Steve J Gamblin

List of Publications by Year
in descending order

90 papers	20,591 citations	23567 58 h-index	45317 90 g-index
99 all docs	99 docs citations	99 times ranked	28414 citing authors

#	Article	IF	Citations
1	Omicron neutralising antibodies after third COVID-19 vaccine dose in patients with cancer. Lancet, The, 2022, 399, 905-907.	13.7	60
2	Immune responses following third COVID-19 vaccination are reduced in patients with hematological malignancies compared to patients with solid cancer. Cancer Cell, 2022, 40, 114-116.	16.8	50
3	Evolution of the SARS-CoV-2 spike protein in the human host. Nature Communications, 2022, 13, 1178.	12.8	44
4	Hemagglutinin Structure and Activities. Cold Spring Harbor Perspectives in Medicine, 2021, 11, a038638.	6.2	23
5	Structure and binding properties of Pangolin-CoV spike glycoprotein inform the evolution of SARS-CoV-2. Nature Communications, 2021, 12, 837.	12.8	55
6	The effect of the D614G substitution on the structure of the spike glycoprotein of SARS-CoV-2. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	7.1	131
7	Neutralising antibody activity against SARS-CoV-2 VOCs B.1.617.2 and B.1.351 by BNT162b2 vaccination. Lancet, The, 2021, 397, 2331-2333.	13.7	490
8	Reduced antibody cross-reactivity following infection with B.1.1.7 than with parental SARS-CoV-2 strains. ELife, 2021, 10, .	6.0	42
9	AZD1222-induced neutralising antibody activity against SARS-CoV-2 Delta VOC. Lancet, The, 2021, 398, 207-209.	13.7	112
10	Favorable antibody responses to human coronaviruses in children and adolescents with autoimmune rheumatic diseases. Med, 2021, 2, 1093-1109.e6.	4.4	6
11	Heterologous humoral immunity to human and zoonotic coronaviruses: Aiming for the achilles heel. Seminars in Immunology, 2021, 55, 101507.	5.6	16
12	Functional antibody and T cell immunity following SARS-CoV-2 infection, including by variants of concern, in patients with cancer: the CAPTURE study. Nature Cancer, 2021, 2, 1321-1337.	13.2	66
13	Adaptive immunity and neutralizing antibodies against SARS-CoV-2 variants of concern following vaccination in patients with cancer: the CAPTURE study. Nature Cancer, 2021, 2, 1305-1320.	13.2	123
14	Tissue-specific and interferon-inducible expression of nonfunctional ACE2 through endogenous retroelement co-option. Nature Genetics, 2020, 52, 1294-1302.	21.4	82
15	Hemagglutinin Traits Determine Transmission of Avian A/H10N7 Influenza Virus between Mammals. Cell Host and Microbe, 2020, 28, 602-613.e7.	11.0	20
16	Receptor binding and priming of the spike protein of SARS-CoV-2 for membrane fusion. Nature, 2020, 588, 327-330.	27.8	684
17	Antibody-mediated disruption of the SARS-CoV-2 spike glycoprotein. Nature Communications, 2020, 11, 5337.	12.8	43
18	Preexisting and de novo humoral immunity to SARS-CoV-2 in humans. Science, 2020, 370, 1339-1343.	12.6	735

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19	Structural transitions in influenza haemagglutinin at membrane fusionÂpH. Nature, 2020, 583, 150-153.	27.8	87
20	Scalable and robust SARS-CoV-2 testing in an academic center. Nature Biotechnology, 2020, 38, 927-931.	17.5	32
21	SARS-CoV-2 and bat RaTG13 spike glycoprotein structures inform on virus evolution and furin-cleavage effects. Nature Structural and Molecular Biology, 2020, 27, 763-767.	8.2	471
22	Pandemic peak SARS-CoV-2 infection and seroconversion rates in London frontline health-care workers. Lancet, The, 2020, 396, e6-e7.	13.7	196
23	A key to unlocking chromatin revealed by complex structures. Nature, 2019, 573, 355-356.	27.8	3
24	G-tract RNA removes Polycomb repressive complex 2 from genes. Nature Structural and Molecular Biology, 2019, 26, 899-909.	8.2	86
25	Influenza hemagglutinin membrane anchor. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 10112-10117.	7.1	115
26	The structure of the RbBP5 Î²-propeller domain reveals a surface with potential nucleic acid binding sites. Nucleic Acids Research, 2018, 46, 3802-3812.	14.5	11
27	Phosphorylation of AMPK by upstream kinases is required for activity in mammalian cells. Biochemical Journal, 2017, 474, 3059-3073.	3.7	117
28	Structure and Function Analysis of an Antibody Recognizing All Influenza A Subtypes. Cell, 2016, 166, 596-608.	28.9	320
29	Structural basis of oncogenic histone H3K27M inhibition of human polycomb repressive complex 2. Nature Communications, 2016, 7, 11316.	12.8	326
30	Evolving Catalytic Properties of the MLL Family SET Domain. Structure, 2015, 23, 1921-1933.	3.3	67
31	Jarid2 Methylation via the PRC2 Complex Regulates H3K27me3 Deposition during Cell Differentiation. Molecular Cell, 2015, 57, 769-783.	9.7	229
32	Structures of complexes formed by H5 influenza hemagglutinin with a potent broadly neutralizing human monoclonal antibody. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 9430-9435.	7.1	38
33	Recent evolution of equine influenza and the origin of canine influenza. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 11175-11180.	7.1	54
34	A Novel I221L Substitution in Neuraminidase Confers High-Level Resistance to Oseltamivir in Influenza B Viruses. Journal of Infectious Diseases, 2014, 210, 1260-1269.	4.0	26
35	Enhanced human receptor binding by H5 haemagglutinins. Virology, 2014, 456-457, 179-187.	2.4	22
36	Receptor binding by H10 influenza viruses. Nature, 2014, 511, 475-477.	27.8	69

