

# Jason Gorman

## List of Publications by Year in descending order

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73  
papers

9,981  
citations

94433

37  
h-index

85541

71  
g-index

81  
all docs

81  
docs citations

81  
times ranked

10868  
citing authors

#	ARTICLE	IF	CITATIONS
1	A single residue in influenza virus H2 hemagglutinin enhances the breadth of the B cell response elicited by H2 vaccination. <i>Nature Medicine</i> , 2022, 28, 373-382.	30.7	16
2	Development of Neutralization Breadth against Diverse HIV-1 by Increasing Ab-Ag Interface on V2. <i>Advanced Science</i> , 2022, , 2200063.	11.2	3
3	Antigenic analysis of the HIV-1 envelope trimer implies small differences between structural states 1 and 2. <i>Journal of Biological Chemistry</i> , 2022, 298, 101819.	3.4	9
4	Structure of an influenza group 2-neutralizing antibody targeting the hemagglutinin stem supersite. <i>Structure</i> , 2022, , .	3.3	1
5	Tyrosine O-sulfation proteoforms affect HIV-1 monoclonal antibody potency. <i>Scientific Reports</i> , 2022, 12, 8433.	3.3	8
6	Highly protective antimalarial antibodies via precision library generation and yeast display screening. <i>Journal of Experimental Medicine</i> , 2022, 219, .	8.5	9
7	Broad coverage of neutralization-resistant SIV strains by second-generation SIV-specific antibodies targeting the region involved in binding CD4. <i>PLoS Pathogens</i> , 2022, 18, e1010574.	4.7	6
8	Recapitulation of HIV-1 Env-antibody coevolution in macaques leading to neutralization breadth. <i>Science</i> , 2021, 371, .	12.6	49
9	A matrix of structure-based designs yields improved VRC01-class antibodies for HIV-1 therapy and prevention. <i>MAbs</i> , 2021, 13, 1946918.	5.2	11
10	Anti-V2 antibodies virus vulnerability revealed by envelope V1 deletion in HIV vaccine candidates. <i>IScience</i> , 2021, 24, 102047.	4.1	16
11	Structural basis of malaria RIFIN binding by LILRB1-containing antibodies. <i>Nature</i> , 2021, 592, 639-643.	27.8	8
12	Potent SARS-CoV-2 neutralizing antibodies directed against spike N-terminal domain target a single supersite. <i>Cell Host and Microbe</i> , 2021, 29, 819-833.e7.	11.0	444
13	Sequence-Signature Optimization Enables Improved Identification of Human HV6-1-Derived Class Antibodies That Neutralize Diverse Influenza A Viruses. <i>Frontiers in Immunology</i> , 2021, 12, 662909.	4.8	0
14	Structural basis of LAIR1 targeting by polymorphic Plasmodium RIFINs. <i>Nature Communications</i> , 2021, 12, 4226.	12.8	1
15	Interprotomer disulfide-stabilized variants of the human metapneumovirus fusion glycoprotein induce high titer-neutralizing responses. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	7.1	20
16	Extended antibody-framework-to-antigen distance observed exclusively with broad HIV-1-neutralizing antibodies recognizing glycan-dense surfaces. <i>Nature Communications</i> , 2021, 12, 6470.	12.8	3
17	Structure-Based Design with Tag-Based Purification and In-Process Biotinylation Enable Streamlined Development of SARS-CoV-2 Spike Molecular Probes. <i>Cell Reports</i> , 2020, 33, 108322.	6.4	59
18	Cryo-EM Structures of SARS-CoV-2 Spike without and with ACE2 Reveal a pH-Dependent Switch to Mediate Endosomal Positioning of Receptor-Binding Domains. <i>Cell Host and Microbe</i> , 2020, 28, 867-879.e5.	11.0	316

