

Stephen Anthony Cusack

List of Publications by Year in Descending Order

Source: <https://exaly.com/author-pdf/6856895/stephen-anthony-cusack-publications-by-year.pdf>

Version: 2024-04-20

This document has been generated based on the publications and citations recorded by exaly.com. For the latest version of this publication list, visit the link given above.

The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

87
papers

8,064
citations

41
h-index

89
g-index

97
ext. papers

9,169
ext. citations

16.8
avg, IF

5.92
L-index

#	Paper	IF	Citations
87	Structural snapshots of La Crosse virus polymerase reveal the mechanisms underlying Peribunyaviridae replication and transcription.. <i>Nature Communications</i> , 2022 , 13, 902	17.4	0
86	Type B and type A influenza polymerases have evolved distinct binding interfaces to recruit the RNA polymerase II CTD. <i>PLoS Pathogens</i> , 2022 , 18, e1010328	7.6	0
85	Structure and Function of Influenza Polymerase. <i>Cold Spring Harbor Perspectives in Medicine</i> , 2021 , 11,	5.4	21
84	Conformational changes in Lassa virus L protein associated with promoter binding and RNA synthesis activity. <i>Nature Communications</i> , 2021 , 12, 7018	17.4	4
83	Errors in the deposited SFTSV L protein structure. <i>Nature Microbiology</i> , 2021 , 6, 549-550	26.6	1
82	Influenza Virus RNA-Dependent RNA Polymerase and the Host Transcriptional Apparatus. <i>Annual Review of Biochemistry</i> , 2021 , 90, 321-348	29.1	7
81	The Cap-Snatching Mechanism of Bunyaviruses. <i>Trends in Microbiology</i> , 2020 , 28, 293-303	12.4	23
80	Molecular basis of the multifaceted functions of human leucyl-tRNA synthetase in protein synthesis and beyond. <i>Nucleic Acids Research</i> , 2020 , 48, 4946-4959	20.1	9
79	Molecular basis of host-adaptation interactions between influenza virus polymerase PB2 subunit and ANP32A. <i>Nature Communications</i> , 2020 , 11, 3656	17.4	18
78	NCBP3 positively impacts mRNA biogenesis. <i>Nucleic Acids Research</i> , 2020 , 48, 10413-10427	20.1	6
77	Pre-initiation and elongation structures of full-length La Crosse virus polymerase reveal functionally important conformational changes. <i>Nature Communications</i> , 2020 , 11, 3590	17.4	13
76	A Structure-Based Model for the Complete Transcription Cycle of Influenza Polymerase. <i>Cell</i> , 2020 , 181, 877-893.e21	56.2	43
75	Structural and functional characterization of the severe fever with thrombocytopenia syndrome virus L protein. <i>Nucleic Acids Research</i> , 2020 , 48, 5749-5765	20.1	15
74	Structural snapshots of actively transcribing influenza polymerase. <i>Nature Structural and Molecular Biology</i> , 2019 , 26, 460-470	17.6	41
73	Capped RNA primer binding to influenza polymerase and implications for the mechanism of cap-binding inhibitors. <i>Nucleic Acids Research</i> , 2018 , 46, 956-971	20.1	34
72	Structural analysis of human ARS2 as a platform for co-transcriptional RNA sorting. <i>Nature Communications</i> , 2018 , 9, 1701	17.4	24
71	Kinetic Origin of Substrate Specificity in Post-Transfer Editing by Leucyl-tRNA Synthetase. <i>Journal of Molecular Biology</i> , 2018 , 430, 1-16	6.5	14