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37	Changes in the hemagglutinin of H5N1 viruses during human infection â€“ Influence on receptor binding. Virology, 2013, 447, 326-337.	2.4	34
38	Receptor binding by a ferret-transmissible H5 avian influenza virus. Nature, 2013, 497, 392-396.	27.8	194
39	Receptor binding by an H7N9 influenza virus from humans. Nature, 2013, 499, 496-499.	27.8	284
40	Structural basis of AMPK regulation by small molecule activators. Nature Communications, 2013, 4, 3017.	12.8	432
41	H1N1 2009 Pandemic Influenza Virus: Resistance of the I223R Neuraminidase Mutant Explained by Kinetic and Structural Analysis. PLoS Pathogens, 2012, 8, e1002914.	4.7	72
42	Evolution of the receptor binding properties of the influenza A(H3N2) hemagglutinin. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 21474-21479.	7.1	250
43	A Human Antibody Recognizing a Conserved Epitope of H5 Hemagglutinin Broadly Neutralizes Highly Pathogenic Avian Influenza H5N1 Viruses. Journal of Virology, 2012, 86, 2978-2989.	3.4	60
44	ADP Regulates SNF1, the Saccharomyces cerevisiae Homolog of AMP-Activated Protein Kinase. Cell Metabolism, 2011, 14, 707-714.	16.2	146
45	Structure of mammalian AMPK and its regulation by ADP. Nature, 2011, 472, 230-233.	27.8	761
46	AMP-activated protein kinase: also regulated by ADP?. Trends in Biochemical Sciences, 2011, 36, 470-477.	7.5	153
47	A Neutralizing Antibody Selected from Plasma Cells That Binds to Group 1 and Group 2 Influenza A Hemagglutinins. Science, 2011, 333, 850-856.	12.6	1,092
48	AMP-activated protein kinase: nature's energy sensor. Nature Chemical Biology, 2011, 7, 512-518.	8.0	350
49	Reading, writing and editing methylated lysines on histone tails: new insights from recent structural studies. Current Opinion in Structural Biology, 2010, 20, 730-738.	5.7	61
50	Influenza Hemagglutinin and Neuraminidase Membrane Glycoproteins. Journal of Biological Chemistry, 2010, 285, 28403-28409.	3.4	491
51	Crystal Structure of the LasA Virulence Factor from Pseudomonas aeruginosa: Substrate Specificity and Mechanism of M23 Metallopeptidases. Journal of Molecular Biology, 2010, 396, 908-923.	4.2	58
52	Structures of receptor complexes formed by hemagglutinins from the Asian Influenza pandemic of 1957. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 17175-17180.	7.1	159
53	Role of the polycomb protein EED in the propagation of repressive histone marks. Nature, 2009, 461, 762-767.	27.8	1,018
54	Crystal structures of oseltamivir-resistant influenza virus neuraminidase mutants. Nature, 2008, 453, 1258-1261.	27.8	475

