

Steve J Gamblin

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/158626/publications.pdf>

Version: 2024-02-01

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	The Structural Basis for 14-3-3:Phosphopeptide Binding Specificity. <i>Cell</i> , 1997, 91, 961-971.	28.9	1,509
2	A Neutralizing Antibody Selected from Plasma Cells That Binds to Group 1 and Group 2 Influenza A Hemagglutinins. <i>Science</i> , 2011, 333, 850-856.	12.6	1,092
3	Role of the polycomb protein EED in the propagation of repressive histone marks. <i>Nature</i> , 2009, 461, 762-767.	27.8	1,018
4	Structure and mechanism of DNA topoisomerase II. <i>Nature</i> , 1996, 379, 225-232.	27.8	813
5	Structure of mammalian AMPK and its regulation by ADP. <i>Nature</i> , 2011, 472, 230-233.	27.8	761
6	The structure of H5N1 avian influenza neuraminidase suggests new opportunities for drug design. <i>Nature</i> , 2006, 443, 45-49.	27.8	735
7	Preexisting and de novo humoral immunity to SARS-CoV-2 in humans. <i>Science</i> , 2020, 370, 1339-1343.	12.6	735
8	Regulation of p53 activity through lysine methylation. <i>Nature</i> , 2004, 432, 353-360.	27.8	706
9	Receptor binding and priming of the spike protein of SARS-CoV-2 for membrane fusion. <i>Nature</i> , 2020, 588, 327-330.	27.8	684
10	Haemagglutinin mutations responsible for the binding of H5N1 influenza A viruses to human-type receptors. <i>Nature</i> , 2006, 444, 378-382.	27.8	594
11	Structural basis for AMP binding to mammalian AMP-activated protein kinase. <i>Nature</i> , 2007, 449, 496-500.	27.8	498
12	Influenza Hemagglutinin and Neuraminidase Membrane Glycoproteins. <i>Journal of Biological Chemistry</i> , 2010, 285, 28403-28409.	3.4	491
13	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.	13.7	490
14	Crystal structures of oseltamivir-resistant influenza virus neuraminidase mutants. <i>Nature</i> , 2008, 453, 1258-1261.	27.8	475
15	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.	8.2	471
16	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, 153-166.	9.7	467
17	Structure of a 14-3-3 protein and implications for coordination of multiple signalling pathways. <i>Nature</i> , 1995, 376, 188-191.	27.8	444
18	Structural basis of AMPK regulation by small molecule activators. <i>Nature Communications</i> , 2013, 4, 3017.	12.8	432

#	ARTICLE	IF	CITATIONS
19	Structure at 1.65Å of RhoA and its GTPase-activating protein in complex with a transition-state analogue. <i>Nature</i> , 1997, 389, 758-762.	27.8	420
20	AMP-activated protein kinase: nature's energy sensor. <i>Nature Chemical Biology</i> , 2011, 7, 512-518.	8.0	350
21	Structure and catalytic mechanism of the human histone methyltransferase SET7/9. <i>Nature</i> , 2003, 421, 652-656.	27.8	346
22	Structural basis of oncogenic histone H3K27M inhibition of human polycomb repressive complex 2. <i>Nature Communications</i> , 2016, 7, 11316.	12.8	326
23	Structure and Function Analysis of an Antibody Recognizing All Influenza A Subtypes. <i>Cell</i> , 2016, 166, 596-608.	28.9	320
24	Structure of the TPR Domain of p67phox in Complex with Rac-GTP. <i>Molecular Cell</i> , 2000, 6, 899-907.	9.7	295
25	The structure of simian virus 40 refined at 3.1 Å resolution. <i>Structure</i> , 1996, 4, 165-182.	3.3	291
26	Receptor binding by an H7N9 influenza virus from humans. <i>Nature</i> , 2013, 499, 496-499.	27.8	284
27	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, 17736-17741.	7.1	273
28	Crystal structure of a small G protein in complex with the GTPase-activating protein rhoGAP. <i>Nature</i> , 1997, 388, 693-697.	27.8	264
29	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, 21474-21479.	7.1	250
30	Jarid2 Methylation via the PRC2 Complex Regulates H3K27me3 Deposition during Cell Differentiation. <i>Molecular Cell</i> , 2015, 57, 769-783.	9.7	229
31	Crystal Structure and Functional Analysis of the Histone Methyltransferase SET7/9. <i>Cell</i> , 2002, 111, 105-115.	28.9	198
32	Pandemic peak SARS-CoV-2 infection and seroconversion rates in London frontline health-care workers. <i>Lancet</i> , The, 2020, 396, e6-e7.	13.7	196
33	Receptor binding by a ferret-transmissible H5 avian influenza virus. <i>Nature</i> , 2013, 497, 392-396.	27.8	194
34	Specificity and mechanism of the histone methyltransferase Pr-Set7. <i>Genes and Development</i> , 2005, 19, 1444-1454.	5.9	159
35	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, 17175-17180.	7.1	159
36	AMP-activated protein kinase: also regulated by ADP?. <i>Trends in Biochemical Sciences</i> , 2011, 36, 470-477.	7.5	153