70	Molecular mechanism of influenza A NS1-mediated TRIM25 recognition and inhibition. <i>Nature Communications</i> , 2018 , 9, 1820	17.4	76
69	RIP2 filament formation is required for NOD2 dependent NF- κ B signalling. <i>Nature Communications</i> , 2018 , 9, 4043	17.4	36
68	Characterization of influenza virus variants induced by treatment with the endonuclease inhibitor baloxavir marboxil. <i>Scientific Reports</i> , 2018 , 8, 9633	4.9	206
67	Structural insights into RNA synthesis by the influenza virus transcription-replication machine. <i>Virus Research</i> , 2017 , 234, 103-117	6.4	102
66	Targeting CPSF3 as a new approach to control toxoplasmosis. <i>EMBO Molecular Medicine</i> , 2017 , 9, 385-394	4.2	37
65	An in vitro fluorescence based study of initiation of RNA synthesis by influenza B polymerase. <i>Nucleic Acids Research</i> , 2017 , 45, 3353-3368	20.1	39
64	Structural basis of an essential interaction between influenza polymerase and Pol II CTD. <i>Nature</i> , 2017 , 541, 117-121	50.4	66
63	Structural insights into reptarenavirus cap-snatching machinery. <i>PLoS Pathogens</i> , 2017 , 13, e1006400	7.6	17
62	Structural basis for mutually exclusive co-transcriptional nuclear cap-binding complexes with either NELF-E or ARS2. <i>Nature Communications</i> , 2017 , 8, 1302	17.4	14
61	Structures of the inactive and active states of RIP2 kinase inform on the mechanism of activation. <i>PLoS ONE</i> , 2017 , 12, e0177161	3.7	18
60	Cryo-electron microscopy structure of La Crosse orthobunyavirus polymerase in presence or absence of viral RNA 2016 , 9-10		
59	Discovery of Novel Oral Protein Synthesis Inhibitors of Mycobacterium tuberculosis That Target Leucyl-tRNA Synthetase. <i>Antimicrobial Agents and Chemotherapy</i> , 2016 , 60, 6271-80	5.9	61
58	Cryptosporidium and Toxoplasma Parasites Are Inhibited by a Benzoxaborole Targeting Leucyl-tRNA Synthetase. <i>Antimicrobial Agents and Chemotherapy</i> , 2016 , 60, 5817-27	5.9	41
57	Structural characterization of antibiotic self-immunity tRNA synthetase in plant tumour biocontrol agent. <i>Nature Communications</i> , 2016 , 7, 12928	17.4	9
56	Antimalarial Benzoxaboroles Target Plasmodium falciparum Leucyl-tRNA Synthetase. <i>Antimicrobial Agents and Chemotherapy</i> , 2016 , 60, 4886-95	5.9	39
55	Influenza Polymerase Can Adopt an Alternative Configuration Involving a Radical Repacking of PB2 Domains. <i>Molecular Cell</i> , 2016 , 61, 125-37	17.6	92
54	Towards a structural understanding of RNA synthesis by negative strand RNA viral polymerases. <i>Current Opinion in Structural Biology</i> , 2016 , 36, 75-84	8.1	51
53	Time-Resolved Visualisation of Nearly-Native Influenza A Virus Progeny Ribonucleoproteins and Their Individual Components in Live Infected Cells. <i>PLoS ONE</i> , 2016 , 11, e0149986	3.7	10

