

Steve J Gamblin

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94
papers

16,310
citations

54
h-index

99
g-index

99
ext. papers

18,853
ext. citations

22.9
avg, IF

6.27
L-index

#	Paper	IF	Citations
94	The structural basis for 14-3-3:phosphopeptide binding specificity. <i>Cell</i> , 1997 , 91, 961-71	56.2	1348
93	A neutralizing antibody selected from plasma cells that binds to group 1 and group 2 influenza A hemagglutinins. <i>Science</i> , 2011 , 333, 850-6	33.3	891
92	Role of the polycomb protein EED in the propagation of repressive histone marks. <i>Nature</i> , 2009 , 461, 762-7	50.4	849
91	Structure and mechanism of DNA topoisomerase II. <i>Nature</i> , 1996 , 379, 225-32	50.4	723
90	The structure of H5N1 avian influenza neuraminidase suggests new opportunities for drug design. <i>Nature</i> , 2006 , 443, 45-9	50.4	648
89	Structure of mammalian AMPK and its regulation by ADP. <i>Nature</i> , 2011 , 472, 230-3	50.4	633
88	Regulation of p53 activity through lysine methylation. <i>Nature</i> , 2004 , 432, 353-60	50.4	620
87	Haemagglutinin mutations responsible for the binding of H5N1 influenza A viruses to human-type receptors. <i>Nature</i> , 2006 , 444, 378-82	50.4	491
86	Preexisting and de novo humoral immunity to SARS-CoV-2 in humans. <i>Science</i> , 2020 , 370, 1339-1343	33.3	441
85	Structural basis for AMP binding to mammalian AMP-activated protein kinase. <i>Nature</i> , 2007 , 449, 496-509	50.4	434
84	Structural analysis of 14-3-3 phosphopeptide complexes identifies a dual role for the nuclear export signal of 14-3-3 in ligand binding. <i>Molecular Cell</i> , 1999 , 4, 153-66	17.6	428
83	Crystal structures of oseltamivir-resistant influenza virus neuraminidase mutants. <i>Nature</i> , 2008 , 453, 1258-61	50.4	419
82	Structure of a 14-3-3 protein and implications for coordination of multiple signalling pathways. <i>Nature</i> , 1995 , 376, 188-91	50.4	402
81	Influenza hemagglutinin and neuraminidase membrane glycoproteins. <i>Journal of Biological Chemistry</i> , 2010 , 285, 28403-9	5.4	382
80	Structure at 1.65 Å of RhoA and its GTPase-activating protein in complex with a transition-state analogue. <i>Nature</i> , 1997 , 389, 758-62	50.4	376
79	Receptor binding and priming of the spike protein of SARS-CoV-2 for membrane fusion. <i>Nature</i> , 2020 , 588, 327-330	50.4	339
78	Structural basis of AMPK regulation by small molecule activators. <i>Nature Communications</i> , 2013 , 4, 3017	17.4	333

