

# Robyn L Stanfield

## List of Publications by Year in descending order

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66  
papers

6,740  
citations

117453

34  
h-index

106150

65  
g-index

67  
all docs

67  
docs citations

67  
times ranked

6163  
citing authors

#	ARTICLE	IF	CITATIONS
1	Crystal Structure of a Soluble Cleaved HIV-1 Envelope Trimer. <i>Science</i> , 2013, 342, 1477-1483.	6.0	793
2	A Potent and Broad Neutralizing Antibody Recognizes and Penetrates the HIV Glycan Shield. <i>Science</i> , 2011, 334, 1097-1103.	6.0	644
3	Broadly Neutralizing Anti-HIV Antibody 4E10 Recognizes a Helical Conformation of a Highly Conserved Fusion-Associated Motif in gp41. <i>Immunity</i> , 2005, 22, 163-173.	6.6	410
4	Hepatitis C Virus E2 Envelope Glycoprotein Core Structure. <i>Science</i> , 2013, 342, 1090-1094.	6.0	374
5	HIV Vaccine Design to Target Germline Precursors of Glycan-Dependent Broadly Neutralizing Antibodies. <i>Immunity</i> , 2016, 45, 483-496.	6.6	335
6	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.	3.6	314
7	Crystal Structure of a Shark Single-Domain Antibody V Region in Complex with Lysozyme. <i>Science</i> , 2004, 305, 1770-1773.	6.0	282
8	Contrasting IgG Structures Reveal Extreme Asymmetry and Flexibility. <i>Journal of Molecular Biology</i> , 2002, 319, 9-18.	2.0	246
9	Antibody Elbow Angles are Influenced by their Light Chain Class. <i>Journal of Molecular Biology</i> , 2006, 357, 1566-1574.	2.0	229
10	Open and closed structures reveal allostery and pliability in the HIV-1 envelope spike. <i>Nature</i> , 2017, 547, 360-363.	13.7	217
11	Affinity Maturation of a Potent Family of HIV Antibodies Is Primarily Focused on Accommodating or Avoiding Glycans. <i>Immunity</i> , 2015, 43, 1053-1063.	6.6	200
12	Structural Rationale for the Broad Neutralization of HIV-1 by Human Monoclonal Antibody 447-52D. <i>Structure</i> , 2004, 12, 193-204.	1.6	185
13	Receptor mimicry by antibody F045â€‘092 facilitates universal binding to the H3 subtype of influenza virus. <i>Nature Communications</i> , 2014, 5, 3614.	5.8	175
14	Rapid elicitation of broadly neutralizing antibodies to HIV by immunization in cows. <i>Nature</i> , 2017, 548, 108-111.	13.7	154
15	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.	4.2	151
16	Murine Antibody Responses to Cleaved Soluble HIV-1 Envelope Trimers Are Highly Restricted in Specificity. <i>Journal of Virology</i> , 2015, 89, 10383-10398.	1.5	148
17	Maturation of Shark Single-domain (IgNAR) Antibodies: Evidence for Induced-fit Binding. <i>Journal of Molecular Biology</i> , 2007, 367, 358-372.	2.0	127
18	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, 6093-6105.	1.5	113

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19	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, 501-512.	1.2	97
20	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.	6.6	96
21	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, 8451-8462.	1.5	92
22	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, 1846-1851.	3.3	91
23	Crystallographic Identification of Lipid as an Integral Component of the Epitope of HIV Broadly Neutralizing Antibody 4E10. <i>Immunity</i> , 2016, 44, 21-31.	6.6	87
24	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, 2099-2108.	2.5	69
25	Structure of 2G12 Fab in Complex with Soluble and Fully Glycosylated HIV-1 Env by Negative-Stain Single-Particle Electron Microscopy. <i>Journal of Virology</i> , 2014, 88, 10177-10188.	1.5	67
26	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.	2.1	58
27	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.	3.3	56
28	Conservation and diversity in the ultralong third heavy-chain complementarity-determining region of bovine antibodies. <i>Science Immunology</i> , 2016, 1, .	5.6	52
29	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.	3.3	52
30	Structure of a cleavage-independent HIV Env recapitulates the glycoprotein architecture of the native cleaved trimer. <i>Nature Communications</i> , 2018, 9, 1956.	5.8	50
31	Detect, correct, retract: How to manage incorrect structural models. <i>FEBS Journal</i> , 2018, 285, 444-466.	2.2	49
32	Recurring conformation of the human immunodeficiency virus type 1 gp120 V3 loop. <i>Virology</i> , 2003, 315, 159-173.	1.1	48
33	Cofactor-Mediated Conformational Dynamics Promote Product Release From <i>Escherichia coli</i> Dihydrofolate Reductase via an Allosteric Pathway. <i>Journal of the American Chemical Society</i> , 2015, 137, 9459-9468.	6.6	45
34	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, 2617-2628.	2.0	44
35	Structural Insights into the Lipid A Transport Pathway in MsbA. <i>Structure</i> , 2019, 27, 1114-1123.e3.	1.6	41
36	The Unusual Genetics and Biochemistry of Bovine Immunoglobulins. <i>Advances in Immunology</i> , 2018, 137, 135-164.	1.1	36

