

Robyn L Stanfield

List of Publications by Citations

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

66

papers

5,360

citations

31

h-index

67

g-index

67

ext. papers

6,268

ext. citations

13.6

avg, IF

5.2

L-index

#	Paper	IF	Citations
66	Crystal structure of a soluble cleaved HIV-1 envelope trimer. <i>Science</i> , 2013 , 342, 1477-83	33.3	687
65	A potent and broad neutralizing antibody recognizes and penetrates the HIV glycan shield. <i>Science</i> , 2011 , 334, 1097-103	33.3	576
64	Broadly neutralizing anti-HIV antibody 4E10 recognizes a helical conformation of a highly conserved fusion-associated motif in gp41. <i>Immunity</i> , 2005 , 22, 163-73	32.3	379
63	Hepatitis C virus E2 envelope glycoprotein core structure. <i>Science</i> , 2013 , 342, 1090-4	33.3	300
62	Supersite of immune vulnerability on the glycosylated face of HIV-1 envelope glycoprotein gp120. <i>Nature Structural and Molecular Biology</i> , 2013 , 20, 796-803	17.6	274
61	Crystal structure of a shark single-domain antibody V region in complex with lysozyme. <i>Science</i> , 2004 , 305, 1770-3	33.3	235
60	HIV Vaccine Design to Target Germline Precursors of Glycan-Dependent Broadly Neutralizing Antibodies. <i>Immunity</i> , 2016 , 45, 483-496	32.3	232
59	Contrasting IgG structures reveal extreme asymmetry and flexibility. <i>Journal of Molecular Biology</i> , 2002 , 319, 9-18	6.5	209
58	Antibody elbow angles are influenced by their light chain class. <i>Journal of Molecular Biology</i> , 2006 , 357, 1566-74	6.5	185
57	Structural rationale for the broad neutralization of HIV-1 by human monoclonal antibody 447-52D. <i>Structure</i> , 2004 , 12, 193-204	5.2	174
56	Affinity Maturation of a Potent Family of HIV Antibodies Is Primarily Focused on Accommodating or Avoiding Glycans. <i>Immunity</i> , 2015 , 43, 1053-63	32.3	170
55	Open and closed structures reveal allostery and pliability in the HIV-1 envelope spike. <i>Nature</i> , 2017 , 547, 360-363	50.4	155
54	Receptor mimicry by antibody F045-092 facilitates universal binding to the H3 subtype of influenza virus. <i>Nature Communications</i> , 2014 , 5, 3614	17.4	130
53	Crystal structures of human immunodeficiency virus type 1 (HIV-1) neutralizing antibody 2219 in complex with three different V3 peptides reveal a new binding mode for HIV-1 cross-reactivity. <i>Journal of Virology</i> , 2006 , 80, 6093-105	6.6	111
52	Murine Antibody Responses to Cleaved Soluble HIV-1 Envelope Trimers Are Highly Restricted in Specificity. <i>Journal of Virology</i> , 2015 , 89, 10383-98	6.6	105
51	Design and crystal structure of a native-like HIV-1 envelope trimer that engages multiple broadly neutralizing antibody precursors in vivo. <i>Journal of Experimental Medicine</i> , 2017 , 214, 2573-2590	16.6	100
50	Rapid elicitation of broadly neutralizing antibodies to HIV by immunization in cows. <i>Nature</i> , 2017 , 548, 108-111	50.4	99

