

Stephen C Graham

List of Publications by Year in descending order

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Version: 2024-02-01

72
papers

3,224
citations

136885

32
h-index

168321

53
g-index

94
all docs

94
docs citations

94
times ranked

5609
citing authors

#	ARTICLE	IF	CITATIONS
1	The crystal structure of vaccinia virus protein E2 and perspectives on the prediction of novel viral protein folds. <i>Journal of General Virology</i> , 2022, 103, .	1.3	8
2	<i>Contour</i>: A semi-automated segmentation and quantitation tool for cryo-soft-X-ray tomography. <i>Biological Imaging</i> , 2022, 2, .	1.0	6
3	SARS-CoV-2 Spike has broad tropism for mammalian ACE2 proteins yet exhibits a distinct pattern of receptor usage when compared to other Î²-coronavirus Spike proteins. <i>Access Microbiology</i> , 2022, 4, .	0.2	1
4	Near-native state imaging by cryo-soft-X-ray tomography reveals remodelling of multiple cellular organelles during HSV-1 infection. <i>PLoS Pathogens</i> , 2022, 18, e1010629.	2.1	12
5	Application of error-prone PCR to functionally probe the morbillivirus Haemagglutinin protein. <i>Journal of General Virology</i> , 2021, 102, .	1.3	2
6	pUL21 is a viral phosphatase adaptor that promotes herpes simplex virus replication and spread. <i>PLoS Pathogens</i> , 2021, 17, e1009824.	2.1	19
7	Investigating molecular mechanisms of 2A-stimulated ribosomal pausing and frameshifting in <i>Theilovirus</i>. <i>Nucleic Acids Research</i> , 2021, 49, 11938-11958.	6.5	11
8	A Tetrameric Assembly of Saposin A: Increasing Structural Diversity in Lipid Transfer Proteins. <i>Contact (Thousand Oaks (Ventura County, Calif))</i> , 2021, 4, 251525642110523.	0.4	1
9	Structural and molecular basis for Cardiovirus 2A protein as a viral gene expression switch. <i>Nature Communications</i> , 2021, 12, 7166.	5.8	18
10	Temporal Proteomic Analysis of Herpes Simplex Virus 1 Infection Reveals Cell-Surface Remodeling via pUL56-Mediated GOPC Degradation. <i>Cell Reports</i> , 2020, 33, 108235.	2.9	29
11	The SARS-CoV-2 Spike protein has a broad tropism for mammalian ACE2 proteins. <i>PLoS Biology</i> , 2020, 18, e3001016.	2.6	169
12	Insights into herpesvirus assembly from the structure of the pUL7:pUL51 complex. <i>ELife</i> , 2020, 9, .	2.8	27
13	Non-native fold of the putative VPS39 zinc finger domain. <i>Wellcome Open Research</i> , 2020, 5, 154.	0.9	2
14	Non-native fold of the putative VPS39 zinc finger domain. <i>Wellcome Open Research</i> , 2020, 5, 154.	0.9	3
15	The SARS-CoV-2 Spike protein has a broad tropism for mammalian ACE2 proteins. , 2020, 18, e3001016.		0
16	The SARS-CoV-2 Spike protein has a broad tropism for mammalian ACE2 proteins. , 2020, 18, e3001016.		0
17	The SARS-CoV-2 Spike protein has a broad tropism for mammalian ACE2 proteins. , 2020, 18, e3001016.		0
18	The SARS-CoV-2 Spike protein has a broad tropism for mammalian ACE2 proteins. , 2020, 18, e3001016.		0