#	ARTICLE	IF	CITATIONS
37	Specificity Determinants of Recruitment Peptides Bound to Phospho-CDK2/Cyclin A. <i>Biochemistry</i> , 2002, 41, 15625-15634.	2.5	152
38	ADP Regulates SNF1, the <i>Saccharomyces cerevisiae</i> Homolog of AMP-Activated Protein Kinase. <i>Cell Metabolism</i> , 2011, 14, 707-714.	16.2	146
39	SET domains and histone methylation. <i>Current Opinion in Structural Biology</i> , 2003, 13, 699-705.	5.7	144
40	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, 317-335.	4.2	137
41	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, .	7.1	131
42	Antibiotic Recognition by Binuclear Metallo-β-Lactamases Revealed by X-ray Crystallography#. <i>Journal of the American Chemical Society</i> , 2005, 127, 14439-14444.	13.7	123
43	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, 1305-1320.	13.2	123
44	The structure of the GTPase-activating domain from p50rhoGAP. <i>Nature</i> , 1997, 385, 458-461.	27.8	121
45	Phosphorylation of AMPK by upstream kinases is required for activity in mammalian cells. <i>Biochemical Journal</i> , 2017, 474, 3059-3073.	3.7	117
46	Influenza hemagglutinin membrane anchor. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 10112-10117.	7.1	115
47	AZD1222-induced neutralising antibody activity against SARS-CoV-2 Delta VOC. <i>Lancet, The</i> , 2021, 398, 207-209.	13.7	112
48	Activity and specificity of human aldolases. <i>Journal of Molecular Biology</i> , 1991, 219, 573-576.	4.2	111
49	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, 14669-14679.	2.5	100
50	MgF3 ²⁻ as a Transition State Analog of Phosphoryl Transfer. <i>Chemistry and Biology</i> , 2002, 9, 375-381.	6.0	97
51	Structural transitions in influenza haemagglutinin at membrane fusion pH. <i>Nature</i> , 2020, 583, 150-153.	27.8	87
52	G-tract RNA removes Polycomb repressive complex 2 from genes. <i>Nature Structural and Molecular Biology</i> , 2019, 26, 899-909.	8.2	86
53	Tissue-specific and interferon-inducible expression of nonfunctional ACE2 through endogenous retroelement co-option. <i>Nature Genetics</i> , 2020, 52, 1294-1302.	21.4	82
54	GTPase-activating proteins and their complexes. <i>Current Opinion in Structural Biology</i> , 1998, 8, 195-201.	5.7	78