49	Maturation of shark single-domain (IgNAR) antibodies: evidence for induced-fit binding. <i>Journal of Molecular Biology</i> , 2007 , 367, 358-72	6.5	97
48	A conformational switch in human immunodeficiency virus gp41 revealed by the structures of overlapping epitopes recognized by neutralizing antibodies. <i>Journal of Virology</i> , 2009 , 83, 8451-62	6.6	85
47	Structural analysis, selection, and ontogeny of the shark new antigen receptor (IgNAR): identification of a new locus preferentially expressed in early development. <i>Immunogenetics</i> , 2002 , 54, 501-12	3.2	81
46	First molecular and biochemical analysis of in vivo affinity maturation in an ectothermic vertebrate. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006 , 103, 1846-51	11.5	75
45	Crystallographic Identification of Lipid as an Integral Component of the Epitope of HIV Broadly Neutralizing Antibody 4E10. <i>Immunity</i> , 2016 , 44, 21-31	32.3	67
44	Glycine Substitution at Helix-to-Coil Transitions Facilitates the Structural Determination of a Stabilized Subtype C HIV Envelope Glycoprotein. <i>Immunity</i> , 2017 , 46, 792-803.e3	32.3	59
43	Complete epitopes for vaccine design derived from a crystal structure of the broadly neutralizing antibodies PGT128 and 8ANC195 in complex with an HIV-1 Env trimer. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2015 , 71, 2099-108		54
42	Structure of 2G12 Fab2 in complex with soluble and fully glycosylated HIV-1 Env by negative-stain single-particle electron microscopy. <i>Journal of Virology</i> , 2014 , 88, 10177-88	6.6	53
41	Recurring conformation of the human immunodeficiency virus type 1 gp120 V3 loop. <i>Virology</i> , 2003 , 315, 159-73	3.6	46
40	Lipid interactions and angle of approach to the HIV-1 viral membrane of broadly neutralizing antibody 10E8: Insights for vaccine and therapeutic design. <i>PLoS Pathogens</i> , 2017 , 13, e1006212	7.6	42
39	Cofactor-Mediated Conformational Dynamics Promote Product Release From Escherichia coli Dihydrofolate Reductase via an Allosteric Pathway. <i>Journal of the American Chemical Society</i> , 2015 , 137, 9459-68	16.4	37
38	Conservation and diversity in the ultralong third heavy-chain complementarity-determining region of bovine antibodies. <i>Science Immunology</i> , 2016 , 1,	28	34
37	Role of the CBP catalytic core in intramolecular SUMOylation and control of histone H3 acetylation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017 , 114, E5335-E5342	11.5	33
36	Structure of Hepatitis C Virus Envelope Glycoprotein E1 Antigenic Site 314-324 in Complex with Antibody IGH526. <i>Journal of Molecular Biology</i> , 2015 , 427, 2617-28	6.5	32
35	Detect, correct, retract: How to manage incorrect structural models. <i>FEBS Journal</i> , 2018 , 285, 444-466	5.7	31
34	Stabilization of amyloidogenic immunoglobulin light chains by small molecules. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019 , 116, 8360-8369	11.5	30
33	Structure of a cleavage-independent HIV Env recapitulates the glycoprotein architecture of the native cleaved trimer. <i>Nature Communications</i> , 2018 , 9, 1956	17.4	28
32	Selection of nanobodies with broad neutralizing potential against primary HIV-1 strains using soluble subtype C gp140 envelope trimers. <i>Scientific Reports</i> , 2017 , 7, 8390	4.9	27