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19	The SARS-CoV-2 Spike protein has a broad tropism for mammalian ACE2 proteins. , 2020, 18, e3001016.		0
20	The SARS-CoV-2 Spike protein has a broad tropism for mammalian ACE2 proteins. , 2020, 18, e3001016.		0
21	Molecular models should not be published without the corresponding atomic coordinates. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 11099-11100.	3.3	4
22	Molecular basis of cullin-3 (Cul3) ubiquitin ligase subversion by vaccinia virus protein A55. Journal of Biological Chemistry, 2019, 294, 6416-6429.	1.6	14
23	Parallel adaptation of rabbit populations to myxoma virus. Science, 2019, 363, 1319-1326.	6.0	124
24	The lipid transfer protein Saposin B does not directly bind CD1d for lipid antigen loading. Wellcome Open Research, 2019, 4, 117.	0.9	4
25	The lipid transfer protein Saposin B does not directly bind CD1d for lipid antigen loading. Wellcome Open Research, 2019, 4, 117.	0.9	1
26	The mechanism of glycosphingolipid degradation revealed by a GALC-SapA complex structure. Nature Communications, 2018, 9, 151.	5.8	37
27	IFIT3 and IFIT2/3 promote IFIT1-mediated translation inhibition by enhancing binding to non-self RNA. Nucleic Acids Research, 2018, 46, 5269-5285.	6.5	72
28	Structure-Guided Identification of a Nonhuman Morbillivirus with Zoonotic Potential. Journal of Virology, 2018, 92, .	1.5	23
29	Proteomic and Biochemical Comparison of the Cellular Interaction Partners of Human VPS33A and VPS33B. Journal of Molecular Biology, 2018, 430, 2153-2163.	2.0	21
30	VPS18 recruits VPS41 to the human HOPS complex via a RING-RING interaction. Biochemical Journal, 2017, 474, 3615-3626.	1.7	23
31	Cellular and viral peptides bind multiple sites on the N-terminal domain of clathrin. Traffic, 2017, 18, 44-57.	1.3	30
32	Dual Function of the pUL7-pUL51 Tegument Protein Complex in Herpes Simplex Virus 1 Infection. Journal of Virology, 2017, 91, .	1.5	44
33	Using selenomethionyl derivatives to assign sequence in low-resolution structures of the AP2 clathrin adaptor. Acta Crystallographica Section D: Structural Biology, 2016, 72, 336-345.	1.1	1
34	A Conserved Interaction between a C-Terminal Motif in Norovirus VPg and the HEAT-1 Domain of eIF4G Is Essential for Translation Initiation. PLoS Pathogens, 2016, 12, e1005379.	2.1	40
35	Tegument Assembly and Secondary Envelopment of Alphaherpesviruses. Viruses, 2015, 7, 5084-5114.	1.5	164
36	Vaccinia Virus Protein A49 Is an Unexpected Member of the B-cell Lymphoma (Bcl)-2 Protein Family. Journal of Biological Chemistry, 2015, 290, 5991-6002.	1.6	49

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37	Recruitment of <scp>VPS33A</scp> to <scp>HOPS</scp> by <scp>VPS16</scp> Is Required for Lysosome Fusion with Endosomes and Autophagosomes. <i>Traffic</i> , 2015, 16, 727-742.	1.3	122
38	AP2 controls clathrin polymerization with a membrane-activated switch. <i>Science</i> , 2014, 345, 459-463.	6.0	185
39	Structure of a VP1-VP3 Complex Suggests How Birnaviruses Package the VP1 Polymerase. <i>Journal of Virology</i> , 2013, 87, 3229-3236.	1.5	15
40	Syntaxin binding mechanism and disease-causing mutations in Munc18-2. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, E4482-91.	3.3	70
41	Structural basis of Vps33A recruitment to the human HOPS complex by Vps16. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 13345-13350.	3.3	79
42	Structural snapshots illustrate the catalytic cycle of Î²-galactocerebrosidase, the defective enzyme in Krabbe disease. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 20479-20484.	3.3	39
43	The Molecular Basis for the Endocytosis of Small R-SNAREs by the Clathrin Adaptor CALM. <i>Cell</i> , 2011, 147, 1118-1131.	13.5	172
44	How vaccinia virus has evolved to subvert the host immune response. <i>Journal of Structural Biology</i> , 2011, 175, 127-134.	1.3	66
45	Insights into the Evolution of a Complex Virus from the Crystal Structure of Vaccinia Virus D13. <i>Structure</i> , 2011, 19, 1011-1020.	1.6	78
46	PCNA directs type 2 RNase H activity on DNA replication and repair substrates. <i>Nucleic Acids Research</i> , 2011, 39, 3652-3666.	6.5	112
47	Mapping the Î²B Kinase Î² (IKKÎ²)-binding Interface of the B14 Protein, a Vaccinia Virus Inhibitor of IKKÎ²-mediated Activation of Nuclear Factor Î²B. <i>Journal of Biological Chemistry</i> , 2011, 286, 20727-20735.	1.6	48
48	The Structure of the Human RNase H2 Complex Defines Key Interaction Interfaces Relevant to Enzyme Function and Human Disease. <i>Journal of Biological Chemistry</i> , 2011, 286, 10530-10539.	1.6	94
49	Insights into Krabbe disease from structures of galactocerebrosidase. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 15169-15173.	3.3	87
50	The N-Terminus of the RNA Polymerase from Infectious Pancreatic Necrosis Virus Is the Determinant of Genome Attachment. <i>PLoS Pathogens</i> , 2011, 7, e1002085.	2.1	34
51	Inhibition of Apoptosis and NF-Î²B Activation by Vaccinia Protein N1 Occur via Distinct Binding Surfaces and Make Different Contributions to Virulence. <i>PLoS Pathogens</i> , 2011, 7, e1002430.	2.1	73
52	Genomics and structure/function studies of Rhabdoviridae proteins involved in replication and transcription. <i>Antiviral Research</i> , 2010, 87, 149-161.	1.9	57
53	Structure of the Nucleoprotein Binding Domain of Mokola Virus Phosphoprotein. <i>Journal of Virology</i> , 2010, 84, 1089-1096.	1.5	27
54	Unusual Molecular Architecture of the Machupo Virus Attachment Glycoprotein. <i>Journal of Virology</i> , 2009, 83, 8259-8265.	1.5	71