#	ARTICLE	IF	CITATIONS
55	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, 283-289.	2.6	73
56	H1N1 2009 Pandemic Influenza Virus: Resistance of the I223R Neuraminidase Mutant Explained by Kinetic and Structural Analysis. <i>PLoS Pathogens</i> , 2012, 8, e1002914.	4.7	72
57	Receptor binding by H10 influenza viruses. <i>Nature</i> , 2014, 511, 475-477.	27.8	69
58	Evolving Catalytic Properties of the MLL Family SET Domain. <i>Structure</i> , 2015, 23, 1921-1933.	3.3	67
59	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.	13.2	66
60	Reading, writing and editing methylated lysines on histone tails: new insights from recent structural studies. <i>Current Opinion in Structural Biology</i> , 2010, 20, 730-738.	5.7	61
61	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, 2978-2989.	3.4	60
62	Omicron neutralising antibodies after third COVID-19 vaccine dose in patients with cancer. <i>Lancet, The</i> , 2022, 399, 905-907.	13.7	60
63	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, 908-923.	4.2	58
64	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, 1087-1095.	4.2	57
65	Structure and binding properties of Pangolin-CoV spike glycoprotein inform the evolution of SARS-CoV-2. <i>Nature Communications</i> , 2021, 12, 837.	12.8	55
66	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, 11175-11180.	7.1	54
67	Comment on "The Pentacovalent Phosphorus Intermediate of a Phosphoryl Transfer Reaction". <i>Science</i> , 2003, 301, 1184c-1184.	12.6	50
68	Immune responses following third COVID-19 vaccination are reduced in patients with hematological malignancies compared to patients with solid cancer. <i>Cancer Cell</i> , 2022, 40, 114-116.	16.8	50
69	Evolution of the SARS-CoV-2 spike protein in the human host. <i>Nature Communications</i> , 2022, 13, 1178.	12.8	44
70	Antibody-mediated disruption of the SARS-CoV-2 spike glycoprotein. <i>Nature Communications</i> , 2020, 11, 5337.	12.8	43
71	Reduced antibody cross-reactivity following infection with B.1.1.7 than with parental SARS-CoV-2 strains. <i>ELife</i> , 2021, 10, .	6.0	42
72	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, 9430-9435.	7.1	38

#	ARTICLE	IF	CITATIONS
73	Changes in the hemagglutinin of H5N1 viruses during human infection – Influence on receptor binding. <i>Virology</i> , 2013, 447, 326-337.	2.4	34
74	Support for shared ancestry of GAPs. <i>Nature</i> , 1998, 392, 448-448.	27.8	32
75	Scalable and robust SARS-CoV-2 testing in an academic center. <i>Nature Biotechnology</i> , 2020, 38, 927-931.	17.5	32
76	A knot or not a knot? SETting the record –straight–™ on proteins. <i>Computational Biology and Chemistry</i> , 2003, 27, 11-15.	2.3	28
77	A Novel I221L Substitution in Neuraminidase Confers High-Level Resistance to Oseltamivir in Influenza B Viruses. <i>Journal of Infectious Diseases</i> , 2014, 210, 1260-1269.	4.0	26
78	Hemagglutinin Structure and Activities. <i>Cold Spring Harbor Perspectives in Medicine</i> , 2021, 11, a038638.	6.2	23
79	Enhanced human receptor binding by H5 haemagglutinins. <i>Virology</i> , 2014, 456-457, 179-187.	2.4	22
80	Hemagglutinin Traits Determine Transmission of Avian A/H10N7 Influenza Virus between Mammals. <i>Cell Host and Microbe</i> , 2020, 28, 602-613.e7.	11.0	20
81	Heterologous humoral immunity to human and zoonotic coronaviruses: Aiming for the achilles heel. <i>Seminars in Immunology</i> , 2021, 55, 101507.	5.6	16
82	The structure of the RbBP5 β -propeller domain reveals a surface with potential nucleic acid binding sites. <i>Nucleic Acids Research</i> , 2018, 46, 3802-3812.	14.5	11
83	Nuclear transport: what a kary-on!. <i>Structure</i> , 1999, 7, R199-R204.	3.3	7
84	Crystallization of a ternary complex of lactate dehydrogenase from <i>Bacillus stearothermophilus</i> . <i>Journal of Molecular Biology</i> , 1988, 204, 1041-1043.	4.2	6
85	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, 1263-1264.	4.2	6
86	Favorable antibody responses to human coronaviruses in children and adolescents with autoimmune rheumatic diseases. <i>Med</i> , 2021, 2, 1093-1109.e6.	4.4	6
87	6 Structure of SET domain protein lysine methyltransferases. <i>The Enzymes</i> , 2006, 24, 155-178.	1.7	5
88	A key to unlocking chromatin revealed by complex structures. <i>Nature</i> , 2019, 573, 355-356.	27.8	3
89	The effects of cryoprotectant on crystal stability. <i>Journal of Crystal Growth</i> , 1996, 168, 244-247.	1.5	1
90	Hemagglutinin Traits Determine Transmission of Avian A/H10N7 Virus between Mammals. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0