52	Atomic Structure and Biochemical Characterization of an RNA Endonuclease in the N Terminus of Andes Virus L Protein. <i>PLoS Pathogens</i> , 2016 , 12, e1005635	7.6	23
51	Comparative Structural and Functional Analysis of Bunyavirus and Arenavirus Cap-Snatching Endonucleases. <i>PLoS Pathogens</i> , 2016 , 12, e1005636	7.6	55
50	Structural Analysis of dsRNA Binding to Anti-viral Pattern Recognition Receptors LGP2 and MDA5. <i>Molecular Cell</i> , 2016 , 62, 586-602	17.6	82
49	Aminoacetylation Reaction Catalyzed by Leucyl-tRNA Synthetase Operates via a Self-Assisted Mechanism Using a Conserved Residue and the Aminoacyl Substrate. <i>Journal of Physical Chemistry B</i> , 2016 , 120, 4388-98	3.4	5
48	Analysis of the Resistance Mechanism of a Benzoxaborole Inhibitor Reveals Insight into the Leucyl-tRNA Synthetase Editing Mechanism. <i>ACS Chemical Biology</i> , 2015 , 10, 2277-85	4.9	19
47	An RNA Hybridization Assay for Screening Influenza A Virus Polymerase Inhibitors Using the Entire Ribonucleoprotein Complex. <i>Assay and Drug Development Technologies</i> , 2015 , 13, 488-506	2.1	6
46	Crystal structure of the RNA-dependent RNA polymerase from influenza C virus. <i>Nature</i> , 2015 , 527, 114-7	30.4	116
45	Kinetic discrimination of self/non-self RNA by the ATPase activity of RIG-I and MDA5. <i>BMC Biology</i> , 2015 , 13, 54	7.3	39
44	Structural Insights into Bunyavirus Replication and Its Regulation by the vRNA Promoter. <i>Cell</i> , 2015 , 161, 1267-79	56.2	120
43	Crystal structure of vaccinia virus mRNA capping enzyme provides insights into the mechanism and evolution of the capping apparatus. <i>Structure</i> , 2014 , 22, 452-65	5.2	29
42	Structure of influenza A polymerase bound to the viral RNA promoter. <i>Nature</i> , 2014 , 516, 355-60	50.4	321
41	Structural insight into cap-snatching and RNA synthesis by influenza polymerase. <i>Nature</i> , 2014 , 516, 361-5	50.4	299
40	The physiological target for LeuRS translational quality control is norvaline. <i>EMBO Journal</i> , 2014 , 33, 1639-53	13	47
39	Segmented negative strand RNA virus nucleoprotein structure. <i>Current Opinion in Virology</i> , 2014 , 5, 7-15	7.5	29
38	RNA clamping by Vasa assembles a piRNA amplifier complex on transposon transcripts. <i>Cell</i> , 2014 , 157, 1698-711	56.2	149
37	RIG-I self-oligomerization is either dispensable or very transient for signal transduction. <i>PLoS ONE</i> , 2014 , 9, e108770	3.7	8
36	Crystal structure of a signal recognition particle Alu domain in the elongation arrest conformation. <i>Rna</i> , 2014 , 20, 1955-62	5.8	6
35	Comparative structural and functional analysis of orthomyxovirus polymerase cap-snatching domains. <i>PLoS ONE</i> , 2014 , 9, e84973	3.7	12

34	New 7-methylguanine derivatives targeting the influenza polymerase PB2 cap-binding domain. <i>Journal of Medicinal Chemistry</i> , 2013 , 56, 8915-30	8.3	57
33	Systems to establish bunyavirus genome replication in the absence of transcription. <i>Journal of Virology</i> , 2013 , 87, 8205-12	6.6	24
32	CBC-ARS2 stimulates 3' end maturation of multiple RNA families and favors cap-proximal processing. <i>Nature Structural and Molecular Biology</i> , 2013 , 20, 1358-66	17.6	102
31	Influenza A virus progeny vRNP trafficking in live infected cells studied with the virus-encoded fluorescently tagged PB2 protein. <i>Vaccine</i> , 2012 , 30, 7411-7	4.1	37
30	Structural analysis of specific metal chelating inhibitor binding to the endonuclease domain of influenza pH1N1 (2009) polymerase. <i>PLoS Pathogens</i> , 2012 , 8, e1002831	7.6	123
29	Structural dynamics of the aminoacylation and proofreading functional cycle of bacterial leucyl-tRNA synthetase. <i>Nature Structural and Molecular Biology</i> , 2012 , 19, 677-84	17.6	111
28	Structural basis for the activation of innate immune pattern-recognition receptor RIG-I by viral RNA. <i>Cell</i> , 2011 , 147, 423-35	56.2	439
27	Mutational and metal binding analysis of the endonuclease domain of the influenza virus polymerase PA subunit. <i>Journal of Virology</i> , 2010 , 84, 9096-104	6.6	72
26	Structure and RNA recognition by the snRNA and snoRNA transport factor PHAX. <i>Rna</i> , 2010 , 16, 1205-16	5.8	13
25	Bunyaviridae RNA polymerases (L-protein) have an N-terminal, influenza-like endonuclease domain, essential for viral cap-dependent transcription. <i>PLoS Pathogens</i> , 2010 , 6, e1001101	7.6	176
24	Towards an atomic resolution understanding of the influenza virus replication machinery. <i>Current Opinion in Structural Biology</i> , 2010 , 20, 104-13	8.1	89
23	The cap-snatching endonuclease of influenza virus polymerase resides in the PA subunit. <i>Nature</i> , 2009 , 458, 914-8	50.4	542
22	Crystal structures of the human and fungal cytosolic Leucyl-tRNA synthetase editing domains: A structural basis for the rational design of antifungal benzoxaboroles. <i>Journal of Molecular Biology</i> , 2009 , 390, 196-207	6.5	80
21	The structural basis for cap binding by influenza virus polymerase subunit PB2. <i>Nature Structural and Molecular Biology</i> , 2008 , 15, 500-6	17.6	380
20	Host determinant residue lysine 627 lies on the surface of a discrete, folded domain of influenza virus polymerase PB2 subunit. <i>PLoS Pathogens</i> , 2008 , 4, e1000136	7.6	143
19	Structure and nuclear import function of the C-terminal domain of influenza virus polymerase PB2 subunit. <i>Nature Structural and Molecular Biology</i> , 2007 , 14, 229-33	17.6	245
18	An antifungal agent inhibits an aminoacyl-tRNA synthetase by trapping tRNA in the editing site. <i>Science</i> , 2007 , 316, 1759-61	33.3	469
17	Solution structure of NOD1 CARD and mutational analysis of its interaction with the CARD of downstream kinase RICK. <i>Journal of Molecular Biology</i> , 2007 , 365, 160-74	6.5	62