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19	Real-Time Conformational Dynamics of SARS-CoV-2 Spikes on Virus Particles. <i>Cell Host and Microbe</i> , 2020, 28, 880-891.e8.	11.0	153
20	Potent neutralizing antibodies against multiple epitopes on SARS-CoV-2 spike. <i>Nature</i> , 2020, 584, 450-456.	27.8	1,337
21	Disulfide stabilization of human norovirus GI.1 virus-like particles focuses immune response toward blockade epitopes. <i>Npj Vaccines</i> , 2020, 5, 110.	6.0	6
22	Subnanometer structures of HIV-1 envelope trimers on aldrithiol-2-inactivated virus particles. <i>Nature Structural and Molecular Biology</i> , 2020, 27, 726-734.	8.2	55
23	Structure of Super-Potent Antibody CAP256-VRC26.25 in Complex with HIV-1 Envelope Reveals a Combined Mode of Trimer-Apex Recognition. <i>Cell Reports</i> , 2020, 31, 107488.	6.4	53
24	Antibody Lineages with Vaccine-Induced Antigen-Binding Hotspots Develop Broad HIV Neutralization. <i>Cell</i> , 2019, 178, 567-584.e19.	28.9	106
25	Somatic hypermutation to counter a globally rare viral immunotype drove off-track antibodies in the CAP256-VRC26 HIV-1 V2-directed bNAbs lineage. <i>PLoS Pathogens</i> , 2019, 15, e1008005.	4.7	6
26	Blocking $\alpha 4 \beta 7$ integrin binding to SIV does not improve virologic control. <i>Science</i> , 2019, 365, 1033-1036.	12.6	31
27	Isolation and Structure of an Antibody that Fully Neutralizes Isolate SIVmac239 Reveals Functional Similarity of SIV and HIV Glycan Shields. <i>Immunity</i> , 2019, 51, 724-734.e4.	14.3	13
28	Longitudinal Analysis Reveals Early Development of Three MPER-Directed Neutralizing Antibody Lineages from an HIV-1-Infected Individual. <i>Immunity</i> , 2019, 50, 677-691.e13.	14.3	77
29	Associating HIV-1 envelope glycoprotein structures with states on the virus observed by smFRET. <i>Nature</i> , 2019, 568, 415-419.	27.8	156
30	Rational design and in vivo selection of SHIVs encoding transmitted/founder subtype C HIV-1 envelopes. <i>PLoS Pathogens</i> , 2019, 15, e1007632.	4.7	20
31	Sequencing HIV-neutralizing antibody exons and introns reveals detailed aspects of lineage maturation. <i>Nature Communications</i> , 2018, 9, 4136.	12.8	11
32	Select gp120 V2 domain specific antibodies derived from HIV and SIV infection and vaccination inhibit gp120 binding to $\alpha 4 \beta 7$ . <i>PLoS Pathogens</i> , 2018, 14, e1007278.	4.7	29
33	HIV-1 Env trimer opens through an asymmetric intermediate in which individual protomers adopt distinct conformations. <i>ELife</i> , 2018, 7, .	6.0	127
34	Epitope-based vaccine design yields fusion peptide-directed antibodies that neutralize diverse strains of HIV-1. <i>Nature Medicine</i> , 2018, 24, 857-867.	30.7	256
35	Interdomain Stabilization Impairs CD4 Binding and Improves Immunogenicity of the HIV-1 Envelope Trimer. <i>Cell Host and Microbe</i> , 2018, 23, 832-844.e6.	11.0	43
36	Ontogeny-based immunogens for the induction of V2-directed HIV broadly neutralizing antibodies. <i>Immunological Reviews</i> , 2017, 275, 217-229.	6.0	27

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37	Structure-Based Design of a Soluble Prefusion-Closed HIV-1 Env Trimer with Reduced CD4 Affinity and Improved Immunogenicity. <i>Journal of Virology</i> , 2017, 91, .	3.4	81
38	Virus-like Particles Identify an HIV V1V2 Apex-Binding Neutralizing Antibody that Lacks a Protruding Loop. <i>Immunity</i> , 2017, 46, 777-791.e10.	14.3	81
39	Single-Molecule FRET Delineates Asymmetric Trimer Conformations during HIV-1 Entry. <i>Biophysical Journal</i> , 2017, 112, 177a.	0.5	3
40	Conformational Changes in HIV-1 Env Trimer Induced by a Single CD4 as Revealed by Cryo-EM. <i>Microscopy and Microanalysis</i> , 2017, 23, 1190-1191.	0.4	0
41	Structure and Recognition of a Novel HIV-1 gp120-gp41 Interface Antibody that Caused MPER Exposure through Viral Escape. <i>PLoS Pathogens</i> , 2017, 13, e1006074.	4.7	33
42	Targeted Isolation of Antibodies Directed against Major Sites of SIV Env Vulnerability. <i>PLoS Pathogens</i> , 2016, 12, e1005537.	4.7	51
43	Fusion peptide of HIV-1 as a site of vulnerability to neutralizing antibody. <i>Science</i> , 2016, 352, 828-833.	12.6	310
44	Structure of an N276-Dependent HIV-1 Neutralizing Antibody Targeting a Rare V5 Glycan Hole Adjacent to the CD4 Binding Site. <i>Journal of Virology</i> , 2016, 90, 10220-10235.	3.4	32
45	Somatic Hypermutation-Induced Changes in the Structure and Dynamics of HIV-1 Broadly Neutralizing Antibodies. <i>Structure</i> , 2016, 24, 1346-1357.	3.3	35
46	Envelope residue 375 substitutions in simianâ€“human immunodeficiency viruses enhance CD4 binding and replication in rhesus macaques. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, E3413-22.	7.1	170
47	Structures of HIV-1 Env V1V2 with broadly neutralizing antibodies reveal commonalities that enable vaccine design. <i>Nature Structural and Molecular Biology</i> , 2016, 23, 81-90.	8.2	162
48	New Member of the V1V2-Directed CAP256-VRC26 Lineage That Shows Increased Breadth and Exceptional Potency. <i>Journal of Virology</i> , 2016, 90, 76-91.	3.4	205
49	Single-Chain Soluble BG505.SOSIP gp140 Trimers as Structural and Antigenic Mimics of Mature Closed HIV-1 Env. <i>Journal of Virology</i> , 2015, 89, 5318-5329.	3.4	125
50	Conformational Dynamics of Single HIV-1 Envelope Proteins on the Surface of Native Virions. <i>Biophysical Journal</i> , 2015, 108, 362a-363a.	0.5	0
51	AAV-expressed eCD4-Ig provides durable protection from multiple SHIV challenges. <i>Nature</i> , 2015, 519, 87-91.	27.8	265
52	Crystal structure, conformational fixation and entry-related interactions of mature ligand-free HIV-1 Env. <i>Nature Structural and Molecular Biology</i> , 2015, 22, 522-531.	8.2	333
53	Viral variants that initiate and drive maturation of V1V2-directed HIV-1 broadly neutralizing antibodies. <i>Nature Medicine</i> , 2015, 21, 1332-1336.	30.7	215
54	Developmental pathway for potent V1V2-directed HIV-neutralizing antibodies. <i>Nature</i> , 2014, 509, 55-62.	27.8	681