77	Structure and catalytic mechanism of the human histone methyltransferase SET7/9. <i>Nature</i> , 2003 , 421, 652-6	50.4	304
76	Neutralising antibody activity against SARS-CoV-2 VOCs B.1.617.2 and B.1.351 by BNT162b2 vaccination. <i>Lancet, The</i> , 2021 , 397, 2331-2333	40	293
75	AMP-activated protein kinase: nature's energy sensor. <i>Nature Chemical Biology</i> , 2011 , 7, 512-8	11.7	292
74	SARS-CoV-2 and bat RaTG13 spike glycoprotein structures inform on virus evolution and furin-cleavage effects. <i>Nature Structural and Molecular Biology</i> , 2020 , 27, 763-767	17.6	273
73	The structure of simian virus 40 refined at 3.1 Å resolution. <i>Structure</i> , 1996 , 4, 165-82	5.2	268
72	Structure of the TPR domain of p67phox in complex with Rac.GTP. <i>Molecular Cell</i> , 2000 , 6, 899-907	17.6	258
71	Structural basis of oncogenic histone H3K27M inhibition of human polycomb repressive complex 2. <i>Nature Communications</i> , 2016 , 7, 11316	17.4	245
70	Receptor binding by an H7N9 influenza virus from humans. <i>Nature</i> , 2013 , 499, 496-9	50.4	244
69	Crystal structure of a small G protein in complex with the GTPase-activating protein rhoGAP. <i>Nature</i> , 1997 , 388, 693-7	50.4	240
68	Structure and Function Analysis of an Antibody Recognizing All Influenza A Subtypes. <i>Cell</i> , 2016 , 166, 596-608	56.2	228
67	Structure of influenza hemagglutinin in complex with an inhibitor of membrane fusion. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008 , 105, 17736-41	11.5	220
66	Evolution of the receptor binding properties of the influenza A(H3N2) hemagglutinin. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012 , 109, 21474-9	11.5	194
65	Crystal structure and functional analysis of the histone methyltransferase SET7/9. <i>Cell</i> , 2002 , 111, 105-15	56.2	173
64	Jarid2 Methylation via the PRC2 Complex Regulates H3K27me3 Deposition during Cell Differentiation. <i>Molecular Cell</i> , 2015 , 57, 769-783	17.6	172
63	Receptor binding by a ferret-transmissible H5 avian influenza virus. <i>Nature</i> , 2013 , 497, 392-6	50.4	167
62	Pandemic peak SARS-CoV-2 infection and seroconversion rates in London frontline health-care workers. <i>Lancet, The</i> , 2020 , 396, e6-e7	40	144
61	Specificity and mechanism of the histone methyltransferase Pr-Set7. <i>Genes and Development</i> , 2005 , 19, 1444-54	12.6	144
60	Structures of receptor complexes formed by hemagglutinins from the Asian Influenza pandemic of 1957. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009 , 106, 17175-80	11.5	141

59	Specificity determinants of recruitment peptides bound to phospho-CDK2/cyclin A. <i>Biochemistry</i> , 2002 , 41, 15625-34	3.2	139
58	AMP-activated protein kinase: also regulated by ADP?. <i>Trends in Biochemical Sciences</i> , 2011 , 36, 470-7	10.3	132
57	SET domains and histone methylation. <i>Current Opinion in Structural Biology</i> , 2003 , 13, 699-705	8.1	128
56	ADP regulates SNF1, the <i>Saccharomyces cerevisiae</i> homolog of AMP-activated protein kinase. <i>Cell Metabolism</i> , 2011 , 14, 707-14	24.6	124
55	Structure of a ternary complex of an allosteric lactate dehydrogenase from <i>Bacillus stearothermophilus</i> at 2.5 Å resolution. <i>Journal of Molecular Biology</i> , 1992 , 223, 317-35	6.5	116
54	Antibiotic recognition by binuclear metallo-beta-lactamases revealed by X-ray crystallography. <i>Journal of the American Chemical Society</i> , 2005 , 127, 14439-44	16.4	107
53	The structure of the GTPase-activating domain from p50rhoGAP. <i>Nature</i> , 1997 , 385, 458-61	50.4	101
52	Activity and specificity of human aldolases. <i>Journal of Molecular Biology</i> , 1991 , 219, 573-6	6.5	95
51	Structure of the complex of calmodulin with the target sequence of calmodulin-dependent protein kinase I: studies of the kinase activation mechanism. <i>Biochemistry</i> , 2002 , 41, 14669-79	3.2	89
50	MgF(3)(-) as a transition state analog of phosphoryl transfer. <i>Chemistry and Biology</i> , 2002 , 9, 375-81		86
49	Phosphorylation of AMPK by upstream kinases is required for activity in mammalian cells. <i>Biochemical Journal</i> , 2017 , 474, 3059-3073	3.8	81
48	GTPase-activating proteins and their complexes. <i>Current Opinion in Structural Biology</i> , 1998 , 8, 195-201	8.1	72
47	The structure of a thermally stable 3-phosphoglycerate kinase and a comparison with its mesophilic equivalent. <i>Proteins: Structure, Function and Bioinformatics</i> , 1993 , 15, 283-9	4.2	68
46	Influenza hemagglutinin membrane anchor. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018 , 115, 10112-10117	11.5	61
45	H1N1 2009 pandemic influenza virus: resistance of the I223R neuraminidase mutant explained by kinetic and structural analysis. <i>PLoS Pathogens</i> , 2012 , 8, e1002914	7.6	60
44	Pre-existing and de novo humoral immunity to SARS-CoV-2 in humans		59
43	The effect of the D614G substitution on the structure of the spike glycoprotein of SARS-CoV-2. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021 , 118,	11.5	59
42	Receptor binding by H10 influenza viruses. <i>Nature</i> , 2014 , 511, 475-7	50.4	56