16	Specificity of recognition of mRNA 5'cap by human nuclear cap-binding complex. <i>Rna</i> , 2005 , 11, 1355-63	5.8	55
15	Large-scale induced fit recognition of an m(7)GpppG cap analogue by the human nuclear cap-binding complex. <i>EMBO Journal</i> , 2002 , 21, 5548-57	13	154
14	Crystal structure of the human nuclear cap binding complex. <i>Molecular Cell</i> , 2001 , 8, 383-96	17.6	115
13	Hierarchical assembly of the Alu domain of the mammalian signal recognition particle. <i>Rna</i> , 2001 , 7, 731-40	5.8	30
12	The 2 A crystal structure of leucyl-tRNA synthetase and its complex with a leucyl-adenylate analogue. <i>EMBO Journal</i> , 2000 , 19, 2351-61	13	223
11	A triple beta-spiral in the adenovirus fibre shaft reveals a new structural motif for a fibrous protein. <i>Nature</i> , 1999 , 401, 935-8	50.4	279
10	Escherichia coli SecA shape and dimensions. <i>FEBS Letters</i> , 1998 , 436, 277-82	3.8	40
9	The structure of the Escherichia coli EF-Tu.EF-Ts complex at 2.5 A resolution. <i>Nature</i> , 1996 , 379, 511-8	50.4	275
8	Eleven down and nine to go. <i>Nature Structural Biology</i> , 1995 , 2, 824-31		173
7	Crystallization of the seryl-tRNA synthetase:tRNAs ^(ser) complex of Escherichia coli. <i>FEBS Letters</i> , 1993 , 324, 167-70	3.8	32
6	Sequence, structural and evolutionary relationships between class 2 aminoacyl-tRNA synthetases. <i>Nucleic Acids Research</i> , 1991 , 19, 3489-98	20.1	245
5	A second class of synthetase structure revealed by X-ray analysis of Escherichia coli seryl-tRNA synthetase at 2.5 A. <i>Nature</i> , 1990 , 347, 249-55	50.4	602
4	Direct measurement of hydration-related dynamic changes in lysozyme using inelastic neutron scattering spectroscopy. <i>Journal of Biomolecular Structure and Dynamics</i> , 1987 , 4, 583-8	3.6	33
3	Variation of longitudinal acoustic velocity at gigahertz frequencies with water content in rat-tail tendon fibers. <i>Biopolymers</i> , 1984 , 23, 337-51	2.2	32
2	Inelastic neutron scattering analysis of hexokinase dynamics and its modification on binding of glucose. <i>Nature</i> , 1982 , 300, 84-6	50.4	51
1	Mechanistic insights into RNA binding and RNA-regulated RIG-I ubiquitination by TRIM25		5