31	Crystal structure of the HIV neutralizing antibody 2G12 in complex with a bacterial oligosaccharide analog of mammalian oligomannose. <i>Glycobiology</i> , 2015 , 25, 412-9	5.8	23
30	X-Ray Crystallographic Studies of Antibody-Peptide Complexes. <i>ImmunoMethods</i> , 1993 , 3, 211-221		21
29	The Unusual Genetics and Biochemistry of Bovine Immunoglobulins. <i>Advances in Immunology</i> , 2018 , 137, 135-164	5.6	20
28	Defining the Structural Basis for Allosteric Product Release from E. coli Dihydrofolate Reductase Using NMR Relaxation Dispersion. <i>Journal of the American Chemical Society</i> , 2017 , 139, 11233-11240	16.4	19
27	Oligomannose Glycopeptide Conjugates Elicit Antibodies Targeting the Glycan Core Rather than Its Extremities. <i>ACS Central Science</i> , 2019 , 5, 237-249	16.8	18
26	Structure-based design of a protein immunogen that displays an HIV-1 gp41 neutralizing epitope. <i>Journal of Molecular Biology</i> , 2011 , 414, 460-76	6.5	17
25	Structural Basis of Pan-Ebolavirus Neutralization by an Antibody Targeting the Glycoprotein Fusion Loop. <i>Cell Reports</i> , 2018 , 24, 2723-2732.e4	10.6	17
24	Nucleotide insertions and deletions complement point mutations to massively expand the diversity created by somatic hypermutation of antibodies. <i>Journal of Biological Chemistry</i> , 2014 , 289, 33557-67	5.4	16
23	Structural basis of broad HIV neutralization by a vaccine-induced cow antibody. <i>Science Advances</i> , 2020 , 6, eaba0468	14.3	14
22	Antibody Structure. <i>Microbiology Spectrum</i> , 2014 , 2,	8.9	14
21	Crystallization, sequence, and preliminary crystallographic data for an antipeptide Fab 50.1 and peptide complexes with the principal neutralizing determinant of HIV-1 gp120. <i>Proteins: Structure, Function and Bioinformatics</i> , 1992 , 14, 499-508	4.2	14
20	Structural Insights into the Lipid A Transport Pathway in MsbA. <i>Structure</i> , 2019 , 27, 1114-1123.e3	5.2	13
19	Specific recognition of a DNA immunogen by its elicited antibody. <i>Journal of Molecular Biology</i> , 2007 , 370, 183-95	6.5	13
18	CH ₃ Hydrogen Bonds Mediate Highly Specific Recognition of Methylated CpG Sites by the Zinc Finger Protein Kaiso. <i>Biochemistry</i> , 2018 , 57, 2109-2120	3.2	10
17	Functional convergence of a germline-encoded neutralizing antibody response in rhesus macaques immunized with HCV envelope glycoproteins. <i>Immunity</i> , 2021 , 54, 781-796.e4	32.3	10
16	Structural basis for cooperative regulation of KIX-mediated transcription pathways by the HTLV-1 HBZ activation domain. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018 , 115, 10040-10045	11.5	10
15	Structural studies of human HIV-1 V3 antibodies. <i>Human Antibodies</i> , 2005 , 14, 73-80	1.3	10
14	An alternate conformation of HCV E2 neutralizing face as an additional vaccine target. <i>Science Advances</i> , 2020 , 6, eabb5642	14.3	9

13	Single-component multilayered self-assembling nanoparticles presenting rationally designed glycoprotein trimers as Ebola virus vaccines. <i>Nature Communications</i> , 2021 , 12, 2633	17.4	8
12	Structural basis for differential recognition of phosphohistidine-containing peptides by 1-pHis and 3-pHis monoclonal antibodies. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021 , 118,	11.5	8
11	Crystal structure determination of anti-DNA Fab A52. <i>Proteins: Structure, Function and Bioinformatics</i> , 2014 , 82, 1674-8	4.2	6
10	The Impact of Sustained Immunization Regimens on the Antibody Response to Oligomannose Glycans. <i>ACS Chemical Biology</i> , 2020 , 15, 789-798	4.9	4
9	A Conformational Switch in the Zinc Finger Protein Kaiso Mediates Differential Readout of Specific and Methylated DNA Sequences. <i>Biochemistry</i> , 2020 , 59, 1909-1926	3.2	3
8	A Dynamic Switch in Inactive p38 γ Leads to an Excited State on the Pathway to an Active Kinase. <i>Biochemistry</i> , 2019 , 58, 5160-5172	3.2	3
7	50 γ Years of structural immunology. <i>Journal of Biological Chemistry</i> , 2021 , 296, 100745	5.4	3
6	Never too late for endothelin. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2019 , 75, 45-46	1.1	2
5	Determination of antibody structures. <i>Methods in Molecular Biology</i> , 2014 , 1131, 395-406	1.4	2
4	Discovery of Small-Molecule Nonfluorescent Inhibitors of Fluorogen-Fluorogen Activating Protein Binding Pair. <i>Journal of Biomolecular Screening</i> , 2016 , 21, 74-87		1
3	Antibody Molecular Structure51-66		1
2	Antibody Structure49-62		1
1	The molecular basis of allostery in a facilitated dissociation process. <i>Structure</i> , 2021 , 29, 1327-1338.e5	5.2	1