41	Reading, writing and editing methylated lysines on histone tails: new insights from recent structural studies. <i>Current Opinion in Structural Biology</i> , 2010 , 20, 730-8	8.1	54
40	Crystal structure of the transcription elongation/anti-termination factor NusA from <i>Mycobacterium tuberculosis</i> at 1.7 Å resolution. <i>Journal of Molecular Biology</i> , 2001 , 314, 1087-95	6.5	54
39	Tissue-specific and interferon-inducible expression of nonfunctional ACE2 through endogenous retroelement co-option. <i>Nature Genetics</i> , 2020 , 52, 1294-1302	36.3	54
38	AZD1222-induced neutralising antibody activity against SARS-CoV-2 Delta VOC. <i>Lancet, The</i> , 2021 , 398, 207-209	40	52
37	A human antibody recognizing a conserved epitope of H5 hemagglutinin broadly neutralizes highly pathogenic avian influenza H5N1 viruses. <i>Journal of Virology</i> , 2012 , 86, 2978-89	6.6	51
36	G-tract RNA removes Polycomb repressive complex 2 from genes. <i>Nature Structural and Molecular Biology</i> , 2019 , 26, 899-909	17.6	49
35	Evolving Catalytic Properties of the MLL Family SET Domain. <i>Structure</i> , 2015 , 23, 1921-1933	5.2	49
34	Comment on "The pentacovalent phosphorus intermediate of a phosphoryl transfer reaction". <i>Science</i> , 2003 , 301, 1184; author reply 1184	33.3	48
33	Recent evolution of equine influenza and the origin of canine influenza. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014 , 111, 11175-80	11.5	42
32	Crystal structure of the LasA virulence factor from <i>Pseudomonas aeruginosa</i> : substrate specificity and mechanism of M23 metallopeptidases. <i>Journal of Molecular Biology</i> , 2010 , 396, 908-23	6.5	42
31	Structures of complexes formed by H5 influenza hemagglutinin with a potent broadly neutralizing human monoclonal antibody. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015 , 112, 9430-5	11.5	34
30	Structural transitions in influenza haemagglutinin at membrane fusion pH. <i>Nature</i> , 2020 , 583, 150-153	50.4	32
29	Support for shared ancestry of GAPs. <i>Nature</i> , 1998 , 392, 448-9	50.4	29
28	Changes in the hemagglutinin of H5N1 viruses during human infection--influence on receptor binding. <i>Virology</i> , 2013 , 447, 326-37	3.6	27
27	Reduced antibody cross-reactivity following infection with B.1.1.7 than with parental SARS-CoV-2 strains. <i>ELife</i> , 2021 , 10,	8.9	26
26	Adaptive immunity and neutralizing antibodies against SARS-CoV-2 variants of concern following vaccination in patients with cancer: The CAPTURE study.. <i>Nature Cancer</i> , 2021 , 2, 1321-1337	15.4	24
25	Antibody-mediated disruption of the SARS-CoV-2 spike glycoprotein. <i>Nature Communications</i> , 2020 , 11, 5337	17.4	23
24	Structure and binding properties of Pangolin-CoV spike glycoprotein inform the evolution of SARS-CoV-2. <i>Nature Communications</i> , 2021 , 12, 837	17.4	23

