Robyn L Stanfield

List of Publications by Year
in descending order

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	50ÂYears of structural immunology. Journal of Biological Chemistry, 2021, 296, 100745.	1.6	15
2	Structural basis for differential recognition of phosphohistidine-containing peptides by 1-pHis and 3-pHis monoclonal antibodies. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	3.3	13
3	Functional convergence of a germline-encoded neutralizing antibody response in rhesus macaques immunized with HCV envelope glycoproteins. Immunity, 2021, 54, 781-796.e4.	6.6	23
4	Single-component multilayered self-assembling nanoparticles presenting rationally designed glycoprotein trimers as Ebola virus vaccines. Nature Communications, 2021, 12, 2633.	5.8	25
5	The molecular basis of allostery in a facilitated dissociation process. Structure, 2021, 29, 1327-1338.e5.	1.6	6
6	An alternate conformation of HCV E2 neutralizing face as an additional vaccine target. Science Advances, 2020, 6, eabb5642.	4.7	26
7	A Conformational Switch in the Zinc Finger Protein Kaiso Mediates Differential Readout of Specific and Methylated DNA Sequences. Biochemistry, 2020, 59, 1909-1926.	1.2	7
8	Structural basis of broad HIV neutralization by a vaccine-induced cow antibody. Science Advances, 2020, 6, eaba0468.	4.7	31
9	The Impact of Sustained Immunization Regimens on the Antibody Response to Oligomannose Glycans. ACS Chemical Biology, 2020, 15, 789-798.	1.6	9
10	Structural Insights into the Lipid A Transport Pathway in MsbA. Structure, 2019, 27, 1114-1123.e3.	1.6	41
11	Stabilization of amyloidogenic immunoglobulin light chains by small molecules. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 8360-8369.	3.3	52
12	Oligomannose Glycopeptide Conjugates Elicit Antibodies Targeting the Glycan Core Rather than Its Extremities. ACS Central Science, 2019, 5, 237-249.	5.3	33
13	A Dynamic Switch in Inactive p38Î³ Leads to an Excited State on the Pathway to an Active Kinase. Biochemistry, 2019, 58, 5160-5172.	1.2	7
14	Never too late for endothelin. Acta Crystallographica Section F, Structural Biology Communications, 2019, 75, 45-46.	0.4	2
15	CHÂ·Â·Â·O Hydrogen Bonds Mediate Highly Specific Recognition of Methylated CpG Sites by the Zinc Finger Protein Kaiso. Biochemistry, 2018, 57, 2109-2120.	1.2	19
16	Detect, correct, retract: How to manage incorrect structural models. FEBS Journal, 2018, 285, 444-466.	2.2	49
17	Structural Basis of Pan-Ebolavirus Neutralization by an Antibody Targeting the Glycoprotein Fusion Loop. Cell Reports, 2018, 24, 2723-2732.e4.	2.9	26
18	Structural basis for cooperative regulation of KIX-mediated transcription pathways by the HTLV-1 HBZ activation domain. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 10040-10045.	3.3	18

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19	Structure of a cleavage-independent HIV Env recapitulates the glycoprotein architecture of the native cleaved trimer. Nature Communications, 2018, 9, 1956.	5.8	50
20	The Unusual Genetics and Biochemistry of Bovine Immunoglobulins. Advances in Immunology, 2018, 137, 135-164.	1.1	36
21	Glycine Substitution at Helix-to-Coil Transitions Facilitates the Structural Determination of a Stabilized Subtype C HIV Envelope Glycoprotein. Immunity, 2017, 46, 792-803.e3.	6.6	96
22	Role of the CBP catalytic core in intramolecular SUMOylation and control of histone H3 acetylation. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, E5335-E5342.	3.3	56
23	Design and crystal structure of a native-like HIV-1 envelope trimer that engages multiple broadly neutralizing antibody precursors in vivo. Journal of Experimental Medicine, 2017, 214, 2573-2590.	4.2	151
24	Selection of nanobodies with broad neutralizing potential against primary HIV-1 strains using soluble subtype C gp140 envelope trimers. Scientific Reports, 2017, 7, 8390.	1.6	31
25	Defining the Structural Basis for Allosteric Product Release from E. coli Dihydrofolate Reductase Using NMR Relaxation Dispersion. Journal of the American Chemical Society, 2017, 139, 11233-11240.	6.6	27
26	Rapid elicitation of broadly neutralizing antibodies to HIV by immunization in cows. Nature, 2017, 548, 108-111.	13.7	154
27	Open and closed structures reveal allostery and pliability in the HIV-1 envelope spike. Nature, 2017, 547, 360-363.	13.7	217
28	Lipid interactions and angle of approach to the HIV-1 viral membrane of broadly neutralizing antibody 10E8: Insights for vaccine and therapeutic design. PLoS Pathogens, 2017, 13, e1006212.	2.1	58
29	HIV Vaccine Design to Target Germline Precursors of Glycan-Dependent Broadly Neutralizing Antibodies. Immunity, 2016, 45, 483-496.	6.6	335
30	Conservation and diversity in the ultralong third heavy-chain complementarity-determining region of bovine antibodies. Science Immunology, 2016, 1, .	5.6	52
31	Crystallographic Identification of Lipid as an Integral Component of the Epitope of HIV Broadly Neutralizing Antibody 4E10. Immunity, 2016, 44, 21-31.	6.6	87
32	Discovery of Small-Molecule Nonfluorescent Inhibitors of Fluorogenâ€“Fluorogen Activating Protein Binding Pair. Journal of Biomolecular Screening, 2016, 21, 74-87.	2.6	2
33	Affinity Maturation of a Potent Family of HIV Antibodies Is Primarily Focused on Accommodating or Avoiding Glycans. Immunity, 2015, 43, 1053-1063.	6.6	200
34	Structure of Hepatitis C Virus Envelope Glycoprotein E1 Antigenic Site 314â€“324 in Complex with Antibody IGH526. Journal of Molecular Biology, 2015, 427, 2617-2628.	2.0	44
35	Cofactor-Mediated Conformational Dynamics Promote Product Release From Escherichia coli Dihydrofolate Reductase via an Allosteric Pathway. Journal of the American Chemical Society, 2015, 137, 9459-9468.	6.6	45
36	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. Acta Crystallographica Section D: Biological Crystallography, 2015, 71, 2099-2108.	2.5	69