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37	Oligomannose Glycopeptide Conjugates Elicit Antibodies Targeting the Glycan Core Rather than Its Extremities. <i>ACS Central Science</i> , 2019, 5, 237-249.	5.3	33
38	Antibody Structure. <i>Microbiology Spectrum</i> , 2014, 2, .	1.2	31
39	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.	1.6	31
40	Structural basis of broad HIV neutralization by a vaccine-induced cow antibody. <i>Science Advances</i> , 2020, 6, eaba0468.	4.7	31
41	Crystal structure of the HIV neutralizing antibody 2G12 in complex with a bacterial oligosaccharide analog of mammalian oligomannose. <i>Glycobiology</i> , 2015, 25, 412-419.	1.3	27
42	Defining the Structural Basis for Allosteric Product Release from <i>E. coli</i> Dihydrofolate Reductase Using NMR Relaxation Dispersion. <i>Journal of the American Chemical Society</i> , 2017, 139, 11233-11240.	6.6	27
43	Structural Basis of Pan-Ebolavirus Neutralization by an Antibody Targeting the Glycoprotein Fusion Loop. <i>Cell Reports</i> , 2018, 24, 2723-2732.e4.	2.9	26
44	An alternate conformation of HCV E2 neutralizing face as an additional vaccine target. <i>Science Advances</i> , 2020, 6, eabb5642.	4.7	26
45	Single-component multilayered self-assembling nanoparticles presenting rationally designed glycoprotein trimers as Ebola virus vaccines. <i>Nature Communications</i> , 2021, 12, 2633.	5.8	25
46	X-Ray Crystallographic Studies of Antibody–Peptide Complexes. <i>ImmunoMethods</i> , 1993, 3, 211-221.	0.8	24
47	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.	6.6	23
48	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, 33557-33567.	1.6	22
49	Structure-Based Design of a Protein Immunogen that Displays an HIV-1 gp41 Neutralizing Epitope. <i>Journal of Molecular Biology</i> , 2011, 414, 460-476.	2.0	20
50	CH <sub>2</sub> -OH Hydrogen Bonds Mediate Highly Specific Recognition of Methylated CpG Sites by the Zinc Finger Protein Kaiso. <i>Biochemistry</i> , 2018, 57, 2109-2120.	1.2	19
51	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.	3.3	18
52	Unraveling the mysteries of T cell recognition. <i>Nature Immunology</i> , 2001, 2, 579-581.	7.0	17
53	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.	1.5	16
54	50 Years of structural immunology. <i>Journal of Biological Chemistry</i> , 2021, 296, 100745.	1.6	15

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55	Specific Recognition of a DNA Immunogen by its Elicited Antibody. <i>Journal of Molecular Biology</i> , 2007, 370, 183-195.	2.0	13
56	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, .	3.3	13
57	Structural studies of human HIV-1 V3 antibodies. <i>Human Antibodies</i> , 2005, 14, 73-80.	0.6	10
58	The Impact of Sustained Immunization Regimens on the Antibody Response to Oligomannose Glycans. <i>ACS Chemical Biology</i> , 2020, 15, 789-798.	1.6	9
59	Crystal structure determination of anti- $\alpha$ DNA Fab A52. <i>Proteins: Structure, Function and Bioinformatics</i> , 2014, 82, 1674-1678.	1.5	7
60	A Dynamic Switch in Inactive p38 <sup><math>\beta</math></sup> Leads to an Excited State on the Pathway to an Active Kinase. <i>Biochemistry</i> , 2019, 58, 5160-5172.	1.2	7
61	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.	1.2	7
62	The molecular basis of allostery in a facilitated dissociation process. <i>Structure</i> , 2021, 29, 1327-1338.e5.	1.6	6
63	Discovery of Small-Molecule Nonfluorescent Inhibitors of Fluorogen-Fluorogen Activating Protein Binding Pair. <i>Journal of Biomolecular Screening</i> , 2016, 21, 74-87.	2.6	2
64	Determination of Antibody Structures. <i>Methods in Molecular Biology</i> , 2014, 1131, 395-406.	0.4	2
65	Never too late for endothelin. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2019, 75, 45-46.	0.4	2
66	Antibody Structure. , 0, , 49-62.		1