23	A novel I221L substitution in neuraminidase confers high-level resistance to oseltamivir in influenza B viruses. <i>Journal of Infectious Diseases</i> , 2014 , 210, 1260-9	7	22
22	A knot or not a knot? SETting the record BstraightPon proteins. <i>Computational Biology and Chemistry</i> , 2003 , 27, 11-5	3.6	22
21	Scalable and robust SARS-CoV-2 testing in an academic center. <i>Nature Biotechnology</i> , 2020 , 38, 927-931	44.5	18
20	Enhanced human receptor binding by H5 haemagglutinins. <i>Virology</i> , 2014 , 456-457, 179-87	3.6	17
19	Functional antibody and T cell immunity following SARS-CoV-2 infection, including by variants of concern, in patients with cancer: the CAPTURE study.. <i>Nature Cancer</i> , 2021 , 2, 1321-1337	15.4	17
18	Hemagglutinin Traits Determine Transmission of Avian A/H10N7 Influenza Virus between Mammals. <i>Cell Host and Microbe</i> , 2020 , 28, 602-613.e7	23.4	11
17	Immune responses following third COVID-19 vaccination are reduced in patients with hematological malignancies compared to patients with solid cancer.. <i>Cancer Cell</i> , 2021 ,	24.3	10
16	Omicron neutralising antibodies after third COVID-19 vaccine dose in patients with cancer.. <i>Lancet, The</i> , 2022 ,	40	9
15	The structure of the RbBP5 Epropeller domain reveals a surface with potential nucleic acid binding sites. <i>Nucleic Acids Research</i> , 2018 , 46, 3802-3812	20.1	9
14	Hemagglutinin Structure and Activities. <i>Cold Spring Harbor Perspectives in Medicine</i> , 2021 , 11,	5.4	7
13	Nuclear transport: what a kary-on!. <i>Structure</i> , 1999 , 7, R199-204	5.2	7
12	6 Structure of SET domain protein lysine methyltransferases. <i>The Enzymes</i> , 2006 , 24, 155-78	2.3	5
11	Purification, crystallization and preliminary X-ray analysis of the 3-phosphoglycerate kinase from <i>Bacillus stearothermophilus</i> . <i>Journal of Molecular Biology</i> , 1992 , 227, 1263-4	6.5	5
10	Crystallization of a ternary complex of lactate dehydrogenase from <i>Bacillus stearothermophilus</i> . <i>Journal of Molecular Biology</i> , 1988 , 204, 1041-3	6.5	5
9	Heterologous humoral immunity to human and zoonotic coronaviruses: Aiming for the achilles heel. <i>Seminars in Immunology</i> , 2021 , 55, 101507	10.7	5
8	Reduced antibody cross-reactivity following infection with B.1.1.7 than with parental SARS-CoV-2 strains		5
7	Evolution of the SARS-CoV-2 spike protein in the human host.. <i>Nature Communications</i> , 2022 , 13, 1178	17.4	5
6	Influenza glycoproteins: Hemagglutinin and neuraminidase 2013 , 67-100		4

5	Structure and binding properties of Pangolin-CoV Spike glycoprotein inform the evolution of SARS-CoV-2.	2
4	Adaptive immunity to SARS-CoV-2 in cancer patients: The CAPTURE study	2
3	The effects of cryoprotectant on crystal stability. <i>Journal of Crystal Growth</i> , 1996 , 168, 244-247	1.6 1
2	Broad human and animal coronavirus neutralisation by SARS-CoV-2 S2-targeted vaccination	1
1	Favorable antibody responses to human coronaviruses in children and adolescents with autoimmune rheumatic diseases. <i>Med</i> , 2021 , 2, 1093-1109.e6	31.7 1