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37	Murine Antibody Responses to Cleaved Soluble HIV-1 Envelope Trimers Are Highly Restricted in Specificity. Journal of Virology, 2015, 89, 10383-10398.	1.5	148
38	Crystal structure of the HIV neutralizing antibody 2G12 in complex with a bacterial oligosaccharide analog of mammalian oligomannose. Glycobiology, 2015, 25, 412-419.	1.3	27
39	Receptor mimicry by antibody F045â€“092 facilitates universal binding to the H3 subtype of influenza virus. Nature Communications, 2014, 5, 3614.	5.8	175
40	Nucleotide Insertions and Deletions Complement Point Mutations to Massively Expand the Diversity Created by Somatic Hypermutation of Antibodies. Journal of Biological Chemistry, 2014, 289, 33557-33567.	1.6	22
41	Crystal structure determination of antiâ€ÐNA Fab A52. Proteins: Structure, Function and Bioinformatics, 2014, 82, 1674-1678.	1.5	7
42	Structure of 2G12 Fab ₂ in Complex with Soluble and Fully Glycosylated HIV-1 Env by Negative-Stain Single-Particle Electron Microscopy. Journal of Virology, 2014, 88, 10177-10188.	1.5	67
43	Antibody Structure. Microbiology Spectrum, 2014, 2, .	1.2	31
44	Determination of Antibody Structures. Methods in Molecular Biology, 2014, 1131, 395-406.	0.4	2
45	Crystal Structure of a Soluble Cleaved HIV-1 Envelope Trimer. Science, 2013, 342, 1477-1483.	6.0	793
46	Hepatitis C Virus E2 Envelope Glycoprotein Core Structure. Science, 2013, 342, 1090-1094.	6.0	374
47	Supersite of immune vulnerability on the glycosylated face of HIV-1 envelope glycoprotein gp120. Nature Structural and Molecular Biology, 2013, 20, 796-803.	3.6	314
48	Structure-Based Design of a Protein Immunogen that Displays an HIV-1 gp41 Neutralizing Epitope. Journal of Molecular Biology, 2011, 414, 460-476.	2.0	20
49	A Potent and Broad Neutralizing Antibody Recognizes and Penetrates the HIV Glycan Shield. Science, 2011, 334, 1097-1103.	6.0	644
50	A Conformational Switch in Human Immunodeficiency Virus gp41 Revealed by the Structures of Overlapping Epitopes Recognized by Neutralizing Antibodies. Journal of Virology, 2009, 83, 8451-8462.	1.5	92
51	Maturation of Shark Single-domain (IgNAR) Antibodies: Evidence for Induced-fit Binding. Journal of Molecular Biology, 2007, 367, 358-372.	2.0	127
52	Specific Recognition of a DNA Immunogen by its Elicited Antibody. Journal of Molecular Biology, 2007, 370, 183-195.	2.0	13
53	Antibody Elbow Angles are Influenced by their Light Chain Class. Journal of Molecular Biology, 2006, 357, 1566-1574.	2.0	229
54	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. Journal of Virology, 2006, 80, 6093-6105.	1.5	113

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55	First molecular and biochemical analysis of in vivo affinity maturation in an ectothermic vertebrate. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 1846-1851.	3.3	91
56	Broadly Neutralizing Anti-HIV Antibody 4E10 Recognizes a Helical Conformation of a Highly Conserved Fusion-Associated Motif in gp41. Immunity, 2005, 22, 163-173.	6.6	410
57	Structural studies of human HIV-1 V3 antibodies. Human Antibodies, 2005, 14, 73-80.	0.6	10
58	Structural Rationale for the Broad Neutralization of HIV-1 by Human Monoclonal Antibody 447-52D. Structure, 2004, 12, 193-204.	1.6	185
59	Crystal Structure of a Shark Single-Domain Antibody V Region in Complex with Lysozyme. Science, 2004, 305, 1770-1773.	6.0	282
60	Recurring conformation of the human immunodeficiency virus type 1 gp120 V3 loop. Virology, 2003, 315, 159-173.	1.1	48
61	Contrasting IgG Structures Reveal Extreme Asymmetry and Flexibility. Journal of Molecular Biology, 2002, 319, 9-18.	2.0	246
62	Structural analysis, selection, and ontogeny of the shark new antigen receptor (IgNAR): identification of a new locus preferentially expressed in early development. Immunogenetics, 2002, 54, 501-512.	1.2	97
63	Unraveling the mysteries of Î³Î´ T cell recognition. Nature Immunology, 2001, 2, 579-581.	7.0	17
64	X-Ray Crystallographic Studies of Antibodyâ€“Peptide Complexes. ImmunoMethods, 1993, 3, 211-221.	0.8	24
65	Crystallization, sequence, and preliminary crystallographic data for an antipeptide Fab 50.1 and peptide complexes with the principal neutralizing determinant of HIV-1 gpl20. Proteins: Structure, Function and Bioinformatics, 1992, 14, 499-508.	1.5	16
66	Antibody Structure. , 0, , 49-62.		1