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55	Structure of Signal-regulatory Protein $\hat{\pm}$. Journal of Biological Chemistry, 2009, 284, 26613-26619.	1.6	35
56	Functional characteristics of HIV-1 subtype C compatible with increased heterosexual transmissibility. Aids, 2009, 23, 1047-1057.	1.0	19
57	Semi-automated microseeding of nanolitre crystallization experiments. Acta Crystallographica Section F: Structural Biology Communications, 2008, 64, 14-18.	0.7	31
58	Expression, purification and crystallization of a lyssavirus matrix (M) protein. Acta Crystallographica Section F: Structural Biology Communications, 2008, 64, 258-262.	0.7	17
59	Crystal structure of Spa40, the specificity switch for the <i>Shigella flexneri</i> type III secretion system. Molecular Microbiology, 2008, 69, 267-276.	1.2	55
60	Paired Receptor Specificity Explained by Structures of Signal Regulatory Proteins Alone and Complexed with CD47. Molecular Cell, 2008, 31, 266-277.	4.5	171
61	Complexes of mutants of Escherichia coli aminopeptidase P and the tripeptide substrate ValProLeu. Archives of Biochemistry and Biophysics, 2008, 469, 200-208.	1.4	19
62	Rhabdovirus Matrix Protein Structures Reveal a Novel Mode of Self-Association. PLoS Pathogens, 2008, 4, e1000251.	2.1	71
63	Vaccinia Virus Proteins A52 and B14 Share a Bcl-2 Like Fold but Have Evolved to Inhibit NF- $\hat{\rho}$ B rather than Apoptosis. PLoS Pathogens, 2008, 4, e1000128.	2.1	136
64	Structures of Ligand-free and Inhibitor Complexes of Dihydroorotase from Escherichia coli: Implications for Loop Movement in Inhibitor Design. Journal of Molecular Biology, 2007, 370, 812-825.	2.0	35
65	Structure of CrmE, a Virus-encoded Tumour Necrosis Factor Receptor. Journal of Molecular Biology, 2007, 372, 660-671.	2.0	43
66	Kinetic and Crystallographic Analysis of Mutant Escherichia coli Aminopeptidase P: Insights into Substrate Recognition and the Mechanism of Catalysis. Biochemistry, 2006, 45, 964-975.	1.2	41
67	Stabilization of a binary protein complex by intein-mediated cyclization. Protein Science, 2006, 15, 2612-2618.	3.1	29
68	Structural and Functional Implications of Metal Ion Selection in Aminopeptidase P, a Metalloprotease with a Dinuclear Metal Center. Biochemistry, 2005, 44, 13820-13836.	1.2	41
69	Structure of Escherichia coli aminopeptidase P in complex with the inhibitor apstatin. Acta Crystallographica Section D: Biological Crystallography, 2004, 60, 1770-1779.	2.5	29
70	Crystallization of GcnA, an N-acetyl- $\hat{2}$ -D-glucosaminidase, from Streptococcus gordonii. Acta Crystallographica Section D: Biological Crystallography, 2004, 60, 1910-1911.	2.5	1
71	An orthorhombic form of Escherichia coli aminopeptidase P at 2.4 Å resolution. Acta Crystallographica Section D: Biological Crystallography, 2003, 59, 897-902.	2.5	19
72	Crystallization of FLINC4, an intramolecular LMO4 IdB1 complex. Acta Crystallographica Section D: Biological Crystallography, 2003, 59, 1484-1486.	2.5	10