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55	Conformational dynamics of single HIV-1 envelope trimers on the surface of native virions. <i>Science</i> , 2014, 346, 759-763.	12.6	439
56	Structure and immune recognition of trimeric pre-fusion HIV-1 Env. <i>Nature</i> , 2014, 514, 455-461.	27.8	702
57	Transplanting Supersites of HIV-1 Vulnerability. <i>PLoS ONE</i> , 2014, 9, e99881.	2.5	51
58	The promoter-search mechanism of <i>Escherichia coli</i> RNA polymerase is dominated by three-dimensional diffusion. <i>Nature Structural and Molecular Biology</i> , 2013, 20, 174-181.	8.2	110
59	Vaccine Induction of Antibodies against a Structurally Heterogeneous Site of Immune Pressure within HIV-1 Envelope Protein Variable Regions 1 and 2. <i>Immunity</i> , 2013, 38, 176-186.	14.3	374
60	Target search dynamics during post-replicative mismatch repair. <i>Cell Cycle</i> , 2013, 12, 537-538.	2.6	2
61	N332-Directed Broadly Neutralizing Antibodies Use Diverse Modes of HIV-1 Recognition: Inferences from Heavy-Light Chain Complementation of Function. <i>PLoS ONE</i> , 2013, 8, e55701.	2.5	38
62	A Short Segment of the HIV-1 gp120 V1/V2 Region Is a Major Determinant of Resistance to V1/V2 Neutralizing Antibodies. <i>Journal of Virology</i> , 2012, 86, 8319-8323.	3.4	76
63	Single-molecule imaging reveals target-search mechanisms during DNA mismatch repair. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, E3074-83.	7.1	156
64	Structure of HIV-1 gp120 V1/V2 domain with broadly neutralizing antibody PG9. <i>Nature</i> , 2011, 480, 336-343.	27.8	794
65	Visualizing one-dimensional diffusion of eukaryotic DNA repair factors along a chromatin lattice. <i>Nature Structural and Molecular Biology</i> , 2010, 17, 932-938.	8.2	175
66	Nanofabricated Racks of Aligned and Anchored DNA Substrates for Single-Molecule Imaging. <i>Langmuir</i> , 2010, 26, 1372-1379.	3.5	62
67	DNA Curtains for High-Throughput Single-Molecule Optical Imaging. <i>Methods in Enzymology</i> , 2010, 472, 293-315.	1.0	116
68	Visualizing one-dimensional diffusion of proteins along DNA. <i>Nature Structural and Molecular Biology</i> , 2008, 15, 768-774.	8.2	247
69	Dynamic Basis for One-Dimensional DNA Scanning by the Mismatch Repair Complex Msh2-Msh6. <i>Molecular Cell</i> , 2007, 28, 359-370.	9.7	215
70	Crystal structures of the tryptophan repressor binding protein WrbA and complexes with flavin mononucleotide. <i>Protein Science</i> , 2005, 14, 3004-3012.	7.6	23
71	Structure of <i>Escherichia coli</i> YfdW, a type III CoA transferase. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2004, 60, 507-511.	2.5	12
72	Structure of serine acetyltransferase from <i>Haemophilus influenzae</i> Rd. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2004, 60, 1600-1605.	2.5	31

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73	Structure of Antibody CAP256-VRC26.25 in Complex with HIV-1 Envelope Reveals a Combined Mode of Trimer-Apex Recognition. SSRN Electronic Journal, 0, , .	0.4	1