

Stephen C Graham

List of Publications by Year in descending order

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72
papers

3,224
citations

136740

32
h-index

168136

53
g-index

94
all docs

94
docs citations

94
times ranked

5609
citing authors

#	ARTICLE	IF	CITATIONS
1	AP2 controls clathrin polymerization with a membrane-activated switch. <i>Science</i> , 2014, 345, 459-463.	6.0	185
2	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
3	Paired Receptor Specificity Explained by Structures of Signal Regulatory Proteins Alone and Complexed with CD47. <i>Molecular Cell</i> , 2008, 31, 266-277.	4.5	171
4	The SARS-CoV-2 Spike protein has a broad tropism for mammalian ACE2 proteins. <i>PLoS Biology</i> , 2020, 18, e3001016.	2.6	169
5	Tegument Assembly and Secondary Envelopment of Alphaherpesviruses. <i>Viruses</i> , 2015, 7, 5084-5114.	1.5	164
6	Vaccinia Virus Proteins A52 and B14 Share a Bcl-2-like Fold but Have Evolved to Inhibit NF- κ B rather than Apoptosis. <i>PLoS Pathogens</i> , 2008, 4, e1000128.	2.1	136
7	Parallel adaptation of rabbit populations to myxoma virus. <i>Science</i> , 2019, 363, 1319-1326.	6.0	124
8	Recruitment of VPS33A to HOPS by VPS16 Is Required for Lysosome Fusion with Endosomes and Autophagosomes. <i>Traffic</i> , 2015, 16, 727-742.	1.3	122
9	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
10	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
11	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
12	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
13	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
14	Inhibition of Apoptosis and NF- κ B 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
15	IFIT3 and IFIT2/3 promote IFIT1-mediated translation inhibition by enhancing binding to non-self RNA. <i>Nucleic Acids Research</i> , 2018, 46, 5269-5285.	6.5	72
16	Rhabdovirus Matrix Protein Structures Reveal a Novel Mode of Self-Association. <i>PLoS Pathogens</i> , 2008, 4, e1000251.	2.1	71
17	Unusual Molecular Architecture of the Machupo Virus Attachment Glycoprotein. <i>Journal of Virology</i> , 2009, 83, 8259-8265.	1.5	71
18	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

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19	How vaccinia virus has evolved to subvert the host immune response. <i>Journal of Structural Biology</i> , 2011, 175, 127-134.	1.3	66
20	Genomics and structure/function studies of Rhabdoviridae proteins involved in replication and transcription. <i>Antiviral Research</i> , 2010, 87, 149-161.	1.9	57
21	Crystal structure of Spa40, the specificity switch for the <i>Shigella flexneri</i> type III secretion system. <i>Molecular Microbiology</i> , 2008, 69, 267-276.	1.2	55
22	Vaccinia Virus Protein A49 Is an Unexpected Member of the B-cell Lymphoma (Bcl)-2 Protein Family. <i>Journal of Biological Chemistry</i> , 2015, 290, 5991-6002.	1.6	49
23	Mapping the I κ B Kinase I κ B (IKK β)-binding Interface of the B14 Protein, a Vaccinia Virus Inhibitor of IKK β -mediated Activation of Nuclear Factor I κ B. <i>Journal of Biological Chemistry</i> , 2011, 286, 20727-20735.	1.6	48
24	Dual Function of the pUL7-pUL51 Tegument Protein Complex in Herpes Simplex Virus 1 Infection. <i>Journal of Virology</i> , 2017, 91, .	1.5	44
25	Structure of CrmE, a Virus-encoded Tumour Necrosis Factor Receptor. <i>Journal of Molecular Biology</i> , 2007, 372, 660-671.	2.0	43
26	Structural and Functional Implications of Metal Ion Selection in Aminopeptidase P, a Metalloprotease with a Dinuclear Metal Center. <i>Biochemistry</i> , 2005, 44, 13820-13836.	1.2	41
27	Kinetic and Crystallographic Analysis of Mutant <i>Escherichia coli</i> Aminopeptidase P: Insights into Substrate Recognition and the Mechanism of Catalysis. <i>Biochemistry</i> , 2006, 45, 964-975.	1.2	41
28	A Conserved Interaction between a C-Terminal Motif in Norovirus VPg and the HEAT-1 Domain of eIF4G Is Essential for Translation Initiation. <i>PLoS Pathogens</i> , 2016, 12, e1005379.	2.1	40
29	Structural snapshots illustrate the catalytic cycle of I β -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
30	The mechanism of glycosphingolipid degradation revealed by a GALC-SapA complex structure. <i>Nature Communications</i> , 2018, 9, 151.	5.8	37
31	Structures of Ligand-free and Inhibitor Complexes of Dihydroorotase from <i>Escherichia coli</i> : Implications for Loop Movement in Inhibitor Design. <i>Journal of Molecular Biology</i> , 2007, 370, 812-825.	2.0	35
32	Structure of Signal-regulatory Protein I β . <i>Journal of Biological Chemistry</i> , 2009, 284, 26613-26619.	1.6	35
33	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
34	Semi-automated microseeding of nanolitre crystallization experiments. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2008, 64, 14-18.	0.7	31
35	Cellular and viral peptides bind multiple sites on the N-terminal domain of clathrin. <i>Traffic</i> , 2017, 18, 44-57.	1.3	30
36	Structure of <i>Escherichia coli</i> aminopeptidase P in complex with the inhibitor apstatin. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2004, 60, 1770-1779.	2.5	29

