31	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
32	Cryptosporidium and Toxoplasma Parasites Are Inhibited by a Benzoxaborole Targeting Leucyl-tRNA Synthetase. Antimicrobial Agents and Chemotherapy, 2016, 60, 5817-5827.	1.4	55
33	Structural characterization of antibiotic self-immunity tRNA synthetase in plant tumour biocontrol agent. Nature Communications, 2016, 7, 12928.	5.8	15
34	Antimalarial Benzoxaboroles Target Plasmodium falciparum Leucyl-tRNA Synthetase. Antimicrobial Agents and Chemotherapy, 2016, 60, 4886-4895.	1.4	58
35	Influenza Polymerase Can Adopt an Alternative Configuration Involving a Radical Repacking of PB2 Domains. Molecular Cell, 2016, 61, 125-137.	4.5	123
36	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

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37	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
38	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
39	Comparative Structural and Functional Analysis of Bunyavirus and Arenavirus Cap-Snatching Endonucleases. PLoS Pathogens, 2016, 12, e1005636.	2.1	84
40	Structural Insights into Bunyavirus Replication and Its Regulation by the vRNA Promoter. Cell, 2015, 161, 1267-1279.	13.5	164
41	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
42	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
43	Crystal structure of the RNA-dependent RNA polymerase from influenza C virus. Nature, 2015, 527, 114-117.	13.7	145
44	Kinetic discrimination of self/non-self RNA by the ATPase activity of RIG-I and MDA5. BMC Biology, 2015, 13, 54.	1.7	47
45	RIG-I Self-Oligomerization Is Either Dispensable or Very Transient for Signal Transduction. PLoS ONE, 2014, 9, e108770.	1.1	10
46	Crystal structure of a signal recognition particleAludomain in the elongation arrest conformation. Rna, 2014, 20, 1955-1962.	1.6	8
47	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
48	Structure of influenza A polymerase bound to the viral RNA promoter. Nature, 2014, 516, 355-360.	13.7	404
49	Structural insight into cap-snatching and RNA synthesis by influenza polymerase. Nature, 2014, 516, 361-366.	13.7	376
50	The physiological target for Leu<scp>RS</scp> translational quality control is norvaline. EMBO Journal, 2014, 33, 1639-1653.	3.5	58
51	Segmented negative strand RNA virus nucleoprotein structure. Current Opinion in Virology, 2014, 5, 7-15.	2.6	35
52	RNA Clamping by Vasa Assembles a piRNA Amplifier Complex on Transposon Transcripts. Cell, 2014, 157, 1698-1711.	13.5	208
53	Comparative Structural and Functional Analysis of Orthomyxovirus Polymerase Cap-Snatching Domains. PLoS ONE, 2014, 9, e84973.	1.1	18
54	New 7-Methylguanine Derivatives Targeting the Influenza Polymerase PB2 Cap-Binding Domain. Journal of Medicinal Chemistry, 2013, 56, 8915-8930.	2.9	64

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55	Systems To Establish Bunyavirus Genome Replication in the Absence of Transcription. Journal of Virology, 2013, 87, 8205-8212.	1.5	32
56	CBCâ€“ARS2 stimulates 3â€²-end maturation of multiple RNA families and favors cap-proximal processing. Nature Structural and Molecular Biology, 2013, 20, 1358-1366.	3.6	143
57	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
58	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
59	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
60	Structural Basis for the Activation of Innate Immune Pattern-Recognition Receptor RIG-I by Viral RNA. Cell, 2011, 147, 423-435.	13.5	543
61	Towards an atomic resolution understanding of the influenza virus replication machinery. Current Opinion in Structural Biology, 2010, 20, 104-113.	2.6	95
62	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
63	Structure and RNA recognition by the snRNA and snoRNA transport factor PHAX. Rna, 2010, 16, 1205-1216.	1.6	18
64	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
65	The cap-snatching endonuclease of influenza virus polymerase resides in the PA subunit. Nature, 2009, 458, 914-918.	13.7	630
66	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
67	The structural basis for cap binding by influenza virus polymerase subunit PB2. Nature Structural and Molecular Biology, 2008, 15, 500-506.	3.6	436
68	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
69	An Antifungal Agent Inhibits an Aminoacyl-tRNA Synthetase by Trapping tRNA in the Editing Site. Science, 2007, 316, 1759-1761.	6.0	556
70	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
71	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
72	Specificity of recognition of mRNA 5' cap by human nuclear cap-binding complex. Rna, 2005, 11, 1355-1363.	1.6	59

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73	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
74	Crystal Structure of the Human Nuclear Cap Binding Complex. Molecular Cell, 2001, 8, 383-396.	4.5	126
75	Hierarchical assembly of the Alu domain of the mammalian signal recognition particle. Rna, 2001, 7, 731-740.	1.6	31
76	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
77	A triple Î²-spiral in the adenovirus fibreÂshaft reveals a new structural motif for a fibrous protein. Nature, 1999, 401, 935-938.	13.7	310
78	Escherichia coliSecA shape and dimensions. FEBS Letters, 1998, 436, 277-282.	1.3	46
79	The structure of the Escherichia coli EF-TuÂ· EF-Ts complex at 2.5 Ã… resolution. Nature, 1996, 379, 511-518.	13.7	307
80	Eleven down and nine to go. Nature Structural Biology, 1995, 2, 824-831.	9.7	192
81	Crystallization of the seryl-tRNA synthetase: tRNAsercomplex ofEscherichia coli. FEBS Letters, 1993, 324, 167-170.	1.3	36
82	Sequence, structural and evolutionary relationships between class 2 aminoacyl-tRNA synthetases. Nucleic Acids Research, 1991, 19, 3489-3498.	6.5	270
83	A second class of synthetase structure revealed by X-ray analysis of Escherichia coli seryl-tRNA synthetase at 2.5 Ã…. Nature, 1990, 347, 249-255.	13.7	667
84	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
85	Variation of longitudinal acoustic velocity at gigahertz frequencies with water content in rat-tail tendon fibers. Biopolymers, 1984, 23, 337-351.	1.2	39
86	Inelastic neutron scattering analysis of hexokinase dynamics and its modification on binding of glucose. Nature, 1982, 300, 84-86.	13.7	56