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55	Structure of influenza hemagglutinin in complex with an inhibitor of membrane fusion. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 17736-17741.	7.1	273
56	Structural basis for AMP binding to mammalian AMP-activated protein kinase. Nature, 2007, 449, 496-500.	27.8	498
57	6 Structure of SET domain protein lysine methyltransferases. The Enzymes, 2006, 24, 155-178.	1.7	5
58	The structure of H5N1 avian influenza neuraminidase suggests new opportunities for drug design. Nature, 2006, 443, 45-49.	27.8	735
59	Haemagglutinin mutations responsible for the binding of H5N1 influenza A viruses to human-type receptors. Nature, 2006, 444, 378-382.	27.8	594
60	Specificity and mechanism of the histone methyltransferase Pr-Set7. Genes and Development, 2005, 19, 1444-1454.	5.9	159
61	Antibiotic Recognition by Binuclear Metallo-Î²-Lactamases Revealed by X-ray Crystallography#. Journal of the American Chemical Society, 2005, 127, 14439-14444.	13.7	123
62	Regulation of p53 activity through lysine methylation. Nature, 2004, 432, 353-360.	27.8	706
63	SET domains and histone methylation. Current Opinion in Structural Biology, 2003, 13, 699-705.	5.7	144
64	A knot or not a knot? SETting the record â€˜straightâ€™ on proteins. Computational Biology and Chemistry, 2003, 27, 11-15.	2.3	28
65	Structure and catalytic mechanism of the human histone methyltransferase SET7/9. Nature, 2003, 421, 652-656.	27.8	346
66	Comment on "The Pentacovalent Phosphorus Intermediate of a Phosphoryl Transfer Reaction". Science, 2003, 301, 1184c-1184.	12.6	50
67	Structure of the Complex of Calmodulin with the Target Sequence of Calmodulin-Dependent Protein Kinase I:Â Studies of the Kinase Activation Mechanismâ€¡. Biochemistry, 2002, 41, 14669-14679.	2.5	100
68	Crystal Structure and Functional Analysis of the Histone Methyltransferase SET7/9. Cell, 2002, 111, 105-115.	28.9	198
69	MgF3â^' as a Transition State Analog of Phosphoryl Transfer. Chemistry and Biology, 2002, 9, 375-381.	6.0	97
70	Specificity Determinants of Recruitment Peptides Bound to Phospho-CDK2/Cyclin Aâ€‚â€¡. Biochemistry, 2002, 41, 15625-15634.	2.5	152
71	Crystal structure of the transcription elongation/anti-termination factor NusA from Mycobacterium tuberculosis at 1.7 Ã... resolution. Journal of Molecular Biology, 2001, 314, 1087-1095.	4.2	57
72	Structure of the TPR Domain of p67phox in Complex with RacÂ·GTP. Molecular Cell, 2000, 6, 899-907.	9.7	295

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73	Nuclear transport: what a kary-on!. Structure, 1999, 7, R199-R204.	3.3	7
74	Structural Analysis of 14-3-3 Phosphopeptide Complexes Identifies a Dual Role for the Nuclear Export Signal of 14-3-3 in Ligand Binding. Molecular Cell, 1999, 4, 153-166.	9.7	467
75	Support for shared ancestry of GAPs. Nature, 1998, 392, 448-448.	27.8	32
76	GTPase-activating proteins and their complexes. Current Opinion in Structural Biology, 1998, 8, 195-201.	5.7	78
77	The Structural Basis for 14-3-3:Phosphopeptide Binding Specificity. Cell, 1997, 91, 961-971.	28.9	1,509
78	The structure of the GTPase-activating domain from p50rhoGAP. Nature, 1997, 385, 458-461.	27.8	121
79	Structure at 1.65â€‰Ã... of RhoA and its GTPase-activating protein in complex with a transition-state analogue. Nature, 1997, 389, 758-762.	27.8	420
80	Crystal structure of a small G protein in complex with the GTPase-activating protein rhoGAP. Nature, 1997, 388, 693-697.	27.8	264
81	The structure of simian virus 40 refined at 3.1 Ã¥ resolution. Structure, 1996, 4, 165-182.	3.3	291
82	The effects of cryoprotectant on crystal stability. Journal of Crystal Growth, 1996, 168, 244-247.	1.5	1
83	Structure and mechanism of DNA topoisomerase II. Nature, 1996, 379, 225-232.	27.8	813
84	Structure of a 14-3-3 protein and implications for coordination of multiple signalling pathways. Nature, 1995, 376, 188-191.	27.8	444
85	The structure of a thermally stable 3-phosphoglycerate kinase and a comparison with its mesophilic equivalent. Proteins: Structure, Function and Bioinformatics, 1993, 15, 283-289.	2.6	73
86	Purification, crystallization and preliminary X-ray analysis of the 3-phosphoglycerate kinase from Bacillus stearothermophilus. Journal of Molecular Biology, 1992, 227, 1263-1264.	4.2	6
87	Structure of a ternary complex of an allosteric lactate dehydrogenase from Bacillus stearothermophilus at 2Â·5 Ã... resolution. Journal of Molecular Biology, 1992, 223, 317-335.	4.2	137
88	Activity and specificity of human aldolases. Journal of Molecular Biology, 1991, 219, 573-576.	4.2	111
89	Crystallization of a ternary complex of lactate dehydrogenase from Bacillus stearothermophilus. Journal of Molecular Biology, 1988, 204, 1041-1043.	4.2	6
90	Hemagglutinin Traits Determine Transmission of Avian A/H10N7 Virus between Mammals. SSRN Electronic Journal, 0, , .	0.4	0