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37	Stabilization of a binary protein complex by intein-mediated cyclization. <i>Protein Science</i> , 2006, 15, 2612-2618.	3.1	29
38	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
39	Structure of the Nucleoprotein Binding Domain of Mokola Virus Phosphoprotein. <i>Journal of Virology</i> , 2010, 84, 1089-1096.	1.5	27
40	Insights into herpesvirus assembly from the structure of the pUL7:pUL51 complex. <i>ELife</i> , 2020, 9, .	2.8	27
41	VPS18 recruits VPS41 to the human HOPS complex via a RING-RING interaction. <i>Biochemical Journal</i> , 2017, 474, 3615-3626.	1.7	23
42	Structure-Guided Identification of a Nonhuman Morbillivirus with Zoonotic Potential. <i>Journal of Virology</i> , 2018, 92, .	1.5	23
43	Proteomic and Biochemical Comparison of the Cellular Interaction Partners of Human VPS33A and VPS33B. <i>Journal of Molecular Biology</i> , 2018, 430, 2153-2163.	2.0	21
44	An orthorhombic form of <i>Escherichia coli</i> aminopeptidase P at 2.4 Å resolution. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2003, 59, 897-902.	2.5	19
45	Complexes of mutants of <i>Escherichia coli</i> aminopeptidase P and the tripeptide substrate ValProLeu. <i>Archives of Biochemistry and Biophysics</i> , 2008, 469, 200-208.	1.4	19
46	Functional characteristics of HIV-1 subtype C compatible with increased heterosexual transmissibility. <i>Aids</i> , 2009, 23, 1047-1057.	1.0	19
47	pUL21 is a viral phosphatase adaptor that promotes herpes simplex virus replication and spread. <i>PLoS Pathogens</i> , 2021, 17, e1009824.	2.1	19
48	Structural and molecular basis for Cardiovirus 2A protein as a viral gene expression switch. <i>Nature Communications</i> , 2021, 12, 7166.	5.8	18
49	Expression, purification and crystallization of a lyssavirus matrix (M) protein. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2008, 64, 258-262.	0.7	17
50	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
51	Molecular basis of cullin-3 (Cul3) ubiquitin ligase subversion by vaccinia virus protein A55. <i>Journal of Biological Chemistry</i> , 2019, 294, 6416-6429.	1.6	14
52	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
53	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
54	Crystallization of FLINC4, an intramolecular LMO4-Idb1 complex. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2003, 59, 1484-1486.	2.5	10

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55	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
56	<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
57	Molecular models should not be published without the corresponding atomic coordinates. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 11099-11100.	3.3	4
58	The lipid transfer protein Saposin B does not directly bind CD1d for lipid antigen loading. <i>Wellcome Open Research</i> , 2019, 4, 117.	0.9	4
59	Non-native fold of the putative VPS39 zinc finger domain. <i>Wellcome Open Research</i> , 2020, 5, 154.	0.9	3
60	Application of error-prone PCR to functionally probe the morbillivirus Haemagglutinin protein. <i>Journal of General Virology</i> , 2021, 102, .	1.3	2
61	Non-native fold of the putative VPS39 zinc finger domain. <i>Wellcome Open Research</i> , 2020, 5, 154.	0.9	2
62	Crystallization of GcnA, an N-acetyl- β -D-glucosaminidase, from <i>Streptococcus gordonii</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2004, 60, 1910-1911.	2.5	1
63	Using selenomethionyl derivatives to assign sequence in low-resolution structures of the AP2 clathrin adaptor. <i>Acta Crystallographica Section D: Structural Biology</i> , 2016, 72, 336-345.	1.1	1
64	The lipid transfer protein Saposin B does not directly bind CD1d for lipid antigen loading. <i>Wellcome Open Research</i> , 2019, 4, 117.	0.9	1
65	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
66	SARS-CoV-2 Spike has broad tropism for mammalian ACE2 proteins yet exhibits a distinct pattern of receptor usage when compared to other β -coronavirus Spike proteins. <i>Access Microbiology</i> , 2022, 4, .	0.2	1
67	The SARS-CoV-2 Spike protein has a broad tropism for mammalian ACE2 proteins. , 2020, 18, e3001016.		0
68	The SARS-CoV-2 Spike protein has a broad tropism for mammalian ACE2 proteins. , 2020, 18, e3001016.		0
69	The SARS-CoV-2 Spike protein has a broad tropism for mammalian ACE2 proteins. , 2020, 18, e3001016.		0
70	The SARS-CoV-2 Spike protein has a broad tropism for mammalian ACE2 proteins. , 2020, 18, e3001016.		0
71	The SARS-CoV-2 Spike protein has a broad tropism for mammalian ACE2 proteins. , 2020, 18, e3001016.		0
72	The SARS-CoV-2 Spike protein has a broad tropism for mammalian ACE2 proteins. , 2020, 18, e3001016.		0